SUPPLEMENTARY MATERIAL

Data S1. Supplemental Methods

Major Resources Table

• Animal (*in vivo* studies)

Species	Vendor or Source	Background Strain	Sex	Persistent ID / URL
αMHC-rtTA (tON) transgenic mouse	Wende LAB, UAB	FVB/NJ strain	F/M	https://doi.org/10.1161/JAHA.119.013039; https://doi.org/10.2337/db19-1057

• Genetically Modified Animals (*in vivo* studies)

	Species	Vendor or Source	Background Strain	Other information	Persistent ID / URL
Control: Male / Female	tON – mG4H	Wende LAB, UAB	FVB/NJ	Single transgenic	https://doi.org/10.1161/JAHA.119.013039; https://doi.org/10.2337/db19-1057
TRE-mycGLUT4 (mG4H): Male / Female	tON + mG4H	Wende LAB, UAB	FVB/NJ	Double transgenic	https://doi.org/10.1161/JAHA.119.013039; https://doi.org/10.2337/db19-1057

• Data & Code Availability

Description	Source / Repository	Persistent ID / URL
RNA sequencing data	NCBI GEO database	GSE275229
Methyl sequencing data	NCBI GEO database	GSE275229
R code history	GitHub repository	https://github.com/bakshisayan/mG4H-OFF-Bakshi-Wende-2024.git

ARRIVE GUIDELINES

• Study design (mRNA sequencing and reduced representation bisulfite sequencing)

Groups	Sex	Age	Number (prior to experiment)	Number (after termination)	Littermates (Yes/No)	Other description
Con-ON	M	8-10 weeks	3	3	YES	Single transgenic mice (tON or mG4H) with DOX diet
mG4H-ON	M	8-10 weeks	3	3	YES	Double transgenic mice (tON + mG4H) with DOX diet
Con-OFF	M	8-10 weeks	3	3	YES	Single transgenic mice (tON or mG4H) with DOX diet for 2

						weeks and back to chow diet for another 2 weeks
mG4H-OFF	M	8-10 weeks	3	3	YES	Double transgenic mice (tON + mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks

• Study design (transverse aortic constriction and echocardiography)

Groups	Sex	Age	Number (prior to experiment)	Number (after termination)	Littermates (Yes/No)	Other description
Con-OFF-Sham	M	12-14 weeks	14	12	YES	Single transgenic mice (tON or mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by sham surgery
Con-OFF-TAC	M	12-14 weeks	22	15	YES	Single transgenic mice (tON or mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by TAC surgery
mG4H-OFF-Sham	M	12-14 weeks	11	5	YES	Double transgenic mice (tON + mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by sham surgery
mG4H-OFF-TAC	M	12-14 weeks	19	10	YES	Double transgenic mice (tON + mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by TAC surgery
Con-OFF-Sham	F	12-14 weeks	11	9	YES	Single transgenic mice (tON or mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by sham surgery
Con-OFF-TAC	F	12-14 weeks	19	14	YES	Single transgenic mice (tON or mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by TAC surgery

mG4H-OFF-Sham	F	12-14 weeks	12	9	YES	Double transgenic mice (tON + mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by sham surgery
mG4H-OFF-TAC	F	12-14 weeks	20	15	YES	Double transgenic mice (tON + mG4H) with DOX diet for 2 weeks and back to chow diet for another 2 weeks; followed by TAC surgery

Sample Size

The sample size is determined by experimental usage, echocardiography, and cardiac function measurement.

Inclusion Criteria

All experimental mice were included in all groups, except for the fight wound or adverse event.

Exclusion Criteria

In this study, mice wounded during fighting were excluded.

Randomization

The experimental cohorts come from 14–16 breeding pairings. 25% of littermates are double transgenic as mG4H, while 50% of littermates are single transgenic as Control, according to the Madelaine possibility. Each mouse ID is assigned to a random sequence.

Blinding

After characterizing the genotype of the mice, all experimental sheets are labeled only with their assigned ID at random sequences to ensure that the groups remain blinded throughout the study until the final analysis data are obtained. Each cage contains mice from both the control and experimental groups.

Data S2. RAW UNEDITED BLOTS.

Figure S1

Figure S1: MYC

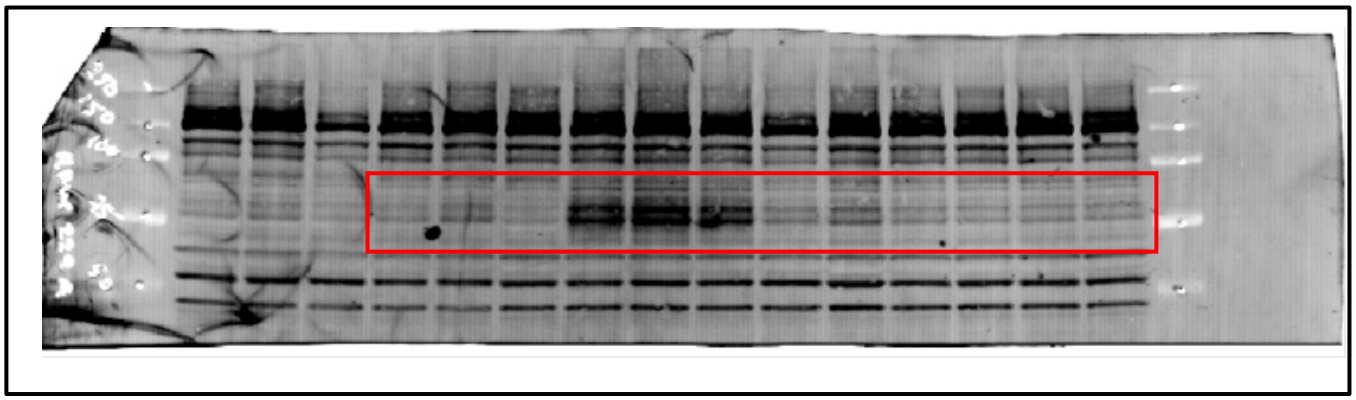
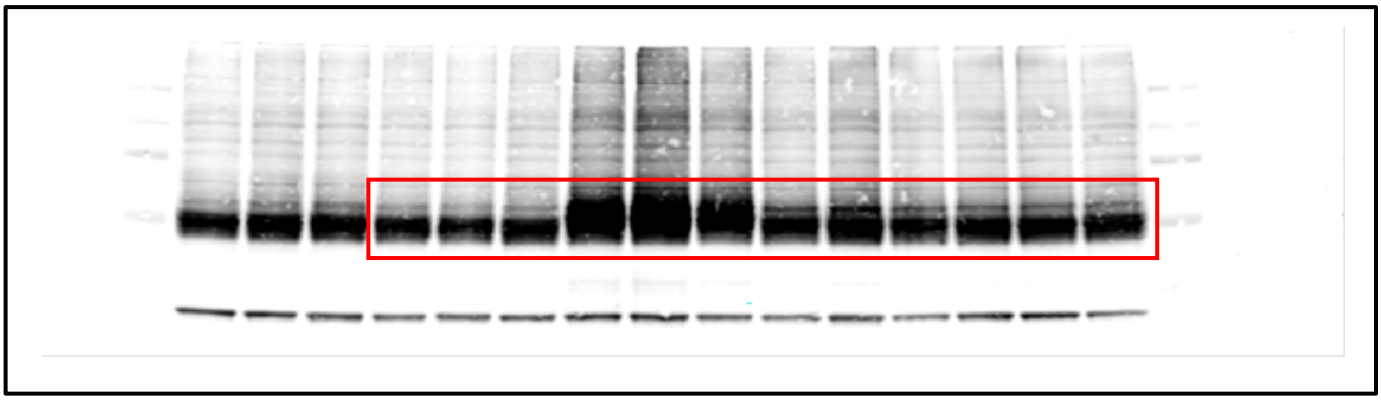


Figure S1: GLUT4



• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610009L18Rik	ENSMUSG00000043644	RIKEN cDNA 0610009L18 gene	5.210	0.0000	0.0000
1110004F10Rik	ENSMUSG00000030663	RIKEN cDNA 1110004F10 gene	1.621	0.0000	0.0000
1110018N20Rik	ENSMUSG00000085151	RIKEN cDNA 1110018N20 gene	2.369	0.0000	0.0000
1110032F04Rik	ENSMUSG00000046999	RIKEN cDNA 1110032F04 gene	3.754	0.0004	0.0015
1110038F14Rik	ENSMUSG00000063236	RIKEN cDNA 1110038F14 gene	1.663	0.0000	0.0000
1110065P20Rik	ENSMUSG00000078570	RIKEN cDNA 1110065P20 gene	2.464	0.0001	0.0005
1190005I06Rik	ENSMUSG00000043687	RIKEN cDNA 1190005I06 gene	6.380	0.0000	0.0000
1300002E11Rik	ENSMUSG00000097290	RIKEN cDNA 1300002E11 gene	2.439	0.0000	0.0000
1500009L16Rik	ENSMUSG00000087651	RIKEN cDNA 1500009L16 gene	1.666	0.0002	0.0006
1600014C23Rik	ENSMUSG00000094690	RIKEN cDNA 1600014C23 gene	2.765	0.0069	0.0174
1700001G17Rik	ENSMUSG00000103746	RIKEN cDNA 1700001G17 gene	3.576	0.0275	0.0580
1700008J07Rik	ENSMUSG00000101225	RIKEN cDNA 1700008J07 gene	1.513	0.0025	0.0071
1700018L02Rik	ENSMUSG00000100075	RIKEN cDNA 1700018L02 gene	1.706	0.0489	0.0949
1700034H15Rik	ENSMUSG00000055833	RIKEN cDNA 1700034H15 gene	2.371	0.0002	0.0009
1700034P13Rik	ENSMUSG00000097893	RIKEN cDNA 1700034P13 gene	4.363	0.0443	0.0871
1700040L08Rik	ENSMUSG00000107406	RIKEN cDNA 1700040L08 gene	27.172	0.0010	0.0032
1700052K11Rik	ENSMUSG00000099681	RIKEN cDNA 1700052K11 gene	1.592	0.0079	0.0196
1700056E22Rik	ENSMUSG00000044854	RIKEN cDNA 1700056E22 gene	3.228	0.0002	0.0007
1700084E18Rik	ENSMUSG00000100747	RIKEN cDNA 1700084E18 gene	4.583	0.0000	0.0000
1700095B10Rik	ENSMUSG00000098230	RIKEN cDNA 1700095B10 gene	22.426	0.0000	0.0000
1700096K18Rik	ENSMUSG00000101856	RIKEN cDNA 1700096K18 gene	1.531	0.0203	0.0446
1700105P06Rik	ENSMUSG00000099923	RIKEN cDNA 1700105P06 gene	4.930	0.0254	0.0541
1700119I11Rik	ENSMUSG00000082488	RIKEN cDNA 1700119I11 gene	26.015	0.0001	0.0004
1810037I17Rik	ENSMUSG00000054091	RIKEN cDNA 1810037I17 gene	1.711	0.0000	0.0000
1810049J17Rik	ENSMUSG00000097221	RIKEN cDNA 1810049J17 gene	50.484	0.0000	0.0000
2010001A14Rik	ENSMUSG00000087165	RIKEN cDNA 2010001A14 gene	4.281	0.0000	0.0000
2010007H06Rik	ENSMUSG00000044694	RIKEN cDNA 2010007H06 gene	1.952	0.0072	0.0179
2300009A05Rik	ENSMUSG00000032403	RIKEN cDNA 2300009A05 gene	2.517	0.0000	0.0000
2310009B15Rik	ENSMUSG00000079283	RIKEN cDNA 2310009B15 gene	1.508	0.0007	0.0023
2310010J17Rik	ENSMUSG00000097162	RIKEN cDNA 2310010J17 gene	2.945	0.0000	0.0000
2310015K22Rik	ENSMUSG00000101257	RIKEN cDNA 2310015K22 gene	2.377	0.0213	0.0464
2310016D23Rik	ENSMUSG00000085965	RIKEN cDNA 2310016D23 gene	3.064	0.0290	0.0606
2310061I04Rik	ENSMUSG00000050705	RIKEN cDNA 2310061I04 gene	3.196	0.0000	0.0001
2410004B18Rik	ENSMUSG00000036873	RIKEN cDNA 2410004B18 gene	2.307	0.0000	0.0000
2410022M11Rik	ENSMUSG00000100017	RIKEN cDNA 2410022M11 gene	3.434	0.0000	0.0000
2510039O18Rik	ENSMUSG00000044496	RIKEN cDNA 2510039O18 gene	1.785	0.0002	0.0008
2610037D02Rik	ENSMUSG00000097536	RIKEN cDNA 2610037D02 gene	1.736	0.0465	0.0908
2610306M01Rik	ENSMUSG00000100164	RIKEN cDNA 2610306M01 gene	2.273	0.0000	0.0000
2810002D19Rik	ENSMUSG00000045464	RIKEN cDNA 2810002D19 gene	2.606	0.0000	0.0000
2810457G06Rik	ENSMUSG00000115410	RIKEN cDNA 2810457G06 gene	5.018	0.0073	0.0181

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
2900005J15Rik	ENSMUSG00000043833	RIKEN cDNA 2900005J15 gene	2.860	0.0044	0.0116
2900089D17Rik	ENSMUSG00000087484	RIKEN cDNA 2900089D17 gene	2.209	0.0004	0.0013
3110021N24Rik	ENSMUSG00000094958	RIKEN cDNA 3110021N24 gene	9.782	0.0000	0.0000
3110040N11Rik	ENSMUSG00000025102	RIKEN cDNA 3110040N11 gene	1.579	0.0000	0.0000
3110082I17Rik	ENSMUSG00000053553	RIKEN cDNA 3110082I17 gene	1.796	0.0000	0.0000
3830403N18Rik	ENSMUSG00000031125	RIKEN cDNA 3830403N18 gene	1.802	0.0230	0.0497
3830408C21Rik	ENSMUSG00000071181	RIKEN cDNA 3830408C21 gene	1.624	0.0163	0.0367
4833403J16Rik	ENSMUSG00000107481	RIKEN cDNA 4833403J16 gene	1.656	0.0126	0.0293
4833438C02Rik	ENSMUSG00000118087	RIKEN cDNA 4833438C02 gene	1.765	0.0074	0.0183
4921504A21Rik	ENSMUSG00000097626	RIKEN cDNA 4921504A21 gene	2.006	0.0000	0.0000
4921524J17Rik	ENSMUSG00000036934	RIKEN cDNA 4921524J17 gene	1.759	0.0000	0.0000
4921531C22Rik	ENSMUSG00000085704	RIKEN cDNA 4921531C22 gene	2.556	0.0000	0.0000
4930412F12Rik	ENSMUSG00000110289	RIKEN cDNA 4930412F12 gene	5.261	0.0000	0.0001
4930500M09Rik	ENSMUSG00000044306	RIKEN cDNA 4930500M09 gene	18.436	0.0070	0.0174
4930507D05Rik	ENSMUSG00000097129	RIKEN cDNA 4930507D05 gene	3.447	0.0001	0.0005
4930526A20Rik	ENSMUSG00000085521	RIKEN cDNA 4930526A20 gene	22.888	0.0000	0.0000
4930577N17Rik	ENSMUSG00000087440	RIKEN cDNA 4930577N17 gene	7.547	0.0000	0.0000
4930578M01Rik	ENSMUSG00000097587	RIKEN cDNA 4930578M01 gene	1.956	0.0052	0.0134
4930589O11Rik	ENSMUSG00000107195	RIKEN cDNA 4930589O11 gene	2.410	0.0049	0.0127
4930590J08Rik	ENSMUSG00000034063	RIKEN cDNA 4930590J08 gene	2.139	0.0329	0.0675
4930597O21Rik	ENSMUSG00000053442	RIKEN cDNA 4930597O21 gene	28.932	0.0169	0.0380
4931403E22Rik	ENSMUSG00000093772	RIKEN cDNA 4931403E22 gene	29.442	0.0000	0.0000
4931428F04Rik	ENSMUSG00000014837	RIKEN cDNA 4931428F04 gene	1.541	0.0216	0.0471
4931440P22Rik	ENSMUSG00000074580	RIKEN cDNA 4931440P22 gene	9.222	0.0000	0.0000
4933412E12Rik	ENSMUSG00000112627	RIKEN cDNA 4933412E12 gene	1.612	0.0187	0.0414
4933415A04Rik	ENSMUSG00000045877	RIKEN cDNA 4933415A04 gene	4.537	0.0002	0.0008
4933421O10Rik	ENSMUSG00000085037	RIKEN cDNA 4933421O10 gene	2.476	0.0000	0.0000
4933427D14Rik	ENSMUSG00000107877	RIKEN cDNA 4933427D14 gene	3.101	0.0028	0.0077
4933440N22Rik	ENSMUSG00000042087	RIKEN cDNA 4933440N22 gene	2.372	0.0044	0.0117
5330438D12Rik	ENSMUSG00000052291	RIKEN cDNA 5330438D12 gene	1.995	0.0066	0.0167
5330439K02Rik	ENSMUSG00000097827	RIKEN cDNA 5330439K02 gene	5.154	0.0000	0.0000
5430414B19Rik	ENSMUSG00000114419	RIKEN cDNA 5430414B19 gene	3.102	0.0091	0.0220

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5430416N02Rik	ENSMUSG00000097772	RIKEN cDNA 5430416N02 gene	2.712	0.0001	0.0005
5730409E04Rik	ENSMUSG00000073755	RIKEN cDNA 5730409E04Rik gene	1.559	0.0000	0.0000
5730414N17Rik	ENSMUSG00000116506	RIKEN cDNA 5730414N17 gene	2.354	0.0001	0.0005
5730480H06Rik	ENSMUSG00000029089	RIKEN cDNA 5730480H06 gene	2.456	0.0000	0.0000
5830454E08Rik	ENSMUSG00000052658	RIKEN cDNA 5830454E08 gene	2.044	0.0070	0.0175
5930420M18Rik	ENSMUSG00000107201	RIKEN cDNA 5930420M18 gene	1.903	0.0329	0.0677
6330418K02Rik	ENSMUSG00000085227	RIKEN cDNA 6330418K02 gene	1.842	0.0205	0.0450
6330562C20Rik	ENSMUSG00000093424	RIKEN cDNA 6330562C20 gene	2.880	0.0004	0.0014
6430573P05Rik	ENSMUSG00000102545	RIKEN cDNA 6430573P05 gene	3.704	0.0000	0.0000
6530402F18Rik	ENSMUSG00000079499	RIKEN cDNA 6530402F18 gene	3.284	0.0000	0.0000
6720427I07Rik	ENSMUSG00000097375	RIKEN cDNA 6720427I07 gene	1.800	0.0000	0.0000
6820431F20Rik	ENSMUSG00000071796	RIKEN cDNA 6820431F20 gene	1.836	0.0334	0.0685
9030407P20Rik	ENSMUSG00000097343	RIKEN cDNA 9030407P20 gene	1.697	0.0088	0.0214
9130017K11Rik	ENSMUSG00000055134	RIKEN cDNA 9130017K11 gene	2.217	0.0284	0.0595
9130230N09Rik	ENSMUSG00000092626	RIKEN cDNA 9130230N09 gene	4.363	0.0033	0.0090
9130401M01Rik	ENSMUSG00000101892	RIKEN cDNA 9130401M01 gene	2.115	0.0000	0.0000
9230111E07Rik	ENSMUSG00000087624	RIKEN cDNA 9230111E07 gene	9.302	0.0022	0.0063
9230116N13Rik	ENSMUSG00000097403	RIKEN cDNA 9230116N13 gene	1.663	0.0413	0.0822
9330121J05Rik	ENSMUSG00000103502	RIKEN cDNA 9330121J05 gene	15.129	0.0159	0.0360
9330160F10Rik	ENSMUSG00000072809	RIKEN cDNA 9330160F10 gene	2.987	0.0000	0.0001
9330162012Rik	ENSMUSG00000086448	cDNA RIKEN 9330162012 gene	3.854	0.0000	0.0000
9330162G02Rik	ENSMUSG00000109536	RIKEN cDNA 9330162G02 gene	1.986	0.0005	0.0017
9430062P05Rik	ENSMUSG00000104263	RIKEN cDNA 9430062P05 gene	3.148	0.0003	0.0010
9530085L11Rik	ENSMUSG00000107742	RIKEN cDNA 9530085L11 gene	2.367	0.0046	0.0119
9930021J03Rik	ENSMUSG00000046138	RIKEN cDNA 9930021J03 gene	1.649	0.0000	0.0000
A230072E10Rik	ENSMUSG00000084771	RIKEN cDNA A230072E10 gene	3.671	0.0388	0.0778
A330041J22Rik	ENSMUSG00000087466	RIKEN cDNA A330041J22 gene	6.539	0.0000	0.0000
A430027H14Rik	ENSMUSG00000104507	RIKEN cDNA A430027H14 gene	4.436	0.0174	0.0389
A530017D24Rik	ENSMUSG00000072847	RIKEN cDNA A530017D24 gene	1.634	0.0000	0.0000
A530058N18Rik	ENSMUSG00000092201	RIKEN cDNA A530058N18 gene	4.198	0.0000	0.0000
A630019I02Rik	ENSMUSG00000114968	RIKEN cDNA A630019I02 gene	13.032	0.0000	0.0000
A630072M18Rik	ENSMUSG00000101013	RIKEN cDNA A630072M18 gene	1.771	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
A830035O19Rik	ENSMUSG00000111329	RIKEN cDNA A830035O19 gene	2.006	0.0029	0.0080
A930004J17Rik	ENSMUSG00000102602	RIKEN cDNA A930004J17 gene	1.810	0.0431	0.0852
A930015D03Rik	ENSMUSG00000092368	RIKEN cDNA A930015D03 gene	1.924	0.0000	0.0001
A930016O22Rik	ENSMUSG00000040705	RIKEN cDNA A930016O22 gene	6.746	0.0000	0.0000
A930018P22Rik	ENSMUSG00000032671	RIKEN cDNA A930018P22 gene	9.505	0.0000	0.0000
A930035D04Rik	ENSMUSG00000052241	RIKEN cDNA A930035D04 gene	6.313	0.0000	0.0000
AA465934	ENSMUSG00000093483	expressed sequence AA465934	1.954	0.0137	0.0315
Aatf	ENSMUSG00000018697	apoptosis antagonizing transcription factor	2.126	0.0000	0.0000
AB124611	ENSMUSG00000057191	cDNA sequence AB124611	1.738	0.0314	0.0650
Abcf1	ENSMUSG00000038762	ATP-binding cassette, sub-family F (GCN20), member 1	1.840	0.0000	0.0000
Abhd11os	ENSMUSG00000085042	abhydrolase domain containing 11, opposite strand	4.459	0.0039	0.0104
Abhd17a	ENSMUSG00000003346	abhydrolase domain containing 17A	2.262	0.0000	0.0000
Abhd17b	ENSMUSG00000047368	abhydrolase domain containing 17B	1.858	0.0000	0.0000
Abl2	ENSMUSG00000026596	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	1.685	0.0000	0.0000
Abr	ENSMUSG00000017631	active BCR-related gene	1.553	0.0000	0.0000
Abra	ENSMUSG00000042895	actin-binding Rho activating protein	1.717	0.0136	0.0314
Abracl	ENSMUSG00000078453	ABRA C-terminal like	2.431	0.0000	0.0000
Acaca	ENSMUSG00000020532	acetyl-Coenzyme A carboxylase alpha	1.729	0.0000	0.0001
Acbd3	ENSMUSG00000026499	acyl-Coenzyme A binding domain containing 3	3.473	0.0000	0.0000
Acbd5	ENSMUSG00000026781	acyl-Coenzyme A binding domain containing 5	1.756	0.0000	0.0000
Acbd6	ENSMUSG00000033701	acyl-Coenzyme A binding domain containing 6	3.941	0.0000	0.0000
Acin1	ENSMUSG00000022185	apoptotic chromatin condensation inducer 1	1.902	0.0000	0.0000
Acot1	ENSMUSG00000072949	acyl-CoA thioesterase 1	2.370	0.0000	0.0000
Acot4	ENSMUSG00000052392	acyl-CoA thioesterase 4	2.991	0.0000	0.0000
Acsl3	ENSMUSG00000032883	acyl-CoA synthetase long-chain family member 3	1.553	0.0000	0.0001
Acsm5	ENSMUSG00000030972	acyl-CoA synthetase medium-chain family member 5	1.508	0.0224	0.0486
Actr3-ps	ENSMUSG00000082319	actin related protein 3, pseudogene	2.589	0.0000	0.0000
Acvr1b	ENSMUSG00000000532	activin A receptor, type 1B	1.739	0.0000	0.0000
Acvr2a	ENSMUSG00000052155	activin receptor IIA	1.507	0.0000	0.0000
Acvr2b	ENSMUSG00000061393	activin receptor IIB	1.699	0.0001	0.0002
Adam1a	ENSMUSG00000072647	a disintegrin and metallopeptidase domain 1a	2.605	0.0046	0.0119
Adam23	ENSMUSG00000025964	a disintegrin and metallopeptidase domain 23	2.078	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Adamts19	ENSMUSG00000053441	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19	2.118	0.0015	0.0045
Adat2	ENSMUSG00000019808	adenosine deaminase, tRNA-specific 2	2.550	0.0000	0.0000
Adcy5	ENSMUSG00000022840	adenylate cyclase 5	1.571	0.0019	0.0054
Adgrb2	ENSMUSG00000028782	adhesion G protein-coupled receptor B2	1.856	0.0140	0.0322
Adipor1	ENSMUSG00000026457	adiponectin receptor 1	1.613	0.0000	0.0000
Adnp	ENSMUSG00000051149	activity-dependent neuroprotective protein	25.375	0.0000	0.0000
Adra1d	ENSMUSG00000027335	adrenergic receptor, alpha 1d	2.452	0.0000	0.0002
Adra2c	ENSMUSG00000045318	adrenergic receptor, alpha 2c	4.255	0.0003	0.0010
Adrb1	ENSMUSG00000035283	adrenergic receptor, beta 1	3.139	0.0000	0.0000
Adss	ENSMUSG00000015961	adenylosuccinate synthetase, non muscle	1.898	0.0000	0.0000
Adssl1	ENSMUSG00000011148	adenylosuccinate synthetase like 1	1.626	0.0000	0.0002
Aebp2	ENSMUSG00000030232	AE binding protein 2	2.644	0.0000	0.0000
Afg3l2	ENSMUSG00000024527	AFG3-like AAA ATPase 2	1.568	0.0000	0.0000
Aga	ENSMUSG00000031521	aspartylglucosaminidase	1.848	0.0000	0.0000
Agap3	ENSMUSG00000023353	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	2.265	0.0000	0.0000
Agpat5	ENSMUSG00000031467	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.704	0.0000	0.0000
Agtpbp1	ENSMUSG00000021557	ATP/GTP binding protein 1	1.726	0.0000	0.0001
Ahcyl1	ENSMUSG00000027893	S-adenosylhomocysteine hydrolase-like 1	2.125	0.0000	0.0000
Ahcyl2	ENSMUSG00000029772	S-adenosylhomocysteine hydrolase-like 2	1.562	0.0000	0.0000
Ahsa2	ENSMUSG00000020288	AHA1, activator of heat shock protein ATPase 2	1.656	0.0000	0.0000
AI662270	ENSMUSG00000087107	expressed sequence AI662270	4.132	0.0000	0.0002
Aif1	ENSMUSG00000024397	allograft inflammatory factor 1	2.331	0.0029	0.0080
Aifm1	ENSMUSG00000036932	apoptosis-inducing factor, mitochondrion-associated 1	2.012	0.0000	0.0000
Ak6	ENSMUSG00000078941	adenylate kinase 6	2.347	0.0000	0.0000
Akap7	ENSMUSG00000039166	A kinase (PRKA) anchor protein 7	1.961	0.0000	0.0000
Akap8	ENSMUSG00000024045	A kinase (PRKA) anchor protein 8	2.100	0.0000	0.0000
Akap9	ENSMUSG00000040407	A kinase (PRKA) anchor protein (yotiao) 9	1.512	0.0003	0.0009
Akirin1	ENSMUSG00000023075	akirin 1	2.189	0.0000	0.0000
Akirin2	ENSMUSG00000028291	akirin 2	2.638	0.0000	0.0000
Akt3	ENSMUSG00000019699	thymoma viral proto-oncogene 3	1.537	0.0000	0.0000
Aktip	ENSMUSG00000031667	AKT interacting protein	1.648	0.0000	0.0000
Aldh5a1	ENSMUSG00000035936	aldhehyde dehydrogenase family 5, subfamily A1	1.573	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Aldoa	ENSMUSG00000114515	aldolase A, fructose-bisphosphate	3.882	0.0015	0.0044
Aldoart1	ENSMUSG00000059343	aldolase 1 A, retrogene 1	8.690	0.0000	0.0000
Alkbh2	ENSMUSG00000044339	alkB homolog 2, alpha-ketoglutarate-dependent dioxygenase	2.018	0.0000	0.0000
Alyref	ENSMUSG00000025134	Aly/REF export factor	6.207	0.0000	0.0000
Alyref2	ENSMUSG00000060244	Aly/REF export factor 2	1.812	0.0009	0.0027
Ammecr1	ENSMUSG00000042225	AMMECR nuclear protein 1	1.974	0.0000	0.0000
Anapc13	ENSMUSG00000035048	anaphase promoting complex subunit 13	4.213	0.0000	0.0000
Anapc15	ENSMUSG00000030649	anaphase promoting complex C subunit 15	2.097	0.0000	0.0000
Angptl1	ENSMUSG00000033544	angiopoietin-like 1	1.555	0.0239	0.0512
Ank1	ENSMUSG00000031543	ankyrin 1, erythroid	1.945	0.0000	0.0000
Ankhd1	ENSMUSG00000024483	ankyrin repeat and KH domain containing 1	1.757	0.0000	0.0000
Ankmy1	ENSMUSG00000034212	ankyrin repeat and MYND domain containing 1	9.800	0.0006	0.0020
Ankrd11	ENSMUSG00000035569	ankyrin repeat domain 11	1.506	0.0000	0.0000
Ankrd35	ENSMUSG00000038354	ankyrin repeat domain 35	1.987	0.0167	0.0376
Ankrd37	ENSMUSG00000050914	ankyrin repeat domain 37	2.033	0.0012	0.0036
Ankrd40	ENSMUSG00000020864	ankyrin repeat domain 40	2.182	0.0000	0.0000
Ankrd63	ENSMUSG00000078137	ankyrin repeat domain 63	1.803	0.0172	0.0385
Ano8	ENSMUSG00000034863	anoctamin 8	3.905	0.0000	0.0000
Anp32a	ENSMUSG00000032249	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	2.317	0.0000	0.0000
Anp32b	ENSMUSG00000028333	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	7.305	0.0000	0.0000
Anp32e	ENSMUSG00000015749	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	2.708	0.0000	0.0000
Anxa5	ENSMUSG00000027712	annexin A5	1.842	0.0000	0.0000
Ap1ar	ENSMUSG00000074238	adaptor-related protein complex 1 associated regulatory protein	1.738	0.0000	0.0000
Ap1g1	ENSMUSG00000031731	adaptor protein complex AP-1, gamma 1 subunit	1.535	0.0000	0.0000
Ap3b1	ENSMUSG00000021686	adaptor-related protein complex 3, beta 1 subunit	1.793	0.0000	0.0000
Ap3s1	ENSMUSG00000024480	adaptor-related protein complex 3, sigma 1 subunit	3.382	0.0000	0.0000
Ap4s1	ENSMUSG00000020955	adaptor-related protein complex AP-4, sigma 1	2.122	0.0000	0.0000
Apba1	ENSMUSG00000024897	amyloid beta (A4) precursor protein binding, family A, member 1	1.770	0.0031	0.0084
Apip	ENSMUSG00000010911	APAF1 interacting protein	1.543	0.0000	0.0000
Aplp2	ENSMUSG00000031996	amyloid beta (A4) precursor-like protein 2	1.509	0.0000	0.0000
Apobr	ENSMUSG00000042759	apolipoprotein B receptor	1.997	0.0044	0.0117
Apol10b	ENSMUSG00000050014	apolipoprotein L 10B	2.216	0.0013	0.0039

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Apold1	ENSMUSG00000090698	apolipoprotein L domain containing 1	1.873	0.0002	0.0007
Apoo-ps	ENSMUSG00000049233	apolipoprotein O, pseudogene	1.891	0.0001	0.0002
App	ENSMUSG00000022892	amyloid beta (A4) precursor protein	1.566	0.0000	0.0000
Appbp2os	ENSMUSG00000085628	amyloid beta precursor protein (cytoplasmic tail) binding protein 2, opposite strand	5.475	0.0168	0.0377
Aqp4	ENSMUSG00000024411	aquaporin 4	1.651	0.0058	0.0147
Arf3	ENSMUSG00000051853	ADP-ribosylation factor 3	2.283	0.0000	0.0000
Arf5	ENSMUSG00000020440	ADP-ribosylation factor 5	2.546	0.0000	0.0000
Arf6	ENSMUSG00000044147	ADP-ribosylation factor 6	3.998	0.0000	0.0000
Arglu1	ENSMUSG00000040459	arginine and glutamate rich 1	3.016	0.0000	0.0000
Arhgap11a	ENSMUSG00000041219	Rho GTPase activating protein 11A	2.475	0.0000	0.0000
Arhgap19	ENSMUSG00000025154	Rho GTPase activating protein 19	1.897	0.0000	0.0000
Arhgap23	ENSMUSG00000049807	Rho GTPase activating protein 23	2.589	0.0000	0.0000
Arhgap30	ENSMUSG00000048865	Rho GTPase activating protein 30	2.002	0.0001	0.0003
Arhgap44	ENSMUSG00000033389	Rho GTPase activating protein 44	1.664	0.0000	0.0001
Arhgdig	ENSMUSG00000073433	Rho GDP dissociation inhibitor (GDI) gamma	1.562	0.0414	0.0824
Arhgef9	ENSMUSG00000025656	CDC42 guanine nucleotide exchange factor (GEF) 9	1.714	0.0000	0.0000
Arid1a	ENSMUSG00000007880	AT rich interactive domain 1A (SWI-like)	1.592	0.0000	0.0001
Arid4a	ENSMUSG00000048118	AT rich interactive domain 4A (RBP1-like)	2.183	0.0000	0.0000
Arid4b	ENSMUSG00000039219	AT rich interactive domain 4B (RBP1-like)	1.894	0.0000	0.0000
Arih1	ENSMUSG00000025234	ariadne RBR E3 ubiquitin protein ligase 1	1.791	0.0000	0.0000
Arl1	ENSMUSG00000060904	ADP-ribosylation factor-like 1	1.981	0.0000	0.0000
Arl10	ENSMUSG00000025870	ADP-ribosylation factor-like 10	2.700	0.0000	0.0000
Arl13b	ENSMUSG00000022911	ADP-ribosylation factor-like 13B	1.866	0.0000	0.0000
Arl2bp	ENSMUSG00000031776	ADP-ribosylation factor-like 2 binding protein	1.504	0.0000	0.0000
Arl4a	ENSMUSG00000047446	ADP-ribosylation factor-like 4A	2.153	0.0001	0.0002
Arl4c	ENSMUSG00000049866	ADP-ribosylation factor-like 4C	1.924	0.0000	0.0000
Arl4d	ENSMUSG00000034936	ADP-ribosylation factor-like 4D	1.660	0.0003	0.0011
Arl5b	ENSMUSG00000017418	ADP-ribosylation factor-like 5B	1.545	0.0000	0.0000
Arl6ip4	ENSMUSG00000029404	ADP-ribosylation factor-like 6 interacting protein 4	1.790	0.0000	0.0000
Arl6ip5	ENSMUSG00000035199	ADP-ribosylation factor-like 6 interacting protein 5	1.747	0.0000	0.0000
Arl6ip6	ENSMUSG00000026960	ADP-ribosylation factor-like 6 interacting protein 6	1.845	0.0000	0.0000
Arl8a	ENSMUSG00000026426	ADP-ribosylation factor-like 8A	2.604	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Armc8	ENSMUSG00000032468	armadillo repeat containing 8	1.518	0.0000	0.0000
Armcx4	ENSMUSG00000049804	armadillo repeat containing, X-linked 4	2.551	0.0000	0.0000
Armcx6	ENSMUSG00000050394	armadillo repeat containing, X-linked 6	2.657	0.0000	0.0000
Armh4	ENSMUSG00000036242	armadillo-like helical domain containing 4	1.590	0.0000	0.0000
Arnt	ENSMUSG00000015522	aryl hydrocarbon receptor nuclear translocator	1.654	0.0000	0.0000
Arpc2	ENSMUSG00000006304	actin related protein 2/3 complex, subunit 2	1.593	0.0000	0.0000
Arpc5l	ENSMUSG00000026755	actin related protein 2/3 complex, subunit 5-like	1.522	0.0000	0.0000
Arpp19	ENSMUSG00000007656	cAMP-regulated phosphoprotein 19	1.919	0.0000	0.0000
Arrdc4	ENSMUSG00000042659	arrestin domain containing 4	2.146	0.0000	0.0000
Asf1a	ENSMUSG00000019857	anti-silencing function 1A histone chaperone	2.616	0.0000	0.0000
Ash2l	ENSMUSG00000031575	ASH2 like histone lysine methyltransferase complex subunit	2.302	0.0000	0.0000
Asph	ENSMUSG00000028207	aspartate-beta-hydroxylase	2.046	0.0000	0.0000
Asrgl1	ENSMUSG00000024654	asparaginase like 1	1.951	0.0000	0.0000
Atad1	ENSMUSG00000013662	ATPase family, AAA domain containing 1	1.940	0.0000	0.0000
Atad2	ENSMUSG00000022360	ATPase family, AAA domain containing 2	2.313	0.0000	0.0000
Atad2b	ENSMUSG00000052812	ATPase family, AAA domain containing 2B	1.984	0.0000	0.0000
Atad3a	ENSMUSG00000029036	ATPase family, AAA domain containing 3A	2.149	0.0000	0.0000
Atf1	ENSMUSG00000023027	activating transcription factor 1	2.810	0.0000	0.0000
Atf2	ENSMUSG00000027104	activating transcription factor 2	1.565	0.0000	0.0000
Atf5	ENSMUSG00000038539	activating transcription factor 5	3.062	0.0000	0.0000
Atg10	ENSMUSG00000021619	autophagy related 10	1.725	0.0000	0.0000
Atg3	ENSMUSG00000022663	autophagy related 3	4.076	0.0000	0.0000
Atn1	ENSMUSG00000004263	atrophin 1	6.372	0.0000	0.0000
Atp11b	ENSMUSG00000037400	ATPase, class VI, type 11B	2.024	0.0000	0.0000
Atp13a3	ENSMUSG00000022533	ATPase type 13A3	1.613	0.0000	0.0000
Atp1b1	ENSMUSG00000026576	ATPase, Na+/K+ transporting, beta 1 polypeptide	1.593	0.0000	0.0000
Atp1b3	ENSMUSG00000032412	ATPase, Na+/K+ transporting, beta 3 polypeptide	1.853	0.0000	0.0000
Atp23	ENSMUSG00000025436	ATP23 metallopeptidase and ATP synthase assembly factor homolog	1.541	0.0292	0.0609
Atp2a2	ENSMUSG00000029467	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	1.878	0.0000	0.0000
Atp6v1g1	ENSMUSG00000039105	ATPase, H+ transporting, lysosomal V1 subunit G1	1.987	0.0000	0.0000
Atrx	ENSMUSG00000031229	ATRX, chromatin remodeler	1.710	0.0000	0.0000
Atxn7	ENSMUSG00000021738	ataxin 7	1.779	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Aven	ENSMUSG00000003604	apoptosis, caspase activation inhibitor	4.911	0.0000	0.0000
AW046200	ENSMUSG00000110419	expressed sequence AW046200	3.660	0.0001	0.0003
Axin1	ENSMUSG00000024182	axin 1	1.567	0.0007	0.0021
Axin2	ENSMUSG00000000142	axin 2	1.835	0.0002	0.0007
Azin1	ENSMUSG00000037458	antizyme inhibitor 1	1.721	0.0000	0.0000
B230216N24Rik	ENSMUSG00000089706	RIKEN cDNA B230216N24 gene	2.020	0.0469	0.0915
B230322F03Rik	ENSMUSG00000097509	RIKEN cDNA B230322F03 gene	2.451	0.0034	0.0091
B230377A18Rik	ENSMUSG00000104195	RIKEN cDNA B230377A18 gene	8.191	0.0000	0.0000
B330016D10Rik	ENSMUSG00000048406	RIKEN cDNA B330016D10 gene	2.360	0.0000	0.0000
B3gnt2	ENSMUSG00000051650	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	14.044	0.0000	0.0000
B430219N15Rik	ENSMUSG00000085211	RIKEN cDNA B430219N15 gene	4.043	0.0003	0.0010
B430319F04Rik	ENSMUSG00000110062	RIKEN cDNA B430319F04 gene	3.483	0.0365	0.0738
B430319G15Rik	ENSMUSG00000103622	RIKEN cDNA B430319G15 gene	1.925	0.0162	0.0366
B4galt1	ENSMUSG00000028413	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	1.509	0.0000	0.0000
B4galt2	ENSMUSG00000028541	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	3.571	0.0000	0.0000
B630019K06Rik	ENSMUSG00000052364	RIKEN cDNA B630019K06 gene	2.132	0.0003	0.0012
B930094E09Rik	ENSMUSG00000092124	RIKEN cDNA B930094E09 gene	1.594	0.0120	0.0281
Bag1	ENSMUSG00000028416	BCL2-associated athanogene 1	2.497	0.0000	0.0000
Basp1	ENSMUSG00000045763	brain abundant, membrane attached signal protein 1	8.773	0.0000	0.0000
Baz1a	ENSMUSG00000035021	bromodomain adjacent to zinc finger domain 1A	1.734	0.0003	0.0009
Baz1b	ENSMUSG00000002748	bromodomain adjacent to zinc finger domain, 1B	2.344	0.0000	0.0000
Baz2b	ENSMUSG00000026987	bromodomain adjacent to zinc finger domain, 2B	1.514	0.0000	0.0000
Bbc3	ENSMUSG00000002083	BCL2 binding component 3	5.699	0.0000	0.0000
Bbof1	ENSMUSG00000057265	basal body orientation factor 1	1.582	0.0012	0.0035
Bbs5	ENSMUSG00000063145	Bardet-Biedl syndrome 5 (human)	1.578	0.0000	0.0001
Bbx	ENSMUSG00000022641	bobby sox HMG box containing	1.624	0.0000	0.0000
BC002189	ENSMUSG00000104465	cDNA sequence BC002189	2.664	0.0103	0.0247
BC005537	ENSMUSG00000019132	cDNA sequence BC005537	1.568	0.0008	0.0025
BC005624	ENSMUSG00000026851	cDNA sequence BC005624	2.291	0.0000	0.0000
Bcas2	ENSMUSG00000005687	BCAS2 pre-mRNA processing factor	1.714	0.0000	0.0000
Bcat1	ENSMUSG00000030268	branched chain aminotransferase 1, cytosolic	1.552	0.0256	0.0543
Bccip	ENSMUSG00000030983	BRCA2 and CDKN1A interacting protein	2.553	0.0000	0.0000

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Bcl2a1b	ENSMUSG00000089929	B cell leukemia/lymphoma 2 related protein A1b	18.966	0.0078	0.0192
Bcl2l2	ENSMUSG00000089682	BCL2-like 2	2.090	0.0000	0.0000
Bcl3	ENSMUSG00000053175	B cell leukemia/lymphoma 3	3.629	0.0000	0.0000
Bcl6b	ENSMUSG00000000317	B cell CLL/lymphoma 6, member B	1.723	0.0004	0.0013
Bcl7c	ENSMUSG00000030814	B cell CLL/lymphoma 7C	5.806	0.0000	0.0000
Bdp1	ENSMUSG00000049658	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	1.952	0.0000	0.0000
Bean1	ENSMUSG00000031872	brain expressed, associated with Nedd4, 1	1.637	0.0216	0.0471
Becn1	ENSMUSG00000035086	beclin 1, autophagy related	1.958	0.0000	0.0000
Begain	ENSMUSG00000040867	brain-enriched guanylate kinase-associated	3.612	0.0106	0.0254
Bend5	ENSMUSG00000028545	BEN domain containing 5	1.787	0.0000	0.0000
Bex1	ENSMUSG00000050071	brain expressed X-linked 1	1.754	0.0075	0.0185
Bex4	ENSMUSG00000047844	brain expressed X-linked 4	4.390	0.0080	0.0196
Bfsp1	ENSMUSG00000027420	beaded filament structural protein 1, in lens-CP94	1.977	0.0119	0.0280
Bhlhe22	ENSMUSG00000025128	basic helix-loop-helix family, member e22	2.597	0.0038	0.0100
Bhlhe41	ENSMUSG00000030256	basic helix-loop-helix family, member e41	2.720	0.0000	0.0000
Bicd2	ENSMUSG00000037933	BICD cargo adaptor 2	1.666	0.0000	0.0000
Bloc1s4	ENSMUSG00000060708	biogenesis of lysosomal organelles complex-1, subunit 4, cappuccino	3.365	0.0000	0.0000
Bmi1	ENSMUSG00000026739	Bmi1 polycomb ring finger oncogene	1.605	0.0000	0.0000
Bmpr1a	ENSMUSG00000021796	bone morphogenetic protein receptor, type 1A	1.642	0.0000	0.0000
Bmpr1b	ENSMUSG00000052430	bone morphogenetic protein receptor, type 1B	3.024	0.0000	0.0002
Bms1	ENSMUSG00000030138	BMS1, ribosome biogenesis factor	2.490	0.0000	0.0000
Bmx	ENSMUSG00000031377	BMX non-receptor tyrosine kinase	1.815	0.0002	0.0007
Bnip2	ENSMUSG00000011958	BCL2/adenovirus E1B interacting protein 2	1.884	0.0000	0.0000
Bod1	ENSMUSG00000044502	biorientation of chromosomes in cell division 1	1.559	0.0000	0.0000
Bod1l	ENSMUSG00000061755	biorientation of chromosomes in cell division 1-like	1.898	0.0000	0.0000
Borcs6	ENSMUSG00000045176	BLOC-1 related complex subunit 6	2.977	0.0000	0.0001
Bpnt1	ENSMUSG00000026617	3'(2'), 5'-bisphosphate nucleotidase 1	1.552	0.0010	0.0031
Bpnt2	ENSMUSG00000066324	3'(2'), 5'-bisphosphate nucleotidase 2	1.611	0.0000	0.0000
Brd7	ENSMUSG00000031660	bromodomain containing 7	1.613	0.0000	0.0000
Brd9	ENSMUSG00000057649	bromodomain containing 9	1.529	0.0000	0.0000
Brf1	ENSMUSG00000011158	BRF1, RNA polymerase III transcription initiation factor 90 kDa subunit	1.722	0.0000	0.0000
Bri3	ENSMUSG00000047843	brain protein I3	7.344	0.0000	0.0000

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Brsk1	ENSMUSG00000035390	BR serine/threonine kinase 1	2.030	0.0001	0.0002
Btbd1	ENSMUSG00000025103	BTB (POZ) domain containing 1	2.444	0.0000	0.0000
Btbd10	ENSMUSG00000038187	BTB (POZ) domain containing 10	1.621	0.0000	0.0000
Btbd19	ENSMUSG00000073771	BTB (POZ) domain containing 19	1.772	0.0139	0.0319
Btf3	ENSMUSG00000021660	basic transcription factor 3	1.941	0.0000	0.0000
Btf3l4	ENSMUSG00000028568	basic transcription factor 3-like 4	2.240	0.0000	0.0000
Btg1	ENSMUSG00000036478	BTG anti-proliferation factor 1	4.328	0.0000	0.0000
Btg3	ENSMUSG00000022863	BTG anti-proliferation factor 3	2.838	0.0000	0.0000
Btla	ENSMUSG00000052013	B and T lymphocyte associated	2.178	0.0225	0.0488
Bub1b	ENSMUSG00000040084	BUB1B, mitotic checkpoint serine/threonine kinase	2.468	0.0008	0.0026
Bud13	ENSMUSG00000032077	BUD13 homolog	1.611	0.0000	0.0000
C030015A19Rik	ENSMUSG00000108181	RIKEN cDNA C030015A19 gene	1.645	0.0473	0.0923
C030037D09Rik	ENSMUSG00000087574	RIKEN cDNA C030037D09 gene	1.504	0.0002	0.0007
C130074G19Rik	ENSMUSG00000039349	RIKEN cDNA C130074G19 gene	2.344	0.0000	0.0000
C130080G10Rik	ENSMUSG00000092397	RIKEN cDNA C130080G10 gene	1.605	0.0003	0.0009
C1galt1c1	ENSMUSG00000048970	C1GALT1-specific chaperone 1	1.818	0.0000	0.0000
C1qc	ENSMUSG00000036896	complement component 1, q subcomponent, C chain	4.478	0.0003	0.0009
C1qtnf9	ENSMUSG00000071347	C1q and tumor necrosis factor related protein 9	1.686	0.0001	0.0005
C1rb	ENSMUSG00000098470	complement component 1, r subcomponent B	3.681	0.0000	0.0000
C230013L11Rik	ENSMUSG00000117171	RIKEN cDNA C230013L11 gene	5.086	0.0000	0.0000
C230096K16Rik	ENSMUSG00000106205	RIKEN cDNA C230096K16 gene	3.997	0.0000	0.0000
C2cd4b	ENSMUSG00000091956	C2 calcium-dependent domain containing 4B	2.258	0.0431	0.0851
C2cd4d	ENSMUSG00000091648	C2 calcium-dependent domain containing 4D	12.776	0.0015	0.0045
C330011M18Rik	ENSMUSG00000056753	RIKEN cDNA C330011M18 gene	2.001	0.0000	0.0000
C430014B12Rik	ENSMUSG00000097564	RIKEN cDNA C430014B12 gene	3.941	0.0000	0.0002
C430049B03Rik	ENSMUSG00000087365	RIKEN cDNA C430049B03 gene	2.739	0.0015	0.0044
C5ar1	ENSMUSG00000049130	complement component 5a receptor 1	2.330	0.0000	0.0001
C630043F03Rik	ENSMUSG00000084910	RIKEN cDNA C630043F03 gene	3.117	0.0000	0.0000
Caap1	ENSMUSG00000028578	caspase activity and apoptosis inhibitor 1	2.132	0.0000	0.0000
Cab39	ENSMUSG00000036707	calcium binding protein 39	2.034	0.0000	0.0000
Cables1	ENSMUSG00000040957	CDK5 and Abl enzyme substrate 1	1.894	0.0000	0.0000
Cables2	ENSMUSG00000038990	CDK5 and Abl enzyme substrate 2	1.663	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cacfd1	ENSMUSG00000015488	calcium channel flower domain containing 1	2.143	0.0000	0.0000
Cacna2d2	ENSMUSG00000010066	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.702	0.0119	0.0280
Cacng7	ENSMUSG00000069806	calcium channel, voltage-dependent, gamma subunit 7	2.223	0.0000	0.0000
Cacul1	ENSMUSG00000033417	CDK2 associated, cullin domain 1	1.607	0.0000	0.0001
Cadm1	ENSMUSG00000032076	cell adhesion molecule 1	1.649	0.0002	0.0008
Cadm3	ENSMUSG00000005338	cell adhesion molecule 3	1.671	0.0427	0.0844
Cadps2	ENSMUSG00000017978	Ca2+-dependent activator protein for secretion 2	1.506	0.0387	0.0776
Cald1	ENSMUSG00000029761	caldesmon 1	1.927	0.0000	0.0000
Calm2	ENSMUSG00000036438	calmodulin 2	2.332	0.0000	0.0000
Calm3	ENSMUSG00000019370	calmodulin 3	2.343	0.0000	0.0000
Calr	ENSMUSG00000003814	calreticulin	1.702	0.0000	0.0000
Camk1	ENSMUSG00000030272	calcium/calmodulin-dependent protein kinase I	2.493	0.0000	0.0000
Camk2d	ENSMUSG00000053819	calcium/calmodulin-dependent protein kinase II, delta	1.618	0.0000	0.0000
Camk2n1	ENSMUSG00000046447	calcium/calmodulin-dependent protein kinase II inhibitor 1	5.358	0.0000	0.0000
Camk2n2	ENSMUSG00000051146	calcium/calmodulin-dependent protein kinase II inhibitor 2	3.200	0.0000	0.0000
Camkmt	ENSMUSG00000071037	calmodulin-lysine N-methyltransferase	2.150	0.0000	0.0002
Camsap2	ENSMUSG00000041570	calmodulin regulated spectrin-associated protein family, member 2	1.654	0.0000	0.0000
Canx	ENSMUSG00000020368	calnexin	1.795	0.0000	0.0000
Caprin1	ENSMUSG00000027184	cell cycle associated protein 1	1.945	0.0000	0.0000
Carnmt1	ENSMUSG00000024726	carnosine N-methyltransferase 1	3.294	0.0000	0.0000
Casc1	ENSMUSG00000043541	cancer susceptibility candidate 1	2.636	0.0448	0.0879
Casc3	ENSMUSG00000078676	cancer susceptibility candidate 3	1.967	0.0000	0.0000
Casq1	ENSMUSG00000007122	calsequestrin 1	1.516	0.0337	0.0690
Castor2	ENSMUSG00000015944	cytosolic arginine sensor for mTORC1 subunit 2	1.694	0.0033	0.0090
Casz1	ENSMUSG00000028977	castor zinc finger 1	1.851	0.0000	0.0000
Cavin1	ENSMUSG00000004044	caveolae associated 1	2.460	0.0000	0.0000
Cbfb	ENSMUSG00000031885	core binding factor beta	2.615	0.0000	0.0000
Cbx1	ENSMUSG00000018666	chromobox 1	2.642	0.0000	0.0000
Cbx3	ENSMUSG00000029836	chromobox 3	2.486	0.0000	0.0000
Cbx5	ENSMUSG00000009575	chromobox 5	1.632	0.0000	0.0000
Ccar1	ENSMUSG00000020074	cell division cycle and apoptosis regulator 1	2.464	0.0000	0.0000
Ccdc112	ENSMUSG00000071855	coiled-coil domain containing 112	1.555	0.0360	0.0729

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ccdc117	ENSMUSG00000020482	coiled-coil domain containing 117	2.112	0.0000	0.0000
Ccdc12	ENSMUSG00000019659	coiled-coil domain containing 12	1.863	0.0000	0.0000
Ccdc122	ENSMUSG00000034795	coiled-coil domain containing 122	2.290	0.0000	0.0000
Ccdc124	ENSMUSG00000007721	coiled-coil domain containing 124	2.263	0.0000	0.0000
Ccdc142os	ENSMUSG00000087578	coiled-coil domain containing 142, opposite strand	1.720	0.0168	0.0378
Ccdc146	ENSMUSG00000064280	coiled-coil domain containing 146	1.849	0.0000	0.0000
Ccdc173	ENSMUSG00000070883	coiled-coil domain containing 173	3.320	0.0000	0.0000
Ccdc174	ENSMUSG00000034083	coiled-coil domain containing 174	1.826	0.0000	0.0000
Ccdc18	ENSMUSG00000056531	coiled-coil domain containing 18	2.735	0.0251	0.0535
Ccdc181	ENSMUSG00000026578	coiled-coil domain containing 181	1.894	0.0000	0.0000
Ccdc191	ENSMUSG00000022701	coiled-coil domain containing 191	1.952	0.0000	0.0001
Ccdc25	ENSMUSG00000022035	coiled-coil domain containing 25	2.111	0.0000	0.0000
Ccdc28b	ENSMUSG00000028795	coiled coil domain containing 28B	1.506	0.0010	0.0030
Ccdc34	ENSMUSG00000027160	coiled-coil domain containing 34	3.968	0.0000	0.0000
Ccdc43	ENSMUSG00000020925	coiled-coil domain containing 43	1.525	0.0000	0.0000
Ccdc47	ENSMUSG00000078622	coiled-coil domain containing 47	2.602	0.0000	0.0000
Ccdc50	ENSMUSG00000038127	coiled-coil domain containing 50	1.570	0.0000	0.0000
Ccdc66	ENSMUSG00000046753	coiled-coil domain containing 66	1.502	0.0001	0.0003
Ccdc71l	ENSMUSG00000090946	coiled-coil domain containing 71 like	3.095	0.0000	0.0000
Ccdc82	ENSMUSG00000079084	coiled-coil domain containing 82	1.911	0.0000	0.0000
Ccdc85b	ENSMUSG00000095098	coiled-coil domain containing 85B	3.463	0.0002	0.0006
Ccdc85c	ENSMUSG00000084883	coiled-coil domain containing 85C	1.741	0.0000	0.0000
Ccdc88a	ENSMUSG00000032740	coiled coil domain containing 88A	1.524	0.0000	0.0000
Ccdc9	ENSMUSG00000041375	coiled-coil domain containing 9	1.987	0.0000	0.0000
Ccdc91	ENSMUSG00000030301	coiled-coil domain containing 91	1.943	0.0000	0.0000
Cchcr1	ENSMUSG00000040312	coiled-coil alpha-helical rod protein 1	1.557	0.0069	0.0173
Ccm2l	ENSMUSG00000027474	cerebral cavernous malformation 2-like	1.549	0.0021	0.0060
Ccnd1	ENSMUSG00000070348	cyclin D1	2.050	0.0001	0.0004
Ccng2	ENSMUSG00000029385	cyclin G2	2.429	0.0000	0.0000
Ccni	ENSMUSG00000063015	cyclin I	2.340	0.0000	0.0000
Ccnj	ENSMUSG00000025010	cyclin J	2.412	0.0000	0.0000
Ccnt1	ENSMUSG00000011960	cyclin T1	1.530	0.0000	0.0000

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Ccnyl1	ENSMUSG00000070871	cyclin Y-like 1	1.578	0.0001	0.0005
Ccs	ENSMUSG00000034108	copper chaperone for superoxide dismutase	1.831	0.0000	0.0000
Ccsap	ENSMUSG00000031971	centriole, cilia and spindle associated protein	3.235	0.0000	0.0000
Ccz1	ENSMUSG00000029617	CCZ1 vacuolar protein trafficking and biogenesis associated	2.053	0.0000	0.0000
Cd163	ENSMUSG00000008845	CD163 antigen	1.780	0.0135	0.0313
Cd2	ENSMUSG00000027863	CD2 antigen	3.337	0.0040	0.0107
Cd209f	ENSMUSG00000051906	CD209f antigen	1.747	0.0518	0.0997
Cd300a	ENSMUSG00000034652	CD300A molecule	1.755	0.0081	0.0199
Cd3e	ENSMUSG00000032093	CD3 antigen, epsilon polypeptide	3.972	0.0000	0.0000
Cd44	ENSMUSG00000005087	CD44 antigen	1.688	0.0100	0.0241
Cd63	ENSMUSG00000025351	CD63 antigen	1.665	0.0000	0.0000
Cd72	ENSMUSG00000028459	CD72 antigen	2.879	0.0125	0.0291
Cd9	ENSMUSG00000030342	CD9 antigen	1.913	0.0000	0.0000
Cdc25a	ENSMUSG00000032477	cell division cycle 25A	1.693	0.0000	0.0000
Cdc26	ENSMUSG00000066149	cell division cycle 26	1.988	0.0000	0.0000
Cdc37	ENSMUSG00000019471	cell division cycle 37	2.061	0.0000	0.0000
Cdc37l1	ENSMUSG00000024780	cell division cycle 37-like 1	1.517	0.0214	0.0467
Cdk11b	ENSMUSG00000029062	cyclin-dependent kinase 11B	2.385	0.0000	0.0000
Cdk13	ENSMUSG00000041297	cyclin-dependent kinase 13	1.851	0.0000	0.0000
Cdk17	ENSMUSG00000020015	cyclin-dependent kinase 17	1.777	0.0000	0.0000
Cdk18	ENSMUSG00000026437	cyclin-dependent kinase 18	1.563	0.0000	0.0000
Cdk2ap1	ENSMUSG00000029394	CDK2 (cyclin-dependent kinase 2)-associated protein 1	2.197	0.0000	0.0001
Cdk5rap3	ENSMUSG00000018669	CDK5 regulatory subunit associated protein 3	1.800	0.0000	0.0000
Cdk8	ENSMUSG00000029635	cyclin-dependent kinase 8	1.852	0.0000	0.0000
Cdkl3	ENSMUSG00000020389	cyclin-dependent kinase-like 3	1.630	0.0001	0.0002
Cdkn1c	ENSMUSG00000037664	cyclin-dependent kinase inhibitor 1C (P57)	4.230	0.0000	0.0000
Cdkn2c	ENSMUSG00000028551	cyclin dependent kinase inhibitor 2C	2.091	0.0000	0.0000
Cdnf	ENSMUSG00000039496	cerebral dopamine neurotrophic factor	1.848	0.0000	0.0000
Cdr2	ENSMUSG00000030878	cerebellar degeneration-related 2	2.279	0.0000	0.0000
Cdr2l	ENSMUSG00000050910	cerebellar degeneration-related protein 2-like	2.006	0.0000	0.0000
Cds1	ENSMUSG00000029330	CDP-diacylglycerol synthase 1	1.760	0.0008	0.0025
Cdv3	ENSMUSG00000032803	carnitine deficiency-associated gene expressed in ventricle 3	2.896	0.0000	0.0000

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Cdyl	ENSMUSG00000059288	chromodomain protein, Y chromosome-like	1.797	0.0000	0.0000
Cebpa	ENSMUSG00000034957	CCAAT/enhancer binding protein (C/EBP), alpha	4.478	0.0000	0.0000
Cebpb	ENSMUSG00000056501	CCAAT/enhancer binding protein (C/EBP), beta	11.498	0.0000	0.0000
Cebpd	ENSMUSG00000071637	CCAAT/enhancer binding protein (C/EBP), delta	3.492	0.0213	0.0465
Cebpg	ENSMUSG00000056216	CCAAT/enhancer binding protein (C/EBP), gamma	1.759	0.0000	0.0000
Cebpz	ENSMUSG00000024081	CCAAT/enhancer binding protein zeta	1.602	0.0000	0.0000
Celf1	ENSMUSG00000005506	CUGBP, Elav-like family member 1	1.604	0.0000	0.0000
Cemip2	ENSMUSG00000024754	cell migration inducing hyaluronidase 2	1.685	0.0000	0.0000
Cenpb	ENSMUSG00000068267	centromere protein B	1.643	0.0000	0.0000
Cenpe	ENSMUSG00000045328	centromere protein E	2.205	0.0023	0.0066
Cenpf	ENSMUSG00000026605	centromere protein F	1.671	0.0060	0.0153
Cenph	ENSMUSG00000045273	centromere protein H	2.640	0.0443	0.0872
Cenps	ENSMUSG00000073705	centromere protein S	1.968	0.0046	0.0121
Cenpv	ENSMUSG00000018509	centromere protein V	2.600	0.0000	0.0000
Cep126	ENSMUSG00000040729	centrosomal protein 126	1.565	0.0015	0.0044
Cep170	ENSMUSG00000057335	centrosomal protein 170	1.522	0.0000	0.0000
Cep250	ENSMUSG00000038241	centrosomal protein 250	1.682	0.0000	0.0000
Cep290	ENSMUSG00000019971	centrosomal protein 290	1.542	0.0000	0.0001
Cep63	ENSMUSG00000032534	centrosomal protein 63	2.280	0.0000	0.0000
Cep83	ENSMUSG00000020024	centrosomal protein 83	2.278	0.0000	0.0000
Cep89	ENSMUSG00000023072	centrosomal protein 89	1.737	0.0000	0.0000
Cep97	ENSMUSG00000022604	centrosomal protein 97	2.136	0.0000	0.0000
Cers3	ENSMUSG00000030510	ceramide synthase 3	2.081	0.0462	0.0904
Cetn3	ENSMUSG00000021537	centrin 3	4.023	0.0000	0.0000
Cfap298	ENSMUSG00000022972	cilia and flagella associate protien 298	2.087	0.0000	0.0000
Cfap36	ENSMUSG00000020462	cilia and flagella associated protein 36	1.799	0.0000	0.0000
Cfdp1	ENSMUSG00000031954	craniofacial development protein 1	2.788	0.0000	0.0000
Cflar	ENSMUSG00000026031	CASP8 and FADD-like apoptosis regulator	1.746	0.0000	0.0000
Cgas	ENSMUSG00000032344	cyclic GMP-AMP synthase	1.730	0.0090	0.0219
Cgnl1	ENSMUSG00000032232	cingulin-like 1	1.503	0.0000	0.0000
Cgref1	ENSMUSG00000029161	cell growth regulator with EF hand domain 1	4.750	0.0000	0.0000
Chaf1a	ENSMUSG00000002835	chromatin assembly factor 1, subunit A (p150)	2.259	0.0000	0.0000

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Chaserr	ENSMUSG00000101970	CHD2 adjacent suppressive regulatory RNA	3.468	0.0000	0.0000
Chchd4	ENSMUSG00000034203	coiled-coil-helix-coiled-coil-helix domain containing 4	1.683	0.0000	0.0000
Chd1	ENSMUSG00000023852	chromodomain helicase DNA binding protein 1	1.879	0.0000	0.0000
Chd2	ENSMUSG00000078671	chromodomain helicase DNA binding protein 2	1.790	0.0000	0.0000
Chd4	ENSMUSG00000063870	chromodomain helicase DNA binding protein 4	1.812	0.0000	0.0000
Chgb	ENSMUSG00000027350	chromogranin B	2.261	0.0132	0.0307
Chic2	ENSMUSG00000029229	cysteine-rich hydrophobic domain 2	5.125	0.0000	0.0000
Chmp3	ENSMUSG00000053119	charged multivesicular body protein 3	1.994	0.0000	0.0000
Chmp4b	ENSMUSG00000038467	charged multivesicular body protein 4B	2.337	0.0000	0.0000
Chmp4c	ENSMUSG00000027536	charged multivesicular body protein 4C	1.749	0.0000	0.0000
Chmp5	ENSMUSG00000028419	charged multivesicular body protein 5	1.517	0.0000	0.0000
Chmp7	ENSMUSG00000034190	charged multivesicular body protein 7	2.262	0.0000	0.0000
Chrna2	ENSMUSG00000022041	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	2.468	0.0025	0.0071
Chst14	ENSMUSG00000074916	carbohydrate sulfotransferase 14	1.802	0.0000	0.0001
Chst2	ENSMUSG00000033350	carbohydrate sulfotransferase 2	3.099	0.0000	0.0000
Chsy1	ENSMUSG00000032640	chondroitin sulfate synthase 1	2.336	0.0000	0.0000
Chuk	ENSMUSG00000025199	conserved helix-loop-helix ubiquitous kinase	1.713	0.0000	0.0000
Cib2	ENSMUSG00000037493	calcium and integrin binding family member 2	3.185	0.0000	0.0000
Cideb	ENSMUSG00000022219	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	1.582	0.0279	0.0586
Cir1	ENSMUSG00000041777	corepressor interacting with RBPJ, 1	1.964	0.0004	0.0014
Cirbp	ENSMUSG00000045193	cold inducible RNA binding protein	1.774	0.0001	0.0004
Cited2	ENSMUSG00000039910	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1.902	0.0023	0.0064
Cited4	ENSMUSG00000070803	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	4.217	0.0001	0.0003
Ckap4	ENSMUSG00000046841	cytoskeleton-associated protein 4	2.019	0.0000	0.0000
Clasrp	ENSMUSG00000061028	CLK4-associating serine/arginine rich protein	1.539	0.0068	0.0171
Cldnd1	ENSMUSG00000022744	claudin domain containing 1	1.652	0.0000	0.0000
Clint1	ENSMUSG00000006169	clathrin interactor 1	1.778	0.0000	0.0000
Clk1	ENSMUSG00000026034	CDC-like kinase 1	1.744	0.0032	0.0087
Clptm1	ENSMUSG00000002981	cleft lip and palate associated transmembrane protein 1	1.881	0.0000	0.0002
Clpx	ENSMUSG00000015357	caseinolytic mitochondrial matrix peptidase chaperone subunit	1.659	0.0004	0.0013
Clspn	ENSMUSG00000042489	claspin	2.281	0.0117	0.0275
Cltb	ENSMUSG00000047547	clathrin, light polypeptide (Lcb)	2.478	0.0000	0.0000

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Cluap1	ENSMUSG00000014232	clusterin associated protein 1	2.049	0.0000	0.0000
Cmas	ENSMUSG00000030282	cytidine monophospho-N-acetylneuraminic acid synthetase	2.833	0.0000	0.0000
Cmpk1	ENSMUSG00000028719	cytidine monophosphate (UMP-CMP) kinase 1	2.144	0.0000	0.0000
Cmtm4	ENSMUSG00000096188	CKLF-like MARVEL transmembrane domain containing 4	1.666	0.0000	0.0000
Cmtm6	ENSMUSG00000032434	CKLF-like MARVEL transmembrane domain containing 6	1.602	0.0000	0.0000
Cnbd2	ENSMUSG00000038085	cyclic nucleotide binding domain containing 2	1.594	0.0166	0.0374
Cngb1	ENSMUSG00000031789	cyclic nucleotide gated channel beta 1	1.617	0.0069	0.0173
Cnih2	ENSMUSG00000024873	cornichon family AMPA receptor auxiliary protein 2	3.461	0.0504	0.0972
Cnnm2	ENSMUSG00000064105	cyclin M2	1.691	0.0002	0.0007
Cnot11	ENSMUSG00000003135	CCR4-NOT transcription complex, subunit 11	2.110	0.0000	0.0000
Cnot6l	ENSMUSG00000034724	CCR4-NOT transcription complex, subunit 6-like	1.580	0.0000	0.0000
Cnpy4	ENSMUSG00000036968	canopy FGF signaling regulator 4	1.814	0.0000	0.0000
Cntf	ENSMUSG00000079415	ciliary neurotrophic factor	8.064	0.0035	0.0095
Col13a1	ENSMUSG00000058806	collagen, type XIII, alpha 1	2.403	0.0025	0.0070
Col20a1	ENSMUSG00000016356	collagen, type XX, alpha 1	1.794	0.0014	0.0042
Col7a1	ENSMUSG00000025650	collagen, type VII, alpha 1	2.364	0.0432	0.0853
Commd1	ENSMUSG00000051355	COMM domain containing 1	1.725	0.0000	0.0000
Cop1	ENSMUSG00000040782	COP1, E3 ubiquitin ligase	1.813	0.0000	0.0000
Coprs	ENSMUSG00000031458	coordinator of PRMT5, differentiation stimulator	1.837	0.0000	0.0001
Copz2	ENSMUSG00000018672	coatomer protein complex, subunit zeta 2	3.014	0.0000	0.0000
Cox11	ENSMUSG00000020544	cytochrome c oxidase assembly protein 11, copper chaperone	3.073	0.0000	0.0000
Cox17	ENSMUSG00000046516	cytochrome c oxidase assembly protein 17, copper chaperone	2.264	0.0004	0.0012
Cox20	ENSMUSG00000026500	cytochrome c oxidase assembly protein 20	1.809	0.0000	0.0000
Cox7c	ENSMUSG00000017778	cytochrome c oxidase subunit 7C	2.732	0.0000	0.0000
Cpe	ENSMUSG00000037852	carboxypeptidase E	2.105	0.0000	0.0000
Cpeb2	ENSMUSG00000039782	cytoplasmic polyadenylation element binding protein 2	2.822	0.0000	0.0000
Cpeb4	ENSMUSG00000020300	cytoplasmic polyadenylation element binding protein 4	1.631	0.0000	0.0000
Cpne2	ENSMUSG00000034361	copine II	1.593	0.0125	0.0293
Cpox	ENSMUSG00000022742	coproporphyrinogen oxidase	2.986	0.0000	0.0000
Cracr2b	ENSMUSG00000048200	calcium release activated channel regulator 2B	1.563	0.0000	0.0000
Creb3	ENSMUSG00000028466	cAMP responsive element binding protein 3	2.724	0.0000	0.0000
Creb3l1	ENSMUSG00000027230	cAMP responsive element binding protein 3-like 1	1.848	0.0001	0.0003

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Crebzf	ENSMUSG00000051451	CREB/ATF bZIP transcription factor	3.044	0.0000	0.0000
Creld2	ENSMUSG00000023272	cysteine-rich with EGF-like domains 2	1.850	0.0000	0.0000
Crim1	ENSMUSG00000024074	cysteine rich transmembrane BMP regulator 1 (chordin like)	1.593	0.0000	0.0000
Crispld1	ENSMUSG00000025776	cysteine-rich secretory protein LCCL domain containing 1	1.935	0.0000	0.0000
Crk	ENSMUSG00000017776	v-crk avian sarcoma virus CT10 oncogene homolog	1.651	0.0000	0.0000
Crlf1	ENSMUSG00000007888	cytokine receptor-like factor 1	4.081	0.0032	0.0086
Crls1	ENSMUSG00000027357	cardiolipin synthase 1	1.962	0.0000	0.0000
Crnkl1	ENSMUSG00000001767	crooked neck pre-mRNA splicing factor 1	1.818	0.0000	0.0000
Csde1	ENSMUSG00000068823	cold shock domain containing E1, RNA binding	1.978	0.0000	0.0000
Csk	ENSMUSG00000032312	c-src tyrosine kinase	1.939	0.0000	0.0000
Csnk1g3	ENSMUSG00000073563	casein kinase 1, gamma 3	2.210	0.0000	0.0000
Csnk2a1	ENSMUSG00000074698	casein kinase 2, alpha 1 polypeptide	2.408	0.0000	0.0000
Cspp1	ENSMUSG00000056763	centrosome and spindle pole associated protein 1	1.797	0.0000	0.0000
Csrnp2	ENSMUSG00000044636	cysteine-serine-rich nuclear protein 2	1.637	0.0027	0.0075
Csrp2	ENSMUSG00000020186	cysteine and glycine-rich protein 2	2.325	0.0000	0.0000
Ctcf	ENSMUSG00000005698	CCCTC-binding factor	1.666	0.0000	0.0000
Ctdnep1	ENSMUSG00000018559	CTD nuclear envelope phosphatase 1	1.670	0.0001	0.0004
Ctdp1	ENSMUSG00000033323	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	1.916	0.0000	0.0000
Ctf1	ENSMUSG00000042340	cardiotrophin 1	1.548	0.0035	0.0095
Ctnnb1	ENSMUSG00000006932	catenin (cadherin associated protein), beta 1	1.549	0.0000	0.0000
Ctnnbl1	ENSMUSG00000027649	catenin, beta like 1	1.764	0.0000	0.0000
Ctnnd1	ENSMUSG00000034101	catenin (cadherin associated protein), delta 1	2.490	0.0000	0.0000
Cul4a	ENSMUSG00000031446	cullin 4A	2.249	0.0000	0.0000
Cul5	ENSMUSG00000032030	cullin 5	1.690	0.0000	0.0000
Cutal	ENSMUSG00000026870	cutA divalent cation tolerance homolog-like	2.334	0.0000	0.0002
Cutc	ENSMUSG00000025193	cutC copper transporter	2.321	0.0000	0.0000
Cwc15	ENSMUSG00000004096	CWC15 spliceosome-associated protein	2.050	0.0000	0.0000
Cwc27	ENSMUSG00000021715	CWC27 spliceosome-associated protein	3.630	0.0000	0.0000
Cwf19l2	ENSMUSG00000025898	CWF19-like 2, cell cycle control (S. pombe)	1.792	0.0000	0.0000
Cyb5d1	ENSMUSG00000044795	cytochrome b5 domain containing 1	2.085	0.0000	0.0000
Cyb5r4	ENSMUSG00000032872	cytochrome b5 reductase 4	2.446	0.0000	0.0000
Cyp51	ENSMUSG00000001467	cytochrome P450, family 51	1.662	0.0000	0.0000

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Cyrib	ENSMUSG00000022378	CYFIP related Rac1 interactor B	2.152	0.0000	0.0000
Cys1	ENSMUSG00000062563	cystin 1	3.275	0.0000	0.0000
Cyth2	ENSMUSG00000003269	cytohesin 2	1.963	0.0001	0.0005
D030034A15Rik	ENSMUSG00000111055	RIKEN cDNA D030034A15 gene	1.751	0.0226	0.0489
D030056L22Rik	ENSMUSG00000047044	RIKEN cDNA D030056L22 gene	2.139	0.0000	0.0000
D030062O11Rik	ENSMUSG00000103710	RIKEN cDNA D030062O11 gene	3.483	0.0144	0.0329
D330050I16Rik	ENSMUSG00000117959	RIKEN cDNA D330050I16 gene	7.677	0.0000	0.0000
D630033A02Rik	ENSMUSG00000112237	RIKEN cDNA D630033A02 gene	5.503	0.0000	0.0000
D7Bwg0826e	ENSMUSG00000109198	DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed	6.122	0.0226	0.0488
D830013O20Rik	ENSMUSG00000056359	RIKEN cDNA D830013O20 gene	1.665	0.0000	0.0001
D830036C21Rik	ENSMUSG00000108854	RIKEN cDNA D830036C21 gene	4.104	0.0010	0.0030
D830050J10Rik	ENSMUSG00000107994	RIKEN cDNA D830050J10 gene	4.504	0.0000	0.0000
D8Ertd738e	ENSMUSG00000019362	DNA segment, Chr 8, ERATO Doi 738, expressed	1.746	0.0000	0.0000
D930007J09Rik	ENSMUSG00000042874	RIKEN cDNA D930007J09 gene	2.837	0.0040	0.0106
Dact1	ENSMUSG00000044548	dishevelled-binding antagonist of beta-catenin 1	1.773	0.0008	0.0026
Dact3	ENSMUSG00000078794	dishevelled-binding antagonist of beta-catenin 3	7.079	0.0000	0.0000
Dazap1	ENSMUSG00000069565	DAZ associated protein 1	2.470	0.0000	0.0000
Dbf4	ENSMUSG00000002297	DBF4 zinc finger	1.907	0.0012	0.0037
Dbn1	ENSMUSG00000034675	drebrin 1	1.566	0.0043	0.0113
Dbndd2	ENSMUSG00000017734	dysbindin (dystrobrevin binding protein 1) domain containing 2	2.239	0.0000	0.0000
Dbp	ENSMUSG00000059824	D site albumin promoter binding protein	3.059	0.0023	0.0064
Dcaf13	ENSMUSG00000022300	DDB1 and CUL4 associated factor 13	1.761	0.0000	0.0000
Dctn5	ENSMUSG00000030868	dynactin 5	1.803	0.0000	0.0000
Dcun1d1	ENSMUSG00000027708	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	2.014	0.0000	0.0000
Dcun1d5	ENSMUSG00000032002	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	4.345	0.0000	0.0000
Ddi2	ENSMUSG00000078515	DNA-damage inducible protein 2	1.717	0.0000	0.0000
Ddrgk1	ENSMUSG00000068290	DDRGK domain containing 1	1.853	0.0000	0.0000
Ddx10	ENSMUSG00000053289	DEAD box helicase 10	2.554	0.0000	0.0000
Ddx19b	ENSMUSG00000033658	DEAD box helicase 19b	1.744	0.0000	0.0000
Ddx21	ENSMUSG00000020075	DExD box helicase 21	1.601	0.0000	0.0000
Ddx23	ENSMUSG00000003360	DEAD box helicase 23	1.568	0.0000	0.0000
Ddx27	ENSMUSG00000017999	DEAD box helicase 27	2.138	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ddx3x	ENSMUSG00000000787	DEAD box helicase 3, X-linked	2.538	0.0000	0.0000
Ddx3y	ENSMUSG00000069045	DEAD box helicase 3, Y-linked	1.885	0.0000	0.0000
Ddx42	ENSMUSG00000020705	DEAD box helicase 42	1.687	0.0000	0.0000
Ddx46	ENSMUSG00000021500	DEAD box helicase 46	2.173	0.0000	0.0000
Ddx55	ENSMUSG00000029389	DEAD box helicase 55	1.876	0.0000	0.0000
Deaf1	ENSMUSG00000058886	DEAF1, transcription factor	1.666	0.0021	0.0060
Decr1	ENSMUSG00000028223	2,4-dienoyl CoA reductase 1, mitochondrial	2.116	0.0000	0.0000
Dek	ENSMUSG00000021377	DEK proto-oncogene (DNA binding)	2.481	0.0000	0.0000
Dennd6a	ENSMUSG00000040818	DENN/MADD domain containing 6A	1.556	0.0000	0.0000
Denr	ENSMUSG00000023106	density-regulated protein	2.483	0.0000	0.0000
Depdc1b	ENSMUSG00000021697	DEP domain containing 1B	2.438	0.0061	0.0154
Desi1	ENSMUSG00000022472	desumoylating isopeptidase 1	1.710	0.0027	0.0074
Desi2	ENSMUSG00000026502	desumoylating isopeptidase 2	1.660	0.0000	0.0000
Dexi	ENSMUSG00000038055	dexamethasone-induced transcript	3.297	0.0000	0.0000
Dgcr8	ENSMUSG00000022718	DGCR8, microprocessor complex subunit	1.549	0.0000	0.0000
Dhdh	ENSMUSG00000011382	dihydrodiol dehydrogenase (dimeric)	2.213	0.0000	0.0000
Dhh	ENSMUSG00000023000	desert hedgehog	2.007	0.0343	0.0700
Dhrs4	ENSMUSG00000022210	dehydrogenase/reductase (SDR family) member 4	2.550	0.0000	0.0000
Dhrs7	ENSMUSG00000021094	dehydrogenase/reductase (SDR family) member 7	1.917	0.0000	0.0000
Diaph1	ENSMUSG00000024456	diaphanous related formin 1	1.661	0.0000	0.0000
Dld	ENSMUSG00000020664	dihydrolipoamide dehydrogenase	1.613	0.0000	0.0000
Dleu2	ENSMUSG00000097589	deleted in lymphocytic leukemia, 2	1.812	0.0002	0.0008
Dmrt2	ENSMUSG00000048138	doublesex and mab-3 related transcription factor 2	9.422	0.0402	0.0803
Dmrta2	ENSMUSG00000047143	doublesex and mab-3 related transcription factor like family A2	6.913	0.0001	0.0004
Dnaja1	ENSMUSG00000028410	DnaJ heat shock protein family (Hsp40) member A1	1.547	0.0000	0.0000
Dnaja2	ENSMUSG00000031701	DnaJ heat shock protein family (Hsp40) member A2	1.624	0.0000	0.0000
Dnaja4	ENSMUSG00000032285	DnaJ heat shock protein family (Hsp40) member A4	2.584	0.0000	0.0000
Dnajb11	ENSMUSG00000004460	DnaJ heat shock protein family (Hsp40) member B11	3.931	0.0000	0.0000
Dnajb2	ENSMUSG00000026203	DnaJ heat shock protein family (Hsp40) member B2	2.028	0.0000	0.0000
Dnajb6	ENSMUSG00000029131	DnaJ heat shock protein family (Hsp40) member B6	2.145	0.0000	0.0000
Dnajb6-ps	ENSMUSG00000091905	DnaJ heat shock protein family (Hsp40) member B6, pseudogene	11.852	0.0000	0.0000
Dnajb9	ENSMUSG00000014905	DnaJ heat shock protein family (Hsp40) member B9	1.842	0.0001	0.0003

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dnajc11	ENSMUSG00000039768	DnaJ heat shock protein family (Hsp40) member C11	1.838	0.0000	0.0000
Dnajc12	ENSMUSG00000036764	DnaJ heat shock protein family (Hsp40) member C12	1.654	0.0001	0.0002
Dnajc14	ENSMUSG00000025354	DnaJ heat shock protein family (Hsp40) member C14	1.767	0.0000	0.0000
Dnajc2	ENSMUSG00000029014	DnaJ heat shock protein family (Hsp40) member C2	2.378	0.0000	0.0000
Dnajc21	ENSMUSG00000044224	DnaJ heat shock protein family (Hsp40) member C21	4.289	0.0000	0.0000
Dnajc25	ENSMUSG00000070972	DnaJ heat shock protein family (Hsp40) member C25	2.380	0.0000	0.0000
Dnajc3	ENSMUSG00000022136	DnaJ heat shock protein family (Hsp40) member C3	1.661	0.0000	0.0001
Dnajc8	ENSMUSG00000054405	DnaJ heat shock protein family (Hsp40) member C8	3.239	0.0000	0.0000
Dnlz	ENSMUSG00000075467	DNL-type zinc finger	2.955	0.0000	0.0000
Dnm1	ENSMUSG00000026825	dynamin 1	1.760	0.0004	0.0015
Dnttip1	ENSMUSG00000017299	deoxynucleotidyltransferase, terminal, interacting protein 1	2.732	0.0000	0.0000
Dnttip2	ENSMUSG00000039756	deoxynucleotidyltransferase, terminal, interacting protein 2	1.539	0.0156	0.0353
Dok5	ENSMUSG00000027560	docking protein 5	2.177	0.0003	0.0009
Donson	ENSMUSG00000022960	downstream neighbor of SON	1.826	0.0006	0.0019
Dpcd	ENSMUSG00000041035	deleted in primary ciliary dyskinesia	2.474	0.0000	0.0000
Dpf1	ENSMUSG00000030584	double PHD fingers 1	3.665	0.0239	0.0513
Dpy30	ENSMUSG00000024067	dpy-30, histone methyltransferase complex regulatory subunit	1.585	0.0000	0.0000
Dpysl2	ENSMUSG00000022048	dihydropyrimidinase-like 2	1.547	0.0000	0.0000
Dpysl3	ENSMUSG00000024501	dihydropyrimidinase-like 3	1.585	0.0187	0.0414
Drap1	ENSMUSG00000024914	Dr1 associated protein 1 (negative cofactor 2 alpha)	3.913	0.0000	0.0000
Dtwd2	ENSMUSG00000024505	DTW domain containing 2	2.372	0.0000	0.0000
Dusp26	ENSMUSG00000039661	dual specificity phosphatase 26 (putative)	2.837	0.0000	0.0000
Dusp27	ENSMUSG00000026564	dual specificity phosphatase 27 (putative)	2.489	0.0000	0.0000
Dusp6	ENSMUSG00000019960	dual specificity phosphatase 6	1.746	0.0000	0.0001
Dusp7	ENSMUSG00000053716	dual specificity phosphatase 7	1.550	0.0000	0.0000
Dusp8	ENSMUSG00000037887	dual specificity phosphatase 8	1.951	0.0003	0.0012
Dut	ENSMUSG00000027203	deoxyuridine triphosphatase	1.738	0.0000	0.0001
Dync1li2	ENSMUSG00000035770	dynein, cytoplasmic 1 light intermediate chain 2	2.319	0.0000	0.0000
Dync2i1	ENSMUSG00000042050	dynein 2 intermediate chain 1	1.606	0.0008	0.0024
Dynll2	ENSMUSG00000020483	dynein light chain LC8-type 2	2.265	0.0000	0.0000
Dynlt2b	ENSMUSG00000014075	dynein light chain Tctex-type 2B	2.303	0.0000	0.0000
Dynlt3	ENSMUSG00000031176	dynein light chain Tctex-type 3	2.401	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dyrk1a	ENSMUSG00000022897	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	1.519	0.0000	0.0001
Dyrk1b	ENSMUSG00000002409	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b	1.516	0.0069	0.0173
E130102H24Rik	ENSMUSG00000086782	RIKEN cDNA E130102H24 gene	1.947	0.0122	0.0285
E130201H02Rik	ENSMUSG00000044141	RIKEN cDNA E130201H02 gene	9.858	0.0009	0.0027
E130208F15Rik	ENSMUSG00000074210	RIKEN cDNA E130208F15 gene	5.658	0.0000	0.0000
E2f1	ENSMUSG00000027490	E2F transcription factor 1	1.904	0.0062	0.0158
E2f3	ENSMUSG00000016477	E2F transcription factor 3	1.716	0.0000	0.0000
E2f4	ENSMUSG00000014859	E2F transcription factor 4	1.655	0.0000	0.0000
E2f5	ENSMUSG00000027552	E2F transcription factor 5	1.599	0.0011	0.0034
E330034L11Rik	ENSMUSG00000106383	RIKEN cDNA E330034L11 gene	1.771	0.0044	0.0116
Ebag9	ENSMUSG00000022339	estrogen receptor-binding fragment-associated gene 9	3.561	0.0000	0.0000
Echdc1	ENSMUSG00000019883	enoyl Coenzyme A hydratase domain containing 1	1.958	0.0000	0.0000
Edem3	ENSMUSG00000043019	ER degradation enhancer, mannosidase alpha-like 3	2.060	0.0000	0.0000
Edn1	ENSMUSG00000021367	endothelin 1	1.571	0.0030	0.0083
Eea1	ENSMUSG00000036499	early endosome antigen 1	1.810	0.0000	0.0000
Eed	ENSMUSG00000030619	embryonic ectoderm development	1.788	0.0000	0.0000
Eef1akmt2	ENSMUSG00000030960	EEF1A lysine methyltransferase 2	1.520	0.0013	0.0039
Eef1b2	ENSMUSG00000025967	eukaryotic translation elongation factor 1 beta 2	1.580	0.0000	0.0000
Eef2-ps2	ENSMUSG00000082575	eukaryotic translation elongation factor 2, pseudogene 2	1.579	0.0328	0.0675
Efcab2	ENSMUSG00000026495	EF-hand calcium binding domain 2	2.246	0.0000	0.0000
Efhd1	ENSMUSG00000026255	EF hand domain containing 1	1.898	0.0000	0.0002
Efnb1	ENSMUSG00000031217	ephrin B1	1.699	0.0002	0.0006
Efnb2	ENSMUSG00000001300	ephrin B2	1.937	0.0000	0.0000
Egln2	ENSMUSG00000058709	egl-9 family hypoxia-inducible factor 2	1.932	0.0001	0.0002
Egr1	ENSMUSG00000038418	early growth response 1	2.301	0.0113	0.0267
Ehbp1	ENSMUSG00000042302	EH domain binding protein 1	2.036	0.0000	0.0000
Ehbp1l1	ENSMUSG00000024937	EH domain binding protein 1-like 1	1.527	0.0000	0.0000
Ei24	ENSMUSG00000062762	etoposide induced 2.4 mRNA	2.136	0.0000	0.0000
Eid1	ENSMUSG00000091337	EP300 interacting inhibitor of differentiation 1	3.089	0.0000	0.0000
Eid2	ENSMUSG00000046058	EP300 interacting inhibitor of differentiation 2	4.388	0.0000	0.0000
Eid2b	ENSMUSG00000070705	EP300 interacting inhibitor of differentiation 2B	2.576	0.0000	0.0000
Eif1a	ENSMUSG00000057561	eukaryotic translation initiation factor 1A	1.698	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Eif1ad	ENSMUSG00000024841	eukaryotic translation initiation factor 1A domain containing	2.143	0.0000	0.0000
Eif2s2	ENSMUSG00000074656	eukaryotic translation initiation factor 2, subunit 2 (beta)	1.560	0.0000	0.0000
Eif2s3x	ENSMUSG00000035150	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	1.700	0.0000	0.0000
Eif3a	ENSMUSG00000024991	eukaryotic translation initiation factor 3, subunit A	3.646	0.0000	0.0000
Eif3b	ENSMUSG00000056076	eukaryotic translation initiation factor 3, subunit B	2.767	0.0000	0.0000
Eif3f	ENSMUSG00000031029	eukaryotic translation initiation factor 3, subunit F	2.203	0.0001	0.0003
Eif3j1	ENSMUSG00000027236	eukaryotic translation initiation factor 3, subunit J1	4.837	0.0000	0.0000
Eif3j2	ENSMUSG00000043424	eukaryotic translation initiation factor 3, subunit J2	2.839	0.0000	0.0000
Eif3s6-ps1	ENSMUSG00000081629	eukaryotic translation initiation factor 3, subunit 6, pseudogene 1	2.428	0.0439	0.0866
Eif4a2	ENSMUSG00000022884	eukaryotic translation initiation factor 4A2	1.788	0.0000	0.0000
Eif4e2	ENSMUSG00000026254	eukaryotic translation initiation factor 4E member 2	2.015	0.0000	0.0000
Eif4g1	ENSMUSG00000045983	eukaryotic translation initiation factor 4, gamma 1	1.914	0.0000	0.0000
Eif5b	ENSMUSG00000026083	eukaryotic translation initiation factor 5B	2.772	0.0000	0.0000
Elac1	ENSMUSG00000036941	elaC ribonuclease Z 1	1.667	0.0000	0.0000
Ell2	ENSMUSG00000001542	elongation factor for RNA polymerase II 2	2.223	0.0000	0.0000
Eln	ENSMUSG00000029675	elastin	2.468	0.0000	0.0000
Eloc	ENSMUSG00000079658	elongin C	2.140	0.0000	0.0000
Emc10	ENSMUSG00000008140	ER membrane protein complex subunit 10	2.270	0.0000	0.0000
Enah	ENSMUSG00000022995	ENAH actin regulator	1.742	0.0000	0.0000
Endog	ENSMUSG00000015337	endonuclease G	2.557	0.0000	0.0001
Engase	ENSMUSG00000033857	endo-beta-N-acetylglucosaminidase	2.510	0.0000	0.0000
Enho	ENSMUSG00000028445	energy homeostasis associated	2.408	0.0000	0.0000
Enkur	ENSMUSG00000026679	enkurin, TRPC channel interacting protein	1.526	0.0151	0.0344
Entr1	ENSMUSG00000026927	endosome associated trafficking regulator 1	1.522	0.0000	0.0000
Eny2	ENSMUSG00000022338	ENY2 transcription and export complex 2 subunit	1.795	0.0000	0.0000
Epb41l2	ENSMUSG00000019978	erythrocyte membrane protein band 4.1 like 2	1.503	0.0000	0.0000
Epha7	ENSMUSG00000028289	Eph receptor A7	1.853	0.0000	0.0000
Epha8	ENSMUSG00000028661	Eph receptor A8	4.322	0.0351	0.0715
Epop	ENSMUSG00000043439	elongin BC and polycomb repressive complex 2 associated protein	2.764	0.0224	0.0486
Erh	ENSMUSG00000021131	ERH mRNA splicing and mitosis factor	4.003	0.0000	0.0000
Eri3	ENSMUSG00000033423	exoribonuclease 3	2.104	0.0000	0.0001
Erich3	ENSMUSG00000078161	glutamate rich 3	1.788	0.0317	0.0656

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Erlec1	ENSMUSG00000020311	endoplasmic reticulum lectin 1	1.831	0.0000	0.0000
Esf1	ENSMUSG00000045624	ESF1 nucleolar pre-rRNA processing protein homolog	2.031	0.0000	0.0000
Esm1	ENSMUSG00000042379	endothelial cell-specific molecule 1	2.685	0.0000	0.0002
Espn	ENSMUSG00000028943	espin	2.006	0.0000	0.0001
Esrra	ENSMUSG00000024955	estrogen related receptor, alpha	1.893	0.0000	0.0000
Etf1	ENSMUSG00000024360	eukaryotic translation termination factor 1	1.631	0.0000	0.0000
Etfa	ENSMUSG00000032314	electron transferring flavoprotein, alpha polypeptide	1.502	0.0000	0.0000
Etfb	ENSMUSG00000004610	electron transferring flavoprotein, beta polypeptide	1.810	0.0000	0.0000
Etfdh	ENSMUSG00000027809	electron transferring flavoprotein, dehydrogenase	1.639	0.0000	0.0000
Etnk1	ENSMUSG00000030275	ethanolamine kinase 1	1.580	0.0000	0.0000
Eva1b	ENSMUSG00000050212	eva-1 homolog B (C. elegans)	2.660	0.0000	0.0001
Evl	ENSMUSG00000021262	Ena-vasodilator stimulated phosphoprotein	2.321	0.0000	0.0000
Ewsr1	ENSMUSG00000009079	Ewing sarcoma breakpoint region 1	2.459	0.0000	0.0000
Exo5	ENSMUSG00000028629	exonuclease 5	1.742	0.0000	0.0000
Exoc8	ENSMUSG00000074030	exocyst complex component 8	1.691	0.0000	0.0000
Exosc2	ENSMUSG00000039356	exosome component 2	2.122	0.0000	0.0000
Exosc3	ENSMUSG00000028322	exosome component 3	2.480	0.0000	0.0000
Exosc7	ENSMUSG00000025785	exosome component 7	2.058	0.0000	0.0000
Exosc9	ENSMUSG00000027714	exosome component 9	2.259	0.0000	0.0000
Ezh2	ENSMUSG00000029687	enhancer of zeste 2 polycomb repressive complex 2 subunit	2.326	0.0000	0.0000
F830016B08Rik	ENSMUSG00000090942	RIKEN cDNA F830016B08 gene	4.547	0.0000	0.0000
Fabp4	ENSMUSG00000062515	fatty acid binding protein 4, adipocyte	2.411	0.0000	0.0000
Fabp5	ENSMUSG00000027533	fatty acid binding protein 5, epidermal	2.223	0.0000	0.0000
Fabp7	ENSMUSG00000019874	fatty acid binding protein 7, brain	2.240	0.0010	0.0031
Fahd1	ENSMUSG00000045316	fumarylacetoacetate hydrolase domain containing 1	2.353	0.0000	0.0000
Faim	ENSMUSG00000032463	Fas apoptotic inhibitory molecule	2.939	0.0000	0.0000
Fam104a	ENSMUSG00000041629	family with sequence similarity 104, member A	2.482	0.0000	0.0000
Fam110d	ENSMUSG00000050105	family with sequence similarity 110, member D	1.864	0.0052	0.0134
Fam122a	ENSMUSG00000074922	family with sequence similarity 122, member A	4.496	0.0000	0.0000
Fam133b	ENSMUSG00000058503	family with sequence similarity 133, member B	2.065	0.0000	0.0000
Fam149a	ENSMUSG00000070044	family with sequence similarity 149, member A	1.786	0.0004	0.0014
Fam149b	ENSMUSG00000039599	family with sequence similarity 149, member B	2.111	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fam161a	ENSMUSG00000049811	family with sequence similarity 161, member A	1.698	0.0026	0.0071
Fam171a2	ENSMUSG00000034685	family with sequence similarity 171, member A2	4.995	0.0000	0.0000
Fam174a	ENSMUSG00000051185	family with sequence similarity 174, member A	2.361	0.0000	0.0000
Fam181b	ENSMUSG00000051515	family with sequence similarity 181, member B	1.529	0.0439	0.0866
Fam193a	ENSMUSG00000037210	family with sequence homology 193, member A	1.529	0.0000	0.0000
Fam199x	ENSMUSG00000042595	family with sequence similarity 199, X-linked	1.502	0.0000	0.0001
Fam204a	ENSMUSG00000057858	family with sequence similarity 204, member A	2.856	0.0000	0.0000
Fam216a	ENSMUSG00000029463	family with sequence similarity 216, member A	2.563	0.0000	0.0002
Fam219a	ENSMUSG00000028439	family with sequence similarity 219, member A	1.671	0.0000	0.0000
Fam219b	ENSMUSG00000032305	family with sequence similarity 219, member B	2.015	0.0001	0.0002
Fam241a	ENSMUSG00000050549	family with sequence similarity 241, member A	5.066	0.0000	0.0000
Fam3c	ENSMUSG00000029672	FAM3 metabolism regulating signaling molecule C	3.623	0.0000	0.0000
Fam50a	ENSMUSG00000001962	family with sequence similarity 50, member A	2.655	0.0000	0.0000
Fam53c	ENSMUSG00000034300	family with sequence similarity 53, member C	2.074	0.0000	0.0000
Fam76b	ENSMUSG00000037808	family with sequence similarity 76, member B	1.824	0.0000	0.0000
Fam78b	ENSMUSG00000060568	family with sequence similarity 78, member B	1.501	0.0019	0.0055
Fam89a	ENSMUSG00000043068	family with sequence similarity 89, member A	2.718	0.0000	0.0001
Fam8a1	ENSMUSG00000069237	family with sequence similarity 8, member A1	2.555	0.0000	0.0000
Fancf	ENSMUSG00000092118	Fanconi anemia, complementation group F	1.700	0.0149	0.0340
Faxc	ENSMUSG00000028246	failed axon connections homolog	2.120	0.0024	0.0067
Fbl	ENSMUSG00000046865	fibrillarin	2.559	0.0000	0.0000
Fbrs	ENSMUSG00000042423	fibrosin	1.899	0.0000	0.0002
Fbxl14	ENSMUSG00000030019	F-box and leucine-rich repeat protein 14	3.239	0.0000	0.0000
Fbxl17	ENSMUSG00000023965	F-box and leucine-rich repeat protein 17	1.588	0.0015	0.0044
Fbxl19	ENSMUSG00000030811	F-box and leucine-rich repeat protein 19	2.173	0.0000	0.0002
Fbxl3	ENSMUSG00000022124	F-box and leucine-rich repeat protein 3	1.942	0.0000	0.0000
Fbxo28	ENSMUSG00000047539	F-box protein 28	1.576	0.0000	0.0000
Fbxo30	ENSMUSG00000047648	F-box protein 30	1.822	0.0001	0.0003
Fbxo4	ENSMUSG00000022184	F-box protein 4	1.836	0.0000	0.0001
Fbxo45	ENSMUSG00000035764	F-box protein 45	2.090	0.0000	0.0000
Fbxw11	ENSMUSG00000020271	F-box and WD-40 domain protein 11	1.730	0.0000	0.0000
Fbxw4	ENSMUSG00000040913	F-box and WD-40 domain protein 4	1.714	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fbxw7	ENSMUSG00000028086	F-box and WD-40 domain protein 7	1.714	0.0000	0.0000
Fdx2	ENSMUSG00000079677	ferredoxin 2	17.450	0.0488	0.0946
Fgf16	ENSMUSG00000031230	fibroblast growth factor 16	2.684	0.0000	0.0000
Fgf20	ENSMUSG00000031603	fibroblast growth factor 20	8.023	0.0000	0.0000
Fgf9	ENSMUSG00000021974	fibroblast growth factor 9	1.915	0.0000	0.0000
Fgfbp3	ENSMUSG00000047632	fibroblast growth factor binding protein 3	3.120	0.0000	0.0000
Fhad1	ENSMUSG00000051435	forkhead-associated (FHA) phosphopeptide binding domain 1	3.545	0.0113	0.0267
Fhip2b	ENSMUSG00000022095	FHF complex subunit HOOK interacting protein 2B	2.420	0.0000	0.0000
Fignl1	ENSMUSG00000035455	fidgetin-like 1	2.080	0.0123	0.0288
Fignl2	ENSMUSG00000095440	fidgetin-like 2	2.131	0.0002	0.0006
Filip1	ENSMUSG00000034898	filamin A interacting protein 1	1.825	0.0000	0.0000
Fip1l1	ENSMUSG00000029227	FIP1 like 1 (S. cerevisiae)	1.797	0.0000	0.0000
Firre	ENSMUSG00000085396	functional intergenic repeating RNA element	1.799	0.0125	0.0291
Fjx1	ENSMUSG00000075012	four jointed box 1	3.491	0.0049	0.0127
Fkbp1a	ENSMUSG00000032966	FK506 binding protein 1a	2.007	0.0000	0.0000
Fkbp1b	ENSMUSG00000020635	FK506 binding protein 1b	2.444	0.0060	0.0154
Fkbp2	ENSMUSG00000056629	FK506 binding protein 2	4.010	0.0000	0.0000
Fkbp8	ENSMUSG00000019428	FK506 binding protein 8	1.530	0.0000	0.0000
Fkbp9	ENSMUSG00000029781	FK506 binding protein 9	1.843	0.0000	0.0000
Fkbpl	ENSMUSG00000033739	FK506 binding protein-like	2.276	0.0000	0.0000
Flvcr1	ENSMUSG00000066595	feline leukemia virus subgroup C cellular receptor 1	1.663	0.0000	0.0000
Fmnl2	ENSMUSG00000036053	formin-like 2	1.677	0.0000	0.0000
Fmr1	ENSMUSG00000000838	fragile X messenger ribonucleoprotein 1	1.517	0.0000	0.0001
Fn3krp	ENSMUSG00000039253	fructosamine 3 kinase related protein	1.556	0.0001	0.0002
Fnbp1l	ENSMUSG00000039735	formin binding protein 1-like	1.985	0.0000	0.0000
Fndc4	ENSMUSG00000038552	fibronectin type III domain containing 4	2.410	0.0000	0.0000
Fnta	ENSMUSG00000015994	farnesyltransferase, CAAX box, alpha	2.346	0.0000	0.0000
Fosl2	ENSMUSG00000029135	fos-like antigen 2	1.542	0.0414	0.0824
Foxc1	ENSMUSG00000050295	forkhead box C1	3.647	0.0000	0.0000
Foxd1	ENSMUSG00000078302	forkhead box D1	8.112	0.0135	0.0311
Foxd2	ENSMUSG00000055210	forkhead box D2	4.276	0.0000	0.0000
Foxd3	ENSMUSG00000067261	forkhead box D3	5.484	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Foxf1	ENSMUSG00000042812	forkhead box F1	3.655	0.0002	0.0008
Foxj3	ENSMUSG00000032998	forkhead box J3	1.745	0.0001	0.0002
Foxk2	ENSMUSG00000039275	forkhead box K2	1.639	0.0000	0.0000
Foxn3	ENSMUSG00000033713	forkhead box N3	1.509	0.0003	0.0011
Foxo4	ENSMUSG00000042903	forkhead box O4	1.653	0.0000	0.0000
Foxo6	ENSMUSG00000052135	forkhead box O6	5.344	0.0000	0.0000
Foxp1	ENSMUSG00000030067	forkhead box P1	1.523	0.0000	0.0001
Foxp4	ENSMUSG00000023991	forkhead box P4	2.831	0.0000	0.0000
Foxq1	ENSMUSG00000038415	forkhead box Q1	3.873	0.0194	0.0429
Fra10ac1	ENSMUSG00000054237	FRA10AC1 homolog (human)	3.077	0.0000	0.0000
Frat1	ENSMUSG00000067199	frequently rearranged in advanced T cell lymphomas	2.698	0.0000	0.0000
Frat2	ENSMUSG00000047604	frequently rearranged in advanced T cell lymphomas 2	6.004	0.0000	0.0000
Frg1	ENSMUSG00000031590	FSHD region gene 1	1.812	0.0000	0.0000
Fst	ENSMUSG00000021765	follistatin	1.749	0.0175	0.0391
Fth1-ps	ENSMUSG00000084289	ferritin heavy polypeptide 1, pseudogene	3.424	0.0033	0.0091
Ftsj3	ENSMUSG00000020706	FtsJ RNA methyltransferase homolog 3 (E. coli)	2.051	0.0000	0.0000
Fubp1	ENSMUSG00000028034	far upstream element (FUSE) binding protein 1	2.407	0.0000	0.0000
Fubp3	ENSMUSG00000026843	far upstream element (FUSE) binding protein 3	2.522	0.0000	0.0000
Fv1	ENSMUSG00000070583	Friend virus susceptibility 1	2.909	0.0000	0.0000
Fxr1	ENSMUSG00000027680	FMR1 autosomal homolog 1	1.539	0.0000	0.0000
Fxr2	ENSMUSG00000018765	FMR1 autosomal homolog 2	1.848	0.0000	0.0000
Fyb	ENSMUSG00000022148	FYN binding protein	1.557	0.0155	0.0351
Fyn	ENSMUSG00000019843	Fyn proto-oncogene	3.192	0.0000	0.0000
Fzd1	ENSMUSG00000044674	frizzled class receptor 1	2.615	0.0000	0.0000
Fzd2	ENSMUSG00000050288	frizzled class receptor 2	1.980	0.0001	0.0004
Fzd5	ENSMUSG00000045005	frizzled class receptor 5	1.595	0.0000	0.0000
Fzd6	ENSMUSG00000022297	frizzled class receptor 6	2.000	0.0000	0.0000
Fzd7	ENSMUSG00000041075	frizzled class receptor 7	1.864	0.0000	0.0000
Fzd8	ENSMUSG00000036904	frizzled class receptor 8	1.692	0.0009	0.0029
Gadd45a	ENSMUSG00000036390	growth arrest and DNA-damage-inducible 45 alpha	2.166	0.0000	0.0000
Galnt1	ENSMUSG00000000420	polypeptide N-acetylgalactosaminyltransferase 1	1.980	0.0000	0.0000
Galnt2	ENSMUSG00000089704	polypeptide N-acetylgalactosaminyltransferase 2	108.290	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gar1	ENSMUSG00000028010	GAR1 ribonucleoprotein	2.015	0.0000	0.0000
Gas1	ENSMUSG00000052957	growth arrest specific 1	2.798	0.0000	0.0000
Gas2l1	ENSMUSG00000034201	growth arrest-specific 2 like 1	2.109	0.0002	0.0007
Gas5	ENSMUSG00000053332	growth arrest specific 5	3.296	0.0000	0.0000
Gas8	ENSMUSG00000040220	growth arrest specific 8	2.196	0.0000	0.0000
Gata6	ENSMUSG00000005836	GATA binding protein 6	1.886	0.0000	0.0000
Gatad1	ENSMUSG00000007415	GATA zinc finger domain containing 1	2.069	0.0000	0.0000
Gatad2b	ENSMUSG00000042390	GATA zinc finger domain containing 2B	1.594	0.0004	0.0013
Gbp3	ENSMUSG00000028268	guanylate binding protein 3	1.793	0.0061	0.0154
Gcfc2	ENSMUSG00000035125	GC-rich sequence DNA binding factor 2	1.879	0.0004	0.0013
Gch1	ENSMUSG00000037580	GTP cyclohydrolase 1	2.191	0.0000	0.0000
Gclc	ENSMUSG00000032350	glutamate-cysteine ligase, catalytic subunit	1.784	0.0003	0.0009
Gcsh	ENSMUSG00000034424	glycine cleavage system protein H (aminomethyl carrier)	1.779	0.0000	0.0000
Gdf11	ENSMUSG00000025352	growth differentiation factor 11	1.599	0.0056	0.0143
Gdf6	ENSMUSG00000051279	growth differentiation factor 6	2.246	0.0009	0.0027
Gemin2	ENSMUSG00000060121	gem nuclear organelle associated protein 2	1.716	0.0000	0.0000
Gemin6	ENSMUSG00000055760	gem nuclear organelle associated protein 6	1.536	0.0004	0.0015
Get4	ENSMUSG00000025858	golgi to ER traffic protein 4	1.664	0.0038	0.0100
Gfra2	ENSMUSG00000022103	glial cell line derived neurotrophic factor family receptor alpha 2	1.550	0.0158	0.0358
Ggct	ENSMUSG00000002797	gamma-glutamyl cyclotransferase	2.098	0.0000	0.0000
Gid4	ENSMUSG00000018415	GID complex subunit 4, VID24 homolog	1.696	0.0000	0.0000
Gid8	ENSMUSG00000027573	GID complex subunit 8	1.707	0.0000	0.0000
Gigyf2	ENSMUSG00000048000	GRB10 interacting GYF protein 2	1.627	0.0000	0.0000
Gimap4	ENSMUSG00000054435	GTPase, IMAP family member 4	2.326	0.0000	0.0000
Gimap7	ENSMUSG00000043931	GTPase, IMAP family member 7	2.739	0.0379	0.0761
Gimap8	ENSMUSG00000064262	GTPase, IMAP family member 8	1.677	0.0000	0.0000
Ginm1	ENSMUSG00000040006	glycoprotein integral membrane 1	2.147	0.0000	0.0000
Gins2	ENSMUSG00000031821	GINS complex subunit 2 (Psf2 homolog)	1.593	0.0261	0.0553
Gja1	ENSMUSG00000050953	gap junction protein, alpha 1	1.728	0.0000	0.0000
Gjc1	ENSMUSG00000034520	gap junction protein, gamma 1	1.809	0.0000	0.0000
Gjc2	ENSMUSG00000043448	gap junction protein, gamma 2	2.752	0.0023	0.0066
Gkap1	ENSMUSG00000021552	G kinase anchoring protein 1	2.326	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Glcci1	ENSMUSG00000029638	glucocorticoid induced transcript 1	13.434	0.0000	0.0000
Glce	ENSMUSG00000032252	glucuronyl C5-epimerase	1.531	0.0000	0.0002
Glrx2	ENSMUSG00000018196	glutaredoxin 2 (thioltransferase)	1.997	0.0000	0.0000
Glrx5	ENSMUSG00000021102	glutaredoxin 5	3.953	0.0000	0.0000
Gls	ENSMUSG00000026103	glutaminase	1.618	0.0000	0.0000
Gm10036	ENSMUSG00000058064	predicted gene 10036	2.196	0.0382	0.0768
Gm10052	ENSMUSG00000058922	predicted pseudogene 10052	16.128	0.0000	0.0000
Gm10060	ENSMUSG00000110669	predicted gene 10060	2.871	0.0001	0.0004
Gm10069	ENSMUSG00000059659	predicted gene 10069	1.940	0.0001	0.0003
Gm10074	ENSMUSG00000101932	predicted gene 10074	5.211	0.0435	0.0858
Gm10086	ENSMUSG00000060730	predicted pseudogene 10086	10.022	0.0000	0.0000
Gm10095	ENSMUSG00000113555	predicted gene 10095	1.892	0.0001	0.0004
Gm10125	ENSMUSG00000063087	predicted gene 10125	2.030	0.0042	0.0111
Gm10167	ENSMUSG00000066554	predicted pseudogene 10167	1.972	0.0014	0.0041
Gm10209	ENSMUSG00000108080	predicted gene 10209	6.902	0.0000	0.0000
Gm10222	ENSMUSG00000067736	predicted gene 10222	2.232	0.0066	0.0167
Gm10232	ENSMUSG00000068141	predicted pseudogene 10232	5.991	0.0000	0.0000
Gm10244	ENSMUSG00000068601	predicted gene 10244	6.414	0.0000	0.0000
Gm10293	ENSMUSG00000070490	predicted pseudogene 10293	1.537	0.0179	0.0398
Gm10366	ENSMUSG00000115767	predicted gene 10366	2.770	0.0024	0.0067
Gm10371	ENSMUSG00000072589	predicted gene 10371	16.411	0.0000	0.0000
Gm10461	ENSMUSG00000107277	predicted gene 10461	1.826	0.0017	0.0051
Gm10524	ENSMUSG00000097141	predicted gene 10524	2.319	0.0000	0.0000
Gm10575	ENSMUSG00000073787	predicted gene 10575	1.789	0.0006	0.0018
Gm10638	ENSMUSG00000074178	predicted gene 10638	11.484	0.0000	0.0000
Gm10642	ENSMUSG00000074213	predicted gene 10642	6.780	0.0000	0.0000
Gm10705	ENSMUSG00000074506	predicted gene 10705	6.025	0.0000	0.0000
Gm10762	ENSMUSG00000074807	predicted gene 10762	2.782	0.0000	0.0000
Gm10817	ENSMUSG00000117710	predicted gene 10817	2.790	0.0271	0.0571
Gm10925	ENSMUSG00000100862	predicted gene 10925	33.630	0.0000	0.0000
Gm11175	ENSMUSG00000080058	predicted gene 11175	15.629	0.0000	0.0000
Gm11221	ENSMUSG00000082998	predicted gene 11221	6.253	0.0163	0.0367

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm11478	ENSMUSG00000083992	predicted gene 11478	3.354	0.0000	0.0000
Gm11560	ENSMUSG00000086688	predicted gene 11560	3.088	0.0000	0.0000
Gm11581	ENSMUSG00000083355	predicted gene 11581	2.542	0.0147	0.0337
Gm11642	ENSMUSG00000086794	predicted gene 11642	3.004	0.0000	0.0000
Gm11696	ENSMUSG00000056687	predicted gene 11696	2.728	0.0000	0.0000
Gm11748	ENSMUSG00000087036	predicted gene 11748	169.340	0.0000	0.0000
Gm11837	ENSMUSG00000086587	predicted gene 11837	2.478	0.0022	0.0063
Gm11847	ENSMUSG00000060989	predicted gene 11847	5.469	0.0081	0.0199
Gm11940	ENSMUSG00000087692	predicted gene 11940	1.708	0.0059	0.0151
Gm11973	ENSMUSG00000086839	predicted gene 11973	5.426	0.0000	0.0002
Gm12101	ENSMUSG00000083990	predicted gene 12101	3.291	0.0010	0.0030
Gm12129	ENSMUSG00000082587	predicted gene 12129	8.596	0.0026	0.0071
Gm12138	ENSMUSG00000082087	predicted gene 12138	9.402	0.0000	0.0000
Gm12184	ENSMUSG00000078154	predicted gene 12184	2.040	0.0000	0.0000
Gm12191	ENSMUSG00000083061	predicted gene 12191	5.492	0.0000	0.0000
Gm12295	ENSMUSG00000085162	predicted gene 12295	1.975	0.0000	0.0001
Gm12312	ENSMUSG00000082145	predicted gene 12312	2.290	0.0000	0.0001
Gm12338	ENSMUSG00000081485	predicted gene 12338	1.754	0.0000	0.0000
Gm12366	ENSMUSG00000082762	predicted gene 12366	3.908	0.0383	0.0770
Gm12444	ENSMUSG00000082194	predicted gene 12444	6.299	0.0116	0.0274
Gm12473	ENSMUSG00000086043	predicted gene 12473	38.870	0.0044	0.0116
Gm12693	ENSMUSG00000083179	predicted gene 12693	8.071	0.0000	0.0000
Gm12844	ENSMUSG00000084260	predicted gene 12844	2.576	0.0196	0.0433
Gm12905	ENSMUSG00000085875	predicted gene 12905	3.434	0.0004	0.0013
Gm12966	ENSMUSG00000070729	predicted gene 12966	4.794	0.0000	0.0000
Gm12992	ENSMUSG00000085667	predicted gene 12992	2.367	0.0000	0.0000
Gm12999	ENSMUSG00000087352	predicted gene 12999	2.200	0.0024	0.0067
Gm13091	ENSMUSG00000085213	predicted gene 13091	3.034	0.0102	0.0244
Gm13136	ENSMUSG00000081179	predicted gene 13136	2.953	0.0196	0.0433
Gm13161	ENSMUSG00000082248	predicted gene 13161	25.616	0.0000	0.0000
Gm13162	ENSMUSG00000082779	predicted pseudogene 13162	10.596	0.0268	0.0566
Gm13179	ENSMUSG00000086018	predicted gene 13179	8.513	0.0317	0.0655

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm13243	ENSMUSG00000094417	predicted gene 13243	9.605	0.0002	0.0006
Gm13339	ENSMUSG00000082884	predicted gene 13339	2.884	0.0001	0.0004
Gm13341	ENSMUSG00000083863	predicted gene 13341	2.114	0.0000	0.0000
Gm13369	ENSMUSG00000083796	predicted gene 13369	17.939	0.0049	0.0127
Gm13394	ENSMUSG00000083773	predicted gene 13394	1.527	0.0000	0.0000
Gm13421	ENSMUSG00000085929	predicted gene 13421	3.669	0.0139	0.0319
Gm13430	ENSMUSG00000083101	predicted gene 13430	29.264	0.0196	0.0432
Gm13453	ENSMUSG00000083240	predicted gene 13453	3.128	0.0000	0.0000
Gm13577	ENSMUSG00000082127	predicted gene 13577	8.188	0.0000	0.0000
Gm13594	ENSMUSG00000086881	predicted gene 13594	14.909	0.0000	0.0000
Gm13601	ENSMUSG00000087467	predicted gene 13601	15.796	0.0002	0.0008
Gm13712	ENSMUSG00000082534	predicted gene 13712	7.147	0.0000	0.0000
Gm13736	ENSMUSG00000082908	predicted gene 13736	1.523	0.0000	0.0000
Gm13889	ENSMUSG00000087006	predicted gene 13889	3.173	0.0000	0.0000
Gm14057	ENSMUSG00000089662	predicted gene 14057	1.932	0.0113	0.0268
Gm14221	ENSMUSG00000078956	predicted gene 14221	3.165	0.0001	0.0003
Gm14322	ENSMUSG00000078864	predicted gene 14322	2.367	0.0073	0.0182
Gm14398	ENSMUSG00000083993	predicted gene 14398	9.793	0.0000	0.0001
Gm14890	ENSMUSG00000081209	predicted gene 14890	6.492	0.0011	0.0034
Gm14964	ENSMUSG00000052188	predicted gene 14964	2.257	0.0001	0.0002
Gm15163	ENSMUSG00000085711	predicted gene 15163	3.976	0.0000	0.0000
Gm15270	ENSMUSG00000087400	predicted gene 15270	1.652	0.0027	0.0074
Gm15283	ENSMUSG00000087700	predicted gene 15283	1.602	0.0026	0.0071
Gm15285	ENSMUSG00000081277	predicted gene 15285	4.734	0.0000	0.0000
Gm15327	ENSMUSG00000085204	predicted gene 15327	3.512	0.0054	0.0140
Gm15387	ENSMUSG00000082585	predicted gene 15387	5.600	0.0372	0.0751
Gm15419	ENSMUSG00000084783	predicted gene 15419	5.651	0.0122	0.0286
Gm15441	ENSMUSG00000074398	predicted gene 15441	6.200	0.0000	0.0000
Gm15469	ENSMUSG00000107265	predicted gene 15469	3.990	0.0450	0.0883
Gm15500	ENSMUSG00000086583	predicted pseudogene 15500	1.581	0.0144	0.0329
Gm15542	ENSMUSG00000083396	predicted gene 15542	3.790	0.0000	0.0001
Gm15543	ENSMUSG00000086863	predicted gene 15543	1.809	0.0012	0.0036

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm15583	ENSMUSG00000080078	predicted gene 15583	2.118	0.0078	0.0192
Gm15609	ENSMUSG00000086602	predicted gene 15609	9.153	0.0000	0.0000
Gm15610	ENSMUSG00000078183	predicted gene 15610	1.767	0.0000	0.0002
Gm15706	ENSMUSG00000086013	predicted gene 15706	1.929	0.0106	0.0254
Gm15728	ENSMUSG00000086075	predicted gene 15728	2.309	0.0204	0.0448
Gm15801	ENSMUSG00000096592	predicted gene 15801	16.999	0.0000	0.0000
Gm15816	ENSMUSG00000086741	predicted gene 15816	3.288	0.0000	0.0000
Gm15853	ENSMUSG00000103400	predicted gene 15853	3.204	0.0000	0.0000
Gm15856	ENSMUSG00000086527	predicted gene 15856	9.545	0.0008	0.0026
Gm15860	ENSMUSG00000087336	predicted gene 15860	4.691	0.0000	0.0000
Gm15867	ENSMUSG00000089812	predicted gene 15867	5.828	0.0022	0.0062
Gm15906	ENSMUSG00000087416	predicted gene 15906	79.916	0.0000	0.0000
Gm15952	ENSMUSG00000085655	predicted gene 15952	12.740	0.0000	0.0000
Gm16089	ENSMUSG00000081228	predicted gene 16089	2.094	0.0020	0.0057
Gm16124	ENSMUSG00000086914	predicted gene 16124	3.339	0.0000	0.0000
Gm16136	ENSMUSG00000089804	predicted gene 16136	2.169	0.0013	0.0040
Gm16140	ENSMUSG00000084085	predicted gene 16140	2.693	0.0250	0.0533
Gm16409	ENSMUSG00000075581	predicted gene 16409	5.594	0.0019	0.0056
Gm16437	ENSMUSG00000024761	predicted pseudogene 16437	2.198	0.0065	0.0164
Gm16576	ENSMUSG00000087543	predicted gene 16576	1.553	0.0001	0.0003
Gm16701	ENSMUSG00000097823	predicted gene, 16701	2.181	0.0059	0.0150
Gm16861	ENSMUSG00000097397	predicted gene, 16861	3.673	0.0039	0.0105
Gm16933	ENSMUSG00000086289	predicted gene, 16933	53.949	0.0007	0.0022
Gm17082	ENSMUSG00000090674	predicted gene 17082	30.775	0.0021	0.0059
Gm17092	ENSMUSG00000091623	predicted gene 17092	12.983	0.0000	0.0000
Gm17108	ENSMUSG00000091133	predicted gene 17108	10.843	0.0001	0.0003
Gm17110	ENSMUSG00000090779	predicted gene 17110	25.660	0.0000	0.0000
Gm17251	ENSMUSG00000090952	predicted gene, 17251	2.675	0.0000	0.0000
Gm17349	ENSMUSG00000091604	predicted gene, 17349	14.749	0.0000	0.0002
Gm17382	ENSMUSG00000078838	predicted gene, 17382	4.519	0.0022	0.0062
Gm17428	ENSMUSG00000090889	predicted gene, 17428	5.052	0.0000	0.0000
Gm17606	ENSMUSG00000091306	predicted gene, 17606	27.424	0.0008	0.0024

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm17661	ENSMUSG00000091037	predicted gene, 17661	25.268	0.0000	0.0000
Gm18588	ENSMUSG00000093402	predicted gene, 18588	1.801	0.0132	0.0307
Gm18706	ENSMUSG00000109882	predicted gene, 18706	3.401	0.0502	0.0968
Gm18860	ENSMUSG00000110569	predicted gene, 18860	1.838	0.0000	0.0001
Gm18911	ENSMUSG00000116438	predicted gene, 18911	4.956	0.0012	0.0037
Gm19221	ENSMUSG00000113491	predicted gene, 19221	13.120	0.0018	0.0053
Gm19426	ENSMUSG00000097187	predicted gene, 19426	1.883	0.0031	0.0085
Gm2000	ENSMUSG00000078193	predicted gene 2000	1.553	0.0005	0.0016
Gm20033	ENSMUSG00000097640	predicted gene, 20033	8.475	0.0000	0.0000
Gm20091	ENSMUSG00000094249	predicted gene, 20091	4.548	0.0054	0.0139
Gm20186	ENSMUSG00000106874	predicted gene, 20186	2.711	0.0003	0.0010
Gm2027	ENSMUSG00000112795	predicted gene 2027	4.972	0.0137	0.0315
Gm20300	ENSMUSG00000111080	predicted gene, 20300	1.589	0.0000	0.0000
Gm20379	ENSMUSG00000100622	predicted gene, 20379	17.264	0.0014	0.0041
Gm20400	ENSMUSG00000092500	predicted gene 20400	6.000	0.0041	0.0110
Gm20421	ENSMUSG00000092483	predicted gene 20421	7.029	0.0001	0.0003
Gm20517	ENSMUSG00000023984	predicted gene 20517	2.730	0.0289	0.0604
Gm20522	ENSMUSG00000092241	predicted gene 20522	2.191	0.0018	0.0053
Gm20544	ENSMUSG00000092569	predicted gene 20544	3.162	0.0000	0.0000
Gm2058	ENSMUSG00000074903	predicted gene 2058	3.531	0.0000	0.0000
Gm20721	ENSMUSG00000090625	predicted gene, 20721	20.669	0.0000	0.0000
Gm21399	ENSMUSG00000094530	predicted gene, 21399	2.183	0.0000	0.0001
Gm21596	ENSMUSG00000096006	predicted gene, 21596	10.607	0.0000	0.0000
Gm21926	ENSMUSG00000116995	predicted gene, 21926	1.815	0.0000	0.0001
Gm22009	ENSMUSG00000089417	predicted gene, 22009	3.306	0.0000	0.0000
Gm22953	ENSMUSG00000080374	predicted gene, 22953	3.584	0.0111	0.0264
Gm2296	ENSMUSG00000118653	predicted gene 2296	4.175	0.0001	0.0004
Gm2308	ENSMUSG00000092257	predicted gene 2308	1.780	0.0052	0.0136
Gm23119	ENSMUSG00000089235	predicted gene, 23119	8.743	0.0003	0.0011
Gm23969	ENSMUSG00000065258	predicted gene, 23969	26.854	0.0017	0.0050
Gm24045	ENSMUSG00000065047	predicted gene, 24045	4.761	0.0188	0.0416
Gm2451	ENSMUSG00000106574	predicted pseudogene 2451	3.982	0.0331	0.0679

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm24616	ENSMUSG00000065208	predicted gene, 24616	15.563	0.0321	0.0662
Gm2619	ENSMUSG00000091199	predicted gene 2619	49.105	0.0004	0.0012
Gm26549	ENSMUSG00000097217	predicted gene, 26549	2.176	0.0119	0.0281
Gm26558	ENSMUSG00000097025	predicted gene, 26558	8.242	0.0008	0.0025
Gm26588	ENSMUSG00000097730	predicted gene, 26588	2.249	0.0156	0.0354
Gm26590	ENSMUSG00000097533	predicted gene, 26590	2.949	0.0425	0.0842
Gm26631	ENSMUSG00000097445	predicted gene, 26631	18.006	0.0000	0.0000
Gm26648	ENSMUSG00000097275	predicted gene, 26648	7.167	0.0032	0.0088
Gm26793	ENSMUSG00000096999	predicted gene, 26793	1.662	0.0516	0.0993
Gm26881	ENSMUSG00000096974	predicted gene, 26881	1.828	0.0000	0.0000
Gm26910	ENSMUSG00000097835	predicted gene, 26910	2.963	0.0000	0.0001
Gm27151	ENSMUSG00000098739	predicted gene 27151	4.892	0.0499	0.0965
Gm28035	ENSMUSG00000099041	predicted gene, 28035	14.137	0.0074	0.0184
Gm28043	ENSMUSG00000098374	predicted gene, 28043	6.878	0.0004	0.0013
Gm28187	ENSMUSG00000099375	predicted gene 28187	7.245	0.0081	0.0199
Gm2830	ENSMUSG00000086567	predicted gene 2830	3.053	0.0000	0.0000
Gm28424	ENSMUSG00000101037	predicted gene 28424	2.518	0.0442	0.0870
Gm28437	ENSMUSG00000101111	predicted gene 28437	5.104	0.0000	0.0000
Gm28439	ENSMUSG00000100131	predicted gene 28439	6.353	0.0000	0.0000
Gm28523	ENSMUSG00000100707	predicted gene 28523	2.045	0.0012	0.0036
Gm28529	ENSMUSG00000101320	predicted gene 28529	5.973	0.0000	0.0000
Gm28661	ENSMUSG00000102070	predicted gene 28661	3.037	0.0000	0.0000
Gm29015	ENSMUSG00000101680	predicted gene 29015	1.946	0.0077	0.0191
Gm29216	ENSMUSG00000101249	predicted gene 29216	21.481	0.0000	0.0000
Gm29246	ENSMUSG00000102062	predicted gene 29246	5.342	0.0000	0.0000
Gm29346	ENSMUSG00000101386	predicted gene 29346	3.317	0.0034	0.0091
Gm2962	ENSMUSG00000089838	predicted pseudogene 2962	6.306	0.0000	0.0000
Gm29629	ENSMUSG00000099874	predicted gene 29629	76.072	0.0000	0.0000
Gm30698	ENSMUSG00000111090	predicted gene, 30698	4.337	0.0457	0.0895
Gm30735	ENSMUSG00000105168	predicted gene, 30735	3.034	0.0005	0.0016
Gm30934	ENSMUSG00000111082	predicted gene, 30934	2.230	0.0428	0.0846
Gm31166	ENSMUSG00000109695	predicted gene, 31166	4.855	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm31659	ENSMUSG00000110489	predicted gene, 31659	1.620	0.0002	0.0006
Gm3200	ENSMUSG00000097388	predicted pseudogene 3200	1.807	0.0014	0.0042
Gm32282	ENSMUSG00000117648	predicted gene, 32282	2.690	0.0001	0.0005
Gm32391	ENSMUSG00000104011	predicted gene, 32391	1.558	0.0034	0.0092
Gm32699	ENSMUSG00000113528	predicted gene, 32699	2.844	0.0002	0.0006
Gm33023	ENSMUSG00000110652	predicted gene, 33023	1.919	0.0074	0.0183
Gm3411	ENSMUSG00000079396	predicted gene 3411	6.702	0.0362	0.0734
Gm34220	ENSMUSG00000114045	predicted gene, 34220	7.154	0.0000	0.0000
Gm35558	ENSMUSG00000113662	predicted gene, 35558	2.950	0.0000	0.0000
Gm36235	ENSMUSG00000113930	predicted gene, 36235	6.272	0.0356	0.0723
Gm3625	ENSMUSG00000118449	predicted gene 3625	1.762	0.0000	0.0001
Gm3650	ENSMUSG00000097891	predicted gene 3650	1.832	0.0108	0.0257
Gm36989	ENSMUSG00000102496	predicted gene, 36989	3.360	0.0137	0.0316
Gm37083	ENSMUSG00000102852	predicted gene, 37083	6.392	0.0116	0.0274
Gm37116	ENSMUSG00000103574	predicted gene, 37116	4.033	0.0000	0.0000
Gm37120	ENSMUSG00000103966	predicted gene, 37120	8.710	0.0058	0.0147
Gm37123	ENSMUSG00000103039	predicted gene, 37123	2.699	0.0012	0.0037
Gm3716	ENSMUSG00000105402	predicted gene 3716	1.664	0.0368	0.0742
Gm37194	ENSMUSG00000102189	predicted gene, 37194	46.655	0.0000	0.0000
Gm37201	ENSMUSG00000103658	predicted gene, 37201	5.417	0.0000	0.0000
Gm37309	ENSMUSG00000103046	predicted gene, 37309	3.108	0.0207	0.0454
Gm37376	ENSMUSG00000102349	predicted gene, 37376	7.111	0.0227	0.0490
Gm37415	ENSMUSG00000103864	predicted gene, 37415	5.504	0.0108	0.0257
Gm37499	ENSMUSG00000103901	predicted gene, 37499	1.919	0.0251	0.0535
Gm37563	ENSMUSG00000104040	predicted gene, 37563	5.969	0.0508	0.0978
Gm3788	ENSMUSG00000094392	predicted gene 3788	39.980	0.0003	0.0010
Gm38190	ENSMUSG00000102302	predicted gene, 38190	2.881	0.0116	0.0274
Gm38393	ENSMUSG00000000948	predicted gene, 38393	2.682	0.0000	0.0000
Gm39302	ENSMUSG00000111172	predicted gene, 39302	3.415	0.0004	0.0014
Gm40466	ENSMUSG00000110649	predicted gene, 40466	1.552	0.0362	0.0733
Gm40477	ENSMUSG00000113940	predicted gene, 40477	2.361	0.0115	0.0272
Gm4076	ENSMUSG00000096449	predicted gene 4076	2.002	0.0000	0.0001

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm40841	ENSMUSG00000113216	predicted gene, 40841	2.328	0.0160	0.0361
Gm41381	ENSMUSG00000118456	predicted gene, 41381	7.068	0.0000	0.0000
Gm41505	ENSMUSG00000116641	predicted gene, 41505	2.212	0.0176	0.0392
Gm41717	ENSMUSG00000117919	predicted gene, 41717	1.659	0.0005	0.0018
Gm41757	ENSMUSG00000118163	predicted gene, 41757	7.538	0.0216	0.0470
Gm41760	ENSMUSG00000117992	predicted gene, 41760	2.241	0.0000	0.0000
Gm42432	ENSMUSG00000105962	predicted gene 42432	1.946	0.0046	0.0120
Gm42462	ENSMUSG00000104728	predicted gene 42462	5.047	0.0021	0.0061
Gm42517	ENSMUSG00000105867	predicted gene 42517	4.908	0.0000	0.0000
Gm42547	ENSMUSG00000106990	predicted gene 42547	2.019	0.0000	0.0001
Gm42549	ENSMUSG00000107320	predicted gene 42549	3.197	0.0101	0.0242
Gm42596	ENSMUSG00000105482	predicted gene 42596	30.511	0.0000	0.0001
Gm42636	ENSMUSG00000104682	predicted gene 42636	1.672	0.0276	0.0581
Gm42690	ENSMUSG00000106391	predicted gene 42690	3.136	0.0378	0.0761
Gm42734	ENSMUSG00000106999	predicted gene 42734	3.487	0.0014	0.0042
Gm42819	ENSMUSG00000105728	predicted gene 42819	3.269	0.0001	0.0004
Gm42901	ENSMUSG00000104850	predicted gene 42901	1.796	0.0195	0.0430
Gm42922	ENSMUSG00000104605	predicted gene 42922	7.141	0.0000	0.0001
Gm42984	ENSMUSG00000104784	predicted gene 42984	9.296	0.0000	0.0000
Gm43034	ENSMUSG00000106662	predicted gene 43034	1.843	0.0013	0.0039
Gm43075	ENSMUSG00000105004	predicted gene 43075	10.020	0.0000	0.0000
Gm43196	ENSMUSG00000107017	predicted gene 43196	2.433	0.0299	0.0622
Gm43361	ENSMUSG00000106375	predicted gene 43361	17.021	0.0000	0.0000
Gm43457	ENSMUSG00000106678	predicted gene 43457	2.066	0.0291	0.0609
Gm43579	ENSMUSG00000107191	predicted gene 43579	10.975	0.0194	0.0428
Gm4366	ENSMUSG00000107383	predicted gene 4366	2.433	0.0000	0.0000
Gm43808	ENSMUSG00000107086	predicted gene 43808	10.235	0.0008	0.0026
Gm43961	ENSMUSG00000107549	predicted gene, 43961	4.409	0.0422	0.0836
Gm44126	ENSMUSG00000107770	predicted gene, 44126	4.162	0.0237	0.0508
Gm44136	ENSMUSG00000107524	predicted gene, 44136	4.134	0.0398	0.0796
Gm44250	ENSMUSG00000107881	predicted gene, 44250	1.532	0.0000	0.0000
Gm44423	ENSMUSG00000108064	predicted gene, 44423	3.592	0.0036	0.0097

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm44570	ENSMUSG00000109194	predicted gene 44570	5.751	0.0004	0.0014
Gm44616	ENSMUSG00000108701	predicted gene 44616	1.939	0.0231	0.0498
Gm4473	ENSMUSG00000086522	predicted gene 4473	3.397	0.0024	0.0066
Gm44731	ENSMUSG00000108190	predicted gene 44731	4.211	0.0010	0.0030
Gm44732	ENSMUSG00000108934	predicted gene 44732	23.224	0.0000	0.0000
Gm44899	ENSMUSG00000109008	predicted gene 44899	4.612	0.0000	0.0000
Gm44954	ENSMUSG00000109205	predicted gene 44954	2.058	0.0084	0.0205
Gm45051	ENSMUSG00000108435	predicted gene 45051	2.122	0.0089	0.0217
Gm45112	ENSMUSG00000109304	predicted gene 45112	2.128	0.0095	0.0229
Gm4524	ENSMUSG00000090257	predicted gene 4524	3.096	0.0001	0.0002
Gm45246	ENSMUSG00000109645	predicted gene 45246	4.575	0.0000	0.0000
Gm45250	ENSMUSG00000110317	predicted gene 45250	2.607	0.0026	0.0071
Gm45371	ENSMUSG00000109954	predicted gene 45371	13.887	0.0105	0.0252
Gm45380	ENSMUSG00000110360	predicted gene 45380	1.887	0.0010	0.0031
Gm45494	ENSMUSG00000110161	predicted gene 45494	3.468	0.0000	0.0000
Gm45507	ENSMUSG00000109881	predicted gene 45507	59.209	0.0002	0.0007
Gm45527	ENSMUSG00000109618	predicted gene 45527	3.215	0.0181	0.0403
Gm45605	ENSMUSG00000109829	predicted gene 45605	1.837	0.0410	0.0817
Gm45760	ENSMUSG00000110711	predicted gene 45760	6.328	0.0100	0.0240
Gm45930	ENSMUSG00000113681	predicted gene, 45930	2.984	0.0356	0.0723
Gm4617	ENSMUSG00000096544	predicted pseudogene 4617	6.130	0.0000	0.0000
Gm46404	ENSMUSG00000113440	predicted gene, 46404	1.824	0.0001	0.0004
Gm4673	ENSMUSG00000097750	predicted gene 4673	2.163	0.0010	0.0030
Gm47155	ENSMUSG00000114019	predicted gene, 47155	3.508	0.0000	0.0000
Gm47205	ENSMUSG00000111312	predicted gene, 47205	5.476	0.0018	0.0053
Gm4734	ENSMUSG00000106208	predicted gene 4734	4.841	0.0363	0.0735
Gm47483	ENSMUSG00000111496	predicted gene, 47483	2.462	0.0237	0.0508
Gm47484	ENSMUSG00000113529	predicted gene, 47484	2.984	0.0002	0.0006
Gm4754	ENSMUSG00000106895	predicted gene 4754	6.436	0.0027	0.0074
Gm47572	ENSMUSG00000112922	predicted gene, 47572	2.929	0.0000	0.0000
Gm47644	ENSMUSG00000112734	predicted gene, 47644	7.461	0.0000	0.0000
Gm47766	ENSMUSG00000112336	predicted gene, 47766	140.587	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm48069	ENSMUSG00000111547	predicted gene, 48069	1.731	0.0259	0.0550
Gm4811	ENSMUSG00000113263	predicted gene 4811	1.822	0.0215	0.0469
Gm48226	ENSMUSG00000112302	predicted gene, 48226	2.120	0.0000	0.0000
Gm4835	ENSMUSG00000043223	predicted pseudogene 4835	7.835	0.0000	0.0000
Gm4841	ENSMUSG00000068606	predicted gene 4841	33.154	0.0000	0.0000
Gm48488	ENSMUSG00000114433	predicted gene, 48488	2.982	0.0378	0.0761
Gm4853	ENSMUSG00000081473	predicted pseudogene 4853	1.901	0.0310	0.0641
Gm48604	ENSMUSG00000111291	predicted gene, 48604	2.759	0.0000	0.0000
Gm48623	ENSMUSG00000112941	predicted gene, 48623	3.022	0.0112	0.0264
Gm4864	ENSMUSG00000112003	predicted gene 4864	1.909	0.0069	0.0172
Gm48667	ENSMUSG00000113964	predicted gene, 48667	12.841	0.0001	0.0002
Gm48705	ENSMUSG00000114834	predicted gene, 48705	44.248	0.0005	0.0015
Gm48768	ENSMUSG00000112346	predicted gene, 48768	2.620	0.0000	0.0000
Gm48878	ENSMUSG00000112794	predicted gene, 48878	1.865	0.0242	0.0519
Gm48933	ENSMUSG00000115003	predicted gene, 48933	13.294	0.0000	0.0001
Gm4895	ENSMUSG00000044268	predicted gene 4895	2.987	0.0004	0.0014
Gm49041	ENSMUSG00000115026	predicted gene, 49041	2.039	0.0029	0.0081
Gm49130	ENSMUSG00000115234	predicted gene, 49130	10.337	0.0000	0.0000
Gm49207	ENSMUSG00000115497	predicted gene, 49207	5.158	0.0168	0.0378
Gm49227	ENSMUSG00000115469	predicted gene, 49227	9.079	0.0332	0.0681
Gm49326	ENSMUSG00000113294	predicted gene, 49326	4.696	0.0069	0.0173
Gm49330	ENSMUSG00000113234	predicted gene, 49330	64.478	0.0001	0.0005
Gm49336	ENSMUSG00000114797	predicted gene, 49336	1.594	0.0000	0.0000
Gm49492	ENSMUSG00000116180	predicted gene, 49492	1.774	0.0000	0.0000
Gm49540	ENSMUSG00000116272	predicted gene, 49540	3.560	0.0000	0.0001
Gm49544	ENSMUSG00000116262	predicted gene, 49544	36.236	0.0000	0.0000
Gm49741	ENSMUSG00000116571	predicted gene, 49741	7.085	0.0000	0.0000
Gm49759	ENSMUSG00000111394	predicted gene, 49759	1.917	0.0099	0.0238
Gm49774	ENSMUSG00000116657	predicted gene, 49774	2.987	0.0046	0.0121
Gm49864	ENSMUSG00000117255	predicted gene, 49864	6.155	0.0000	0.0001
Gm49883	ENSMUSG00000117113	predicted gene, 49883	1.840	0.0168	0.0378
Gm49894	ENSMUSG00000117069	predicted gene, 49894	2.836	0.0391	0.0784

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm50069	ENSMUSG00000117634	predicted gene, 50069	3.131	0.0001	0.0003
Gm50107	ENSMUSG00000118239	predicted gene, 50107	2.019	0.0192	0.0425
Gm50144	ENSMUSG00000118184	predicted gene, 50144	2.806	0.0000	0.0001
Gm50163	ENSMUSG00000118030	predicted gene, 50163	5.794	0.0184	0.0410
Gm50240	ENSMUSG00000117725	predicted gene, 50240	1.600	0.0009	0.0027
Gm50251	ENSMUSG00000117839	predicted gene, 50251	8.871	0.0001	0.0003
Gm50253	ENSMUSG00000117819	predicted gene, 50253	4.923	0.0000	0.0000
Gm50464	ENSMUSG00000118487	predicted gene, 50464	3.223	0.0486	0.0943
Gm5112	ENSMUSG00000107868	predicted gene 5112	1.683	0.0156	0.0353
Gm5216	ENSMUSG00000116398	predicted gene 5216	30.621	0.0000	0.0000
Gm527	ENSMUSG00000047227	predicted gene 527	2.038	0.0000	0.0000
Gm53012	ENSMUSG00000118504	predicted gene, 53012	2.304	0.0001	0.0004
Gm53023	ENSMUSG00000118572	predicted gene, 53023	17.987	0.0000	0.0000
Gm5335	ENSMUSG00000098035	predicted gene 5335	2.548	0.0140	0.0322
Gm5422	ENSMUSG00000039684	predicted pseudogene 5422	5.018	0.0000	0.0000
Gm5469	ENSMUSG00000116083	predicted gene 5469	14.974	0.0000	0.0001
Gm55094	ENSMUSG00002075524	predicted gene, 55094	4.466	0.0171	0.0383
Gm55118	ENSMUSG00002076173	predicted gene, 55118	22.681	0.0000	0.0000
Gm5512	ENSMUSG00000112693	predicted gene 5512	23.691	0.0000	0.0000
Gm5526	ENSMUSG00000084817	predicted pseudogene 5526	4.952	0.0040	0.0107
Gm55276	ENSMUSG00002075551	predicted gene, 55276	6.726	0.0000	0.0002
Gm5550	ENSMUSG00000106419	predicted gene 5550	6.852	0.0291	0.0608
Gm55594	ENSMUSG00000095562	predicted gene, 55594	7.931	0.0000	0.0000
Gm55632	ENSMUSG00002075486	predicted gene, 55632	53.764	0.0000	0.0000
Gm55936	ENSMUSG00002075188	predicted gene, 55936	12.613	0.0001	0.0003
Gm55944	ENSMUSG00002076463	predicted gene, 55944	29.197	0.0000	0.0000
Gm5602	ENSMUSG00000086108	predicted gene 5602	2.473	0.0001	0.0003
Gm5611	ENSMUSG00000090602	predicted gene 5611	3.653	0.0229	0.0494
Gm56171	ENSMUSG00002075501	predicted gene, 56171	21.274	0.0000	0.0000
Gm56228	ENSMUSG00002075075	predicted gene, 56228	3.899	0.0000	0.0000
Gm56257	ENSMUSG00002075231	predicted gene, 56257	20.838	0.0000	0.0000
Gm56350	ENSMUSG00000103009	predicted gene, 56350	2.333	0.0001	0.0003

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm56478	ENSMUSG00002076074	predicted gene, 56478	3.933	0.0000	0.0000
Gm5778	ENSMUSG00000091825	predicted gene 5778	3.262	0.0004	0.0012
Gm5805	ENSMUSG00000061848	predicted gene 5805	13.100	0.0000	0.0000
Gm5828	ENSMUSG00000091020	predicted gene 5828	1.956	0.0121	0.0283
Gm5881	ENSMUSG00000107747	predicted gene 5881	7.284	0.0137	0.0316
Gm5898	ENSMUSG00000081788	predicted gene 5898	6.047	0.0000	0.0000
Gm5909	ENSMUSG00000082491	predicted gene 5909	2.091	0.0009	0.0029
Gm5921	ENSMUSG00000074034	predicted gene 5921	2.401	0.0256	0.0543
Gm6123	ENSMUSG00000103922	predicted gene 6123	1.615	0.0295	0.0616
Gm6139	ENSMUSG00000057244	predicted gene 6139	4.335	0.0020	0.0057
Gm6155	ENSMUSG00000068629	predicted pseudogene 6155	4.492	0.0028	0.0078
Gm6161	ENSMUSG00000081441	predicted gene 6161	5.043	0.0020	0.0057
Gm6204	ENSMUSG00000105879	predicted gene 6204	11.616	0.0000	0.0000
Gm6254	ENSMUSG00000066538	predicted gene 6254	5.657	0.0043	0.0113
Gm6277	ENSMUSG00000097440	predicted gene 6277	2.485	0.0001	0.0004
Gm6363	ENSMUSG00000114993	predicted gene 6363	27.220	0.0007	0.0022
Gm6392	ENSMUSG00000115503	predicted gene 6392	2.977	0.0226	0.0489
Gm6397	ENSMUSG00000089640	predicted gene 6397	13.166	0.0000	0.0002
Gm6430	ENSMUSG00000044757	predicted gene 6430	3.129	0.0101	0.0242
Gm6433	ENSMUSG00000083382	predicted gene 6433	5.788	0.0006	0.0019
Gm6445	ENSMUSG00000100141	predicted gene 6445	7.773	0.0000	0.0001
Gm6451	ENSMUSG00000084166	predicted gene 6451	2.148	0.0203	0.0446
Gm6467	ENSMUSG00000117327	predicted gene 6467	1.971	0.0124	0.0289
Gm6477	ENSMUSG00000111877	predicted gene 6477	4.849	0.0006	0.0018
Gm6556	ENSMUSG00000097806	predicted gene 6556	2.966	0.0172	0.0385
Gm6560	ENSMUSG00000104913	predicted gene 6560	1.608	0.0030	0.0083
Gm6579	ENSMUSG00000109565	predicted gene 6579	8.649	0.0046	0.0121
Gm6598	ENSMUSG00000107143	predicted gene 6598	3.348	0.0194	0.0429
Gm6682	ENSMUSG00000091269	predicted gene 6682	2.658	0.0016	0.0048
Gm6728	ENSMUSG00000091408	predicted gene 6728	3.012	0.0000	0.0000
Gm6758	ENSMUSG00000081118	predicted gene 6758	6.338	0.0266	0.0562
Gm6793	ENSMUSG00000092086	predicted gene 6793	8.382	0.0002	0.0008

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm6807	ENSMUSG00000057605	predicted gene 6807	2.186	0.0377	0.0758
Gm6863	ENSMUSG00000043483	predicted gene 6863	1.543	0.0362	0.0733
Gm6877	ENSMUSG00000083557	predicted pseudogene 6877	3.357	0.0115	0.0272
Gm6916	ENSMUSG00000108608	predicted pseudogene 6916	3.222	0.0000	0.0000
Gm7008	ENSMUSG00000035983	predicted gene 7008	2.005	0.0325	0.0669
Gm7224	ENSMUSG00000083623	predicted gene 7224	1.961	0.0219	0.0477
Gm7292	ENSMUSG00000104222	predicted gene 7292	2.981	0.0000	0.0000
Gm7327	ENSMUSG00000050900	predicted gene 7327	2.086	0.0017	0.0050
Gm7334	ENSMUSG00000044645	predicted gene 7334	2.644	0.0267	0.0563
Gm7335	ENSMUSG00000067189	predicted gene 7335	5.257	0.0335	0.0686
Gm7390	ENSMUSG00000110644	predicted gene 7390	8.611	0.0000	0.0000
Gm7432	ENSMUSG00000109610	predicted gene 7432	4.468	0.0154	0.0350
Gm7466	ENSMUSG00000117359	predicted gene 7466	3.739	0.0030	0.0083
Gm7467	ENSMUSG00000098449	predicted gene 7467	7.725	0.0000	0.0000
Gm7517	ENSMUSG00000115700	predicted gene 7517	2.723	0.0411	0.0817
Gm7591	ENSMUSG00000114349	predicted gene 7591	4.202	0.0000	0.0000
Gm7666	ENSMUSG00000067547	predicted pseudogene 7666	1.525	0.0023	0.0066
Gm7729	ENSMUSG00000046636	predicted gene 7729	6.372	0.0000	0.0000
Gm7803	ENSMUSG00000083754	predicted gene 7803	9.674	0.0183	0.0408
Gm7809	ENSMUSG00000099397	predicted gene 7809	4.518	0.0000	0.0000
Gm7859	ENSMUSG00000116089	predicted gene 7859	2.321	0.0016	0.0048
Gm7887	ENSMUSG00000044211	predicted gene 7887	2.494	0.0000	0.0000
Gm7895	ENSMUSG00000100347	predicted gene 7895	2.588	0.0058	0.0147
Gm7984	ENSMUSG00000049891	predicted gene 7984	1.504	0.0292	0.0610
Gm8066	ENSMUSG00000106237	predicted gene 8066	8.323	0.0000	0.0000
Gm8098	ENSMUSG00000073073	predicted gene 8098	2.810	0.0028	0.0076
Gm8116	ENSMUSG00000059422	predicted gene 8116	5.384	0.0000	0.0000
Gm8130	ENSMUSG00000116637	predicted gene 8130	2.201	0.0214	0.0466
Gm8225	ENSMUSG00000068604	predicted gene 8225	2.975	0.0066	0.0167
Gm8228	ENSMUSG00000099779	predicted gene 8228	2.852	0.0231	0.0498
Gm8319	ENSMUSG00000108528	predicted gene 8319	4.595	0.0216	0.0470
Gm8451	ENSMUSG00000099471	predicted gene 8451	10.399	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm8643	ENSMUSG00000102809	predicted gene 8643	5.548	0.0341	0.0697
Gm8797	ENSMUSG00000103034	predicted pseudogene 8797	3.774	0.0366	0.0739
Gm8806	ENSMUSG00000083367	predicted gene 8806	5.591	0.0005	0.0016
Gm8826	ENSMUSG00000102268	predicted gene 8826	16.633	0.0012	0.0036
Gm8991	ENSMUSG00000059179	predicted pseudogene 8991	85.606	0.0000	0.0000
Gm9104	ENSMUSG00000061242	predicted gene 9104	9.986	0.0029	0.0080
Gm9162	ENSMUSG00000098044	predicted gene 9162	12.419	0.0000	0.0000
Gm9276	ENSMUSG00000118377	predicted gene 9276	3.171	0.0506	0.0975
Gm9358	ENSMUSG00000098199	predicted gene 9358	7.773	0.0000	0.0000
Gm9392	ENSMUSG00000087298	predicted pseudogene 9392	16.835	0.0000	0.0000
Gm9431	ENSMUSG00000083468	predicted gene 9431	13.672	0.0001	0.0003
Gm9530	ENSMUSG00000096950	predicted gene 9530	4.048	0.0331	0.0679
Gm9761	ENSMUSG00000034437	predicted gene 9761	2.862	0.0000	0.0001
Gm9800	ENSMUSG00000045799	predicted gene 9800	35.976	0.0000	0.0000
Gm9812	ENSMUSG00000046747	predicted gene 9812	6.378	0.0000	0.0000
Gm9856	ENSMUSG00000110945	predicted gene 9856	1.753	0.0488	0.0947
Gm9870	ENSMUSG00000052154	predicted gene 9870	2.429	0.0000	0.0001
Gm9887	ENSMUSG00000052673	predicted gene 9887	4.087	0.0000	0.0000
Gm9905	ENSMUSG00000053358	predicted gene 9905	4.043	0.0000	0.0000
Gm9910	ENSMUSG00000103469	predicted gene 9910	2.992	0.0440	0.0867
Gm9939	ENSMUSG00000054247	predicted gene 9939	2.141	0.0004	0.0012
Gm9988	ENSMUSG00000055968	predicted gene 9988	4.627	0.0230	0.0496
Gmfb	ENSMUSG00000062014	glia maturation factor, beta	1.668	0.0000	0.0000
Gmfg	ENSMUSG00000060791	glia maturation factor, gamma	2.114	0.0000	0.0001
Gmpr2	ENSMUSG00000002326	guanosine monophosphate reductase 2	1.770	0.0000	0.0000
Gnao1	ENSMUSG00000031748	guanine nucleotide binding protein, alpha O	1.645	0.0003	0.0010
Gnb1	ENSMUSG00000029064	guanine nucleotide binding protein (G protein), beta 1	1.549	0.0000	0.0000
Gng10	ENSMUSG00000038607	guanine nucleotide binding protein (G protein), gamma 10	4.396	0.0198	0.0437
Gng11	ENSMUSG00000032766	guanine nucleotide binding protein (G protein), gamma 11	1.592	0.0004	0.0013
Gngt2	ENSMUSG00000038811	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	1.907	0.0000	0.0000
Gnl1	ENSMUSG00000024429	guanine nucleotide binding protein-like 1	1.790	0.0000	0.0000
Gnl3	ENSMUSG00000042354	guanine nucleotide binding protein-like 3 (nucleolar)	1.580	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Golga4	ENSMUSG00000038708	golgi autoantigen, golgin subfamily a, 4	2.268	0.0000	0.0000
Golim4	ENSMUSG00000034109	golgi integral membrane protein 4	2.143	0.0000	0.0000
Golph3	ENSMUSG00000022200	golgi phosphoprotein 3	2.438	0.0000	0.0000
Gopc	ENSMUSG00000019861	golgi associated PDZ and coiled-coil motif containing	1.677	0.0000	0.0000
Gpat3	ENSMUSG00000029314	glycerol-3-phosphate acyltransferase 3	1.640	0.0005	0.0016
Gpatch11	ENSMUSG00000050668	G patch domain containing 11	1.985	0.0000	0.0000
Gpatch3	ENSMUSG00000028850	G patch domain containing 3	2.865	0.0000	0.0000
Gpatch4	ENSMUSG00000028069	G patch domain containing 4	4.780	0.0000	0.0000
Gpc3	ENSMUSG00000055653	glypican 3	1.518	0.0473	0.0922
Gpc4	ENSMUSG00000031119	glypican 4	2.084	0.0000	0.0000
Gpi-ps	ENSMUSG00000043192	glucose-6-phosphate isomerase, pseudogene	1.570	0.0251	0.0535
Gpr27	ENSMUSG00000072875	G protein-coupled receptor 27	3.686	0.0000	0.0000
Gpr62	ENSMUSG00000091735	G protein-coupled receptor 62	4.437	0.0113	0.0268
Gps2	ENSMUSG00000023170	G protein pathway suppressor 2	2.621	0.0000	0.0000
Gpx4-ps2	ENSMUSG00000110841	glutathione peroxidase 4, pseudogene 2	1.597	0.0000	0.0000
Grik3	ENSMUSG00000001985	glutamate receptor, ionotropic, kainate 3	1.711	0.0351	0.0714
Grik5	ENSMUSG00000003378	glutamate receptor, ionotropic, kainate 5 (gamma 2)	2.112	0.0000	0.0000
Grin2d	ENSMUSG00000002771	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	2.904	0.0001	0.0004
Grk3	ENSMUSG00000042249	G protein-coupled receptor kinase 3	1.517	0.0001	0.0003
Grsf1	ENSMUSG00000044221	G-rich RNA sequence binding factor 1	1.787	0.0000	0.0000
Gsg1l	ENSMUSG00000046182	GSG1-like	2.672	0.0000	0.0000
Gsk3a	ENSMUSG00000057177	glycogen synthase kinase 3 alpha	1.534	0.0000	0.0000
Gsk3b	ENSMUSG00000022812	glycogen synthase kinase 3 beta	1.644	0.0000	0.0000
Gspt1	ENSMUSG00000062203	G1 to S phase transition 1	1.597	0.0000	0.0000
Gspt2	ENSMUSG00000071723	G1 to S phase transition 2	1.938	0.0123	0.0287
Gsr	ENSMUSG00000031584	glutathione reductase	2.369	0.0000	0.0000
Gsta4	ENSMUSG00000032348	glutathione S-transferase, alpha 4	1.564	0.0000	0.0000
Gstp-ps	ENSMUSG00000103653	glutathione S-transferase, pi, pseudogene	2.772	0.0000	0.0000
Gtf2a1	ENSMUSG00000020962	general transcription factor II A, 1	2.672	0.0000	0.0000
Gtf2e1	ENSMUSG00000022828	general transcription factor II E, polypeptide 1 (alpha subunit)	1.533	0.0001	0.0002
Gtf2f1	ENSMUSG00000002658	general transcription factor IIF, polypeptide 1	2.523	0.0000	0.0000
Gtf2f2	ENSMUSG00000067995	general transcription factor IIF, polypeptide 2	1.507	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gtf2h3	ENSMUSG00000029387	general transcription factor IIH, polypeptide 3	1.671	0.0003	0.0011
Gtf3c6	ENSMUSG00000019837	general transcription factor IIIC, polypeptide 6, alpha	2.843	0.0000	0.0000
Gtpbp4	ENSMUSG00000021149	GTP binding protein 4	1.765	0.0000	0.0000
Guf1	ENSMUSG00000029208	GUF1 homolog, GTPase	1.620	0.0000	0.0000
Gvin2	ENSMUSG00000078606	GTPase, very large interferon inducible, family member 2	1.868	0.0078	0.0193
Gxylt1	ENSMUSG00000036197	glucoside xylosyltransferase 1	2.036	0.0000	0.0000
H19	ENSMUSG00000000031	H19, imprinted maternally expressed transcript	2.117	0.0001	0.0005
H1f10	ENSMUSG00000044927	H1.10 linker histone	6.314	0.0000	0.0000
H1f2	ENSMUSG00000036181	H1.2 linker histone, cluster member	1.643	0.0000	0.0002
H2aw	ENSMUSG00000078851	H2A.W histone	4.017	0.0000	0.0000
H2-Bl	ENSMUSG00000073406	histocompatibility 2, blastocyst	1.792	0.0001	0.0003
H2-Ke6	ENSMUSG00000073422	H2-K region expressed gene 6	6.860	0.0305	0.0634
H3f3a	ENSMUSG00000060743	H3.3 histone A	1.534	0.0000	0.0000
Habp4	ENSMUSG00000021476	hyaluronic acid binding protein 4	1.756	0.0000	0.0000
Hace1	ENSMUSG00000038822	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	1.674	0.0000	0.0000
Hand2	ENSMUSG00000038193	heart and neural crest derivatives expressed 2	4.248	0.0000	0.0000
Haus3	ENSMUSG00000079555	HAUS augmin-like complex, subunit 3	1.929	0.0000	0.0000
Hccs	ENSMUSG00000031352	holocytochrome c synthetase	2.194	0.0000	0.0002
Hcls1	ENSMUSG00000022831	hematopoietic cell specific Lyn substrate 1	2.319	0.0000	0.0000
Hcn2	ENSMUSG00000020331	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	3.753	0.0000	0.0000
Hcn4	ENSMUSG00000032338	hyperpolarization-activated, cyclic nucleotide-gated K+ 4	2.219	0.0000	0.0001
Hdac2	ENSMUSG00000019777	histone deacetylase 2	4.277	0.0000	0.0000
Hdac7	ENSMUSG00000022475	histone deacetylase 7	1.529	0.0000	0.0000
Hdgf	ENSMUSG00000004897	heparin binding growth factor	1.837	0.0000	0.0000
Hdgfl3	ENSMUSG00000025104	HDGF like 3	2.294	0.0000	0.0000
Hdnr	ENSMUSG00000097910	Hand2 downstream lncRNA	1.781	0.0001	0.0005
Heca	ENSMUSG00000039879	hdc homolog, cell cycle regulator	1.706	0.0001	0.0003
Herc2	ENSMUSG00000030451	HECT and RLD domain containing E3 ubiquitin protein ligase 2	1.591	0.0000	0.0000
Herpud2	ENSMUSG00000008429	HERPUD family member 2	1.686	0.0002	0.0007
Hes1	ENSMUSG00000022528	hes family bHLH transcription factor 1	2.920	0.0000	0.0000
Hey2	ENSMUSG00000019789	hairy/enhancer-of-split related with YRPW motif 2	1.829	0.0019	0.0054
Hgsnat	ENSMUSG00000037260	heparan-alpha-glucosaminide N-acetyltransferase	1.563	0.0003	0.0011

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hic1	ENSMUSG00000043099	hypermethylated in cancer 1	3.295	0.0000	0.0000
Hirip3	ENSMUSG00000042606	HIRA interacting protein 3	3.419	0.0000	0.0000
Hjv	ENSMUSG00000038403	hemojuvelin BMP co-receptor	2.128	0.0000	0.0000
Hk1	ENSMUSG00000037012	hexokinase 1	1.713	0.0000	0.0000
Hlf	ENSMUSG00000003949	hepatic leukemia factor	1.514	0.0000	0.0000
Hmg20b	ENSMUSG00000020232	high mobility group 20B	2.095	0.0001	0.0003
Hmga1	ENSMUSG00000046711	high mobility group AT-hook 1	5.143	0.0000	0.0000
Hmga1b	ENSMUSG00000078249	high mobility group AT-hook 1B	4.119	0.0000	0.0000
Hmgb1	ENSMUSG00000066551	high mobility group box 1	1.681	0.0000	0.0000
Hmgb1-ps7	ENSMUSG00000092281	high-mobility group high mobility group box 1, pseudogene 7	17.209	0.0000	0.0000
Hmgb2	ENSMUSG00000054717	high mobility group box 2	1.742	0.0000	0.0000
Hmgb3	ENSMUSG00000015217	high mobility group box 3	2.906	0.0000	0.0000
Hmgcs1	ENSMUSG00000093930	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1.805	0.0000	0.0000
Hmgn1	ENSMUSG00000040681	high mobility group nucleosomal binding domain 1	1.747	0.0000	0.0000
Hmgn3	ENSMUSG00000066456	high mobility group nucleosomal binding domain 3	3.847	0.0000	0.0000
Hmgn5	ENSMUSG00000031245	high-mobility group nucleosome binding domain 5	6.826	0.0000	0.0000
Hnrnpa0	ENSMUSG00000007836	heterogeneous nuclear ribonucleoprotein A0	4.069	0.0000	0.0000
Hnrnpa1	ENSMUSG00000046434	heterogeneous nuclear ribonucleoprotein A1	2.442	0.0000	0.0000
Hnrnpa1l2-ps2	ENSMUSG00000021927	heterogeneous nuclear ribonucleoprotein A1-like 2, pseudogene 2	59.076	0.0000	0.0000
Hnrnpa2b1	ENSMUSG00000004980	heterogeneous nuclear ribonucleoprotein A2/B1	2.665	0.0000	0.0000
Hnrnpa3	ENSMUSG00000059005	heterogeneous nuclear ribonucleoprotein A3	4.842	0.0000	0.0000
Hnrnpab	ENSMUSG00000020358	heterogeneous nuclear ribonucleoprotein A/B	4.438	0.0000	0.0000
Hnrnpc	ENSMUSG00000060373	heterogeneous nuclear ribonucleoprotein C	1.652	0.0000	0.0000
Hnrnpd	ENSMUSG00000000568	heterogeneous nuclear ribonucleoprotein D	3.351	0.0000	0.0000
Hnrnpdl	ENSMUSG00000029328	heterogeneous nuclear ribonucleoprotein D-like	1.957	0.0000	0.0000
Hnrnpf	ENSMUSG00000042079	heterogeneous nuclear ribonucleoprotein F	1.600	0.0000	0.0000
Hnrnph1	ENSMUSG00000007850	heterogeneous nuclear ribonucleoprotein H1	3.319	0.0000	0.0000
Hnrnph2	ENSMUSG00000045427	heterogeneous nuclear ribonucleoprotein H2	2.561	0.0000	0.0000
Hnrnph3	ENSMUSG00000020069	heterogeneous nuclear ribonucleoprotein H3	2.736	0.0000	0.0000
Hnrnpk	ENSMUSG00000021546	heterogeneous nuclear ribonucleoprotein K	1.804	0.0000	0.0000
Hnrnpl	ENSMUSG00000015165	heterogeneous nuclear ribonucleoprotein L	1.992	0.0000	0.0000
Hnrnpll	ENSMUSG00000024095	heterogeneous nuclear ribonucleoprotein L-like	2.477	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hnrnpm	ENSMUSG00000059208	heterogeneous nuclear ribonucleoprotein M	3.747	0.0000	0.0000
Hnrnpr	ENSMUSG00000066037	heterogeneous nuclear ribonucleoprotein R	2.730	0.0000	0.0000
Hnrnpu	ENSMUSG00000039630	heterogeneous nuclear ribonucleoprotein U	3.396	0.0000	0.0000
Hnrnpul1	ENSMUSG00000040725	heterogeneous nuclear ribonucleoprotein U-like 1	2.605	0.0000	0.0000
Hnrnpul2	ENSMUSG00000071659	heterogeneous nuclear ribonucleoprotein U-like 2	2.984	0.0000	0.0000
Homer1	ENSMUSG00000007617	homer scaffolding protein 1	1.723	0.0000	0.0000
Homer2	ENSMUSG00000025813	homer scaffolding protein 2	1.566	0.0000	0.0000
Hook1	ENSMUSG00000028572	hook microtubule tethering protein 1	1.647	0.0000	0.0001
Hook3	ENSMUSG00000037234	hook microtubule tethering protein 3	1.521	0.0000	0.0000
Hoxa5	ENSMUSG00000038253	homeobox A5	2.280	0.0285	0.0597
Hoxb2	ENSMUSG00000075588	homeobox B2	2.142	0.0085	0.0209
Hoxb3os	ENSMUSG00000084844	homeobox B3 and homeobox B2, opposite strand	2.291	0.0012	0.0037
Hoxd8	ENSMUSG00000027102	homeobox D8	2.305	0.0032	0.0087
Hoxd9	ENSMUSG00000043342	homeobox D9	3.857	0.0021	0.0059
Hpf1	ENSMUSG00000038005	histone PARylation factor 1	1.954	0.0000	0.0000
Hpse	ENSMUSG00000035273	heparanase	1.598	0.0297	0.0618
Hras	ENSMUSG00000025499	Harvey rat sarcoma virus oncogene	2.864	0.0000	0.0000
Hrc	ENSMUSG00000038239	histidine rich calcium binding protein	2.092	0.0000	0.0000
Hs3st3a1	ENSMUSG00000047759	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	2.140	0.0016	0.0046
Hs3st3b1	ENSMUSG00000070407	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	2.003	0.0000	0.0002
Hsd17b4	ENSMUSG00000024507	hydroxysteroid (17-beta) dehydrogenase 4	2.160	0.0000	0.0000
Hsd3b7	ENSMUSG00000042289	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	2.646	0.0127	0.0295
Hsdl2	ENSMUSG00000028383	hydroxysteroid dehydrogenase like 2	3.108	0.0000	0.0000
Hsp90aa1	ENSMUSG00000021270	heat shock protein 90, alpha (cytosolic), class A member 1	1.504	0.0003	0.0010
Hsp90ab1	ENSMUSG00000023944	heat shock protein 90 alpha (cytosolic), class B member 1	2.053	0.0000	0.0000
Hsp90b1	ENSMUSG00000020048	heat shock protein 90, beta (Grp94), member 1	2.058	0.0000	0.0000
Hspa14	ENSMUSG00000109865	heat shock protein 14	1.570	0.0000	0.0000
Hspa4	ENSMUSG00000020361	heat shock protein 4	2.591	0.0000	0.0000
Hspa5	ENSMUSG00000026864	heat shock protein 5	1.569	0.0000	0.0000
Hspa9	ENSMUSG00000024359	heat shock protein 9	1.761	0.0000	0.0000
Hspd1	ENSMUSG00000025980	heat shock protein 1 (chaperonin)	2.284	0.0000	0.0000
Hspd1-ps3	ENSMUSG00000058809	heat shock protein 1 (chaperonin), pseudogene 3	1.609	0.0346	0.0707

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hspe1	ENSMUSG00000073676	heat shock protein 1 (chaperonin 10)	1.847	0.0000	0.0000
Hspe1-rs1	ENSMUSG00000117621	heat shock protein 1 (chaperonin 10), related sequence 1	3.697	0.0000	0.0000
Hsph1	ENSMUSG00000029657	heat shock 105kDa/110kDa protein 1	1.616	0.0001	0.0005
Htatsf1	ENSMUSG00000067873	HIV TAT specific factor 1	3.078	0.0000	0.0000
Htr7	ENSMUSG00000024798	5-hydroxytryptamine (serotonin) receptor 7	1.740	0.0152	0.0346
Hyi	ENSMUSG00000006395	hydroxypyruvate isomerase (putative)	1.555	0.0145	0.0332
Hypk	ENSMUSG00000027245	huntingtin interacting protein K	3.092	0.0000	0.0000
Ibtk	ENSMUSG00000035941	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1.642	0.0000	0.0000
Ier2	ENSMUSG00000053560	immediate early response 2	1.922	0.0116	0.0274
Ier5	ENSMUSG00000056708	immediate early response 5	4.031	0.0000	0.0000
Ier5l	ENSMUSG00000089762	immediate early response 5-like	3.251	0.0000	0.0000
Iffo2	ENSMUSG00000041025	intermediate filament family orphan 2	1.653	0.0000	0.0000
Ifi202b	ENSMUSG00000026535	interferon activated gene 202B	1.555	0.0058	0.0149
Ifi204	ENSMUSG00000073489	interferon activated gene 204	2.113	0.0000	0.0001
Ifi35	ENSMUSG00000010358	interferon-induced protein 35	1.502	0.0000	0.0000
Ifit2	ENSMUSG00000045932	interferon-induced protein with tetratricopeptide repeats 2	1.570	0.0011	0.0033
Ifit3	ENSMUSG00000074896	interferon-induced protein with tetratricopeptide repeats 3	1.995	0.0004	0.0012
Ifit3b	ENSMUSG00000062488	interferon-induced protein with tetratricopeptide repeats 3B	2.344	0.0001	0.0003
Ifrd1	ENSMUSG00000001627	interferon-related developmental regulator 1	2.967	0.0000	0.0000
Ift57	ENSMUSG00000032965	intraflagellar transport 57	2.346	0.0000	0.0000
Ift80	ENSMUSG00000027778	intraflagellar transport 80	1.570	0.0001	0.0002
Iftap	ENSMUSG00000027165	intraflagellar transport associated protein	1.570	0.0000	0.0000
Igf2	ENSMUSG00000048583	insulin-like growth factor 2	3.078	0.0000	0.0000
Igfbp7	ENSMUSG00000036256	insulin-like growth factor binding protein 7	1.905	0.0001	0.0003
Igsf11	ENSMUSG00000022790	immunoglobulin superfamily, member 11	1.644	0.0080	0.0197
Igsf9b	ENSMUSG00000034275	immunoglobulin superfamily, member 9B	1.746	0.0034	0.0092
Igtp	ENSMUSG00000078853	interferon gamma induced GTPase	1.794	0.0103	0.0247
Iigp1	ENSMUSG00000054072	interferon inducible GTPase 1	2.084	0.0179	0.0398
Ik	ENSMUSG00000024474	IK cytokine	2.324	0.0000	0.0000
Il17d	ENSMUSG00000050222	interleukin 17D	2.826	0.0000	0.0001
Ilkap	ENSMUSG00000026309	integrin-linked kinase-associated serine/threonine phosphatase 2C	1.605	0.0000	0.0000
Ilrun	ENSMUSG00000056692	inflammation and lipid regulator with UBA-like and NBR1-like domains	1.903	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Impa2	ENSMUSG00000024525	inositol monophosphatase 2	2.483	0.0000	0.0000
Inafm1	ENSMUSG00000091811	InaF motif containing 1	2.554	0.0000	0.0001
Inafm2	ENSMUSG00000074918	InaF motif containing 2	3.452	0.0000	0.0000
Incenp	ENSMUSG00000024660	inner centromere protein	2.177	0.0000	0.0000
Ing2	ENSMUSG00000063049	inhibitor of growth family, member 2	1.957	0.0000	0.0001
Ing5	ENSMUSG00000026283	inhibitor of growth family, member 5	1.557	0.0000	0.0001
Inhba	ENSMUSG00000041324	inhibin beta-A	2.352	0.0000	0.0002
Inhbb	ENSMUSG00000037035	inhibin beta-B	2.663	0.0000	0.0000
Inka2	ENSMUSG00000048458	inka box actin regulator 2	1.637	0.0080	0.0196
Ino80b	ENSMUSG00000030034	INO80 complex subunit B	3.322	0.0000	0.0000
Ino80dos	ENSMUSG00000084799	INO80 complex subunit D, opposite strand	2.048	0.0001	0.0004
Inpp5a	ENSMUSG00000025477	inositol polyphosphate-5-phosphatase A	1.770	0.0000	0.0000
Ints13	ENSMUSG00000040250	integrator complex subunit 13	1.553	0.0000	0.0000
Ints8	ENSMUSG00000040738	integrator complex subunit 8	1.527	0.0000	0.0000
Ipo8	ENSMUSG00000040029	importin 8	1.803	0.0000	0.0000
Ipp	ENSMUSG00000028696	IAP promoted placental gene	1.592	0.0000	0.0000
Iqsec2	ENSMUSG00000041115	IQ motif and Sec7 domain 2	2.290	0.0000	0.0000
Irak1bp1	ENSMUSG00000032251	interleukin-1 receptor-associated kinase 1 binding protein 1	1.717	0.0050	0.0130
Irak4	ENSMUSG00000059883	interleukin-1 receptor-associated kinase 4	1.727	0.0000	0.0000
Irf2bp2	ENSMUSG00000051495	interferon regulatory factor 2 binding protein 2	2.520	0.0000	0.0000
Irgm2	ENSMUSG00000069874	immunity-related GTPase family M member 2	1.589	0.0108	0.0256
Irx1	ENSMUSG00000060969	Iroquois homeobox 1	3.042	0.0000	0.0000
Irx2	ENSMUSG00000001504	Iroquois homeobox 2	2.947	0.0000	0.0001
Irx3	ENSMUSG00000031734	Iroquois related homeobox 3	4.333	0.0000	0.0000
Irx3os	ENSMUSG00000046413	iroquois homeobox 3, opposite strand	3.078	0.0005	0.0017
Irx5	ENSMUSG00000031737	Iroquois homeobox 5	2.626	0.0000	0.0000
Iscu	ENSMUSG00000025825	iron-sulfur cluster assembly enzyme	3.680	0.0000	0.0000
Ism1	ENSMUSG00000074766	isthmin 1, angiogenesis inhibitor	2.163	0.0156	0.0353
Itgam	ENSMUSG00000030786	integrin alpha M	2.784	0.0000	0.0000
Itgb1	ENSMUSG00000025809	integrin beta 1 (fibronectin receptor beta)	2.303	0.0000	0.0000
Itgbl1	ENSMUSG00000032925	integrin, beta-like 1	2.618	0.0000	0.0000
Itpripl2	ENSMUSG00000095115	inositol 1,4,5-triphosphate receptor interacting protein-like 2	2.246	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Itsn1	ENSMUSG00000022957	intersectin 1 (SH3 domain protein 1A)	1.735	0.0000	0.0000
Iws1	ENSMUSG00000024384	IWS1, SUPT6 interacting protein	2.074	0.0000	0.0000
Jakmip3	ENSMUSG00000056856	janus kinase and microtubule interacting protein 3	5.782	0.0326	0.0672
Jdp2	ENSMUSG00000034271	Jun dimerization protein 2	1.867	0.0004	0.0012
Jmjd7	ENSMUSG00000098789	jumonji domain containing 7	5.996	0.0346	0.0706
Jmy	ENSMUSG00000021690	junction-mediating and regulatory protein	1.734	0.0002	0.0008
Jph2	ENSMUSG00000017817	junctophilin 2	3.007	0.0000	0.0000
Jund	ENSMUSG00000071076	jun D proto-oncogene	9.236	0.0000	0.0000
Junos	ENSMUSG00000087366	jun proto-oncogene, opposite strand	1.803	0.0185	0.0412
K230015D01Rik	ENSMUSG00000110630	RIKEN cDNA K230015D01 gene	2.713	0.0001	0.0002
Kansl2	ENSMUSG00000022992	KAT8 regulatory NSL complex subunit 2	2.110	0.0000	0.0000
Kantr	ENSMUSG00000087403	Kdm5c adjacent non-coding transcript	1.712	0.0002	0.0008
Katnbl1	ENSMUSG00000027132	katanin p80 subunit B like 1	1.602	0.0001	0.0002
Kbtbd2	ENSMUSG00000059486	kelch repeat and BTB (POZ) domain containing 2	1.512	0.0000	0.0000
Kcmf1	ENSMUSG00000055239	potassium channel modulatory factor 1	1.986	0.0000	0.0000
Kcna4	ENSMUSG00000042604	potassium voltage-gated channel, shaker-related subfamily, member 4	1.862	0.0273	0.0576
Kcnab3	ENSMUSG00000018470	potassium voltage-gated channel, shaker-related subfamily, beta member 3	2.359	0.0013	0.0038
Kcnb1	ENSMUSG00000050556	potassium voltage gated channel, Shab-related subfamily, member 1	1.707	0.0000	0.0000
Kcnd3os	ENSMUSG00000074346	potassium voltage-gated channel, Shal-related family, member 3, opposite strand	2.472	0.0005	0.0015
Kcng2	ENSMUSG00000059852	potassium voltage-gated channel, subfamily G, member 2	1.889	0.0000	0.0000
Kcng4	ENSMUSG00000045246	potassium voltage-gated channel, subfamily G, member 4	3.295	0.0067	0.0169
Kcnh2	ENSMUSG00000038319	potassium voltage-gated channel, subfamily H (eag-related), member 2	1.539	0.0250	0.0533
Kcnj10	ENSMUSG00000044708	potassium inwardly-rectifying channel, subfamily J, member 10	2.386	0.0154	0.0350
Kcnj12	ENSMUSG00000042529	potassium inwardly-rectifying channel, subfamily J, member 12	1.951	0.0000	0.0001
Kcnk2	ENSMUSG00000037624	potassium channel, subfamily K, member 2	1.535	0.0005	0.0017
Kctd1	ENSMUSG00000036225	potassium channel tetramerisation domain containing 1	1.870	0.0000	0.0000
Kctd13	ENSMUSG00000030685	potassium channel tetramerisation domain containing 13	2.155	0.0006	0.0019
Kctd18	ENSMUSG00000054770	potassium channel tetramerisation domain containing 18	1.880	0.0000	0.0000
Kctd2	ENSMUSG00000016940	potassium channel tetramerisation domain containing 2	2.576	0.0000	0.0000
Kctd3	ENSMUSG00000026608	potassium channel tetramerisation domain containing 3	1.971	0.0000	0.0000
Kctd6	ENSMUSG00000021752	potassium channel tetramerisation domain containing 6	2.243	0.0000	0.0000
Kctd9	ENSMUSG00000034327	potassium channel tetramerisation domain containing 9	1.795	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kdm1a	ENSMUSG00000036940	lysine (K)-specific demethylase 1A	2.328	0.0000	0.0000
Kdm5d	ENSMUSG00000056673	lysine (K)-specific demethylase 5D	1.535	0.0000	0.0000
Kdm6b	ENSMUSG00000018476	KDM1 lysine (K)-specific demethylase 6B	1.983	0.0001	0.0003
Kdr	ENSMUSG00000062960	kinase insert domain protein receptor	1.658	0.0000	0.0001
Khdrbs1	ENSMUSG00000028790	KH domain containing, RNA binding, signal transduction associated 1	1.821	0.0000	0.0000
Khdrbs3	ENSMUSG00000022332	KH domain containing, RNA binding, signal transduction associated 3	1.787	0.0000	0.0000
Khsrp	ENSMUSG00000007670	KH-type splicing regulatory protein	3.241	0.0000	0.0000
Kif14	ENSMUSG00000041498	kinesin family member 14	2.437	0.0022	0.0064
Kif1c	ENSMUSG00000020821	kinesin family member 1C	1.693	0.0000	0.0000
Kif20b	ENSMUSG00000024795	kinesin family member 20B	2.364	0.0001	0.0002
Kif21a	ENSMUSG00000022629	kinesin family member 21A	1.583	0.0000	0.0000
Kif2a	ENSMUSG00000021693	kinesin family member 2A	1.765	0.0000	0.0000
Kif3a	ENSMUSG00000018395	kinesin family member 3A	2.002	0.0000	0.0000
Kifbp	ENSMUSG00000036955	kinesin family binding protein	1.633	0.0000	0.0000
Klf10	ENSMUSG00000037465	Kruppel-like factor 10	2.045	0.0000	0.0000
Klf11	ENSMUSG00000020653	Kruppel-like factor 11	1.794	0.0000	0.0000
Klf16	ENSMUSG00000035397	Kruppel-like factor 16	1.853	0.0000	0.0000
Klf2	ENSMUSG00000055148	Kruppel-like factor 2 (lung)	2.888	0.0000	0.0000
Klf3	ENSMUSG00000029178	Kruppel-like factor 3 (basic)	1.843	0.0000	0.0000
Klf4	ENSMUSG00000003032	Kruppel-like factor 4 (gut)	1.994	0.0000	0.0000
Klf5	ENSMUSG00000005148	Kruppel-like factor 5	2.749	0.0194	0.0429
Klhdc2	ENSMUSG00000020978	kelch domain containing 2	2.165	0.0000	0.0000
Klhdc4	ENSMUSG00000040263	kelch domain containing 4	2.171	0.0000	0.0000
Klhdc8b	ENSMUSG00000032609	kelch domain containing 8B	1.751	0.0001	0.0003
Klhl12	ENSMUSG00000026455	kelch-like 12	1.636	0.0000	0.0000
Klhl2	ENSMUSG00000031605	kelch-like 2, Mayven	1.705	0.0014	0.0042
Klhl20	ENSMUSG00000026705	kelch-like 20	1.653	0.0000	0.0000
Klhl31	ENSMUSG00000044938	kelch-like 31	1.668	0.0000	0.0000
Klhl8	ENSMUSG00000029312	kelch-like 8	1.536	0.0000	0.0000
Klhl9	ENSMUSG00000070923	kelch-like 9	1.583	0.0000	0.0000
Klrg2	ENSMUSG00000071537	killer cell lectin-like receptor subfamily G, member 2	2.194	0.0288	0.0603
Kmt5b	ENSMUSG00000045098	lysine methyltransferase 5B	1.542	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kpna2	ENSMUSG00000018362	karyopherin (importin) alpha 2	2.139	0.0000	0.0000
Kpna4	ENSMUSG00000027782	karyopherin (importin) alpha 4	1.788	0.0000	0.0000
Kpnb1	ENSMUSG00000001440	karyopherin (importin) beta 1	1.522	0.0000	0.0000
Kras	ENSMUSG00000030265	Kirsten rat sarcoma viral oncogene homolog	2.105	0.0000	0.0000
Krcc1	ENSMUSG00000053012	lysine-rich coiled-coil 1	1.915	0.0000	0.0000
Ktn1	ENSMUSG00000021843	kinectin 1	1.537	0.0000	0.0000
Lacc1	ENSMUSG00000044350	laccase domain containing 1	1.667	0.0002	0.0008
Lactb	ENSMUSG00000032370	lactamase, beta	2.281	0.0000	0.0000
Lamtor3	ENSMUSG00000091512	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3	1.640	0.0000	0.0000
Larp1b	ENSMUSG00000025762	La ribonucleoprotein domain family, member 1B	2.440	0.0000	0.0000
Larp4b	ENSMUSG00000033499	La ribonucleoprotein domain family, member 4B	1.563	0.0000	0.0000
Larp6	ENSMUSG00000034839	La ribonucleoprotein domain family, member 6	2.064	0.0006	0.0019
Las1l	ENSMUSG00000057421	LAS1-like (S. cerevisiae)	1.566	0.0000	0.0000
Lat2	ENSMUSG00000040751	linker for activation of T cells family, member 2	1.891	0.0026	0.0074
Lats2	ENSMUSG00000021959	large tumor suppressor 2	1.911	0.0000	0.0000
Lbhd1	ENSMUSG00000096740	LBH domain containing 1	1.991	0.0001	0.0005
Lca5l	ENSMUSG00000045275	Leber congenital amaurosis 5-like	2.355	0.0000	0.0000
Ldhb	ENSMUSG00000030246	lactate dehydrogenase B	1.690	0.0000	0.0000
Ldlrad4	ENSMUSG00000024544	low density lipoprotein receptor class A domain containing 4	1.907	0.0000	0.0000
Lemd2	ENSMUSG00000044857	LEM domain containing 2	3.168	0.0000	0.0000
Lemd3	ENSMUSG00000048661	LEM domain containing 3	2.389	0.0000	0.0000
Leng1	ENSMUSG00000078813	leukocyte receptor cluster (LRC) member 1	2.706	0.0000	0.0000
Leng8	ENSMUSG00000035545	leukocyte receptor cluster (LRC) member 8	1.743	0.0037	0.0098
Leo1	ENSMUSG00000042487	Leo1, Paf1/RNA polymerase II complex component	1.976	0.0000	0.0000
Lgals4	ENSMUSG00000053964	lectin, galactose binding, soluble 4	1.820	0.0130	0.0301
Lgi3	ENSMUSG00000033595	leucine-rich repeat LGI family, member 3	2.131	0.0000	0.0000
Lgr4	ENSMUSG00000050199	leucine-rich repeat-containing G protein-coupled receptor 4	1.523	0.0000	0.0000
Lhfp	ENSMUSG00000048332	lipoma HMGIC fusion partner	1.623	0.0000	0.0000
Lhfpl4	ENSMUSG00000042873	lipoma HMGIC fusion partner-like protein 4	4.201	0.0000	0.0000
Lig1	ENSMUSG00000056394	ligase I, DNA, ATP-dependent	1.674	0.0003	0.0009
Lin7a	ENSMUSG00000019906	lin-7 homolog A, crumbs cell polarity complex component	2.012	0.0053	0.0137
Lin7c	ENSMUSG00000027162	lin-7 homolog C, crumbs cell polarity complex component	1.706	0.0000	0.0000

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Lingo1	ENSMUSG00000049556	leucine rich repeat and Ig domain containing 1	2.719	0.0050	0.0129
Lipo4	ENSMUSG00000079344	lipase, member O4	2.870	0.0000	0.0000
Lix1l	ENSMUSG00000049288	Lix1-like	1.661	0.0000	0.0000
Llph-ps1	ENSMUSG00000081459	LLP homolog, pseudogene 1	6.582	0.0168	0.0377
Llph-ps2	ENSMUSG00000083364	LLP homolog, pseudogene 2	19.242	0.0000	0.0000
Lmln	ENSMUSG00000022802	leishmanolysin-like (metallopeptidase M8 family)	1.553	0.0012	0.0036
Lmnb1	ENSMUSG00000024590	lamin B1	2.010	0.0000	0.0002
Lmo2	ENSMUSG00000032698	LIM domain only 2	2.379	0.0000	0.0000
Lmod1	ENSMUSG00000048096	leiomodin 1 (smooth muscle)	2.508	0.0000	0.0000
Lmod2	ENSMUSG00000029683	leiomodin 2 (cardiac)	2.623	0.0000	0.0000
Lmod3	ENSMUSG00000044086	leiomodin 3 (fetal)	1.716	0.0218	0.0475
Lmtk3	ENSMUSG00000062044	lemur tyrosine kinase 3	10.326	0.0137	0.0316
Lncob1	ENSMUSG00000092381	lncRNA osteoblastogenesis associated 1	4.900	0.0007	0.0022
Lonp1	ENSMUSG00000041168	lon peptidase 1, mitochondrial	2.056	0.0000	0.0000
Lonrf1	ENSMUSG00000039633	LON peptidase N-terminal domain and ring finger 1	2.705	0.0000	0.0000
Lpar1	ENSMUSG00000038668	lysophosphatidic acid receptor 1	2.286	0.0000	0.0000
Lpar4	ENSMUSG00000049929	lysophosphatidic acid receptor 4	1.748	0.0009	0.0029
Lpcat1	ENSMUSG00000021608	lysophosphatidylcholine acyltransferase 1	2.011	0.0000	0.0000
Lpcat4	ENSMUSG00000027134	lysophosphatidylcholine acyltransferase 4	2.440	0.0000	0.0000
Lrch1	ENSMUSG00000068015	leucine-rich repeats and calponin homology (CH) domain containing 1	1.638	0.0002	0.0007
Lrfn1	ENSMUSG00000030600	leucine rich repeat and fibronectin type III domain containing 1	4.063	0.0000	0.0000
Lrfn4	ENSMUSG00000045045	leucine rich repeat and fibronectin type III domain containing 4	2.691	0.0000	0.0000
Lrp6	ENSMUSG00000030201	low density lipoprotein receptor-related protein 6	1.601	0.0000	0.0000
Lrrc15	ENSMUSG00000052316	leucine rich repeat containing 15	12.936	0.0008	0.0026
Lrrc47	ENSMUSG00000029028	leucine rich repeat containing 47	4.454	0.0000	0.0000
Lrrc58	ENSMUSG00000034158	leucine rich repeat containing 58	1.537	0.0407	0.0812
Lrrc75a	ENSMUSG00000046417	leucine rich repeat containing 75A	1.634	0.0008	0.0025
Lrrc8a	ENSMUSG00000007476	leucine rich repeat containing 8A VRAC subunit A	1.722	0.0029	0.0080
Lrrfip1	ENSMUSG00000026305	leucine rich repeat (in FLII) interacting protein 1	1.531	0.0000	0.0000
Lrrfip2	ENSMUSG00000032497	leucine rich repeat (in FLII) interacting protein 2	1.541	0.0000	0.0001
Lsg1	ENSMUSG00000022538	large 60S subunit nuclear export GTPase 1	1.663	0.0000	0.0000
Lsm14a	ENSMUSG00000066568	LSM14A mRNA processing body assembly factor	1.754	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lsm3	ENSMUSG00000034192	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated	1.696	0.0001	0.0005
Lsm4	ENSMUSG00000031848	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated	2.029	0.0002	0.0008
Lsm5	ENSMUSG00000091625	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated	1.733	0.0001	0.0003
Lsm6	ENSMUSG00000031683	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated	2.996	0.0000	0.0000
Lsm8	ENSMUSG00000044155	LSM8 homolog, U6 small nuclear RNA associated	2.652	0.0000	0.0000
Ltb4r2	ENSMUSG00000040432	leukotriene B4 receptor 2	2.841	0.0141	0.0325
Ltbp1	ENSMUSG00000001870	latent transforming growth factor beta binding protein 1	1.722	0.0000	0.0000
Ltv1	ENSMUSG00000019814	LTV1 ribosome biogenesis factor	2.123	0.0000	0.0000
Luc7l2	ENSMUSG00000029823	LUC7-like 2 (S. cerevisiae)	2.126	0.0000	0.0000
Luc7l3	ENSMUSG00000020863	LUC7-like 3 (S. cerevisiae)	2.284	0.0000	0.0000
Lurap1l	ENSMUSG00000048706	leucine rich adaptor protein 1-like	1.574	0.0069	0.0173
Ly75	ENSMUSG00000026980	lymphocyte antigen 75	1.599	0.0019	0.0055
Lyar	ENSMUSG00000067367	Ly1 antibody reactive clone	1.758	0.0000	0.0000
Lyrm4	ENSMUSG00000046573	LYR motif containing 4	2.012	0.0000	0.0000
Macf1	ENSMUSG00000028649	microtubule-actin crosslinking factor 1	1.514	0.0000	0.0000
Maco1	ENSMUSG00000028826	macoilin 1	2.131	0.0000	0.0000
Macrod1	ENSMUSG00000036278	mono-ADP ribosylhydrolase 1	2.273	0.0000	0.0000
Macrod2	ENSMUSG00000068205	mono-ADP ribosylhydrolase 2	2.301	0.0000	0.0000
Mad1l1	ENSMUSG00000029554	MAD1 mitotic arrest deficient 1-like 1	1.719	0.0000	0.0000
Madd	ENSMUSG00000040687	MAP-kinase activating death domain	1.518	0.0000	0.0000
Maf	ENSMUSG00000055435	avian musculoaponeurotic fibrosarcoma oncogene homolog	2.664	0.0000	0.0000
Mafa	ENSMUSG00000047591	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (avian)	7.029	0.0000	0.0000
Maff	ENSMUSG00000042622	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	2.293	0.0369	0.0745
Mafk	ENSMUSG00000018143	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	1.575	0.0499	0.0964
Magohb	ENSMUSG00000030188	mago homolog B, exon junction complex core component	1.820	0.0001	0.0003
Mak16	ENSMUSG00000031578	MAK16 homolog	2.214	0.0000	0.0000
Malat1	ENSMUSG00000092341	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	3.422	0.0009	0.0027
Malsu1	ENSMUSG00000029815	mitochondrial assembly of ribosomal large subunit 1	2.034	0.0000	0.0000
Manf	ENSMUSG00000032575	mesencephalic astrocyte-derived neurotrophic factor	1.778	0.0000	0.0000
Map1lc3a	ENSMUSG00000027602	microtubule-associated protein 1 light chain 3 alpha	2.632	0.0000	0.0000
Map2k2	ENSMUSG00000035027	mitogen-activated protein kinase kinase 2	2.206	0.0001	0.0003
Map2k5	ENSMUSG00000058444	mitogen-activated protein kinase kinase 5	1.717	0.0002	0.0006

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Map2k7	ENSMUSG00000002948	mitogen-activated protein kinase kinase 7	1.868	0.0000	0.0000
Map3k10	ENSMUSG00000040390	mitogen-activated protein kinase kinase kinase 10	3.154	0.0000	0.0000
Map3k5	ENSMUSG00000071369	mitogen-activated protein kinase kinase kinase 5	1.813	0.0000	0.0000
Map4	ENSMUSG00000032479	microtubule-associated protein 4	1.577	0.0000	0.0000
Map4k4	ENSMUSG00000026074	mitogen-activated protein kinase kinase kinase kinase 4	2.345	0.0000	0.0000
Map7	ENSMUSG00000019996	microtubule-associated protein 7	2.143	0.0000	0.0000
Map7d1	ENSMUSG00000028849	MAP7 domain containing 1	2.382	0.0000	0.0000
Map7d2	ENSMUSG00000041020	MAP7 domain containing 2	2.540	0.0000	0.0002
Mapk14	ENSMUSG00000053436	mitogen-activated protein kinase 14	1.538	0.0000	0.0000
Mapk1ip1l	ENSMUSG00000021840	mitogen-activated protein kinase 1 interacting protein 1-like	1.830	0.0000	0.0000
Mapk9	ENSMUSG00000020366	mitogen-activated protein kinase 9	1.548	0.0000	0.0000
Mapkapk5	ENSMUSG00000029454	MAP kinase-activated protein kinase 5	20.690	0.0000	0.0000
Mapre1	ENSMUSG00000027479	microtubule-associated protein, RP/EB family, member 1	1.520	0.0000	0.0000
Marchf1	ENSMUSG00000036469	membrane associated ring-CH-type finger 1	1.555	0.0375	0.0755
Marchf11	ENSMUSG00000022269	membrane associated ring-CH-type finger 11	4.881	0.0000	0.0000
Marchf2	ENSMUSG00000079557	membrane associated ring-CH-type finger 2	1.517	0.0000	0.0000
Marchf5	ENSMUSG00000023307	membrane associated ring-CH-type finger 5	2.968	0.0000	0.0000
Marchf8	ENSMUSG00000025702	membrane associated ring-CH-type finger 8	1.732	0.0000	0.0000
Marchf9	ENSMUSG00000040502	membrane associated ring-CH-type finger 9	4.783	0.0000	0.0000
Marcks	ENSMUSG00000069662	myristoylated alanine rich protein kinase C substrate	3.884	0.0000	0.0000
Marcksl1	ENSMUSG00000047945	MARCKS-like 1	2.243	0.0001	0.0003
Mark2	ENSMUSG00000024969	MAP/microtubule affinity regulating kinase 2	1.615	0.0000	0.0000
Mark3	ENSMUSG00000007411	MAP/microtubule affinity regulating kinase 3	1.789	0.0000	0.0000
Mark4	ENSMUSG00000030397	MAP/microtubule affinity regulating kinase 4	2.647	0.0000	0.0000
Mat2a	ENSMUSG00000053907	methionine adenosyltransferase II, alpha	1.507	0.0000	0.0000
Max	ENSMUSG00000059436	Max protein	1.756	0.0000	0.0000
Maz	ENSMUSG00000030678	MYC-associated zinc finger protein (purine-binding transcription factor)	2.529	0.0000	0.0000
Mbd1	ENSMUSG00000024561	methyl-CpG binding domain protein 1	1.513	0.0283	0.0593
Mbd2	ENSMUSG00000024513	methyl-CpG binding domain protein 2	3.308	0.0000	0.0000
Mbd3	ENSMUSG00000035478	methyl-CpG binding domain protein 3	1.669	0.0000	0.0001
Mbtd1	ENSMUSG00000059474	mbt domain containing 1	1.757	0.0000	0.0000
Mbtps2	ENSMUSG00000046873	membrane-bound transcription factor peptidase, site 2	1.580	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mcat	ENSMUSG00000048755	malonyl CoA:ACP acyltransferase (mitochondrial)	1.524	0.0000	0.0000
Mcl1	ENSMUSG00000038612	myeloid cell leukemia sequence 1	2.344	0.0000	0.0000
Mcur1	ENSMUSG00000021371	mitochondrial calcium uniporter regulator 1	1.546	0.0000	0.0001
Mdfic	ENSMUSG00000041390	MyoD family inhibitor domain containing	2.271	0.0000	0.0000
Mdn1	ENSMUSG00000058006	midasin AAA ATPase 1	1.700	0.0000	0.0000
Mecomos	ENSMUSG00000085702	MDS1 and EVI1 complex locus, opposite strand	10.093	0.0000	0.0001
Med13	ENSMUSG00000034297	mediator complex subunit 13	1.765	0.0000	0.0000
Med16	ENSMUSG00000013833	mediator complex subunit 16	1.578	0.0000	0.0000
Med30	ENSMUSG00000038622	mediator complex subunit 30	3.167	0.0000	0.0000
Medag	ENSMUSG00000029659	mesenteric estrogen dependent adipogenesis	3.143	0.0000	0.0000
Meig1	ENSMUSG00000026650	meiosis expressed gene 1	1.569	0.0025	0.0070
Meis1	ENSMUSG00000020160	Meis homeobox 1	1.518	0.0002	0.0006
Meox1	ENSMUSG00000001493	mesenchyme homeobox 1	2.021	0.0214	0.0466
Mepce	ENSMUSG00000029726	methylphosphate capping enzyme	1.551	0.0000	0.0000
Mesd	ENSMUSG00000038503	mesoderm development LRP chaperone	1.706	0.0000	0.0000
Metap2	ENSMUSG00000036112	methionine aminopeptidase 2	1.848	0.0000	0.0000
Metrnl	ENSMUSG00000039208	meteorin, glial cell differentiation regulator-like	1.954	0.0000	0.0000
Mettl14	ENSMUSG00000028114	methyltransferase like 14	2.299	0.0000	0.0000
Mettl5	ENSMUSG00000051730	methyltransferase like 5	3.602	0.0000	0.0000
Mettl6	ENSMUSG00000021891	methyltransferase like 6	1.583	0.0000	0.0000
Mex3a	ENSMUSG00000074480	mex3 RNA binding family member A	2.265	0.0002	0.0009
Mex3c	ENSMUSG00000037253	mex3 RNA binding family member C	1.803	0.0000	0.0000
Mex3d	ENSMUSG00000048696	mex3 RNA binding family member D	2.435	0.0000	0.0000
Mfn1	ENSMUSG00000027668	mitofusin 1	2.044	0.0000	0.0000
Mfsd1	ENSMUSG00000027775	major facilitator superfamily domain containing 1	1.895	0.0000	0.0000
Mfsd12	ENSMUSG00000034854	major facilitator superfamily domain containing 12	1.505	0.0001	0.0005
Mfsd6	ENSMUSG00000041439	major facilitator superfamily domain containing 6	1.578	0.0000	0.0000
Mgat4b	ENSMUSG00000036620	mannoside acetylglucosaminyltransferase 4, isoenzyme B	2.500	0.0000	0.0000
Mhrt	ENSMUSG00000097652	myosin heavy chain associated RNA transcript	2.276	0.0000	0.0000
Mib1	ENSMUSG00000024294	MIB E3 ubiquitin protein ligase 1	2.082	0.0000	0.0000
Micos13	ENSMUSG00000049760	mitochondrial contact site and cristae organizing system subunit 13	1.579	0.0000	0.0000
Micu2	ENSMUSG00000021973	mitochondrial calcium uptake 2	1.782	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Midn	ENSMUSG00000035621	midnolin	1.806	0.0013	0.0038
Mios	ENSMUSG00000042447	meiosis regulator for oocyte development	2.686	0.0000	0.0000
Mipep	ENSMUSG00000021993	mitochondrial intermediate peptidase	1.574	0.0000	0.0000
Mipol1	ENSMUSG00000047022	mirror-image polydactyly 1	1.725	0.0000	0.0002
Mir762	ENSMUSG00000076454	microRNA 762	9.594	0.0001	0.0002
Mir8091	ENSMUSG00000098286	microRNA 8091	4.280	0.0001	0.0004
Mir8116	ENSMUSG00000099145	microRNA 8116	4.576	0.0272	0.0573
Mkrn1	ENSMUSG00000029922	makorin, ring finger protein, 1	2.666	0.0000	0.0000
Mlec	ENSMUSG00000048578	malectin	1.577	0.0000	0.0000
Mlf2	ENSMUSG00000030120	myeloid leukemia factor 2	1.634	0.0005	0.0017
Mlkl	ENSMUSG00000012519	mixed lineage kinase domain-like	1.551	0.0007	0.0022
Mllt6	ENSMUSG00000038437	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6	1.539	0.0000	0.0000
Mlycd	ENSMUSG00000074064	malonyl-CoA decarboxylase	1.914	0.0000	0.0000
Mmadhc	ENSMUSG00000026766	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	1.786	0.0000	0.0000
Mmd	ENSMUSG00000003948	monocyte to macrophage differentiation-associated	1.749	0.0006	0.0019
Mmp14	ENSMUSG00000000957	matrix metallopeptidase 14 (membrane-inserted)	1.534	0.0068	0.0170
Mnat1	ENSMUSG00000021103	menage a trois 1	1.963	0.0000	0.0000
Mnd1	ENSMUSG00000033752	meiotic nuclear divisions 1	2.179	0.0021	0.0060
Mob1b	ENSMUSG00000006262	MOB kinase activator 1B	1.549	0.0000	0.0000
Mob3c	ENSMUSG00000028709	MOB kinase activator 3C	1.523	0.0002	0.0007
Mocs2	ENSMUSG00000015536	molybdenum cofactor synthesis 2	1.645	0.0000	0.0000
Mocs3	ENSMUSG00000074576	molybdenum cofactor synthesis 3	2.193	0.0002	0.0008
Mon1b	ENSMUSG00000078908	MON1 homolog B, secretory traffciking associated	1.600	0.0000	0.0000
Morc4	ENSMUSG00000031434	microrchidia 4	1.500	0.0014	0.0043
Morf4l1	ENSMUSG00000062270	mortality factor 4 like 1	1.664	0.0000	0.0000
Morrbid	ENSMUSG00000074813	myeloid RNA regulator of BCL2L11 induced cell death	1.659	0.0003	0.0011
Mospd3	ENSMUSG00000037221	motile sperm domain containing 3	5.440	0.0000	0.0000
Mpeg1	ENSMUSG00000046805	macrophage expressed gene 1	1.639	0.0043	0.0113
Mphosph10	ENSMUSG00000030521	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	1.703	0.0000	0.0000
Mphosph6	ENSMUSG00000031843	M phase phosphoprotein 6	2.679	0.0000	0.0000
Mphosph8	ENSMUSG00000079184	M-phase phosphoprotein 8	1.881	0.0000	0.0000
Mplkip	ENSMUSG00000012429	M-phase specific PLK1 intereacting protein	2.655	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mpnd	ENSMUSG00000003199	MPN domain containing	1.814	0.0000	0.0000
Mreg	ENSMUSG00000039395	melanoregulin	2.552	0.0000	0.0000
Mrfap1	ENSMUSG00000055302	Morf4 family associated protein 1	1.996	0.0000	0.0000
Mrgbp	ENSMUSG00000027569	MRG/MORF4L binding protein	2.261	0.0000	0.0000
Mrm1	ENSMUSG00000018405	mitochondrial rRNA methyltransferase 1	1.526	0.0002	0.0006
Mrpl16	ENSMUSG00000024683	mitochondrial ribosomal protein L16	1.722	0.0000	0.0000
Mrpl18	ENSMUSG00000057388	mitochondrial ribosomal protein L18	1.505	0.0000	0.0000
Mrpl43	ENSMUSG00000025208	mitochondrial ribosomal protein L43	1.856	0.0000	0.0000
Mrpl50	ENSMUSG00000044018	mitochondrial ribosomal protein L50	1.658	0.0000	0.0000
Mrpl9	ENSMUSG00000028140	mitochondrial ribosomal protein L9	2.006	0.0000	0.0000
Mrps25	ENSMUSG00000014551	mitochondrial ribosomal protein S25	1.633	0.0000	0.0000
Mrps35	ENSMUSG00000040112	mitochondrial ribosomal protein S35	1.548	0.0000	0.0000
Mrps5	ENSMUSG00000027374	mitochondrial ribosomal protein S5	2.187	0.0000	0.0000
Mrto4	ENSMUSG00000028741	mRNA turnover 4, ribosome maturation factor	1.762	0.0001	0.0004
Msantd3	ENSMUSG00000039693	Myb/SANT-like DNA-binding domain containing 3	2.308	0.0000	0.0000
Msi1	ENSMUSG00000054256	musashi RNA-binding protein 1	1.666	0.0127	0.0295
Msi2	ENSMUSG00000069769	musashi RNA-binding protein 2	1.606	0.0000	0.0000
Msl1	ENSMUSG00000052915	male specific lethal 1	2.742	0.0000	0.0000
Msl2	ENSMUSG00000066415	MSL complex subunit 2	1.685	0.0000	0.0000
Msl3l2	ENSMUSG00000047669	MSL3 like 2	2.257	0.0061	0.0154
Msrb3	ENSMUSG00000051236	methionine sulfoxide reductase B3	1.820	0.0000	0.0000
mt-Atp6	ENSMUSG00000064357	mitochondrially encoded ATP synthase 6	162.310	0.0000	0.0000
mt-Atp8	ENSMUSG00000064356	mitochondrially encoded ATP synthase 8	587.642	0.0000	0.0000
Mtch1	ENSMUSG00000024012	mitochondrial carrier 1	2.193	0.0000	0.0000
Mtcl1	ENSMUSG00000052105	microtubule crosslinking factor 1	2.280	0.0000	0.0000
mt-Co2	ENSMUSG00000064354	mitochondrially encoded cytochrome c oxidase II	67.767	0.0000	0.0000
mt-Co3	ENSMUSG00000064358	mitochondrially encoded cytochrome c oxidase III	39.237	0.0000	0.0000
Mtdh	ENSMUSG00000022255	metadherin	1.780	0.0000	0.0000
Mterf1a	ENSMUSG00000040429	mitochondrial transcription termination factor 1a	1.875	0.0001	0.0005
Mthfd2l	ENSMUSG00000029376	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	2.980	0.0000	0.0000
Mthfs	ENSMUSG00000066442	5, 10-methenyltetrahydrofolate synthetase	2.118	0.0247	0.0528
Mtif2	ENSMUSG00000020459	mitochondrial translational initiation factor 2	1.908	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
mt-Nd2	ENSMUSG00000064345	mitochondrially encoded NADH dehydrogenase 2	1.562	0.0000	0.0000
mt-Nd4l	ENSMUSG00000065947	mitochondrially encoded NADH dehydrogenase 4L	1312.905	0.0000	0.0000
mt-Nd5	ENSMUSG00000064367	mitochondrially encoded NADH dehydrogenase 5	1.862	0.0000	0.0000
mt-Nd6	ENSMUSG00000064368	mitochondrially encoded NADH dehydrogenase 6	9.718	0.0000	0.0000
Mtres1	ENSMUSG00000019797	mitochondrial transcription rescue factor 1	2.366	0.0000	0.0000
Mtrf1l	ENSMUSG00000019774	mitochondrial translational release factor 1-like	2.351	0.0000	0.0000
mt-Te	ENSMUSG00000064369	mitochondrially encoded tRNA glutamic acid	2.991	0.0003	0.0010
mt-Tq	ENSMUSG00000064343	mitochondrially encoded tRNA glutamine	3.651	0.0000	0.0000
Mtx2	ENSMUSG00000027099	metaxin 2	1.718	0.0000	0.0000
Mtx3	ENSMUSG00000021704	metaxin 3	1.949	0.0002	0.0008
Mxra7	ENSMUSG00000020814	matrix-remodelling associated 7	4.263	0.0000	0.0000
Myadm	ENSMUSG00000068566	myeloid-associated differentiation marker	2.248	0.0000	0.0000
Mycbp	ENSMUSG00000028647	MYC binding protein	1.507	0.0000	0.0000
Mycl	ENSMUSG00000028654	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived	2.704	0.0016	0.0048
Myef2	ENSMUSG00000027201	myelin basic protein expression factor 2, repressor	2.550	0.0000	0.0000
Myef2l	ENSMUSG00000049230	myelin expression factor 2 like	8.853	0.0000	0.0000
Myh10	ENSMUSG00000020900	myosin, heavy polypeptide 10, non-muscle	1.729	0.0000	0.0000
Myh11	ENSMUSG00000018830	myosin, heavy polypeptide 11, smooth muscle	1.754	0.0000	0.0001
Myh14	ENSMUSG00000030739	myosin, heavy polypeptide 14	1.915	0.0000	0.0000
Myh6	ENSMUSG00000040752	myosin, heavy polypeptide 6, cardiac muscle, alpha	1.772	0.0000	0.0000
Myh7b	ENSMUSG00000074652	myosin, heavy chain 7B, cardiac muscle, beta	1.599	0.0095	0.0230
Myh9	ENSMUSG00000022443	myosin, heavy polypeptide 9, non-muscle	2.075	0.0000	0.0000
Myl12b	ENSMUSG00000034868	myosin, light chain 12B, regulatory	2.745	0.0000	0.0000
Mylk	ENSMUSG00000022836	myosin, light polypeptide kinase	1.773	0.0000	0.0000
Myo18b	ENSMUSG00000072720	myosin XVIIIb	1.567	0.0000	0.0000
Mypop	ENSMUSG00000048481	Myb-related transcription factor, partner of profilin	1.798	0.0095	0.0229
Myzap	ENSMUSG00000041361	myocardial zonula adherens protein	1.554	0.0001	0.0003
N4bp2os	ENSMUSG00000106978	NEDD4 binding protein 2, opposite strand	8.537	0.0000	0.0000
Naa15	ENSMUSG00000063273	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	1.629	0.0000	0.0000
Naa30	ENSMUSG00000036282	N(alpha)-acetyltransferase 30, NatC catalytic subunit	3.124	0.0000	0.0000
Naa50	ENSMUSG00000022698	N(alpha)-acetyltransferase 50, NatE catalytic subunit	2.713	0.0000	0.0000
Nab2	ENSMUSG00000025402	Ngfi-A binding protein 2	1.637	0.0003	0.0012

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nacc2	ENSMUSG00000026932	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	1.511	0.0010	0.0030
Nadk2	ENSMUSG00000022253	NAD kinase 2, mitochondrial	1.589	0.0002	0.0008
Naf1	ENSMUSG00000014907	nuclear assembly factor 1 ribonucleoprotein	3.636	0.0000	0.0000
Naif1	ENSMUSG00000039164	nuclear apoptosis inducing factor 1	1.964	0.0000	0.0000
Nanos3	ENSMUSG00000056155	nanos C2HC-type zinc finger 3	2.737	0.0072	0.0180
Nap1l4	ENSMUSG00000059119	nucleosome assembly protein 1-like 4	1.504	0.0000	0.0000
Nasp	ENSMUSG00000028693	nuclear autoantigenic sperm protein (histone-binding)	3.303	0.0000	0.0000
Nat10	ENSMUSG00000027185	N-acetyltransferase 10	1.571	0.0000	0.0000
Nat8l	ENSMUSG00000048142	N-acetyltransferase 8-like	1.931	0.0023	0.0065
Nbl1	ENSMUSG00000041120	NBL1, DAN family BMP antagonist	1.557	0.0271	0.0572
Ncam2	ENSMUSG00000022762	neural cell adhesion molecule 2	18.665	0.0109	0.0259
Ncbp1	ENSMUSG00000028330	nuclear cap binding protein subunit 1	1.811	0.0000	0.0000
Ncbp3	ENSMUSG00000020783	nuclear cap binding subunit 3	1.735	0.0000	0.0000
Nck1	ENSMUSG00000032475	non-catalytic region of tyrosine kinase adaptor protein 1	1.574	0.0000	0.0000
Nck2	ENSMUSG00000066877	non-catalytic region of tyrosine kinase adaptor protein 2	1.881	0.0000	0.0000
Ncl	ENSMUSG00000026234	nucleolin	2.915	0.0000	0.0000
Ncoa4	ENSMUSG00000056234	nuclear receptor coactivator 4	1.577	0.0000	0.0000
Ncoa5	ENSMUSG00000039804	nuclear receptor coactivator 5	1.843	0.0000	0.0000
Ndc80	ENSMUSG00000024056	NDC80 kinetochore complex component	2.040	0.0300	0.0625
Ndfip2	ENSMUSG00000053253	Nedd4 family interacting protein 2	2.799	0.0000	0.0000
Ndufa12	ENSMUSG00000020022	NADH:ubiquinone oxidoreductase subunit A12	1.519	0.0000	0.0000
Ndufa5	ENSMUSG00000023089	NADH:ubiquinone oxidoreductase subunit A5	3.161	0.0000	0.0000
Ndufa9	ENSMUSG00000000399	NADH:ubiquinone oxidoreductase subunit A9	1.908	0.0000	0.0000
Ndufaf6	ENSMUSG00000050323	NADH:ubiquinone oxidoreductase complex assembly factor 6	3.047	0.0000	0.0000
Ndufb3	ENSMUSG00000026032	NADH:ubiquinone oxidoreductase subunit B3	1.867	0.0000	0.0000
Ndufb9	ENSMUSG00000022354	NADH:ubiquinone oxidoreductase subunit B9	1.686	0.0000	0.0000
Ndufs6b	ENSMUSG00000083820	NADH:ubiquinone oxidoreductase subunit S6B	4.034	0.0000	0.0001
Nectin1	ENSMUSG00000032012	nectin cell adhesion molecule 1	1.528	0.0253	0.0538
Nedd8	ENSMUSG00000010376	neural precursor cell expressed, developmentally down-regulated gene 8	1.769	0.0000	0.0000
Nek2	ENSMUSG00000026622	NIMA (never in mitosis gene a)-related expressed kinase 2	1.859	0.0154	0.0349
Nek7	ENSMUSG00000026393	NIMA (never in mitosis gene a)-related expressed kinase 7	2.034	0.0000	0.0000
Nemf	ENSMUSG00000020982	nuclear export mediator factor	2.050	0.0000	0.0000

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Nenf	ENSMUSG00000037499	neuron derived neurotrophic factor	1.510	0.0372	0.0751
Nes	ENSMUSG00000004891	nestin	2.168	0.0000	0.0001
Net1	ENSMUSG00000021215	neuroepithelial cell transforming gene 1	1.956	0.0000	0.0000
Nexn	ENSMUSG00000039103	nexilin	3.192	0.0000	0.0000
Nfatc2	ENSMUSG00000027544	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2	1.934	0.0017	0.0050
Nfe2l1	ENSMUSG00000038615	nuclear factor, erythroid derived 2,-like 1	1.728	0.0000	0.0000
Nfia	ENSMUSG00000028565	nuclear factor I/A	1.589	0.0000	0.0000
Nfix	ENSMUSG00000001911	nuclear factor I/X	2.099	0.0000	0.0000
Nfkbiz	ENSMUSG00000035356	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	1.506	0.0192	0.0425
Nfxl1	ENSMUSG00000072889	nuclear transcription factor, X-box binding-like 1	2.180	0.0000	0.0000
Nfyb	ENSMUSG00000020248	nuclear transcription factor-Y beta	3.118	0.0000	0.0000
Nipa2	ENSMUSG00000030452	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	1.586	0.0000	0.0001
Nkapd1	ENSMUSG00000059820	NKAP domain containing 1	1.910	0.0000	0.0000
Nkd1	ENSMUSG00000031661	naked cuticle 1	2.384	0.0078	0.0192
Nkiras1	ENSMUSG00000021772	NFKB inhibitor interacting Ras-like protein 1	2.214	0.0000	0.0000
Nkrf	ENSMUSG00000044149	NF-kappaB repressing factor	1.572	0.0003	0.0012
Nlgn2	ENSMUSG00000051790	neuroligin 2	1.522	0.0006	0.0018
Nlrp5-ps	ENSMUSG00000041596	NLR family, pyrin domain containing 5, pseudogene	2.499	0.0263	0.0556
Noc2l	ENSMUSG00000095567	NOC2 like nucleolar associated transcriptional repressor	1.924	0.0000	0.0000
Noc3l	ENSMUSG00000024999	NOC3 like DNA replication regulator	1.681	0.0000	0.0000
Nog	ENSMUSG00000048616	noggin	5.558	0.0019	0.0054
Nol10	ENSMUSG00000061458	nucleolar protein 10	1.590	0.0000	0.0000
Nol7	ENSMUSG00000063200	nucleolar protein 7	3.346	0.0000	0.0000
Nol8	ENSMUSG00000021392	nucleolar protein 8	1.559	0.0000	0.0000
Nom1	ENSMUSG00000001569	nucleolar protein with MIF4G domain 1	1.560	0.0000	0.0000
Nono	ENSMUSG00000031311	non-POU-domain-containing, octamer binding protein	2.364	0.0000	0.0000
Nop14	ENSMUSG00000036693	NOP14 nucleolar protein	1.773	0.0000	0.0000
Nop58	ENSMUSG00000026020	NOP58 ribonucleoprotein	2.006	0.0000	0.0000
Nop9	ENSMUSG00000019297	NOP9 nucleolar protein	1.912	0.0000	0.0000
Norad	ENSMUSG00000102869	non-coding RNA activated by DNA damage	2.515	0.0000	0.0000
Nos1ap	ENSMUSG00000038473	nitric oxide synthase 1 (neuronal) adaptor protein	1.878	0.0043	0.0112
Notumos	ENSMUSG00000053613	notum palmitoleoyl-protein carboxylesterase, opposite strand	4.916	0.0019	0.0055

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nova2	ENSMUSG00000030411	NOVA alternative splicing regulator 2	2.290	0.0000	0.0000
Npepps	ENSMUSG00000001441	aminopeptidase puromycin sensitive	1.570	0.0000	0.0000
Nphp1	ENSMUSG00000027378	nephronophthisis 1 (juvenile) homolog (human)	1.796	0.0000	0.0000
Npm1	ENSMUSG00000057113	nucleophosmin 1	3.260	0.0000	0.0000
Nr1d2	ENSMUSG00000021775	nuclear receptor subfamily 1, group D, member 2	1.558	0.0000	0.0000
Nr2f1	ENSMUSG00000069171	nuclear receptor subfamily 2, group F, member 1	3.391	0.0000	0.0000
Nr2f2	ENSMUSG00000030551	nuclear receptor subfamily 2, group F, member 2	2.604	0.0000	0.0000
Nr2f6	ENSMUSG00000002393	nuclear receptor subfamily 2, group F, member 6	3.935	0.0000	0.0000
Nr4a2	ENSMUSG00000026826	nuclear receptor subfamily 4, group A, member 2	2.251	0.0020	0.0058
Nrarp	ENSMUSG00000078202	Notch-regulated ankyrin repeat protein	2.231	0.0000	0.0000
Nrd1	ENSMUSG00000053510	nardilysin, N-arginine dibasic convertase, NRD convertase 1	2.125	0.0000	0.0000
Nrgn	ENSMUSG00000053310	neurogranin	9.877	0.0000	0.0000
Nrk	ENSMUSG00000052854	Nik related kinase	1.835	0.0097	0.0233
Nrp2	ENSMUSG00000025969	neuropilin 2	1.610	0.0005	0.0017
Nrtn	ENSMUSG00000039481	neurturin	10.540	0.0000	0.0000
Nrxn2	ENSMUSG00000033768	neurexin II	2.645	0.0001	0.0004
Nsa2	ENSMUSG00000060739	NSA2 ribosome biogenesis homolog	3.467	0.0000	0.0000
Nsa2-ps1	ENSMUSG00000118353	NSA2 ribosome biogenesis homolog, pseudogene 1	3.611	0.0067	0.0168
Nsmce1	ENSMUSG00000030750	NSE1 homolog, SMC5-SMC6 complex component	1.575	0.0000	0.0000
Nsmce3	ENSMUSG00000070520	NSE3 homolog, SMC5-SMC6 complex component	2.401	0.0000	0.0000
Nsmce4a	ENSMUSG00000040331	NSE4 homolog A, SMC5-SMC6 complex component	2.197	0.0000	0.0000
Nsrp1	ENSMUSG00000037958	nuclear speckle regulatory protein 1	3.970	0.0000	0.0000
Nsun2	ENSMUSG00000021595	NOL1/NOP2/Sun domain family member 2	1.625	0.0000	0.0000
Nt5c1a	ENSMUSG00000054958	5'-nucleotidase, cytosolic IA	1.740	0.0151	0.0343
Ntn4	ENSMUSG00000020019	netrin 4	1.962	0.0000	0.0000
Ntng2	ENSMUSG00000035513	netrin G2	1.696	0.0032	0.0087
Nucb2	ENSMUSG00000030659	nucleobindin 2	2.018	0.0000	0.0000
Nucks1	ENSMUSG00000026434	nuclear casein kinase and cyclin-dependent kinase substrate 1	2.168	0.0000	0.0000
Nudc	ENSMUSG00000028851	nudC nuclear distribution protein	3.147	0.0000	0.0000
Nudc-ps1	ENSMUSG00000110331	nuclear distribution gene C homolog (Aspergillus), pseudogene 1	1.705	0.0000	0.0001
Nudt3	ENSMUSG00000024213	nudix (nucleotide diphosphate linked moiety X)-type motif 3	2.887	0.0000	0.0000
Nudt4	ENSMUSG00000020029	nudix (nucleoside diphosphate linked moiety X)-type motif 4	3.308	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nudt6	ENSMUSG00000050174	nudix (nucleoside diphosphate linked moiety X)-type motif 6	3.386	0.0000	0.0000
Nudt9	ENSMUSG00000029310	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2.127	0.0000	0.0000
Nuf2	ENSMUSG00000026683	NUF2, NDC80 kinetochore complex component	2.569	0.0234	0.0503
Nup107	ENSMUSG00000052798	nucleoporin 107	1.546	0.0000	0.0000
Nup50	ENSMUSG00000016619	nucleoporin 50	1.543	0.0000	0.0000
Nus1	ENSMUSG00000023068	NUS1 dehydrodolichyl diphosphate synthase subunit	1.600	0.0000	0.0000
Nutf2-ps1	ENSMUSG00000071497	nuclear transport factor 2, pseudogene 1	6.719	0.0000	0.0000
Nxn	ENSMUSG00000020844	nucleoredoxin	1.586	0.0014	0.0041
Oaf	ENSMUSG00000032014	out at first homolog	1.605	0.0179	0.0399
Obi1	ENSMUSG00000022120	ORC ubiquitin ligase 1	1.743	0.0000	0.0000
Ociad2	ENSMUSG00000029153	OCIA domain containing 2	1.835	0.0000	0.0000
Odad4	ENSMUSG00000006784	outer dynein arm complex subunit 4	23.190	0.0000	0.0000
Odc1	ENSMUSG00000011179	ornithine decarboxylase, structural 1	1.765	0.0000	0.0001
Oga	ENSMUSG00000025220	O-GlcNAcase	1.545	0.0000	0.0001
Ogfrl1	ENSMUSG00000026158	opioid growth factor receptor-like 1	2.680	0.0000	0.0000
Olfm1	ENSMUSG00000026833	olfactomedin 1	2.350	0.0000	0.0000
Orai1	ENSMUSG00000049686	ORAI calcium release-activated calcium modulator 1	3.008	0.0000	0.0000
Osbpl10	ENSMUSG00000040875	oxysterol binding protein-like 10	1.663	0.0007	0.0022
Osbpl9	ENSMUSG00000028559	oxysterol binding protein-like 9	1.659	0.0000	0.0000
Otogl	ENSMUSG00000091455	otogelin-like	17.238	0.0075	0.0186
Otud1	ENSMUSG00000043415	OTU domain containing 1	3.134	0.0000	0.0000
Otud3	ENSMUSG00000041161	OTU domain containing 3	2.111	0.0000	0.0000
Otud4	ENSMUSG00000036990	OTU domain containing 4	1.746	0.0000	0.0000
Otud6b	ENSMUSG00000040550	OTU domain containing 6B	2.047	0.0000	0.0000
Otud7b	ENSMUSG00000038495	OTU domain containing 7B	1.976	0.0000	0.0000
Otulin	ENSMUSG00000046034	OTU deubiquitinase with linear linkage specificity	2.565	0.0000	0.0000
Otulinl	ENSMUSG00000056069	OTU deubiquitinase with linear linkage specificity like	2.025	0.0001	0.0002
Oxr1	ENSMUSG00000022307	oxidation resistance 1	1.722	0.0000	0.0000
Oxsr1	ENSMUSG00000036737	oxidative-stress responsive 1	1.811	0.0000	0.0000
P3h3	ENSMUSG00000023191	prolyl 3-hydroxylase 3	1.673	0.0067	0.0168
P4ha3	ENSMUSG00000051048	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III	3.218	0.0434	0.0856

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pabpc4	ENSMUSG00000011257	poly(A) binding protein, cytoplasmic 4	1.615	0.0000	0.0000
Pabpn1	ENSMUSG00000022194	poly(A) binding protein, nuclear 1	12.246	0.0000	0.0000
Pacsin3	ENSMUSG00000027257	protein kinase C and casein kinase substrate in neurons 3	1.713	0.0000	0.0000
Paf1	ENSMUSG00000003437	Paf1, RNA polymerase II complex component	2.592	0.0000	0.0000
Pafah1b2	ENSMUSG00000003131	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2	1.718	0.0000	0.0000
Paip1	ENSMUSG00000025451	polyadenylate binding protein-interacting protein 1	2.708	0.0000	0.0000
Palm3	ENSMUSG00000047986	paralemmin 3	3.332	0.0007	0.0023
Pals2	ENSMUSG00000038388	protein associated with LIN7 2, MAGUK family member	1.848	0.0000	0.0000
Pan3	ENSMUSG00000029647	PAN3 poly(A) specific ribonuclease subunit	1.739	0.0000	0.0000
Pank1	ENSMUSG00000033610	pantothenate kinase 1	1.709	0.0000	0.0000
Pank2	ENSMUSG00000037514	pantothenate kinase 2	2.451	0.0000	0.0000
Paqr3	ENSMUSG00000055725	progestin and adipoQ receptor family member III	1.875	0.0001	0.0003
Paqr4	ENSMUSG00000023909	progestin and adipoQ receptor family member IV	2.292	0.0000	0.0000
Paqr9	ENSMUSG00000064225	progestin and adipoQ receptor family member IX	1.887	0.0000	0.0000
Pard3	ENSMUSG00000025812	par-3 family cell polarity regulator	1.939	0.0000	0.0000
Pard6b	ENSMUSG00000044641	par-6 family cell polarity regulator beta	2.305	0.0000	0.0000
Parg	ENSMUSG00000021911	poly (ADP-ribose) glycohydrolase	1.600	0.0000	0.0000
Parn	ENSMUSG00000022685	poly(A)-specific ribonuclease (deadenylation nuclease)	1.689	0.0000	0.0000
Particl	ENSMUSG00000108591	promoter of Mat2a antisense radiation induced circulating long non-coding RNA	3.070	0.0000	0.0000
Patl1	ENSMUSG00000046139	protein associated with topoisomerase II homolog 1 (yeast)	1.532	0.0001	0.0002
Pawr	ENSMUSG00000035873	PRKC, apoptosis, WT1, regulator	4.498	0.0000	0.0000
Paxbp1	ENSMUSG00000022974	PAX3 and PAX7 binding protein 1	1.739	0.0000	0.0000
Pbdc1	ENSMUSG00000031226	polysaccharide biosynthesis domain containing 1	2.534	0.0000	0.0000
Pbx2	ENSMUSG00000034673	pre B cell leukemia homeobox 2	1.875	0.0000	0.0000
Pcbd2	ENSMUSG00000021496	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	6.811	0.0000	0.0000
Pcdhb16	ENSMUSG00000047910	protocadherin beta 16	1.772	0.0017	0.0051
Pcdhb20	ENSMUSG00000046191	protocadherin beta 20	2.060	0.0000	0.0000
Pcdhb22	ENSMUSG00000073591	protocadherin beta 22	1.521	0.0144	0.0330
Pcf11	ENSMUSG00000041328	PCF11 cleavage and polyadenylation factor subunit	1.735	0.0000	0.0000
Pcgf3	ENSMUSG00000033623	polycomb group ring finger 3	2.076	0.0000	0.0000
Pcgf6	ENSMUSG00000025050	polycomb group ring finger 6	1.857	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pcm1	ENSMUSG00000031592	pericentriolar material 1	1.685	0.0000	0.0000
Pcmt1	ENSMUSG00000019795	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.543	0.0000	0.0000
Pcmtd2	ENSMUSG00000027589	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	1.608	0.0000	0.0000
Pcna	ENSMUSG00000027342	proliferating cell nuclear antigen	1.818	0.0000	0.0000
Pcnp	ENSMUSG00000071533	PEST proteolytic signal containing nuclear protein	1.513	0.0000	0.0000
Pcyox1l	ENSMUSG00000024579	prenylcysteine oxidase 1 like	1.657	0.0266	0.0563
Pcyt1b	ENSMUSG00000035246	phosphate cytidylyltransferase 1, choline, beta isoform	2.438	0.0320	0.0661
Pdap1	ENSMUSG00000029623	PDGFA associated protein 1	2.608	0.0000	0.0000
Pdcd4	ENSMUSG00000024975	programmed cell death 4	2.551	0.0000	0.0000
Pdcd5	ENSMUSG00000030417	programmed cell death 5	2.973	0.0000	0.0000
Pdcd5-ps	ENSMUSG00000102824	programmed cell death 5, pseudogene	1.713	0.0017	0.0050
Pdcd7	ENSMUSG00000041837	programmed cell death 7	5.032	0.0000	0.0000
Pdcl	ENSMUSG00000009030	phosducin-like	1.708	0.0000	0.0000
Pdcl3	ENSMUSG00000026078	phosducin-like 3	2.777	0.0000	0.0000
Pde3b	ENSMUSG00000030671	phosphodiesterase 3B, cGMP-inhibited	2.169	0.0004	0.0012
Pde6d	ENSMUSG00000026239	phosphodiesterase 6D, cGMP-specific, rod, delta	2.011	0.0000	0.0000
Pdgfa	ENSMUSG00000025856	platelet derived growth factor, alpha	1.507	0.0004	0.0012
Pdgfb	ENSMUSG00000000489	platelet derived growth factor, B polypeptide	1.828	0.0000	0.0000
Pdha1	ENSMUSG00000031299	pyruvate dehydrogenase E1 alpha 1	1.531	0.0000	0.0000
Pdhb	ENSMUSG00000021748	pyruvate dehydrogenase (lipoamide) beta	2.214	0.0000	0.0000
Pdia6	ENSMUSG00000020571	protein disulfide isomerase associated 6	1.747	0.0000	0.0000
Pdk1	ENSMUSG00000006494	pyruvate dehydrogenase kinase, isoenzyme 1	1.521	0.0000	0.0000
Pdk4	ENSMUSG00000019577	pyruvate dehydrogenase kinase, isoenzyme 4	3.703	0.0001	0.0003
Pdzd11	ENSMUSG00000015668	PDZ domain containing 11	1.530	0.0000	0.0000
Pdzd4	ENSMUSG00000002006	PDZ domain containing 4	1.811	0.0001	0.0004
Pdzd9	ENSMUSG00000030887	PDZ domain containing 9	8.897	0.0043	0.0114
Pdzrn4	ENSMUSG00000036218	PDZ domain containing RING finger 4	2.283	0.0087	0.0213
Peg12	ENSMUSG00000070526	paternally expressed 12	1.787	0.0176	0.0392
Peg3	ENSMUSG00000002265	paternally expressed 3	1.842	0.0002	0.0008
Peli1	ENSMUSG00000020134	pellino 1	1.746	0.0005	0.0015
Pet100	ENSMUSG00000087687	PET100 homolog	2.148	0.0000	0.0000
Pex11a	ENSMUSG00000030545	peroxisomal biogenesis factor 11 alpha	1.509	0.0000	0.0000

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Pex13	ENSMUSG00000020283	peroxisomal biogenesis factor 13	1.757	0.0003	0.0009
Pfdn2	ENSMUSG00000006412	prefoldin 2	2.919	0.0000	0.0000
Pfdn4	ENSMUSG00000052033	prefoldin 4	1.548	0.0000	0.0001
Pfdn6	ENSMUSG00000024309	prefoldin subunit 6	1.854	0.0000	0.0000
Pfn4	ENSMUSG00000020639	profilin family, member 4	1.535	0.0224	0.0485
Pgrmc2	ENSMUSG00000049940	progesterone receptor membrane component 2	2.410	0.0000	0.0000
Phactr3	ENSMUSG00000027525	phosphatase and actin regulator 3	3.466	0.0000	0.0000
Phc2	ENSMUSG00000028796	polyhomeotic 2	1.568	0.0002	0.0008
Phf1	ENSMUSG00000024193	PHD finger protein 1	1.902	0.0000	0.0000
Phf10	ENSMUSG00000023883	PHD finger protein 10	1.783	0.0000	0.0000
Phf12	ENSMUSG00000037791	PHD finger protein 12	1.513	0.0009	0.0028
Phf13	ENSMUSG00000047777	PHD finger protein 13	2.270	0.0000	0.0000
Phf14	ENSMUSG00000029629	PHD finger protein 14	1.605	0.0000	0.0000
Phf8	ENSMUSG00000041229	PHD finger protein 8	1.685	0.0000	0.0000
Phlda3	ENSMUSG00000041801	pleckstrin homology like domain, family A, member 3	1.699	0.0149	0.0339
Phldb3	ENSMUSG00000074277	pleckstrin homology like domain, family B, member 3	2.701	0.0097	0.0234
Phospho1	ENSMUSG00000050860	phosphatase, orphan 1	12.572	0.0000	0.0000
Phox2a	ENSMUSG00000007946	paired-like homeobox 2a	3.301	0.0004	0.0012
Phtf1	ENSMUSG00000058388	putative homeodomain transcription factor 1	2.503	0.0000	0.0000
Pi15	ENSMUSG00000067780	peptidase inhibitor 15	1.574	0.0000	0.0001
Pi4k2b	ENSMUSG00000029186	phosphatidylinositol 4-kinase type 2 beta	1.951	0.0011	0.0034
Pick1	ENSMUSG00000068206	protein interacting with C kinase 1	1.598	0.0004	0.0013
Pikfyve	ENSMUSG00000025949	phosphoinositide kinase, FYVE type zinc finger containing	1.626	0.0000	0.0000
Pilra	ENSMUSG00000046245	paired immunoglobin-like type 2 receptor alpha	2.440	0.0016	0.0048
Pin4	ENSMUSG00000079480	peptidyl-prolyl cis/trans isomerase, NIMA-interacting, 4 (parvulin)	4.648	0.0000	0.0000
Pip4k2b	ENSMUSG00000018547	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	1.634	0.0000	0.0000
Pip4p1	ENSMUSG00000035953	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 1	1.951	0.0000	0.0001
Pitpna	ENSMUSG00000017781	phosphatidylinositol transfer protein, alpha	2.662	0.0000	0.0000
Pitpnb	ENSMUSG00000050017	phosphatidylinositol transfer protein, beta	1.847	0.0000	0.0000
Pitx3	ENSMUSG00000025229	paired-like homeodomain transcription factor 3	5.374	0.0000	0.0001
Pja2	ENSMUSG00000024083	praja ring finger ubiquitin ligase 2	1.519	0.0000	0.0000
Pkd2	ENSMUSG00000034462	polycystin 2, transient receptor potential cation channel	1.971	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pkdcc	ENSMUSG00000024247	protein kinase domain containing, cytoplasmic	1.791	0.0001	0.0002
Pkib	ENSMUSG00000019876	protein kinase inhibitor beta, cAMP dependent, testis specific	1.801	0.0182	0.0406
Pkm	ENSMUSG00000032294	pyruvate kinase, muscle	2.658	0.0000	0.0000
Pkp2	ENSMUSG00000041957	plakophilin 2	1.634	0.0003	0.0010
Pla2g12a	ENSMUSG00000027999	phospholipase A2, group XIIA	2.686	0.0000	0.0000
Plaa	ENSMUSG00000028577	phospholipase A2, activating protein	1.583	0.0000	0.0000
Plcl1	ENSMUSG00000038349	phospholipase C-like 1	1.544	0.0004	0.0014
Plekha1	ENSMUSG00000040268	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	2.258	0.0000	0.0000
Plekha3	ENSMUSG00000002733	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	2.026	0.0000	0.0000
Plekha8	ENSMUSG00000005225	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	1.568	0.0000	0.0000
Plekhd1	ENSMUSG00000066438	pleckstrin homology domain containing, family D (with coiled-coil domains) member 1	4.113	0.0149	0.0340
Plekhf2	ENSMUSG00000049969	pleckstrin homology domain containing, family F (with FYVE domain) member 2	1.860	0.0000	0.0001
Plekhh3	ENSMUSG00000035172	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	2.052	0.0001	0.0005
Plekhj1	ENSMUSG00000035278	pleckstrin homology domain containing, family J member 1	2.498	0.0000	0.0000
Plin1	ENSMUSG00000030546	perilipin 1	3.828	0.0062	0.0156
Plk4	ENSMUSG00000025758	polo like kinase 4	1.572	0.0086	0.0211
Plod2	ENSMUSG00000032374	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1.813	0.0000	0.0000
Plpp6	ENSMUSG00000040105	phospholipid phosphatase 6	1.754	0.0000	0.0000
Plppr2	ENSMUSG00000040563	phospholipid phosphatase related 2	1.924	0.0003	0.0010
Pm20d2	ENSMUSG00000054659	peptidase M20 domain containing 2	2.281	0.0000	0.0001
Pnisr	ENSMUSG00000028248	PNN interacting serine/arginine-rich	2.413	0.0000	0.0000
Pnma8b	ENSMUSG00000070802	PNMA family member 8B	1.509	0.0007	0.0021
Pnn	ENSMUSG00000020994	pinin	4.660	0.0000	0.0000
Pnrc1	ENSMUSG00000040128	proline-rich nuclear receptor coactivator 1	2.517	0.0000	0.0000
Pole4	ENSMUSG00000030042	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.865	0.0031	0.0084
Polr1c	ENSMUSG00000067148	polymerase (RNA) I polypeptide C	1.750	0.0000	0.0000
Polr1has	ENSMUSG00000036214	RNA polymerase I subunit H, antisense	1.728	0.0000	0.0000
Polr2m	ENSMUSG00000032199	polymerase (RNA) II (DNA directed) polypeptide M	1.830	0.0000	0.0000
Polr3d	ENSMUSG00000000776	polymerase (RNA) III (DNA directed) polypeptide D	1.517	0.0000	0.0001
Polr3g	ENSMUSG00000035834	polymerase (RNA) III (DNA directed) polypeptide G	2.318	0.0000	0.0000
Polr3gl	ENSMUSG00000028104	polymerase (RNA) III (DNA directed) polypeptide G like	1.992	0.0000	0.0000
Pou3f1	ENSMUSG00000090125	POU domain, class 3, transcription factor 1	5.364	0.0000	0.0001

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ppargc1a	ENSMUSG00000029167	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	1.589	0.0000	0.0001
Ppat	ENSMUSG00000029246	phosphoribosyl pyrophosphate amidotransferase	1.690	0.0000	0.0000
Ppfibp1	ENSMUSG00000016487	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.169	0.0000	0.0000
Ppid	ENSMUSG00000027804	peptidylprolyl isomerase D (cyclophilin D)	2.133	0.0000	0.0000
Ppig	ENSMUSG00000042133	peptidyl-prolyl isomerase G (cyclophilin G)	3.375	0.0000	0.0000
Ppil3	ENSMUSG00000026035	peptidylprolyl isomerase (cyclophilin)-like 3	2.115	0.0000	0.0000
Ppil4	ENSMUSG00000015757	peptidylprolyl isomerase (cyclophilin)-like 4	2.108	0.0000	0.0000
Ppm1a	ENSMUSG00000021096	protein phosphatase 1A, magnesium dependent, alpha isoform	2.450	0.0000	0.0000
Ppm1b	ENSMUSG00000061130	protein phosphatase 1B, magnesium dependent, beta isoform	3.075	0.0000	0.0000
Ppm1e	ENSMUSG00000046442	protein phosphatase 1E (PP2C domain containing)	1.509	0.0135	0.0312
Ppm1g	ENSMUSG00000029147	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	2.121	0.0000	0.0000
Ppme1	ENSMUSG00000030718	protein phosphatase methylesterase 1	1.527	0.0000	0.0000
Ppp1cb	ENSMUSG00000014956	protein phosphatase 1 catalytic subunit beta	2.016	0.0000	0.0000
Ppp1cc	ENSMUSG00000004455	protein phosphatase 1 catalytic subunit gamma	1.676	0.0000	0.0000
Ppp1ccb	ENSMUSG00000100153	protein phosphatase 1 catalytic subunit gamma B	1.636	0.0491	0.0951
Ppp1r11	ENSMUSG00000036398	protein phosphatase 1, regulatory inhibitor subunit 11	2.191	0.0000	0.0000
Ppp1r12a	ENSMUSG00000019907	protein phosphatase 1, regulatory subunit 12A	1.976	0.0000	0.0000
Ppp1r14a	ENSMUSG00000037166	protein phosphatase 1, regulatory inhibitor subunit 14A	3.535	0.0000	0.0000
Ppp1r14b	ENSMUSG00000056612	protein phosphatase 1, regulatory inhibitor subunit 14B	3.916	0.0000	0.0000
Ppp1r14c	ENSMUSG00000040653	protein phosphatase 1, regulatory inhibitor subunit 14C	1.512	0.0114	0.0268
Ppp1r18os	ENSMUSG00000087443	protein phosphatase 1, regulatory subunit 18, opposite strand	3.009	0.0372	0.0750
Ppp1r1a	ENSMUSG00000022490	protein phosphatase 1, regulatory inhibitor subunit 1A	2.276	0.0002	0.0007
Ppp1r1b	ENSMUSG00000061718	protein phosphatase 1, regulatory inhibitor subunit 1B	2.202	0.0036	0.0096
Ppp1r2-ps4	ENSMUSG00000059237	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 4	3.337	0.0018	0.0052
Ppp1r35	ENSMUSG00000029725	protein phosphatase 1, regulatory subunit 35	4.189	0.0000	0.0000
Ppp1r3b	ENSMUSG00000046794	protein phosphatase 1, regulatory subunit 3B	1.885	0.0004	0.0014
Ppp1r3e	ENSMUSG00000072494	protein phosphatase 1, regulatory subunit 3E	2.903	0.0038	0.0101
Ppp1r3f	ENSMUSG00000039556	protein phosphatase 1, regulatory subunit 3F	4.485	0.0000	0.0000
Ppp1r9b	ENSMUSG00000038976	protein phosphatase 1, regulatory subunit 9B	3.857	0.0000	0.0000
Ppp2ca	ENSMUSG00000020349	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	1.820	0.0000	0.0000
Ppp2r5a	ENSMUSG00000026626	protein phosphatase 2, regulatory subunit B', alpha	2.227	0.0000	0.0000
Ppp2r5e	ENSMUSG00000021051	protein phosphatase 2, regulatory subunit B', epsilon	1.586	0.0004	0.0012

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ppp3ca	ENSMUSG00000028161	protein phosphatase 3, catalytic subunit, alpha isoform	1.517	0.0000	0.0000
Ppp3cc	ENSMUSG00000022092	protein phosphatase 3, catalytic subunit, gamma isoform	2.039	0.0000	0.0000
Ppp4c	ENSMUSG00000030697	protein phosphatase 4, catalytic subunit	2.443	0.0000	0.0000
Ppp4r1l-ps	ENSMUSG00000055897	protein phosphatase 4, regulatory subunit 1-like, pseudogene	1.968	0.0000	0.0000
Ppp4r2	ENSMUSG00000052144	protein phosphatase 4, regulatory subunit 2	1.758	0.0000	0.0000
Ppp4r3a	ENSMUSG00000041846	protein phosphatase 4 regulatory subunit 3A	1.979	0.0000	0.0000
Ppwd1	ENSMUSG00000021713	peptidylprolyl isomerase domain and WD repeat containing 1	1.702	0.0000	0.0000
Prc1	ENSMUSG00000038943	protein regulator of cytokinesis 1	1.732	0.0269	0.0568
Prcd	ENSMUSG00000075410	photoreceptor disc component	1.874	0.0092	0.0223
Prdm10	ENSMUSG00000042496	PR domain containing 10	1.524	0.0000	0.0000
Prdm8	ENSMUSG00000035456	PR domain containing 8	4.430	0.0004	0.0012
Prkag2	ENSMUSG00000028944	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.808	0.0000	0.0000
Prkar1a	ENSMUSG00000020612	protein kinase, cAMP dependent regulatory, type I, alpha	1.650	0.0000	0.0000
Prkar2b	ENSMUSG00000002997	protein kinase, cAMP dependent regulatory, type II beta	1.681	0.0141	0.0323
Prkci	ENSMUSG00000037643	protein kinase C, iota	2.052	0.0000	0.0000
Prkg1	ENSMUSG00000052920	protein kinase, cGMP-dependent, type I	1.787	0.0000	0.0000
Prkrip1	ENSMUSG00000039737	Prkr interacting protein 1 (IL11 inducible)	1.550	0.0000	0.0000
Prmt9	ENSMUSG00000037134	protein arginine methyltransferase 9	2.296	0.0000	0.0000
Procr	ENSMUSG00000027611	protein C receptor, endothelial	1.903	0.0007	0.0023
Prpf18	ENSMUSG00000039449	pre-mRNA processing factor 18	1.578	0.0000	0.0000
Prpf3	ENSMUSG00000015748	pre-mRNA processing factor 3	2.193	0.0000	0.0000
Prpf31	ENSMUSG00000008373	pre-mRNA processing factor 31	2.594	0.0000	0.0000
Prpf38a	ENSMUSG00000063800	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	1.564	0.0000	0.0000
Prpf38b	ENSMUSG00000027881	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	3.004	0.0000	0.0000
Prpf40a	ENSMUSG00000061136	pre-mRNA processing factor 40A	1.617	0.0000	0.0000
Prpf4b	ENSMUSG00000021413	pre-mRNA processing factor 4B	1.514	0.0001	0.0003
Prph	ENSMUSG00000023484	peripherin	3.652	0.0207	0.0454
Prr18	ENSMUSG00000055945	proline rich 18	2.895	0.0149	0.0340
Prr33	ENSMUSG00000043795	proline rich 33	1.885	0.0000	0.0001
Prr5	ENSMUSG00000036106	proline rich 5 (renal)	2.207	0.0000	0.0000
Prr7	ENSMUSG00000034686	proline rich 7 (synaptic)	6.984	0.0000	0.0000
Prrg3	ENSMUSG00000033361	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	1.565	0.0006	0.0020

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Prrg4	ENSMUSG00000027171	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	1.789	0.0175	0.0392
Prrx2	ENSMUSG00000039476	paired related homeobox 2	4.541	0.0003	0.0009
Psd	ENSMUSG00000037126	pleckstrin and Sec7 domain containing	2.400	0.0107	0.0255
Psip1	ENSMUSG00000028484	PC4 and SFRS1 interacting protein 1	2.345	0.0000	0.0000
Psma3	ENSMUSG00000060073	proteasome subunit alpha 3	1.529	0.0000	0.0000
Psma5	ENSMUSG00000068749	proteasome subunit alpha 5	1.728	0.0000	0.0000
Psma5-ps	ENSMUSG00000050490	proteasome subunit alpha 5, pseudogene	2.666	0.0181	0.0404
Psmb7	ENSMUSG00000026750	proteasome (prosome, macropain) subunit, beta type 7	1.916	0.0000	0.0000
Psmd10	ENSMUSG00000031429	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	1.837	0.0000	0.0000
Psmd14	ENSMUSG00000026914	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	2.357	0.0000	0.0000
Psmd7	ENSMUSG00000039067	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.550	0.0002	0.0008
Psme2b	ENSMUSG00000078153	protease (prosome, macropain) activator subunit 2B	1.697	0.0007	0.0023
Pspc1	ENSMUSG00000021938	paraspeckle protein 1	1.538	0.0021	0.0059
Ptch1	ENSMUSG00000021466	patched 1	1.631	0.0007	0.0021
Pten	ENSMUSG00000013663	phosphatase and tensin homolog	1.763	0.0000	0.0000
Ptger1	ENSMUSG00000019464	prostaglandin E receptor 1 (subtype EP1)	2.484	0.0068	0.0170
Ptges2	ENSMUSG00000026820	prostaglandin E synthase 2	1.737	0.0000	0.0000
Ptges3	ENSMUSG00000071072	prostaglandin E synthase 3	3.143	0.0000	0.0000
Ptgr1	ENSMUSG00000028378	prostaglandin reductase 1	1.545	0.0010	0.0029
Ptgr2	ENSMUSG00000072946	prostaglandin reductase 2	1.780	0.0000	0.0000
Pth1r	ENSMUSG00000032492	parathyroid hormone 1 receptor	1.658	0.0025	0.0069
Ptma	ENSMUSG00000026238	prothymosin alpha	7.683	0.0000	0.0000
Ptms	ENSMUSG00000030122	parathymosin	5.617	0.0000	0.0000
Ptov1	ENSMUSG00000038502	prostate tumor over expressed gene 1	1.606	0.0067	0.0169
Ptp4a1	ENSMUSG00000026064	protein tyrosine phosphatase 4a1	6.018	0.0003	0.0012
Ptp4a2	ENSMUSG00000028788	protein tyrosine phosphatase 4a2	1.686	0.0000	0.0000
Ptp4a3	ENSMUSG00000059895	protein tyrosine phosphatase 4a3	1.700	0.0000	0.0001
Ptpn11	ENSMUSG00000043733	protein tyrosine phosphatase, non-receptor type 11	1.618	0.0002	0.0007
Ptpn9	ENSMUSG00000032290	protein tyrosine phosphatase, non-receptor type 9	1.682	0.0005	0.0015
Ptpra	ENSMUSG00000027303	protein tyrosine phosphatase, receptor type, A	1.658	0.0000	0.0000
Ptprk	ENSMUSG00000019889	protein tyrosine phosphatase, receptor type, K	1.716	0.0000	0.0000
Ptx3	ENSMUSG00000027832	pentraxin related gene	3.254	0.0026	0.0072

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pum3	ENSMUSG00000041360	pumilio RNA-binding family member 3	1.642	0.0000	0.0000
Pura	ENSMUSG00000043991	purine rich element binding protein A	1.770	0.0000	0.0000
Purb	ENSMUSG00000094483	purine rich element binding protein B	1.666	0.0000	0.0000
Pwwp2a	ENSMUSG00000044950	PWWP domain containing 2A	2.368	0.0000	0.0000
Pxdc1	ENSMUSG00000021411	PX domain containing 1	2.640	0.0000	0.0000
Pygo1	ENSMUSG00000034910	pygopus 1	2.044	0.0000	0.0000
Pygo2	ENSMUSG00000047824	pygopus 2	1.669	0.0000	0.0000
Qki	ENSMUSG00000062078	quaking, KH domain containing RNA binding	2.097	0.0000	0.0000
R3hcc1	ENSMUSG00000034194	R3H domain and coiled-coil containing 1	2.935	0.0000	0.0000
R3hdm4	ENSMUSG00000035781	R3H domain containing 4	1.856	0.0000	0.0000
Rab10os	ENSMUSG00000079179	RAB10, member RAS oncogene family, opposite strand	1.729	0.0000	0.0002
Rab11fip4	ENSMUSG00000017639	RAB11 family interacting protein 4 (class II)	4.229	0.0059	0.0150
Rab12	ENSMUSG00000023460	RAB12, member RAS oncogene family	1.617	0.0000	0.0000
Rab18	ENSMUSG00000073639	RAB18, member RAS oncogene family	2.611	0.0000	0.0000
Rab21	ENSMUSG00000020132	RAB21, member RAS oncogene family	2.084	0.0000	0.0000
Rab22a	ENSMUSG00000027519	RAB22A, member RAS oncogene family	2.160	0.0000	0.0000
Rab24	ENSMUSG00000034789	RAB24, member RAS oncogene family	2.441	0.0000	0.0000
Rab27a	ENSMUSG00000032202	RAB27A, member RAS oncogene family	1.560	0.0101	0.0242
Rab28	ENSMUSG00000029128	RAB28, member RAS oncogene family	2.918	0.0000	0.0000
Rab2a	ENSMUSG00000047187	RAB2A, member RAS oncogene family	2.079	0.0000	0.0000
Rab43	ENSMUSG00000030055	RAB43, member RAS oncogene family	9.546	0.0000	0.0000
Rab5a	ENSMUSG00000017831	RAB5A, member RAS oncogene family	1.830	0.0000	0.0000
Rab5if	ENSMUSG00000027637	RAB5 interacting factor	3.150	0.0000	0.0000
Rab6a	ENSMUSG00000030704	RAB6A, member RAS oncogene family	1.776	0.0000	0.0000
Rab8a	ENSMUSG00000003037	RAB8A, member RAS oncogene family	2.866	0.0000	0.0000
Rabgap1l	ENSMUSG00000026721	RAB GTPase activating protein 1-like	1.679	0.0000	0.0000
Rabggtb	ENSMUSG00000038975	Rab geranylgeranyl transferase, b subunit	1.670	0.0000	0.0000
Rabl3	ENSMUSG00000022827	RAB, member RAS oncogene family-like 3	1.528	0.0000	0.0000
Rac1	ENSMUSG00000001847	Rac family small GTPase 1	1.894	0.0000	0.0000
Rad23b	ENSMUSG00000028426	RAD23 homolog B, nucleotide excision repair protein	2.081	0.0000	0.0000
Rad50	ENSMUSG00000020380	RAD50 double strand break repair protein	1.567	0.0000	0.0000
Rad51c	ENSMUSG00000007646	RAD51 paralog C	1.771	0.0014	0.0042

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rad54l2	ENSMUSG00000040661	RAD54 like 2 (S. cerevisiae)	1.521	0.0000	0.0000
Rala	ENSMUSG00000008859	v-ral simian leukemia viral oncogene A (ras related)	2.229	0.0000	0.0000
Ramac	ENSMUSG00000038646	RNA guanine-7 methyltransferase activating subunit	2.317	0.0000	0.0000
Ranbp1	ENSMUSG00000005732	RAN binding protein 1	2.568	0.0000	0.0000
Ranbp9	ENSMUSG00000038546	RAN binding protein 9	1.768	0.0034	0.0093
Rap1a	ENSMUSG00000068798	RAS-related protein 1a	2.551	0.0000	0.0000
Rap1b	ENSMUSG00000052681	RAS related protein 1b	2.175	0.0000	0.0000
Rap2b	ENSMUSG00000036894	RAP2B, member of RAS oncogene family	2.030	0.0000	0.0000
Rars	ENSMUSG00000018848	arginyl-tRNA synthetase	1.505	0.0000	0.0000
Rasl10b	ENSMUSG00000020684	RAS-like, family 10, member B	1.749	0.0000	0.0000
Rassf3	ENSMUSG00000025795	Ras association (RalGDS/AF-6) domain family member 3	2.157	0.0000	0.0000
Rbfox2	ENSMUSG00000033565	RNA binding protein, fox-1 homolog (C. elegans) 2	1.567	0.0000	0.0000
Rbm15b	ENSMUSG00000074102	RNA binding motif protein 15B	1.576	0.0000	0.0000
Rbm17	ENSMUSG00000037197	RNA binding motif protein 17	4.626	0.0000	0.0000
Rbm24	ENSMUSG00000038132	RNA binding motif protein 24	2.410	0.0000	0.0000
Rbm25	ENSMUSG00000010608	RNA binding motif protein 25	3.062	0.0000	0.0000
Rbm3	ENSMUSG00000031167	RNA binding motif (RNP1, RRM) protein 3	2.211	0.0000	0.0000
Rbm33	ENSMUSG00000048271	RNA binding motif protein 33	1.786	0.0007	0.0021
Rbm39	ENSMUSG00000027620	RNA binding motif protein 39	1.605	0.0000	0.0000
Rbm4	ENSMUSG00000094936	RNA binding motif protein 4	1.886	0.0001	0.0005
Rbm45	ENSMUSG00000042369	RNA binding motif protein 45	2.051	0.0000	0.0000
Rbm47	ENSMUSG00000070780	RNA binding motif protein 47	1.874	0.0276	0.0580
Rbm6	ENSMUSG00000032582	RNA binding motif protein 6	1.819	0.0000	0.0000
Rbm8a	ENSMUSG00000038374	RNA binding motif protein 8a	2.233	0.0000	0.0000
Rbms1	ENSMUSG00000026970	RNA binding motif, single stranded interacting protein 1	1.580	0.0000	0.0000
Rbpj-ps3	ENSMUSG00000079575	recombination signal binding protein for immunoglobulin kappa J region, pseudogene 3	1.804	0.0000	0.0000
Rbpms	ENSMUSG00000031586	RNA binding protein gene with multiple splicing	3.990	0.0000	0.0000
Rc3h2	ENSMUSG00000075376	ring finger and CCCH-type zinc finger domains 2	1.558	0.0000	0.0000
Rcan2	ENSMUSG00000039601	regulator of calcineurin 2	1.769	0.0000	0.0000
Rcn1	ENSMUSG00000005973	reticulocalbin 1	1.877	0.0000	0.0000
Rcn2	ENSMUSG00000032320	reticulocalbin 2	1.523	0.0000	0.0000
Rdh10	ENSMUSG00000025921	retinol dehydrogenase 10 (all-trans)	1.743	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rdx	ENSMUSG00000032050	radixin	1.581	0.0000	0.0000
Rell1	ENSMUSG00000047881	RELT-like 1	1.846	0.0000	0.0000
Rell2	ENSMUSG00000044024	RELT-like 2	3.097	0.0499	0.0965
Renbp	ENSMUSG00000031387	renin binding protein	1.938	0.0000	0.0000
Rest	ENSMUSG00000029249	RE1-silencing transcription factor	2.088	0.0000	0.0000
Rev1	ENSMUSG00000026082	REV1, DNA directed polymerase	1.543	0.0069	0.0172
Rexo2	ENSMUSG00000032026	RNA exonuclease 2	1.516	0.0000	0.0000
Rfk	ENSMUSG00000024712	riboflavin kinase	2.024	0.0000	0.0000
Rflnb	ENSMUSG00000020846	refilin B	2.419	0.0000	0.0000
Rfxap	ENSMUSG00000036615	regulatory factor X-associated protein	4.609	0.0000	0.0000
Rgmb	ENSMUSG00000048027	repulsive guidance molecule family member B	1.565	0.0000	0.0000
Rgs16	ENSMUSG00000026475	regulator of G-protein signaling 16	1.714	0.0299	0.0622
Rgs7	ENSMUSG00000026527	regulator of G protein signaling 7	1.901	0.0013	0.0039
Rhbdl1	ENSMUSG00000025735	rhomboid like 1	4.482	0.0275	0.0578
Rhbdl3	ENSMUSG00000017692	rhomboid like 3	4.708	0.0000	0.0000
Rheb	ENSMUSG00000028945	Ras homolog enriched in brain	2.254	0.0000	0.0000
Rhoa	ENSMUSG00000007815	ras homolog family member A	2.111	0.0000	0.0000
Rhot2	ENSMUSG00000025733	ras homolog family member T2	1.710	0.0000	0.0000
Rhox2h	ENSMUSG00000079627	reproductive homeobox 2H	5.269	0.0156	0.0354
Rhox5	ENSMUSG00000095180	reproductive homeobox 5	1.623	0.0191	0.0423
Ribc1	ENSMUSG00000025257	RIB43A domain with coiled-coils 1	2.023	0.0128	0.0298
Rida	ENSMUSG00000022323	reactive intermediate imine deaminase A homolog	1.960	0.0000	0.0000
Rilpl1	ENSMUSG00000029392	Rab interacting lysosomal protein-like 1	1.581	0.0000	0.0001
Rims4	ENSMUSG00000035226	regulating synaptic membrane exocytosis 4	1.967	0.0013	0.0038
Ring1	ENSMUSG00000024325	ring finger protein 1	2.136	0.0000	0.0001
Riox1	ENSMUSG00000046791	ribosomal oxygenase 1	2.040	0.0030	0.0083
Ripk1	ENSMUSG00000021408	receptor (TNFRSF)-interacting serine-threonine kinase 1	1.723	0.0000	0.0000
Rnd3	ENSMUSG00000017144	Rho family GTPase 3	1.775	0.0000	0.0000
Rnf10	ENSMUSG00000041740	ring finger protein 10	2.875	0.0000	0.0000
Rnf103	ENSMUSG00000052656	ring finger protein 103	2.434	0.0000	0.0000
Rnf11	ENSMUSG00000028557	ring finger protein 11	2.116	0.0000	0.0000
Rnf111	ENSMUSG00000032217	ring finger 111	1.640	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rnf113a2	ENSMUSG00000098134	ring finger protein 113A2	2.151	0.0000	0.0000
Rnf125	ENSMUSG00000033107	ring finger protein 125	1.943	0.0001	0.0002
Rnf146	ENSMUSG00000038876	ring finger protein 146	2.053	0.0000	0.0000
Rnf149	ENSMUSG00000048234	ring finger protein 149	2.457	0.0000	0.0000
Rnf152	ENSMUSG00000047496	ring finger protein 152	1.688	0.0000	0.0000
Rnf166	ENSMUSG00000014470	ring finger protein 166	1.610	0.0000	0.0001
Rnf168	ENSMUSG00000014074	ring finger protein 168	1.749	0.0000	0.0000
Rnf187	ENSMUSG00000020496	ring finger protein 187	1.696	0.0001	0.0004
Rnf19a	ENSMUSG00000022280	ring finger protein 19A	1.515	0.0001	0.0002
Rnf19b	ENSMUSG00000028793	ring finger protein 19B	2.190	0.0000	0.0000
Rnf20	ENSMUSG00000028309	ring finger protein 20	1.945	0.0000	0.0000
Rnf214	ENSMUSG00000042790	ring finger protein 214	1.652	0.0000	0.0000
Rnf217	ENSMUSG00000063760	ring finger protein 217	1.798	0.0000	0.0000
Rnf220	ENSMUSG00000028677	ring finger protein 220	2.106	0.0000	0.0000
Rnf227	ENSMUSG00000043419	ring finger protein 227	1.887	0.0301	0.0625
Rnf38	ENSMUSG00000035696	ring finger protein 38	1.573	0.0023	0.0066
Rnps1	ENSMUSG00000034681	RNA binding protein with serine rich domain 1	2.942	0.0000	0.0000
Rock1	ENSMUSG00000024290	Rho-associated coiled-coil containing protein kinase 1	2.451	0.0000	0.0000
Rock2	ENSMUSG00000020580	Rho-associated coiled-coil containing protein kinase 2	1.806	0.0000	0.0000
Rora	ENSMUSG00000032238	RAR-related orphan receptor alpha	1.520	0.0240	0.0514
Rp1	ENSMUSG00000025900	retinitis pigmentosa 1 (human)	1.767	0.0149	0.0339
Rp9	ENSMUSG00000032239	retinitis pigmentosa 9 (human)	2.809	0.0000	0.0000
Rpf2	ENSMUSG00000038510	ribosome production factor 2 homolog	1.652	0.0000	0.0000
Rpia	ENSMUSG00000053604	ribose 5-phosphate isomerase A	2.390	0.0000	0.0000
Rpl11	ENSMUSG00000059291	ribosomal protein L11	2.844	0.0000	0.0000
Rpl13a	ENSMUSG00000074129	ribosomal protein L13A	1.745	0.0000	0.0001
Rpl14-ps1	ENSMUSG00000046721	ribosomal protein L14, pseudogene 1	1.735	0.0000	0.0000
Rpl15-ps6	ENSMUSG00000057262	ribosomal protein L15, pseudogene 6	9.077	0.0000	0.0002
Rpl24	ENSMUSG00000098274	ribosomal protein L24	5.499	0.0202	0.0444
Rpl30-ps11	ENSMUSG00000081461	ribosomal protein L30, pseudogene 11	2.858	0.0415	0.0824
Rpl31-ps17	ENSMUSG00000072255	ribosomal protein L31, pseudogene 17	5.151	0.0212	0.0463
Rpl5	ENSMUSG00000058558	ribosomal protein L5	2.597	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpl5-ps2	ENSMUSG00000082064	ribisomal protein L5, pseudogene 2	5.263	0.0000	0.0000
Rpl9	ENSMUSG00000047215	ribosomal protein L9	2.184	0.0000	0.0000
Rpl9-ps7	ENSMUSG00000047965	ribosomal protein L9, pseudogene 7	6.635	0.0000	0.0000
Rprml	ENSMUSG00000046215	reprimo-like	5.679	0.0010	0.0030
Rps12-ps4	ENSMUSG00000109509	ribosomal protein S12, pseudogene 4	7.743	0.0050	0.0130
Rps14	ENSMUSG00000024608	ribosomal protein S14	1.841	0.0000	0.0000
Rps18	ENSMUSG00000008668	ribosomal protein S18	2.072	0.0000	0.0000
Rps18-ps4	ENSMUSG00000097346	ribosomal protein S18, pseudogene 4	5.804	0.0007	0.0022
Rps19bp1	ENSMUSG00000051518	ribosomal protein S19 binding protein 1	1.948	0.0100	0.0240
Rps2	ENSMUSG00000044533	ribosomal protein S2	2.789	0.0000	0.0002
Rps23-ps1	ENSMUSG00000100755	ribosomal protein S23, pseudogene 1	1.713	0.0127	0.0296
Rps2-ps10	ENSMUSG00000091957	ribosomal protein S2, pseudogene 10	8.445	0.0000	0.0000
Rps2-ps11	ENSMUSG00000104280	ribosomal protein S2, pseudogene 11	5.221	0.0016	0.0048
Rps2-ps13	ENSMUSG00000081684	ribosomal protein S2, pseudogene 13	3.766	0.0005	0.0017
Rps2-ps6	ENSMUSG00000095427	ribosomal protein S2, pseudogene 6	5.053	0.0069	0.0172
Rps2-ps8	ENSMUSG00000118161	ribosomal protein S2, pseudogene 8	2.797	0.0454	0.0889
Rps3	ENSMUSG00000030744	ribosomal protein S3	1.821	0.0000	0.0000
Rps6	ENSMUSG00000028495	ribosomal protein S6	1.667	0.0000	0.0000
Rps6ka6	ENSMUSG00000025665	ribosomal protein S6 kinase polypeptide 6	4.872	0.0004	0.0013
Rps6kb1	ENSMUSG00000020516	ribosomal protein S6 kinase, polypeptide 1	1.685	0.0000	0.0000
Rps6-ps3	ENSMUSG00000082465	ribosomal protein S6, pseudogene 3	23.307	0.0013	0.0039
Rps7	ENSMUSG00000061477	ribosomal protein S7	1.555	0.0000	0.0000
Rpusd2	ENSMUSG00000027324	RNA pseudouridylate synthase domain containing 2	2.045	0.0000	0.0000
Rras	ENSMUSG00000038387	related RAS viral (r-ras) oncogene	1.907	0.0000	0.0000
Rras2	ENSMUSG00000055723	related RAS viral (r-ras) oncogene 2	2.198	0.0000	0.0000
Rrbp1	ENSMUSG00000027422	ribosome binding protein 1	1.594	0.0000	0.0000
Rrp1	ENSMUSG00000061032	ribosomal RNA processing 1	2.124	0.0000	0.0000
Rrp15	ENSMUSG00000001305	ribosomal RNA processing 15 homolog	2.410	0.0000	0.0000
Rrp9	ENSMUSG00000041506	ribosomal RNA processing 9, U3 small nucleolar RNA binding protein	1.892	0.0000	0.0000
Rsad2	ENSMUSG00000020641	radical S-adenosyl methionine domain containing 2	1.520	0.0000	0.0001
Rsbn1l	ENSMUSG00000039968	round spermatid basic protein 1-like	1.604	0.0000	0.0000
Rsf1	ENSMUSG00000035623	remodeling and spacing factor 1	1.823	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rsl24d1	ENSMUSG00000032215	ribosomal L24 domain containing 1	2.718	0.0000	0.0000
Rsph1	ENSMUSG00000024033	radial spoke head 1 homolog (Chlamydomonas)	1.767	0.0160	0.0362
Rsph3a	ENSMUSG00000073471	radial spoke 3A homolog (Chlamydomonas)	2.553	0.0000	0.0000
Rsph3b	ENSMUSG00000023806	radial spoke 3B homolog (Chlamydomonas)	2.758	0.0000	0.0000
Rsrc2	ENSMUSG00000029422	arginine/serine-rich coiled-coil 2	2.053	0.0000	0.0000
Rsu1	ENSMUSG00000026727	Ras suppressor protein 1	1.553	0.0000	0.0000
Rtca	ENSMUSG00000000339	RNA 3'-terminal phosphate cyclase	1.564	0.0000	0.0000
Rtcb	ENSMUSG00000001783	RNA 2',3'-cyclic phosphate and 5'-OH ligase	1.838	0.0000	0.0000
Rtn4	ENSMUSG00000020458	reticulon 4	2.375	0.0000	0.0000
Rtn4ip1	ENSMUSG00000019864	reticulon 4 interacting protein 1	1.962	0.0000	0.0000
Rtn4r	ENSMUSG00000043811	reticulon 4 receptor	2.594	0.0468	0.0914
Rtn4rl2	ENSMUSG00000050896	reticulon 4 receptor-like 2	2.423	0.0219	0.0476
Rtp3	ENSMUSG00000066319	receptor transporter protein 3	1.734	0.0001	0.0003
Rufy1	ENSMUSG00000020375	RUN and FYVE domain containing 1	2.909	0.0000	0.0000
Rufy3	ENSMUSG00000029291	RUN and FYVE domain containing 3	1.855	0.0000	0.0000
Ruvbl1	ENSMUSG00000030079	RuvB-like protein 1	1.738	0.0000	0.0000
Rwdd3	ENSMUSG00000028133	RWD domain containing 3	1.588	0.0059	0.0151
Rwdd4a	ENSMUSG00000031568	RWD domain containing 4A	1.600	0.0000	0.0000
S1pr5	ENSMUSG00000045087	sphingosine-1-phosphate receptor 5	1.842	0.0018	0.0051
Safb	ENSMUSG00000071054	scaffold attachment factor B	2.179	0.0000	0.0000
Safb2	ENSMUSG00000042625	scaffold attachment factor B2	1.608	0.0001	0.0003
Sall4	ENSMUSG00000027547	spalt like transcription factor 4	2.151	0.0003	0.0011
Samd1	ENSMUSG00000079003	sterile alpha motif domain containing 1	3.077	0.0000	0.0000
Samd4	ENSMUSG00000021838	sterile alpha motif domain containing 4	1.724	0.0000	0.0000
Sap18	ENSMUSG00000021963	Sin3-associated polypeptide 18	1.782	0.0000	0.0000
Sap18b	ENSMUSG00000061104	Sin3-associated polypeptide 18B	2.785	0.0001	0.0002
Sap30	ENSMUSG00000031609	sin3 associated polypeptide	5.097	0.0000	0.0000
Sap30l	ENSMUSG00000020519	SAP30-like	9.281	0.0000	0.0000
Sarnp	ENSMUSG00000078427	SAP domain containing ribonucleoprotein	2.000	0.0000	0.0000
Sars	ENSMUSG00000068739	seryl-aminoacyl-tRNA synthetase	1.607	0.0000	0.0000
Sart1	ENSMUSG00000039148	squamous cell carcinoma antigen recognized by T cells 1	2.800	0.0000	0.0000
Sart3	ENSMUSG00000018974	squamous cell carcinoma antigen recognized by T cells 3	2.307	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Satb1	ENSMUSG00000023927	special AT-rich sequence binding protein 1	2.183	0.0000	0.0000
Satb2	ENSMUSG00000038331	special AT-rich sequence binding protein 2	2.040	0.0262	0.0555
Sbds	ENSMUSG00000025337	SBDS ribosome maturation factor	1.981	0.0000	0.0000
Sbk2	ENSMUSG00000030433	SH3-binding domain kinase family, member 2	2.431	0.0000	0.0000
Sbno1	ENSMUSG00000038095	strawberry notch 1	1.743	0.0000	0.0000
Scaf4	ENSMUSG00000022983	SR-related CTD-associated factor 4	2.253	0.0000	0.0000
Scamp1	ENSMUSG00000021687	secretory carrier membrane protein 1	1.668	0.0000	0.0000
Scand1	ENSMUSG00000046229	SCAN domain-containing 1	12.419	0.0000	0.0000
Scarf2	ENSMUSG00000012017	scavenger receptor class F, member 2	2.800	0.0000	0.0000
Scarna2	ENSMUSG00000088185	small Cajal body-specific RNA 2	9.050	0.0054	0.0139
Schip1	ENSMUSG00000027777	schwannomin interacting protein 1	2.751	0.0000	0.0000
Sclt1	ENSMUSG00000059834	sodium channel and clathrin linker 1	1.569	0.0002	0.0008
Scn2b	ENSMUSG00000070304	sodium channel, voltage-gated, type II, beta	2.237	0.0033	0.0090
Scx	ENSMUSG00000034161	scleraxis	3.765	0.0000	0.0000
Sdc4	ENSMUSG00000017009	syndecan 4	2.489	0.0000	0.0000
Sdccag8	ENSMUSG00000026504	serologically defined colon cancer antigen 8	1.712	0.0000	0.0000
Sde2	ENSMUSG00000038806	SDE2 telomere maintenance homolog (S. pombe)	1.571	0.0000	0.0000
Sdf2l1	ENSMUSG00000022769	stromal cell-derived factor 2-like 1	1.658	0.0105	0.0251
Sdha	ENSMUSG00000021577	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.592	0.0000	0.0000
Sdhaf1	ENSMUSG00000074211	succinate dehydrogenase complex assembly factor 1	2.592	0.0000	0.0000
Sec11a	ENSMUSG00000025724	SEC11 homolog A, signal peptidase complex subunit	1.951	0.0000	0.0000
Sec11c	ENSMUSG00000024516	SEC11 homolog C, signal peptidase complex subunit	1.645	0.0000	0.0000
Sec62	ENSMUSG00000027706	SEC62 homolog (S. cerevisiae)	2.440	0.0000	0.0000
Sec63	ENSMUSG00000019802	SEC63-like (S. cerevisiae)	1.680	0.0000	0.0000
Secisbp2l	ENSMUSG00000035093	SECIS binding protein 2-like	2.076	0.0000	0.0000
Selenoi	ENSMUSG00000075703	selenoprotein I	1.698	0.0000	0.0000
Selenot	ENSMUSG00000075700	selenoprotein T	1.808	0.0000	0.0000
Sem1	ENSMUSG00000042541	SEM1, 26S proteasome complex subunit	2.070	0.0000	0.0000
Sema6b	ENSMUSG00000001227	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	3.892	0.0000	0.0000
Sema6c	ENSMUSG00000038777	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	2.642	0.0000	0.0000
Senp6	ENSMUSG00000034252	SUMO/sentrin specific peptidase 6	1.623	0.0000	0.0000
Septin10	ENSMUSG00000019917	septin 10	2.413	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Septin7	ENSMUSG00000001833	septin 7	2.494	0.0000	0.0000
Serbp1	ENSMUSG00000036371	serpine1 mRNA binding protein 1	3.088	0.0000	0.0000
Serinc4	ENSMUSG00000046110	serine incorporator 4	3.692	0.0477	0.0928
Serpina1b	ENSMUSG00000071178	serine (or cysteine) preptidase inhibitor, clade A, member 1B	1.564	0.0423	0.0838
Sertad4	ENSMUSG00000016262	SERTA domain containing 4	1.540	0.0173	0.0388
Set	ENSMUSG00000054766	SET nuclear oncogene	3.405	0.0000	0.0000
Setd3	ENSMUSG00000056770	SET domain containing 3	1.785	0.0000	0.0000
Setd6	ENSMUSG00000031671	SET domain containing 6	2.936	0.0000	0.0000
Setx	ENSMUSG00000043535	senataxin	1.511	0.0000	0.0000
Sf1	ENSMUSG00000024949	splicing factor 1	1.503	0.0000	0.0001
Sf3a1	ENSMUSG00000002129	splicing factor 3a, subunit 1	1.965	0.0000	0.0000
Sf3b2	ENSMUSG00000024853	splicing factor 3b, subunit 2	1.724	0.0000	0.0000
Sfpq	ENSMUSG00000028820	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	4.390	0.0000	0.0000
Sfr1	ENSMUSG00000025066	SWI5 dependent recombination repair 1	2.605	0.0000	0.0000
Sfrp5	ENSMUSG00000018822	secreted frizzled-related sequence protein 5	2.961	0.0001	0.0004
Sfswap	ENSMUSG00000029439	splicing factor SWAP	2.222	0.0000	0.0000
Sgpp1	ENSMUSG00000021054	sphingosine-1-phosphate phosphatase 1	1.800	0.0000	0.0000
Sh3bgr	ENSMUSG00000040666	SH3-binding domain glutamic acid-rich protein	1.913	0.0000	0.0000
Sh3gl3	ENSMUSG00000030638	SH3-domain GRB2-like 3	3.969	0.0000	0.0000
Sh3pxd2a	ENSMUSG00000053617	SH3 and PX domains 2A	1.534	0.0000	0.0000
Shc3	ENSMUSG00000021448	src homology 2 domain-containing transforming protein C3	2.249	0.0022	0.0063
Shc4	ENSMUSG00000035109	SHC (Src homology 2 domain containing) family, member 4	1.868	0.0001	0.0004
Shf	ENSMUSG00000033256	Src homology 2 domain containing F	2.168	0.0000	0.0000
Shoc2	ENSMUSG00000024976	Shoc2, leucine rich repeat scaffold protein	1.734	0.0000	0.0000
Shox2	ENSMUSG00000027833	short stature homeobox 2	2.636	0.0225	0.0488
Shroom3	ENSMUSG00000029381	shroom family member 3	1.944	0.0002	0.0008
Siah1a	ENSMUSG00000036840	siah E3 ubiquitin protein ligase 1A	2.229	0.0000	0.0000
Siah2	ENSMUSG00000036432	siah E3 ubiquitin protein ligase 2	3.072	0.0000	0.0000
Sinhcaf	ENSMUSG00000039985	SIN3-HDAC complex associated factor	2.382	0.0000	0.0001
Six1	ENSMUSG00000051367	sine oculis-related homeobox 1	1.826	0.0255	0.0542
Six4	ENSMUSG00000034460	sine oculis-related homeobox 4	1.565	0.0018	0.0052
Skap2	ENSMUSG00000059182	src family associated phosphoprotein 2	1.570	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Skil	ENSMUSG00000027660	SKI-like	1.659	0.0000	0.0000
Slain1	ENSMUSG00000055717	SLAIN motif family, member 1	4.566	0.0249	0.0531
Slbp	ENSMUSG00000004642	stem-loop binding protein	1.752	0.0000	0.0000
Slc12a2	ENSMUSG00000024597	solute carrier family 12, member 2	1.755	0.0000	0.0000
Slc16a1	ENSMUSG00000032902	solute carrier family 16 (monocarboxylic acid transporters), member 1	1.536	0.0001	0.0003
Slc16a10	ENSMUSG00000019838	solute carrier family 16 (monocarboxylic acid transporters), member 10	1.537	0.0009	0.0028
Slc16a11	ENSMUSG00000040938	solute carrier family 16 (monocarboxylic acid transporters), member 11	4.951	0.0002	0.0008
Slc17a7	ENSMUSG00000070570	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	1.766	0.0000	0.0001
Slc22a3	ENSMUSG00000023828	solute carrier family 22 (organic cation transporter), member 3	1.648	0.0194	0.0429
Slc24a3	ENSMUSG00000063873	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	1.596	0.0001	0.0003
Slc25a15	ENSMUSG00000031482	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	1.608	0.0000	0.0000
Slc25a32	ENSMUSG00000022299	solute carrier family 25, member 32	1.796	0.0000	0.0000
Slc25a38	ENSMUSG00000032519	solute carrier family 25, member 38	1.558	0.0038	0.0100
Slc29a4	ENSMUSG00000050822	solute carrier family 29 (nucleoside transporters), member 4	2.859	0.0024	0.0068
Slc30a1	ENSMUSG00000037434	solute carrier family 30 (zinc transporter), member 1	1.566	0.0000	0.0000
Slc30a5	ENSMUSG00000021629	solute carrier family 30 (zinc transporter), member 5	1.686	0.0000	0.0000
Slc35a2	ENSMUSG00000031156	solute carrier family 35 (UDP-galactose transporter), member A2	1.624	0.0000	0.0000
Slc35a3	ENSMUSG00000027957	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	2.103	0.0000	0.0000
Slc35d1	ENSMUSG00000028521	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	1.638	0.0000	0.0000
Slc35g1	ENSMUSG00000044026	solute carrier family 35, member G1	1.560	0.0042	0.0111
Slc49a4	ENSMUSG00000022848	solute carrier family 49 member 4	1.955	0.0000	0.0000
Slc4a1ap	ENSMUSG00000029141	solute carrier family 4 (anion exchanger), member 1, adaptor protein	1.738	0.0000	0.0000
Slc5a1	ENSMUSG00000011034	solute carrier family 5 (sodium/glucose cotransporter), member 1	2.020	0.0018	0.0053
Slc6a8	ENSMUSG00000019558	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	2.025	0.0000	0.0000
Slc7a6os	ENSMUSG00000033106	solute carrier family 7, member 6 opposite strand	1.504	0.0001	0.0005
Slc8a2	ENSMUSG00000030376	solute carrier family 8 (sodium/calcium exchanger), member 2	1.636	0.0118	0.0278
Slc8a3	ENSMUSG00000079055	solute carrier family 8 (sodium/calcium exchanger), member 3	3.917	0.0239	0.0513
Slco5a1	ENSMUSG00000025938	solute carrier organic anion transporter family, member 5A1	1.728	0.0000	0.0000
Slfn5	ENSMUSG00000054404	schlafen 5	1.625	0.0000	0.0000
Slk	ENSMUSG00000025060	STE20-like kinase	1.780	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slmap	ENSMUSG00000021870	sarcolemma associated protein	2.387	0.0000	0.0000
Sltm	ENSMUSG00000032212	SAFB-like, transcription modulator	1.783	0.0001	0.0003
Smad1	ENSMUSG00000031681	SMAD family member 1	1.768	0.0000	0.0000
Smad2	ENSMUSG00000024563	SMAD family member 2	1.534	0.0000	0.0000
Smad4	ENSMUSG00000024515	SMAD family member 4	1.942	0.0000	0.0000
Smad6	ENSMUSG00000036867	SMAD family member 6	2.440	0.0000	0.0000
Smad7	ENSMUSG00000025880	SMAD family member 7	4.345	0.0000	0.0000
Smagp	ENSMUSG00000053559	small cell adhesion glycoprotein	2.736	0.0000	0.0000
Smap1	ENSMUSG00000026155	small ArfGAP 1	1.797	0.0000	0.0000
Smap2	ENSMUSG00000032870	small ArfGAP 2	1.789	0.0000	0.0000
Smarca2	ENSMUSG00000024921	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	2.234	0.0000	0.0000
Smarca5	ENSMUSG00000031715	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	2.508	0.0000	0.0000
Smarca5-ps	ENSMUSG00000052912	SWI/SNF related, matrix associated, actin depenent ragulator of chromatin, subfamily a, member 5, pseudogene	2.606	0.0203	0.0446
Smarcc2	ENSMUSG00000025369	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	1.916	0.0000	0.0000
Smarcd3	ENSMUSG00000028949	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	3.538	0.0000	0.0000
Smarce1	ENSMUSG00000037935	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	1.796	0.0000	0.0000
Smc1a	ENSMUSG00000041133	structural maintenance of chromosomes 1A	1.958	0.0000	0.0000
Smc2	ENSMUSG00000028312	structural maintenance of chromosomes 2	1.653	0.0059	0.0150
Smc3	ENSMUSG00000024974	structural maintenance of chromosomes 3	2.267	0.0000	0.0000
Smc5	ENSMUSG00000024943	structural maintenance of chromosomes 5	1.716	0.0000	0.0000
Smc6	ENSMUSG00000020608	structural maintenance of chromosomes 6	2.177	0.0000	0.0000
Smco4	ENSMUSG00000058173	single-pass membrane protein with coiled-coil domains 4	2.362	0.0000	0.0000
Smim10l1	ENSMUSG00000072704	small integral membrane protein 10 like 1	2.150	0.0000	0.0000
Smim13	ENSMUSG00000091264	small integral membrane protein 13	1.686	0.0000	0.0000
Smim19	ENSMUSG00000031534	small integral membrane protein 19	1.798	0.0001	0.0003
Smim36	ENSMUSG00000110344	small integral membrane protein 36	1.545	0.0000	0.0000
Smkr-ps	ENSMUSG00000045709	smal lysine rich protein 1, pseudogene	5.414	0.0475	0.0925
Smndc1	ENSMUSG00000025024	survival motor neuron domain containing 1	2.037	0.0000	0.0000
Smox	ENSMUSG00000027333	spermine oxidase	1.575	0.0001	0.0005

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sms	ENSMUSG00000071708	spermine synthase	1.508	0.0000	0.0001
Snapc5	ENSMUSG00000032398	small nuclear RNA activating complex, polypeptide 5	1.768	0.0000	0.0000
Snca	ENSMUSG00000025889	synuclein, alpha	3.489	0.0001	0.0003
Snhg12	ENSMUSG00000086290	small nucleolar RNA host gene 12	1.603	0.0353	0.0718
Snhg14	ENSMUSG00000100826	small nucleolar RNA host gene 14	2.586	0.0005	0.0016
Snhg3	ENSMUSG00000085241	small nucleolar RNA host gene 3	2.719	0.0000	0.0000
Snhg4	ENSMUSG00000117869	small nucleolar RNA host gene 4	2.115	0.0001	0.0004
Snhg5	ENSMUSG00000097195	small nucleolar RNA host gene 5	2.210	0.0027	0.0075
Snhg8	ENSMUSG00000104960	small nucleolar RNA host gene 8	2.077	0.0000	0.0000
Snora73b	ENSMUSG00000065353	small nucleolar RNA, H/ACA box 73b	5.434	0.0000	0.0000
Snord104	ENSMUSG00000065126	small nucleolar RNA, C/D box 104	2.246	0.0076	0.0188
Snord55	ENSMUSG00000092680	small nucleolar RNA, C/D box 55	53.000	0.0001	0.0004
Snord72	ENSMUSG00000077737	small nucleolar RNA, C/D box 72	5.083	0.0004	0.0015
Snrnp27	ENSMUSG00000001158	small nuclear ribonucleoprotein 27 (U4/U6.U5)	2.062	0.0000	0.0000
Snrnp35	ENSMUSG00000029402	small nuclear ribonucleoprotein 35 (U11/U12)	1.897	0.0000	0.0000
Snrnp48	ENSMUSG00000021431	small nuclear ribonucleoprotein 48 (U11/U12)	3.246	0.0000	0.0000
Snrnp70	ENSMUSG00000063511	small nuclear ribonucleoprotein 70 (U1)	1.511	0.0019	0.0055
Snrpd1	ENSMUSG00000002477	small nuclear ribonucleoprotein D1	2.073	0.0000	0.0000
Snrpn	ENSMUSG00000102252	small nuclear ribonucleoprotein N	2.143	0.0000	0.0000
Snw1	ENSMUSG00000021039	SNW domain containing 1	1.820	0.0000	0.0000
Snx12	ENSMUSG00000046032	sorting nexin 12	1.756	0.0000	0.0000
Snx18	ENSMUSG00000042364	sorting nexin 18	1.517	0.0012	0.0036
Snx2	ENSMUSG00000034484	sorting nexin 2	1.564	0.0000	0.0000
Snx4	ENSMUSG00000022808	sorting nexin 4	1.560	0.0000	0.0000
Snx7	ENSMUSG00000028007	sorting nexin 7	2.484	0.0000	0.0000
Snx9	ENSMUSG00000002365	sorting nexin 9	1.651	0.0000	0.0000
Soat1	ENSMUSG00000026600	sterol O-acyltransferase 1	1.516	0.0013	0.0039
Sobp	ENSMUSG00000038248	sine oculis binding protein	2.163	0.0000	0.0000
Socs6	ENSMUSG00000056153	suppressor of cytokine signaling 6	2.059	0.0000	0.0000
Socs7	ENSMUSG00000038485	suppressor of cytokine signaling 7	2.546	0.0000	0.0000
Sox10	ENSMUSG00000033006	SRY (sex determining region Y)-box 10	2.367	0.0021	0.0060
Sox12	ENSMUSG00000051817	SRY (sex determining region Y)-box 12	4.549	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sox30	ENSMUSG00000040489	SRY (sex determining region Y)-box 30	3.479	0.0205	0.0450
Sox4	ENSMUSG00000076431	SRY (sex determining region Y)-box 4	2.768	0.0000	0.0000
Sp110	ENSMUSG00000070034	Sp110 nuclear body protein	1.803	0.0006	0.0019
Spaca6	ENSMUSG00000080316	sperm acrosome associated 6	2.005	0.0140	0.0323
Spata48	ENSMUSG00000020191	spermatogenesis associated 48	7.575	0.0000	0.0000
Spata5	ENSMUSG00000027722	spermatogenesis associated 5	1.996	0.0000	0.0000
Spata5l1	ENSMUSG00000118663	spermatogenesis associated 5-like 1	1.670	0.0031	0.0086
Spata6l	ENSMUSG00000064202	spermatogenesis associated 6 like	1.573	0.0000	0.0000
Spats2	ENSMUSG00000051934	spermatogenesis associated, serine-rich 2	1.675	0.0000	0.0000
Spcs2	ENSMUSG00000035227	signal peptidase complex subunit 2 homolog (S. cerevisiae)	2.145	0.0000	0.0000
Speg	ENSMUSG00000026207	SPEG complex locus	1.572	0.0002	0.0007
Spg7	ENSMUSG00000000738	SPG7, paraplegin matrix AAA peptidase subunit	2.077	0.0000	0.0000
Spi1	ENSMUSG00000002111	spleen focus forming virus (SFFV) proviral integration oncogene	2.041	0.0123	0.0287
Spin4	ENSMUSG00000071722	spindlin family, member 4	1.646	0.0336	0.0688
Spn	ENSMUSG00000051457	sialophorin	1.976	0.0053	0.0137
Spop	ENSMUSG00000057522	speckle-type BTB/POZ protein	2.387	0.0000	0.0000
Spopl	ENSMUSG00000026771	speckle-type BTB/POZ protein-like	2.125	0.0000	0.0000
Sppl3	ENSMUSG00000029550	signal peptide peptidase 3	1.929	0.0000	0.0000
Spred2	ENSMUSG00000045671	sprouty-related EVH1 domain containing 2	2.022	0.0000	0.0000
Spring1	ENSMUSG00000032840	SREBF pathway regulator in golgi 1	1.630	0.0000	0.0000
Sprtn	ENSMUSG00000031986	SprT-like N-terminal domain	1.637	0.0000	0.0000
Spry1	ENSMUSG00000037211	sprouty RTK signaling antagonist 1	1.561	0.0010	0.0031
Spta1	ENSMUSG00000026532	spectrin alpha, erythrocytic 1	1.602	0.0008	0.0025
Srcap	ENSMUSG00000053877	Snf2-related CREBBP activator protein	2.138	0.0000	0.0001
Srek1	ENSMUSG00000032621	splicing regulatory glutamine/lysine-rich protein 1	1.905	0.0000	0.0000
Srf	ENSMUSG00000015605	serum response factor	3.890	0.0000	0.0000
Srfbp1	ENSMUSG00000024528	serum response factor binding protein 1	1.827	0.0000	0.0000
Srm	ENSMUSG00000006442	spermidine synthase	1.853	0.0033	0.0089
Srp14	ENSMUSG00000009549	signal recognition particle 14	1.957	0.0000	0.0000
Srp54a	ENSMUSG00000073079	signal recognition particle 54A	1.905	0.0000	0.0000
Srp54c	ENSMUSG00000079108	signal recognition particle 54C	3.154	0.0000	0.0000
Srrd	ENSMUSG00000029346	SRR1 domain containing	2.832	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Srrt	ENSMUSG00000037364	serrate RNA effector molecule homolog (Arabidopsis)	2.566	0.0000	0.0000
Srsf1	ENSMUSG00000018379	serine and arginine-rich splicing factor 1	3.252	0.0000	0.0000
Srsf10	ENSMUSG00000028676	serine and arginine-rich splicing factor 10	1.533	0.0007	0.0021
Srsf11	ENSMUSG00000055436	serine and arginine-rich splicing factor 11	2.017	0.0000	0.0000
Srsf2	ENSMUSG00000034120	serine and arginine-rich splicing factor 2	2.306	0.0000	0.0000
Srsf4	ENSMUSG00000028911	serine and arginine-rich splicing factor 4	1.549	0.0000	0.0000
Srsf5	ENSMUSG00000021134	serine and arginine-rich splicing factor 5	2.060	0.0000	0.0000
Srsf6	ENSMUSG00000016921	serine and arginine-rich splicing factor 6	1.546	0.0000	0.0000
Srsf9	ENSMUSG00000029538	serine and arginine-rich splicing factor 9	2.381	0.0000	0.0000
Ss18l1	ENSMUSG00000039086	SS18, nBAF chromatin remodeling complex subunit like 1	2.288	0.0000	0.0000
Ssb	ENSMUSG00000068882	Sjogren syndrome antigen B	2.208	0.0000	0.0000
Ssbp1	ENSMUSG00000029911	single-stranded DNA binding protein 1	2.864	0.0000	0.0000
Ssbp3	ENSMUSG00000061887	single-stranded DNA binding protein 3	2.160	0.0000	0.0000
Ssbp4	ENSMUSG00000070003	single stranded DNA binding protein 4	3.125	0.0000	0.0000
Ssr3	ENSMUSG00000027828	signal sequence receptor, gamma	1.558	0.0000	0.0000
Ssrp1	ENSMUSG00000027067	structure specific recognition protein 1	1.549	0.0000	0.0000
Ssx2ip	ENSMUSG00000036825	synovial sarcoma, X 2 interacting protein	1.659	0.0000	0.0000
St13	ENSMUSG00000022403	suppression of tumorigenicity 13	1.590	0.0000	0.0000
St3gal4	ENSMUSG00000032038	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	1.593	0.0007	0.0021
St3gal5	ENSMUSG00000056091	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1.762	0.0000	0.0000
Stard10	ENSMUSG00000030688	START domain containing 10	1.528	0.0000	0.0000
Stard5	ENSMUSG00000046027	StAR-related lipid transfer (START) domain containing 5	1.561	0.0009	0.0029
Stbd1	ENSMUSG00000047963	starch binding domain 1	3.476	0.0000	0.0000
Stc2	ENSMUSG00000020303	stanniocalcin 2	2.081	0.0000	0.0000
Steap4	ENSMUSG00000012428	STEAP family member 4	1.502	0.0021	0.0060
Stim2	ENSMUSG00000039156	stromal interaction molecule 2	2.159	0.0000	0.0000
Stk11	ENSMUSG00000003068	serine/threonine kinase 11	1.651	0.0000	0.0000
Stk24	ENSMUSG00000063410	serine/threonine kinase 24	1.824	0.0000	0.0000
Stk32c	ENSMUSG00000015981	serine/threonine kinase 32C	1.725	0.0044	0.0116
Stk40	ENSMUSG00000042608	serine/threonine kinase 40	1.730	0.0000	0.0000
Strbp	ENSMUSG00000026915	spermatid perinuclear RNA binding protein	1.976	0.0000	0.0000
Strn3	ENSMUSG00000020954	striatin, calmodulin binding protein 3	3.154	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Stt3b	ENSMUSG00000032437	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	2.574	0.0000	0.0000
Stx11	ENSMUSG00000039232	syntaxin 11	1.737	0.0033	0.0089
Stx4a	ENSMUSG00000030805	syntaxin 4A (placental)	1.535	0.0000	0.0000
Stx6	ENSMUSG00000026470	syntaxin 6	1.672	0.0022	0.0062
Suco	ENSMUSG00000040297	SUN domain containing ossification factor	1.569	0.0000	0.0000
Suds3	ENSMUSG00000066900	suppressor of defective silencing 3 homolog (S. cerevisiae)	2.501	0.0000	0.0000
Sugct	ENSMUSG00000055137	succinyl-CoA glutarate-CoA transferase	1.517	0.0142	0.0326
Sumf1	ENSMUSG00000030101	sulfatase modifying factor 1	2.010	0.0000	0.0000
Sumo1	ENSMUSG00000026021	small ubiquitin-like modifier 1	1.927	0.0000	0.0000
Suox	ENSMUSG00000049858	sulfite oxidase	1.804	0.0000	0.0000
Supt16	ENSMUSG00000035726	SPT16, facilitates chromatin remodeling subunit	1.899	0.0000	0.0000
Suz12	ENSMUSG00000017548	SUZ12 polycomb repressive complex 2 subunit	1.868	0.0000	0.0000
Svbp	ENSMUSG00000028643	small vasohibin binding protein	2.583	0.0000	0.0000
Swap70	ENSMUSG00000031015	SWA-70 protein	1.757	0.0000	0.0000
Syap1	ENSMUSG00000031357	synapse associated protein 1	2.093	0.0000	0.0000
Syde2	ENSMUSG00000036863	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	1.675	0.0000	0.0001
Syf2	ENSMUSG00000028821	SYF2 homolog, RNA splicing factor (S. cerevisiae)	2.319	0.0000	0.0000
Syn3	ENSMUSG00000059602	synapsin III	2.592	0.0226	0.0489
Sync	ENSMUSG00000001333	syncoilin	1.748	0.0000	0.0000
Syncrip	ENSMUSG00000032423	synaptotagmin binding, cytoplasmic RNA interacting protein	1.596	0.0000	0.0000
Synj2bp	ENSMUSG00000090935	synaptojanin 2 binding protein	1.799	0.0000	0.0000
Synm	ENSMUSG00000030554	synemin, intermediate filament protein	1.615	0.0000	0.0001
Synpo2	ENSMUSG00000050315	synaptopodin 2	1.621	0.0000	0.0000
Syp	ENSMUSG00000031144	synaptophysin	2.686	0.0000	0.0000
Syt7	ENSMUSG00000024743	synaptotagmin VII	1.694	0.0007	0.0023
Szrd1	ENSMUSG00000040842	SUZ RNA binding domain containing 1	1.599	0.0000	0.0000
Taf1	ENSMUSG00000031314	TATA-box binding protein associated factor 1	1.543	0.0000	0.0000
Taf10	ENSMUSG00000043866	TATA-box binding protein associated factor 10	5.602	0.0000	0.0000
Taf12	ENSMUSG00000028899	TATA-box binding protein associated factor 12	1.719	0.0000	0.0000
Taf13	ENSMUSG00000048100	TATA-box binding protein associated factor 13	2.103	0.0000	0.0000
Taf15	ENSMUSG00000020680	TATA-box binding protein associated factor 15	4.208	0.0000	0.0000
Taf1a	ENSMUSG00000072258	TATA-box binding protein associated factor, RNA polymerase I, A	1.755	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Taf3	ENSMUSG00000025782	TATA-box binding protein associated factor 3	2.252	0.0000	0.0000
Taf4	ENSMUSG00000039117	TATA-box binding protein associated factor 4	1.590	0.0000	0.0000
Taf5	ENSMUSG00000025049	TATA-box binding protein associated factor 5	3.071	0.0000	0.0000
Tagln	ENSMUSG00000032085	transgelin	1.610	0.0077	0.0191
Tamalin	ENSMUSG00000000531	trafficking regulator and scaffold protein tamalin	2.994	0.0000	0.0000
Taok3	ENSMUSG00000061288	TAO kinase 3	1.514	0.0006	0.0019
Tardbp	ENSMUSG00000041459	TAR DNA binding protein	1.961	0.0000	0.0000
Tarsl2	ENSMUSG00000030515	threonyl-tRNA synthetase-like 2	1.802	0.0000	0.0000
Tbc1d12	ENSMUSG00000048720	TBC1D12: TBC1 domain family, member 12	1.983	0.0000	0.0000
Tbc1d20	ENSMUSG00000027465	TBC1 domain family, member 20	2.053	0.0000	0.0000
Tbca	ENSMUSG00000042043	tubulin cofactor A	1.820	0.0000	0.0000
Tbcc	ENSMUSG00000036430	tubulin-specific chaperone C	2.878	0.0000	0.0000
Tbcel	ENSMUSG00000037287	tubulin folding cofactor E-like	1.951	0.0000	0.0000
Tbk1	ENSMUSG00000020115	TANK-binding kinase 1	1.508	0.0001	0.0005
Tbkbp1	ENSMUSG00000038517	TBK1 binding protein 1	2.221	0.0000	0.0001
Tbpl1	ENSMUSG00000071359	TATA box binding protein-like 1	1.572	0.0000	0.0000
Tbx1	ENSMUSG00000009097	T-box 1	3.566	0.0000	0.0000
Tbx15	ENSMUSG00000027868	T-box 15	1.969	0.0226	0.0488
Tbx2	ENSMUSG00000000093	T-box 2	3.685	0.0000	0.0000
Tbx3	ENSMUSG00000018604	T-box 3	1.612	0.0002	0.0007
Tcea1-ps1	ENSMUSG00000067869	transcription elongation factor A (SII) 1, pseudogene 1	2.277	0.0016	0.0047
Tceal1	ENSMUSG00000049536	transcription elongation factor A (SII)-like 1	1.736	0.0001	0.0002
Tceal8	ENSMUSG00000051579	transcription elongation factor A (SII)-like 8	1.590	0.0000	0.0001
Tceal9	ENSMUSG00000042712	transcription elongation factor A like 9	1.756	0.0000	0.0000
Tcerg1	ENSMUSG00000024498	transcription elongation regulator 1 (CA150)	2.207	0.0000	0.0000
Tcf15	ENSMUSG00000068079	transcription factor 15	3.610	0.0000	0.0000
Tcf3	ENSMUSG00000020167	transcription factor 3	1.787	0.0000	0.0001
Tcf7l1	ENSMUSG00000055799	transcription factor 7 like 1 (T cell specific, HMG box)	1.572	0.0000	0.0002
Tchh	ENSMUSG00000052415	trichohyalin	1.624	0.0013	0.0039
Tchp	ENSMUSG00000002486	trichoplein, keratin filament binding	2.225	0.0000	0.0000
Tcp11l1	ENSMUSG00000027175	t-complex 11 like 1	2.281	0.0000	0.0000
Tcte2	ENSMUSG00000038347	t-complex-associated testis expressed 2	1.905	0.0281	0.0591

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tdg	ENSMUSG00000034674	thymine DNA glycosylase	2.833	0.0000	0.0002
Tdp2	ENSMUSG00000035958	tyrosyl-DNA phosphodiesterase 2	2.029	0.0000	0.0000
Tdrkh	ENSMUSG00000041912	tudor and KH domain containing protein	1.605	0.0011	0.0032
Tead2	ENSMUSG00000030796	TEA domain family member 2	1.846	0.0005	0.0015
Tead3	ENSMUSG00000002249	TEA domain family member 3	2.271	0.0000	0.0000
Tent4a	ENSMUSG00000034575	terminal nucleotidyltransferase 4A	1.974	0.0000	0.0000
Tent4b	ENSMUSG00000036779	terminal nucleotidyltransferase 4B	3.414	0.0000	0.0000
Terf1	ENSMUSG00000025925	telomeric repeat binding factor 1	2.903	0.0000	0.0000
Tes3-ps	ENSMUSG00000113255	testis derived transcript 3, pseudogene	1.592	0.0029	0.0080
Tesc	ENSMUSG00000029359	tescalcin	2.997	0.0000	0.0000
Tesk1	ENSMUSG00000028458	testis specific protein kinase 1	2.055	0.0000	0.0000
Tex30	ENSMUSG00000026049	testis expressed 30	2.117	0.0000	0.0000
Tex9	ENSMUSG00000090626	testis expressed gene 9	1.902	0.0048	0.0125
Tfam	ENSMUSG00000003923	transcription factor A, mitochondrial	1.804	0.0000	0.0000
Tfdp1	ENSMUSG00000038482	transcription factor Dp 1	2.104	0.0000	0.0000
Tfec	ENSMUSG00000029553	transcription factor EC	2.494	0.0330	0.0678
Tfpt	ENSMUSG00000006335	TCF3 (E2A) fusion partner	2.945	0.0000	0.0000
Tgfb1	ENSMUSG00000002603	transforming growth factor, beta 1	2.356	0.0000	0.0000
Tgfb3	ENSMUSG00000021253	transforming growth factor, beta 3	1.739	0.0000	0.0001
Tgs1	ENSMUSG00000028233	trimethylguanosine synthase 1	1.521	0.0000	0.0000
Thap12	ENSMUSG00000030753	THAP domain containing 12	1.627	0.0000	0.0000
Thg1l	ENSMUSG00000011254	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	2.325	0.0000	0.0000
Thoc2	ENSMUSG00000037475	THO complex 2	1.662	0.0000	0.0000
Thoc2l	ENSMUSG00000097392	THO complex subunit 2-like	2.143	0.0000	0.0000
Thra	ENSMUSG00000058756	thyroid hormone receptor alpha	1.806	0.0000	0.0000
Thumpd1	ENSMUSG00000030942	THUMP domain containing 1	2.615	0.0000	0.0000
Timeless	ENSMUSG00000039994	timeless circadian clock 1	2.244	0.0000	0.0000
Timm10	ENSMUSG00000027076	translocase of inner mitochondrial membrane 10	1.625	0.0000	0.0000
Timm29	ENSMUSG00000048429	translocase of inner mitochondrial membrane 29	2.030	0.0000	0.0000
Timm44	ENSMUSG00000002949	translocase of inner mitochondrial membrane 44	1.696	0.0000	0.0000
Timm8b	ENSMUSG00000039016	translocase of inner mitochondrial membrane 8B	1.681	0.0000	0.0000
Timmdc1	ENSMUSG00000002846	translocase of inner mitochondrial membrane domain containing 1	1.657	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Timp2	ENSMUSG00000017466	tissue inhibitor of metalloproteinase 2	1.672	0.0000	0.0002
Tle1	ENSMUSG00000008305	transducin-like enhancer of split 1	2.292	0.0000	0.0000
Tle5	ENSMUSG00000054452	TLE family member 5, transcriptional modulator	3.122	0.0000	0.0000
Tlk1	ENSMUSG00000041997	tousled-like kinase 1	1.577	0.0000	0.0000
Tlk2	ENSMUSG00000020694	tousled-like kinase 2 (Arabidopsis)	1.866	0.0000	0.0000
Tlnrd1	ENSMUSG00000070462	talin rod domain containing 1	2.550	0.0017	0.0050
Tm6sf1	ENSMUSG00000038623	transmembrane 6 superfamily member 1	2.042	0.0000	0.0000
Tm9sf3	ENSMUSG00000025016	transmembrane 9 superfamily member 3	2.175	0.0000	0.0000
Tma7	ENSMUSG00000091537	translational machinery associated 7	1.501	0.0000	0.0000
Tma7-ps	ENSMUSG00000059058	translational machinery associated 7 homolog (S. cerevisiae), pseudogene	2.935	0.0000	0.0000
Tmbim6	ENSMUSG00000023010	transmembrane BAX inhibitor motif containing 6	1.542	0.0000	0.0000
Tmc7	ENSMUSG00000042246	transmembrane channel-like gene family 7	1.777	0.0000	0.0000
Tmco6	ENSMUSG00000006850	transmembrane and coiled-coil domains 6	2.001	0.0000	0.0000
Tmed9	ENSMUSG00000058569	transmembrane p24 trafficking protein 9	1.630	0.0000	0.0000
Tmem101	ENSMUSG00000020921	transmembrane protein 101	3.265	0.0000	0.0000
Tmem127	ENSMUSG00000034850	transmembrane protein 127	1.752	0.0000	0.0000
Tmem138	ENSMUSG00000024666	transmembrane protein 138	1.755	0.0010	0.0031
Tmem150a	ENSMUSG00000055912	transmembrane protein 150A	2.177	0.0000	0.0000
Tmem158	ENSMUSG00000054871	transmembrane protein 158	5.720	0.0000	0.0000
Tmem160	ENSMUSG00000019158	transmembrane protein 160	5.004	0.0000	0.0000
Tmem164	ENSMUSG00000047045	transmembrane protein 164	1.806	0.0001	0.0005
Tmem165	ENSMUSG00000029234	transmembrane protein 165	3.166	0.0000	0.0000
Tmem170b	ENSMUSG00000087370	transmembrane protein 170B	1.579	0.0002	0.0007
Tmem181b-ps	ENSMUSG00000096780	transmembrane protein 181B, pseudogene	8.958	0.0002	0.0007
Tmem192	ENSMUSG00000025521	transmembrane protein 192	1.913	0.0000	0.0000
Tmem196	ENSMUSG00000048004	transmembrane protein 196	2.298	0.0000	0.0000
Tmem200b	ENSMUSG00000070720	transmembrane protein 200B	3.610	0.0000	0.0000
Tmem201	ENSMUSG00000044700	transmembrane protein 201	1.519	0.0001	0.0004
Tmem243	ENSMUSG00000079659	transmembrane protein 243, mitochondrial	1.861	0.0000	0.0000
Tmem248	ENSMUSG00000053094	transmembrane protein 248	1.622	0.0000	0.0000
Tmem250-ps	ENSMUSG00000087679	transmembrane protein 250, pseudogene	2.022	0.0003	0.0011
Tmem251	ENSMUSG00000046675	transmembrane protein 251	2.307	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem252	ENSMUSG00000048572	transmembrane protein 252	4.392	0.0349	0.0712
Tmem259	ENSMUSG00000013858	transmembrane protein 259	2.365	0.0000	0.0000
Tmem263	ENSMUSG00000060935	transmembrane protein 263	1.799	0.0000	0.0000
Tmem30a	ENSMUSG00000032328	transmembrane protein 30A	1.734	0.0000	0.0000
Tmem38b	ENSMUSG00000028420	transmembrane protein 38B	1.770	0.0005	0.0018
Tmem51os1	ENSMUSG00000073728	Tmem51 opposite strand 1	2.798	0.0002	0.0008
Tmem64	ENSMUSG00000043252	transmembrane protein 64	1.825	0.0000	0.0000
Tmem65	ENSMUSG00000062373	transmembrane protein 65	2.228	0.0000	0.0000
Tmem87a	ENSMUSG00000033808	transmembrane protein 87A	1.806	0.0000	0.0000
Tmf1	ENSMUSG00000030059	TATA element modulatory factor 1	1.596	0.0000	0.0001
Tmpo	ENSMUSG00000019961	thymopoietin	1.855	0.0000	0.0000
Tmx1	ENSMUSG00000021072	thioredoxin-related transmembrane protein 1	2.124	0.0000	0.0000
Tmx4	ENSMUSG00000034723	thioredoxin-related transmembrane protein 4	1.505	0.0000	0.0000
Tnfrsf11a	ENSMUSG00000026321	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	2.126	0.0005	0.0015
Tnfsf10	ENSMUSG00000039304	tumor necrosis factor (ligand) superfamily, member 10	1.516	0.0092	0.0222
Tnip2	ENSMUSG00000059866	TNFAIP3 interacting protein 2	2.079	0.0000	0.0000
Tnks2	ENSMUSG00000024811	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	1.802	0.0000	0.0000
Tnnc1	ENSMUSG00000091898	troponin C, cardiac/slow skeletal	2.063	0.0000	0.0000
Tnnt1	ENSMUSG00000064179	troponin T1, skeletal, slow	1.631	0.0000	0.0000
Tnnt2	ENSMUSG00000026414	troponin T2, cardiac	3.295	0.0000	0.0000
Tnnt3	ENSMUSG00000061723	troponin T3, skeletal, fast	2.659	0.0153	0.0347
Tnrc18	ENSMUSG00000039477	trinucleotide repeat containing 18	1.771	0.0000	0.0000
Tnrc6b	ENSMUSG00000047888	trinucleotide repeat containing 6b	1.502	0.0000	0.0000
Tnrc6c	ENSMUSG00000025571	trinucleotide repeat containing 6C	2.091	0.0000	0.0000
Tob1	ENSMUSG00000037573	transducer of ErbB-2.1	1.774	0.0000	0.0000
Tom1l1	ENSMUSG00000020541	target of myb1-like 1 (chicken)	1.602	0.0000	0.0000
Tomm70a	ENSMUSG00000022752	translocase of outer mitochondrial membrane 70A	2.173	0.0000	0.0000
Tomt	ENSMUSG00000078630	transmembrane O-methyltransferase	10.047	0.0019	0.0054
Top1	ENSMUSG00000070544	topoisomerase (DNA) I	2.284	0.0000	0.0000
Top2a	ENSMUSG00000020914	topoisomerase (DNA) II alpha	1.869	0.0168	0.0377
Tox	ENSMUSG00000041272	thymocyte selection-associated high mobility group box	2.366	0.0000	0.0001
Tox2	ENSMUSG00000074607	TOX high mobility group box family member 2	2.414	0.0000	0.0001

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tpbg	ENSMUSG00000035274	trophoblast glycoprotein	1.834	0.0281	0.0590
Tpm1	ENSMUSG00000032366	tropomyosin 1, alpha	1.597	0.0000	0.0000
Tpm2	ENSMUSG00000028464	tropomyosin 2, beta	1.621	0.0004	0.0015
Tpm3	ENSMUSG00000027940	tropomyosin 3, gamma	2.598	0.0000	0.0000
Tpm3-rs7	ENSMUSG00000058126	tropomyosin 3, related sequence 7	3.147	0.0000	0.0001
Tpm4	ENSMUSG00000031799	tropomyosin 4	1.638	0.0000	0.0002
Tpr	ENSMUSG00000006005	translocated promoter region, nuclear basket protein	1.765	0.0000	0.0000
Tpt1	ENSMUSG00000060126	tumor protein, translationally-controlled 1	1.874	0.0000	0.0000
Traf3ip1	ENSMUSG00000034292	TRAF3 interacting protein 1	2.754	0.0000	0.0000
Trak1	ENSMUSG00000032536	trafficking protein, kinesin binding 1	1.719	0.0000	0.0000
Trappc3	ENSMUSG00000028847	trafficking protein particle complex 3	1.915	0.0000	0.0000
Trappc6b	ENSMUSG00000020993	trafficking protein particle complex 6B	3.242	0.0000	0.0000
Trim27	ENSMUSG00000021326	tripartite motif-containing 27	2.473	0.0000	0.0000
Trim34a	ENSMUSG00000056144	tripartite motif-containing 34A	1.947	0.0004	0.0013
Trim44	ENSMUSG00000027189	tripartite motif-containing 44	1.900	0.0000	0.0000
Trim47	ENSMUSG00000020773	tripartite motif-containing 47	1.814	0.0061	0.0155
Trim68	ENSMUSG00000073968	tripartite motif-containing 68	1.579	0.0000	0.0000
Trim72	ENSMUSG00000042828	tripartite motif-containing 72	2.000	0.0000	0.0000
Trim8	ENSMUSG00000025034	tripartite motif-containing 8	3.322	0.0000	0.0000
Triobp	ENSMUSG00000033088	TRIO and F-actin binding protein	1.503	0.0000	0.0000
Trip13	ENSMUSG00000021569	thyroid hormone receptor interactor 13	2.418	0.0024	0.0068
Trir	ENSMUSG00000041203	telomerase RNA component interacting RNase	13.228	0.0000	0.0000
Trmt10a	ENSMUSG00000004127	tRNA methyltransferase 10A	2.105	0.0000	0.0000
Trmt10c	ENSMUSG00000044763	tRNA methyltransferase 10C, mitochondrial RNase P subunit	1.507	0.0000	0.0000
Trnau1ap	ENSMUSG00000028898	tRNA selenocysteine 1 associated protein 1	1.685	0.0025	0.0070
Trnp1	ENSMUSG00000056596	TMF1-regulated nuclear protein 1	2.927	0.0111	0.0263
Trp53bp2	ENSMUSG00000026510	transformation related protein 53 binding protein 2	1.735	0.0000	0.0000
Trp53rka	ENSMUSG00000039725	transformation related protein 53 regulating kinase A	1.845	0.0000	0.0000
Trp53rkb	ENSMUSG00000042854	transformation related protein 53 regulating kinase B	2.232	0.0000	0.0000
Trub1	ENSMUSG00000025086	TruB pseudouridine (psi) synthase family member 1	2.264	0.0000	0.0000
Tsc22d2	ENSMUSG00000027806	TSC22 domain family, member 2	2.715	0.0000	0.0000
Tsen34	ENSMUSG00000035585	tRNA splicing endonuclease subunit 34	3.060	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tslp	ENSMUSG00000024379	thymic stromal lymphopoietin	2.324	0.0001	0.0002
Tsnax	ENSMUSG00000056820	translin-associated factor X	1.846	0.0000	0.0000
Tspan17	ENSMUSG00000025875	tetraspanin 17	2.588	0.0000	0.0000
Tspan5	ENSMUSG00000028152	tetraspanin 5	1.654	0.0002	0.0007
Tspyl1	ENSMUSG00000047514	testis-specific protein, Y-encoded-like 1	1.507	0.0002	0.0007
Tspyl2	ENSMUSG00000041096	TSPY-like 2	2.089	0.0000	0.0000
Tsr1	ENSMUSG00000038335	TSR1 20S rRNA accumulation	1.644	0.0000	0.0000
Tstd3	ENSMUSG00000028251	thiosulfate sulfurtransferase (rhodanese)-like domain containing 3	1.699	0.0000	0.0000
Ttc1	ENSMUSG00000041278	tetratricopeptide repeat domain 1	1.673	0.0000	0.0000
Ttc30a1	ENSMUSG00000075271	tetratricopeptide repeat domain 30A1	1.623	0.0033	0.0089
Ttc33	ENSMUSG00000022151	tetratricopeptide repeat domain 33	1.687	0.0000	0.0000
Ttc39c	ENSMUSG00000024424	tetratricopeptide repeat domain 39C	1.526	0.0010	0.0029
Ttc9	ENSMUSG00000042734	tetratricopeptide repeat domain 9	2.262	0.0006	0.0020
Ttll11	ENSMUSG00000026885	tubulin tyrosine ligase-like family, member 11	3.552	0.0000	0.0000
Tuba1a	ENSMUSG00000072235	tubulin, alpha 1A	1.705	0.0039	0.0103
Tuba1b	ENSMUSG00000023004	tubulin, alpha 1B	1.977	0.0005	0.0015
Tubb1	ENSMUSG00000016255	tubulin, beta 1 class VI	3.052	0.0354	0.0719
Tubb2a	ENSMUSG00000058672	tubulin, beta 2A class IIA	1.868	0.0000	0.0000
Tubb4b-ps1	ENSMUSG00000095159	tubulin, beta 4B class IVB, pseudogene 1	16.059	0.0000	0.0000
Tusc1	ENSMUSG00000054000	tumor suppressor candidate 1	4.275	0.0000	0.0000
Tut7	ENSMUSG00000035248	terminal uridylyl transferase 7	1.765	0.0000	0.0000
Tvp23b	ENSMUSG00000014177	trans-golgi network vesicle protein 23B	2.147	0.0000	0.0000
Twist1	ENSMUSG00000035799	twist basic helix-loop-helix transcription factor 1	2.509	0.0001	0.0002
Twist2	ENSMUSG00000007805	twist basic helix-loop-helix transcription factor 2	5.081	0.0000	0.0000
Txnip	ENSMUSG00000038393	thioredoxin interacting protein	1.649	0.0005	0.0015
U2surp	ENSMUSG00000032407	U2 snRNP-associated SURP domain containing	1.728	0.0000	0.0000
Uba3	ENSMUSG00000030061	ubiquitin-like modifier activating enzyme 3	2.295	0.0000	0.0000
Uba5	ENSMUSG00000032557	ubiquitin-like modifier activating enzyme 5	1.796	0.0000	0.0000
Uba52	ENSMUSG00000090137	ubiquitin A-52 residue ribosomal protein fusion product 1	19.384	0.0000	0.0000
Ube2d1	ENSMUSG00000019927	ubiquitin-conjugating enzyme E2D 1	1.779	0.0000	0.0000
Ube2d2a	ENSMUSG00000091896	ubiquitin-conjugating enzyme E2D 2A	1.990	0.0000	0.0001
Ube2d3	ENSMUSG00000078578	ubiquitin-conjugating enzyme E2D 3	1.998	0.0000	0.0000

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Ube2e2	ENSMUSG00000058317	ubiquitin-conjugating enzyme E2E 2	1.697	0.0000	0.0000
Ube2g2	ENSMUSG00000009293	ubiquitin-conjugating enzyme E2G 2	1.841	0.0000	0.0000
Ube2h	ENSMUSG00000039159	ubiquitin-conjugating enzyme E2H	3.095	0.0000	0.0000
Ube2j2	ENSMUSG00000023286	ubiquitin-conjugating enzyme E2J 2	2.595	0.0000	0.0000
Ube2k	ENSMUSG00000029203	ubiquitin-conjugating enzyme E2K	1.985	0.0000	0.0000
Ube2m	ENSMUSG00000005575	ubiquitin-conjugating enzyme E2M	2.338	0.0000	0.0000
Ube2q1	ENSMUSG00000042572	ubiquitin-conjugating enzyme E2Q family member 1	2.995	0.0000	0.0000
Ube2q2	ENSMUSG00000032307	ubiquitin-conjugating enzyme E2Q family member 2	1.953	0.0000	0.0000
Ube2r2	ENSMUSG00000036241	ubiquitin-conjugating enzyme E2R 2	3.692	0.0000	0.0000
Ube2s	ENSMUSG00000060860	ubiquitin-conjugating enzyme E2S	6.037	0.0000	0.0000
Ube2v2	ENSMUSG00000022674	ubiquitin-conjugating enzyme E2 variant 2	1.788	0.0001	0.0004
Ube2w	ENSMUSG00000025939	ubiquitin-conjugating enzyme E2W (putative)	1.649	0.0000	0.0000
Ubfd1	ENSMUSG00000030870	ubiquitin family domain containing 1	2.127	0.0000	0.0000
Ubqln4	ENSMUSG00000008604	ubiquilin 4	1.742	0.0000	0.0001
Ubtd2	ENSMUSG00000044949	ubiquitin domain containing 2	2.622	0.0000	0.0000
Ubtf	ENSMUSG00000020923	upstream binding transcription factor, RNA polymerase I	2.648	0.0000	0.0000
Ubxn1	ENSMUSG00000071655	UBX domain protein 1	2.035	0.0000	0.0000
Uchl5	ENSMUSG00000018189	ubiquitin carboxyl-terminal esterase L5	1.603	0.0000	0.0000
Uck2	ENSMUSG00000026558	uridine-cytidine kinase 2	1.613	0.0023	0.0064
Ucp3	ENSMUSG00000032942	uncoupling protein 3 (mitochondrial, proton carrier)	1.631	0.0127	0.0296
Ugcg	ENSMUSG00000028381	UDP-glucose ceramide glucosyltransferase	1.819	0.0000	0.0000
Ugt1a7c	ENSMUSG00000090124	UDP glucuronosyltransferase 1 family, polypeptide A7C	3.472	0.0000	0.0002
Uhmk1	ENSMUSG00000026667	U2AF homology motif (UHM) kinase 1	1.609	0.0000	0.0000
Uhrf2	ENSMUSG00000024817	ubiquitin-like, containing PHD and RING finger domains 2	1.756	0.0001	0.0003
Uimc1	ENSMUSG00000025878	ubiquitin interaction motif containing 1	2.337	0.0000	0.0000
Ulk4	ENSMUSG00000040936	unc-51-like kinase 4	5.500	0.0040	0.0107
Unc119	ENSMUSG00000002058	unc-119 lipid binding chaperone	2.868	0.0000	0.0000
Upf1	ENSMUSG00000058301	UPF1 regulator of nonsense transcripts homolog (yeast)	2.065	0.0000	0.0000
Upf2	ENSMUSG00000043241	UPF2 regulator of nonsense transcripts homolog (yeast)	2.204	0.0000	0.0000
Upf3a	ENSMUSG00000038398	UPF3 regulator of nonsense transcripts homolog A (yeast)	3.316	0.0000	0.0000
Upf3b	ENSMUSG00000036572	UPF3 regulator of nonsense transcripts homolog B (yeast)	2.200	0.0000	0.0000
Upp2	ENSMUSG00000026839	uridine phosphorylase 2	5.696	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Uqcrb	ENSMUSG00000021520	ubiquinol-cytochrome c reductase binding protein	2.496	0.0000	0.0000
Uri1	ENSMUSG00000030421	URI1, prefoldin-like chaperone	1.581	0.0000	0.0001
Urm1	ENSMUSG00000069020	ubiquitin related modifier 1	1.643	0.0000	0.0000
Usf2	ENSMUSG00000058239	upstream transcription factor 2	2.971	0.0000	0.0000
Usp1	ENSMUSG00000028560	ubiquitin specific peptidase 1	2.146	0.0000	0.0000
Usp12	ENSMUSG00000029640	ubiquitin specific peptidase 12	1.652	0.0000	0.0000
Usp2	ENSMUSG00000032010	ubiquitin specific peptidase 2	1.655	0.0031	0.0085
Usp27x	ENSMUSG00000046269	ubiquitin specific peptidase 27, X chromosome	3.055	0.0000	0.0000
Usp31	ENSMUSG00000063317	ubiquitin specific peptidase 31	1.854	0.0000	0.0000
Usp47	ENSMUSG00000059263	ubiquitin specific peptidase 47	1.681	0.0000	0.0000
Ust	ENSMUSG00000047712	uronyl-2-sulfotransferase	1.527	0.0013	0.0038
Utp14b	ENSMUSG00000079470	UTP14B small subunit processome component	2.567	0.0001	0.0002
Utp18	ENSMUSG00000054079	UTP18 small subunit processome component	4.081	0.0000	0.0000
Utp3	ENSMUSG00000070697	UTP3 small subunit processome component	2.827	0.0000	0.0000
Uvrag	ENSMUSG00000035354	UV radiation resistance associated gene	1.573	0.0128	0.0298
Vamp1	ENSMUSG00000030337	vesicle-associated membrane protein 1	1.588	0.0000	0.0001
Vamp2	ENSMUSG00000020894	vesicle-associated membrane protein 2	1.962	0.0000	0.0000
Vamp3	ENSMUSG00000028955	vesicle-associated membrane protein 3	1.606	0.0000	0.0000
Vamp4	ENSMUSG00000026696	vesicle-associated membrane protein 4	1.548	0.0000	0.0000
Vamp8	ENSMUSG00000050732	vesicle-associated membrane protein 8	2.770	0.0000	0.0000
Vangl2	ENSMUSG00000026556	VANGL planar cell polarity 2	1.677	0.0000	0.0000
Vapa	ENSMUSG00000024091	vesicle-associated membrane protein, associated protein A	1.878	0.0000	0.0000
Vapb	ENSMUSG00000054455	vesicle-associated membrane protein, associated protein B and C	2.181	0.0000	0.0000
Vcp	ENSMUSG00000028452	valosin containing protein	1.989	0.0000	0.0000
Vdac1	ENSMUSG00000020402	voltage-dependent anion channel 1	1.831	0.0000	0.0000
Vdac3-ps1	ENSMUSG00000075053	voltage-dependent anion channel 3, pseudogene 1	3.988	0.0000	0.0000
Vegfa	ENSMUSG00000023951	vascular endothelial growth factor A	2.180	0.0000	0.0000
Vegfb	ENSMUSG00000024962	vascular endothelial growth factor B	1.717	0.0000	0.0002
Vhl	ENSMUSG00000033933	von Hippel-Lindau tumor suppressor	1.510	0.0000	0.0000
Vopp1	ENSMUSG00000037788	vesicular, overexpressed in cancer, prosurvival protein 1	1.783	0.0000	0.0000
Vps45	ENSMUSG00000015747	vacuolar protein sorting 45	1.629	0.0000	0.0000
Vstm2l	ENSMUSG00000037843	V-set and transmembrane domain containing 2-like	4.707	0.0081	0.0200

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Vwc2	ENSMUSG00000050830	von Willebrand factor C domain containing 2	4.001	0.0000	0.0000
Wapl	ENSMUSG00000041408	WAPL cohesin release factor	1.975	0.0000	0.0000
Wasf3	ENSMUSG00000029636	WASP family, member 3	1.543	0.0097	0.0234
Wbp11	ENSMUSG00000030216	WW domain binding protein 11	1.670	0.0000	0.0000
Wbp4	ENSMUSG00000022023	WW domain binding protein 4	1.748	0.0000	0.0000
Wdr26	ENSMUSG00000038733	WD repeat domain 26	1.835	0.0000	0.0000
Wdr31	ENSMUSG00000028391	WD repeat domain 31	2.151	0.0191	0.0422
Wdr43	ENSMUSG00000041057	WD repeat domain 43	1.904	0.0000	0.0000
Whamm	ENSMUSG00000045795	WAS protein homolog associated with actin, golgi membranes and microtubules	1.531	0.0329	0.0676
Whrn	ENSMUSG00000039137	whirlin	2.314	0.0000	0.0000
Wnt5a	ENSMUSG00000021994	wingless-type MMTV integration site family, member 5A	2.197	0.0000	0.0000
Wnt5b	ENSMUSG00000030170	wingless-type MMTV integration site family, member 5B	2.298	0.0000	0.0002
Wnt9a	ENSMUSG00000000126	wingless-type MMTV integration site family, member 9A	1.521	0.0004	0.0014
Wrnip1	ENSMUSG00000021400	Werner helicase interacting protein 1	1.943	0.0000	0.0001
Wsb1	ENSMUSG00000017677	WD repeat and SOCS box-containing 1	1.774	0.0000	0.0000
Wtap	ENSMUSG00000060475	WT1 associating protein	3.047	0.0000	0.0000
Wtip	ENSMUSG00000036459	WT1 interacting protein	2.812	0.0000	0.0000
Xirp2	ENSMUSG00000027022	xin actin-binding repeat containing 2	1.585	0.0045	0.0117
Xkr6	ENSMUSG00000035067	X-linked Kx blood group related 6	1.620	0.0151	0.0343
Xkr8	ENSMUSG00000037752	X-linked Kx blood group related 8	1.756	0.0000	0.0001
Xlr	ENSMUSG00000054626	X-linked lymphocyte-regulated	1.696	0.0051	0.0131
Xndc1	ENSMUSG00000099481	Xrcc1 N-terminal domain containing 1	1.744	0.0189	0.0419
Xpa	ENSMUSG00000028329	xeroderma pigmentosum, complementation group A	3.005	0.0000	0.0000
Xylt2	ENSMUSG00000020868	xylosyltransferase II	1.555	0.0338	0.0692
Yae1d1	ENSMUSG00000075054	Yae1 domain containing 1	1.536	0.0002	0.0008
Yap1	ENSMUSG00000053110	yes-associated protein 1	1.512	0.0000	0.0000
Ybx1	ENSMUSG00000028639	Y box protein 1	4.441	0.0000	0.0000
Ybx2	ENSMUSG00000018554	Y box protein 2	2.499	0.0000	0.0000
Ybx3	ENSMUSG00000030189	Y box protein 3	3.668	0.0000	0.0000
Yeats4	ENSMUSG00000020171	YEATS domain containing 4	2.539	0.0000	0.0000
Yes1	ENSMUSG00000014932	YES proto-oncogene 1, Src family tyrosine kinase	1.611	0.0000	0.0000
Yipf4	ENSMUSG00000024072	Yip1 domain family, member 4	1.885	0.0000	0.0000

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Yipf6	ENSMUSG00000047694	Yip1 domain family, member 6	1.677	0.0000	0.0000
Ykt6	ENSMUSG00000002741	YKT6 v-SNARE homolog (S. cerevisiae)	1.945	0.0000	0.0000
Ylpm1	ENSMUSG00000021244	YLP motif containing 1	1.713	0.0000	0.0000
Ypel3	ENSMUSG00000042675	yippee like 3	4.519	0.0000	0.0000
Ypel5	ENSMUSG00000039770	yippee like 5	1.891	0.0000	0.0000
Yrdc	ENSMUSG00000028889	yrdC domain containing (E.coli)	1.821	0.0001	0.0005
Ythdc1	ENSMUSG00000035851	YTH domain containing 1	2.576	0.0000	0.0000
Ythdf1	ENSMUSG00000038848	YTH N6-methyladenosine RNA binding protein 1	1.830	0.0000	0.0000
Ywhae	ENSMUSG00000020849	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2.865	0.0000	0.0000
Ywhah	ENSMUSG00000018965	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	3.246	0.0000	0.0000
Ywhaz	ENSMUSG00000022285	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	2.442	0.0000	0.0000
Yy1	ENSMUSG00000021264	YY1 transcription factor	2.482	0.0000	0.0000
Zadh2	ENSMUSG00000049090	zinc binding alcohol dehydrogenase, domain containing 2	1.535	0.0000	0.0000
Zbtb10	ENSMUSG00000069114	zinc finger and BTB domain containing 10	1.841	0.0000	0.0000
Zbtb11os1	ENSMUSG00000102101	zinc finger and BTB domain containing 11, opposite strand 1	4.356	0.0000	0.0000
Zbtb12	ENSMUSG00000049823	zinc finger and BTB domain containing 12	1.736	0.0000	0.0000
Zbtb18	ENSMUSG00000063659	zinc finger and BTB domain containing 18	1.670	0.0000	0.0000
Zbtb41	ENSMUSG00000033964	zinc finger and BTB domain containing 41	1.783	0.0000	0.0000
Zbtb42	ENSMUSG00000037638	zinc finger and BTB domain containing 42	1.621	0.0001	0.0002
Zbtb44	ENSMUSG00000047412	zinc finger and BTB domain containing 44	2.028	0.0000	0.0000
Zbtb6	ENSMUSG00000066798	zinc finger and BTB domain containing 6	1.571	0.0000	0.0000
Zbtb7a	ENSMUSG00000035011	zinc finger and BTB domain containing 7a	2.480	0.0000	0.0000
Zc3h11a	ENSMUSG00000102976	zinc finger CCCH type containing 11A	2.044	0.0000	0.0000
Zc3h12d	ENSMUSG00000039981	zinc finger CCCH type containing 12D	3.238	0.0003	0.0011
Zc3h13	ENSMUSG00000022000	zinc finger CCCH type containing 13	2.308	0.0000	0.0000
Zc3h15	ENSMUSG00000027091	zinc finger CCCH-type containing 15	2.534	0.0000	0.0000
Zc3h18	ENSMUSG00000017478	zinc finger CCCH-type containing 18	1.566	0.0000	0.0000
Zc3h8	ENSMUSG00000027387	zinc finger CCCH type containing 8	1.727	0.0000	0.0001
Zcchc10	ENSMUSG00000018239	zinc finger, CCHC domain containing 10	2.679	0.0000	0.0000
Zcchc17	ENSMUSG00000028772	zinc finger, CCHC domain containing 17	1.700	0.0000	0.0000

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Zcchc2	ENSMUSG00000038866	zinc finger, CCHC domain containing 2	1.739	0.0000	0.0000
Zcchc3	ENSMUSG00000074682	zinc finger, CCHC domain containing 3	2.161	0.0000	0.0000
Zcrb1	ENSMUSG00000022635	zinc finger CCHC-type and RNA binding motif 1	2.252	0.0000	0.0000
Zcwpw1	ENSMUSG00000037108	zinc finger, CW type with PWWP domain 1	2.253	0.0002	0.0007
Zdhhc14	ENSMUSG00000034265	zinc finger, DHHC domain containing 14	1.700	0.0001	0.0005
Zdhhc2	ENSMUSG00000039470	zinc finger, DHHC domain containing 2	1.656	0.0005	0.0016
Zdhhc7	ENSMUSG00000031823	zinc finger, DHHC domain containing 7	1.793	0.0000	0.0000
Zeb2os	ENSMUSG00000052248	zinc finger E-box binding homeobox 2, opposite strand	4.609	0.0000	0.0000
Zfand1	ENSMUSG00000039795	zinc finger, AN1-type domain 1	1.507	0.0009	0.0029
Zfand6	ENSMUSG00000030629	zinc finger, AN1-type domain 6	1.506	0.0000	0.0000
Zfas1	ENSMUSG00000074578	zinc finger, NFX1-type containing 1, antisense RNA 1	2.953	0.0000	0.0002
Zfp207	ENSMUSG00000017421	zinc finger protein 207	2.027	0.0000	0.0000
Zfp217	ENSMUSG00000052056	zinc finger protein 217	1.524	0.0000	0.0000
Zfp251	ENSMUSG00000022526	zinc finger protein 251	1.613	0.0000	0.0000
Zfp280b	ENSMUSG00000049764	zinc finger protein 280B	1.599	0.0000	0.0000
Zfp326	ENSMUSG00000029290	zinc finger protein 326	1.619	0.0000	0.0000
Zfp329	ENSMUSG00000057894	zinc finger protein 329	1.633	0.0030	0.0083
Zfp330	ENSMUSG00000031711	zinc finger protein 330	2.721	0.0000	0.0000
Zfp335os	ENSMUSG00000085436	zinc finger protein 335, opposite strand	3.336	0.0000	0.0000
Zfp362	ENSMUSG00000028799	zinc finger protein 362	1.603	0.0000	0.0000
Zfp369	ENSMUSG00000021514	zinc finger protein 369	1.734	0.0000	0.0000
Zfp36l1	ENSMUSG00000021127	zinc finger protein 36, C3H type-like 1	1.512	0.0000	0.0000
Zfp36l2	ENSMUSG00000045817	zinc finger protein 36, C3H type-like 2	2.881	0.0000	0.0000
Zfp445	ENSMUSG00000047036	zinc finger protein 445	1.533	0.0000	0.0001
Zfp451	ENSMUSG00000042197	zinc finger protein 451	1.774	0.0000	0.0000
Zfp462	ENSMUSG00000060206	zinc finger protein 462	1.652	0.0000	0.0000
Zfp513	ENSMUSG00000043059	zinc finger protein 513	2.424	0.0000	0.0000
Zfp579	ENSMUSG00000051550	zinc finger protein 579	1.948	0.0055	0.0141
Zfp593	ENSMUSG00000028840	zinc finger protein 593	2.825	0.0003	0.0011
Zfp622	ENSMUSG00000052253	zinc finger protein 622	4.051	0.0000	0.0000
Zfp628	ENSMUSG00000074406	zinc finger protein 628	1.678	0.0033	0.0089
Zfp641	ENSMUSG00000022987	zinc finger protein 641	1.547	0.0003	0.0009

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**
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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp667	ENSMUSG00000054893	zinc finger protein 667	1.855	0.0000	0.0000
Zfp703	ENSMUSG00000085795	zinc finger protein 703	2.014	0.0005	0.0017
Zfp710	ENSMUSG00000048897	zinc finger protein 710	1.579	0.0000	0.0000
Zfp740	ENSMUSG00000046897	zinc finger protein 740	1.607	0.0000	0.0000
Zfp787	ENSMUSG00000046792	zinc finger protein 787	1.787	0.0000	0.0000
Zfp821	ENSMUSG00000031728	zinc finger protein 821	2.266	0.0000	0.0000
Zfp827	ENSMUSG00000071064	zinc finger protein 827	2.050	0.0000	0.0000
Zfp830	ENSMUSG00000046010	zinc finger protein 830	2.568	0.0000	0.0000
Zfp839	ENSMUSG00000021271	zinc finger protein 839	2.315	0.0000	0.0000
Zfp84	ENSMUSG00000046185	zinc finger protein 84	1.916	0.0000	0.0000
Zfp870	ENSMUSG00000095325	zinc finger protein 870	1.564	0.0000	0.0000
Zfp938	ENSMUSG00000062931	zinc finger protein 938	3.868	0.0000	0.0000
Zfp982	ENSMUSG00000078496	zinc finger protein 982	1.756	0.0001	0.0004
Zfp991	ENSMUSG00000067916	zinc finger protein 991	1.653	0.0093	0.0226
Zfpm1	ENSMUSG00000049577	zinc finger protein, multitype 1	3.704	0.0000	0.0000
Zfr2	ENSMUSG00000034949	zinc finger RNA binding protein 2	1.543	0.0039	0.0104
Zfta	ENSMUSG00000053080	zinc finger translocation associated	2.333	0.0000	0.0000
Zgpat	ENSMUSG00000027582	zinc finger, CCCH-type with G patch domain	1.532	0.0046	0.0121
Zmat2	ENSMUSG00000001383	zinc finger, matrin type 2	3.074	0.0000	0.0000
Zmynd11	ENSMUSG00000021156	zinc finger, MYND domain containing 11	1.547	0.0000	0.0000
Zmynd19	ENSMUSG00000026974	zinc finger, MYND domain containing 19	1.906	0.0000	0.0000
Znhit6	ENSMUSG00000074182	zinc finger, HIT type 6	2.387	0.0000	0.0000
Znrf1	ENSMUSG00000033545	zinc and ring finger 1	2.403	0.0000	0.0000
Znrf2	ENSMUSG00000058446	zinc and ring finger 2	2.448	0.0000	0.0000
Zpbp	ENSMUSG00000020193	zona pellucida binding protein	2.641	0.0003	0.0009
Zranb1	ENSMUSG00000030967	zinc finger, RAN-binding domain containing 1	1.583	0.0034	0.0092
Zranb2	ENSMUSG00000028180	zinc finger, RAN-binding domain containing 2	2.054	0.0000	0.0000
Zrsr1	ENSMUSG00000044068	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	1.899	0.0000	0.0000
Zrsr2	ENSMUSG00000031370	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	3.234	0.0000	0.0000
Zscan29	ENSMUSG00000050619	zinc finger SCAN domains 29	1.818	0.0000	0.0000
Zswim4	ENSMUSG00000035671	zinc finger SWIM-type containing 4	1.592	0.0034	0.0092
Zswim9	ENSMUSG00000070814	zinc finger SWIM-type containing 9	1.962	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zxdc	ENSMUSG00000034430	ZXD family zinc finger C	1.743	0.0021	0.0061
	ENSMUSG00000095742		25.900	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610005C13Rik	ENSMUSG00000109644	RIKEN cDNA 0610005C13 gene	-3.817	0.0470	0.0917
0610012D04Rik	ENSMUSG00000089755	RIKEN cDNA 0610012D04 gene	-4.077	0.0085	0.0209
0610012G03Rik	ENSMUSG00000107002	RIKEN cDNA 0610012G03 gene	-2.366	0.0000	0.0000
0610025J13Rik	ENSMUSG00000046683	RIKEN cDNA 0610025J13 gene	-1.779	0.0223	0.0483
1010001B22Rik	ENSMUSG00000097863	RIKEN cDNA 1010001B22 gene	-4.589	0.0002	0.0006
1110002O04Rik	ENSMUSG00000102531	RIKEN cDNA 1110002O04 gene	-5.920	0.0039	0.0103
1110017D15Rik	ENSMUSG00000028441	RIKEN cDNA 1110017D15 gene	-8.878	0.0367	0.0742
1110019D14Rik	ENSMUSG00000097616	RIKEN cDNA 1110019D14 gene	-2.850	0.0046	0.0120
1110038B12Rik	ENSMUSG00000092203	RIKEN cDNA 1110038B12 gene	-2.944	0.0001	0.0003
1190007I07Rik	ENSMUSG00000063320	RIKEN cDNA 1190007I07 gene	-2.644	0.0000	0.0000
1600020E01Rik	ENSMUSG00000097048	RIKEN cDNA 1600020E01 gene	-1.650	0.0162	0.0365
1700001O22Rik	ENSMUSG00000044320	RIKEN cDNA 1700001O22 gene	-2.240	0.0030	0.0081
1700003E16Rik	ENSMUSG00000030030	RIKEN cDNA 1700003E16 gene	-4.314	0.0144	0.0329
1700007L15Rik	ENSMUSG00000097318	RIKEN cDNA 1700007L15 gene	-2.294	0.0027	0.0076
1700008O03Rik	ENSMUSG00000008028	RIKEN cDNA 1700008O03 gene	-16.044	0.0159	0.0360
1700017B05Rik	ENSMUSG00000032300	RIKEN cDNA 1700017B05 gene	-2.071	0.0000	0.0001
1700037H04Rik	ENSMUSG00000027327	RIKEN cDNA 1700037H04 gene	-1.710	0.0002	0.0008
1700088E04Rik	ENSMUSG00000033029	RIKEN cDNA 1700088E04 gene	-2.017	0.0023	0.0064
1700101I11Rik	ENSMUSG00000097675	RIKEN cDNA 1700101I11 gene	-1.603	0.0150	0.0341
1700102H20Rik	ENSMUSG00000116852	RIKEN cDNA 1700102H20 gene	-5.244	0.0047	0.0122
1700120C14Rik	ENSMUSG00000100599	RIKEN cDNA 1700120C14 gene	-2.581	0.0000	0.0000
1810021B22Rik	ENSMUSG00000087331	RIKEN cDNA 1810021B22 gene	-2.405	0.0000	0.0000
1810024B03Rik	ENSMUSG00000044145	RIKEN cDNA 1810024B03 gene	-3.933	0.0002	0.0006
1810044D09Rik	ENSMUSG00000100680	RIKEN cDNA 1810044D09 gene	-3.576	0.0000	0.0000
1810055G02Rik	ENSMUSG00000035372	RIKEN cDNA 1810055G02 gene	-1.813	0.0000	0.0001
1810058I24Rik	ENSMUSG00000073155	RIKEN cDNA 1810058I24 gene	-2.756	0.0000	0.0000
2210408F21Rik	ENSMUSG00000087380	RIKEN cDNA 2210408F21 gene	-1.586	0.0000	0.0000
2310001K24Rik	ENSMUSG00000053353	RIKEN cDNA 2310001K24 gene	-2.838	0.0103	0.0247
2310002D06Rik	ENSMUSG00000112701	RIKEN cDNA 2310002D06 gene	-7.044	0.0000	0.0002
2310011J03Rik	ENSMUSG00000020133	RIKEN cDNA 2310011J03 gene	-1.854	0.0000	0.0000
2310015A16Rik	ENSMUSG00000117879	RIKEN cDNA 2310015A16 gene	-1.658	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
2310015D24Rik	ENSMUSG00000099411	RIKEN cDNA 2310015D24 gene	-2.284	0.0156	0.0355
2310016G11Rik	ENSMUSG00000070574	RIKEN cDNA 2310016G11 gene	-2.362	0.0005	0.0017
2310022A10Rik	ENSMUSG00000049643	RIKEN cDNA 2310022A10 gene	-1.954	0.0000	0.0000
2310039H08Rik	ENSMUSG00000062619	RIKEN cDNA 2310039H08 gene	-3.036	0.0000	0.0000
2310039L15Rik	ENSMUSG00000100550	RIKEN cDNA 2310039L15 gene	-1.565	0.0411	0.0817
2410002F23Rik	ENSMUSG00000045411	RIKEN cDNA 2410002F23 gene	-1.786	0.0001	0.0004
2410006H16Rik	ENSMUSG00000086841	RIKEN cDNA 2410006H16 gene	-2.017	0.0242	0.0519
2510002D24Rik	ENSMUSG00000071632	RIKEN cDNA 2510002D24 gene	-1.845	0.0000	0.0000
2700038G22Rik	ENSMUSG00000097180	RIKEN cDNA 2700038G22 gene	-1.983	0.0061	0.0155
2700046G09Rik	ENSMUSG00000097787	RIKEN cDNA 2700046G09 gene	-1.838	0.0026	0.0073
2700062C07Rik	ENSMUSG00000024273	RIKEN cDNA 2700062C07 gene	-2.643	0.0000	0.0000
2810039B14Rik	ENSMUSG00000099034	RIKEN cDNA 2810039B14 gene	-2.741	0.0067	0.0168
2810403D21Rik	ENSMUSG00000086629	RIKEN cDNA 2810403D21 gene	-3.087	0.0000	0.0000
2810455O05Rik	ENSMUSG00000085030	RIKEN cDNA 2810455O05 gene	-13.210	0.0057	0.0146
2900009J06Rik	ENSMUSG00000102014	RIKEN cDNA 2900009J06 gene	-2.244	0.0126	0.0293
3000002C10Rik	ENSMUSG00000070282	RIKEN cDNA 3000002C10 gene	-1.634	0.0399	0.0797
3110070M22Rik	ENSMUSG00000074635	RIKEN cDNA 3110070M22 gene	-4.350	0.0000	0.0000
4833408A19Rik	ENSMUSG00000118132	RIKEN cDNA 4833408A19 gene	-1.934	0.0110	0.0262
4930466K18Rik	ENSMUSG00000112332	RIKEN cDNA 4930466K18 gene	-2.044	0.0355	0.0721
4930522O17Rik	ENSMUSG00000086947	RIKEN cDNA 4930522O17 gene	-2.576	0.0471	0.0918
4930523C07Rik	ENSMUSG00000090394	RIKEN cDNA 4930523C07 gene	-1.605	0.0000	0.0001
4930547M16Rik	ENSMUSG00000097890	RIKEN cDNA 4930547M16 gene	-8.266	0.0223	0.0483
4930592C13Rik	ENSMUSG00000105834	RIKEN cDNA 4930592C13 gene	-21.376	0.0018	0.0051
4931414P19Rik	ENSMUSG00000022179	RIKEN cDNA 4931414P19 gene	-1.960	0.0000	0.0000
4933404O12Rik	ENSMUSG00000097908	RIKEN cDNA 4933404O12 gene	-1.505	0.0502	0.0968
4933406P04Rik	ENSMUSG00000069713	RIKEN cDNA 4933406P04 gene	-4.158	0.0000	0.0001
4933434E20Rik	ENSMUSG00000027942	RIKEN cDNA 4933434E20 gene	-2.262	0.0000	0.0000
4933436F18Rik	ENSMUSG00000104380	RIKEN cDNA 4933436F18 gene	-8.164	0.0517	0.0996
5033430I15Rik	ENSMUSG00000038152	RIKEN cDNA 5033430I15 gene	-3.415	0.0000	0.0000
5330411O13Rik	ENSMUSG00000108603	RIKEN cDNA 5330411O13 gene	-17.348	0.0080	0.0197
5430403G16Rik	ENSMUSG00000072763	RIKEN cDNA 5430403G16 gene	-1.749	0.0307	0.0637

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
5430405H02Rik	ENSMUSG00000085741	RIKEN cDNA 5430405H02 gene	-1.720	0.0022	0.0061
5830405F06Rik	ENSMUSG00000103586	RIKEN cDNA 5830405F06 gene	-8.446	0.0307	0.0637
5830408C22Rik	ENSMUSG00000110148	RIKEN cDNA 5830408C22 gene	-2.471	0.0357	0.0725
5830448L01Rik	ENSMUSG00000115007	RIKEN cDNA 5830448L01 gene	-2.100	0.0130	0.0303
5930430L01Rik	ENSMUSG00000106951	RIKEN cDNA 5930430L01 gene	-1.768	0.0000	0.0000
6030443J06Rik	ENSMUSG00000097207	RIKEN cDNA 6030443J06 gene	-1.933	0.0155	0.0352
6330549D23Rik	ENSMUSG00000045327	RIKEN cDNA 6330549D23 gene	-3.016	0.0060	0.0154
9130604C24Rik	ENSMUSG00000105851	RIKEN cDNA 9130604C24 gene	-2.990	0.0125	0.0291
9230114K14Rik	ENSMUSG00000097145	RIKEN cDNA 9230114K14 gene	-1.814	0.0001	0.0003
9330102E08Rik	ENSMUSG00000107879	RIKEN cDNA 9330102E08 gene	-1.559	0.0062	0.0158
9430091E24Rik	ENSMUSG00000084808	RIKEN cDNA 9430091E24 gene	-2.639	0.0258	0.0548
9530020I12Rik	ENSMUSG00000112041	RIKEN cDNA 9530020I12 gene	-2.903	0.0350	0.0713
9930111J21Rik1	ENSMUSG00000069893	RIKEN cDNA 9930111J21 gene 1	-2.032	0.0001	0.0003
A130051J06Rik	ENSMUSG00000097643	RIKEN cDNA A130051J0 gene	-10.474	0.0316	0.0653
A230065N10Rik	ENSMUSG00000092071	RIKEN cDNA A230065N10 gene	-2.334	0.0313	0.0647
A330009N23Rik	ENSMUSG00000097915	RIKEN cDNA A330009N23 gene	-1.897	0.0161	0.0364
A430005L14Rik	ENSMUSG00000047613	RIKEN cDNA A430005L14 gene	-1.676	0.0000	0.0000
A430057M04Rik	ENSMUSG00000090564	RIKEN cDNA A430057M04 gene	-10.089	0.0389	0.0780
A530013C23Rik	ENSMUSG00000006462	RIKEN cDNA A530013C23 gene	-1.910	0.0231	0.0498
A530016L24Rik	ENSMUSG00000043122	RIKEN cDNA A530016L24 gene	-3.042	0.0000	0.0000
A630072L19Rik	ENSMUSG00000097160	RIKEN cDNA A630072L19 gene	-10.635	0.0085	0.0207
A730020M07Rik	ENSMUSG00000044522	RIKEN cDNA A730020M07 gene	-2.535	0.0000	0.0000
A930004D18Rik	ENSMUSG00000054057	RIKEN cDNA A930004D18 gene	-1.842	0.0017	0.0050
A930005H10Rik	ENSMUSG00000054426	RIKEN cDNA A930005H10 gene	-1.654	0.0000	0.0001
A930015P04Rik	ENSMUSG00000114526	RIKEN cDNA A930015P04 gene	-11.325	0.0473	0.0923
A930017K11Rik	ENSMUSG00000025727	RIKEN cDNA A930017K11 gene	-8.164	0.0054	0.0139
A930029G22Rik	ENSMUSG00000096988	RIKEN cDNA A930029G22 gene	-1.645	0.0516	0.0994
AA986860	ENSMUSG00000042510	expressed sequence AA986860	-1.644	0.0432	0.0853
Aars2	ENSMUSG00000023938	alanyl-tRNA synthetase 2, mitochondrial	-1.895	0.0000	0.0000
Aass	ENSMUSG00000029695	aminoadipate-semialdehyde synthase	-2.759	0.0019	0.0055
Aatk	ENSMUSG00000025375	apoptosis-associated tyrosine kinase	-1.697	0.0001	0.0005

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Abat	ENSMUSG00000057880	4-aminobutyrate aminotransferase	-6.029	0.0000	0.0000
Abca2	ENSMUSG00000026944	ATP-binding cassette, sub-family A (ABC1), member 2	-2.013	0.0000	0.0000
Abca3	ENSMUSG00000024130	ATP-binding cassette, sub-family A (ABC1), member 3	-2.208	0.0000	0.0000
Abca7	ENSMUSG00000035722	ATP-binding cassette, sub-family A (ABC1), member 7	-1.786	0.0007	0.0021
Abcb6	ENSMUSG00000026198	ATP-binding cassette, sub-family B (MDR/TAP), member 6	-5.685	0.0004	0.0013
Abcb8	ENSMUSG00000028973	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-2.056	0.0000	0.0000
Abcb9	ENSMUSG00000029408	ATP-binding cassette, sub-family B (MDR/TAP), member 9	-2.439	0.0000	0.0000
Abcc8	ENSMUSG00000040136	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-2.802	0.0000	0.0000
Abcd1	ENSMUSG00000031378	ATP-binding cassette, sub-family D (ALD), member 1	-1.731	0.0000	0.0000
Abhd11	ENSMUSG00000040532	abhydrolase domain containing 11	-1.514	0.0000	0.0000
Abhd14b	ENSMUSG00000042073	abhydrolase domain containing 14b	-3.185	0.0000	0.0000
Abhd15	ENSMUSG00000000686	abhydrolase domain containing 15	-1.764	0.0336	0.0688
Abhd3	ENSMUSG00000002475	abhydrolase domain containing 3	-1.748	0.0002	0.0007
Abhd4	ENSMUSG00000040997	abhydrolase domain containing 4	-2.696	0.0000	0.0000
Abhd8	ENSMUSG00000007950	abhydrolase domain containing 8	-2.337	0.0000	0.0000
Abi3	ENSMUSG00000018381	ABI family member 3	-1.667	0.0000	0.0000
Abitram	ENSMUSG00000038827	actin binding transcription modulator	-1.733	0.0000	0.0001
Acaa1a	ENSMUSG00000036138	acetyl-Coenzyme A acyltransferase 1A	-1.602	0.0000	0.0000
Acad10	ENSMUSG00000029456	acyl-Coenzyme A dehydrogenase family, member 10	-2.676	0.0000	0.0000
Acad11	ENSMUSG00000090150	acyl-Coenzyme A dehydrogenase family, member 11	-1.676	0.0000	0.0000
Acad12	ENSMUSG00000042647	acyl-Coenzyme A dehydrogenase family, member 12	-2.028	0.0000	0.0000
Acad9	ENSMUSG00000027710	acyl-Coenzyme A dehydrogenase family, member 9	-1.614	0.0000	0.0000
Acads	ENSMUSG00000029545	acyl-Coenzyme A dehydrogenase, short chain	-2.959	0.0000	0.0000
Accs	ENSMUSG00000040272	1-aminocyclopropane-1-carboxylate synthase (non-functional)	-1.690	0.0001	0.0004
Acd	ENSMUSG00000038000	adrenocortical dysplasia	-1.892	0.0000	0.0000
Ace	ENSMUSG00000020681	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	-2.300	0.0000	0.0000
Ache	ENSMUSG00000023328	acetylcholinesterase	-1.943	0.0000	0.0002
Ackr2	ENSMUSG00000044534	atypical chemokine receptor 2	-1.572	0.0450	0.0883
Ackr3	ENSMUSG00000044337	atypical chemokine receptor 3	-1.859	0.0000	0.0000
Acot8	ENSMUSG00000017307	acyl-CoA thioesterase 8	-2.147	0.0000	0.0000
Acp1	ENSMUSG00000044573	acid phosphatase 1, soluble	-2.183	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Acp2	ENSMUSG00000002103	acid phosphatase 2, lysosomal	-2.042	0.0000	0.0000
Acp5	ENSMUSG00000001348	acid phosphatase 5, tartrate resistant	-2.555	0.0072	0.0180
Acr	ENSMUSG00000022622	acrosin prepropeptide	-6.176	0.0067	0.0167
Acta1	ENSMUSG00000031972	actin alpha 1, skeletal muscle	-1.743	0.0164	0.0369
Actc1	ENSMUSG00000068614	actin, alpha, cardiac muscle 1	-1.805	0.0000	0.0000
Actg1	ENSMUSG00000062825	actin, gamma, cytoplasmic 1	-2.495	0.0000	0.0000
Acy1	ENSMUSG00000023262	aminoacylase 1	-1.859	0.0000	0.0000
Acy3	ENSMUSG00000024866	aspartoacylase (aminoacylase) 3	-4.088	0.0000	0.0000
Ada	ENSMUSG00000017697	adenosine deaminase	-3.484	0.0004	0.0012
Adam15	ENSMUSG00000028041	a disintegrin and metallopeptidase domain 15 (metargidin)	-1.810	0.0000	0.0000
Adamtsl4	ENSMUSG00000015850	ADAMTS-like 4	-1.751	0.0001	0.0002
Adamtsl5	ENSMUSG00000043822	ADAMTS-like 5	-1.842	0.0000	0.0000
Adar	ENSMUSG00000027951	adenosine deaminase, RNA-specific	-1.736	0.0000	0.0000
Adck1	ENSMUSG00000021044	aarF domain containing kinase 1	-2.013	0.0000	0.0000
Adck5	ENSMUSG00000022550	aarF domain containing kinase 5	-1.551	0.0275	0.0578
Adcy4	ENSMUSG00000022220	adenylate cyclase 4	-1.960	0.0000	0.0000
Adgre1	ENSMUSG00000004730	adhesion G protein-coupled receptor E1	-1.566	0.0083	0.0204
Adgre5	ENSMUSG00000002885	adhesion G protein-coupled receptor E5	-1.792	0.0000	0.0000
Adgrf3	ENSMUSG00000067642	adhesion G protein-coupled receptor F3	-12.967	0.0392	0.0784
Adgrg1	ENSMUSG00000031785	adhesion G protein-coupled receptor G1	-2.189	0.0004	0.0013
Adgrg3	ENSMUSG00000060470	adhesion G protein-coupled receptor G3	-7.248	0.0000	0.0000
Adhfe1	ENSMUSG00000025911	alcohol dehydrogenase, iron containing, 1	-1.788	0.0000	0.0000
Adig	ENSMUSG00000044405	adipogenin	-3.442	0.0009	0.0027
Adora2b	ENSMUSG00000018500	adenosine A2b receptor	-2.693	0.0125	0.0293
Adsl	ENSMUSG00000022407	adenylosuccinate lyase	-2.259	0.0000	0.0000
Aebp1	ENSMUSG00000020473	AE binding protein 1	-2.077	0.0003	0.0010
Afmid	ENSMUSG00000017718	arylformamidase	-2.886	0.0000	0.0002
Agmat	ENSMUSG00000040706	agmatine ureohydrolase (agmatinase)	-3.224	0.0121	0.0284
Agmo	ENSMUSG00000050103	alkylglycerol monooxygenase	-2.059	0.0013	0.0040
Agpat1	ENSMUSG00000034254	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	-1.817	0.0000	0.0000
Agpat2	ENSMUSG00000026922	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	-1.612	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Agt	ENSMUSG00000031980	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-2.258	0.0165	0.0372
Ahcy	ENSMUSG00000027597	S-adenosylhomocysteine hydrolase	-3.356	0.0000	0.0000
Ahrr	ENSMUSG00000021575	aryl-hydrocarbon receptor repressor	-1.647	0.0130	0.0302
AI413582	ENSMUSG00000062753	expressed sequence AI413582	-2.795	0.0000	0.0000
AI467606	ENSMUSG00000045165	expressed sequence AI467606	-2.458	0.0001	0.0003
AI661453	ENSMUSG00000034382	expressed sequence AI661453	-2.348	0.0021	0.0060
Aimp2	ENSMUSG00000029610	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	-1.537	0.0000	0.0000
AK157302	ENSMUSG00000078139	cDNA sequence AK157302	-2.867	0.0000	0.0000
Ak3l2-ps	ENSMUSG00000081957	adenylate kinase 3-like 2, pseudogene	-4.356	0.0001	0.0003
Akip1	ENSMUSG00000031023	A kinase (PRKA) interacting protein 1	-1.567	0.0001	0.0002
Akna	ENSMUSG00000039158	AT-hook transcription factor	-1.896	0.0000	0.0000
Akr1b10	ENSMUSG00000061758	aldo-keto reductase family 1, member B10 (aldose reductase)	-1.857	0.0000	0.0000
Akr1b3	ENSMUSG00000001642	aldo-keto reductase family 1, member B3 (aldose reductase)	-1.545	0.0000	0.0000
Akr1b8	ENSMUSG00000029762	aldo-keto reductase family 1, member B8	-1.694	0.0001	0.0005
Akr7a5	ENSMUSG00000028743	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	-3.746	0.0000	0.0000
Akt2-ps	ENSMUSG00000084347	thymoma viral proto-oncogene 2, pseudogene	-2.957	0.0001	0.0003
Alad	ENSMUSG00000028393	aminolevulinate, delta-, dehydratase	-3.262	0.0000	0.0000
Aldh16a1	ENSMUSG00000007833	aldehyde dehydrogenase 16 family, member A1	-1.630	0.0000	0.0000
Aldh18a1	ENSMUSG00000025007	aldehyde dehydrogenase 18 family, member A1	-1.543	0.0103	0.0246
Aldh1b1	ENSMUSG00000035561	aldehyde dehydrogenase 1 family, member B1	-1.611	0.0000	0.0000
Aldh1l1	ENSMUSG00000030088	aldehyde dehydrogenase 1 family, member L1	-2.318	0.0009	0.0027
Aldh3b3	ENSMUSG00000037263	aldehyde dehydrogenase 3 family, member B3	-3.691	0.0377	0.0759
Aldh4a1	ENSMUSG00000028737	aldehyde dehydrogenase 4 family, member A1	-1.700	0.0000	0.0000
Aldh6a1	ENSMUSG00000021238	aldehyde dehydrogenase family 6, subfamily A1	-1.604	0.0000	0.0000
Alg1	ENSMUSG00000039427	asparagine-linked glycosylation 1 (beta-1,4-mannosyltransferase)	-1.970	0.0000	0.0000
Alg12	ENSMUSG00000035845	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase)	-2.463	0.0000	0.0000
Alg3	ENSMUSG00000033809	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase)	-1.662	0.0001	0.0002
Alg8	ENSMUSG00000035704	asparagine-linked glycosylation 8 (alpha-1,3-glucosyltransferase)	-2.121	0.0000	0.0000
Alkbh4	ENSMUSG00000039754	alkB homolog 4, lysine demethylase	-1.759	0.0004	0.0014
Alkbh6	ENSMUSG00000042831	alkB homolog 6	-2.001	0.0000	0.0000
Alkbh7	ENSMUSG00000002661	alkB homolog 7	-3.977	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Alox5ap	ENSMUSG00000060063	arachidonate 5-lipoxygenase activating protein	-2.304	0.0000	0.0001
Als2cl	ENSMUSG00000044037	ALS2 C-terminal like	-1.573	0.0031	0.0085
Amd2	ENSMUSG00000063953	S-adenosylmethionine decarboxylase 2	-1.954	0.0075	0.0185
Amdhd2	ENSMUSG00000036820	amidohydrolase domain containing 2	-1.542	0.0039	0.0103
Amhr2	ENSMUSG00000023047	anti-Mullerian hormone type 2 receptor	-4.068	0.0046	0.0121
Amigo3	ENSMUSG00000032593	adhesion molecule with Ig like domain 3	-3.723	0.0002	0.0007
Amz2	ENSMUSG00000020610	archaelysin family metallopeptidase 2	-1.593	0.0000	0.0000
Anapc16	ENSMUSG00000020107	anaphase promoting complex subunit 16	-1.723	0.0001	0.0003
Angel1	ENSMUSG00000021257	angel homolog 1	-1.682	0.0000	0.0000
Angpt4	ENSMUSG00000027460	angiopoietin 4	-4.402	0.0313	0.0647
Angptl3	ENSMUSG00000028553	angiopoietin-like 3	-1.849	0.0231	0.0498
Angptl6	ENSMUSG00000038742	angiopoietin-like 6	-1.916	0.0000	0.0001
Ankrd23	ENSMUSG00000067653	ankyrin repeat domain 23	-2.587	0.0000	0.0000
Ankrd39	ENSMUSG00000079610	ankyrin repeat domain 39	-1.680	0.0003	0.0010
Ankrd46	ENSMUSG00000048307	ankyrin repeat domain 46	-1.515	0.0000	0.0000
Ankrd55	ENSMUSG00000049985	ankyrin repeat domain 55	-4.088	0.0001	0.0005
Anpep	ENSMUSG00000039062	alanyl (membrane) aminopeptidase	-1.765	0.0003	0.0011
Ap1b1	ENSMUSG00000009090	adaptor protein complex AP-1, beta 1 subunit	-1.717	0.0000	0.0000
Ap1g2	ENSMUSG00000040701	adaptor protein complex AP-1, gamma 2 subunit	-1.714	0.0001	0.0002
Ap1m1	ENSMUSG00000003033	adaptor-related protein complex AP-1, mu subunit 1	-1.507	0.0000	0.0000
Ap2a1	ENSMUSG00000060279	adaptor-related protein complex 2, alpha 1 subunit	-1.866	0.0000	0.0000
Ap2m1-ps	ENSMUSG00000081272	adaptor-related protein complex 2, mu 1 subunit, pseudogene	-3.051	0.0000	0.0000
Ap2s1	ENSMUSG00000008036	adaptor-related protein complex 2, sigma 1 subunit	-1.690	0.0000	0.0000
Ap3s1-ps1	ENSMUSG00000085611	adaptor-related protein complex 3, sigma 1 subunit, pseudogene 1	-9.573	0.0206	0.0452
Ap5b1	ENSMUSG00000049562	adaptor-related protein complex 5, beta 1 subunit	-2.322	0.0000	0.0000
Ap5m1	ENSMUSG00000036291	adaptor-related protein complex 5, mu 1 subunit	-1.569	0.0000	0.0000
Ap5z1	ENSMUSG00000039623	adaptor-related protein complex 5, zeta 1 subunit	-1.768	0.0000	0.0000
Apba3	ENSMUSG00000004931	amyloid beta (A4) precursor protein-binding, family A, member 3	-2.583	0.0000	0.0000
Apc2	ENSMUSG00000020135	APC regulator of WNT signaling pathway 2	-2.337	0.0000	0.0001
Apeh	ENSMUSG00000032590	acylpeptide hydrolase	-2.202	0.0000	0.0000
Aph1a	ENSMUSG00000015750	aph1 homolog A, gamma secretase subunit	-1.560	0.0000	0.0000

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Aph1b	ENSMUSG00000032375	aph1 homolog B, gamma secretase subunit	-2.306	0.0000	0.0000
Aph1c	ENSMUSG00000053040	aph1 homolog C, gamma secretase subunit	-2.520	0.0001	0.0002
Apobec1	ENSMUSG00000040613	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	-1.711	0.0001	0.0005
Apoc1	ENSMUSG00000040564	apolipoprotein C-I	-3.227	0.0329	0.0677
Aprt	ENSMUSG00000006589	adenine phosphoribosyl transferase	-2.369	0.0000	0.0000
Aqp1	ENSMUSG00000004655	aquaporin 1	-1.805	0.0101	0.0243
Aqp8	ENSMUSG00000030762	aquaporin 8	-2.154	0.0028	0.0076
Arap3	ENSMUSG00000024451	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	-1.508	0.0000	0.0000
Arc	ENSMUSG00000022602	activity regulated cytoskeletal-associated protein	-2.114	0.0168	0.0378
Arfip1	ENSMUSG00000074513	ADP-ribosylation factor interacting protein 1	-2.027	0.0000	0.0000
Arhgap1	ENSMUSG00000027247	Rho GTPase activating protein 1	-2.071	0.0000	0.0000
Arhgap27	ENSMUSG00000034255	Rho GTPase activating protein 27	-1.960	0.0027	0.0074
Arhgap33	ENSMUSG00000036882	Rho GTPase activating protein 33	-1.905	0.0055	0.0141
Arhgap9	ENSMUSG00000040345	Rho GTPase activating protein 9	-2.271	0.0000	0.0000
Arhgdia	ENSMUSG00000025132	Rho GDP dissociation inhibitor (GDI) alpha	-2.110	0.0000	0.0000
Arhgef10	ENSMUSG00000071176	Rho guanine nucleotide exchange factor (GEF) 10	-1.629	0.0006	0.0018
Arhgef10l	ENSMUSG00000040964	Rho guanine nucleotide exchange factor (GEF) 10-like	-1.560	0.0000	0.0000
Arhgef16	ENSMUSG00000029032	Rho guanine nucleotide exchange factor (GEF) 16	-3.774	0.0004	0.0012
Arhgef40	ENSMUSG00000004562	Rho guanine nucleotide exchange factor (GEF) 40	-1.923	0.0000	0.0000
Arl15	ENSMUSG00000042348	ADP-ribosylation factor-like 15	-1.800	0.0000	0.0000
Arl2	ENSMUSG00000024944	ADP-ribosylation factor-like 2	-1.847	0.0000	0.0000
Arl6	ENSMUSG00000022722	ADP-ribosylation factor-like 6	-1.799	0.0000	0.0000
Armc2	ENSMUSG00000071324	armadillo repeat containing 2	-1.536	0.0136	0.0315
Armc5	ENSMUSG00000042178	armadillo repeat containing 5	-1.545	0.0000	0.0000
Armc6	ENSMUSG00000002343	armadillo repeat containing 6	-2.063	0.0000	0.0000
Armc9	ENSMUSG00000062590	armadillo repeat containing 9	-1.658	0.0001	0.0005
Arpc1b	ENSMUSG00000029622	actin related protein 2/3 complex, subunit 1B	-1.577	0.0000	0.0000
Arpc3	ENSMUSG00000029465	actin related protein 2/3 complex, subunit 3	-2.173	0.0000	0.0000
Arrdc1	ENSMUSG00000026972	arrestin domain containing 1	-2.118	0.0001	0.0003
Arsa	ENSMUSG00000022620	arylsulfatase A	-1.705	0.0000	0.0000
Arsb	ENSMUSG00000042082	arylsulfatase B	-1.866	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Arsg	ENSMUSG00000020604	arylsulfatase G	-2.173	0.0000	0.0000
Art1	ENSMUSG00000030996	ADP-ribosyltransferase 1	-1.938	0.0000	0.0000
Art3	ENSMUSG00000034842	ADP-ribosyltransferase 3	-1.646	0.0035	0.0095
Art4	ENSMUSG00000030217	ADP-ribosyltransferase 4	-1.897	0.0011	0.0034
Arv1	ENSMUSG00000031982	ARV1 homolog, fatty acid homeostasis modulator	-1.995	0.0000	0.0000
Asb11	ENSMUSG00000031382	ankyrin repeat and SOCS box-containing 11	-1.763	0.0000	0.0001
Asb14	ENSMUSG00000021898	ankyrin repeat and SOCS box-containing 14	-2.295	0.0000	0.0000
Asb18	ENSMUSG00000067081	ankyrin repeat and SOCS box-containing 18	-1.702	0.0000	0.0000
Asb2	ENSMUSG00000021200	ankyrin repeat and SOCS box-containing 2	-1.900	0.0000	0.0000
Asb6	ENSMUSG00000039483	ankyrin repeat and SOCS box-containing 6	-2.590	0.0000	0.0000
Ascc1	ENSMUSG00000044475	activating signal cointegrator 1 complex subunit 1	-2.205	0.0000	0.0000
Asf1b	ENSMUSG00000005470	anti-silencing function 1B histone chaperone	-1.648	0.0186	0.0413
Asl	ENSMUSG00000025533	argininosuccinate lyase	-2.254	0.0000	0.0000
Asns	ENSMUSG00000029752	asparagine synthetase	-1.721	0.0148	0.0338
Asnsd1	ENSMUSG00000026095	asparagine synthetase domain containing 1	-1.517	0.0006	0.0019
Aspa	ENSMUSG00000020774	aspartoacylase	-1.969	0.0024	0.0066
Aspg	ENSMUSG00000037686	asparaginase	-6.945	0.0017	0.0051
Atat1	ENSMUSG00000024426	alpha tubulin acetyltransferase 1	-1.828	0.0002	0.0006
Atf6b	ENSMUSG00000015461	activating transcription factor 6 beta	-1.733	0.0000	0.0000
Atg2a	ENSMUSG00000024773	autophagy related 2A	-2.751	0.0000	0.0000
Atg4a-ps	ENSMUSG00000087119	autophagy related 4A, pseudogene	-2.439	0.0224	0.0486
Atg4d	ENSMUSG00000002820	autophagy related 4D, cysteine peptidase	-1.637	0.0000	0.0000
Atg7	ENSMUSG00000030314	autophagy related 7	-1.662	0.0000	0.0000
Atg9a	ENSMUSG00000033124	autophagy related 9A	-2.449	0.0000	0.0000
Atoh8	ENSMUSG00000037621	atonal bHLH transcription factor 8	-1.827	0.0123	0.0289
Atox1	ENSMUSG00000018585	antioxidant 1 copper chaperone	-3.492	0.0000	0.0000
Atp10a	ENSMUSG00000025324	ATPase, class V, type 10A	-1.507	0.0218	0.0474
Atp13a1	ENSMUSG00000031862	ATPase type 13A1	-2.007	0.0000	0.0000
Atp1a3	ENSMUSG00000040907	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-2.237	0.0187	0.0414
Atp5d	ENSMUSG00000003072	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-3.893	0.0000	0.0000
Atp5g2	ENSMUSG00000062683	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	-4.492	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Atp5l	ENSMUSG00000038717	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	-6.749	0.0000	0.0000
Atp5mpl	ENSMUSG00000021290	ATP synthase membrane subunit 6.8PL	-1.536	0.0000	0.0000
Atp5o	ENSMUSG00000022956	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-2.394	0.0000	0.0000
Atp5pb-ps	ENSMUSG00000044751	ATP synthase peripheral stalk-membrane subunit b, pseudogene	-1.573	0.0347	0.0708
Atp6ap1	ENSMUSG00000019087	ATPase, H+ transporting, lysosomal accessory protein 1	-1.591	0.0000	0.0000
Atp6v0c	ENSMUSG00000024121	ATPase, H+ transporting, lysosomal V0 subunit C	-5.543	0.0000	0.0000
Atp6v0c-ps2	ENSMUSG00000080242	ATPase, H+ transporting, lysosomal V0 subunit C, pseudogene 2	-8.443	0.0000	0.0000
Atp6v0d1	ENSMUSG00000013160	ATPase, H+ transporting, lysosomal V0 subunit D1	-2.975	0.0000	0.0000
Atp6v0e	ENSMUSG00000015575	ATPase, H+ transporting, lysosomal V0 subunit E	-1.712	0.0000	0.0000
Atp6v0e2	ENSMUSG00000039347	ATPase, H+ transporting, lysosomal V0 subunit E2	-2.109	0.0000	0.0000
Atp6v1b2	ENSMUSG00000006273	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.573	0.0000	0.0000
Atp6v1f	ENSMUSG00000004285	ATPase, H+ transporting, lysosomal V1 subunit F	-1.637	0.0000	0.0000
Atraid	ENSMUSG00000013622	all-trans retinoic acid induced differentiation factor	-1.731	0.0000	0.0000
Atrip	ENSMUSG00000025646	ATR interacting protein	-2.086	0.0000	0.0000
Atxn10	ENSMUSG00000016541	ataxin 10	-1.620	0.0000	0.0000
Atxn7l2	ENSMUSG00000048997	ataxin 7-like 2	-2.172	0.0002	0.0006
AU021092	ENSMUSG00000051669	expressed sequence AU021092	-3.793	0.0000	0.0000
Aunip	ENSMUSG00000078521	aurora kinase A and ninein interacting protein	-3.747	0.0137	0.0316
Aurkaip1	ENSMUSG00000065990	aurora kinase A interacting protein 1	-2.395	0.0000	0.0000
Avpi1	ENSMUSG00000018821	arginine vasopressin-induced 1	-1.925	0.0000	0.0000
AW112010	ENSMUSG00000075010	expressed sequence AW112010	-2.761	0.0000	0.0000
B230319C09Rik	ENSMUSG00000051844	RIKEN cDNA B230319C09 gene	-3.116	0.0247	0.0527
B2m	ENSMUSG00000060802	beta-2 microglobulin	-2.407	0.0000	0.0000
B3galt4	ENSMUSG00000067370	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	-3.086	0.0000	0.0000
B3galt6	ENSMUSG00000050796	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	-1.907	0.0101	0.0242
B3gnt9	ENSMUSG00000069920	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	-1.737	0.0028	0.0078
B3gntl1	ENSMUSG00000046605	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	-2.035	0.0003	0.0012
B4galt3	ENSMUSG00000052423	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	-1.629	0.0000	0.0000
B9d2	ENSMUSG00000063439	B9 protein domain 2	-3.457	0.0000	0.0000
Bace2	ENSMUSG00000040605	beta-site APP-cleaving enzyme 2	-1.835	0.0001	0.0004
Bag6	ENSMUSG00000024392	BCL2-associated athanogene 6	-1.529	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Bahcc1	ENSMUSG00000039741	BAH domain and coiled-coil containing 1	-1.547	0.0000	0.0001
Baiap2	ENSMUSG00000025372	brain-specific angiogenesis inhibitor 1-associated protein 2	-3.222	0.0054	0.0138
Baiap2l2	ENSMUSG00000018126	BAI1-associated protein 2-like 2	-17.551	0.0022	0.0062
Baiap3	ENSMUSG00000047507	BAI1-associated protein 3	-3.522	0.0005	0.0017
Bak1	ENSMUSG00000057789	BCL2-antagonist/killer 1	-2.229	0.0000	0.0000
Bambi-ps1	ENSMUSG00000081219	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus laevis)	-2.197	0.0022	0.0061
Banf2os	ENSMUSG00000086384	barrier to autointegration factor 2, opposite strand	-2.747	0.0002	0.0008
BB218582	ENSMUSG00000085218	expressed sequence BB218582	-1.697	0.0051	0.0132
Bbln	ENSMUSG00000039195	bublin coiled coil protein	-1.886	0.0000	0.0000
Bbs4	ENSMUSG00000025235	Bardet-Biedl syndrome 4 (human)	-2.576	0.0000	0.0000
BC002059	ENSMUSG00000060149	cDNA sequence BC002059	-1.760	0.0000	0.0000
BC004004	ENSMUSG00000052712	cDNA sequence BC004004	-2.423	0.0000	0.0000
BC024063	ENSMUSG00000112160	cDNA sequence BC024063	-1.727	0.0378	0.0761
BC024978	ENSMUSG00000078786	cDNA sequence BC024978	-1.645	0.0000	0.0000
BC029722	ENSMUSG00000074649	cDNA sequence BC029722	-1.653	0.0000	0.0000
BC049352	ENSMUSG00000091996	cDNA sequence BC049352	-8.033	0.0375	0.0756
BC049762	ENSMUSG00000045942	cDNA sequence BC049762	-4.039	0.0208	0.0455
BC055324	ENSMUSG00000041406	cDNA sequence BC055324	-2.264	0.0031	0.0084
Bcam	ENSMUSG00000002980	basal cell adhesion molecule	-1.802	0.0000	0.0000
Bcar3	ENSMUSG00000028121	breast cancer anti-estrogen resistance 3	-1.648	0.0000	0.0001
Bcas3	ENSMUSG00000059439	BCAS3 microtubule associated cell migration factor	-1.903	0.0000	0.0000
Bcat2	ENSMUSG00000030826	branched chain aminotransferase 2, mitochondrial	-1.838	0.0000	0.0000
Bckdha	ENSMUSG00000060376	branched chain ketoacid dehydrogenase E1, alpha polypeptide	-2.778	0.0000	0.0000
Bckdhb	ENSMUSG00000032263	branched chain ketoacid dehydrogenase E1, beta polypeptide	-1.911	0.0000	0.0000
Bckdk	ENSMUSG00000030802	branched chain ketoacid dehydrogenase kinase	-2.215	0.0000	0.0000
Bcl2l12	ENSMUSG00000003190	BCL2-like 12 (proline rich)	-1.788	0.0003	0.0010
Bdh1	ENSMUSG00000046598	3-hydroxybutyrate dehydrogenase, type 1	-3.671	0.0000	0.0000
Bdkrb2	ENSMUSG00000021070	bradykinin receptor, beta 2	-2.029	0.0000	0.0000
Best1	ENSMUSG00000037418	bestrophin 1	-3.640	0.0309	0.0641
Best3	ENSMUSG00000020169	bestrophin 3	-2.362	0.0000	0.0000
Bfsp2	ENSMUSG00000032556	beaded filament structural protein 2, phakinin	-13.214	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Bgn	ENSMUSG00000031375	biglycan	-2.084	0.0000	0.0002
Bicra	ENSMUSG00000070808	BRD4 interacting chromatin remodeling complex associated protein	-1.562	0.0001	0.0005
Bicral	ENSMUSG00000036568	BRD4 interacting chromatin remodeling complex associated protein like	-1.634	0.0000	0.0000
Bid	ENSMUSG00000004446	BH3 interacting domain death agonist	-2.660	0.0003	0.0010
Bik	ENSMUSG00000016758	BCL2-interacting killer	-2.093	0.0000	0.0000
Blnk	ENSMUSG00000061132	B cell linker	-2.080	0.0000	0.0001
Bloc1s1	ENSMUSG00000090247	biogenesis of lysosomal organelles complex-1, subunit 1	-2.215	0.0001	0.0003
Bloc1s2	ENSMUSG00000057506	biogenesis of lysosomal organelles complex-1, subunit 2	-1.547	0.0003	0.0010
Bloc1s6	ENSMUSG00000005804	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin	-1.788	0.0000	0.0000
Blvrb	ENSMUSG00000040466	biliverdin reductase B (flavin reductase (NADPH))	-2.796	0.0000	0.0000
Bmp7	ENSMUSG00000008999	bone morphogenetic protein 7	-1.580	0.0151	0.0343
Bmyc	ENSMUSG00000049086	brain expressed myelocytomatosis oncogene	-2.444	0.0000	0.0000
Bnc1	ENSMUSG00000025105	basonuclin 1	-22.445	0.0028	0.0077
Bnc2	ENSMUSG00000028487	basonuclin 2	-2.073	0.0176	0.0392
Bnip1	ENSMUSG00000024191	BCL2/adenovirus E1B interacting protein 1	-2.046	0.0000	0.0000
Boc	ENSMUSG00000022687	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein	-1.993	0.0000	0.0000
Bok	ENSMUSG00000026278	BCL2-related ovarian killer	-2.668	0.0000	0.0000
Bola1	ENSMUSG00000015943	bolA-like 1 (E. coli)	-3.627	0.0000	0.0000
Bop1	ENSMUSG00000022557	block of proliferation 1	-2.287	0.0000	0.0000
Borcs5	ENSMUSG00000042992	BLOC-1 related complex subunit 5	-1.584	0.0000	0.0000
Borcs8	ENSMUSG00000002345	BLOC-1 related complex subunit 8	-1.670	0.0000	0.0000
Brat1	ENSMUSG00000000148	BRCA1-associated ATM activator 1	-1.736	0.0000	0.0000
Brd3os	ENSMUSG00000109946	bromodomain containing 3, opposite strand	-3.193	0.0000	0.0000
Brf2	ENSMUSG00000031487	BRF2, RNA polymerase III transcription initiation factor 50kDa subunit	-1.870	0.0000	0.0000
Brk1	ENSMUSG00000033940	BRICK1, SCAR/WAVE actin-nucleating complex subunit	-1.618	0.0000	0.0000
Brme1	ENSMUSG00000008129	break repair meiotic recombinase recruitment factor 1	-4.440	0.0080	0.0197
Bscl2	ENSMUSG00000071657	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	-2.090	0.0000	0.0000
Bst1	ENSMUSG00000029082	bone marrow stromal cell antigen 1	-9.558	0.0000	0.0000
Bst2	ENSMUSG00000046718	bone marrow stromal cell antigen 2	-2.116	0.0000	0.0000
Btbd3	ENSMUSG00000062098	BTB (POZ) domain containing 3	-1.522	0.0000	0.0000
Btbd6	ENSMUSG00000002803	BTB (POZ) domain containing 6	-2.941	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Btd	ENSMUSG00000021900	biotinidase	-2.430	0.0000	0.0000
Bud23	ENSMUSG00000005378	BUD23, rRNA methyltransferase and ribosome maturation factor	-1.811	0.0000	0.0000
C030006K11Rik	ENSMUSG00000116138	RIKEN cDNA C030006K11 gene	-1.729	0.0000	0.0000
C030013G03Rik	ENSMUSG00000117314	RIKEN cDNA C030013G03 gene	-4.509	0.0025	0.0071
C1qtnf12	ENSMUSG00000023571	C1q and tumor necrosis factor related 12	-3.214	0.0000	0.0000
C1qtnf2	ENSMUSG00000046491	C1q and tumor necrosis factor related protein 2	-2.346	0.0001	0.0005
C1qtnf6	ENSMUSG00000022440	C1q and tumor necrosis factor related protein 6	-2.079	0.0000	0.0000
C1ra	ENSMUSG00000055172	complement component 1, r subcomponent A	-1.685	0.0001	0.0003
C1s2	ENSMUSG00000079343	complement component 1, s subcomponent 2	-2.384	0.0000	0.0002
C2	ENSMUSG00000024371	complement component 2 (within H-2S)	-2.232	0.0468	0.0913
C2cd3	ENSMUSG00000047248	C2 calcium-dependent domain containing 3	-1.606	0.0000	0.0000
C77080	ENSMUSG00000050390	expressed sequence C77080	-1.704	0.0000	0.0001
C87436	ENSMUSG00000046679	expressed sequence C87436	-2.000	0.0000	0.0000
C8g	ENSMUSG00000015083	complement component 8, gamma polypeptide	-3.691	0.0002	0.0007
Cabin1	ENSMUSG00000020196	calcineurin binding protein 1	-1.969	0.0000	0.0000
Cacna1i	ENSMUSG00000022416	calcium channel, voltage-dependent, alpha 1I subunit	-17.754	0.0061	0.0156
Cacna1s	ENSMUSG00000026407	calcium channel, voltage-dependent, L type, alpha 1S subunit	-2.739	0.0000	0.0000
Cacnb1	ENSMUSG00000020882	calcium channel, voltage-dependent, beta 1 subunit	-1.581	0.0000	0.0002
Cacng6	ENSMUSG00000078815	calcium channel, voltage-dependent, gamma subunit 6	-13.164	0.0111	0.0264
Calhm2	ENSMUSG00000033033	calcium homeostasis modulator family member 2	-2.099	0.0000	0.0000
Camkk1	ENSMUSG00000020785	calcium/calmodulin-dependent protein kinase kinase 1, alpha	-1.563	0.0295	0.0616
Cand2	ENSMUSG00000030319	cullin-associated and neddylation-dissociated 2 (putative)	-2.133	0.0000	0.0000
Capg	ENSMUSG00000056737	capping protein (actin filament), gelsolin-like	-1.620	0.0025	0.0069
Capn15	ENSMUSG00000037326	calpain 15	-1.673	0.0000	0.0001
Capn3	ENSMUSG00000079110	calpain 3	-1.752	0.0277	0.0582
Capn6	ENSMUSG00000067276	calpain 6	-4.622	0.0034	0.0093
Capns1	ENSMUSG00000001794	calpain, small subunit 1	-2.217	0.0000	0.0000
Car15	ENSMUSG00000090236	carbonic anhydrase 15	-6.382	0.0131	0.0304
Car7	ENSMUSG00000031883	carbonic anhydrase 7	-2.864	0.0000	0.0000
Carm1	ENSMUSG00000032185	coactivator-associated arginine methyltransferase 1	-1.983	0.0000	0.0000
Carmil3	ENSMUSG00000022211	capping protein regulator and myosin 1 linker 3	-2.520	0.0000	0.0000

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Carns1	ENSMUSG00000075289	carnosine synthase 1	-1.843	0.0000	0.0001
Caskin2	ENSMUSG00000034471	CASK-interacting protein 2	-2.738	0.0000	0.0000
Cav2	ENSMUSG00000000058	caveolin 2	-1.837	0.0000	0.0000
Cbarp	ENSMUSG00000035640	calcium channel, voltage-dependent, beta subunit associated regulatory protein	-2.041	0.0004	0.0014
Cblc	ENSMUSG00000040525	Casitas B-lineage lymphoma c	-2.883	0.0140	0.0322
Cbr1	ENSMUSG00000051483	carbonyl reductase 1	-1.519	0.0000	0.0000
Cbs	ENSMUSG00000024039	cystathionine beta-synthase	-9.551	0.0358	0.0726
Cbx2	ENSMUSG00000025577	chromobox 2	-1.633	0.0004	0.0013
Ccdc106	ENSMUSG00000035228	coiled-coil domain containing 106	-10.328	0.0168	0.0378
Ccdc107	ENSMUSG00000028461	coiled-coil domain containing 107	-2.951	0.0000	0.0000
Ccdc159	ENSMUSG00000006241	coiled-coil domain containing 159	-2.731	0.0000	0.0000
Ccdc166	ENSMUSG00000098176	coiled-coil domain containing 166	-2.290	0.0001	0.0004
Ccdc17	ENSMUSG00000034035	coiled-coil domain containing 17	-2.366	0.0021	0.0059
Ccdc184	ENSMUSG00000029875	coiled-coil domain containing 184	-1.816	0.0291	0.0607
Ccdc22	ENSMUSG00000031143	coiled-coil domain containing 22	-7.467	0.0002	0.0008
Ccdc68	ENSMUSG00000038903	coiled-coil domain containing 68	-2.133	0.0265	0.0559
Ccdc69	ENSMUSG00000049588	coiled-coil domain containing 69	-1.788	0.0177	0.0395
Ccdc86	ENSMUSG00000024732	coiled-coil domain containing 86	-2.512	0.0000	0.0000
Ccdc90b	ENSMUSG00000030613	coiled-coil domain containing 90B	-1.527	0.0000	0.0001
Ccl12	ENSMUSG00000035352	chemokine (C-C motif) ligand 12	-5.028	0.0021	0.0060
Ccl21a	ENSMUSG00000094686	chemokine (C-C motif) ligand 21A (serine)	-2.821	0.0000	0.0001
Ccl24	ENSMUSG00000004814	chemokine (C-C motif) ligand 24	-2.638	0.0034	0.0092
Ccl5	ENSMUSG00000035042	chemokine (C-C motif) ligand 5	-2.671	0.0300	0.0624
Ccn4	ENSMUSG00000005124	cellular communication network factor 4	-1.880	0.0005	0.0016
Ccnd3	ENSMUSG00000034165	cyclin D3	-1.517	0.0000	0.0000
Ccnq	ENSMUSG00000049489	cyclin Q	-1.629	0.0000	0.0000
Ccrl2	ENSMUSG00000043953	chemokine (C-C motif) receptor-like 2	-2.039	0.0000	0.0001
Cd109	ENSMUSG00000046186	CD109 antigen	-1.657	0.0138	0.0318
Cd14	ENSMUSG00000051439	CD14 antigen	-2.645	0.0000	0.0000
Cd151	ENSMUSG00000025510	CD151 antigen	-2.097	0.0000	0.0000
Cd180	ENSMUSG00000021624	CD180 antigen	-1.964	0.0272	0.0572

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cd209b	ENSMUSG00000065987	CD209b antigen	-3.148	0.0338	0.0692
Cd247	ENSMUSG00000005763	CD247 antigen	-3.474	0.0010	0.0032
Cd27	ENSMUSG00000030336	CD27 antigen	-29.790	0.0003	0.0011
Cd300lb	ENSMUSG00000063193	CD300 molecule like family member B	-2.457	0.0194	0.0429
Cd300ld	ENSMUSG00000034641	CD300 molecule like family member d	-1.779	0.0068	0.0170
Cd302	ENSMUSG00000060703	CD302 antigen	-1.753	0.0000	0.0000
Cd320	ENSMUSG00000002308	CD320 antigen	-3.285	0.0000	0.0000
Cd34	ENSMUSG00000016494	CD34 antigen	-1.518	0.0000	0.0002
Cd40	ENSMUSG00000017652	CD40 antigen	-2.069	0.0002	0.0008
Cd46	ENSMUSG00000016493	CD46 antigen, complement regulatory protein	-1.750	0.0156	0.0353
Cd52	ENSMUSG00000000682	CD52 antigen	-3.257	0.0035	0.0096
Cd59b	ENSMUSG00000068686	CD59b antigen	-2.709	0.0000	0.0000
Cd68	ENSMUSG00000018774	CD68 antigen	-1.786	0.0020	0.0057
Cd7	ENSMUSG00000025163	CD7 antigen	-20.063	0.0030	0.0081
Cd74	ENSMUSG00000024610	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-2.456	0.0001	0.0002
Cd82	ENSMUSG00000027215	CD82 antigen	-1.664	0.0000	0.0001
Cd83	ENSMUSG00000015396	CD83 antigen	-1.869	0.0037	0.0099
Cda	ENSMUSG00000028755	cytidine deaminase	-4.657	0.0001	0.0003
Cdc42ep2	ENSMUSG00000045664	CDC42 effector protein (Rho GTPase binding) 2	-1.686	0.0000	0.0001
Cdcp3	ENSMUSG00000006204	CUB domain containing protein 3	-3.964	0.0000	0.0000
Cdh13	ENSMUSG00000031841	cadherin 13	-1.546	0.0000	0.0000
Cdh15	ENSMUSG00000031962	cadherin 15	-17.090	0.0045	0.0119
Cdh16	ENSMUSG00000031881	cadherin 16	-5.483	0.0000	0.0000
Cdh23	ENSMUSG00000012819	cadherin 23 (otocadherin)	-2.338	0.0000	0.0000
Cdh3	ENSMUSG00000061048	cadherin 3	-6.154	0.0389	0.0779
Cdh4	ENSMUSG00000000305	cadherin 4	-3.064	0.0000	0.0000
Cdhr3	ENSMUSG00000035860	cadherin-related family member 3	-2.936	0.0356	0.0723
Cdin1	ENSMUSG00000040282	CDAN1 interacting nuclease 1	-1.764	0.0009	0.0027
Cdip1	ENSMUSG00000004071	cell death inducing Trp53 target 1	-1.761	0.0000	0.0000
Cdipt	ENSMUSG00000030682	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	-1.846	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cdk20	ENSMUSG00000021483	cyclin-dependent kinase 20	-2.171	0.0002	0.0006
Cdk2ap2	ENSMUSG00000024856	CDK2-associated protein 2	-3.128	0.0000	0.0000
Cdk4	ENSMUSG00000006728	cyclin-dependent kinase 4	-2.044	0.0000	0.0000
Cdpf1	ENSMUSG00000064284	cysteine rich, DPF motif domain containing 1	-2.139	0.0000	0.0000
Cdsn	ENSMUSG00000039518	corneodesmosin	-2.778	0.0004	0.0012
Cdt1	ENSMUSG00000006585	chromatin licensing and DNA replication factor 1	-1.825	0.0087	0.0211
Celsr1	ENSMUSG00000016028	cadherin, EGF LAG seven-pass G-type receptor 1	-2.023	0.0001	0.0004
Cenpa	ENSMUSG00000029177	centromere protein A	-1.560	0.0007	0.0021
Cenpt	ENSMUSG00000036672	centromere protein T	-2.246	0.0030	0.0082
Cenpw	ENSMUSG00000075266	centromere protein W	-2.407	0.0244	0.0522
Cenpx	ENSMUSG00000025144	centromere protein X	-2.338	0.0000	0.0000
Cep295	ENSMUSG00000046111	centrosomal protein 295	-1.540	0.0003	0.0010
Cers2	ENSMUSG00000015714	ceramide synthase 2	-1.551	0.0000	0.0000
Ces1e	ENSMUSG00000061959	carboxylesterase 1E	-2.666	0.0320	0.0661
Ces2e	ENSMUSG00000031886	carboxylesterase 2E	-2.547	0.0018	0.0053
Cfap126	ENSMUSG00000026649	cilia and flagella associated protein 126	-1.609	0.0407	0.0811
Cfap20	ENSMUSG00000031796	cilia and flagella associated protein 20	-1.732	0.0000	0.0000
Cfap300	ENSMUSG00000053070	cilia and flagella associated protein 300	-3.282	0.0001	0.0003
Cfap410	ENSMUSG00000020284	cilia and flagella associated protein 410	-2.156	0.0000	0.0000
Cfap418	ENSMUSG00000059482	cilia and flagella associated protein 418	-1.542	0.0048	0.0125
Cfap54	ENSMUSG00000020014	cilia and flagella associated protein 54	-1.901	0.0014	0.0041
Chac1	ENSMUSG00000027313	ChaC, cation transport regulator 1	-2.902	0.0342	0.0700
Chchd1	ENSMUSG00000063787	coiled-coil-helix-coiled-coil-helix domain containing 1	-3.418	0.0000	0.0000
Chchd2	ENSMUSG00000070493	coiled-coil-helix-coiled-coil-helix domain containing 2	-1.611	0.0000	0.0000
Chchd2-ps	ENSMUSG00000094320	coiled-coil-helix-coiled-coil-helix domain containing 2, pseudogene	-12.941	0.0000	0.0000
Chchd5	ENSMUSG00000037938	coiled-coil-helix-coiled-coil-helix domain containing 5	-1.655	0.0000	0.0000
Chchd6	ENSMUSG00000030086	coiled-coil-helix-coiled-coil-helix domain containing 6	-1.508	0.0000	0.0001
Chpf2	ENSMUSG00000038181	chondroitin polymerizing factor 2	-1.782	0.0008	0.0026
Chrd	ENSMUSG00000006958	chordin	-1.943	0.0024	0.0068
Chrna1	ENSMUSG00000027107	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	-37.453	0.0008	0.0025
Chst12	ENSMUSG00000036599	carbohydrate sulfotransferase 12	-2.328	0.0000	0.0000

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Chst7	ENSMUSG00000037347	carbohydrate (N-acetylglucosamino) sulfotransferase 7	-1.956	0.0002	0.0006
Churc1	ENSMUSG00000090258	churchill domain containing 1	-2.977	0.0000	0.0000
Ciao3	ENSMUSG00000002280	cytosolic iron-sulfur assembly component 3	-2.185	0.0000	0.0000
Cib1	ENSMUSG00000030538	calcium and integrin binding 1 (calmyrin)	-1.778	0.0000	0.0000
Cib3	ENSMUSG00000074240	calcium and integrin binding family member 3	-12.143	0.0001	0.0002
Cipc	ENSMUSG00000034157	CLOCK interacting protein, circadian	-1.837	0.0001	0.0003
Cisd3	ENSMUSG00000078695	CDGSH iron sulfur domain 3	-2.206	0.0000	0.0000
Cish	ENSMUSG00000032578	cytokine inducible SH2-containing protein	-3.152	0.0000	0.0000
Ckb	ENSMUSG00000001270	creatine kinase, brain	-5.942	0.0000	0.0000
Ckm	ENSMUSG00000030399	creatine kinase, muscle	-2.310	0.0000	0.0000
Clba1	ENSMUSG00000037594	clathrin binding box of aftiphilin containing 1	-1.865	0.0004	0.0014
Clcn7	ENSMUSG00000036636	chloride channel, voltage-sensitive 7	-1.666	0.0000	0.0000
Cldn10	ENSMUSG00000022132	claudin 10	-12.612	0.0498	0.0962
Cldn15	ENSMUSG00000001739	claudin 15	-3.144	0.0003	0.0009
Cldn5	ENSMUSG00000041378	claudin 5	-1.803	0.0000	0.0002
Clec10a	ENSMUSG00000000318	C-type lectin domain family 10, member A	-1.704	0.0158	0.0358
Clec2d	ENSMUSG00000030157	C-type lectin domain family 2, member d	-2.971	0.0000	0.0000
Clec2e	ENSMUSG00000030155	C-type lectin domain family 2, member e	-4.498	0.0098	0.0237
Clec3b	ENSMUSG00000025784	C-type lectin domain family 3, member b	-3.558	0.0000	0.0000
Clec4a1	ENSMUSG00000049037	C-type lectin domain family 4, member a1	-1.681	0.0149	0.0340
Clec4a3	ENSMUSG00000043832	C-type lectin domain family 4, member a3	-1.733	0.0360	0.0730
Clec4f	ENSMUSG00000014542	C-type lectin domain family 4, member f	-14.337	0.0176	0.0392
Clic1	ENSMUSG00000007041	chloride intracellular channel 1	-2.347	0.0000	0.0000
Clic3	ENSMUSG00000015093	chloride intracellular channel 3	-15.986	0.0056	0.0144
Clpb	ENSMUSG00000001829	ClpB caseinolytic peptidase B	-1.524	0.0000	0.0000
Clpp	ENSMUSG00000002660	caseinolytic mitochondrial matrix peptidase proteolytic subunit	-1.767	0.0000	0.0000
Clu	ENSMUSG00000022037	clusterin	-1.890	0.0000	0.0000
Cmtm3	ENSMUSG00000031875	CKLF-like MARVEL transmembrane domain containing 3	-2.660	0.0000	0.0000
Cmtm5	ENSMUSG00000040759	CKLF-like MARVEL transmembrane domain containing 5	-4.397	0.0167	0.0375
Cmtm8	ENSMUSG00000041012	CKLF-like MARVEL transmembrane domain containing 8	-1.793	0.0000	0.0000
Cmtr1	ENSMUSG00000024019	cap methyltransferase 1	-1.781	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cnep1r1	ENSMUSG00000036810	CTD nuclear envelope phosphatase 1 regulatory subunit 1	-1.657	0.0000	0.0000
Cngb3	ENSMUSG00000056494	cyclic nucleotide gated channel beta 3	-2.028	0.0099	0.0237
Cnih1	ENSMUSG00000015759	cornichon family AMPA receptor auxiliary protein 1	-1.532	0.0000	0.0000
Cnksr1	ENSMUSG00000028841	connector enhancer of kinase suppressor of Ras 1	-4.882	0.0000	0.0000
Cnn3	ENSMUSG00000053931	calponin 3, acidic	-1.995	0.0000	0.0000
Cnr2	ENSMUSG00000062585	cannabinoid receptor 2 (macrophage)	-1.640	0.0208	0.0455
Cntfr	ENSMUSG00000028444	ciliary neurotrophic factor receptor	-1.923	0.0006	0.0018
Cntnap1	ENSMUSG00000017167	contactin associated protein-like 1	-1.847	0.0045	0.0119
Coa3	ENSMUSG00000017188	cytochrome C oxidase assembly factor 3	-2.298	0.0000	0.0000
Coa6	ENSMUSG00000051671	cytochrome c oxidase assembly factor 6	-1.914	0.0000	0.0000
Coa8	ENSMUSG00000037787	cytochrome c oxidase assembly factor 8	-1.704	0.0000	0.0000
Coasy	ENSMUSG00000001755	Coenzyme A synthase	-1.624	0.0001	0.0002
Cog8	ENSMUSG00000031916	component of oligomeric golgi complex 8	-1.788	0.0000	0.0001
Col4a5	ENSMUSG00000031274	collagen, type IV, alpha 5	-1.988	0.0000	0.0000
Col4a6	ENSMUSG00000031273	collagen, type IV, alpha 6	-1.536	0.0258	0.0548
Col6a5	ENSMUSG00000091345	collagen, type VI, alpha 5	-5.942	0.0000	0.0001
Colec12	ENSMUSG00000036103	collectin sub-family member 12	-1.708	0.0000	0.0000
Commd2	ENSMUSG00000036513	COMM domain containing 2	-1.503	0.0000	0.0000
Commd4	ENSMUSG00000032299	COMM domain containing 4	-3.257	0.0000	0.0000
Commd9	ENSMUSG00000027163	COMM domain containing 9	-2.596	0.0000	0.0000
Comt	ENSMUSG00000000326	catechol-O-methyltransferase	-2.278	0.0000	0.0000
Comtd1	ENSMUSG00000021773	catechol-O-methyltransferase domain containing 1	-4.108	0.0000	0.0000
Cope	ENSMUSG00000055681	coatomer protein complex, subunit epsilon	-3.064	0.0000	0.0000
Cops3	ENSMUSG00000019373	COP9 signalosome subunit 3	-1.934	0.0000	0.0000
Cops6	ENSMUSG00000019494	COP9 signalosome subunit 6	-1.952	0.0000	0.0000
Cops7a	ENSMUSG00000030127	COP9 signalosome subunit 7A	-2.456	0.0000	0.0000
Coq4	ENSMUSG00000026798	coenzyme Q4	-2.395	0.0000	0.0000
Coq6	ENSMUSG00000021235	coenzyme Q6 monooxygenase	-1.786	0.0000	0.0000
Coq8a	ENSMUSG00000026489	coenzyme Q8A	-1.777	0.0000	0.0000
Coq8b	ENSMUSG00000003762	coenzyme Q8B	-1.557	0.0000	0.0000
Coq9	ENSMUSG00000031782	coenzyme Q9	-1.934	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Coro1a	ENSMUSG00000030707	coronin, actin binding protein 1A	-1.737	0.0124	0.0291
Coro1b	ENSMUSG00000024835	coronin, actin binding protein 1B	-2.408	0.0000	0.0000
Coro6	ENSMUSG00000020836	coronin 6	-1.587	0.0000	0.0000
Cox10	ENSMUSG00000042148	heme A:farnesyltransferase cytochrome c oxidase assembly factor 10	-1.818	0.0000	0.0000
Cox14	ENSMUSG00000023020	cytochrome c oxidase assembly protein 14	-1.836	0.0000	0.0000
Cox16	ENSMUSG00000091803	cytochrome c oxidase assembly protein 16	-7.547	0.0000	0.0000
Cox18	ENSMUSG00000035505	cytochrome c oxidase assembly protein 18	-2.022	0.0000	0.0000
Cox4i2	ENSMUSG00000009876	cytochrome c oxidase subunit 4I2	-2.655	0.0000	0.0000
Cox6a1	ENSMUSG00000041697	cytochrome c oxidase subunit 6A1	-1.845	0.0000	0.0000
Cox6a2	ENSMUSG00000030785	cytochrome c oxidase subunit 6A2	-5.350	0.0000	0.0000
Cox6b1	ENSMUSG00000036751	cytochrome c oxidase, subunit 6B1	-2.577	0.0000	0.0000
Cox7a1	ENSMUSG00000074218	cytochrome c oxidase subunit 7A1	-2.924	0.0000	0.0000
Cox7a2	ENSMUSG00000032330	cytochrome c oxidase subunit 7A2	-3.664	0.0000	0.0000
Cox7a2l	ENSMUSG00000024248	cytochrome c oxidase subunit 7A2 like	-2.082	0.0000	0.0000
Cox7b	ENSMUSG00000031231	cytochrome c oxidase subunit 7B	-1.839	0.0000	0.0000
Cox8a	ENSMUSG00000035885	cytochrome c oxidase subunit 8A	-3.913	0.0000	0.0000
Cox8b	ENSMUSG00000025488	cytochrome c oxidase subunit 8B	-1.737	0.0000	0.0000
Cpa1	ENSMUSG00000054446	carboxypeptidase A1, pancreatic	-6.565	0.0423	0.0838
Cpped1	ENSMUSG00000065979	calcineurin-like phosphoesterase domain containing 1	-1.538	0.0000	0.0000
Cpsf1	ENSMUSG00000034022	cleavage and polyadenylation specific factor 1	-1.577	0.0000	0.0000
Cpt1b	ENSMUSG00000078937	carnitine palmitoyltransferase 1b, muscle	-5.923	0.0000	0.0000
Cpt1c	ENSMUSG00000007783	carnitine palmitoyltransferase 1c	-1.776	0.0031	0.0086
Cpt2	ENSMUSG00000028607	carnitine palmitoyltransferase 2	-1.794	0.0000	0.0000
Cptp	ENSMUSG00000029073	ceramide-1-phosphate transfer protein	-1.772	0.0000	0.0001
Cpxm1	ENSMUSG00000027408	carboxypeptidase X 1 (M14 family)	-4.446	0.0000	0.0000
Cpxm2	ENSMUSG00000030862	carboxypeptidase X 2 (M14 family)	-2.388	0.0000	0.0000
Cpz	ENSMUSG00000036596	carboxypeptidase Z	-3.829	0.0425	0.0842
Crat	ENSMUSG00000026853	carnitine acetyltransferase	-2.260	0.0000	0.0000
Crb2	ENSMUSG00000035403	crumbs family member 2	-24.646	0.0038	0.0102
Crb3	ENSMUSG00000044279	crumbs family member 3	-5.182	0.0015	0.0044
Crip2	ENSMUSG00000006356	cysteine rich protein 2	-1.892	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Crlf2	ENSMUSG00000033467	cytokine receptor-like factor 2	-3.627	0.0000	0.0000
Crtc1	ENSMUSG00000003575	CREB regulated transcription coactivator 1	-2.170	0.0000	0.0000
Cryab	ENSMUSG00000032060	crystallin, alpha B	-2.163	0.0000	0.0000
Crybb1	ENSMUSG00000029343	crystallin, beta B1	-2.839	0.0000	0.0000
Crybb3	ENSMUSG00000029352	crystallin, beta B3	-2.638	0.0115	0.0272
Cs	ENSMUSG00000005683	citrate synthase	-1.785	0.0000	0.0000
Csdc2	ENSMUSG00000042109	cold shock domain containing C2, RNA binding	-1.782	0.0014	0.0042
Csf1r	ENSMUSG00000024621	colony stimulating factor 1 receptor	-1.947	0.0000	0.0000
Csf2rb2	ENSMUSG00000071714	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	-2.599	0.0016	0.0046
Csf3r	ENSMUSG00000028859	colony stimulating factor 3 receptor (granulocyte)	-2.406	0.0073	0.0181
Csmd1	ENSMUSG00000060924	CUB and Sushi multiple domains 1	-2.699	0.0119	0.0280
Csnk2a1-ps3	ENSMUSG00000101523	casein kinase 2, alpha 1 polypeptide, pseudogene 3	-1.629	0.0150	0.0342
Csnk2b	ENSMUSG00000024387	casein kinase 2, beta polypeptide	-3.217	0.0000	0.0000
Cspg4	ENSMUSG00000032911	chondroitin sulfate proteoglycan 4	-1.703	0.0000	0.0000
Csrp3	ENSMUSG00000030470	cysteine and glycine-rich protein 3	-1.662	0.0000	0.0000
Cst6	ENSMUSG00000024846	cystatin E/M	-5.301	0.0000	0.0000
Cstf1	ENSMUSG00000027498	cleavage stimulation factor, 3' pre-RNA, subunit 1	-1.873	0.0000	0.0000
Cstpp1	ENSMUSG00000040591	centriolar satellite-associated tubulin polyglutamylase complex regulator 1	-1.594	0.0002	0.0008
Ctbp2	ENSMUSG00000030970	C-terminal binding protein 2	-1.893	0.0000	0.0000
Ctc1	ENSMUSG00000020898	CTS telomere maintenance complex component 1	-1.929	0.0000	0.0000
Cth	ENSMUSG00000028179	cystathionase (cystathionine gamma-lyase)	-2.639	0.0136	0.0314
Ctsa	ENSMUSG00000017760	cathepsin A	-1.750	0.0000	0.0000
Ctsb	ENSMUSG00000021939	cathepsin B	-1.826	0.0000	0.0000
Ctsd	ENSMUSG00000007891	cathepsin D	-4.110	0.0000	0.0000
Ctsf	ENSMUSG00000083282	cathepsin F	-1.514	0.0000	0.0000
Ctu2	ENSMUSG00000049482	cytosolic thiouridylase subunit 2	-2.378	0.0000	0.0000
Cubn	ENSMUSG00000026726	cubilin (intrinsic factor-cobalamin receptor)	-5.154	0.0005	0.0017
Cul9	ENSMUSG00000040327	cullin 9	-1.717	0.0000	0.0000
Cuta	ENSMUSG00000024194	cutA divalent cation tolerance homolog	-1.842	0.0000	0.0000
Cuzd1	ENSMUSG00000040205	CUB and zona pellucida-like domains 1	-3.356	0.0000	0.0000
Cx3cl1	ENSMUSG00000031778	chemokine (C-X3-C motif) ligand 1	-2.326	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cxcr5	ENSMUSG00000047880	chemokine (C-X-C motif) receptor 5	-6.627	0.0383	0.0770
Cyb561a3	ENSMUSG00000034445	cytochrome b561 family, member A3	-1.541	0.0000	0.0001
Cyb561d2	ENSMUSG00000037190	cytochrome b-561 domain containing 2	-3.442	0.0000	0.0000
Cyb5a	ENSMUSG00000024646	cytochrome b5 type A (microsomal)	-3.196	0.0000	0.0000
Cyb5r1	ENSMUSG00000026456	cytochrome b5 reductase 1	-1.575	0.0000	0.0000
Cyba	ENSMUSG00000006519	cytochrome b-245, alpha polypeptide	-1.530	0.0001	0.0004
Cybrd1	ENSMUSG00000027015	cytochrome b reductase 1	-13.597	0.0002	0.0008
Cyfip2	ENSMUSG00000020340	cytoplasmic FMR1 interacting protein 2	-1.737	0.0001	0.0003
Cyp27a1	ENSMUSG00000026170	cytochrome P450, family 27, subfamily a, polypeptide 1	-2.355	0.0000	0.0000
Cyp2d22	ENSMUSG00000061740	cytochrome P450, family 2, subfamily d, polypeptide 22	-2.076	0.0000	0.0000
Cyp2j9	ENSMUSG00000015224	cytochrome P450, family 2, subfamily j, polypeptide 9	-1.837	0.0002	0.0007
Cyp2s1	ENSMUSG00000040703	cytochrome P450, family 2, subfamily s, polypeptide 1	-21.318	0.0000	0.0000
Cyp4f14	ENSMUSG00000024292	cytochrome P450, family 4, subfamily f, polypeptide 14	-13.816	0.0067	0.0169
Cyp4f16	ENSMUSG00000048440	cytochrome P450, family 4, subfamily f, polypeptide 16	-2.234	0.0000	0.0000
Cyp4f17	ENSMUSG00000091586	cytochrome P450, family 4, subfamily f, polypeptide 17	-1.599	0.0060	0.0152
Cyp7b1	ENSMUSG00000039519	cytochrome P450, family 7, subfamily b, polypeptide 1	-2.638	0.0109	0.0258
Cysltr1	ENSMUSG00000052821	cysteinyl leukotriene receptor 1	-1.501	0.0330	0.0677
Cystm1	ENSMUSG00000046727	cysteine-rich transmembrane module containing 1	-2.332	0.0000	0.0000
Cytl1	ENSMUSG00000062329	cytokine-like 1	-3.417	0.0000	0.0000
D330023K18Rik	ENSMUSG00000087269	RIKEN cDNA D330023K18 gene	-2.743	0.0000	0.0000
D5Ertd605e	ENSMUSG00000106820	DNA segment, Chr 5, ERATO Doi 605, expressed	-21.435	0.0011	0.0032
D630003M21Rik	ENSMUSG00000037813	RIKEN cDNA D630003M21 gene	-2.812	0.0000	0.0000
D630024D03Rik	ENSMUSG00000085772	RIKEN cDNA D630024D03 gene	-10.594	0.0003	0.0009
D7Ertd443e	ENSMUSG00000030994	DNA segment, Chr 7, ERATO Doi 443, expressed	-1.941	0.0491	0.0950
D830005E20Rik	ENSMUSG00000112707	RIKEN cDNA D830005E20 gene	-1.708	0.0000	0.0000
Dad1	ENSMUSG00000022174	defender against cell death 1	-3.887	0.0000	0.0000
Dalrd3	ENSMUSG00000019039	DALR anticodon binding domain containing 3	-2.338	0.0000	0.0000
Dap	ENSMUSG00000039168	death-associated protein	-2.863	0.0000	0.0000
Dapp1	ENSMUSG00000028159	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	-1.863	0.0001	0.0005
Dbt	ENSMUSG00000000340	dihydrolipoamide branched chain transacylase E2	-1.543	0.0001	0.0005
Dcaf15	ENSMUSG00000037103	DDB1 and CUL4 associated factor 15	-1.852	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dcaf4	ENSMUSG00000021222	DDB1 and CUL4 associated factor 4	-1.675	0.0002	0.0008
Dcakd	ENSMUSG00000020935	dephospho-CoA kinase domain containing	-2.780	0.0000	0.0000
Dclre1c	ENSMUSG00000026648	DNA cross-link repair 1C	-1.547	0.0091	0.0221
Dcn	ENSMUSG00000019929	decorin	-2.477	0.0000	0.0000
Dctpp1	ENSMUSG00000042462	dCTP pyrophosphatase 1	-2.283	0.0000	0.0000
Dcxr	ENSMUSG00000039450	dicarbonyl L-xylulose reductase	-8.749	0.0000	0.0000
Dda1	ENSMUSG00000074247	DET1 and DDB1 associated 1	-1.900	0.0000	0.0000
Ddost	ENSMUSG00000028757	dolichyl-di-phosphooligosaccharide-protein glycotransferase	-1.678	0.0000	0.0000
Ddt	ENSMUSG00000001666	D-dopachrome tautomerase	-1.809	0.0000	0.0000
Ddx28	ENSMUSG00000045538	DEAD box helicase 28	-2.565	0.0000	0.0000
Ddx31	ENSMUSG00000026806	DEAD/H box helicase 31	-1.519	0.0000	0.0001
Ddx39b	ENSMUSG00000019432	DEAD box helicase 39b	-1.672	0.0000	0.0000
Ddx56	ENSMUSG00000004393	DEAD box helicase 56	-2.166	0.0000	0.0000
Degs1	ENSMUSG00000038633	delta(4)-desaturase, sphingolipid 1	-1.579	0.0000	0.0000
Dele1	ENSMUSG00000024442	DAP3 binding cell death enhancer 1	-3.126	0.0000	0.0000
Dennd4b	ENSMUSG00000042404	DENN/MADD domain containing 4B	-1.506	0.0000	0.0000
Dennd6b	ENSMUSG00000015377	DENN/MADD domain containing 6B	-1.968	0.0000	0.0000
Depdc7	ENSMUSG00000027173	DEP domain containing 7	-1.697	0.0121	0.0284
Depp1	ENSMUSG00000048489	DEPP1 autophagy regulator	-3.180	0.0037	0.0099
Dgki	ENSMUSG00000038665	diacylglycerol kinase, iota	-2.658	0.0122	0.0285
Dgkz	ENSMUSG00000040479	diacylglycerol kinase zeta	-2.247	0.0000	0.0000
Dguok	ENSMUSG00000014554	deoxyguanosine kinase	-2.073	0.0000	0.0000
Dhcr7	ENSMUSG00000058454	7-dehydrocholesterol reductase	-1.611	0.0009	0.0028
Dhodh	ENSMUSG00000031730	dihydroorotate dehydrogenase	-1.645	0.0000	0.0000
Dhrs1	ENSMUSG00000002332	dehydrogenase/reductase (SDR family) member 1	-1.538	0.0000	0.0000
Dhrs11	ENSMUSG00000034449	dehydrogenase/reductase (SDR family) member 11	-2.178	0.0000	0.0000
Dhrs7b	ENSMUSG00000042569	dehydrogenase/reductase (SDR family) member 7B	-1.984	0.0000	0.0000
Dhrs9	ENSMUSG00000027068	dehydrogenase/reductase (SDR family) member 9	-17.059	0.0080	0.0197
Dhx30	ENSMUSG00000032480	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-1.699	0.0000	0.0000
Dhx34	ENSMUSG00000006019	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-2.124	0.0000	0.0000
Dhx35	ENSMUSG00000027655	DEAH (Asp-Glu-Ala-His) box polypeptide 35	-1.586	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dhx37	ENSMUSG00000029480	DEAH (Asp-Glu-Ala-His) box polypeptide 37	-1.912	0.0000	0.0000
Diablo	ENSMUSG00000029433	diablo, IAP-binding mitochondrial protein	-1.664	0.0007	0.0021
Disc1	ENSMUSG00000043051	disrupted in schizophrenia 1	-1.930	0.0135	0.0312
Dlec1	ENSMUSG00000038060	deleted in lung and esophageal cancer 1	-27.172	0.0012	0.0036
Dll4	ENSMUSG00000027314	delta like canonical Notch ligand 4	-2.353	0.0000	0.0000
Dmac1	ENSMUSG00000028398	distal membrane arm assembly complex 1	-1.626	0.0000	0.0000
Dmap1	ENSMUSG00000009640	DNA methyltransferase 1-associated protein 1	-1.791	0.0000	0.0000
Dmkn	ENSMUSG00000060962	dermokine	-9.685	0.0166	0.0374
Dnaaf2	ENSMUSG00000020973	dynein, axonemal assembly factor 2	-2.097	0.0098	0.0235
Dnaaf3	ENSMUSG00000055809	dynein, axonemal assembly factor 3	-1.593	0.0342	0.0699
Dnaaf8	ENSMUSG00000022543	dynein axonemal assembly factor 8	-1.822	0.0021	0.0060
Dnajc15	ENSMUSG00000022013	DnaJ heat shock protein family (Hsp40) member C15	-2.368	0.0000	0.0000
Dnajc19-ps	ENSMUSG00000083854	DnaJ heat shock protein family (Hsp40) member C19, pseudogene	-4.446	0.0085	0.0208
Dnajc30	ENSMUSG00000061118	DnaJ heat shock protein family (Hsp40) member C30	-1.776	0.0000	0.0000
Dnal4	ENSMUSG00000022420	dynein, axonemal, light chain 4	-1.769	0.0000	0.0000
Dnase1l2	ENSMUSG00000024136	deoxyribonuclease 1-like 2	-2.782	0.0198	0.0436
Dnase2a	ENSMUSG00000003812	deoxyribonuclease II alpha	-1.684	0.0000	0.0000
Dnd1	ENSMUSG00000044595	DND microRNA-mediated repression inhibitor 1	-4.697	0.0000	0.0000
Dnpep	ENSMUSG00000026209	aspartyl aminopeptidase	-2.544	0.0000	0.0000
Dohh	ENSMUSG00000078440	deoxyhypusine hydroxylase/monooxygenase	-1.637	0.0000	0.0000
Dok1	ENSMUSG00000068335	docking protein 1	-1.612	0.0119	0.0280
Dok3	ENSMUSG00000035711	docking protein 3	-1.776	0.0341	0.0698
Dok7	ENSMUSG00000044716	docking protein 7	-2.497	0.0000	0.0000
Dolk	ENSMUSG00000075419	dolichol kinase	-1.534	0.0000	0.0000
Dolpp1	ENSMUSG00000026856	dolichyl pyrophosphate phosphatase 1	-1.594	0.0000	0.0001
Dop1b	ENSMUSG00000022946	DOP1 leucine zipper like protein B	-1.986	0.0000	0.0000
Dpagt1	ENSMUSG00000032123	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	-3.776	0.0000	0.0000
Dpep1	ENSMUSG00000019278	dipeptidase 1	-1.786	0.0005	0.0017
Dph1	ENSMUSG00000078789	diphthamide biosynthesis 1	-1.965	0.0000	0.0000
Dph2	ENSMUSG00000028540	DPH2 homolog	-2.336	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dpm2	ENSMUSG00000026810	dolichol-phosphate (beta-D) mannosyltransferase 2	-2.141	0.0000	0.0000
Dpm3	ENSMUSG00000042737	dolichyl-phosphate mannosyltransferase polypeptide 3	-5.332	0.0000	0.0000
Dpp7	ENSMUSG00000026958	dipeptidylpeptidase 7	-4.588	0.0000	0.0000
Dpp9	ENSMUSG00000001229	dipeptidylpeptidase 9	-2.100	0.0000	0.0000
Dpy19l3	ENSMUSG00000043671	dpy-19-like 3 (C. elegans)	-1.621	0.0006	0.0018
Dpysl4	ENSMUSG00000025478	dihydropyrimidinase-like 4	-1.906	0.0000	0.0001
Drc3	ENSMUSG00000056598	dynein regulatory complex subunit 3	-1.640	0.0015	0.0043
Drg2	ENSMUSG00000020537	developmentally regulated GTP binding protein 2	-1.928	0.0000	0.0000
Dstn	ENSMUSG00000015932	destrin	-1.713	0.0000	0.0000
Dus3l	ENSMUSG00000007603	dihydrouridine synthase 3-like (S. cerevisiae)	-1.845	0.0000	0.0000
Dusp13	ENSMUSG00000021768	dual specificity phosphatase 13	-3.937	0.0506	0.0975
Dusp23	ENSMUSG00000026544	dual specificity phosphatase 23	-1.894	0.0000	0.0000
Dxo	ENSMUSG00000040482	decapping exoribonuclease	-2.308	0.0000	0.0000
Dync2i2	ENSMUSG00000039715	dynein 2 intermediate chain 2	-2.260	0.0000	0.0000
Dynll1	ENSMUSG00000009013	dynein light chain LC8-type 1	-1.710	0.0006	0.0019
Dynlt1a	ENSMUSG00000092074	dynein light chain Tctex-type 1A	-6.776	0.0056	0.0145
Dynlt1c	ENSMUSG00000000579	dynein light chain Tctex-type 1C	-11.384	0.0007	0.0023
Dynlt1f	ENSMUSG00000095677	dynein light chain Tctex-type 1F	-4.651	0.0000	0.0001
Dynlt1-ps1	ENSMUSG00000082691	dynein light chain Tctex-type 1, pseuodogene 1	-11.850	0.0096	0.0231
E030042O20Rik	ENSMUSG00000087222	RIKEN cDNA E030042O20 gene	-1.791	0.0157	0.0356
E130310I04Rik	ENSMUSG00000116665	RIKEN cDNA E130310I04 gene	-2.696	0.0002	0.0006
E130317F20Rik	ENSMUSG00000091994	RIKEN cDNA E130317F20 gene	-1.956	0.0045	0.0118
E330011O21Rik	ENSMUSG00000109841	RIKEN cDNA E330011O21 gene	-1.519	0.0062	0.0158
E430024I08Rik	ENSMUSG00000112964	RIKEN cDNA E430024I08 gene	-1.626	0.0001	0.0002
Ear2	ENSMUSG00000072596	eosinophil-associated, ribonuclease A family, member 2	-11.412	0.0169	0.0379
Ebi3	ENSMUSG00000003206	Epstein-Barr virus induced gene 3	-5.355	0.0030	0.0082
Ebpl	ENSMUSG00000021928	emopamil binding protein-like	-1.992	0.0077	0.0189
Ech1	ENSMUSG00000053898	enoyl coenzyme A hydratase 1, peroxisomal	-2.050	0.0000	0.0000
Echdc2	ENSMUSG00000028601	enoyl Coenzyme A hydratase domain containing 2	-1.797	0.0000	0.0000
Echs1	ENSMUSG00000025465	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	-2.237	0.0000	0.0000
Ecm1	ENSMUSG00000028108	extracellular matrix protein 1	-1.761	0.0002	0.0007

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Edc3	ENSMUSG00000038957	enhancer of mRNA decapping 3	-1.937	0.0000	0.0000
Edc4	ENSMUSG00000036270	enhancer of mRNA decapping 4	-1.995	0.0000	0.0000
Edf1	ENSMUSG00000015092	endothelial differentiation-related factor 1	-1.731	0.0000	0.0000
Eef1akmt1	ENSMUSG00000021951	EEF1A alpha lysine methyltransferase 1	-1.845	0.0000	0.0000
Eef1akmt4	ENSMUSG00000115219	EEF1A lysine methyltransferase 4	-3.635	0.0001	0.0002
Eef2	ENSMUSG00000034994	eukaryotic translation elongation factor 2	-1.787	0.0000	0.0000
Eef2kmt	ENSMUSG00000022544	eukaryotic elongation factor 2 lysine methyltransferase	-2.708	0.0000	0.0000
Eefsec	ENSMUSG00000033216	eukaryotic elongation factor, selenocysteine-tRNA-specific	-2.784	0.0000	0.0000
Efemp2	ENSMUSG00000024909	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	-1.519	0.0120	0.0282
Efhc1	ENSMUSG00000041809	EF-hand domain (C-terminal) containing 1	-2.707	0.0056	0.0143
Efna1	ENSMUSG00000027954	ephrin A1	-2.040	0.0000	0.0000
Efna4	ENSMUSG00000028040	ephrin A4	-3.291	0.0061	0.0155
Efs	ENSMUSG00000022203	embryonal Fyn-associated substrate	-1.900	0.0000	0.0001
Eftud2	ENSMUSG00000020929	elongation factor Tu GTP binding domain containing 2	-1.624	0.0000	0.0000
Ehd3	ENSMUSG00000024065	EH-domain containing 3	-1.550	0.0002	0.0006
Eif1	ENSMUSG00000035530	eukaryotic translation initiation factor 1	-2.698	0.0000	0.0000
Eif2b3	ENSMUSG00000028683	eukaryotic translation initiation factor 2B, subunit 3	-1.676	0.0000	0.0000
Eif2d	ENSMUSG00000026427	eukaryotic translation initiation factor 2D	-2.054	0.0000	0.0000
Eif3h	ENSMUSG00000022312	eukaryotic translation initiation factor 3, subunit H	-2.016	0.0000	0.0000
Eif3i	ENSMUSG00000028798	eukaryotic translation initiation factor 3, subunit I	-2.897	0.0000	0.0000
Eif3k	ENSMUSG00000053565	eukaryotic translation initiation factor 3, subunit K	-2.044	0.0000	0.0000
Eif3l	ENSMUSG00000033047	eukaryotic translation initiation factor 3, subunit L	-1.998	0.0000	0.0000
Eif3m	ENSMUSG00000027170	eukaryotic translation initiation factor 3, subunit M	-1.659	0.0000	0.0000
Eif3s6-ps2	ENSMUSG00000091697	eukaryotic translation initiation factor 3, subunit 6, pseudogene 2	-1.982	0.0019	0.0054
Eif5al3-ps	ENSMUSG00000043618	eukaryotic translation initiation factor 5A-like 3, pseudogene	-1.855	0.0000	0.0000
Elmo1	ENSMUSG00000041112	engulfment and cell motility 1	-1.818	0.0012	0.0036
Elmo2	ENSMUSG00000017670	engulfment and cell motility 2	-1.680	0.0000	0.0000
Elmod3	ENSMUSG00000056698	ELMO/CED-12 domain containing 3	-2.106	0.0000	0.0000
Elob	ENSMUSG00000055839	elongin B	-3.186	0.0000	0.0000
Elof1	ENSMUSG00000013822	ELF1 homolog, elongation factor 1	-2.788	0.0000	0.0000
Elovl1	ENSMUSG00000006390	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.873	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Elp4	ENSMUSG00000027167	elongator acetyltransferase complex subunit 4	-1.714	0.0000	0.0000
Elp5	ENSMUSG00000018565	elongator acetyltransferase complex subunit 5	-1.806	0.0000	0.0000
Elp6	ENSMUSG00000054836	elongator acetyltransferase complex subunit 6	-1.665	0.0137	0.0316
Emc3	ENSMUSG00000030286	ER membrane protein complex subunit 3	-1.540	0.0000	0.0000
Emc6	ENSMUSG00000047260	ER membrane protein complex subunit 6	-1.857	0.0000	0.0000
Emcn	ENSMUSG00000054690	endomucin	-1.845	0.0000	0.0000
Emd	ENSMUSG00000001964	emerin	-1.642	0.0000	0.0000
Emilin1	ENSMUSG00000029163	elastin microfibril interfacer 1	-1.627	0.0027	0.0076
Emp2	ENSMUSG00000022505	epithelial membrane protein 2	-1.860	0.0000	0.0000
Emp3	ENSMUSG00000040212	epithelial membrane protein 3	-4.231	0.0000	0.0000
Eng	ENSMUSG00000026814	endoglin	-2.612	0.0000	0.0000
Enkd1	ENSMUSG00000013155	enkurin domain containing 1	-1.996	0.0063	0.0159
Eno1	ENSMUSG00000063524	enolase 1, alpha non-neuron	-1.898	0.0000	0.0000
Eno1b	ENSMUSG00000059040	enolase 1B, retrotransposed	-5.345	0.0000	0.0000
Eno3	ENSMUSG00000060600	enolase 3, beta muscle	-1.869	0.0000	0.0000
Enpep	ENSMUSG00000028024	glutamyl aminopeptidase	-1.723	0.0000	0.0000
Entpd2	ENSMUSG00000015085	ectonucleoside triphosphate diphosphohydrolase 2	-3.789	0.0000	0.0000
Entpd6	ENSMUSG00000033068	ectonucleoside triphosphate diphosphohydrolase 6	-1.884	0.0000	0.0000
Eola1	ENSMUSG00000045237	endothelium and lymphocyte associated ASCH domain 1	-1.849	0.0000	0.0000
Epb41l5	ENSMUSG00000026383	erythrocyte membrane protein band 4.1 like 5	-1.532	0.0028	0.0076
Epdr1	ENSMUSG00000002808	ependymin related protein 1 (zebrafish)	-1.534	0.0093	0.0226
Epg5	ENSMUSG00000039840	ectopic P-granules autophagy protein 5 homolog (C. elegans)	-2.127	0.0000	0.0000
Ephb6	ENSMUSG00000029869	Eph receptor B6	-2.767	0.0016	0.0047
Ephx1	ENSMUSG00000038776	epoxide hydrolase 1, microsomal	-2.074	0.0000	0.0000
Ephx2	ENSMUSG00000022040	epoxide hydrolase 2, cytoplasmic	-1.702	0.0000	0.0000
Ephx3	ENSMUSG00000037577	epoxide hydrolase 3	-2.320	0.0204	0.0448
Epn2	ENSMUSG00000001036	epsin 2	-1.663	0.0000	0.0000
Epn3	ENSMUSG00000010080	epsin 3	-2.928	0.0000	0.0000
Epor	ENSMUSG00000006235	erythropoietin receptor	-1.802	0.0198	0.0437
Eprn	ENSMUSG00000113346	ephemeron, early developmental lncRNA	-1.619	0.0331	0.0679
Eps15l1	ENSMUSG00000006276	epidermal growth factor receptor pathway substrate 15-like 1	-1.531	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ercc1	ENSMUSG00000003549	excision repair cross-complementing rodent repair deficiency, complementation group 1	-1.966	0.0000	0.0000
Ercc2	ENSMUSG00000030400	excision repair cross-complementing rodent repair deficiency, complementation group 2	-2.428	0.0000	0.0000
Ercc6l	ENSMUSG00000051220	excision repair cross-complementing rodent repair deficiency complementation group 6 like	-2.106	0.0033	0.0089
Esd	ENSMUSG00000021996	esterase D/formylglutathione hydrolase	-1.666	0.0000	0.0000
Espl1	ENSMUSG00000058290	extra spindle pole bodies 1, separase	-1.741	0.0302	0.0627
Espnl	ENSMUSG00000049515	espin-like	-11.408	0.0298	0.0620
Esrp2	ENSMUSG00000084128	epithelial splicing regulatory protein 2	-3.611	0.0017	0.0050
Esrrb	ENSMUSG00000021255	estrogen related receptor, beta	-2.066	0.0000	0.0000
Ethe1	ENSMUSG00000064254	ethylmalonic encephalopathy 1	-4.676	0.0000	0.0000
Eva1a	ENSMUSG00000035104	eva-1 homolog A (C. elegans)	-1.970	0.0014	0.0041
Exoc3l4	ENSMUSG00000021280	exocyst complex component 3-like 4	-2.068	0.0008	0.0025
Exoc7	ENSMUSG00000020792	exocyst complex component 7	-1.641	0.0000	0.0000
Exosc5	ENSMUSG00000061286	exosome component 5	-2.395	0.0000	0.0000
Eya4	ENSMUSG00000010461	EYA transcriptional coactivator and phosphatase 4	-3.001	0.0031	0.0085
F420014N23Rik	ENSMUSG00000097331	RIKEN cDNA F420014N23 gene	-18.965	0.0108	0.0258
F8a	ENSMUSG00000078317	factor 8-associated gene A	-1.755	0.0000	0.0000
Faap100	ENSMUSG00000025384	Fanconi anemia core complex associated protein 100	-3.254	0.0000	0.0000
Faap24	ENSMUSG00000030493	Fanconi anemia core complex associated protein 24	-1.973	0.0012	0.0035
Fabp3-ps1	ENSMUSG00000056366	fatty acid binding protein 3, muscle and heart, pseudogene 1	-1.689	0.0000	0.0000
Fads2	ENSMUSG00000024665	fatty acid desaturase 2	-1.698	0.0000	0.0000
Fads6	ENSMUSG00000044788	fatty acid desaturase domain family, member 6	-1.556	0.0001	0.0002
Fah	ENSMUSG00000030630	fumarylacetoacetate hydrolase	-3.348	0.0000	0.0000
Fam110a	ENSMUSG00000027459	family with sequence similarity 110, member A	-2.253	0.0000	0.0000
Fam117a	ENSMUSG00000038893	family with sequence similarity 117, member A	-2.615	0.0000	0.0000
Fam120b	ENSMUSG00000014763	family with sequence similarity 120, member B	-1.819	0.0000	0.0000
Fam13c	ENSMUSG00000043259	family with sequence similarity 13, member C	-1.601	0.0000	0.0000
Fam186b	ENSMUSG00000078907	family with sequence similarity 186, member B	-14.402	0.0185	0.0411
Fam189b	ENSMUSG00000032657	family with sequence similarity 189, member B	-2.721	0.0000	0.0000
Fam205c	ENSMUSG00000050141	family with sequence similarity 205, member C	-6.480	0.0000	0.0000
Fam20a	ENSMUSG00000020614	FAM20A, golgi associated secretory pathway pseudokinase	-2.117	0.0000	0.0002
Fam221b	ENSMUSG00000043633	family with sequence similarity 221, member B	-4.093	0.0023	0.0064

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fam222b	ENSMUSG00000037750	family with sequence similarity 222, member B	-1.610	0.0000	0.0000
Fam229b	ENSMUSG00000051736	family with sequence similarity 229, member B	-3.290	0.0000	0.0000
Fam234a	ENSMUSG00000024187	family with sequence similarity 234, member A	-2.116	0.0000	0.0000
Fam241b	ENSMUSG00000020083	family with sequence similarity 241, member B	-1.830	0.0005	0.0017
Fam53b	ENSMUSG00000030956	family with sequence similarity 53, member B	-1.866	0.0000	0.0000
Fam83e	ENSMUSG00000054161	family with sequence similarity 83, member E	-10.468	0.0015	0.0044
Fam83h	ENSMUSG00000046761	family with sequence similarity 83, member H	-2.071	0.0065	0.0163
Fan1	ENSMUSG00000033458	FANCD2/FANCI-associated nuclease 1	-1.760	0.0000	0.0000
Fanca	ENSMUSG00000032815	Fanconi anemia, complementation group A	-3.032	0.0000	0.0000
Fancb	ENSMUSG00000047757	Fanconi anemia, complementation group B	-1.751	0.0031	0.0084
Fancg	ENSMUSG00000028453	Fanconi anemia, complementation group G	-1.640	0.0038	0.0101
Farp2	ENSMUSG00000034066	FERM, RhoGEF and pleckstrin domain protein 2	-1.648	0.0001	0.0005
Fars2	ENSMUSG00000021420	phenylalanine-tRNA synthetase 2 (mitochondrial)	-2.060	0.0000	0.0000
Farsa	ENSMUSG00000003808	phenylalanyl-tRNA synthetase, alpha subunit	-1.558	0.0000	0.0000
Farsb	ENSMUSG00000026245	phenylalanyl-tRNA synthetase, beta subunit	-2.280	0.0000	0.0000
Fasn	ENSMUSG00000025153	fatty acid synthase	-1.631	0.0008	0.0025
Fastkd3	ENSMUSG00000021532	FAST kinase domains 3	-1.680	0.0001	0.0003
Fat2	ENSMUSG00000055333	FAT atypical cadherin 2	-4.412	0.0014	0.0041
Fau	ENSMUSG00000038274	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	-2.166	0.0000	0.0000
Fbln1	ENSMUSG00000006369	fibulin 1	-1.733	0.0006	0.0019
Fbln2	ENSMUSG00000064080	fibulin 2	-1.877	0.0000	0.0001
Fbln5	ENSMUSG00000021186	fibulin 5	-1.819	0.0000	0.0000
Fbxl13	ENSMUSG00000048520	F-box and leucine-rich repeat protein 13	-5.833	0.0355	0.0722
Fbxl15	ENSMUSG00000025226	F-box and leucine-rich repeat protein 15	-5.361	0.0000	0.0000
Fbxl2	ENSMUSG00000032507	F-box and leucine-rich repeat protein 2	-3.071	0.0134	0.0311
Fbxl22	ENSMUSG00000050503	F-box and leucine-rich repeat protein 22	-2.282	0.0000	0.0000
Fbxl6	ENSMUSG00000022559	F-box and leucine-rich repeat protein 6	-2.877	0.0000	0.0000
Fbxo17	ENSMUSG00000030598	F-box protein 17	-1.678	0.0054	0.0140
Fbxo44	ENSMUSG00000029001	F-box protein 44	-2.106	0.0000	0.0000
Fbxo6	ENSMUSG00000055401	F-box protein 6	-1.817	0.0000	0.0000
Fbxo8	ENSMUSG00000038206	F-box protein 8	-1.632	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fbxw5	ENSMUSG00000015095	F-box and WD-40 domain protein 5	-1.633	0.0000	0.0000
Fbxw9	ENSMUSG00000008167	F-box and WD-40 domain protein 9	-1.606	0.0002	0.0005
Fcer1g	ENSMUSG00000058715	Fc receptor, IgE, high affinity I, gamma polypeptide	-4.322	0.0000	0.0000
Fcgr2b	ENSMUSG00000026656	Fc receptor, IgG, low affinity IIb	-2.146	0.0002	0.0006
Fcgr3	ENSMUSG00000059498	Fc receptor, IgG, low affinity III	-2.656	0.0000	0.0000
Fcna	ENSMUSG00000026938	ficolin A	-1.990	0.0003	0.0010
Fcrls	ENSMUSG00000015852	Fc receptor-like S, scavenger receptor	-1.875	0.0232	0.0500
Fcsk	ENSMUSG00000033703	fucose kinase	-1.714	0.0000	0.0001
Fem1a	ENSMUSG00000043683	fem 1 homolog a	-2.116	0.0000	0.0000
Fer1l5	ENSMUSG00000037432	fer-1-like 5 (C. elegans)	-9.498	0.0013	0.0039
Fermt3	ENSMUSG00000024965	fermitin family member 3	-1.615	0.0059	0.0151
Fetub	ENSMUSG00000022871	fetuin beta	-2.461	0.0107	0.0255
Fgd2	ENSMUSG00000024013	FYVE, RhoGEF and PH domain containing 2	-3.327	0.0008	0.0025
Fgfbp1	ENSMUSG00000048373	fibroblast growth factor binding protein 1	-10.331	0.0055	0.0141
Fgfr3	ENSMUSG00000054252	fibroblast growth factor receptor 3	-1.875	0.0002	0.0006
Fh1	ENSMUSG00000026526	fumarate hydratase 1	-1.657	0.0000	0.0000
Fhdc1	ENSMUSG00000041842	FH2 domain containing 1	-3.024	0.0008	0.0026
Fhip1a	ENSMUSG00000051000	FHF complex subunit HOOK interacting protein 1A	-1.816	0.0000	0.0000
Fhl2	ENSMUSG00000008136	four and a half LIM domains 2	-2.297	0.0000	0.0000
Fhod1	ENSMUSG00000014778	formin homology 2 domain containing 1	-1.634	0.0001	0.0004
Ficd	ENSMUSG00000053334	FIC domain containing	-2.362	0.0000	0.0000
Fitm1	ENSMUSG00000022215	fat storage-inducing transmembrane protein 1	-4.208	0.0000	0.0000
Fkbp10	ENSMUSG00000001555	FK506 binding protein 10	-1.618	0.0000	0.0002
Fkbp11	ENSMUSG00000003355	FK506 binding protein 11	-2.203	0.0000	0.0002
Fkbp15	ENSMUSG00000066151	FK506 binding protein 15	-1.619	0.0000	0.0000
Flad1	ENSMUSG00000042642	flavin adenine dinucleotide synthetase 1	-1.933	0.0000	0.0000
Flnc	ENSMUSG00000068699	filamin C, gamma	-1.716	0.0000	0.0000
Flrt3	ENSMUSG00000051379	fibronectin leucine rich transmembrane protein 3	-3.029	0.0173	0.0386
Flt3l	ENSMUSG00000110206	FMS-like tyrosine kinase 3 ligand	-1.686	0.0370	0.0747
Fn1	ENSMUSG00000026193	fibronectin 1	-1.550	0.0025	0.0069
Fndc1	ENSMUSG00000071984	fibronectin type III domain containing 1	-1.872	0.0081	0.0198

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fndc10	ENSMUSG00000074738	fibronectin type III domain containing 10	-2.102	0.0001	0.0002
Fntb	ENSMUSG00000033373	farnesyltransferase, CAAX box, beta	-1.780	0.0000	0.0000
Focad	ENSMUSG00000038368	focadhesin	-2.057	0.0000	0.0000
Folr2	ENSMUSG00000032725	folate receptor 2 (fetal)	-2.871	0.0000	0.0000
Foxs1	ENSMUSG00000074676	forkhead box S1	-4.574	0.0000	0.0000
Fpgs	ENSMUSG00000009566	folylpolyglutamyl synthetase	-1.843	0.0001	0.0002
Frg2f1	ENSMUSG00000087385	FSHD region gene 2 family member 1	-1.680	0.0003	0.0009
Frmd5	ENSMUSG00000027238	FERM domain containing 5	-1.801	0.0000	0.0001
Frmd8	ENSMUSG00000024816	FERM domain containing 8	-2.619	0.0000	0.0000
Frmd8os	ENSMUSG00000043488	FERM domain containing 8, opposite strand	-2.841	0.0000	0.0000
Frzb	ENSMUSG00000027004	frizzled-related protein	-1.545	0.0040	0.0106
Fscn2	ENSMUSG00000025380	fascin actin-bundling protein 2	-15.709	0.0101	0.0242
Fstl3	ENSMUSG00000020325	follistatin-like 3	-2.208	0.0000	0.0000
Fstl4	ENSMUSG00000036264	follistatin-like 4	-3.061	0.0000	0.0000
Ftl1	ENSMUSG00000050708	ferritin light polypeptide 1	-3.238	0.0000	0.0000
Fuom	ENSMUSG00000025466	fucose mutarotase	-2.056	0.0000	0.0000
Fut7	ENSMUSG00000036587	fucosyltransferase 7	-12.933	0.0247	0.0527
Fuz	ENSMUSG00000011658	fuzzy planar cell polarity protein	-1.677	0.0000	0.0000
Fxn	ENSMUSG00000059363	frataxin	-4.071	0.0000	0.0000
Fxyd1	ENSMUSG00000036570	FXYD domain-containing ion transport regulator 1	-2.503	0.0000	0.0000
Fxyd2	ENSMUSG00000059412	FXYD domain-containing ion transport regulator 2	-3.281	0.0000	0.0000
Fxyd5	ENSMUSG00000009687	FXYD domain-containing ion transport regulator 5	-2.177	0.0000	0.0000
G0s2	ENSMUSG00000009633	G0/G1 switch gene 2	-3.409	0.0000	0.0000
G6pc3	ENSMUSG00000034793	glucose 6 phosphatase, catalytic, 3	-2.628	0.0000	0.0000
G6pdx	ENSMUSG00000031400	glucose-6-phosphate dehydrogenase X-linked	-1.690	0.0000	0.0000
Gaa	ENSMUSG00000025579	glucosidase, alpha, acid	-2.859	0.0000	0.0000
Gabarap	ENSMUSG00000018567	gamma-aminobutyric acid receptor associated protein	-1.528	0.0000	0.0000
Gabrr1	ENSMUSG00000028280	gamma-aminobutyric acid (GABA) C receptor, subunit rho 1	-4.898	0.0215	0.0469
Gadd45g	ENSMUSG00000021453	growth arrest and DNA-damage-inducible 45 gamma	-1.877	0.0030	0.0083
Gal3st2b	ENSMUSG00000093805	galactose-3-O-sulfotransferase 2B	-6.203	0.0000	0.0000
Gal3st3	ENSMUSG00000047658	galactose-3-O-sulfotransferase 3	-2.405	0.0108	0.0258

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Galk1	ENSMUSG00000020766	galactokinase 1	-1.653	0.0000	0.0000
Galm	ENSMUSG00000035473	galactose mutarotase	-1.539	0.0000	0.0000
Galns	ENSMUSG00000015027	galactosamine (N-acetyl)-6-sulfate sulfatase	-1.796	0.0000	0.0000
Galnt18	ENSMUSG00000038296	polypeptide N-acetylgalactosaminyltransferase 18	-1.640	0.0000	0.0000
Galt	ENSMUSG00000036073	galactose-1-phosphate uridyl transferase	-2.655	0.0000	0.0000
Gamt	ENSMUSG00000020150	guanidinoacetate methyltransferase	-2.467	0.0000	0.0000
Ganab	ENSMUSG00000071650	alpha glucosidase 2 alpha neutral subunit	-1.773	0.0000	0.0000
Garre1	ENSMUSG00000066571	granule associated Rac and RHOG effector 1	-1.504	0.0002	0.0007
Gask1b	ENSMUSG00000027955	golgi associated kinase 1B	-1.541	0.0441	0.0869
Gatd3a	ENSMUSG00000053329	glutamine amidotransferase like class 1 domain containing 3A	-1.926	0.0000	0.0000
Gba	ENSMUSG00000028048	glucosidase, beta, acid	-1.675	0.0000	0.0000
Gbp6	ENSMUSG00000104713	guanylate binding protein 6	-10.988	0.0014	0.0042
Gbx2	ENSMUSG00000034486	gastrulation brain homeobox 2	-2.186	0.0146	0.0334
Gcat	ENSMUSG00000006378	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	-1.940	0.0032	0.0086
Gcdh	ENSMUSG00000003809	glutaryl-Coenzyme A dehydrogenase	-1.831	0.0000	0.0000
Gchfr	ENSMUSG00000046814	GTP cyclohydrolase I feedback regulator	-2.698	0.0000	0.0000
Gcn1	ENSMUSG00000041638	GCN1 activator of EIF2AK4	-2.111	0.0000	0.0000
Gde1	ENSMUSG00000033917	glycerophosphodiester phosphodiesterase 1	-1.618	0.0000	0.0000
Gdf15	ENSMUSG00000038508	growth differentiation factor 15	-5.831	0.0000	0.0000
Gdpd3	ENSMUSG00000030703	glycerophosphodiester phosphodiesterase domain containing 3	-1.653	0.0000	0.0000
Gdpgp1	ENSMUSG00000050973	GDP-D-glucose phosphorylase 1	-1.520	0.0024	0.0068
Gemin5	ENSMUSG00000037275	gem nuclear organelle associated protein 5	-1.960	0.0000	0.0000
Gemin6-ps	ENSMUSG00000071237	gem nuclear organelle associated protein 6, pseudogene	-6.579	0.0145	0.0332
Get3	ENSMUSG00000052456	guided entry of tail-anchored proteins factor 3, ATPase	-2.110	0.0000	0.0000
Gfra3	ENSMUSG00000024366	glial cell line derived neurotrophic factor family receptor alpha 3	-4.464	0.0000	0.0001
Ggnbp1	ENSMUSG00000048731	gametogenetin binding protein 1	-2.030	0.0000	0.0000
Ggt5	ENSMUSG00000006344	gamma-glutamyltransferase 5	-2.623	0.0000	0.0000
Ggt7	ENSMUSG00000027603	gamma-glutamyltransferase 7	-1.568	0.0469	0.0915
Gimap1	ENSMUSG00000090019	GTPase, IMAP family member 1	-1.567	0.0063	0.0159
Gipc1	ENSMUSG00000019433	GIPC PDZ domain containing family, member 1	-1.970	0.0000	0.0000
Git2	ENSMUSG00000041890	GIT ArfGAP 2	-1.670	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gja4	ENSMUSG00000050234	gap junction protein, alpha 4	-1.874	0.0001	0.0003
Gkn3	ENSMUSG00000030048	gastrokine 3	-8.422	0.0070	0.0175
Glb1	ENSMUSG00000045594	galactosidase, beta 1	-2.298	0.0000	0.0000
Glb1l2	ENSMUSG00000036395	galactosidase, beta 1-like 2	-4.493	0.0166	0.0374
Glipr1	ENSMUSG00000056888	GLI pathogenesis-related 1 (glioma)	-3.527	0.0020	0.0059
Glis2	ENSMUSG00000014303	GLIS family zinc finger 2	-1.915	0.0000	0.0000
Glmp	ENSMUSG00000001418	glycosylated lysosomal membrane protein	-2.928	0.0000	0.0000
Glo1-ps	ENSMUSG00000075391	glyoxalase 1, pseudogene	-4.006	0.0000	0.0000
Glt8d2	ENSMUSG00000020251	glycosyltransferase 8 domain containing 2	-2.285	0.0030	0.0082
Gm10032	ENSMUSG00000057913	predicted gene 10032	-18.698	0.0091	0.0221
Gm10039	ENSMUSG00000091478	predicted pseudogene 10039	-3.235	0.0000	0.0000
Gm10059	ENSMUSG00000059064	predicted pseudogene 10059	-19.206	0.0020	0.0058
Gm10076	ENSMUSG00000060143	predicted gene 10076	-14.747	0.0000	0.0000
Gm10110	ENSMUSG00000062093	predicted gene 10110	-1.556	0.0000	0.0000
Gm10123	ENSMUSG00000062933	predicted pseudogene 10123	-3.078	0.0129	0.0300
Gm10226	ENSMUSG00000067929	predicted gene 10226	-33.760	0.0000	0.0002
Gm10263	ENSMUSG00000066407	predicted gene 10263	-3.708	0.0000	0.0000
Gm10275	ENSMUSG00000069682	predicted pseudogene 10275	-3.936	0.0000	0.0000
Gm10288	ENSMUSG00000070343	predicted gene 10288	-6.493	0.0000	0.0000
Gm10290	ENSMUSG00000105775	predicted pseudogene 10290	-2.892	0.0427	0.0844
Gm10291	ENSMUSG00000070443	predicted pseudogene 10291	-2.239	0.0011	0.0032
Gm10353	ENSMUSG00000114220	predicted gene 10353	-2.160	0.0185	0.0412
Gm10359	ENSMUSG00000094708	predicted gene 10359	-5.146	0.0099	0.0239
Gm10435	ENSMUSG00000072902	predicted gene 10435	-1.768	0.0025	0.0069
Gm10443	ENSMUSG00000072940	predicted pseudogene 10443	-2.088	0.0347	0.0707
Gm10499	ENSMUSG00000073403	predicted gene 10499	-2.768	0.0000	0.0002
Gm10509	ENSMUSG00000073448	predicted gene 10509	-5.544	0.0000	0.0000
Gm10644	ENSMUSG00000074219	predicted gene 10644	-2.138	0.0003	0.0010
Gm10736	ENSMUSG00000096842	predicted gene 10736	-96.240	0.0000	0.0000
Gm10766	ENSMUSG00000103957	predicted gene 10766	-6.861	0.0346	0.0706
Gm10790	ENSMUSG00000113856	predicted gene 10790	-6.126	0.0362	0.0733

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm10819	ENSMUSG00000075268	predicted gene 10819	-5.790	0.0001	0.0004
Gm11346	ENSMUSG00000085603	predicted gene 11346	-7.208	0.0199	0.0439
Gm11476	ENSMUSG00000085596	predicted gene 11476	-4.720	0.0380	0.0764
Gm11512	ENSMUSG00000081043	predicted gene 11512	-1.830	0.0159	0.0360
Gm11517	ENSMUSG00000081249	predicted gene 11517	-4.277	0.0055	0.0142
Gm11557	ENSMUSG00000082900	predicted gene 11557	-2.894	0.0036	0.0097
Gm11658	ENSMUSG00000081524	predicted gene 11658	-5.332	0.0035	0.0095
Gm11663	ENSMUSG00000082706	predicted gene 11663	-17.380	0.0117	0.0276
Gm11702	ENSMUSG00000084277	predicted gene 11702	-5.776	0.0000	0.0000
Gm11730	ENSMUSG00000087057	predicted gene 11730	-2.597	0.0121	0.0283
Gm11734	ENSMUSG00000085419	predicted gene 11734	-2.143	0.0002	0.0008
Gm11767	ENSMUSG00000085207	predicted gene 11767	-4.672	0.0488	0.0946
Gm11808	ENSMUSG00000068240	predicted gene 11808	-38.553	0.0000	0.0000
Gm11816	ENSMUSG00000086233	predicted gene 11816	-2.052	0.0062	0.0156
Gm11826	ENSMUSG00000083328	predicted gene 11826	-8.806	0.0217	0.0473
Gm11868	ENSMUSG00000050550	predicted gene 11868	-2.023	0.0000	0.0000
Gm11899	ENSMUSG00000087399	predicted gene 11899	-5.882	0.0088	0.0213
Gm11915	ENSMUSG00000086774	predicted gene 11915	-3.341	0.0383	0.0769
Gm11942	ENSMUSG00000094344	predicted gene 11942	-1.625	0.0000	0.0000
Gm11953	ENSMUSG00000082816	predicted gene 11953	-1.691	0.0471	0.0919
Gm11960	ENSMUSG00000081974	predicted gene 11960	-1.719	0.0482	0.0937
Gm11967	ENSMUSG00000084819	predicted gene 11967	-2.459	0.0001	0.0003
Gm11992	ENSMUSG00000040978	predicted gene 11992	-3.100	0.0004	0.0013
Gm12167	ENSMUSG00000085853	predicted gene 12167	-3.747	0.0000	0.0000
Gm12182	ENSMUSG00000083460	predicted gene 12182	-3.024	0.0039	0.0103
Gm12224	ENSMUSG00000085888	predicted gene 12224	-3.075	0.0002	0.0006
Gm12254	ENSMUSG00000085342	predicted gene 12254	-2.117	0.0285	0.0597
Gm12258	ENSMUSG00000072915	predicted gene 12258	-1.785	0.0329	0.0677
Gm12337	ENSMUSG00000084224	predicted gene 12337	-3.614	0.0172	0.0386
Gm12352	ENSMUSG00000084835	predicted gene 12352	-9.487	0.0260	0.0551
Gm12403	ENSMUSG00000082186	predicted gene 12403	-6.112	0.0038	0.0101

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm12409	ENSMUSG00000085876	predicted gene 12409	-2.904	0.0303	0.0630
Gm12439	ENSMUSG00000080850	predicted gene 12439	-1.509	0.0026	0.0073
Gm12481	ENSMUSG00000043770	predicted gene 12481	-2.765	0.0000	0.0000
Gm12537	ENSMUSG00000095042	predicted gene 12537	-3.853	0.0001	0.0004
Gm12586	ENSMUSG00000084401	predicted gene 12586	-7.664	0.0333	0.0682
Gm12663	ENSMUSG00000101316	predicted gene 12663	-2.052	0.0000	0.0000
Gm12715	ENSMUSG00000059195	predicted gene 12715	-4.769	0.0119	0.0281
Gm12724	ENSMUSG00000086249	predicted gene 12724	-14.188	0.0079	0.0196
Gm12727	ENSMUSG00000082768	predicted gene 12727	-10.098	0.0407	0.0811
Gm12751	ENSMUSG00000062554	predicted gene 12751	-5.179	0.0000	0.0000
Gm12854	ENSMUSG00000078238	predicted gene 12854	-17.388	0.0003	0.0009
Gm12864	ENSMUSG00000082143	predicted gene 12864	-21.417	0.0020	0.0057
Gm12993	ENSMUSG00000082063	predicted gene 12993	-3.915	0.0487	0.0945
Gm12996	ENSMUSG00000086417	predicted gene 12996	-2.613	0.0004	0.0012
Gm13092	ENSMUSG00000085787	predicted gene 13092	-9.131	0.0000	0.0000
Gm13192	ENSMUSG00000069188	predicted gene 13192	-12.094	0.0029	0.0080
Gm13245	ENSMUSG00000081998	predicted gene 13245	-10.940	0.0161	0.0363
Gm13375	ENSMUSG00000075514	predicted gene 13375	-1.618	0.0000	0.0000
Gm13436	ENSMUSG00000083716	predicted gene 13436	-2.916	0.0000	0.0000
Gm13456	ENSMUSG00000082536	predicted gene 13456	-3.162	0.0001	0.0005
Gm13578	ENSMUSG00000084104	predicted gene 13578	-4.045	0.0217	0.0472
Gm13668	ENSMUSG00000083072	predicted gene 13668	-10.288	0.0124	0.0290
Gm13881	ENSMUSG00000084756	predicted gene 13881	-1.771	0.0072	0.0180
Gm14022	ENSMUSG00000087151	predicted gene 14022	-2.613	0.0026	0.0073
Gm14026	ENSMUSG00000082274	predicted gene 14026	-2.945	0.0001	0.0003
Gm14048	ENSMUSG00000080989	predicted gene 14048	-2.469	0.0262	0.0554
Gm14091	ENSMUSG00000086421	predicted gene 14091	-17.307	0.0078	0.0193
Gm14097	ENSMUSG00000084839	predicted gene 14097	-1.713	0.0047	0.0122
Gm14111	ENSMUSG00000080870	predicted gene 14111	-2.132	0.0482	0.0937
Gm14121	ENSMUSG00000083325	predicted gene 14121	-2.384	0.0256	0.0545
Gm14130	ENSMUSG00000081494	predicted gene 14130	-7.067	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm14165	ENSMUSG00000081434	predicted gene 14165	-16.119	0.0000	0.0000
Gm14269	ENSMUSG00000084067	predicted gene 14269	-2.921	0.0383	0.0769
Gm14270	ENSMUSG00000084013	predicted gene 14270	-4.289	0.0013	0.0038
Gm14286	ENSMUSG00000087445	predicted gene 14286	-3.956	0.0111	0.0262
Gm14292	ENSMUSG00000061897	predicted gene 14292	-1.809	0.0109	0.0259
Gm14303	ENSMUSG00000081344	predicted gene 14303	-4.016	0.0000	0.0000
Gm14494	ENSMUSG00000083097	predicted gene 14494	-1.874	0.0214	0.0467
Gm14539	ENSMUSG00000084830	predicted gene 14539	-2.494	0.0000	0.0000
Gm14546	ENSMUSG00000086762	predicted gene 14546	-3.606	0.0024	0.0067
Gm15191	ENSMUSG00000082778	predicted gene 15191	-3.646	0.0000	0.0001
Gm15294	ENSMUSG00000081607	predicted gene 15294	-5.467	0.0259	0.0550
Gm15361	ENSMUSG00000083283	predicted pseudogene 15361	-1.659	0.0063	0.0160
Gm15420	ENSMUSG00000087387	predicted gene 15420	-7.958	0.0003	0.0012
Gm15446	ENSMUSG00000090015	predicted gene 15446	-1.508	0.0292	0.0609
Gm15545	ENSMUSG00000087138	predicted gene 15545	-2.077	0.0016	0.0047
Gm15559	ENSMUSG00000086401	predicted gene 15559	-2.668	0.0399	0.0797
Gm15564	ENSMUSG00000086324	predicted gene 15564	-97.879	0.0000	0.0000
Gm15608	ENSMUSG00000112110	predicted gene 15608	-4.815	0.0331	0.0680
Gm15743	ENSMUSG00000086645	predicted gene 15743	-3.384	0.0001	0.0002
Gm15760	ENSMUSG00000080797	predicted gene 15760	-2.798	0.0405	0.0808
Gm15772	ENSMUSG00000062353	predicted gene 15772	-3.167	0.0425	0.0842
Gm15879	ENSMUSG00000084790	predicted gene 15879	-4.162	0.0004	0.0013
Gm15931	ENSMUSG00000081723	predicted gene 15931	-3.123	0.0004	0.0014
Gm15950	ENSMUSG00000089818	predicted gene 15950	-19.935	0.0043	0.0113
Gm15972	ENSMUSG00000086287	predicted gene 15972	-4.557	0.0000	0.0000
Gm15998	ENSMUSG00000086389	predicted gene 15998	-11.058	0.0312	0.0646
Gm1600	ENSMUSG00000116270	predicted gene 1600	-2.089	0.0153	0.0349
Gm16118	ENSMUSG00000089797	predicted gene 16118	-14.160	0.0235	0.0504
Gm16141	ENSMUSG00000087507	predicted gene 16141	-2.716	0.0367	0.0741
Gm16177	ENSMUSG00000082484	predicted gene 16177	-7.529	0.0000	0.0000
Gm16230	ENSMUSG00000087163	predicted gene 16230	-12.725	0.0179	0.0399

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm16251	ENSMUSG00000090075	predicted gene 16251	-3.082	0.0409	0.0815
Gm16283	ENSMUSG00000087020	predicted gene 16283	-4.707	0.0495	0.0957
Gm16364	ENSMUSG00000086915	predicted gene 16364	-4.040	0.0022	0.0064
Gm16374	ENSMUSG00000115205	predicted pseudogene 16374	-4.745	0.0004	0.0013
Gm16378	ENSMUSG00000095762	predicted gene 16378	-3.385	0.0000	0.0000
Gm16380	ENSMUSG00000059830	predicted pseudogene 16380	-1.778	0.0232	0.0499
Gm16439	ENSMUSG00000072594	predicted pseudogene 16439	-2.447	0.0419	0.0832
Gm16494	ENSMUSG00000091775	predicted gene 16494	-6.928	0.0376	0.0758
Gm16537	ENSMUSG00000089671	predicted gene 16537	-1.705	0.0163	0.0368
Gm16574	ENSMUSG00000089769	predicted gene 16574	-2.714	0.0027	0.0075
Gm1673	ENSMUSG00000070858	predicted gene 1673	-4.925	0.0000	0.0001
Gm16793	ENSMUSG00000097357	predicted gene, 16793	-2.710	0.0000	0.0000
Gm17017	ENSMUSG00000090246	predicted gene 17017	-5.679	0.0029	0.0079
Gm17068	ENSMUSG00000078528	predicted gene 17068	-7.283	0.0000	0.0001
Gm17276	ENSMUSG00000097305	predicted gene, 17276	-3.107	0.0003	0.0010
Gm17354	ENSMUSG00000091985	predicted gene, 17354	-1.671	0.0400	0.0799
Gm17455	ENSMUSG00000090439	predicted gene, 17455	-9.587	0.0457	0.0895
Gm17511	ENSMUSG00000090460	predicted gene, 17511	-14.181	0.0000	0.0000
Gm17690	ENSMUSG00000097204	predicted gene, 17690	-2.167	0.0007	0.0021
Gm17709	ENSMUSG00000091952	predicted gene, 17709	-4.849	0.0400	0.0799
Gm17753	ENSMUSG00000115867	predicted gene, 17753	-1.720	0.0379	0.0762
Gm18001	ENSMUSG00000110690	predicted gene, 18001	-6.575	0.0443	0.0872
Gm18095	ENSMUSG00000115856	predicted gene, 18095	-2.827	0.0143	0.0327
Gm18234	ENSMUSG00000116926	predicted gene, 18234	-5.304	0.0000	0.0000
Gm1826	ENSMUSG00000082028	predicted gene 1826	-21.367	0.0039	0.0105
Gm1833	ENSMUSG00000100362	predicted gene 1833	-27.234	0.0005	0.0015
Gm18537	ENSMUSG00000108484	predicted gene, 18537	-3.712	0.0490	0.0950
Gm18584	ENSMUSG00000107853	predicted gene, 18584	-18.476	0.0027	0.0075
Gm18734	ENSMUSG00000092438	predicted gene, 18734	-7.075	0.0028	0.0076
Gm18736	ENSMUSG00000117300	predicted gene, 18736	-2.176	0.0000	0.0000
Gm19277	ENSMUSG00000115924	predicted gene, 19277	-3.606	0.0007	0.0021

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm1943	ENSMUSG00000110528	predicted gene 1943	-7.985	0.0044	0.0115
Gm19522	ENSMUSG00000116903	predicted gene, 19522	-2.113	0.0001	0.0004
Gm19605	ENSMUSG00000113585	predicted gene, 19605	-1.919	0.0057	0.0146
Gm19680	ENSMUSG00000070960	predicted gene, 19680	-5.963	0.0310	0.0643
Gm19710	ENSMUSG00000105552	predicted gene, 19710	-9.585	0.0291	0.0608
Gm20490	ENSMUSG00000092596	predicted gene 20490	-3.201	0.0009	0.0028
Gm20604	ENSMUSG00000041716	predicted gene 20604	-1.605	0.0035	0.0094
Gm20619	ENSMUSG00000093482	predicted gene 20619	-3.024	0.0000	0.0000
Gm20707	ENSMUSG00000093594	predicted gene 20707	-2.440	0.0159	0.0360
Gm20939	ENSMUSG00000095193	predicted gene, 20939	-2.486	0.0248	0.0530
Gm2174	ENSMUSG00000058932	predicted gene 2174	-6.166	0.0008	0.0025
Gm2199	ENSMUSG00000083829	predicted gene 2199	-4.962	0.0319	0.0658
Gm23297	ENSMUSG00000065118	predicted gene, 23297	-14.130	0.0095	0.0231
Gm2383	ENSMUSG00000097628	predicted gene 2383	-5.045	0.0043	0.0113
Gm2420	ENSMUSG00000082305	predicted gene 2420	-7.346	0.0412	0.0819
Gm2423	ENSMUSG00000061724	predicted gene 2423	-5.905	0.0004	0.0013
Gm2445	ENSMUSG00000098113	predicted gene 2445	-2.322	0.0013	0.0039
Gm24474	ENSMUSG00000114005	predicted gene, 24474	-1.758	0.0081	0.0199
Gm25612	ENSMUSG00000077202	predicted gene, 25612	-4.797	0.0338	0.0692
Gm2573	ENSMUSG00000115017	predicted gene 2573	-25.068	0.0000	0.0000
Gm2614	ENSMUSG00000113113	predicted gene 2614	-3.584	0.0025	0.0069
Gm26493	ENSMUSG00000065089	predicted gene, 26493	-11.422	0.0218	0.0474
Gm26620	ENSMUSG00000096968	predicted gene, 26620	-7.102	0.0002	0.0007
Gm26782	ENSMUSG00000097431	predicted gene, 26782	-2.026	0.0000	0.0000
Gm26795	ENSMUSG00000097776	predicted gene, 26795	-1.745	0.0073	0.0181
Gm26877	ENSMUSG00000097373	predicted gene, 26877	-26.866	0.0022	0.0063
Gm26947	ENSMUSG00000098055	predicted gene, 26947	-1.987	0.0231	0.0498
Gm27030	ENSMUSG00000098221	predicted gene, 27030	-4.195	0.0187	0.0415
Gm27045	ENSMUSG00000098211	predicted gene, 27045	-4.848	0.0017	0.0050
Gm27252	ENSMUSG00000098708	predicted gene 27252	-2.720	0.0174	0.0389
Gm2805	ENSMUSG00000116536	predicted gene 2805	-3.926	0.0342	0.0698

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm28119	ENSMUSG00000100158	predicted gene 28119	-8.135	0.0440	0.0867
Gm28231	ENSMUSG00000100782	predicted gene 28231	-2.155	0.0211	0.0462
Gm28438	ENSMUSG00000101939	predicted gene 28438	-2.468	0.0000	0.0000
Gm28455	ENSMUSG00000100490	predicted gene 28455	-18.402	0.0039	0.0104
Gm29188	ENSMUSG00000099622	predicted gene 29188	-2.118	0.0030	0.0082
Gm29668	ENSMUSG00000099835	predicted gene 29668	-4.184	0.0000	0.0000
Gm2a	ENSMUSG00000000594	GM2 ganglioside activator protein	-1.639	0.0000	0.0000
Gm30373	ENSMUSG00000111758	predicted gene, 30373	-2.059	0.0022	0.0063
Gm3052	ENSMUSG00000101462	predicted gene 3052	-7.320	0.0298	0.0621
Gm30556	ENSMUSG00000115180	predicted gene, 30556	-1.776	0.0012	0.0037
Gm30970	ENSMUSG00000115637	predicted gene, 30970	-10.559	0.0000	0.0000
Gm31036	ENSMUSG00000110475	predicted gene, 31036	-11.833	0.0134	0.0311
Gm31663	ENSMUSG00000108994	predicted gene, 31663	-2.004	0.0000	0.0001
Gm32031	ENSMUSG00000109118	predicted gene, 32031	-3.224	0.0000	0.0001
Gm3226	ENSMUSG00000114547	predicted gene 3226	-3.533	0.0004	0.0012
Gm3235	ENSMUSG00000090778	predicted gene 3235	-1.846	0.0507	0.0977
Gm32352	ENSMUSG00000110453	predicted gene, 32352	-2.131	0.0015	0.0044
Gm32591	ENSMUSG00000108015	predicted gene, 32591	-4.992	0.0000	0.0001
Gm33024	ENSMUSG00000107682	predicted gene, 33024	-2.389	0.0434	0.0857
Gm33104	ENSMUSG00000110902	predicted gene, 33104	-14.245	0.0088	0.0214
Gm3325	ENSMUSG00000113836	predicted gene 3325	-2.644	0.0063	0.0159
Gm33424	ENSMUSG00000113101	predicted gene, 33424	-2.609	0.0000	0.0000
Gm33474	ENSMUSG00000106554	predicted gene, 33474	-11.747	0.0121	0.0283
Gm33543	ENSMUSG00000110353	predicted gene, 33543	-1.638	0.0237	0.0509
Gm33609	ENSMUSG00000104736	predicted gene, 33609	-2.981	0.0000	0.0001
Gm3375	ENSMUSG00000107470	predicted gene 3375	-3.164	0.0000	0.0000
Gm3436	ENSMUSG00000096160	predicted pseudogene 3436	-6.682	0.0344	0.0702
Gm34655	ENSMUSG00000110863	predicted gene, 34655	-2.161	0.0344	0.0703
Gm34934	ENSMUSG00000115100	predicted gene, 34934	-2.299	0.0000	0.0000
Gm35021	ENSMUSG00000109714	predicted gene, 35021	-1.733	0.0058	0.0148
Gm35290	ENSMUSG00000117263	predicted gene, 35290	-3.892	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm3534	ENSMUSG00000098192	predicted pseudogene 3534	-3.175	0.0020	0.0058
Gm35438	ENSMUSG00000118209	predicted gene, 35438	-6.079	0.0034	0.0093
Gm3555	ENSMUSG00000089791	predicted pseudogene 3555	-1.527	0.0381	0.0766
Gm35638	ENSMUSG00000113188	predicted gene, 35638	-2.927	0.0078	0.0192
Gm36371	ENSMUSG00000109108	predicted gene, 36371	-1.826	0.0017	0.0050
Gm3646	ENSMUSG00000091937	predicted gene 3646	-1.895	0.0020	0.0059
Gm36535	ENSMUSG00000105376	predicted gene, 36535	-2.184	0.0285	0.0597
Gm36569	ENSMUSG00000102191	predicted gene, 36569	-19.862	0.0021	0.0060
Gm36684	ENSMUSG00000117278	predicted gene, 36684	-2.009	0.0004	0.0014
Gm3671	ENSMUSG00000098232	predicted gene 3671	-2.401	0.0036	0.0097
Gm3695	ENSMUSG00000067224	predicted gene 3695	-3.615	0.0004	0.0013
Gm3699	ENSMUSG00000094955	predicted gene 3699	-5.733	0.0000	0.0002
Gm37486	ENSMUSG00000104126	predicted gene, 37486	-24.320	0.0009	0.0029
Gm3756	ENSMUSG00000091639	predicted gene 3756	-3.647	0.0132	0.0305
Gm37784	ENSMUSG00000102525	predicted gene, 37784	-18.411	0.0053	0.0138
Gm37981	ENSMUSG00000103137	predicted gene, 37981	-10.969	0.0135	0.0312
Gm37986	ENSMUSG00000104212	predicted gene, 37986	-9.003	0.0109	0.0259
Gm3809	ENSMUSG00000097935	predicted gene 3809	-3.830	0.0079	0.0195
Gm38228	ENSMUSG00000103945	predicted gene, 38228	-4.650	0.0443	0.0872
Gm38250	ENSMUSG00000104168	predicted gene, 38250	-2.111	0.0468	0.0915
Gm38534	ENSMUSG00000108634	predicted gene, 38534	-2.664	0.0000	0.0000
Gm38832	ENSMUSG00000108371	predicted gene, 38832	-3.574	0.0417	0.0828
Gm39317	ENSMUSG00000111056	predicted gene, 39317	-4.543	0.0039	0.0103
Gm39469	ENSMUSG00000110834	predicted gene, 39469	-1.866	0.0005	0.0015
Gm4045	ENSMUSG00000108231	predicted gene 4045	-5.050	0.0000	0.0000
Gm40457	ENSMUSG00000108626	predicted gene, 40457	-2.811	0.0000	0.0000
Gm41341	ENSMUSG00000069996	predicted gene, 41341	-3.264	0.0000	0.0002
Gm4149	ENSMUSG00000074800	predicted pseudogene 4149	-35.405	0.0001	0.0004
Gm4217	ENSMUSG00000097954	predicted gene 4217	-1.722	0.0148	0.0338
Gm42208	ENSMUSG00000106140	predicted gene, 42208	-31.318	0.0003	0.0009
Gm42879	ENSMUSG00000106590	predicted gene 42879	-5.923	0.0149	0.0340

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm42917	ENSMUSG00000104985	predicted gene 42917	-13.877	0.0084	0.0206
Gm43080	ENSMUSG00000105556	predicted gene 43080	-1.532	0.0309	0.0640
Gm43247	ENSMUSG00000105406	predicted gene 43247	-4.422	0.0007	0.0023
Gm4353	ENSMUSG00000091900	predicted gene 4353	-2.256	0.0043	0.0112
Gm43660	ENSMUSG00000107352	predicted gene 43660	-3.489	0.0391	0.0783
Gm43667	ENSMUSG00000105135	predicted gene 43667	-2.300	0.0001	0.0005
Gm43691	ENSMUSG00000104776	predicted gene 43691	-5.780	0.0182	0.0404
Gm43814	ENSMUSG00000104654	predicted gene 43814	-6.923	0.0012	0.0036
Gm43823	ENSMUSG00000106224	predicted gene 43823	-3.827	0.0001	0.0005
Gm43860	ENSMUSG00000106928	predicted gene 43860	-3.365	0.0111	0.0264
Gm44386	ENSMUSG00000107689	predicted gene, 44386	-2.983	0.0000	0.0000
Gm45151	ENSMUSG00000108736	predicted gene 45151	-4.996	0.0398	0.0796
Gm4518	ENSMUSG00000098123	predicted gene 4518	-3.366	0.0004	0.0015
Gm45203	ENSMUSG00000108494	predicted gene 45203	-2.349	0.0166	0.0374
Gm45353	ENSMUSG00000109957	predicted gene 45353	-3.581	0.0082	0.0202
Gm45441	ENSMUSG00000110020	predicted gene 45441	-5.292	0.0254	0.0540
Gm45552	ENSMUSG00000110279	predicted gene 45552	-2.266	0.0011	0.0034
Gm45777	ENSMUSG00000110677	predicted gene 45777	-2.772	0.0200	0.0441
Gm45871	ENSMUSG00000110277	predicted gene 45871	-1.731	0.0005	0.0016
Gm4609	ENSMUSG00000078592	predicted gene 4609	-4.227	0.0020	0.0058
Gm4681	ENSMUSG00000115146	predicted gene 4681	-5.205	0.0281	0.0590
Gm47021	ENSMUSG00000113036	predicted gene, 47021	-19.871	0.0016	0.0046
Gm47108	ENSMUSG00000111000	predicted gene, 47108	-3.223	0.0045	0.0119
Gm47283	ENSMUSG00000096768	predicted gene, 47283	-1.955	0.0190	0.0419
Gm47322	ENSMUSG00000113789	predicted gene, 47322	-2.798	0.0086	0.0209
Gm47438	ENSMUSG00000111947	predicted gene, 47438	-18.479	0.0038	0.0102
Gm47547	ENSMUSG00000114196	predicted gene, 47547	-2.432	0.0001	0.0002
Gm47604	ENSMUSG00000110946	predicted gene, 47604	-13.861	0.0000	0.0000
Gm47708	ENSMUSG00000112188	predicted gene, 47708	-8.487	0.0062	0.0157
Gm4800	ENSMUSG00000111759	predicted gene 4800	-4.789	0.0365	0.0738
Gm4815	ENSMUSG00000114733	predicted gene 4815	-41.122	0.0000	0.0001

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm48194	ENSMUSG00000114835	predicted gene, 48194	-4.741	0.0125	0.0293
Gm48336	ENSMUSG00000112952	predicted gene, 48336	-1.909	0.0290	0.0606
Gm48496	ENSMUSG00000112969	predicted gene, 48496	-2.972	0.0006	0.0018
Gm4890	ENSMUSG00000097174	predicted gene 4890	-5.168	0.0517	0.0994
Gm48931	ENSMUSG00000115458	predicted gene, 48931	-2.938	0.0006	0.0019
Gm49024	ENSMUSG00000115575	predicted gene, 49024	-2.172	0.0015	0.0045
Gm49120	ENSMUSG00000115636	predicted gene, 49120	-14.673	0.0045	0.0119
Gm49249	ENSMUSG00000115480	predicted gene, 49249	-15.557	0.0113	0.0268
Gm49327	ENSMUSG00000113536	predicted gene, 49327	-2.139	0.0374	0.0754
Gm49331	ENSMUSG00000114025	predicted gene, 49331	-3.668	0.0000	0.0001
Gm49338	ENSMUSG00000111128	predicted gene, 49338	-2.264	0.0000	0.0000
Gm4935	ENSMUSG00000113405	predicted gene 4935	-3.815	0.0041	0.0110
Gm49390	ENSMUSG00000114898	predicted gene, 49390	-1.788	0.0090	0.0218
Gm49395	ENSMUSG00000114470	predicted gene, 49395	-13.974	0.0081	0.0200
Gm49477	ENSMUSG00000116066	predicted gene, 49477	-1.779	0.0004	0.0013
Gm49486	ENSMUSG00000116121	predicted gene, 49486	-2.514	0.0409	0.0815
Gm4953	ENSMUSG00000061992	predicted pseudogene 4953	-7.623	0.0039	0.0105
Gm49593	ENSMUSG00000116081	predicted gene, 49593	-6.367	0.0106	0.0252
Gm49601	ENSMUSG00000116594	predicted gene, 49601	-6.538	0.0479	0.0933
Gm50114	ENSMUSG00000117692	predicted gene, 50114	-1.642	0.0019	0.0055
Gm50145	ENSMUSG00000117731	predicted gene, 50145	-11.013	0.0000	0.0000
Gm50203	ENSMUSG00000118243	predicted gene, 50203	-17.208	0.0058	0.0147
Gm50357	ENSMUSG00000117951	predicted gene, 50357	-1.750	0.0026	0.0071
Gm5040	ENSMUSG00000111880	predicted gene 5040	-18.682	0.0061	0.0154
Gm50419	ENSMUSG00000118024	predicted gene, 50419	-2.867	0.0051	0.0133
Gm5069	ENSMUSG00000055676	predicted pseudogene 5069	-1.708	0.0001	0.0005
Gm5131	ENSMUSG00000110715	predicted gene 5131	-3.390	0.0000	0.0000
Gm5141	ENSMUSG00000091183	predicted gene 5141	-2.883	0.0037	0.0099
Gm5165	ENSMUSG00000116802	predicted gene 5165	-2.618	0.0000	0.0000
Gm5276	ENSMUSG00000105452	predicted gene 5276	-3.874	0.0001	0.0004
Gm52948	ENSMUSG00000118521	predicted gene, 52948	-50.087	0.0000	0.0001

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5421	ENSMUSG00000097245	predicted gene 5421	-1.936	0.0051	0.0132
Gm5425	ENSMUSG00000111875	predicted gene 5425	-7.285	0.0007	0.0023
Gm5430	ENSMUSG00000098180	predicted gene 5430	-4.081	0.0001	0.0005
Gm5431	ENSMUSG00000058163	predicted gene 5431	-2.106	0.0498	0.0963
Gm5436	ENSMUSG00000042962	predicted pseudogene 5436	-2.753	0.0000	0.0000
Gm5454	ENSMUSG00000047643	predicted gene 5454	-20.462	0.0007	0.0022
Gm5463	ENSMUSG00000114892	predicted gene 5463	-2.174	0.0117	0.0275
Gm54867	ENSMUSG00002075795	predicted gene, 54867	-3.868	0.0159	0.0360
Gm5503	ENSMUSG00000117730	predicted gene 5503	-5.309	0.0000	0.0000
Gm5510	ENSMUSG00000083458	predicted pseudogene 5510	-21.432	0.0037	0.0099
Gm5523	ENSMUSG00000097711	predicted pseudogene 5523	-1.737	0.0277	0.0583
Gm5560	ENSMUSG00000067161	predicted pseudogene 5560	-6.821	0.0002	0.0006
Gm5566	ENSMUSG00000080002	predicted pseudogene 5566	-16.771	0.0000	0.0000
Gm5578	ENSMUSG00000029633	predicted pseudogene 5578	-3.767	0.0117	0.0276
Gm5617	ENSMUSG00000042293	predicted gene 5617	-2.404	0.0000	0.0000
Gm5693	ENSMUSG00000117793	predicted gene 5693	-2.826	0.0002	0.0008
Gm5801	ENSMUSG00000058581	predicted pseudogene 5801	-1.897	0.0056	0.0143
Gm5823	ENSMUSG00000117813	predicted gene 5823	-3.883	0.0000	0.0000
Gm5824	ENSMUSG00000118241	predicted gene 5824	-3.404	0.0206	0.0452
Gm5841	ENSMUSG00000103921	predicted gene 5841	-4.052	0.0107	0.0256
Gm5855	ENSMUSG00000105558	predicted gene 5855	-6.984	0.0000	0.0000
Gm5863	ENSMUSG00000082927	predicted gene 5863	-3.762	0.0002	0.0006
Gm5864	ENSMUSG00000107211	predicted gene 5864	-2.944	0.0050	0.0130
Gm5874	ENSMUSG00000071568	predicted gene 5874	-3.241	0.0001	0.0005
Gm5884	ENSMUSG00000037827	predicted pseudogene 5884	-3.945	0.0000	0.0000
Gm5900	ENSMUSG00000094685	predicted pseudogene 5900	-2.399	0.0000	0.0000
Gm5903	ENSMUSG00000082988	predicted gene 5903	-5.982	0.0457	0.0895
Gm5913	ENSMUSG00000081111	predicted gene 5913	-3.896	0.0006	0.0019
Gm5944	ENSMUSG00000081034	predicted gene 5944	-2.879	0.0489	0.0949
Gm6055	ENSMUSG00000062081	predicted gene 6055	-1.871	0.0088	0.0215
Gm6136	ENSMUSG00000084106	predicted pseudogene 6136	-1.807	0.0406	0.0809

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm6169	ENSMUSG00000057762	predicted gene 6169	-21.506	0.0022	0.0063
Gm6180	ENSMUSG00000053038	predicted pseudogene 6180	-15.440	0.0041	0.0109
Gm6210	ENSMUSG00000107951	predicted gene 6210	-1.794	0.0257	0.0546
Gm6218	ENSMUSG00000112145	predicted gene 6218	-18.704	0.0020	0.0058
Gm6278	ENSMUSG00000116972	predicted gene 6278	-43.639	0.0000	0.0000
Gm6316	ENSMUSG00000078370	predicted pseudogene 6316	-4.937	0.0000	0.0000
Gm6368	ENSMUSG00000080775	predicted gene 6368	-2.980	0.0002	0.0006
Gm6402	ENSMUSG00000117962	predicted pseudogene 6402	-7.876	0.0131	0.0304
Gm6419	ENSMUSG00000072407	predicted gene 6419	-3.262	0.0059	0.0149
Gm6463	ENSMUSG00000098231	predicted gene 6463	-23.061	0.0032	0.0087
Gm6493	ENSMUSG00000090021	predicted gene 6493	-10.622	0.0065	0.0163
Gm6505	ENSMUSG00000070522	predicted pseudogene 6505	-4.180	0.0000	0.0000
Gm6517	ENSMUSG00000082420	predicted gene 6517	-6.052	0.0000	0.0000
Gm6552	ENSMUSG00000117458	predicted gene 6552	-2.978	0.0115	0.0271
Gm6665	ENSMUSG00000091561	predicted gene 6665	-6.075	0.0048	0.0126
Gm6705	ENSMUSG00000116958	predicted gene 6705	-7.970	0.0478	0.0931
Gm6712	ENSMUSG00000072761	predicted gene 6712	-2.611	0.0000	0.0001
Gm6776	ENSMUSG00000047509	predicted pseudogene 6776	-14.448	0.0144	0.0329
Gm6969	ENSMUSG00000066553	predicted pseudogene 6969	-1.786	0.0000	0.0000
Gm6997	ENSMUSG00000115539	predicted gene 6997	-5.615	0.0451	0.0884
Gm7084	ENSMUSG00000114894	predicted gene 7084	-4.535	0.0378	0.0761
Gm7114	ENSMUSG00000100481	predicted gene 7114	-5.360	0.0015	0.0043
Gm7251	ENSMUSG00000069236	predicted pseudogene 7251	-4.999	0.0006	0.0019
Gm7252	ENSMUSG00000114135	predicted gene 7252	-15.760	0.0058	0.0149
Gm7278	ENSMUSG00000080950	predicted gene 7278	-11.654	0.0097	0.0234
Gm7286	ENSMUSG00000098194	predicted gene 7286	-2.887	0.0149	0.0339
Gm7353	ENSMUSG00000055452	predicted pseudogene 7353	-6.274	0.0001	0.0002
Gm7357	ENSMUSG00000102269	predicted gene 7357	-5.557	0.0039	0.0105
Gm7367	ENSMUSG00000047370	predicted pseudogene 7367	-54.323	0.0000	0.0000
Gm7481	ENSMUSG00000098219	predicted gene 7481	-6.572	0.0446	0.0877
Gm7488	ENSMUSG00000039617	predicted gene 7488	-17.783	0.0023	0.0064

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm7507	ENSMUSG00000098142	predicted gene 7507	-2.631	0.0010	0.0029
Gm7536	ENSMUSG00000057036	predicted gene 7536	-10.716	0.0000	0.0000
Gm7543	ENSMUSG00000115738	predicted gene 7543	-6.270	0.0379	0.0763
Gm7598	ENSMUSG00000087390	predicted gene 7598	-2.168	0.0237	0.0508
Gm7607	ENSMUSG00000111085	predicted gene 7607	-15.693	0.0190	0.0421
Gm7633	ENSMUSG00000114606	predicted gene 7633	-3.468	0.0375	0.0756
Gm7658	ENSMUSG00000082935	predicted gene 7658	-1.581	0.0032	0.0087
Gm7665	ENSMUSG00000063628	predicted pseudogene 7665	-19.766	0.0015	0.0045
Gm7832	ENSMUSG00000106917	predicted gene 7832	-3.872	0.0000	0.0000
Gm7879	ENSMUSG00000033036	predicted pseudogene 7879	-4.742	0.0003	0.0011
Gm8075	ENSMUSG00000113321	predicted gene 8075	-6.212	0.0000	0.0000
Gm8100	ENSMUSG00000098056	predicted gene 8100	-3.216	0.0373	0.0751
Gm8121	ENSMUSG00000051116	predicted pseudogene 8121	-1.899	0.0000	0.0001
Gm8186	ENSMUSG00000049124	predicted gene 8186	-4.079	0.0000	0.0001
Gm8189	ENSMUSG00000110298	predicted gene 8189	-1.849	0.0026	0.0074
Gm8210	ENSMUSG00000094497	predicted pseudogene 8210	-3.284	0.0000	0.0000
Gm8216	ENSMUSG00000084303	predicted gene 8216	-19.918	0.0030	0.0082
Gm8330	ENSMUSG00000098048	predicted gene 8330	-4.033	0.0318	0.0656
Gm8349	ENSMUSG00000098208	predicted gene 8349	-1.654	0.0388	0.0778
Gm8355	ENSMUSG00000093798	predicted pseudogene 8355	-2.064	0.0325	0.0670
Gm8606	ENSMUSG00000083362	predicted gene 8606	-27.349	0.0018	0.0053
Gm8615	ENSMUSG00000024437	predicted pseudogene 8615	-2.086	0.0000	0.0001
Gm8666	ENSMUSG00000048709	predicted gene 8666	-4.287	0.0081	0.0199
Gm8692	ENSMUSG00000082755	predicted gene 8692	-7.342	0.0476	0.0927
Gm8730	ENSMUSG00000063696	predicted pseudogene 8730	-15.025	0.0000	0.0000
Gm8741	ENSMUSG00000091655	predicted gene 8741	-13.280	0.0070	0.0174
Gm8756	ENSMUSG00000098238	predicted gene 8756	-2.360	0.0001	0.0005
Gm8825	ENSMUSG00000098105	predicted gene 8825	-3.565	0.0469	0.0915
Gm9008	ENSMUSG00000072476	predicted pseudogene 9008	-2.792	0.0000	0.0001
Gm9108	ENSMUSG00000115819	predicted gene 9108	-3.418	0.0002	0.0008
Gm9164	ENSMUSG00000082322	predicted gene 9164	-3.389	0.0446	0.0877

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm9247	ENSMUSG00000115505	predicted gene 9247	-3.117	0.0028	0.0078
Gm9294	ENSMUSG00000044609	predicted pseudogene 9294	-6.380	0.0241	0.0517
Gm9385	ENSMUSG00000080848	predicted pseudogene 9385	-4.311	0.0000	0.0000
Gm9416	ENSMUSG00000117476	predicted gene 9416	-10.864	0.0441	0.0869
Gm9512	ENSMUSG00000113389	predicted gene 9512	-3.136	0.0100	0.0240
Gm9616	ENSMUSG00000114003	predicted gene 9616	-1.938	0.0338	0.0692
Gm9625	ENSMUSG00000097906	predicted gene 9625	-5.659	0.0000	0.0000
Gm9762	ENSMUSG00000037096	predicted pseudogene 9762	-2.990	0.0001	0.0002
Gm9790	ENSMUSG00000044330	predicted gene 9790	-2.237	0.0028	0.0078
Gm9796	ENSMUSG00000045075	predicted gene 9796	-4.515	0.0036	0.0097
Gm9816	ENSMUSG00000085783	predicted pseudogene 9816	-7.387	0.0025	0.0069
Gm9892	ENSMUSG00000052825	predicted gene 9892	-2.551	0.0001	0.0003
Gm9895	ENSMUSG00000118038	predicted gene 9895	-4.230	0.0003	0.0009
Gm9903	ENSMUSG00000097271	predicted gene 9903	-2.209	0.0173	0.0388
Gm9961	ENSMUSG00000055015	predicted gene 9961	-3.515	0.0188	0.0416
Gmppa	ENSMUSG00000033021	GDP-mannose pyrophosphorylase A	-3.159	0.0000	0.0000
Gna14	ENSMUSG00000024697	guanine nucleotide binding protein, alpha 14	-2.354	0.0092	0.0222
Gna15	ENSMUSG00000034792	guanine nucleotide binding protein, alpha 15	-1.904	0.0487	0.0945
Gnb1l	ENSMUSG00000000884	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-1.632	0.0022	0.0063
Gnb2	ENSMUSG00000029713	guanine nucleotide binding protein (G protein), beta 2	-1.581	0.0000	0.0000
Gnb3	ENSMUSG00000023439	guanine nucleotide binding protein (G protein), beta 3	-2.931	0.0000	0.0000
Gng5	ENSMUSG00000068523	guanine nucleotide binding protein (G protein), gamma 5	-4.058	0.0000	0.0000
Gng7	ENSMUSG00000048240	guanine nucleotide binding protein (G protein), gamma 7	-2.995	0.0000	0.0000
Gnmt	ENSMUSG00000002769	glycine N-methyltransferase	-3.232	0.0001	0.0002
Gnpda1	ENSMUSG00000052102	glucosamine-6-phosphate deaminase 1	-2.057	0.0000	0.0000
Gnpda2	ENSMUSG00000029209	glucosamine-6-phosphate deaminase 2	-1.571	0.0006	0.0020
Gnptg	ENSMUSG00000035521	N-acetylglucosamine-1-phosphotransferase, gamma subunit	-1.722	0.0000	0.0000
Gorasp1	ENSMUSG00000032513	golgi reassembly stacking protein 1	-2.420	0.0000	0.0000
Got1	ENSMUSG00000025190	glutamic-oxaloacetic transaminase 1, soluble	-1.661	0.0012	0.0036
Got2	ENSMUSG00000031672	glutamatic-oxaloacetic transaminase 2, mitochondrial	-1.737	0.0000	0.0000
Got2-ps1	ENSMUSG00000080935	glutamatic-oxaloacetic transaminase 2, mitochondrial, pseudogene 1	-1.683	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gpaa1	ENSMUSG00000022561	GPI anchor attachment protein 1	-3.293	0.0000	0.0000
Gpc2	ENSMUSG00000029510	glypican 2 (cerebroglycan)	-11.106	0.0294	0.0614
Gpd1l	ENSMUSG00000050627	glycerol-3-phosphate dehydrogenase 1-like	-1.833	0.0000	0.0000
Gper1	ENSMUSG00000053647	G protein-coupled estrogen receptor 1	-3.182	0.0000	0.0000
Gpihbp1	ENSMUSG00000022579	GPI-anchored HDL-binding protein 1	-1.837	0.0016	0.0047
Gpr132	ENSMUSG00000021298	G protein-coupled receptor 132	-8.902	0.0072	0.0180
Gpr137	ENSMUSG00000024958	G protein-coupled receptor 137	-2.152	0.0000	0.0000
Gpr137b-ps	ENSMUSG00000097715	G protein-coupled receptor 137B, pseudogene	-2.231	0.0000	0.0000
Gpr137c	ENSMUSG00000049092	G protein-coupled receptor 137C	-1.868	0.0002	0.0009
Gpr146	ENSMUSG00000044197	G protein-coupled receptor 146	-2.197	0.0000	0.0000
Gpr155	ENSMUSG00000041762	G protein-coupled receptor 155	-1.929	0.0000	0.0000
Gpr160	ENSMUSG00000037661	G protein-coupled receptor 160	-2.307	0.0206	0.0451
Gpr182	ENSMUSG00000058396	G protein-coupled receptor 182	-1.761	0.0001	0.0004
Gpr34	ENSMUSG00000040229	G protein-coupled receptor 34	-2.061	0.0073	0.0180
Gpr37l1	ENSMUSG00000026424	G protein-coupled receptor 37-like 1	-1.864	0.0491	0.0951
Gpr89	ENSMUSG00000028096	G protein-coupled receptor 89	-1.802	0.0000	0.0000
Gprc5a	ENSMUSG00000046733	G protein-coupled receptor, family C, group 5, member A	-5.272	0.0038	0.0101
Gprc5c	ENSMUSG00000051043	G protein-coupled receptor, family C, group 5, member C	-2.326	0.0000	0.0000
Gps1	ENSMUSG00000025156	G protein pathway suppressor 1	-2.813	0.0000	0.0000
Gpsm1	ENSMUSG00000026930	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-2.402	0.0000	0.0000
Gpx3	ENSMUSG00000018339	glutathione peroxidase 3	-1.679	0.0002	0.0007
Gpx7	ENSMUSG00000028597	glutathione peroxidase 7	-3.193	0.0000	0.0000
Greb1	ENSMUSG00000036523	gene regulated by estrogen in breast cancer protein	-3.455	0.0449	0.0881
Grhpr	ENSMUSG00000035637	glyoxylate reductase/hydroxypyruvate reductase	-1.601	0.0000	0.0000
Grina	ENSMUSG00000022564	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	-2.135	0.0000	0.0000
Grip2	ENSMUSG00000030098	glutamate receptor interacting protein 2	-2.045	0.0019	0.0054
Grn	ENSMUSG00000034708	granulin	-1.584	0.0000	0.0002
Grpel1	ENSMUSG00000029198	GrpE-like 1, mitochondrial	-1.707	0.0000	0.0000
Grpel2	ENSMUSG00000024580	GrpE-like 2, mitochondrial	-1.530	0.0000	0.0000
Grtp1	ENSMUSG00000038515	GH regulated TBC protein 1	-2.198	0.0001	0.0005

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Grwd1	ENSMUSG00000053801	glutamate-rich WD repeat containing 1	-1.510	0.0000	0.0000
Gsn	ENSMUSG00000026879	gelsolin	-1.789	0.0000	0.0000
Gss	ENSMUSG00000027610	glutathione synthetase	-1.520	0.0001	0.0003
Gstk1	ENSMUSG00000029864	glutathione S-transferase kappa 1	-2.568	0.0000	0.0000
Gstm1	ENSMUSG00000058135	glutathione S-transferase, mu 1	-2.253	0.0000	0.0000
Gstm2	ENSMUSG00000040562	glutathione S-transferase, mu 2	-3.813	0.0000	0.0000
Gstm2-ps1	ENSMUSG00000107369	glutathione S-transferase mu 2 (muscle), pseudogene 1	-4.982	0.0038	0.0103
Gstm7	ENSMUSG00000004035	glutathione S-transferase, mu 7	-2.130	0.0000	0.0000
Gsto1	ENSMUSG00000025068	glutathione S-transferase omega 1	-1.802	0.0000	0.0000
Gstp2	ENSMUSG00000038155	glutathione S-transferase, pi 2	-2.174	0.0281	0.0589
Gstt1	ENSMUSG00000001663	glutathione S-transferase, theta 1	-3.106	0.0000	0.0000
Gstt2	ENSMUSG00000033318	glutathione S-transferase, theta 2	-1.749	0.0020	0.0056
Gstt3	ENSMUSG00000001665	glutathione S-transferase, theta 3	-1.571	0.0160	0.0362
Gtdc1	ENSMUSG00000036890	glycosyltransferase-like domain containing 1	-1.671	0.0000	0.0001
Gtf2h4	ENSMUSG00000001524	general transcription factor II H, polypeptide 4	-3.103	0.0000	0.0000
Gtf3a	ENSMUSG00000016503	general transcription factor III A	-1.675	0.0000	0.0000
Gtpbp8	ENSMUSG00000022668	GTP-binding protein 8 (putative)	-1.526	0.0007	0.0023
Gvin1	ENSMUSG00000045868	GTPase, very large interferon inducible 1	-3.745	0.0012	0.0035
Gypc	ENSMUSG00000090523	glycophorin C	-1.565	0.0000	0.0000
Gys1	ENSMUSG00000003865	glycogen synthase 1, muscle	-1.555	0.0015	0.0045
H13	ENSMUSG00000019188	histocompatibility 13	-1.530	0.0000	0.0000
H2-Ab1	ENSMUSG00000073421	histocompatibility 2, class II antigen A, beta 1	-2.440	0.0006	0.0018
H2ac19	ENSMUSG00000063954	H2A clustered histone 19	-5.848	0.0348	0.0710
H2af-ps2	ENSMUSG00000091383	H2A histone family, pseudogene 2	-14.954	0.0000	0.0000
H2aj	ENSMUSG00000060032	H2J.A histone	-1.636	0.0000	0.0000
H2ax	ENSMUSG00000049932	H2A.X variant histone	-1.757	0.0023	0.0066
H2bc3	ENSMUSG00000075031	H2B clustered histone 3	-2.314	0.0443	0.0872
H2bc4	ENSMUSG00000018102	H2B clustered histone 4	-4.102	0.0000	0.0000
H2bc8	ENSMUSG00000058385	H2B clustered histone 8	-19.127	0.0021	0.0059
H2bu1-ps	ENSMUSG00000080712	H2B.U histone 1, pseudogene	-12.378	0.0118	0.0279
H2-Eb1	ENSMUSG00000060586	histocompatibility 2, class II antigen E beta	-1.998	0.0300	0.0625

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
H2-Oa	ENSMUSG00000024334	histocompatibility 2, O region alpha locus	-4.959	0.0357	0.0724
H2-T22	ENSMUSG00000056116	histocompatibility 2, T region locus 22	-3.172	0.0000	0.0000
H3c15	ENSMUSG00000081058	H3 clustered histone 15	-4.723	0.0000	0.0000
H3f3a-ps1	ENSMUSG00000082284	H3.3 histone A, pseudogene 1	-25.669	0.0002	0.0009
H4c8	ENSMUSG00000060981	H4 clustered histone 8	-4.877	0.0000	0.0000
H4c9	ENSMUSG00000060639	H4 clustered histone 9	-1.999	0.0000	0.0000
Hacd4	ENSMUSG00000028497	3-hydroxyacyl-CoA dehydratase 4	-1.526	0.0105	0.0251
Hadhb	ENSMUSG00000059447	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta	-1.884	0.0000	0.0000
Hadhb-ps	ENSMUSG00000063684	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta, pseudogene	-1.735	0.0000	0.0000
Hagh	ENSMUSG00000024158	hydroxyacyl glutathione hydrolase	-1.871	0.0000	0.0000
Has1	ENSMUSG00000003665	hyaluronan synthase 1	-9.892	0.0442	0.0870
Haus1	ENSMUSG00000041840	HAUS augmin-like complex, subunit 1	-1.543	0.0000	0.0000
Hba-a1	ENSMUSG00000069919	hemoglobin alpha, adult chain 1	-4.927	0.0000	0.0000
Hbb-bs	ENSMUSG00000052305	hemoglobin, beta adult s chain	-3.180	0.0000	0.0000
Hbb-bt	ENSMUSG00000073940	hemoglobin, beta adult t chain	-11.186	0.0000	0.0000
Hcfc1r1	ENSMUSG00000023904	host cell factor C1 regulator 1 (XPO1-dependent)	-4.587	0.0000	0.0000
Hdac10	ENSMUSG00000062906	histone deacetylase 10	-1.748	0.0000	0.0001
Hdac5	ENSMUSG00000008855	histone deacetylase 5	-1.629	0.0000	0.0000
Hdc	ENSMUSG00000027360	histidine decarboxylase	-2.327	0.0002	0.0007
Hddc2	ENSMUSG00000000295	HD domain containing 2	-1.666	0.0005	0.0015
Hdhd3	ENSMUSG00000038422	haloacid dehalogenase-like hydrolase domain containing 3	-2.118	0.0097	0.0233
Heatr6	ENSMUSG00000000976	HEAT repeat containing 6	-1.555	0.0000	0.0000
Hebp1	ENSMUSG00000042770	heme binding protein 1	-1.701	0.0000	0.0000
Hebp2	ENSMUSG00000019853	heme binding protein 2	-1.794	0.0048	0.0124
Hectd4	ENSMUSG00000042744	HECT domain E3 ubiquitin protein ligase 4	-1.701	0.0000	0.0000
Hemk1	ENSMUSG00000032579	HemK methyltransferase family member 1	-1.664	0.0000	0.0000
Herpud1	ENSMUSG00000031770	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	-2.327	0.0428	0.0845
Hexb	ENSMUSG00000021665	hexosaminidase B	-1.559	0.0000	0.0000
Hexdc	ENSMUSG00000039307	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	-1.906	0.0000	0.0000
Hexim2	ENSMUSG00000043372	hexamethylene bis-acetamide inducible 2	-1.750	0.0226	0.0490
Hfe	ENSMUSG00000006611	homeostatic iron regulator	-1.577	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hgh1	ENSMUSG00000022554	HGH1 homolog	-2.363	0.0000	0.0000
Hhatl	ENSMUSG00000032523	hedgehog acyltransferase-like	-2.708	0.0000	0.0000
Hic2	ENSMUSG00000050240	hypermethylated in cancer 2	-1.533	0.0437	0.0862
Hid1	ENSMUSG00000034586	HID1 domain containing	-1.769	0.0027	0.0076
Higd1b	ENSMUSG00000020928	HIG1 domain family, member 1B	-1.683	0.0000	0.0000
Higd2a	ENSMUSG00000025868	HIG1 domain family, member 2A	-2.081	0.0000	0.0000
Hint2	ENSMUSG00000028470	histidine triad nucleotide binding protein 2	-1.947	0.0000	0.0000
Hipk4	ENSMUSG00000040424	homeodomain interacting protein kinase 4	-13.381	0.0121	0.0283
Hk1os	ENSMUSG00000085347	hexokinase 1, opposite strand	-5.118	0.0413	0.0822
Hmbs	ENSMUSG00000032126	hydroxymethylbilane synthase	-2.134	0.0000	0.0000
Hmcn2	ENSMUSG00000055632	hemicentin 2	-2.073	0.0000	0.0000
Hmgcl	ENSMUSG00000028672	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	-2.487	0.0000	0.0000
Hmgn2	ENSMUSG00000003038	high mobility group nucleosomal binding domain 2	-1.686	0.0011	0.0033
Hmgn2-ps	ENSMUSG00000070713	high mobility group nucleosomal binding domain 2, pseudogene	-18.359	0.0013	0.0040
Hmox1	ENSMUSG00000005413	heme oxygenase 1	-3.335	0.0016	0.0046
Hopx	ENSMUSG00000059325	HOP homeobox	-2.186	0.0000	0.0000
Hpcal1	ENSMUSG00000071379	hippocalcin-like 1	-1.925	0.0009	0.0027
Hpcal4	ENSMUSG00000046093	hippocalcin-like 4	-8.139	0.0505	0.0974
Hpdl	ENSMUSG00000043155	4-hydroxyphenylpyruvate dioxygenase-like	-2.725	0.0000	0.0000
Hpgd	ENSMUSG00000031613	hydroxyprostaglandin dehydrogenase 15 (NAD)	-1.565	0.0013	0.0040
Hpn	ENSMUSG00000001249	hepsin	-1.672	0.0016	0.0047
Hps1	ENSMUSG00000025188	HPS1, biogenesis of lysosomal organelles complex 3 subunit 1	-1.790	0.0052	0.0135
Hps4	ENSMUSG00000042328	HPS4, biogenesis of lysosomal organelles complex 3 subunit 2	-1.860	0.0000	0.0000
Hps6	ENSMUSG00000074811	HPS6, biogenesis of lysosomal organelles complex 2 subunit 3	-1.534	0.0000	0.0000
Hrct1	ENSMUSG00000071001	histidine rich carboxyl terminus 1	-2.233	0.0008	0.0024
Hrh1	ENSMUSG00000053004	histamine receptor H1	-2.129	0.0134	0.0309
Hrob	ENSMUSG00000034773	homologous recombination factor with OB-fold	-2.645	0.0421	0.0836
Hs1bp3	ENSMUSG00000020605	HCLS1 binding protein 3	-1.668	0.0000	0.0000
Hs3st1	ENSMUSG00000051022	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-1.773	0.0100	0.0241
Hsd11b1	ENSMUSG00000016194	hydroxysteroid 11-beta dehydrogenase 1	-1.616	0.0022	0.0063
Hsd17b10	ENSMUSG00000025260	hydroxysteroid (17-beta) dehydrogenase 10	-1.922	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hsf1	ENSMUSG00000022556	heat shock factor 1	-2.095	0.0000	0.0000
Hsf4	ENSMUSG00000033249	heat shock transcription factor 4	-1.627	0.0035	0.0094
Hspa1b	ENSMUSG00000090877	heat shock protein 1B	-2.278	0.0073	0.0181
Hspa8	ENSMUSG00000015656	heat shock protein 8	-1.897	0.0000	0.0000
Hspb1	ENSMUSG00000004951	heat shock protein 1	-4.296	0.0000	0.0000
Hspb11	ENSMUSG00000063172	heat shock protein family B (small), member 11	-2.196	0.0000	0.0000
Hspb3	ENSMUSG00000051456	heat shock protein 3	-2.100	0.0001	0.0003
Hspb6	ENSMUSG00000036854	heat shock protein, alpha-crystallin-related, B6	-1.528	0.0000	0.0000
Hspb7	ENSMUSG00000006221	heat shock protein family, member 7 (cardiovascular)	-2.242	0.0000	0.0000
Hspbp1	ENSMUSG00000063802	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	-2.378	0.0000	0.0000
Hspg2	ENSMUSG00000028763	perlecan (heparan sulfate proteoglycan 2)	-2.186	0.0000	0.0000
Htr2b	ENSMUSG00000026228	5-hydroxytryptamine (serotonin) receptor 2B	-39.725	0.0005	0.0017
Htra3	ENSMUSG00000029096	HtrA serine peptidase 3	-3.616	0.0000	0.0000
Hvcn1	ENSMUSG00000064267	hydrogen voltage-gated channel 1	-1.745	0.0027	0.0074
Hyal2	ENSMUSG00000010047	hyaluronoglucosaminidase 2	-3.177	0.0000	0.0000
Hyal3	ENSMUSG00000036091	hyaluronoglucosaminidase 3	-3.640	0.0285	0.0597
Iah1	ENSMUSG00000062054	isoamyl acetate-hydrolyzing esterase 1 homolog	-2.466	0.0000	0.0000
Icam2	ENSMUSG00000001029	intercellular adhesion molecule 2	-3.580	0.0000	0.0000
Id1	ENSMUSG00000042745	inhibitor of DNA binding 1, HLH protein	-4.398	0.0000	0.0000
Id3	ENSMUSG00000007872	inhibitor of DNA binding 3	-2.034	0.0000	0.0000
Ide	ENSMUSG00000056999	insulin degrading enzyme	-1.616	0.0000	0.0000
Idh2	ENSMUSG00000030541	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-1.986	0.0000	0.0000
Idh3g	ENSMUSG00000002010	isocitrate dehydrogenase 3 (NAD+), gamma	-1.872	0.0000	0.0000
Ido1	ENSMUSG00000031551	indoleamine 2,3-dioxygenase 1	-2.161	0.0487	0.0946
Idua	ENSMUSG00000033540	iduronidase, alpha-L	-1.661	0.0000	0.0000
Ier3	ENSMUSG00000003541	immediate early response 3	-2.038	0.0000	0.0000
Ifi203-ps	ENSMUSG00000090222	interferon activated gene 203, pseudogene	-1.592	0.0049	0.0128
Ifi27	ENSMUSG00000064215	interferon, alpha-inducible protein 27	-1.609	0.0000	0.0001
Ifi27l2a	ENSMUSG00000079017	interferon, alpha-inducible protein 27 like 2A	-4.544	0.0000	0.0000
Ifi47	ENSMUSG00000078920	interferon gamma inducible protein 47	-1.602	0.0262	0.0555
Ifit1bl1	ENSMUSG00000079339	interferon induced protein with tetratricpeptide repeats 1B like 1	-1.567	0.0001	0.0003

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ifitm1	ENSMUSG00000025491	interferon induced transmembrane protein 1	-2.228	0.0023	0.0066
Ifitm10	ENSMUSG00000045777	interferon induced transmembrane protein 10	-2.111	0.0046	0.0120
Ifitm3	ENSMUSG00000025492	interferon induced transmembrane protein 3	-1.507	0.0001	0.0004
Ifngr2	ENSMUSG00000022965	interferon gamma receptor 2	-1.794	0.0000	0.0001
Ift140	ENSMUSG00000024169	intraflagellar transport 140	-1.528	0.0006	0.0018
Ift22	ENSMUSG00000007987	intraflagellar transport 22	-1.560	0.0000	0.0000
Ift27	ENSMUSG00000016637	intraflagellar transport 27	-2.057	0.0000	0.0000
Igfals	ENSMUSG00000046070	insulin-like growth factor binding protein, acid labile subunit	-3.090	0.0092	0.0222
Igfbp6	ENSMUSG00000023046	insulin-like growth factor binding protein 6	-1.875	0.0000	0.0001
Ighm	ENSMUSG00000076617	immunoglobulin heavy constant mu	-1.920	0.0013	0.0039
Igkc	ENSMUSG00000076609	immunoglobulin kappa constant	-2.841	0.0008	0.0026
Iglc2	ENSMUSG00000076937	immunoglobulin lambda constant 2	-14.437	0.0416	0.0826
Il10ra	ENSMUSG00000032089	interleukin 10 receptor, alpha	-2.266	0.0001	0.0004
Il11ra1	ENSMUSG00000073889	interleukin 11 receptor, alpha chain 1	-1.783	0.0000	0.0000
Il15	ENSMUSG00000031712	interleukin 15	-1.923	0.0000	0.0000
Il16	ENSMUSG00000001741	interleukin 16	-1.509	0.0002	0.0008
Il17rc	ENSMUSG00000030281	interleukin 17 receptor C	-3.945	0.0000	0.0000
Il18bp	ENSMUSG00000070427	interleukin 18 binding protein	-2.244	0.0000	0.0000
Il1rl2	ENSMUSG00000070942	interleukin 1 receptor-like 2	-2.349	0.0001	0.0004
Il27ra	ENSMUSG00000005465	interleukin 27 receptor, alpha	-2.065	0.0003	0.0010
Il34	ENSMUSG00000031750	interleukin 34	-3.111	0.0000	0.0000
Il3ra	ENSMUSG00000068758	interleukin 3 receptor, alpha chain	-1.556	0.0161	0.0364
Impdh1	ENSMUSG00000003500	inosine monophosphate dehydrogenase 1	-1.675	0.0000	0.0000
Impdh2	ENSMUSG00000062867	inosine monophosphate dehydrogenase 2	-1.530	0.0000	0.0000
Impdh2-ps	ENSMUSG00000071041	inosine monophosphate dehydrogenase 2, pseudogene	-6.549	0.0000	0.0000
Inha	ENSMUSG00000032968	inhibin alpha	-1.869	0.0000	0.0001
Inmt	ENSMUSG00000003477	indolethylamine N-methyltransferase	-2.326	0.0006	0.0018
Inpp5b	ENSMUSG00000028894	inositol polyphosphate-5-phosphatase B	-1.585	0.0000	0.0000
Inpp5j	ENSMUSG00000034570	inositol polyphosphate 5-phosphatase J	-2.134	0.0000	0.0000
Inpp5k	ENSMUSG00000006127	inositol polyphosphate 5-phosphatase K	-1.878	0.0000	0.0000
Insc	ENSMUSG00000048782	INSC spindle orientation adaptor protein	-7.266	0.0020	0.0057

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Insl6	ENSMUSG00000050957	insulin-like 6	-3.794	0.0013	0.0039
Ints1	ENSMUSG00000029547	integrator complex subunit 1	-1.711	0.0000	0.0000
Ints5	ENSMUSG00000071652	integrator complex subunit 5	-1.698	0.0000	0.0000
Ints9	ENSMUSG00000021975	integrator complex subunit 9	-1.967	0.0000	0.0000
Invs	ENSMUSG00000028344	inversin	-1.724	0.0017	0.0049
Ip6k3	ENSMUSG00000024210	inositol hexaphosphate kinase 3	-1.853	0.0068	0.0170
Ipo11	ENSMUSG00000042590	importin 11	-1.539	0.0000	0.0000
Ipo13	ENSMUSG00000033365	importin 13	-1.859	0.0000	0.0000
Ipo4	ENSMUSG00000002319	importin 4	-3.090	0.0000	0.0000
Iqce	ENSMUSG00000036555	IQ motif containing E	-1.502	0.0214	0.0466
Iqgap2	ENSMUSG00000021676	IQ motif containing GTPase activating protein 2	-1.984	0.0000	0.0000
Irf3	ENSMUSG00000003184	interferon regulatory factor 3	-1.508	0.0001	0.0002
Isca2	ENSMUSG00000021241	iron-sulfur cluster assembly 2	-1.559	0.0000	0.0000
Islr	ENSMUSG00000037206	immunoglobulin superfamily containing leucine-rich repeat	-2.594	0.0000	0.0000
Isoc2b	ENSMUSG00000052605	isochorismatase domain containing 2b	-2.153	0.0029	0.0080
Isyna1	ENSMUSG00000019139	myo-inositol 1-phosphate synthase A1	-3.812	0.0000	0.0000
Itga10	ENSMUSG00000090210	integrin, alpha 10	-2.323	0.0108	0.0258
Itga11	ENSMUSG00000032243	integrin alpha 11	-1.709	0.0058	0.0149
Itga3	ENSMUSG00000001507	integrin alpha 3	-1.798	0.0001	0.0003
Itga5	ENSMUSG00000000555	integrin alpha 5 (fibronectin receptor alpha)	-1.913	0.0000	0.0000
Itga7	ENSMUSG00000025348	integrin alpha 7	-1.530	0.0000	0.0000
Itgb3bp	ENSMUSG00000028549	integrin beta 3 binding protein (beta3-endonexin)	-2.138	0.0000	0.0000
Itgb4	ENSMUSG00000020758	integrin beta 4	-1.601	0.0475	0.0925
Itgb7	ENSMUSG00000001281	integrin beta 7	-2.111	0.0286	0.0599
Itih6	ENSMUSG00000087149	inter-alpha-trypsin inhibitor heavy chain family member 6	-5.514	0.0179	0.0398
Itm2a	ENSMUSG00000031239	integral membrane protein 2A	-2.422	0.0000	0.0000
Itm2c	ENSMUSG00000026223	integral membrane protein 2C	-2.132	0.0000	0.0000
Itpa-ps1	ENSMUSG00000081476	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) pseudogene 1	-3.469	0.0043	0.0114
Itpr3	ENSMUSG00000042644	inositol 1,4,5-triphosphate receptor 3	-1.826	0.0000	0.0000
Ivd	ENSMUSG00000027332	isovaleryl coenzyme A dehydrogenase	-2.921	0.0000	0.0000
Izumo4	ENSMUSG00000055862	IZUMO family member 4	-2.180	0.0075	0.0185

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Jagn1	ENSMUSG00000051256	jagunal homolog 1	-2.316	0.0000	0.0000
Jak3	ENSMUSG00000031805	Janus kinase 3	-1.744	0.0062	0.0157
Jam2	ENSMUSG00000053062	junction adhesion molecule 2	-1.877	0.0000	0.0000
Josd2	ENSMUSG00000038695	Josephin domain containing 2	-1.901	0.0000	0.0000
Jrk	ENSMUSG00000046380	jerky	-1.849	0.0000	0.0000
Jtb	ENSMUSG00000027937	jumping translocation breakpoint	-1.562	0.0000	0.0000
Kansl2-ps	ENSMUSG00000097530	KAT8 regulatory NSL complex subunit 2, pseudogene	-2.703	0.0031	0.0084
Kat2b-ps	ENSMUSG00000053208	K(lysine) acetyltransferase 2B, pseudogene	-4.216	0.0458	0.0896
Kat8	ENSMUSG00000030801	K(lysine) acetyltransferase 8	-1.854	0.0000	0.0000
Katnb1	ENSMUSG00000031787	katanin p80 (WD40-containing) subunit B 1	-2.312	0.0000	0.0000
Kcne1	ENSMUSG00000039639	potassium voltage-gated channel, Isk-related subfamily, member 1	-2.127	0.0306	0.0636
Kcne1l	ENSMUSG00000090122	potassium voltage-gated channel, Isk-related family, member 1-like, pseudogene	-4.653	0.0388	0.0778
Kcnj11	ENSMUSG00000096146	potassium inwardly rectifying channel, subfamily J, member 11	-1.655	0.0000	0.0000
Kcnj8	ENSMUSG00000030247	potassium inwardly-rectifying channel, subfamily J, member 8	-1.548	0.0000	0.0000
Kcnk1	ENSMUSG00000033998	potassium channel, subfamily K, member 1	-2.935	0.0066	0.0166
Kcnmb2	ENSMUSG00000037610	potassium large conductance calcium-activated channel, subfamily M, beta member 2	-5.993	0.0197	0.0435
Kcnq1	ENSMUSG00000009545	potassium voltage-gated channel, subfamily Q, member 1	-1.580	0.0000	0.0000
Kcnv2	ENSMUSG00000047298	potassium channel, subfamily V, member 2	-1.603	0.0134	0.0310
Kcp	ENSMUSG00000059022	kielin/chordin-like protein	-1.681	0.0011	0.0033
Kctd21	ENSMUSG00000044952	potassium channel tetramerisation domain containing 21	-1.957	0.0000	0.0000
Kdelr1	ENSMUSG00000002778	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-2.238	0.0000	0.0000
Kdelr2	ENSMUSG00000079111	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	-1.763	0.0000	0.0000
Kdelr3	ENSMUSG00000010830	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	-2.398	0.0000	0.0000
Kif21b	ENSMUSG00000041642	kinesin family member 21B	-1.567	0.0148	0.0338
Kif26a	ENSMUSG00000021294	kinesin family member 26A	-2.168	0.0000	0.0000
Kif26b	ENSMUSG00000026494	kinesin family member 26B	-1.891	0.0001	0.0003
Kif28	ENSMUSG00000087236	kinesin family member 28	-2.179	0.0021	0.0059
Kifc2	ENSMUSG00000004187	kinesin family member C2	-1.596	0.0059	0.0151
Klf8	ENSMUSG00000041649	Kruppel-like factor 8	-4.872	0.0019	0.0054
Klhl22	ENSMUSG00000022750	kelch-like 22	-1.778	0.0000	0.0000
Klhl26	ENSMUSG00000055707	kelch-like 26	-1.851	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Klhl30	ENSMUSG00000026308	kelch-like 30	-2.060	0.0000	0.0000
Klhl40	ENSMUSG00000074001	kelch-like 40	-2.211	0.0000	0.0000
Klk10	ENSMUSG00000030693	kallikrein related-peptidase 10	-5.874	0.0005	0.0016
Klk14	ENSMUSG00000044737	kallikrein related-peptidase 14	-2.110	0.0352	0.0717
Klk8	ENSMUSG00000064023	kallikrein related-peptidase 8	-2.132	0.0000	0.0000
Klra9	ENSMUSG00000033024	killer cell lectin-like receptor subfamily A, member 9	-1.987	0.0061	0.0156
Klrb1c	ENSMUSG00000030325	killer cell lectin-like receptor subfamily B member 1C	-6.688	0.0211	0.0461
Kptn	ENSMUSG00000006021	kaptin	-2.270	0.0000	0.0000
Krba1	ENSMUSG00000042810	KRAB-A domain containing 1	-1.920	0.0000	0.0000
Krt19	ENSMUSG00000020911	keratin 19	-2.996	0.0170	0.0381
Krt80	ENSMUSG00000037185	keratin 80	-1.809	0.0189	0.0418
Krtcap2	ENSMUSG00000042747	keratinocyte associated protein 2	-5.451	0.0000	0.0000
Kti12	ENSMUSG00000073775	KTI12 homolog, chromatin associated	-2.763	0.0000	0.0000
Kyat1	ENSMUSG00000039648	kynurenine aminotransferase 1	-1.706	0.0000	0.0000
Kyat3	ENSMUSG00000040213	kynurenine aminotransferase 3	-2.104	0.0000	0.0000
L1cam	ENSMUSG00000031391	L1 cell adhesion molecule	-1.568	0.0132	0.0305
Lad1	ENSMUSG00000041782	ladinin	-1.921	0.0116	0.0273
Lage3	ENSMUSG00000015289	L antigen family, member 3	-2.274	0.0000	0.0000
Lair1	ENSMUSG00000055541	leukocyte-associated Ig-like receptor 1	-1.919	0.0347	0.0707
Lama5	ENSMUSG00000015647	laminin, alpha 5	-2.669	0.0000	0.0000
Lamb2	ENSMUSG00000052911	laminin, beta 2	-1.936	0.0000	0.0000
Lamc3	ENSMUSG00000026840	laminin gamma 3	-3.068	0.0014	0.0041
Lamtor4	ENSMUSG00000050552	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4	-1.706	0.0000	0.0000
Lancl1	ENSMUSG00000026000	LanC (bacterial lantibiotic synthetase component C)-like 1	-2.696	0.0000	0.0000
Laptm5	ENSMUSG00000028581	lysosomal-associated protein transmembrane 5	-1.881	0.0000	0.0002
Large1	ENSMUSG00000004383	LARGE xylosyl- and glucuronyltransferase 1	-1.591	0.0000	0.0000
Lars2	ENSMUSG00000035202	leucyl-tRNA synthetase, mitochondrial	-8.337	0.0000	0.0000
Lasp1	ENSMUSG00000038366	LIM and SH3 protein 1	-1.862	0.0000	0.0000
Lbp	ENSMUSG00000016024	lipopolysaccharide binding protein	-2.237	0.0056	0.0143
Lcmt2	ENSMUSG00000074890	leucine carboxyl methyltransferase 2	-2.025	0.0000	0.0000
Lcn2	ENSMUSG00000026822	lipocalin 2	-2.903	0.0297	0.0620

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Ldah	ENSMUSG00000037669	lipid droplet associated hydrolase	-1.707	0.0000	0.0000
Ldb3	ENSMUSG00000021798	LIM domain binding 3	-1.661	0.0000	0.0000
Ldhb-ps	ENSMUSG00000045104	lactate dehydrogenase B, pseudogene	-3.221	0.0000	0.0000
Ldhd	ENSMUSG00000031958	lactate dehydrogenase D	-1.806	0.0000	0.0000
Lgals3	ENSMUSG00000050335	lectin, galactose binding, soluble 3	-3.630	0.0002	0.0006
Lgals9	ENSMUSG00000001123	lectin, galactose binding, soluble 9	-1.830	0.0000	0.0000
Lhcgr	ENSMUSG00000024107	luteinizing hormone/choriogonadotropin receptor	-8.884	0.0458	0.0897
Lilra6	ENSMUSG00000030427	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	-2.656	0.0137	0.0316
Limd1	ENSMUSG00000025239	LIM domains containing 1	-1.631	0.0037	0.0099
Lims2	ENSMUSG00000024395	LIM and senescent cell antigen like domains 2	-1.675	0.0000	0.0000
Lin7b	ENSMUSG00000003872	lin-7 homolog B, crumbs cell polarity complex component	-2.149	0.0350	0.0713
Lipe	ENSMUSG00000003123	lipase, hormone sensitive	-1.645	0.0007	0.0023
Lipo3	ENSMUSG00000024766	lipase, member O3	-1.501	0.0458	0.0896
Llgl1	ENSMUSG00000020536	LLGL1 scribble cell polarity complex component	-2.344	0.0000	0.0000
Lman1l	ENSMUSG00000056271	lectin, mannose-binding 1 like	-4.126	0.0001	0.0003
Lmbr1l	ENSMUSG00000022999	limb region 1 like	-1.647	0.0171	0.0384
Lmf1	ENSMUSG00000002279	lipase maturation factor 1	-2.595	0.0000	0.0000
Lmf2	ENSMUSG00000022614	lipase maturation factor 2	-1.947	0.0000	0.0000
Lnx1	ENSMUSG00000029228	ligand of numb-protein X 1	-1.830	0.0066	0.0165
Lnx2	ENSMUSG00000016520	ligand of numb-protein X 2	-1.568	0.0079	0.0194
Loxl1	ENSMUSG00000032334	lysyl oxidase-like 1	-2.260	0.0003	0.0012
Loxl3	ENSMUSG00000000693	lysyl oxidase-like 3	-1.581	0.0046	0.0120
Lpin3	ENSMUSG00000027412	lipin 3	-1.647	0.0077	0.0190
Lrfn3	ENSMUSG00000036957	leucine rich repeat and fibronectin type III domain containing 3	-2.313	0.0004	0.0014
Lrg1	ENSMUSG00000037095	leucine-rich alpha-2-glycoprotein 1	-2.337	0.0052	0.0135
Lrp1	ENSMUSG00000040249	low density lipoprotein receptor-related protein 1	-1.904	0.0000	0.0000
Lrp2	ENSMUSG00000027070	low density lipoprotein receptor-related protein 2	-6.754	0.0412	0.0819
Lrrc10	ENSMUSG00000060187	leucine rich repeat containing 10	-2.726	0.0012	0.0037
Lrrc14b	ENSMUSG00000021579	leucine rich repeat containing 14B	-1.616	0.0000	0.0001
Lrrc24	ENSMUSG00000033707	leucine rich repeat containing 24	-1.778	0.0518	0.0997
Lrrc25	ENSMUSG00000049988	leucine rich repeat containing 25	-2.110	0.0015	0.0044

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lrrc28	ENSMUSG00000030556	leucine rich repeat containing 28	-1.993	0.0000	0.0000
Lrrc29	ENSMUSG00000041679	leucine rich repeat containing 29	-3.294	0.0023	0.0064
Lrrc30	ENSMUSG00000073375	leucine rich repeat containing 30	-7.201	0.0000	0.0000
Lrrc32	ENSMUSG00000090958	leucine rich repeat containing 32	-1.853	0.0001	0.0004
Lrrc49	ENSMUSG00000047766	leucine rich repeat containing 49	-1.544	0.0007	0.0023
Lrrc51	ENSMUSG00000064307	leucine rich repeat containing 51	-2.805	0.0000	0.0000
Lrrc70	ENSMUSG00000118423	leucine rich repeat containing 70	-2.391	0.0021	0.0059
Lrrc8c	ENSMUSG00000054720	leucine rich repeat containing 8 family, member C	-1.509	0.0004	0.0014
Lrrk1	ENSMUSG00000015133	leucine-rich repeat kinase 1	-1.661	0.0000	0.0000
Lrrn2	ENSMUSG00000026443	leucine rich repeat protein 2, neuronal	-1.765	0.0284	0.0595
Lrrn4	ENSMUSG00000043110	leucine rich repeat neuronal 4	-22.490	0.0073	0.0181
Lrsam1	ENSMUSG00000026792	leucine rich repeat and sterile alpha motif containing 1	-1.593	0.0000	0.0000
Lrwd1	ENSMUSG00000029703	leucine-rich repeats and WD repeat domain containing 1	-2.092	0.0000	0.0000
Lsm10	ENSMUSG00000050188	U7 snRNP-specific Sm-like protein LSM10	-3.723	0.0000	0.0000
Lsmem2	ENSMUSG00000103409	leucine-rich single-pass membrane protein 2	-1.783	0.0000	0.0002
Lss	ENSMUSG00000033105	lanosterol synthase	-1.573	0.0392	0.0785
Lta4h	ENSMUSG00000015889	leukotriene A4 hydrolase	-1.740	0.0000	0.0000
Ltc4s	ENSMUSG00000020377	leukotriene C4 synthase	-4.029	0.0000	0.0000
Lxn	ENSMUSG00000047557	latexin	-1.576	0.0262	0.0555
Ly6a	ENSMUSG00000075602	lymphocyte antigen 6 complex, locus A	-1.795	0.0000	0.0000
Ly6c1	ENSMUSG00000079018	lymphocyte antigen 6 complex, locus C1	-1.901	0.0000	0.0000
Ly6e	ENSMUSG00000022587	lymphocyte antigen 6 complex, locus E	-2.353	0.0000	0.0000
Ly86	ENSMUSG00000021423	lymphocyte antigen 86	-3.834	0.0000	0.0000
Ly96	ENSMUSG00000025779	lymphocyte antigen 96	-1.558	0.0250	0.0533
Lyl1	ENSMUSG00000034041	lymphoblastomic leukemia 1	-2.405	0.0000	0.0000
Lypd2	ENSMUSG00000022595	Ly6/Plaur domain containing 2	-3.961	0.0001	0.0005
Lypd6	ENSMUSG00000050447	LY6/PLAUR domain containing 6	-2.354	0.0000	0.0000
Lyrm1	ENSMUSG00000030922	LYR motif containing 1	-1.522	0.0040	0.0106
Lyrm2	ENSMUSG00000045854	LYR motif containing 2	-1.639	0.0000	0.0000
Lysmd4	ENSMUSG00000043831	LysM, putative peptidoglycan-binding, domain containing 4	-1.542	0.0000	0.0000
Lyz2	ENSMUSG00000069516	lysozyme 2	-2.036	0.0001	0.0002

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lzts1	ENSMUSG00000036306	leucine zipper, putative tumor suppressor 1	-1.720	0.0041	0.0109
Macroh2a2	ENSMUSG00000020086	macroH2A.2 histone	-1.521	0.0140	0.0323
Mad2l2	ENSMUSG00000029003	MAD2 mitotic arrest deficient-like 2	-1.742	0.0000	0.0000
Mag	ENSMUSG00000036634	myelin-associated glycoprotein	-18.489	0.0026	0.0073
Maged1	ENSMUSG00000025151	MAGE family member D1	-2.286	0.0000	0.0000
Maged2	ENSMUSG00000025268	MAGE family member D2	-2.016	0.0000	0.0000
Magee1	ENSMUSG00000031227	MAGE family member E1	-1.510	0.0115	0.0271
Maml2	ENSMUSG00000031925	mastermind like transcriptional coactivator 2	-1.563	0.0000	0.0001
Maml3	ENSMUSG00000061143	mastermind like transcriptional coactivator 3	-1.593	0.0007	0.0021
Mamld1	ENSMUSG00000059401	mastermind-like domain containing 1	-1.515	0.0094	0.0227
Mamstr	ENSMUSG00000042918	MEF2 activating motif and SAP domain containing transcriptional regulator	-1.788	0.0000	0.0000
Man2b1	ENSMUSG00000005142	mannosidase 2, alpha B1	-1.827	0.0000	0.0000
Man2b2	ENSMUSG00000029119	mannosidase 2, alpha B2	-2.600	0.0000	0.0000
Man2c1	ENSMUSG00000032295	mannosidase, alpha, class 2C, member 1	-1.579	0.0000	0.0000
Manbal	ENSMUSG00000063019	mannosidase, beta A, lysosomal-like	-2.890	0.0000	0.0000
Map1lc3b	ENSMUSG00000031812	microtubule-associated protein 1 light chain 3 beta	-2.027	0.0000	0.0000
Map1s	ENSMUSG00000019261	microtubule-associated protein 1S	-2.684	0.0000	0.0000
Map2k3os	ENSMUSG00000042549	mitogen-activated protein kinase kinase 3, opposite strand	-2.762	0.0000	0.0000
Map3k14	ENSMUSG00000020941	mitogen-activated protein kinase kinase kinase 14	-1.766	0.0000	0.0001
Map3k21	ENSMUSG00000031853	mitogen-activated protein kinase kinase kinase 21	-1.904	0.0029	0.0080
Map6d1	ENSMUSG00000041205	MAP6 domain containing 1	-2.662	0.0256	0.0544
Mapk13	ENSMUSG00000004864	mitogen-activated protein kinase 13	-8.485	0.0002	0.0007
Mapk1ip1	ENSMUSG00000041775	mitogen-activated protein kinase 1 interacting protein 1	-2.094	0.0000	0.0000
Mapk3	ENSMUSG00000063065	mitogen-activated protein kinase 3	-2.475	0.0000	0.0000
Mapkapk3	ENSMUSG00000032577	mitogen-activated protein kinase-activated protein kinase 3	-1.502	0.0000	0.0001
Marchf3	ENSMUSG00000032656	membrane associated ring-CH-type finger 3	-1.730	0.0002	0.0007
Mavs	ENSMUSG00000037523	mitochondrial antiviral signaling protein	-2.424	0.0000	0.0000
Mbp	ENSMUSG00000041607	myelin basic protein	-2.014	0.0000	0.0001
Mcfd2	ENSMUSG00000024150	multiple coagulation factor deficiency 2	-2.024	0.0000	0.0000
Mcm8	ENSMUSG00000027353	minichromosome maintenance 8 homologous recombination repair factor	-1.638	0.0003	0.0010
Mcrip2	ENSMUSG00000025732	MAPK regulated corepressor interacting protein 2	-1.607	0.0008	0.0026

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Mcrs1	ENSMUSG00000037570	microspherule protein 1	-2.702	0.0000	0.0000
Mdfi	ENSMUSG00000032717	MyoD family inhibitor	-2.377	0.0155	0.0353
Mdh1	ENSMUSG00000020321	malate dehydrogenase 1, NAD (soluble)	-1.812	0.0000	0.0000
Mdh2	ENSMUSG00000019179	malate dehydrogenase 2, NAD (mitochondrial)	-2.710	0.0000	0.0000
Mdp1	ENSMUSG00000002329	magnesium-dependent phosphatase 1	-1.519	0.0000	0.0000
Med10	ENSMUSG00000021598	mediator complex subunit 10	-1.720	0.0000	0.0000
Med11	ENSMUSG00000018923	mediator complex subunit 11	-1.537	0.0004	0.0012
Med22	ENSMUSG00000015776	mediator complex subunit 22	-1.758	0.0000	0.0000
Med24	ENSMUSG00000017210	mediator complex subunit 24	-2.225	0.0000	0.0000
Med26	ENSMUSG00000045248	mediator complex subunit 26	-1.547	0.0004	0.0014
Med27	ENSMUSG00000026799	mediator complex subunit 27	-1.831	0.0000	0.0000
Med29	ENSMUSG00000003444	mediator complex subunit 29	-2.496	0.0000	0.0000
Med7	ENSMUSG00000020397	mediator complex subunit 7	-1.518	0.0005	0.0017
Med9	ENSMUSG00000061650	mediator complex subunit 9	-1.706	0.0000	0.0000
Mef2b	ENSMUSG00000079033	myocyte enhancer factor 2B	-2.762	0.0003	0.0009
Megf6	ENSMUSG00000057751	multiple EGF-like-domains 6	-1.951	0.0024	0.0066
Mest	ENSMUSG00000051855	mesoderm specific transcript	-2.207	0.0000	0.0001
Metrn	ENSMUSG00000002274	meteorin, glial cell differentiation regulator	-1.829	0.0000	0.0000
Mettl11b	ENSMUSG00000040113	methyltransferase like 11B	-3.708	0.0002	0.0008
Mettl22	ENSMUSG00000039345	methyltransferase like 22	-3.220	0.0000	0.0000
Mettl23	ENSMUSG00000090266	methyltransferase like 23	-1.587	0.0000	0.0000
Mettl26	ENSMUSG00000025731	methyltransferase like 26	-1.786	0.0000	0.0000
Mettl27	ENSMUSG00000040557	methyltransferase like 27	-1.823	0.0012	0.0037
Mettl5os	ENSMUSG00000085735	methyltransferase like 5, opposite strand	-6.808	0.0144	0.0329
Mfap1b	ENSMUSG00000048222	microfibrillar-associated protein 1B	-2.345	0.0000	0.0000
Mfap2	ENSMUSG00000060572	microfibrillar-associated protein 2	-3.275	0.0000	0.0001
Mfap4	ENSMUSG00000042436	microfibrillar-associated protein 4	-2.562	0.0132	0.0307
Mfge8	ENSMUSG00000030605	milk fat globule EGF and factor V/VIII domain containing	-1.925	0.0000	0.0000
Mfng	ENSMUSG00000018169	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.503	0.0000	0.0001
Mfsd10	ENSMUSG00000001082	major facilitator superfamily domain containing 10	-1.999	0.0000	0.0000
Mfsd11	ENSMUSG00000020818	major facilitator superfamily domain containing 11	-1.753	0.0000	0.0000

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Mfsd13a	ENSMUSG00000025227	major facilitator superfamily domain containing 13a	-1.765	0.0010	0.0030
Mfsd2b	ENSMUSG00000037336	major facilitator superfamily domain containing 2B	-2.142	0.0301	0.0627
Mfsd3	ENSMUSG00000019080	major facilitator superfamily domain containing 3	-3.632	0.0000	0.0000
Mfsd4a	ENSMUSG00000059149	major facilitator superfamily domain containing 4A	-3.160	0.0000	0.0000
Mfsd4b3-ps	ENSMUSG00000071335	major facilitator superfamily domain containing 4B3, pseudogene	-1.772	0.0014	0.0040
Mgmt	ENSMUSG00000054612	O-6-methylguanine-DNA methyltransferase	-1.657	0.0002	0.0008
Mgp	ENSMUSG00000030218	matrix Gla protein	-2.914	0.0000	0.0000
Mgrn1	ENSMUSG00000022517	mahogunin, ring finger 1	-1.703	0.0000	0.0000
Mgst1	ENSMUSG00000008540	microsomal glutathione S-transferase 1	-1.719	0.0052	0.0135
Mgst3	ENSMUSG00000026688	microsomal glutathione S-transferase 3	-3.100	0.0000	0.0000
Micall2	ENSMUSG00000036718	MICAL-like 2	-2.074	0.0000	0.0001
Mid1	ENSMUSG00000035299	midline 1	-1.581	0.0399	0.0798
Mif	ENSMUSG00000033307	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	-3.389	0.0000	0.0000
Mif4gd	ENSMUSG00000020743	MIF4G domain containing	-1.845	0.0000	0.0000
Miip	ENSMUSG00000029022	migration and invasion inhibitory protein	-2.926	0.0000	0.0000
Mindy1	ENSMUSG00000038712	MINDY lysine 48 deubiquitinase 1	-2.339	0.0000	0.0000
Mindy4	ENSMUSG00000038022	MINDY lysine 48 deubiquitinase 4	-1.592	0.0260	0.0551
Mir133a-2	ENSMUSG00000065460	microRNA 133a-2	-30.296	0.0000	0.0000
Mir5125	ENSMUSG00000092981	microRNA 5125	-5.618	0.0007	0.0022
Mir7-1	ENSMUSG00000065434	microRNA 7-1	-37.166	0.0002	0.0006
Mir7666	ENSMUSG00000098431	microRNA 7666	-5.071	0.0238	0.0511
Misp3	ENSMUSG00000074217	MISP family member 3	-2.023	0.0004	0.0014
Mkks	ENSMUSG00000027274	McKusick-Kaufman syndrome	-1.892	0.0000	0.0000
Mllt1	ENSMUSG00000024212	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 1	-1.604	0.0000	0.0000
Mlst8	ENSMUSG00000024142	MTOR associated protein, LST8 homolog (S. cerevisiae)	-1.860	0.0000	0.0000
Mlx	ENSMUSG00000017801	MAX-like protein X	-2.504	0.0000	0.0000
Mmachc	ENSMUSG00000028690	methylmalonic aciduria cblC type, with homocystinuria	-1.640	0.0000	0.0000
Mmel1	ENSMUSG00000058183	membrane metallo-endopeptidase-like 1	-2.378	0.0020	0.0059
Mmp11	ENSMUSG00000000901	matrix metallopeptidase 11	-1.561	0.0009	0.0027
Mmp2	ENSMUSG00000031740	matrix metallopeptidase 2	-1.548	0.0031	0.0084
Mmp23	ENSMUSG00000029061	matrix metallopeptidase 23	-2.329	0.0001	0.0003

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mmp28	ENSMUSG00000020682	matrix metallopeptidase 28 (epilysin)	-1.989	0.0004	0.0014
Mmp9	ENSMUSG00000017737	matrix metallopeptidase 9	-2.725	0.0003	0.0010
Mmrn1	ENSMUSG00000054641	multimerin 1	-1.720	0.0403	0.0804
Mms19	ENSMUSG00000025159	MMS19 cytosolic iron-sulfur assembly component	-2.776	0.0000	0.0000
Mocs1	ENSMUSG00000064120	molybdenum cofactor synthesis 1	-2.025	0.0006	0.0019
Mon1a	ENSMUSG00000032583	MON1 homolog A, secretory traffciking associated	-2.966	0.0000	0.0000
Morf4l1-ps1	ENSMUSG00000116875	mortality factor 4 like 1, pseudogene 1	-2.650	0.0002	0.0007
Mov10	ENSMUSG00000002227	Mov10 RISC complex RNA helicase	-2.037	0.0000	0.0000
Mov10l1	ENSMUSG00000015365	Mov10 like RISC complex RNA helicase 1	-1.522	0.0006	0.0020
Mpc1	ENSMUSG00000023861	mitochondrial pyruvate carrier 1	-3.244	0.0000	0.0000
Mpc1-ps	ENSMUSG00000091498	mitochondrial pyruvate carrier 1, pseudogene	-11.909	0.0000	0.0000
Mpdu1	ENSMUSG00000018761	mannose-P-dolichol utilization defect 1	-1.688	0.0000	0.0000
Mpg	ENSMUSG00000020287	N-methylpurine-DNA glycosylase	-1.663	0.0000	0.0001
Mpp2	ENSMUSG00000017314	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	-1.612	0.0000	0.0002
Mpst	ENSMUSG00000071711	mercaptopyruvate sulfurtransferase	-3.399	0.0000	0.0000
Mpv17	ENSMUSG00000107283	MpV17 mitochondrial inner membrane protein	-1.656	0.0000	0.0000
Mpv17l2	ENSMUSG00000035559	MPV17 mitochondrial membrane protein-like 2	-3.218	0.0000	0.0000
Mrap	ENSMUSG00000039956	melanocortin 2 receptor accessory protein	-2.079	0.0000	0.0000
Mrgprd	ENSMUSG00000051207	MAS-related GPR, member D	-9.947	0.0432	0.0853
Mrgpre	ENSMUSG00000048965	MAS-related GPR, member E	-2.848	0.0000	0.0000
Mrgprf	ENSMUSG00000031070	MAS-related GPR, member F	-5.134	0.0000	0.0000
Mrgprh	ENSMUSG00000059408	MAS-related GPR, member H	-1.569	0.0185	0.0411
Mrip-ps	ENSMUSG00000098404	Mom radiation induced polyposis, pseudogene	-3.083	0.0000	0.0000
Mrm2	ENSMUSG00000029557	mitochondrial rRNA methyltransferase 2	-1.882	0.0005	0.0017
Mroh1	ENSMUSG00000022558	maestro heat-like repeat family member 1	-2.350	0.0000	0.0000
Mrpl10	ENSMUSG00000001445	mitochondrial ribosomal protein L10	-1.543	0.0000	0.0000
Mrpl11	ENSMUSG00000024902	mitochondrial ribosomal protein L11	-1.709	0.0000	0.0000
Mrpl12	ENSMUSG00000039640	mitochondrial ribosomal protein L12	-2.437	0.0000	0.0000
Mrpl14	ENSMUSG00000023939	mitochondrial ribosomal protein L14	-2.839	0.0000	0.0000
Mrpl17	ENSMUSG00000030879	mitochondrial ribosomal protein L17	-1.666	0.0000	0.0000
Mrpl22	ENSMUSG00000020514	mitochondrial ribosomal protein L22	-1.644	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mrpl23	ENSMUSG00000037772	mitochondrial ribosomal protein L23	-2.121	0.0000	0.0000
Mrpl23-ps1	ENSMUSG00000075279	mitichondrial ribosomal protein L23, pseudogene 1	-2.423	0.0126	0.0294
Mrpl27	ENSMUSG00000024414	mitochondrial ribosomal protein L27	-2.084	0.0000	0.0000
Mrpl27-ps	ENSMUSG00000071867	mitochondrial ribosomal protein L27, pseudogene	-11.091	0.0167	0.0376
Mrpl28	ENSMUSG00000024181	mitochondrial ribosomal protein L28	-1.631	0.0000	0.0000
Mrpl3	ENSMUSG00000032563	mitochondrial ribosomal protein L3	-1.655	0.0000	0.0000
Mrpl30	ENSMUSG00000026087	mitochondrial ribosomal protein L30	-2.913	0.0000	0.0000
Mrpl34	ENSMUSG00000034880	mitochondrial ribosomal protein L34	-2.595	0.0000	0.0000
Mrpl36	ENSMUSG00000021607	mitochondrial ribosomal protein L36	-2.355	0.0000	0.0000
Mrpl37	ENSMUSG00000028622	mitochondrial ribosomal protein L37	-1.706	0.0000	0.0000
Mrpl38	ENSMUSG00000020775	mitochondrial ribosomal protein L38	-1.949	0.0000	0.0000
Mrpl4	ENSMUSG00000003299	mitochondrial ribosomal protein L4	-3.175	0.0000	0.0000
Mrpl41	ENSMUSG00000036850	mitochondrial ribosomal protein L41	-1.632	0.0000	0.0000
Mrpl52	ENSMUSG00000010406	mitochondrial ribosomal protein L52	-1.914	0.0000	0.0000
Mrpl54	ENSMUSG00000034932	mitochondrial ribosomal protein L54	-3.850	0.0000	0.0000
Mrpl57	ENSMUSG00000021967	mitochondrial ribosomal protein L57	-2.030	0.0000	0.0000
Mrpl58	ENSMUSG00000018858	mitochondrial ribosomal protein L58	-1.673	0.0000	0.0000
Mrps11	ENSMUSG00000030611	mitochondrial ribosomal protein S11	-2.075	0.0000	0.0000
Mrps12	ENSMUSG00000045948	mitochondrial ribosomal protein S12	-2.251	0.0000	0.0000
Mrps14	ENSMUSG00000058267	mitochondrial ribosomal protein S14	-1.676	0.0000	0.0000
Mrps16	ENSMUSG00000049960	mitochondrial ribosomal protein S16	-1.819	0.0000	0.0000
Mrps17	ENSMUSG00000034211	mitochondrial ribosomal protein S17	-1.563	0.0000	0.0000
Mrps18a	ENSMUSG00000023967	mitochondrial ribosomal protein S18A	-2.505	0.0000	0.0000
Mrps18b	ENSMUSG00000024436	mitochondrial ribosomal protein S18B	-2.747	0.0000	0.0000
Mrps24	ENSMUSG00000020477	mitochondrial ribosomal protein S24	-1.835	0.0040	0.0106
Mrps26	ENSMUSG00000037740	mitochondrial ribosomal protein S26	-1.568	0.0000	0.0000
Mrps27	ENSMUSG00000041632	mitochondrial ribosomal protein S27	-1.739	0.0000	0.0000
Mrps28	ENSMUSG00000040269	mitochondrial ribosomal protein S28	-3.097	0.0000	0.0000
Mrps30	ENSMUSG00000021731	mitochondrial ribosomal protein S30	-2.211	0.0000	0.0000
Mrps34	ENSMUSG00000038880	mitochondrial ribosomal protein S34	-1.503	0.0000	0.0000
Mrps36-ps1	ENSMUSG00000021631	mitichondrial ribosomal protein S36, pseudogene 1	-3.707	0.0003	0.0010

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mrps7	ENSMUSG00000046756	mitchondrial ribosomal protein S7	-1.976	0.0000	0.0000
Mrrf	ENSMUSG00000026887	mitochondrial ribosome recycling factor	-2.045	0.0000	0.0000
Mrtfa	ENSMUSG00000042292	myocardin related transcription factor A	-1.808	0.0000	0.0000
Mrtfb	ENSMUSG00000009569	myocardin related transcription factor B	-1.557	0.0002	0.0008
Ms4a14	ENSMUSG00000099398	membrane-spanning 4-domains, subfamily A, member 14	-2.880	0.0501	0.0967
Ms4a6d	ENSMUSG00000024679	membrane-spanning 4-domains, subfamily A, member 6D	-2.928	0.0001	0.0005
Msantd1	ENSMUSG00000051246	Myb/SANT-like DNA-binding domain containing 1	-5.129	0.0027	0.0075
Msh5	ENSMUSG00000007035	mutS homolog 5	-3.249	0.0091	0.0220
Msln	ENSMUSG00000063011	mesothelin	-16.377	0.0012	0.0037
Msra	ENSMUSG00000054733	methionine sulfoxide reductase A	-1.741	0.0000	0.0000
Msrb1	ENSMUSG00000075705	methionine sulfoxide reductase B1	-2.351	0.0000	0.0000
Mst1r	ENSMUSG00000032584	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	-2.110	0.0002	0.0005
Msto1	ENSMUSG00000068922	misato 1, mitochondrial distribution and morphology regulator	-2.092	0.0000	0.0000
Mt1	ENSMUSG00000031765	metallothionein 1	-2.236	0.0463	0.0905
Mt2	ENSMUSG00000031762	metallothionein 2	-4.938	0.0294	0.0613
Mterf3	ENSMUSG00000021519	mitochondrial transcription termination factor 3	-1.988	0.0000	0.0000
Mtg1	ENSMUSG00000039018	mitochondrial ribosome-associated GTPase 1	-1.892	0.0000	0.0000
Mthfr	ENSMUSG00000029009	methylenetetrahydrofolate reductase	-2.078	0.0000	0.0000
Mtln	ENSMUSG00000051319	mitoregulin	-2.497	0.0000	0.0000
Mtmr10	ENSMUSG00000030522	myotubularin related protein 10	-1.600	0.0049	0.0127
Mtmr11	ENSMUSG00000045934	myotubularin related protein 11	-1.665	0.0037	0.0099
mt-Rnr1	ENSMUSG00000064337	mitochondrially encoded 12S rRNA	-1.801	0.0013	0.0039
mt-Ta	ENSMUSG00000064347	mitochondrially encoded tRNA alanine	-2.826	0.0232	0.0499
mt-Ti	ENSMUSG00000064342	mitochondrially encoded tRNA isoleucine	-2.429	0.0033	0.0090
mt-Tl1	ENSMUSG00000064340	mitochondrially encoded tRNA leucine 1	-44.006	0.0000	0.0001
mt-Tm	ENSMUSG00000064344	mitochondrially encoded tRNA methionine	-12.882	0.0000	0.0000
mt-Tt	ENSMUSG00000064371	mitochondrially encoded tRNA threonine	-12.128	0.0000	0.0000
mt-Tw	ENSMUSG00000064346	mitochondrially encoded tRNA tryptophan	-2.074	0.0008	0.0024
Mtx1	ENSMUSG00000064068	metaxin 1	-1.657	0.0000	0.0000
Muc1	ENSMUSG00000042784	mucin 1, transmembrane	-2.744	0.0350	0.0712
Muc16	ENSMUSG00000109564	mucin 16	-28.942	0.0005	0.0017

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Muc3a	ENSMUSG00000094840	mucin 3A, cell surface associated	-3.630	0.0214	0.0466
Mus81	ENSMUSG00000024906	MUS81 structure-specific endonuclease subunit	-2.482	0.0000	0.0000
Mutyh	ENSMUSG00000028687	mutY DNA glycosylase	-2.301	0.0010	0.0030
Mvd	ENSMUSG00000006517	mevalonate (diphospho) decarboxylase	-1.852	0.0000	0.0000
Myadml2os	ENSMUSG00000084822	myeloid-associated differentiation marker-like 2, opposite strand	-2.800	0.0289	0.0605
Myc	ENSMUSG00000022346	myelocytomatosis oncogene	-1.909	0.0113	0.0268
Myl12a	ENSMUSG00000024048	myosin, light chain 12A, regulatory, non-sarcomeric	-1.510	0.0000	0.0000
Myl2	ENSMUSG00000013936	myosin, light polypeptide 2, regulatory, cardiac, slow	-2.088	0.0000	0.0000
Myl3	ENSMUSG00000059741	myosin, light polypeptide 3	-1.534	0.0000	0.0000
Myl6b	ENSMUSG00000039824	myosin, light polypeptide 6B	-2.034	0.0000	0.0002
Myl9	ENSMUSG00000067818	myosin, light polypeptide 9, regulatory	-2.122	0.0000	0.0000
Myo19	ENSMUSG00000020527	myosin XIX	-1.936	0.0016	0.0046
Myo7a	ENSMUSG00000030761	myosin VIIA	-2.037	0.0000	0.0000
Myo9b	ENSMUSG00000004677	myosin IXb	-1.875	0.0000	0.0000
Myoc	ENSMUSG00000026697	myocilin	-1.949	0.0000	0.0000
Myot	ENSMUSG00000024471	myotilin	-2.452	0.0000	0.0000
Myoz2	ENSMUSG00000028116	myozenin 2	-1.897	0.0000	0.0000
Myrf	ENSMUSG00000036098	myelin regulatory factor	-1.864	0.0001	0.0005
Myrip	ENSMUSG00000041794	myosin VIIA and Rab interacting protein	-1.762	0.0006	0.0018
Mzb1	ENSMUSG00000024353	marginal zone B and B1 cell-specific protein 1	-5.195	0.0001	0.0005
Mzf1	ENSMUSG00000030380	myeloid zinc finger 1	-2.870	0.0153	0.0347
Mzt2	ENSMUSG00000022671	mitotic spindle organizing protein 2	-1.521	0.0004	0.0012
N4bp3	ENSMUSG00000001053	NEDD4 binding protein 3	-1.825	0.0000	0.0000
Naa38	ENSMUSG00000059278	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	-2.569	0.0000	0.0000
Naa60	ENSMUSG00000005982	N(alpha)-acetyltransferase 60, NatF catalytic subunit	-2.429	0.0000	0.0000
Naa80	ENSMUSG00000079334	N(alpha)-acetyltransferase 80, NatH catalytic subunit	-3.031	0.0000	0.0000
Naaa	ENSMUSG00000029413	N-acylethanolamine acid amidase	-1.648	0.0000	0.0001
Nadsyn1	ENSMUSG00000031090	NAD synthetase 1	-1.947	0.0000	0.0000
Naga	ENSMUSG00000022453	N-acetyl galactosaminidase, alpha	-2.394	0.0000	0.0000
Naglu	ENSMUSG00000001751	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	-2.375	0.0000	0.0000
Nagpa	ENSMUSG00000023143	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	-1.672	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Naip2	ENSMUSG00000078945	NLR family, apoptosis inhibitory protein 2	-1.608	0.0041	0.0109
Napa	ENSMUSG00000006024	N-ethylmaleimide sensitive fusion protein attachment protein alpha	-2.563	0.0000	0.0000
Naprt	ENSMUSG00000022574	nicotinate phosphoribosyltransferase	-1.639	0.0000	0.0000
Nat8f1	ENSMUSG00000057103	N-acetyltransferase 8 (GCN5-related) family member 1	-2.413	0.0001	0.0004
Natd1	ENSMUSG00000018931	N-acetyltransferase domain containing 1	-1.830	0.0000	0.0000
Naxd	ENSMUSG00000031505	NAD(P)HX dehydratase	-1.750	0.0000	0.0000
Nbeal2	ENSMUSG00000056724	neurobeachin-like 2	-1.930	0.0000	0.0000
Ncaph2	ENSMUSG00000008690	non-SMC condensin II complex, subunit H2	-1.765	0.0000	0.0000
Ncdn	ENSMUSG00000028833	neurochondrin	-1.990	0.0000	0.0000
Nckap5l	ENSMUSG00000023009	NCK-associated protein 5-like	-3.041	0.0000	0.0000
Nckipsd	ENSMUSG00000032598	NCK interacting protein with SH3 domain	-2.380	0.0000	0.0000
Ncln	ENSMUSG00000020238	nicalin	-3.754	0.0000	0.0000
Ncoa4-ps	ENSMUSG00000021908	nuclear receptor coactivator 4, pseudogene	-4.490	0.0008	0.0024
Ncor2	ENSMUSG00000029478	nuclear receptor co-repressor 2	-1.720	0.0000	0.0000
Ncr1	ENSMUSG00000062524	natural cytotoxicity triggering receptor 1	-3.916	0.0320	0.0661
Ncstn	ENSMUSG00000003458	nicastrin	-1.532	0.0000	0.0000
Ndor1	ENSMUSG00000006471	NADPH dependent diflavin oxidoreductase 1	-1.635	0.0014	0.0041
Ndrg3	ENSMUSG00000027634	N-myc downstream regulated gene 3	-1.514	0.0046	0.0120
Ndufa11	ENSMUSG00000002379	NADH:ubiquinone oxidoreductase subunit A11	-3.010	0.0000	0.0000
Ndufa12-ps	ENSMUSG00000080893	NADH:ubiquinone oxidoreductase subunit A12, pseudogene	-3.769	0.0000	0.0000
Ndufa3	ENSMUSG00000035674	NADH:ubiquinone oxidoreductase subunit A3	-2.330	0.0000	0.0000
Ndufa4l2	ENSMUSG00000040280	Ndufa4, mitochondrial complex associated like 2	-3.035	0.0000	0.0000
Ndufa7	ENSMUSG00000041881	NADH:ubiquinone oxidoreductase subunit A7	-3.018	0.0000	0.0000
Ndufab1-ps	ENSMUSG00000091989	NADH:ubiquinone oxidoreductase subunit AB1b	-2.872	0.0021	0.0060
Ndufaf3	ENSMUSG00000070283	NADH:ubiquinone oxidoreductase complex assembly factor 3	-1.786	0.0000	0.0000
Ndufaf8	ENSMUSG00000078572	NADH:ubiquinone oxidoreductase complex assembly factor 8	-2.100	0.0000	0.0000
Ndufb1	ENSMUSG00000113902	NADH:ubiquinone oxidoreductase subunit B1	-2.426	0.0000	0.0000
Ndufb11	ENSMUSG00000031059	NADH:ubiquinone oxidoreductase subunit B11	-2.609	0.0000	0.0000
Ndufb2	ENSMUSG00000002416	NADH:ubiquinone oxidoreductase subunit B2	-3.772	0.0000	0.0000
Ndufb5	ENSMUSG00000027673	NADH:ubiquinone oxidoreductase subunit B5	-2.289	0.0000	0.0000
Ndufb6	ENSMUSG00000071014	NADH:ubiquinone oxidoreductase subunit B6	-1.794	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ndufc2	ENSMUSG00000030647	NADH:ubiquinone oxidoreductase subunit C2	-1.604	0.0000	0.0000
Ndufs5	ENSMUSG00000028648	NADH:ubiquinone oxidoreductase core subunit S5	-2.772	0.0000	0.0000
Ndufs5-ps	ENSMUSG00000081824	NADH:ubiquinone oxidoreductase core subunit S5, pseudogene	-3.428	0.0000	0.0000
Ndufs7	ENSMUSG00000020153	NADH:ubiquinone oxidoreductase core subunit S7	-3.422	0.0000	0.0000
Ndufs8	ENSMUSG00000059734	NADH:ubiquinone oxidoreductase core subunit S8	-2.315	0.0000	0.0000
Necab3	ENSMUSG00000027489	N-terminal EF-hand calcium binding protein 3	-13.082	0.0021	0.0061
Necap2	ENSMUSG00000028923	NECAP endocytosis associated 2	-1.512	0.0001	0.0002
Neil2	ENSMUSG00000035121	nei like 2 (E. coli)	-1.711	0.0449	0.0882
Nek6	ENSMUSG00000026749	NIMA (never in mitosis gene a)-related expressed kinase 6	-2.160	0.0000	0.0000
Nelfa	ENSMUSG00000029111	negative elongation factor complex member A, Whsc2	-1.609	0.0000	0.0000
Nepn	ENSMUSG00000038624	nephrocan	-2.362	0.0004	0.0013
Neurl1a	ENSMUSG00000006435	neuralized E3 ubiquitin protein ligase 1A	-2.202	0.0000	0.0000
Neurl2	ENSMUSG00000039873	neuralized E3 ubiquitin protein ligase 2	-1.769	0.0000	0.0000
Nfkbib	ENSMUSG00000030595	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta	-4.088	0.0000	0.0000
Nfkbid	ENSMUSG00000036931	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta	-5.302	0.0111	0.0263
Nfkbie	ENSMUSG00000023947	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon	-1.884	0.0179	0.0398
Nfs1	ENSMUSG00000027618	nitrogen fixation gene 1 (S. cerevisiae)	-2.663	0.0000	0.0000
Nfyc	ENSMUSG00000032897	nuclear transcription factor-Y gamma	-1.912	0.0000	0.0000
Nfyc-ps	ENSMUSG00000073233	nuclear transcription factor-Y gamma, pseudogene	-6.348	0.0009	0.0029
Ngf	ENSMUSG00000027859	nerve growth factor	-1.927	0.0000	0.0002
Ngfr	ENSMUSG00000000120	nerve growth factor receptor (TNFR superfamily, member 16)	-2.573	0.0391	0.0783
Nhej1	ENSMUSG00000026162	non-homologous end joining factor 1	-1.553	0.0001	0.0003
Nicn1	ENSMUSG00000032606	nicolin 1	-1.562	0.0000	0.0000
Nid2	ENSMUSG00000021806	nidogen 2	-1.727	0.0000	0.0000
Ninj1	ENSMUSG00000037966	ninjurin 1	-2.763	0.0000	0.0000
Nipal3	ENSMUSG00000028803	NIPA-like domain containing 3	-1.592	0.0000	0.0000
Nipsnap2	ENSMUSG00000029432	nipsnap homolog 2	-1.888	0.0000	0.0000
Nipsnap3b	ENSMUSG00000015247	nipsnap homolog 3B	-1.641	0.0000	0.0000
Nisch	ENSMUSG00000021910	nischarin	-1.799	0.0000	0.0000
Nit1	ENSMUSG00000013997	nitrilase 1	-1.927	0.0000	0.0000
Nit2	ENSMUSG00000022751	nitrilase family, member 2	-1.678	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nkain4	ENSMUSG00000027574	Na+/K+ transporting ATPase interacting 4	-3.689	0.0204	0.0448
Nkiras2	ENSMUSG00000017837	NFKB inhibitor interacting Ras-like protein 2	-1.835	0.0000	0.0000
Nle1	ENSMUSG00000020692	notchless homolog 1	-1.907	0.0002	0.0008
Nlrc3	ENSMUSG00000049871	NLR family, CARD domain containing 3	-1.606	0.0119	0.0280
Nmb	ENSMUSG00000025723	neuromedin B	-4.201	0.0001	0.0005
Nmnat1	ENSMUSG00000028992	nicotinamide nucleotide adenylyltransferase 1	-1.704	0.0000	0.0000
Nmral1	ENSMUSG00000063445	NmrA-like family domain containing 1	-2.564	0.0000	0.0000
Noc4l	ENSMUSG00000033294	NOC4 like	-2.782	0.0000	0.0000
Nod1	ENSMUSG00000038058	nucleotide-binding oligomerization domain containing 1	-2.146	0.0000	0.0000
Nol12	ENSMUSG00000033099	nucleolar protein 12	-1.683	0.0000	0.0000
Nop10	ENSMUSG00000027133	NOP10 ribonucleoprotein	-2.225	0.0000	0.0000
Nos1	ENSMUSG00000029361	nitric oxide synthase 1, neuronal	-11.561	0.0011	0.0033
Nos2	ENSMUSG00000020826	nitric oxide synthase 2, inducible	-1.517	0.0129	0.0300
Nos3	ENSMUSG00000028978	nitric oxide synthase 3, endothelial cell	-1.916	0.0000	0.0000
Nosip	ENSMUSG00000003421	nitric oxide synthase interacting protein	-2.025	0.0000	0.0000
Notch1	ENSMUSG00000026923	notch 1	-1.639	0.0000	0.0000
Nox4	ENSMUSG00000030562	NADPH oxidase 4	-1.786	0.0401	0.0802
Npdc1	ENSMUSG00000015094	neural proliferation, differentiation and control 1	-2.396	0.0000	0.0000
Npepl1	ENSMUSG00000039263	aminopeptidase-like 1	-1.758	0.0000	0.0000
Npffr1	ENSMUSG00000020090	neuropeptide FF receptor 1	-17.225	0.0064	0.0162
Nphp4	ENSMUSG00000039577	nephronophthisis 4 (juvenile) homolog (human)	-2.468	0.0098	0.0236
Nppa	ENSMUSG00000041616	natriuretic peptide type A	-4.261	0.0024	0.0069
Npr1	ENSMUSG00000027931	natriuretic peptide receptor 1	-1.645	0.0000	0.0000
Nprl2	ENSMUSG00000010057	NPR2 like, GATOR1 complex subunit	-3.957	0.0000	0.0000
Nprl3	ENSMUSG00000020289	nitrogen permease regulator-like 3	-2.408	0.0000	0.0000
Npy4r	ENSMUSG00000048337	neuropeptide Y receptor Y4	-3.154	0.0002	0.0009
Nr0b2	ENSMUSG00000037583	nuclear receptor subfamily 0, group B, member 2	-3.954	0.0000	0.0000
Nr1d1	ENSMUSG00000020889	nuclear receptor subfamily 1, group D, member 1	-1.668	0.0002	0.0007
Nr1h2	ENSMUSG00000060601	nuclear receptor subfamily 1, group H, member 2	-3.508	0.0000	0.0000
Nr1h3	ENSMUSG00000002108	nuclear receptor subfamily 1, group H, member 3	-1.615	0.0001	0.0003
Nr4a1	ENSMUSG00000023034	nuclear receptor subfamily 4, group A, member 1	-1.825	0.0072	0.0179

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nradd	ENSMUSG00000032491	neurotrophin receptor associated death domain	-2.016	0.0368	0.0743
Nrap	ENSMUSG00000049134	nebulin-related anchoring protein	-1.557	0.0000	0.0000
Nrbf2	ENSMUSG00000075000	nuclear receptor binding factor 2	-2.849	0.0000	0.0000
Nrde2	ENSMUSG00000021179	nrde-2 necessary for RNA interference, domain containing	-1.867	0.0000	0.0000
Nrm	ENSMUSG00000059791	nurim (nuclear envelope membrane protein)	-2.808	0.0000	0.0000
Nrros	ENSMUSG00000052384	negative regulator of reactive oxygen species	-2.391	0.0000	0.0002
Nsdhl	ENSMUSG00000031349	NAD(P) dependent steroid dehydrogenase-like	-1.777	0.0000	0.0000
Nsun5	ENSMUSG00000000916	NOL1/NOP2/Sun domain family, member 5	-2.322	0.0000	0.0000
Ntan1	ENSMUSG00000022681	N-terminal Asn amidase	-1.673	0.0000	0.0000
Ntmt1	ENSMUSG00000026857	N-terminal Xaa-Pro-Lys N-methyltransferase 1	-1.873	0.0000	0.0000
Ntsr2	ENSMUSG00000020591	neurotensin receptor 2	-2.187	0.0000	0.0000
Nubp2	ENSMUSG00000039183	nucleotide binding protein 2	-1.735	0.0000	0.0000
Nudt14	ENSMUSG00000002804	nudix (nucleoside diphosphate linked moiety X)-type motif 14	-2.616	0.0000	0.0000
Nudt16	ENSMUSG00000032565	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-1.591	0.0000	0.0001
Nudt16l1	ENSMUSG00000022516	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	-1.512	0.0000	0.0000
Nudt17	ENSMUSG00000028100	nudix (nucleoside diphosphate linked moiety X)-type motif 17	-2.766	0.0000	0.0000
Nudt19	ENSMUSG00000034875	nudix (nucleoside diphosphate linked moiety X)-type motif 19	-1.994	0.0000	0.0000
Nudt2	ENSMUSG00000028443	nudix (nucleoside diphosphate linked moiety X)-type motif 2	-3.935	0.0000	0.0000
Nudt22	ENSMUSG00000037349	nudix (nucleoside diphosphate linked moiety X)-type motif 22	-2.484	0.0000	0.0000
Nudt8	ENSMUSG00000110949	nudix (nucleoside diphosphate linked moiety X)-type motif 8	-2.634	0.0019	0.0056
Nup133	ENSMUSG00000039509	nucleoporin 133	-1.666	0.0000	0.0000
Nup188	ENSMUSG00000052533	nucleoporin 188	-1.944	0.0000	0.0000
Nup214	ENSMUSG00000001855	nucleoporin 214	-1.648	0.0000	0.0000
Nup85	ENSMUSG00000020739	nucleoporin 85	-1.621	0.0000	0.0000
Nupr1	ENSMUSG00000030717	nuclear protein transcription regulator 1	-1.701	0.0247	0.0528
Nupr1l	ENSMUSG00000095789	nuclear protein transcriptional regulator 1 like	-6.496	0.0013	0.0039
Nxpe3	ENSMUSG00000075033	neurexophilin and PC-esterase domain family, member 3	-1.735	0.0002	0.0008
Nxpe4	ENSMUSG00000044229	neurexophilin and PC-esterase domain family, member 4	-2.329	0.0059	0.0150
Oas2	ENSMUSG00000032690	2'-5' oligoadenylate synthetase 2	-1.897	0.0186	0.0412
Oaz1	ENSMUSG00000035242	ornithine decarboxylase antizyme 1	-1.750	0.0000	0.0000
Oaz2-ps	ENSMUSG00000083610	ornithine decarboxylase antizyme 2, pseudogene	-4.232	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ocln	ENSMUSG00000021638	occludin	-3.318	0.0329	0.0675
Ogdh	ENSMUSG00000020456	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-1.505	0.0000	0.0000
Ogdhl	ENSMUSG00000021913	oxoglutarate dehydrogenase-like	-2.159	0.0000	0.0000
Ogg1	ENSMUSG00000030271	8-oxoguanine DNA-glycosylase 1	-2.129	0.0000	0.0000
Ogn	ENSMUSG00000021390	osteoglycin	-1.595	0.0014	0.0041
Oip5	ENSMUSG00000072980	Opa interacting protein 5	-3.361	0.0241	0.0516
Olfml1	ENSMUSG00000051041	olfactomedin-like 1	-1.764	0.0072	0.0179
Olfml2a	ENSMUSG00000046618	olfactomedin-like 2A	-1.790	0.0001	0.0003
Olfr78	ENSMUSG00000043366	olfactory receptor 78	-2.660	0.0006	0.0021
Oplah	ENSMUSG00000022562	5-oxoprolinase (ATP-hydrolysing)	-1.845	0.0000	0.0000
Opn3	ENSMUSG00000026525	opsin 3	-1.721	0.0251	0.0534
Opn4	ENSMUSG00000021799	opsin 4 (melanopsin)	-2.313	0.0001	0.0003
Orc5	ENSMUSG00000029012	origin recognition complex, subunit 5	-1.927	0.0000	0.0000
Ormdl2	ENSMUSG00000025353	ORM1-like 2 (S. cerevisiae)	-2.004	0.0000	0.0000
Osbp2	ENSMUSG00000020435	oxysterol binding protein 2	-1.636	0.0000	0.0000
Osbpl5	ENSMUSG00000037606	oxysterol binding protein-like 5	-1.612	0.0001	0.0004
Oser1	ENSMUSG00000035399	oxidative stress responsive serine rich 1	-1.554	0.0035	0.0094
Osgepl1	ENSMUSG00000026096	O-sialoglycoprotein endopeptidase-like 1	-2.146	0.0000	0.0000
Osgin1	ENSMUSG00000074063	oxidative stress induced growth inhibitor 1	-3.014	0.0001	0.0003
Osmr	ENSMUSG00000022146	oncostatin M receptor	-1.745	0.0003	0.0009
Osr1	ENSMUSG00000048387	odd-skipped related transcription factor 1	-2.861	0.0000	0.0001
Otub1	ENSMUSG00000024767	OTU domain, ubiquitin aldehyde binding 1	-1.617	0.0000	0.0000
Oxa1l	ENSMUSG00000000959	oxidase assembly 1-like	-1.567	0.0000	0.0000
Oxld1	ENSMUSG00000039670	oxidoreductase like domain containing 1	-2.124	0.0000	0.0000
P2rx6	ENSMUSG00000022758	purinergic receptor P2X, ligand-gated ion channel, 6	-1.728	0.0034	0.0092
P2rx7	ENSMUSG00000029468	purinergic receptor P2X, ligand-gated ion channel, 7	-1.559	0.0013	0.0038
P2ry12	ENSMUSG00000036353	purinergic receptor P2Y, G-protein coupled 12	-3.125	0.0001	0.0003
P2ry14	ENSMUSG00000036381	purinergic receptor P2Y, G-protein coupled, 14	-2.281	0.0000	0.0000
P2ry6	ENSMUSG00000048779	pyrimidinergic receptor P2Y, G-protein coupled, 6	-2.467	0.0001	0.0003
P3h1	ENSMUSG00000028641	prolyl 3-hydroxylase 1	-1.887	0.0000	0.0000
Pacc1	ENSMUSG00000026627	proton activated chloride channel 1	-1.851	0.0000	0.0001

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Padi2	ENSMUSG00000028927	peptidyl arginine deiminase, type II	-3.186	0.0000	0.0000
Padi4	ENSMUSG00000025330	peptidyl arginine deiminase, type IV	-23.121	0.0086	0.0209
Pafah2	ENSMUSG00000037366	platelet-activating factor acetylhydrolase 2	-1.654	0.0000	0.0002
Pah	ENSMUSG00000020051	phenylalanine hydroxylase	-5.309	0.0000	0.0000
Pak5	ENSMUSG00000039913	p21 (RAC1) activated kinase 5	-9.604	0.0277	0.0583
Pam16	ENSMUSG00000014301	presequence translocase-asssociated motor 16	-3.436	0.0000	0.0000
Pank4	ENSMUSG00000029056	pantothenate kinase 4	-1.717	0.0000	0.0000
Papln	ENSMUSG00000021223	papilin, proteoglycan-like sulfated glycoprotein	-1.896	0.0054	0.0139
Paqr7	ENSMUSG00000037348	progestin and adipoQ receptor family member VII	-1.840	0.0004	0.0012
Pard6a	ENSMUSG00000005699	par-6 family cell polarity regulator alpha	-2.296	0.0000	0.0000
Parp16	ENSMUSG00000032392	poly (ADP-ribose) polymerase family, member 16	-1.863	0.0000	0.0000
Pars2	ENSMUSG00000043572	prolyl-tRNA synthetase (mitochondrial)(putative)	-1.556	0.0009	0.0028
Parvb	ENSMUSG00000022438	parvin, beta	-1.525	0.0000	0.0000
Patz1	ENSMUSG00000020453	POZ (BTB) and AT hook containing zinc finger 1	-1.836	0.0000	0.0001
Paxx	ENSMUSG00000047617	non-homologous end joining factor	-2.706	0.0000	0.0000
Pbld1	ENSMUSG00000112129	phenazine biosynthesis-like protein domain containing 1	-2.293	0.0289	0.0605
Pcdhga10	ENSMUSG00000102222	protocadherin gamma subfamily A, 10	-1.877	0.0000	0.0001
Pcdhga2	ENSMUSG00000103332	protocadherin gamma subfamily A, 2	-1.967	0.0000	0.0000
Pcdhga3	ENSMUSG00000104346	protocadherin gamma subfamily A, 3	-1.744	0.0056	0.0144
Pcdhga4	ENSMUSG00000103677	protocadherin gamma subfamily A, 4	-2.450	0.0047	0.0124
Pcdhga5	ENSMUSG00000103567	protocadherin gamma subfamily A, 5	-1.895	0.0003	0.0011
Pcdhgc3	ENSMUSG00000102918	protocadherin gamma subfamily C, 3	-1.546	0.0002	0.0006
Pcif1	ENSMUSG00000039849	phosphorylated CTD interacting factor 1	-2.105	0.0000	0.0000
Pcolce	ENSMUSG00000029718	procollagen C-endopeptidase enhancer protein	-2.265	0.0000	0.0000
Pcolce2	ENSMUSG00000015354	procollagen C-endopeptidase enhancer 2	-1.629	0.0000	0.0000
Pcsk4	ENSMUSG00000020131	proprotein convertase subtilisin/kexin type 4	-1.906	0.0010	0.0032
Pcsk6	ENSMUSG00000030513	proprotein convertase subtilisin/kexin type 6	-1.527	0.0002	0.0006
Pcx	ENSMUSG00000024892	pyruvate carboxylase	-2.917	0.0000	0.0000
Pcyt2	ENSMUSG00000025137	phosphate cytidylyltransferase 2, ethanolamine	-1.575	0.0000	0.0000
Pde1b	ENSMUSG00000022489	phosphodiesterase 1B, Ca2+-calmodulin dependent	-1.518	0.0096	0.0231
Pdf	ENSMUSG00000078931	peptide deformylase (mitochondrial)	-4.223	0.0000	0.0000

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Pdgfrb	ENSMUSG00000024620	platelet derived growth factor receptor, beta polypeptide	-2.002	0.0000	0.0000
Pdgfrl	ENSMUSG00000031595	platelet-derived growth factor receptor-like	-3.206	0.0000	0.0000
Pdia5	ENSMUSG00000022844	protein disulfide isomerase associated 5	-2.056	0.0003	0.0010
Pdk2	ENSMUSG00000038967	pyruvate dehydrogenase kinase, isoenzyme 2	-2.008	0.0000	0.0000
Pdk3	ENSMUSG00000035232	pyruvate dehydrogenase kinase, isoenzyme 3	-1.660	0.0059	0.0150
Pdlim1	ENSMUSG00000055044	PDZ and LIM domain 1 (elfin)	-1.734	0.0000	0.0000
Pdlim4	ENSMUSG00000020388	PDZ and LIM domain 4	-2.595	0.0000	0.0000
Pdlim7	ENSMUSG00000021493	PDZ and LIM domain 7	-1.535	0.0000	0.0000
Pdzd3	ENSMUSG00000032105	PDZ domain containing 3	-2.005	0.0008	0.0025
Pear1	ENSMUSG00000028073	platelet endothelial aggregation receptor 1	-2.402	0.0000	0.0000
Pebp1	ENSMUSG00000032959	phosphatidylethanolamine binding protein 1	-1.972	0.0000	0.0000
Peds1	ENSMUSG00000090213	plasmanylethanolamine desaturase 1	-1.708	0.0000	0.0000
Pef1	ENSMUSG00000028779	penta-EF hand domain containing 1	-2.377	0.0000	0.0000
Pelo	ENSMUSG00000042275	pelota mRNA surveillance and ribosome rescue factor	-1.958	0.0000	0.0000
Pemt	ENSMUSG00000000301	phosphatidylethanolamine N-methyltransferase	-2.216	0.0022	0.0061
Penk	ENSMUSG00000045573	preproenkephalin	-1.707	0.0012	0.0035
Pepd	ENSMUSG00000063931	peptidase D	-1.516	0.0000	0.0000
Perm1	ENSMUSG00000078486	PPARGC1 and ESRR induced regulator, muscle 1	-1.554	0.0000	0.0001
Pex10	ENSMUSG00000029047	peroxisomal biogenesis factor 10	-2.807	0.0000	0.0000
Pex26	ENSMUSG00000067825	peroxisomal biogenesis factor 26	-1.557	0.0004	0.0013
Pf4	ENSMUSG00000029373	platelet factor 4	-2.497	0.0009	0.0027
Pfkfb1	ENSMUSG00000025271	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	-2.055	0.0010	0.0031
Pfkfb4	ENSMUSG00000025648	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-3.166	0.0000	0.0000
Pgam1	ENSMUSG00000011752	phosphoglycerate mutase 1	-2.911	0.0000	0.0000
Pgam2	ENSMUSG00000020475	phosphoglycerate mutase 2	-2.164	0.0000	0.0000
Pgap2	ENSMUSG00000030990	post-GPI attachment to proteins 2	-1.748	0.0000	0.0000
Pgap6	ENSMUSG00000024180	post-glycosylphosphatidylinositol attachment to proteins 6	-2.778	0.0000	0.0000
Pgls	ENSMUSG00000031807	6-phosphogluconolactonase	-5.672	0.0000	0.0000
Pgrmc1	ENSMUSG00000006373	progesterone receptor membrane component 1	-1.581	0.0000	0.0000
Pheta1	ENSMUSG00000044134	PH domain containing endocytic trafficking adaptor 1	-1.848	0.0000	0.0000
Phf7	ENSMUSG00000021902	PHD finger protein 7	-1.805	0.0002	0.0006

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Phkg2	ENSMUSG00000030815	phosphorylase kinase, gamma 2 (testis)	-1.877	0.0000	0.0000
Phykpl	ENSMUSG00000020359	5-phosphohydroxy-L-lysine phospholyase	-1.871	0.0000	0.0000
Pi16	ENSMUSG00000024011	peptidase inhibitor 16	-1.761	0.0015	0.0045
Pias3	ENSMUSG00000028101	protein inhibitor of activated STAT 3	-2.026	0.0000	0.0000
Pias4	ENSMUSG00000004934	protein inhibitor of activated STAT 4	-1.668	0.0003	0.0011
Pidd1	ENSMUSG00000025507	p53 induced death domain protein 1	-2.001	0.0067	0.0169
Pierce2	ENSMUSG00000086158	piercer of microtubule wall 2	-2.215	0.0000	0.0000
Pigf	ENSMUSG00000024145	phosphatidylinositol glycan anchor biosynthesis, class F	-2.007	0.0001	0.0002
Pigl	ENSMUSG00000014245	phosphatidylinositol glycan anchor biosynthesis, class L	-1.584	0.0015	0.0045
Pigo	ENSMUSG00000028454	phosphatidylinositol glycan anchor biosynthesis, class O	-2.338	0.0000	0.0000
Pigp	ENSMUSG00000022940	phosphatidylinositol glycan anchor biosynthesis, class P	-1.774	0.0000	0.0000
Pigq	ENSMUSG00000025728	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.787	0.0000	0.0000
Pigs	ENSMUSG00000041958	phosphatidylinositol glycan anchor biosynthesis, class S	-1.844	0.0000	0.0000
Pigt	ENSMUSG00000017721	phosphatidylinositol glycan anchor biosynthesis, class T	-2.397	0.0000	0.0000
Pigv	ENSMUSG00000043257	phosphatidylinositol glycan anchor biosynthesis, class V	-2.035	0.0000	0.0000
Pigz	ENSMUSG00000045625	phosphatidylinositol glycan anchor biosynthesis, class Z	-4.232	0.0000	0.0000
Pih1d1	ENSMUSG00000003423	PIH1 domain containing 1	-2.050	0.0000	0.0000
Pik3ap1	ENSMUSG00000025017	phosphoinositide-3-kinase adaptor protein 1	-1.751	0.0107	0.0255
Pik3r6	ENSMUSG00000046207	phosphoinositide-3-kinase regulatory subunit 5	-1.721	0.0001	0.0003
Pim2	ENSMUSG00000031155	proviral integration site 2	-1.650	0.0142	0.0326
Pin1	ENSMUSG00000032171	peptidyl-prolyl cis/trans isomerase, NIMA-interacting 1	-2.095	0.0000	0.0000
Pip4p2	ENSMUSG00000028221	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 2	-1.692	0.0000	0.0000
Pip5k1b	ENSMUSG00000024867	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-1.776	0.0000	0.0000
Pira12	ENSMUSG00000074417	paired-Ig-like receptor A12	-2.560	0.0105	0.0252
Pisd-ps1	ENSMUSG00000082286	phosphatidylserine decarboxylase, pseudogene 1	-2.344	0.0292	0.0610
Pisd-ps2	ENSMUSG00000023795	phosphatidylserine decarboxylase, pseudogene 2	-2.790	0.0365	0.0739
Pitpnm1	ENSMUSG00000024851	phosphatidylinositol transfer protein, membrane-associated 1	-2.458	0.0000	0.0000
Pitpnm2	ENSMUSG00000029406	phosphatidylinositol transfer protein, membrane-associated 2	-1.735	0.0000	0.0000
Pkd1	ENSMUSG00000032855	polycystin 1, transient receptor potential channel interacting	-1.810	0.0000	0.0000
Pkmyt1	ENSMUSG00000023908	protein kinase, membrane associated tyrosine/threonine 1	-2.569	0.0095	0.0229
Pla1a	ENSMUSG00000002847	phospholipase A1 member A	-1.590	0.0004	0.0012

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Pla2g15	ENSMUSG00000031903	phospholipase A2, group XV	-1.602	0.0000	0.0000
Pla2g4e	ENSMUSG00000050211	phospholipase A2, group IVE	-1.727	0.0195	0.0430
Pla2g6	ENSMUSG00000042632	phospholipase A2, group VI	-1.881	0.0000	0.0000
Plb1	ENSMUSG00000029134	phospholipase B1	-2.118	0.0018	0.0053
Plcd1	ENSMUSG00000010660	phospholipase C, delta 1	-2.170	0.0000	0.0000
Plcd3	ENSMUSG00000020937	phospholipase C, delta 3	-1.816	0.0000	0.0002
Plch2	ENSMUSG00000029055	phospholipase C, eta 2	-4.078	0.0049	0.0129
Pld3	ENSMUSG00000003363	phospholipase D family, member 3	-3.514	0.0000	0.0000
Pld4	ENSMUSG00000052160	phospholipase D family, member 4	-2.962	0.0000	0.0000
Plekha7	ENSMUSG00000045659	pleckstrin homology domain containing, family A member 7	-1.511	0.0247	0.0528
Plekhf1	ENSMUSG00000074170	pleckstrin homology domain containing, family F (with FYVE domain) member 1	-1.844	0.0000	0.0000
Plekhg2	ENSMUSG00000037552	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	-2.099	0.0000	0.0000
Plekhm1	ENSMUSG00000034247	pleckstrin homology domain containing, family M (with RUN domain) member 1	-2.007	0.0000	0.0000
Plekhn1	ENSMUSG00000078485	pleckstrin homology domain containing, family N member 1	-1.792	0.0310	0.0642
Plekho1	ENSMUSG00000015745	pleckstrin homology domain containing, family O member 1	-2.602	0.0000	0.0000
Plet1	ENSMUSG00000032068	placenta expressed transcript 1	-2.946	0.0072	0.0179
Plin4	ENSMUSG00000002831	perilipin 4	-1.977	0.0020	0.0058
Plk5	ENSMUSG00000035486	polo like kinase 5	-4.296	0.0000	0.0000
Pln	ENSMUSG00000038583	phospholamban	-1.679	0.0000	0.0000
Plod1	ENSMUSG00000019055	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-1.572	0.0000	0.0000
Plp2	ENSMUSG00000031146	proteolipid protein 2	-2.962	0.0000	0.0000
Plpbp	ENSMUSG00000031485	pyridoxal phosphate binding protein	-2.415	0.0000	0.0000
Plpp1	ENSMUSG00000021759	phospholipid phosphatase 1	-1.742	0.0000	0.0000
Plpp5	ENSMUSG00000031570	phospholipid phosphatase 5	-1.586	0.0003	0.0010
Plpp7	ENSMUSG00000051373	phospholipid phosphatase 7 (inactive)	-2.204	0.0000	0.0000
Plscr2	ENSMUSG00000032372	phospholipid scramblase 2	-1.707	0.0000	0.0000
Pltp	ENSMUSG00000017754	phospholipid transfer protein	-2.821	0.0000	0.0000
Plxdc1	ENSMUSG00000017417	plexin domain containing 1	-1.767	0.0000	0.0000
Plxna3	ENSMUSG00000031398	plexin A3	-2.496	0.0016	0.0048
Plxnb1	ENSMUSG00000053646	plexin B1	-1.675	0.0000	0.0000
Plxnb2	ENSMUSG00000036606	plexin B2	-2.173	0.0000	0.0000

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Plxnb3	ENSMUSG00000031385	plexin B3	-2.621	0.0000	0.0000
Plxnd1	ENSMUSG00000030123	plexin D1	-1.888	0.0000	0.0000
Pmf1	ENSMUSG00000028066	polyamine-modulated factor 1	-2.402	0.0000	0.0000
Pml	ENSMUSG00000036986	promyelocytic leukemia	-2.128	0.0000	0.0000
Pmp22	ENSMUSG00000018217	peripheral myelin protein 22	-1.551	0.0001	0.0004
Pnck	ENSMUSG00000002012	pregnancy upregulated non-ubiquitously expressed CaM kinase	-2.170	0.0000	0.0000
Pnkd	ENSMUSG00000026179	paroxysmal nonkinesiogenic dyskinesia	-1.916	0.0000	0.0000
Pnkp	ENSMUSG00000002963	polynucleotide kinase 3'- phosphatase	-1.615	0.0000	0.0000
Pno1	ENSMUSG00000020116	partner of NOB1 homolog	-1.506	0.0000	0.0000
Pnp	ENSMUSG00000115338	purine-nucleoside phosphorylase	-2.409	0.0000	0.0000
Pnpla3	ENSMUSG00000041653	patatin-like phospholipase domain containing 3	-4.418	0.0003	0.0010
Pnpo	ENSMUSG00000018659	pyridoxine 5'-phosphate oxidase	-2.937	0.0000	0.0000
Poc1a	ENSMUSG00000023345	POC1 centriolar protein A	-2.093	0.0000	0.0001
Pola2	ENSMUSG00000024833	polymerase (DNA directed), alpha 2	-2.925	0.0000	0.0000
Pold1	ENSMUSG00000038644	polymerase (DNA directed), delta 1, catalytic subunit	-2.192	0.0000	0.0000
Pold2	ENSMUSG00000020471	polymerase (DNA directed), delta 2, regulatory subunit	-2.396	0.0000	0.0000
Pold4	ENSMUSG00000024854	polymerase (DNA-directed), delta 4	-4.686	0.0000	0.0000
Pole	ENSMUSG00000007080	polymerase (DNA directed), epsilon	-1.690	0.0084	0.0205
Pole2	ENSMUSG00000020974	polymerase (DNA directed), epsilon 2 (p59 subunit)	-1.771	0.0318	0.0656
Polg2	ENSMUSG00000020718	polymerase (DNA directed), gamma 2, accessory subunit	-1.875	0.0000	0.0001
Poll	ENSMUSG00000025218	polymerase (DNA directed), lambda	-1.984	0.0000	0.0000
Polm	ENSMUSG00000020474	polymerase (DNA directed), mu	-2.159	0.0000	0.0000
Poln	ENSMUSG00000045102	DNA polymerase N	-3.178	0.0000	0.0000
Polr1b	ENSMUSG00000027395	polymerase (RNA) I polypeptide B	-1.944	0.0000	0.0000
Polr1d	ENSMUSG00000029642	polymerase (RNA) I polypeptide D	-2.094	0.0000	0.0000
Polr2c	ENSMUSG00000031783	polymerase (RNA) II (DNA directed) polypeptide C	-2.849	0.0000	0.0000
Polr2d	ENSMUSG00000024258	polymerase (RNA) II (DNA directed) polypeptide D	-2.061	0.0000	0.0000
Polr2e	ENSMUSG00000004667	polymerase (RNA) II (DNA directed) polypeptide E	-2.515	0.0000	0.0000
Polr2i	ENSMUSG00000019738	polymerase (RNA) II (DNA directed) polypeptide I	-2.195	0.0000	0.0000
Polr2l	ENSMUSG00000038489	polymerase (RNA) II (DNA directed) polypeptide L	-2.354	0.0000	0.0000
Polrmt	ENSMUSG00000020329	polymerase (RNA) mitochondrial (DNA directed)	-1.766	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pop4	ENSMUSG00000030423	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	-2.712	0.0000	0.0000
Pop7	ENSMUSG00000029715	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	-2.823	0.0000	0.0000
Ppan	ENSMUSG00000004100	peter pan homolog	-1.755	0.0000	0.0000
Ppara	ENSMUSG00000022383	peroxisome proliferator activated receptor alpha	-1.545	0.0000	0.0000
Ppard	ENSMUSG00000002250	peroxisome proliferator activator receptor delta	-1.700	0.0000	0.0000
Ppdpf	ENSMUSG00000016344	pancreatic progenitor cell differentiation and proliferation factor	-1.559	0.0000	0.0000
Ppia	ENSMUSG00000071866	peptidylprolyl isomerase A	-1.531	0.0000	0.0000
Ppif	ENSMUSG00000021868	peptidylprolyl isomerase F (cyclophilin F)	-2.011	0.0000	0.0000
Ppil2	ENSMUSG00000022771	peptidylprolyl isomerase (cyclophilin)-like 2	-2.000	0.0000	0.0000
Ppm1j	ENSMUSG00000002228	protein phosphatase 1J	-1.729	0.0000	0.0000
Ppp1r3g	ENSMUSG00000050423	protein phosphatase 1, regulatory subunit 3G	-5.245	0.0230	0.0495
Ppp2r1a	ENSMUSG00000007564	protein phosphatase 2, regulatory subunit A, alpha	-1.523	0.0000	0.0000
Ppp2r3d	ENSMUSG00000093803	protein phosphatase 2 (formerly 2A), regulatory subunit B", delta	-2.044	0.0000	0.0000
Ppp5c	ENSMUSG00000003099	protein phosphatase 5, catalytic subunit	-1.686	0.0000	0.0000
Pqlc3	ENSMUSG00000045679	PQ loop repeat containing	-2.573	0.0014	0.0043
Pradc1	ENSMUSG00000030008	protease-associated domain containing 1	-1.740	0.0000	0.0000
Praf2	ENSMUSG00000031149	PRA1 domain family 2	-4.451	0.0000	0.0000
Prdm5	ENSMUSG00000029913	PR domain containing 5	-1.566	0.0018	0.0052
Prdx2	ENSMUSG00000005161	peroxiredoxin 2	-2.680	0.0000	0.0000
Prdx2-ps1	ENSMUSG00000082431	peroxiredoxin 2, pseudogene 1	-11.154	0.0000	0.0000
Prdx4	ENSMUSG00000025289	peroxiredoxin 4	-2.032	0.0000	0.0000
Prelid1	ENSMUSG00000021486	PRELI domain containing 1	-1.753	0.0000	0.0000
Prelp	ENSMUSG00000041577	proline arginine-rich end leucine-rich repeat	-1.907	0.0007	0.0022
Prickle3	ENSMUSG00000031145	prickle planar cell polarity protein 3	-1.921	0.0002	0.0008
Prim2	ENSMUSG00000026134	DNA primase, p58 subunit	-1.551	0.0038	0.0101
Prima1	ENSMUSG00000041669	proline rich membrane anchor 1	-11.002	0.0086	0.0210
Prkag3	ENSMUSG00000006542	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	-1.501	0.0411	0.0818
Prkar1b	ENSMUSG00000025855	protein kinase, cAMP dependent regulatory, type I beta	-1.672	0.0003	0.0009
Prkcz	ENSMUSG00000029053	protein kinase C, zeta	-3.208	0.0000	0.0000
Prkd2	ENSMUSG00000041187	protein kinase D2	-1.932	0.0000	0.0000
Prkra	ENSMUSG00000002731	protein kinase, interferon inducible double stranded RNA dependent activator	-2.040	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Prlr	ENSMUSG00000005268	prolactin receptor	-1.601	0.0055	0.0141
Prmt2	ENSMUSG00000020230	protein arginine N-methyltransferase 2	-1.588	0.0024	0.0067
Prnp	ENSMUSG00000079037	prion protein	-1.939	0.0000	0.0000
Proscos	ENSMUSG00000091154	proline synthetase co-transcribed, opposite strand	-2.138	0.0000	0.0001
Proser3	ENSMUSG00000036864	proline and serine rich 3	-2.230	0.0001	0.0004
Prpf8	ENSMUSG00000020850	pre-mRNA processing factor 8	-1.567	0.0000	0.0000
Prpsap1	ENSMUSG00000015869	phosphoribosyl pyrophosphate synthetase-associated protein 1	-2.431	0.0000	0.0000
Prpsap2	ENSMUSG00000020528	phosphoribosyl pyrophosphate synthetase-associated protein 2	-1.501	0.0132	0.0306
Prrg2	ENSMUSG00000007837	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	-2.089	0.0000	0.0000
Prss36	ENSMUSG00000070371	protease, serine 36	-2.455	0.0000	0.0000
Psenen	ENSMUSG00000036835	presenilin enhancer gamma secretase subunit	-2.743	0.0000	0.0000
Psenen-ps	ENSMUSG00000056412	presenilin enhancer gamma secretase subunit, pseudogene	-3.771	0.0228	0.0493
Psmb10	ENSMUSG00000031897	proteasome (prosome, macropain) subunit, beta type 10	-1.816	0.0000	0.0000
Psmb3	ENSMUSG00000069744	proteasome (prosome, macropain) subunit, beta type 3	-1.790	0.0000	0.0000
Psmd13	ENSMUSG00000025487	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	-1.530	0.0000	0.0000
Psmd5	ENSMUSG00000026869	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-1.565	0.0000	0.0000
Psmd8	ENSMUSG00000030591	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	-1.623	0.0000	0.0000
Psmf1	ENSMUSG00000032869	proteasome (prosome, macropain) inhibitor subunit 1	-2.152	0.0000	0.0000
Psmg2	ENSMUSG00000024537	proteasome (prosome, macropain) assembly chaperone 2	-2.099	0.0000	0.0000
Psmg3	ENSMUSG00000029551	proteasome (prosome, macropain) assembly chaperone 3	-2.645	0.0000	0.0000
Psmg4	ENSMUSG00000071451	proteasome (prosome, macropain) assembly chaperone 4	-1.676	0.0000	0.0001
Ptbp1	ENSMUSG00000006498	polypyrimidine tract binding protein 1	-2.114	0.0000	0.0000
Ptcd1	ENSMUSG00000029624	pentatricopeptide repeat domain 1	-1.864	0.0000	0.0002
Ptch2	ENSMUSG00000028681	patched 2	-3.857	0.0000	0.0000
Ptgds	ENSMUSG00000015090	prostaglandin D2 synthase (brain)	-4.062	0.0000	0.0000
Ptger4	ENSMUSG00000039942	prostaglandin E receptor 4 (subtype EP4)	-1.757	0.0002	0.0008
Ptgis	ENSMUSG00000017969	prostaglandin I2 (prostacyclin) synthase	-1.579	0.0121	0.0284
Ptpn18	ENSMUSG00000026126	protein tyrosine phosphatase, non-receptor type 18	-1.643	0.0362	0.0733
Ptpn22	ENSMUSG00000027843	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	-2.009	0.0303	0.0630
Ptpn23	ENSMUSG00000036057	protein tyrosine phosphatase, non-receptor type 23	-1.597	0.0000	0.0000
Ptprf	ENSMUSG00000033295	protein tyrosine phosphatase, receptor type, F	-1.510	0.0090	0.0218

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Ptprn	ENSMUSG00000026204	protein tyrosine phosphatase, receptor type, N	-2.038	0.0006	0.0020
Ptprn2	ENSMUSG00000056553	protein tyrosine phosphatase, receptor type, N polypeptide 2	-1.787	0.0142	0.0325
Ptprv	ENSMUSG00000097993	protein tyrosine phosphatase, receptor type, V	-3.838	0.0029	0.0081
Ptrh1	ENSMUSG00000053746	peptidyl-tRNA hydrolase 1 homolog	-2.773	0.0000	0.0000
Ptrhd1	ENSMUSG00000096199	peptidyl-tRNA hydrolase domain containing 1	-1.761	0.0000	0.0000
Pttg1	ENSMUSG00000020415	pituitary tumor-transforming gene 1	-1.581	0.0017	0.0050
Pusl1	ENSMUSG00000051557	pseudouridylate synthase-like 1	-1.754	0.0001	0.0002
Pvr	ENSMUSG00000040511	poliovirus receptor	-1.762	0.0000	0.0000
Pxdn	ENSMUSG00000020674	peroxidasin	-1.808	0.0000	0.0000
Pxmp4	ENSMUSG00000000876	peroxisomal membrane protein 4	-1.712	0.0000	0.0000
Pycard	ENSMUSG00000030793	PYD and CARD domain containing	-2.225	0.0000	0.0001
Pycr1	ENSMUSG00000025140	pyrroline-5-carboxylate reductase 1	-2.275	0.0005	0.0015
Pycr2	ENSMUSG00000026520	pyrroline-5-carboxylate reductase family, member 2	-1.665	0.0001	0.0005
Pycrl	ENSMUSG00000022571	pyrroline-5-carboxylate reductase-like	-2.254	0.0000	0.0000
Pyroxd2	ENSMUSG00000060224	pyridine nucleotide-disulphide oxidoreductase domain 2	-2.789	0.0000	0.0000
Pyurf	ENSMUSG00000043162	Pigy upstream reading frame	-1.587	0.0000	0.0000
Pzp	ENSMUSG00000030359	PZP, alpha-2-macroglobulin like	-2.522	0.0083	0.0202
Qpct	ENSMUSG00000024084	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	-1.823	0.0001	0.0003
Rab11b-ps2	ENSMUSG00000095690	RAB11B, member RAS oncogene family, pseudogene 2	-2.884	0.0000	0.0000
Rab1b	ENSMUSG00000024870	RAB1B, member RAS oncogene family	-1.762	0.0000	0.0000
Rab20	ENSMUSG00000031504	RAB20, member RAS oncogene family	-1.862	0.0000	0.0000
Rab29	ENSMUSG00000026433	RAB29, member RAS oncogene family	-1.901	0.0000	0.0000
Rab33a	ENSMUSG00000031104	RAB33A, member RAS oncogene family	-11.750	0.0113	0.0268
Rab34	ENSMUSG00000002059	RAB34, member RAS oncogene family	-1.877	0.0000	0.0000
Rab36	ENSMUSG00000020175	RAB36, member RAS oncogene family	-4.149	0.0000	0.0000
Rab37	ENSMUSG00000020732	RAB37, member RAS oncogene family	-1.809	0.0106	0.0253
Rab3a	ENSMUSG00000031840	RAB3A, member RAS oncogene family	-2.054	0.0000	0.0000
Rab3d	ENSMUSG00000019066	RAB3D, member RAS oncogene family	-1.641	0.0000	0.0000
Rab3il1	ENSMUSG00000024663	RAB3A interacting protein (rabin3)-like 1	-1.790	0.0041	0.0109
Rab42	ENSMUSG00000089687	RAB42, member RAS oncogene family	-3.867	0.0001	0.0003
Rabac1	ENSMUSG00000003380	Rab acceptor 1 (prenylated)	-2.384	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rabep2	ENSMUSG00000030727	rabaptin, RAB GTPase binding effector protein 2	-1.654	0.0001	0.0003
Rabggta	ENSMUSG00000040472	Rab geranylgeranyl transferase, a subunit	-2.370	0.0000	0.0000
Rabif	ENSMUSG00000042229	RAB interacting factor	-1.666	0.0118	0.0277
Rabl2	ENSMUSG00000022621	RAB, member RAS oncogene family-like 2	-3.894	0.0000	0.0000
Rac2	ENSMUSG00000033220	Rac family small GTPase 2	-2.892	0.0000	0.0001
Rack1	ENSMUSG00000020372	receptor for activated C kinase 1	-3.712	0.0000	0.0000
Rad1	ENSMUSG00000022248	RAD1 checkpoint DNA exonuclease	-1.831	0.0002	0.0007
Rad9a	ENSMUSG00000024824	RAD9 checkpoint clamp component A	-1.840	0.0000	0.0000
Radil	ENSMUSG00000029576	Ras association and DIL domains	-1.884	0.0003	0.0011
Ralgds	ENSMUSG00000026821	ral guanine nucleotide dissociation stimulator	-1.588	0.0000	0.0000
Ramp1	ENSMUSG00000034353	receptor (calcitonin) activity modifying protein 1	-1.508	0.0105	0.0251
Ramp3	ENSMUSG00000041046	receptor (calcitonin) activity modifying protein 3	-1.939	0.0000	0.0000
Ranbp17	ENSMUSG00000040594	RAN binding protein 17	-3.374	0.0004	0.0014
Rap1gap	ENSMUSG00000041351	Rap1 GTPase-activating protein	-1.792	0.0001	0.0004
Rap1gapos	ENSMUSG00000087476	RAP1 GTPase activating protein, opposite strand	-3.243	0.0005	0.0017
Rapsn	ENSMUSG00000002104	receptor-associated protein of the synapse	-1.714	0.0001	0.0003
Rarg	ENSMUSG00000001288	retinoic acid receptor, gamma	-1.806	0.0000	0.0000
Rarres2	ENSMUSG00000009281	retinoic acid receptor responder (tazarotene induced) 2	-2.922	0.0000	0.0000
Rasa4	ENSMUSG00000004952	RAS p21 protein activator 4	-1.676	0.0002	0.0007
Rasgef1c	ENSMUSG00000020374	RasGEF domain family, member 1C	-2.281	0.0292	0.0610
Rasl11a	ENSMUSG00000029641	RAS-like, family 11, member A	-1.557	0.0139	0.0320
Rasl12	ENSMUSG00000041696	RAS-like, family 12	-2.276	0.0000	0.0000
Rassf4	ENSMUSG00000042129	Ras association (RalGDS/AF-6) domain family member 4	-1.611	0.0141	0.0324
Rassf7	ENSMUSG00000038618	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	-1.854	0.0140	0.0322
Raver2	ENSMUSG00000035275	ribonucleoprotein, PTB-binding 2	-1.688	0.0046	0.0121
Rbck1	ENSMUSG00000027466	RanBP-type and C3HC4-type zinc finger containing 1	-2.834	0.0000	0.0000
Rbis	ENSMUSG00000078784	ribosomal biogenesis factor	-1.529	0.0003	0.0009
Rbm22	ENSMUSG00000024604	RNA binding motif protein 22	-1.516	0.0000	0.0000
Rbx1-ps	ENSMUSG00000049832	ring-box 1, pseudogene	-4.941	0.0000	0.0001
Rce1	ENSMUSG00000024889	Ras converting CAAX endopeptidase 1	-2.638	0.0000	0.0000
Rcl1	ENSMUSG00000024785	RNA terminal phosphate cyclase-like 1	-2.012	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rdh12	ENSMUSG00000021123	retinol dehydrogenase 12	-2.835	0.0291	0.0609
Rdh13	ENSMUSG00000008435	retinol dehydrogenase 13 (all-trans and 9-cis)	-1.505	0.0000	0.0001
Rdh5	ENSMUSG00000025350	retinol dehydrogenase 5	-1.891	0.0041	0.0107
Rdm1	ENSMUSG00000010362	RAD52 motif 1	-1.851	0.0000	0.0000
Reep4	ENSMUSG00000033589	receptor accessory protein 4	-1.603	0.0166	0.0374
Reep6	ENSMUSG00000035504	receptor accessory protein 6	-2.458	0.0000	0.0000
Relb	ENSMUSG00000002983	avian reticuloendotheliosis viral (v-rel) oncogene related B	-1.620	0.0001	0.0003
Reln	ENSMUSG00000042453	reelin	-2.376	0.0000	0.0000
Relt	ENSMUSG00000008318	RELT tumor necrosis factor receptor	-1.530	0.0135	0.0311
Rem1	ENSMUSG00000000359	rad and gem related GTP binding protein 1	-1.703	0.0008	0.0025
Reps2	ENSMUSG00000040855	RALBP1 associated Eps domain containing protein 2	-1.681	0.0059	0.0149
Rer1	ENSMUSG00000029048	retention in endoplasmic reticulum sorting receptor 1	-1.782	0.0000	0.0000
Retnla	ENSMUSG00000061100	resistin like alpha	-2.577	0.0001	0.0004
Rfc5	ENSMUSG00000029363	replication factor C (activator 1) 5	-3.031	0.0000	0.0000
Rfng	ENSMUSG00000025158	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.598	0.0000	0.0000
Rfx1	ENSMUSG00000031706	regulatory factor X, 1 (influences HLA class II expression)	-1.581	0.0042	0.0111
Rgcc	ENSMUSG00000022018	regulator of cell cycle	-3.516	0.0000	0.0000
Rgl3	ENSMUSG00000040146	ral guanine nucleotide dissociation stimulator-like 3	-1.793	0.0000	0.0000
Rgs11	ENSMUSG00000024186	regulator of G-protein signaling 11	-2.899	0.0292	0.0610
Rgs12	ENSMUSG00000029101	regulator of G-protein signaling 12	-1.766	0.0000	0.0000
Rgs14	ENSMUSG00000052087	regulator of G-protein signaling 14	-3.122	0.0074	0.0185
Rgs19	ENSMUSG00000002458	regulator of G-protein signaling 19	-2.403	0.0000	0.0000
Rgs3	ENSMUSG00000059810	regulator of G-protein signaling 3	-1.673	0.0000	0.0000
Rhbdd1	ENSMUSG00000026142	rhomboid domain containing 1	-1.601	0.0000	0.0000
Rhbdd2	ENSMUSG00000039917	rhomboid domain containing 2	-1.969	0.0000	0.0000
Rhbdd3	ENSMUSG00000034175	rhomboid domain containing 3	-2.248	0.0000	0.0000
Rhbdf2	ENSMUSG00000020806	rhomboid 5 homolog 2	-2.347	0.0000	0.0000
Rhd	ENSMUSG00000028825	Rh blood group, D antigen	-2.536	0.0000	0.0000
Rhod	ENSMUSG00000041845	ras homolog family member D	-2.966	0.0000	0.0000
Rhof	ENSMUSG00000029449	ras homolog family member F (in filopodia)	-2.556	0.0002	0.0007
Rhog	ENSMUSG00000073982	ras homolog family member G	-1.787	0.0000	0.0000

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Ric8a	ENSMUSG00000025485	RIC8 guanine nucleotide exchange factor A	-1.955	0.0000	0.0000
Riiad1	ENSMUSG00000028139	regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1	-3.061	0.0345	0.0704
Rilp	ENSMUSG00000038195	Rab interacting lysosomal protein	-1.978	0.0000	0.0000
Rimkla	ENSMUSG00000048899	ribosomal modification protein rimK-like family member A	-2.027	0.0088	0.0215
Rimoc1	ENSMUSG00000041935	RAB7A interacting MON1-CCZ1 complex subunit 1	-1.559	0.0000	0.0001
Rin1	ENSMUSG00000024883	Ras and Rab interactor 1	-1.824	0.0077	0.0191
Rint1	ENSMUSG00000028999	RAD50 interactor 1	-1.519	0.0000	0.0000
Ripk3	ENSMUSG00000022221	receptor-interacting serine-threonine kinase 3	-1.700	0.0035	0.0094
Ripor2	ENSMUSG00000036006	RHO family interacting cell polarization regulator 2	-1.659	0.0086	0.0209
Ripor3	ENSMUSG00000074577	RIPOR family member 3	-2.165	0.0427	0.0845
Rita1	ENSMUSG00000029600	RBPJ interacting and tubulin associated 1	-1.978	0.0000	0.0000
Rmnd5b	ENSMUSG00000001054	required for meiotic nuclear division 5 homolog B	-2.987	0.0000	0.0000
Rnase1	ENSMUSG00000035896	ribonuclease, RNase A family, 1 (pancreatic)	-5.670	0.0001	0.0003
Rnase4	ENSMUSG00000021876	ribonuclease, RNase A family 4	-1.885	0.0000	0.0001
Rnd2	ENSMUSG00000001313	Rho family GTPase 2	-1.554	0.0010	0.0032
Rnf113a1	ENSMUSG00000036537	ring finger protein 113A1	-2.968	0.0007	0.0021
Rnf122	ENSMUSG00000039328	ring finger protein 122	-2.014	0.0000	0.0000
Rnf123	ENSMUSG00000041528	ring finger protein 123	-1.563	0.0000	0.0000
Rnf13	ENSMUSG00000036503	ring finger protein 13	-1.604	0.0000	0.0000
Rnf135	ENSMUSG00000020707	ring finger protein 135	-1.640	0.0032	0.0086
Rnf181	ENSMUSG00000055850	ring finger protein 181	-2.162	0.0000	0.0000
Rnf225	ENSMUSG00000033967	ring finger protein 225	-11.142	0.0031	0.0086
Rnf25	ENSMUSG00000026171	ring finger protein 25	-2.785	0.0000	0.0000
Rnf31	ENSMUSG00000047098	ring finger protein 31	-1.681	0.0000	0.0000
Rnf41	ENSMUSG00000025373	ring finger protein 41	-1.745	0.0000	0.0000
Rnh1	ENSMUSG00000038650	ribonuclease/angiogenin inhibitor 1	-1.705	0.0000	0.0000
Rnls	ENSMUSG00000071573	renalase, FAD-dependent amine oxidase	-1.779	0.0000	0.0000
Rnpep	ENSMUSG00000041926	arginyl aminopeptidase (aminopeptidase B)	-1.866	0.0000	0.0000
Rnps1-ps	ENSMUSG00000096403	RNA binding protein with serine rich domain 1, pseudogene	-1.515	0.0001	0.0002
Robo4	ENSMUSG00000032125	roundabout guidance receptor 4	-1.868	0.0000	0.0000
Rogdi	ENSMUSG00000022540	rogdi homolog	-2.285	0.0000	0.0000

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DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Romo1	ENSMUSG00000067847	reactive oxygen species modulator 1	-1.980	0.0000	0.0000
Rpl10	ENSMUSG00000008682	ribosomal protein L10	-2.887	0.0000	0.0000
Rpl10a	ENSMUSG00000037805	ribosomal protein L10A	-2.221	0.0000	0.0000
Rpl10a-ps1	ENSMUSG00000084416	ribosomal protein L10A, pseudogene 1	-2.292	0.0009	0.0028
Rpl12	ENSMUSG00000038900	ribosomal protein L12	-2.581	0.0000	0.0000
Rpl13	ENSMUSG00000000740	ribosomal protein L13	-4.710	0.0000	0.0000
Rpl19-ps11	ENSMUSG00000081094	ribosomal protein L19, pseudogene 11	-2.083	0.0004	0.0015
Rpl21-ps8	ENSMUSG00000061684	ribosomal protein L21, pseudogene 8	-3.312	0.0152	0.0345
Rpl22l1	ENSMUSG00000039221	ribosomal protein L22 like 1	-1.982	0.0000	0.0000
Rpl23a-ps3	ENSMUSG00000078126	ribosomal protein L23A, pseudogene 3	-2.117	0.0330	0.0678
Rpl26	ENSMUSG00000060938	ribosomal protein L26	-4.452	0.0000	0.0000
Rpl27	ENSMUSG00000063316	ribosomal protein L27	-2.849	0.0000	0.0000
Rpl28-ps1	ENSMUSG00000058603	ribosomal protein L28, pseudogene 1	-5.340	0.0114	0.0269
Rpl29	ENSMUSG00000048758	ribosomal protein L29	-2.580	0.0000	0.0000
Rpl3	ENSMUSG00000060036	ribosomal protein L3	-1.966	0.0000	0.0000
Rpl31-ps8	ENSMUSG00000067870	ribosomal protein L31, pseudogene 8	-2.265	0.0054	0.0139
Rpl32	ENSMUSG00000057841	ribosomal protein L32	-3.119	0.0000	0.0000
Rpl32l	ENSMUSG00000111356	ribosomal protein L32-like	-18.469	0.0226	0.0489
Rpl34	ENSMUSG00000062006	ribosomal protein L34	-3.085	0.0000	0.0000
Rpl34-ps1	ENSMUSG00000068396	ribosomal protein L34, pseudogene 1	-4.941	0.0000	0.0000
Rpl34-ps2	ENSMUSG00000061669	ribosomal protein L34, pseudogene 2	-21.281	0.0011	0.0033
Rpl35a	ENSMUSG00000060636	ribosomal protein L35A	-3.280	0.0000	0.0000
Rpl36	ENSMUSG00000057863	ribosomal protein L36	-4.879	0.0000	0.0000
Rpl36a	ENSMUSG00000079435	ribosomal protein L36A	-2.350	0.0000	0.0000
Rpl36-ps12	ENSMUSG00000091845	ribosomal protein L36, pseudogene 12	-5.851	0.0065	0.0163
Rpl37	ENSMUSG00000041841	ribosomal protein L37	-3.486	0.0000	0.0000
Rpl37a	ENSMUSG00000046330	ribosomal protein L37a	-2.715	0.0000	0.0000
Rpl38	ENSMUSG00000057322	ribosomal protein L38	-2.567	0.0000	0.0000
Rpl38-ps2	ENSMUSG00000080921	ribosomal protein L38, pseudogene 2	-10.208	0.0000	0.0000
Rpl39l	ENSMUSG00000039209	ribosomal protein L39-like	-9.128	0.0157	0.0357
Rpl3-ps1	ENSMUSG00000084349	ribosomal protein L3, pseudogene 1	-2.343	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpl6	ENSMUSG00000029614	ribosomal protein L6	-1.504	0.0000	0.0000
Rpl6l	ENSMUSG00000091086	ribosomal protein L6-like	-3.783	0.0047	0.0122
Rpl7	ENSMUSG00000043716	ribosomal protein L7	-1.557	0.0000	0.0000
Rpl8	ENSMUSG00000003970	ribosomal protein L8	-2.366	0.0000	0.0000
Rplp0	ENSMUSG00000067274	ribosomal protein, large, P0	-2.960	0.0000	0.0000
Rplp1	ENSMUSG00000007892	ribosomal protein, large, P1	-4.855	0.0000	0.0000
Rplp2	ENSMUSG00000025508	ribosomal protein, large P2	-1.584	0.0000	0.0000
Rpp21	ENSMUSG00000024446	ribonuclease P 21 subunit	-4.658	0.0000	0.0000
Rpp25l	ENSMUSG00000036114	ribonuclease P/MRP 25 subunit-like	-3.126	0.0000	0.0000
Rpp40	ENSMUSG00000021418	ribonuclease P 40 subunit	-2.410	0.0000	0.0000
Rprd1b	ENSMUSG00000027651	regulation of nuclear pre-mRNA domain containing 1B	-1.612	0.0000	0.0000
Rps10-ps1	ENSMUSG00000060438	ribosomal protein S10, pseudogene 1	-11.687	0.0000	0.0000
Rps10-ps2	ENSMUSG00000099764	ribosomal protein S10, pseudogene 2	-4.500	0.0018	0.0053
Rps11	ENSMUSG00000003429	ribosomal protein S11	-2.023	0.0000	0.0000
Rps12	ENSMUSG00000061983	ribosomal protein S12	-2.399	0.0000	0.0000
Rps13	ENSMUSG00000090862	ribosomal protein S13	-3.186	0.0000	0.0000
Rps13-ps2	ENSMUSG00000069972	ribosomal protein S13, pseudogene 2	-4.558	0.0000	0.0000
Rps15	ENSMUSG00000063457	ribosomal protein S15	-2.483	0.0000	0.0000
Rps15a	ENSMUSG00000008683	ribosomal protein S15A	-2.516	0.0000	0.0000
Rps15a-ps3	ENSMUSG00000084314	ribosomal protein S15A, pseudogene 3	-6.523	0.0061	0.0155
Rps15a-ps4	ENSMUSG00000083757	ribosomal protein S15A, pseudogene 4	-34.308	0.0001	0.0003
Rps15a-ps5	ENSMUSG00000067058	ribosomal protein S15A, pseudogene 5	-6.937	0.0333	0.0684
Rps15a-ps7	ENSMUSG00000081087	ribosomal protein S15A, pseudogene 7	-3.153	0.0010	0.0030
Rps15-ps2	ENSMUSG00000071419	ribosomal protein S15, pseudogene 2	-6.376	0.0005	0.0015
Rps18-ps3	ENSMUSG00000057657	ribosomal protein S18, pseudogene 3	-5.150	0.0129	0.0300
Rps18-ps5	ENSMUSG00000113061	ribosomal protein S18, pseudogene 5	-1.886	0.0000	0.0001
Rps18-ps6	ENSMUSG00000069117	ribosomal protein S18, pseudogene 6	-1.605	0.0000	0.0000
Rps19	ENSMUSG00000040952	ribosomal protein S19	-3.380	0.0000	0.0000
Rps19-ps3	ENSMUSG00000080059	ribosomal protein S19, pseudogene 3	-3.600	0.0003	0.0009
Rps19-ps6	ENSMUSG00000096942	ribosomal protein S19, pseudogene 6	-26.442	0.0002	0.0006
Rps21	ENSMUSG00000039001	ribosomal protein S21	-2.492	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rps24	ENSMUSG00000025290	ribosomal protein S24	-1.552	0.0000	0.0000
Rps24-ps3	ENSMUSG00000081049	ribosomal protein S24, pseudogene 3	-3.728	0.0000	0.0000
Rps25	ENSMUSG00000009927	ribosomal protein S25	-3.112	0.0000	0.0000
Rps26	ENSMUSG00000025362	ribosomal protein S26	-1.562	0.0000	0.0000
Rps27	ENSMUSG00000090733	ribosomal protein S27	-4.340	0.0000	0.0000
Rps27l	ENSMUSG00000036781	ribosomal protein S27-like	-2.236	0.0000	0.0000
Rps27rt	ENSMUSG00000050621	ribosomal protein S27, retrogene	-13.703	0.0000	0.0000
Rps28	ENSMUSG00000067288	ribosomal protein S28	-2.230	0.0000	0.0000
Rps29	ENSMUSG00000034892	ribosomal protein S29	-4.430	0.0000	0.0000
Rps4l	ENSMUSG00000063171	ribosomal protein S4-like	-2.484	0.0000	0.0000
Rps5	ENSMUSG00000012848	ribosomal protein S5	-2.343	0.0000	0.0000
Rps6kb2	ENSMUSG00000024830	ribosomal protein S6 kinase, polypeptide 2	-2.444	0.0000	0.0000
Rps6kl1	ENSMUSG00000019235	ribosomal protein S6 kinase-like 1	-2.410	0.0001	0.0004
Rps7-ps3	ENSMUSG00000095597	ribosomal protein S7, pseudogene 3	-11.492	0.0000	0.0000
Rpsa	ENSMUSG00000032518	ribosomal protein SA	-2.020	0.0000	0.0000
Rpsa-ps10	ENSMUSG00000047676	ribosomal protein SA, pseudogene 10	-4.015	0.0002	0.0007
Rpsa-ps11	ENSMUSG00000082978	ribosomal protein SA, pseudogene 11	-13.939	0.0008	0.0024
Rpsa-ps7	ENSMUSG00000117438	ribosomal protein SA, pseudogene 7	-3.702	0.0451	0.0885
Rpsa-ps9	ENSMUSG00000082895	ribosomal protein SA, pseudogene 9	-3.631	0.0302	0.0628
Rpusd1	ENSMUSG00000041199	RNA pseudouridylate synthase domain containing 1	-2.500	0.0000	0.0000
Rpusd3	ENSMUSG00000051169	RNA pseudouridylate synthase domain containing 3	-2.410	0.0000	0.0000
Rrnad1	ENSMUSG00000004896	ribosomal RNA adenine dimethylase domain containing 1	-1.543	0.0088	0.0214
Rrp36	ENSMUSG00000023971	ribosomal RNA processing 36	-2.268	0.0000	0.0000
Rsl1	ENSMUSG00000058900	regulator of sex limited protein 1	-1.954	0.0137	0.0315
Rsl1d1	ENSMUSG00000005846	ribosomal L1 domain containing 1	-1.561	0.0000	0.0000
Rspo1	ENSMUSG00000028871	R-spondin 1	-2.557	0.0451	0.0884
Rtel1	ENSMUSG00000038685	regulator of telomere elongation helicase 1	-2.036	0.0000	0.0000
Rtl8a	ENSMUSG00000067925	retrotransposon Gag like 8A	-4.605	0.0000	0.0000
Rtl8b	ENSMUSG00000067924	retrotransposon Gag like 8B	-6.103	0.0000	0.0000
Rtl9	ENSMUSG00000085584	retrotransposon Gag like 9	-2.618	0.0400	0.0800
Rtn1	ENSMUSG00000021087	reticulon 1	-1.655	0.0220	0.0478

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rtn2	ENSMUSG00000030401	reticulon 2 (Z-band associated protein)	-1.612	0.0000	0.0000
Rtraf	ENSMUSG00000021807	RNA transcription, translation and transport factor	-1.866	0.0000	0.0000
Rtraf-ps	ENSMUSG00000074479	RNA transcription, translation and transport factor, pseudogene	-2.147	0.0000	0.0000
Rubcn	ENSMUSG00000035629	RUN domain and cysteine-rich domain containing, Beclin 1-interacting protein	-1.549	0.0000	0.0000
Rxfp1	ENSMUSG00000034009	relaxin/insulin-like family peptide receptor 1	-4.718	0.0002	0.0005
S100a11	ENSMUSG00000027907	S100 calcium binding protein A11	-2.100	0.0001	0.0002
S100a13	ENSMUSG00000042312	S100 calcium binding protein A13	-2.366	0.0000	0.0000
S100a6	ENSMUSG00000001025	S100 calcium binding protein A6 (calcyclin)	-3.504	0.0000	0.0000
S100a8	ENSMUSG00000056054	S100 calcium binding protein A8 (calgranulin A)	-2.910	0.0183	0.0406
S100a9	ENSMUSG00000056071	S100 calcium binding protein A9 (calgranulin B)	-2.593	0.0401	0.0801
S1pr4	ENSMUSG00000044199	sphingosine-1-phosphate receptor 4	-3.337	0.0000	0.0001
Samd4b	ENSMUSG00000109336	sterile alpha motif domain containing 4B	-1.638	0.0000	0.0000
Sars2	ENSMUSG00000070699	seryl-aminoacyl-tRNA synthetase 2	-2.210	0.0000	0.0000
Sash3	ENSMUSG00000031101	SAM and SH3 domain containing 3	-2.526	0.0001	0.0003
Sbf1	ENSMUSG00000036529	SET binding factor 1	-1.590	0.0000	0.0000
Sbk1	ENSMUSG00000042978	SH3-binding kinase 1	-1.790	0.0000	0.0000
Sbno2	ENSMUSG00000035673	strawberry notch 2	-1.859	0.0000	0.0000
Scamp2	ENSMUSG00000040188	secretory carrier membrane protein 2	-1.906	0.0000	0.0000
Scamp3	ENSMUSG00000028049	secretory carrier membrane protein 3	-2.027	0.0000	0.0000
Scap	ENSMUSG00000032485	SREBF chaperone	-1.732	0.0000	0.0000
Scarb1	ENSMUSG00000037936	scavenger receptor class B, member 1	-1.656	0.0000	0.0000
Scarf1	ENSMUSG00000038188	scavenger receptor class F, member 1	-1.946	0.0000	0.0000
Scgb1c1	ENSMUSG00000038801	secretoglobin, family 1C, member 1	-6.686	0.0000	0.0000
Scgb3a1	ENSMUSG00000064057	secretoglobin, family 3A, member 1	-2.931	0.0312	0.0646
Scmh1	ENSMUSG00000000085	sex comb on midleg homolog 1	-1.515	0.0000	0.0000
Scn3b	ENSMUSG00000049281	sodium channel, voltage-gated, type III, beta	-1.622	0.0029	0.0080
Scn4a	ENSMUSG00000001027	sodium channel, voltage-gated, type IV, alpha	-1.743	0.0011	0.0032
Scnn1a	ENSMUSG00000030340	sodium channel, nonvoltage-gated 1 alpha	-3.539	0.0000	0.0001
Sco2	ENSMUSG00000091780	SCO2 cytochrome c oxidase assembly protein	-7.675	0.0000	0.0000
Scp2-ps2	ENSMUSG00000058492	sterol carrier protein 2, pseudogene 2	-1.562	0.0058	0.0149
Scrib	ENSMUSG00000022568	scribbled planar cell polarity	-1.566	0.0000	0.0001

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Scube2	ENSMUSG00000007279	signal peptide, CUB domain, EGF-like 2	-1.545	0.0050	0.0130
Sdc1	ENSMUSG00000020592	syndecan 1	-1.504	0.0061	0.0156
Sdhaf4	ENSMUSG00000026154	succinate dehydrogenase complex assembly factor 4	-1.693	0.0001	0.0002
Sdhb	ENSMUSG00000009863	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-2.078	0.0000	0.0000
Sec14l2	ENSMUSG00000003585	SEC14-like lipid binding 2	-2.502	0.0219	0.0476
Sec22a	ENSMUSG00000034473	SEC22 homolog A, vesicle trafficking protein	-1.710	0.0000	0.0000
Sec61a1	ENSMUSG00000030082	Sec61 alpha 1 subunit (S. cerevisiae)	-1.634	0.0000	0.0000
Sec61b	ENSMUSG00000053317	Sec61 beta subunit	-1.734	0.0000	0.0000
Sec61g	ENSMUSG00000078974	SEC61, gamma subunit	-2.849	0.0000	0.0000
Selenbp1	ENSMUSG00000068874	selenium binding protein 1	-2.149	0.0000	0.0000
Selenbp2	ENSMUSG00000068877	selenium binding protein 2	-1.951	0.0007	0.0023
Selenoh	ENSMUSG00000076437	selenoprotein H	-2.336	0.0000	0.0000
Selenom	ENSMUSG00000075702	selenoprotein M	-2.491	0.0000	0.0000
Selenon	ENSMUSG00000050989	selenoprotein N	-1.583	0.0002	0.0007
Selenop	ENSMUSG00000064373	selenoprotein P	-1.629	0.0000	0.0000
Selenos	ENSMUSG00000075701	selenoprotein S	-1.937	0.0000	0.0000
Selplg	ENSMUSG00000048163	selectin, platelet (p-selectin) ligand	-3.134	0.0000	0.0001
Sema3e	ENSMUSG00000063531	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	-3.183	0.0198	0.0436
Sema4a	ENSMUSG00000028064	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	-3.298	0.0000	0.0000
Sema4b	ENSMUSG00000030539	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-1.746	0.0000	0.0000
Sema4d	ENSMUSG00000021451	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	-1.703	0.0000	0.0000
Sema5a	ENSMUSG00000022231	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	-1.676	0.0486	0.0944
Sema5b	ENSMUSG00000052133	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	-4.087	0.0025	0.0071
Sema7a	ENSMUSG00000038264	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	-1.871	0.0000	0.0002
Sergef	ENSMUSG00000030839	secretion regulating guanine nucleotide exchange factor	-1.678	0.0000	0.0002
Serhl	ENSMUSG00000058586	serine hydrolase-like	-1.849	0.0000	0.0000
Serinc2	ENSMUSG00000023232	serine incorporator 2	-2.283	0.0428	0.0845

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Serpina3c	ENSMUSG00000066361	serine (or cysteine) peptidase inhibitor, clade A, member 3C	-2.406	0.0000	0.0001
Serpina3i	ENSMUSG00000079014	serine (or cysteine) peptidase inhibitor, clade A, member 3I	-3.717	0.0125	0.0291
Serpinb10	ENSMUSG00000092572	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	-25.807	0.0022	0.0062
Serpinf1	ENSMUSG00000000753	serine (or cysteine) peptidase inhibitor, clade F, member 1	-2.352	0.0000	0.0001
Serping1	ENSMUSG00000023224	serine (or cysteine) peptidase inhibitor, clade G, member 1	-3.038	0.0000	0.0000
Sesn2	ENSMUSG00000028893	sestrin 2	-1.946	0.0001	0.0003
Setd4	ENSMUSG00000022948	SET domain containing 4	-2.301	0.0005	0.0016
Setmar	ENSMUSG00000034639	SET domain without mariner transposase fusion	-1.549	0.0023	0.0066
Sez6l2	ENSMUSG00000030683	seizure related 6 homolog like 2	-2.523	0.0000	0.0001
Sf3b4	ENSMUSG00000068856	splicing factor 3b, subunit 4	-2.446	0.0000	0.0000
Sf3b5	ENSMUSG00000078348	splicing factor 3b, subunit 5	-3.703	0.0000	0.0000
Sf3b6	ENSMUSG00000037361	splicing factor 3B, subunit 6	-1.948	0.0000	0.0000
Sgca	ENSMUSG00000001508	sarcoglycan, alpha (dystrophin-associated glycoprotein)	-3.500	0.0000	0.0000
Sgf29	ENSMUSG00000030714	SAGA complex associated factor 29	-1.844	0.0000	0.0000
Sgip1	ENSMUSG00000028524	SH3-domain GRB2-like (endophilin) interacting protein 1	-1.747	0.0019	0.0055
Sgsh	ENSMUSG00000005043	N-sulfoglucosamine sulfohydrolase (sulfamidase)	-1.743	0.0000	0.0001
Sgsm3	ENSMUSG00000042303	small G protein signaling modulator 3	-3.179	0.0000	0.0000
Sh2d3c	ENSMUSG00000059013	SH2 domain containing 3C	-2.666	0.0000	0.0000
Sh3bgrl3	ENSMUSG00000028843	SH3 domain binding glutamic acid-rich protein-like 3	-4.065	0.0000	0.0000
Sh3bp1	ENSMUSG00000022436	SH3-domain binding protein 1	-2.901	0.0002	0.0008
Sh3bp4	ENSMUSG00000036206	SH3-domain binding protein 4	-1.534	0.0014	0.0040
Sh3gl1	ENSMUSG00000003200	SH3-domain GRB2-like 1	-2.039	0.0000	0.0000
Sh3glb2	ENSMUSG00000026860	SH3-domain GRB2-like endophilin B2	-2.435	0.0000	0.0000
Sh3tc1	ENSMUSG00000036553	SH3 domain and tetratricopeptide repeats 1	-1.520	0.0048	0.0124
Sh3tc2	ENSMUSG00000045629	SH3 domain and tetratricopeptide repeats 2	-2.328	0.0000	0.0000
Shd	ENSMUSG00000039154	src homology 2 domain-containing transforming protein D	-2.470	0.0017	0.0049
Shisa6	ENSMUSG00000053930	shisa family member 6	-10.299	0.0157	0.0357
Shkbp1	ENSMUSG00000089832	Sh3kbp1 binding protein 1	-2.219	0.0000	0.0000
Shld1	ENSMUSG00000044991	shieldin complex subunit 1	-4.466	0.0000	0.0001
Shmt1	ENSMUSG00000020534	serine hydroxymethyltransferase 1 (soluble)	-1.841	0.0000	0.0000
Shmt2	ENSMUSG00000025403	serine hydroxymethyltransferase 2 (mitochondrial)	-1.726	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Shroom1	ENSMUSG00000018387	shroom family member 1	-1.796	0.0440	0.0867
Sidt1	ENSMUSG00000022696	SID1 transmembrane family, member 1	-1.961	0.0387	0.0777
Sigirr	ENSMUSG00000025494	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	-1.537	0.0005	0.0017
Sik2	ENSMUSG00000037112	salt inducible kinase 2	-1.735	0.0000	0.0001
Sirt2	ENSMUSG00000015149	sirtuin 2	-1.855	0.0000	0.0000
Sirt4	ENSMUSG00000029524	sirtuin 4	-1.667	0.0000	0.0000
Siva1	ENSMUSG00000064326	SIVA1, apoptosis-inducing factor	-1.800	0.0000	0.0000
Six5	ENSMUSG00000040841	sine oculis-related homeobox 5	-1.527	0.0009	0.0027
Slamf8	ENSMUSG00000053318	SLAM family member 8	-2.803	0.0490	0.0949
Slamf9	ENSMUSG00000026548	SLAM family member 9	-2.549	0.0058	0.0147
Slc10a3	ENSMUSG00000032806	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	-2.297	0.0000	0.0000
Slc11a1	ENSMUSG00000026177	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	-3.250	0.0000	0.0000
Slc12a4	ENSMUSG00000017765	solute carrier family 12, member 4	-1.737	0.0000	0.0000
Slc12a8	ENSMUSG00000035506	solute carrier family 12 (potassium/chloride transporters), member 8	-1.901	0.0399	0.0798
Slc12a9	ENSMUSG00000037344	solute carrier family 12 (potassium/chloride transporters), member 9	-1.571	0.0193	0.0426
Slc16a12	ENSMUSG00000009378	solute carrier family 16 (monocarboxylic acid transporters), member 12	-2.022	0.0000	0.0000
Slc16a3	ENSMUSG00000025161	solute carrier family 16 (monocarboxylic acid transporters), member 3	-1.767	0.0324	0.0668
Slc16a8	ENSMUSG00000032988	solute carrier family 16 (monocarboxylic acid transporters), member 8	-3.493	0.0068	0.0171
Slc17a9	ENSMUSG00000023393	solute carrier family 17, member 9	-3.005	0.0377	0.0759
Slc19a1	ENSMUSG00000001436	solute carrier family 19 (folate transporter), member 1	-3.516	0.0000	0.0000
Slc19a3	ENSMUSG00000038496	solute carrier family 19, member 3	-1.950	0.0144	0.0329
Slc1a4	ENSMUSG00000020142	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	-1.875	0.0001	0.0005
Slc1a5	ENSMUSG00000001918	solute carrier family 1 (neutral amino acid transporter), member 5	-1.537	0.0003	0.0009
Slc1a7	ENSMUSG00000008932	solute carrier family 1 (glutamate transporter), member 7	-11.056	0.0064	0.0163
Slc22a21	ENSMUSG00000063652	solute carrier family 22 (organic cation transporter), member 21	-3.209	0.0013	0.0038
Slc22a5	ENSMUSG00000018900	solute carrier family 22 (organic cation transporter), member 5	-2.010	0.0000	0.0000
Slc25a10	ENSMUSG00000025792	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	-3.156	0.0000	0.0000
Slc25a22	ENSMUSG00000019082	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	-1.645	0.0000	0.0001
Slc25a29	ENSMUSG00000021265	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	-3.483	0.0000	0.0000
Slc25a3	ENSMUSG00000061904	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	-1.904	0.0000	0.0000
Slc25a31	ENSMUSG00000069041	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	-3.052	0.0205	0.0449

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc25a34	ENSMUSG00000040740	solute carrier family 25, member 34	-2.037	0.0000	0.0000
Slc25a35	ENSMUSG00000018740	solute carrier family 25, member 35	-1.944	0.0005	0.0017
Slc25a42	ENSMUSG00000002346	solute carrier family 25, member 42	-1.543	0.0000	0.0000
Slc25a45	ENSMUSG00000024818	solute carrier family 25, member 45	-1.871	0.0000	0.0000
Slc25a5	ENSMUSG00000016319	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	-1.551	0.0000	0.0000
Slc26a11	ENSMUSG00000039908	solute carrier family 26, member 11	-1.842	0.0050	0.0130
Slc26a3	ENSMUSG00000001225	solute carrier family 26, member 3	-22.653	0.0014	0.0042
Slc26a6	ENSMUSG00000023259	solute carrier family 26, member 6	-1.824	0.0000	0.0000
Slc27a1	ENSMUSG00000031808	solute carrier family 27 (fatty acid transporter), member 1	-1.588	0.0000	0.0000
Slc29a1	ENSMUSG00000023942	solute carrier family 29 (nucleoside transporters), member 1	-2.286	0.0000	0.0000
Slc29a2	ENSMUSG00000024891	solute carrier family 29 (nucleoside transporters), member 2	-2.880	0.0000	0.0000
Slc2a1	ENSMUSG00000028645	solute carrier family 2 (facilitated glucose transporter), member 1	-2.452	0.0120	0.0281
Slc2a10	ENSMUSG00000027661	solute carrier family 2 (facilitated glucose transporter), member 10	-1.986	0.0003	0.0011
Slc2a12	ENSMUSG00000037490	solute carrier family 2 (facilitated glucose transporter), member 12	-1.990	0.0000	0.0000
Slc2a8	ENSMUSG00000026791	solute carrier family 2, (facilitated glucose transporter), member 8	-3.535	0.0000	0.0000
Slc2a9	ENSMUSG00000005107	solute carrier family 2 (facilitated glucose transporter), member 9	-1.967	0.0003	0.0009
Slc30a6	ENSMUSG00000024069	solute carrier family 30 (zinc transporter), member 6	-1.629	0.0000	0.0000
Slc31a2	ENSMUSG00000066152	solute carrier family 31, member 2	-1.850	0.0000	0.0000
Slc35a4	ENSMUSG00000033272	solute carrier family 35, member A4	-2.119	0.0000	0.0000
Slc35b1	ENSMUSG00000020873	solute carrier family 35, member B1	-1.744	0.0000	0.0000
Slc35c1	ENSMUSG00000049922	solute carrier family 35, member C1	-1.861	0.0000	0.0000
Slc35c2	ENSMUSG00000017664	solute carrier family 35, member C2	-1.854	0.0000	0.0000
Slc35e4	ENSMUSG00000048807	solute carrier family 35, member E4	-1.555	0.0396	0.0792
Slc35f6	ENSMUSG00000029175	solute carrier family 35, member F6	-1.624	0.0000	0.0000
Slc36a2	ENSMUSG00000020264	solute carrier family 36 (proton/amino acid symporter), member 2	-2.546	0.0000	0.0000
Slc37a1	ENSMUSG00000024036	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	-1.901	0.0000	0.0000
Slc37a2	ENSMUSG00000032122	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	-1.792	0.0000	0.0001
Slc38a11	ENSMUSG00000061171	solute carrier family 38, member 11	-1.956	0.0018	0.0051
Slc38a3	ENSMUSG00000010064	solute carrier family 38, member 3	-2.535	0.0000	0.0000
Slc38a7	ENSMUSG00000036534	solute carrier family 38, member 7	-1.837	0.0000	0.0000
Slc39a13	ENSMUSG00000002105	solute carrier family 39 (metal ion transporter), member 13	-1.525	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc39a14	ENSMUSG00000022094	solute carrier family 39 (zinc transporter), member 14	-1.581	0.0000	0.0000
Slc39a3	ENSMUSG00000046822	solute carrier family 39 (zinc transporter), member 3	-1.598	0.0000	0.0000
Slc3a2	ENSMUSG00000010095	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	-2.018	0.0000	0.0000
Slc40a1	ENSMUSG00000025993	solute carrier family 40 (iron-regulated transporter), member 1	-1.823	0.0001	0.0003
Slc41a3	ENSMUSG00000030089	solute carrier family 41, member 3	-1.641	0.0000	0.0000
Slc43a1	ENSMUSG00000027075	solute carrier family 43, member 1	-1.588	0.0445	0.0875
Slc43a3	ENSMUSG00000027074	solute carrier family 43, member 3	-1.526	0.0428	0.0846
Slc46a1	ENSMUSG00000020829	solute carrier family 46, member 1	-3.815	0.0000	0.0001
Slc46a3	ENSMUSG00000029650	solute carrier family 46, member 3	-2.260	0.0000	0.0000
Slc48a1	ENSMUSG00000081534	solute carrier family 48 (heme transporter), member 1	-2.197	0.0000	0.0000
Slc50a1	ENSMUSG00000027953	solute carrier family 50 (sugar transporter), member 1	-3.461	0.0000	0.0000
Slc51a	ENSMUSG00000035699	solute carrier family 51, alpha subunit	-2.498	0.0049	0.0127
Slc52a2	ENSMUSG00000022560	solute carrier protein 52, member 2	-1.954	0.0000	0.0000
Slc5a11	ENSMUSG00000030769	solute carrier family 5 (sodium/glucose cotransporter), member 11	-7.067	0.0456	0.0893
Slc5a6	ENSMUSG00000006641	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	-2.011	0.0000	0.0000
Slc66a1	ENSMUSG00000028744	solute carrier family 66 member 1	-2.838	0.0000	0.0000
Slc6a9	ENSMUSG00000028542	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-1.898	0.0017	0.0050
Slc7a4	ENSMUSG00000022756	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	-3.657	0.0000	0.0000
Slc7a6	ENSMUSG00000031904	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-1.920	0.0000	0.0000
Slc9a1	ENSMUSG00000028854	solute carrier family 9 (sodium/hydrogen exchanger), member 1	-1.912	0.0000	0.0000
Slc9a2	ENSMUSG00000026062	solute carrier family 9 (sodium/hydrogen exchanger), member 2	-1.701	0.0018	0.0053
Slc9a4	ENSMUSG00000026065	solute carrier family 9 (sodium/hydrogen exchanger), member 4	-9.349	0.0009	0.0028
Slc9a8	ENSMUSG00000039463	solute carrier family 9 (sodium/hydrogen exchanger), member 8	-1.556	0.0000	0.0000
Slco2b1	ENSMUSG00000030737	solute carrier organic anion transporter family, member 2b1	-1.683	0.0000	0.0000
Slco4a1	ENSMUSG00000038963	solute carrier organic anion transporter family, member 4a1	-7.382	0.0503	0.0970
Slfn2	ENSMUSG00000072620	schlafen 2	-1.812	0.0000	0.0001
Slfn8	ENSMUSG00000035208	schlafen 8	-1.947	0.0009	0.0027
Slit1	ENSMUSG00000025020	slit guidance ligand 1	-6.744	0.0050	0.0129
Slit3	ENSMUSG00000056427	slit guidance ligand 3	-1.676	0.0109	0.0259
Smarcal1	ENSMUSG00000039354	SWI/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	-2.058	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Smarcb1	ENSMUSG00000000902	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-1.955	0.0000	0.0000
Smco1	ENSMUSG00000046345	single-pass membrane protein with coiled-coil domains 1	-1.895	0.0000	0.0000
Smg9	ENSMUSG00000002210	SMG9 nonsense mediated mRNA decay factor	-1.528	0.0000	0.0000
Smim15	ENSMUSG00000071180	small integral membrane protein 15	-1.588	0.0000	0.0000
Smim27	ENSMUSG00000028407	small integral membrane protein 27	-4.292	0.0000	0.0000
Smim4	ENSMUSG00000058351	small integral membrane protein 4	-1.505	0.0040	0.0105
Smim5	ENSMUSG00000048442	small integral membrane protein 5	-2.451	0.0000	0.0000
Smim8	ENSMUSG00000028295	small integral membrane protein 8	-1.513	0.0000	0.0000
Smpd1	ENSMUSG00000037049	sphingomyelin phosphodiesterase 1, acid lysosomal	-2.319	0.0000	0.0000
Smpd2	ENSMUSG00000019822	sphingomyelin phosphodiesterase 2, neutral	-1.501	0.0000	0.0000
Smpd3	ENSMUSG00000031906	sphingomyelin phosphodiesterase 3, neutral	-3.052	0.0000	0.0000
Smpdl3a	ENSMUSG00000019872	sphingomyelin phosphodiesterase, acid-like 3A	-2.792	0.0000	0.0000
Smpx	ENSMUSG00000041476	small muscle protein, X-linked	-2.143	0.0000	0.0000
Sms-ps	ENSMUSG00000081752	spermine synthase, pseudogene	-3.169	0.0000	0.0000
Smtn	ENSMUSG00000020439	smoothelin	-2.027	0.0000	0.0000
Smyd4	ENSMUSG00000018809	SET and MYND domain containing 4	-1.575	0.0007	0.0021
Snai1	ENSMUSG00000042821	snail family zinc finger 1	-3.271	0.0000	0.0000
Snai2	ENSMUSG00000022676	snail family zinc finger 2	-2.182	0.0000	0.0001
Snai3	ENSMUSG00000006587	snail family zinc finger 3	-10.105	0.0000	0.0000
Snap29	ENSMUSG00000022765	synaptosomal-associated protein 29	-1.534	0.0000	0.0000
Snap47	ENSMUSG00000009894	synaptosomal-associated protein, 47	-2.463	0.0000	0.0000
Snapc2	ENSMUSG00000011837	small nuclear RNA activating complex, polypeptide 2	-2.118	0.0000	0.0000
Snapc4	ENSMUSG00000036281	small nuclear RNA activating complex, polypeptide 4	-1.560	0.0166	0.0374
Snhg18	ENSMUSG00000096956	small nucleolar RNA host gene 18	-1.799	0.0000	0.0000
Snora17	ENSMUSG00000077192	small nucleolar RNA, H/ACA box 17	-13.250	0.0081	0.0199
Snrpb	ENSMUSG00000027404	small nuclear ribonucleoprotein B	-2.514	0.0000	0.0000
Snu13	ENSMUSG00000063480	SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5)	-1.712	0.0000	0.0000
Snx17	ENSMUSG00000029146	sorting nexin 17	-1.769	0.0000	0.0000
Snx32	ENSMUSG00000056185	sorting nexin 32	-1.954	0.0007	0.0022
Socs3	ENSMUSG00000053113	suppressor of cytokine signaling 3	-1.622	0.0297	0.0619

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sox18	ENSMUSG00000046470	SRY (sex determining region Y)-box 18	-3.774	0.0000	0.0000
Sp2	ENSMUSG00000018678	Sp2 transcription factor	-1.600	0.0000	0.0000
Sp3os	ENSMUSG00000063714	trans-acting transcription factor 3, opposite strand	-1.589	0.0007	0.0022
Spata17	ENSMUSG00000026611	spermatogenesis associated 17	-2.800	0.0101	0.0242
Spata2	ENSMUSG00000047030	spermatogenesis associated 2	-1.781	0.0000	0.0000
Spata20	ENSMUSG00000020867	spermatogenesis associated 20	-9.654	0.0000	0.0000
Spata24	ENSMUSG00000024352	spermatogenesis associated 24	-1.819	0.0264	0.0558
Spata2l	ENSMUSG00000033594	spermatogenesis associated 2-like	-1.869	0.0006	0.0019
Spats1	ENSMUSG00000023935	spermatogenesis associated, serine-rich 1	-3.638	0.0001	0.0003
Spats2l	ENSMUSG00000038305	spermatogenesis associated, serine-rich 2-like	-1.542	0.0001	0.0003
Spc24	ENSMUSG00000074476	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-1.578	0.0057	0.0147
Sphk2	ENSMUSG00000057342	sphingosine kinase 2	-2.120	0.0000	0.0000
Spink4	ENSMUSG00000028415	serine peptidase inhibitor, Kazal type 4	-21.589	0.0019	0.0055
Spint2	ENSMUSG00000074227	serine protease inhibitor, Kunitz type 2	-1.689	0.0000	0.0000
Spns1	ENSMUSG00000030741	spinster homolog 1	-3.503	0.0000	0.0000
Spns2	ENSMUSG00000040447	spinster homolog 2	-1.828	0.0000	0.0001
Spns3	ENSMUSG00000020798	spinster homolog 3	-14.310	0.0106	0.0253
Spon2	ENSMUSG00000037379	spondin 2, extracellular matrix protein	-2.496	0.0322	0.0663
Sppl2b	ENSMUSG00000035206	signal peptide peptidase like 2B	-2.472	0.0000	0.0000
Spr	ENSMUSG00000033735	sepiapterin reductase	-2.584	0.0000	0.0000
Sprn	ENSMUSG00000045733	shadow of prion protein	-2.976	0.0001	0.0005
Spr-ps1	ENSMUSG00000068303	sepiapterin reductase pseudogene 1	-11.124	0.0000	0.0000
Spryd4	ENSMUSG00000051346	SPRY domain containing 4	-1.924	0.0000	0.0000
Spsb1	ENSMUSG00000039911	splA/ryanodine receptor domain and SOCS box containing 1	-2.150	0.0001	0.0004
Spsb2	ENSMUSG00000038451	splA/ryanodine receptor domain and SOCS box containing 2	-1.722	0.0201	0.0442
Spsb3	ENSMUSG00000024160	splA/ryanodine receptor domain and SOCS box containing 3	-1.622	0.0000	0.0000
Srd5a3	ENSMUSG00000029233	steroid 5 alpha-reductase 3	-2.134	0.0000	0.0000
Srebf1	ENSMUSG00000020538	sterol regulatory element binding transcription factor 1	-3.033	0.0000	0.0000
Srebf2	ENSMUSG00000022463	sterol regulatory element binding factor 2	-1.768	0.0000	0.0000
Srpk3	ENSMUSG00000002007	serine/arginine-rich protein specific kinase 3	-1.536	0.0003	0.0011
Srpx	ENSMUSG00000090084	sushi-repeat-containing protein	-2.253	0.0001	0.0003

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Srpx2	ENSMUSG00000031253	sushi-repeat-containing protein, X-linked 2	-1.655	0.0002	0.0009
Srr	ENSMUSG00000001323	serine racemase	-1.695	0.0000	0.0000
Ss18l2	ENSMUSG00000032526	SS18, nBAF chromatin remodeling complex subunit like 2	-2.476	0.0000	0.0000
Ssc4d	ENSMUSG00000029699	scavenger receptor cysteine rich family, 4 domains	-2.168	0.0053	0.0137
Ssh3	ENSMUSG00000034616	slingshot protein phosphatase 3	-1.961	0.0001	0.0002
Ssna1	ENSMUSG00000026966	SS nuclear autoantigen 1	-2.733	0.0000	0.0000
Ssu2	ENSMUSG00000034387	ssu-2 homolog (C. elegans)	-1.962	0.0000	0.0000
St3gal1	ENSMUSG00000013846	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-1.518	0.0004	0.0014
St6galnac4	ENSMUSG00000079442	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	-1.722	0.0000	0.0000
Stab1	ENSMUSG00000042286	stabilin 1	-1.888	0.0000	0.0000
Stac2	ENSMUSG00000017400	SH3 and cysteine rich domain 2	-1.933	0.0081	0.0199
Stap2	ENSMUSG00000038781	signal transducing adaptor family member 2	-1.960	0.0000	0.0000
Stard3	ENSMUSG00000018167	START domain containing 3	-1.610	0.0004	0.0012
Stard8	ENSMUSG00000031216	START domain containing 8	-1.752	0.0000	0.0000
Steap3	ENSMUSG00000026389	STEAP family member 3	-1.625	0.0002	0.0005
Sting1	ENSMUSG00000024349	stimulator of interferon response cGAMP interactor 1	-2.319	0.0000	0.0000
Stk11ip	ENSMUSG00000026213	serine/threonine kinase 11 interacting protein	-1.574	0.0060	0.0153
Stk19	ENSMUSG00000061207	serine/threonine kinase 19	-2.127	0.0000	0.0000
Stk25	ENSMUSG00000026277	serine/threonine kinase 25 (yeast)	-1.576	0.0000	0.0000
Stk36	ENSMUSG00000033276	serine/threonine kinase 36	-2.153	0.0355	0.0721
Stmnd1	ENSMUSG00000063529	stathmin domain containing 1	-4.023	0.0420	0.0834
Stn1	ENSMUSG00000042694	STN1, CST complex subunit	-2.335	0.0000	0.0000
Ston1	ENSMUSG00000033855	stonin 1	-1.552	0.0256	0.0545
Stradb	ENSMUSG00000026027	STE20-related kinase adaptor beta	-1.768	0.0000	0.0000
Strip2	ENSMUSG00000039629	striatin interacting protein 2	-1.635	0.0000	0.0000
Strit1	ENSMUSG00000103476	small transmembrane regulator of ion transport 1	-2.653	0.0000	0.0000
Stx5a	ENSMUSG00000010110	syntaxin 5A	-1.653	0.0000	0.0001
Sufu	ENSMUSG00000025231	SUFU negative regulator of hedgehog signaling	-2.203	0.0000	0.0000
Sult1a1	ENSMUSG00000030711	sulfotransferase family 1A, phenol-preferring, member 1	-2.406	0.0076	0.0189
Sult6b2	ENSMUSG00000048473	sulfotransferase family 6B, member 2	-5.108	0.0243	0.0519

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sumf2	ENSMUSG00000025538	sulfatase modifying factor 2	-1.966	0.0000	0.0000
Sun1	ENSMUSG00000036817	Sad1 and UNC84 domain containing 1	-1.545	0.0000	0.0000
Sun3	ENSMUSG00000040985	Sad1 and UNC84 domain containing 3	-5.051	0.0000	0.0000
Supt4a	ENSMUSG00000020485	SPT4A, DSIF elongation factor subunit	-2.227	0.0000	0.0000
Surf1	ENSMUSG00000015790	surfeit gene 1	-1.511	0.0000	0.0000
Susd2	ENSMUSG00000006342	sushi domain containing 2	-2.090	0.0003	0.0011
Suv39h1	ENSMUSG00000039231	suppressor of variegation 3-9 1	-1.853	0.0000	0.0000
Sv2b	ENSMUSG00000053025	synaptic vesicle glycoprotein 2 b	-2.597	0.0011	0.0033
Sv2c	ENSMUSG00000051111	synaptic vesicle glycoprotein 2c	-2.691	0.0276	0.0581
Swi5	ENSMUSG00000044627	SWI5 recombination repair homolog (yeast)	-1.827	0.0000	0.0000
Swsap1	ENSMUSG00000051238	SWIM type zinc finger 7 associated protein 1	-2.630	0.0000	0.0000
Syce2	ENSMUSG00000003824	synaptonemal complex central element protein 2	-10.609	0.0004	0.0013
Syde1	ENSMUSG00000032714	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	-1.592	0.0000	0.0000
Syngr2	ENSMUSG00000048277	synaptogyrin 2	-3.364	0.0000	0.0000
Sys1	ENSMUSG00000045503	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	-1.549	0.0000	0.0000
Syt15	ENSMUSG00000041479	synaptotagmin XV	-1.591	0.0427	0.0844
Syt3	ENSMUSG00000030731	synaptotagmin III	-2.409	0.0000	0.0000
Syt5	ENSMUSG00000004961	synaptotagmin V	-3.466	0.0092	0.0223
Syvn1	ENSMUSG00000024807	synovial apoptosis inhibitor 1, synoviolin	-2.447	0.0000	0.0000
Szt2	ENSMUSG00000033253	SZT2 subunit of KICSTOR complex	-2.202	0.0000	0.0000
Tab1	ENSMUSG00000022414	TGF-beta activated kinase 1/MAP3K7 binding protein 1	-1.944	0.0000	0.0000
Taco1os	ENSMUSG00000085255	translational activator of mitochondrially encoded cytochrome c oxidase I, opposite strand	-7.302	0.0188	0.0417
Tada1	ENSMUSG00000026563	transcriptional adaptor 1	-2.097	0.0000	0.0000
Tada3	ENSMUSG00000048930	transcriptional adaptor 3	-1.651	0.0000	0.0000
Taf1c	ENSMUSG00000031832	TATA-box binding protein associated factor, RNA polymerase I, C	-1.591	0.0027	0.0074
Tafazzin	ENSMUSG00000009995	tafazzin, phospholipid-lysophospholipid transacylase	-1.696	0.0000	0.0000
Tagap	ENSMUSG00000033450	T cell activation Rho GTPase activating protein	-1.734	0.0076	0.0188
Tagln2	ENSMUSG00000026547	transgelin 2	-1.777	0.0000	0.0000
Tamm41	ENSMUSG00000030316	TAM41 mitochondrial translocator assembly and maintenance homolog	-1.616	0.0013	0.0038
Tango2	ENSMUSG00000013539	transport and golgi organization 2	-2.593	0.0000	0.0000
Tap1	ENSMUSG00000037321	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.896	0.0103	0.0247

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tas1r3	ENSMUSG00000029072	taste receptor, type 1, member 3	-3.243	0.0039	0.0103
Tat	ENSMUSG00000001670	tyrosine aminotransferase	-19.793	0.0314	0.0650
Tbc1d10a	ENSMUSG00000034412	TBC1 domain family, member 10a	-1.644	0.0072	0.0179
Tbc1d17	ENSMUSG00000038520	TBC1 domain family, member 17	-2.093	0.0000	0.0000
Tbc1d2	ENSMUSG00000039813	TBC1 domain family, member 2	-2.470	0.0001	0.0003
Tbc1d22a	ENSMUSG00000051864	TBC1 domain family, member 22a	-2.474	0.0000	0.0000
Tbc1d2b	ENSMUSG00000037410	TBC1 domain family, member 2B	-1.628	0.0000	0.0000
Tbc1d5	ENSMUSG00000023923	TBC1 domain family, member 5	-1.678	0.0000	0.0000
Tbc1d7	ENSMUSG00000021368	TBC1 domain family, member 7	-1.746	0.0000	0.0000
Tbc1d8	ENSMUSG00000003134	TBC1 domain family, member 8	-1.539	0.0000	0.0000
Tbc1d9b	ENSMUSG00000036644	TBC1 domain family, member 9B	-1.752	0.0000	0.0000
Tbl3	ENSMUSG00000040688	transducin (beta)-like 3	-2.777	0.0000	0.0000
Tbrg4	ENSMUSG00000000384	transforming growth factor beta regulated gene 4	-1.733	0.0000	0.0000
Tbxa2r	ENSMUSG00000034881	thromboxane A2 receptor	-3.275	0.0000	0.0000
Tcf19	ENSMUSG00000050410	transcription factor 19	-2.054	0.0006	0.0020
Tcf21	ENSMUSG00000045680	transcription factor 21	-2.000	0.0000	0.0000
Tcirg1	ENSMUSG00000001750	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	-2.540	0.0000	0.0000
Tcn2	ENSMUSG00000020432	transcobalamin 2	-2.291	0.0000	0.0000
Tcof1	ENSMUSG00000024613	treacle ribosome biogenesis factor 1	-1.938	0.0000	0.0000
Tcp11l2	ENSMUSG00000020034	t-complex 11 (mouse) like 2	-1.846	0.0002	0.0009
Tcta	ENSMUSG00000039461	T cell leukemia translocation altered gene	-2.868	0.0000	0.0000
Tctn2	ENSMUSG00000118662	tectonic family member 2	-1.508	0.0011	0.0034
Tctn3	ENSMUSG00000025008	tectonic family member 3	-2.581	0.0000	0.0000
Tdg-ps2	ENSMUSG00000085666	thymine DNA glycosylase, pseudogene 2	-2.190	0.0000	0.0001
Tdp1	ENSMUSG00000021177	tyrosyl-DNA phosphodiesterase 1	-1.521	0.0002	0.0006
Tecpr1	ENSMUSG00000066621	tectonin beta-propeller repeat containing 1	-2.061	0.0000	0.0000
Tecr	ENSMUSG00000031708	trans-2,3-enoyl-CoA reductase	-1.818	0.0000	0.0000
Tecrl	ENSMUSG00000049537	trans-2,3-enoyl-CoA reductase-like	-2.510	0.0000	0.0000
Tedc2	ENSMUSG00000024118	tubulin epsilon and delta complex 2	-2.340	0.0041	0.0109
Tef	ENSMUSG00000022389	thyrotroph embryonic factor	-2.211	0.0000	0.0001
Telo2	ENSMUSG00000024170	telomere maintenance 2	-1.707	0.0000	0.0002

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ten1	ENSMUSG00000020778	TEN1 telomerase capping complex subunit	-1.603	0.0012	0.0036
Tep1	ENSMUSG00000006281	telomerase associated protein 1	-1.519	0.0000	0.0000
Tepsin	ENSMUSG00000025377	TEPSIN, adaptor related protein complex 4 accessory protein	-1.985	0.0000	0.0000
Tespa1	ENSMUSG00000034833	thymocyte expressed, positive selection associated 1	-8.837	0.0276	0.0581
Tex11	ENSMUSG00000009670	testis expressed gene 11	-2.032	0.0256	0.0544
Tex261	ENSMUSG00000014748	testis expressed gene 261	-1.540	0.0000	0.0000
Tex38	ENSMUSG00000044556	testis expressed 38	-4.703	0.0069	0.0172
Tex49	ENSMUSG00000022993	testis expressed 49	-16.989	0.0068	0.0170
Tfb2m	ENSMUSG00000026492	transcription factor B2, mitochondrial	-1.683	0.0000	0.0000
Tfg	ENSMUSG00000022757	Trk-fused gene	-1.870	0.0000	0.0000
Tfip11	ENSMUSG00000029345	tuftelin interacting protein 11	-1.697	0.0000	0.0000
Tg	ENSMUSG00000053469	thyroglobulin	-2.383	0.0000	0.0000
Tgfb1i1	ENSMUSG00000030782	transforming growth factor beta 1 induced transcript 1	-2.310	0.0000	0.0000
Tgfbi	ENSMUSG00000035493	transforming growth factor, beta induced	-1.585	0.0011	0.0032
Tgtp1	ENSMUSG00000078922	T cell specific GTPase 1	-2.070	0.0264	0.0558
Tgtp2	ENSMUSG00000078921	T cell specific GTPase 2	-2.582	0.0175	0.0392
Tha1	ENSMUSG00000017713	threonine aldolase 1	-1.592	0.0003	0.0010
Thap3	ENSMUSG00000039759	THAP domain containing, apoptosis associated protein 3	-1.591	0.0006	0.0018
Thap7	ENSMUSG00000022760	THAP domain containing 7	-2.762	0.0000	0.0000
Thbs3	ENSMUSG00000028047	thrombospondin 3	-1.624	0.0066	0.0167
Them4	ENSMUSG00000028145	thioesterase superfamily member 4	-1.912	0.0000	0.0000
Them6	ENSMUSG00000056665	thioesterase superfamily member 6	-1.611	0.0003	0.0009
Thnsl2	ENSMUSG00000054474	threonine synthase-like 2 (bacterial)	-1.625	0.0001	0.0003
Thop1	ENSMUSG00000004929	thimet oligopeptidase 1	-2.183	0.0000	0.0000
Thsd1	ENSMUSG00000031480	thrombospondin, type I, domain 1	-1.598	0.0000	0.0000
Ticam1	ENSMUSG00000047123	toll-like receptor adaptor molecule 1	-3.033	0.0000	0.0000
Tie1	ENSMUSG00000033191	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	-1.643	0.0000	0.0000
Timm13	ENSMUSG00000020219	translocase of inner mitochondrial membrane 13	-2.004	0.0000	0.0000
Timm23	ENSMUSG00000013701	translocase of inner mitochondrial membrane 23	-1.540	0.0000	0.0000
Timm50	ENSMUSG00000003438	translocase of inner mitochondrial membrane 50	-3.079	0.0000	0.0000
Timm9	ENSMUSG00000021079	translocase of inner mitochondrial membrane 9	-2.016	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tkt	ENSMUSG00000021957	transketolase	-2.668	0.0000	0.0000
Tlcd2	ENSMUSG00000038217	TLC domain containing 2	-2.244	0.0000	0.0001
Tlcd3a	ENSMUSG00000069808	TLC domain containing 3A	-2.140	0.0015	0.0045
Tle6	ENSMUSG00000034758	transducin-like enhancer of split 6	-2.642	0.0000	0.0000
Tlr2	ENSMUSG00000027995	toll-like receptor 2	-1.692	0.0034	0.0093
Tlr5	ENSMUSG00000079164	toll-like receptor 5	-1.722	0.0399	0.0797
Tm2d2	ENSMUSG00000031556	TM2 domain containing 2	-2.196	0.0000	0.0000
Tm2d3	ENSMUSG00000078681	TM2 domain containing 3	-1.755	0.0000	0.0000
Tm4sf1	ENSMUSG00000027800	transmembrane 4 superfamily member 1	-1.538	0.0002	0.0006
Tm4sf5	ENSMUSG00000018919	transmembrane 4 superfamily member 5	-12.942	0.0109	0.0260
Tm6sf2	ENSMUSG00000036151	transmembrane 6 superfamily member 2	-2.391	0.0388	0.0778
Tm7sf2	ENSMUSG00000024799	transmembrane 7 superfamily member 2	-1.929	0.0019	0.0055
Tmbim4	ENSMUSG00000020225	transmembrane BAX inhibitor motif containing 4	-1.537	0.0000	0.0000
Tmc4	ENSMUSG00000019734	transmembrane channel-like gene family 4	-2.980	0.0081	0.0199
Tmc6	ENSMUSG00000025572	transmembrane channel-like gene family 6	-2.372	0.0000	0.0000
Tmc8	ENSMUSG00000050106	transmembrane channel-like gene family 8	-1.668	0.0005	0.0017
Tmed1	ENSMUSG00000032180	transmembrane p24 trafficking protein 1	-1.953	0.0000	0.0000
Tmed10-ps	ENSMUSG00000114251	transmembrane p24 trafficking protein 10, pseudogene	-2.155	0.0000	0.0000
Tmed2b	ENSMUSG00000079884	transmembrane p24 trafficking protein 2B	-2.670	0.0003	0.0010
Tmed3	ENSMUSG00000032353	transmembrane p24 trafficking protein 3	-1.829	0.0000	0.0000
Tmem102	ENSMUSG00000089876	transmembrane protein 102	-2.128	0.0145	0.0333
Tmem104	ENSMUSG00000045980	transmembrane protein 104	-1.930	0.0000	0.0000
Tmem106a	ENSMUSG00000034947	transmembrane protein 106A	-1.693	0.0012	0.0037
Tmem107	ENSMUSG00000020895	transmembrane protein 107	-2.119	0.0000	0.0001
Tmem108	ENSMUSG00000042757	transmembrane protein 108	-2.643	0.0000	0.0000
Tmem116	ENSMUSG00000029452	transmembrane protein 116	-2.042	0.0000	0.0001
Tmem119	ENSMUSG00000054675	transmembrane protein 119	-1.886	0.0499	0.0965
Tmem120a	ENSMUSG00000039886	transmembrane protein 120A	-2.582	0.0000	0.0000
Tmem120b	ENSMUSG00000054434	transmembrane protein 120B	-1.850	0.0000	0.0000
Tmem126a	ENSMUSG00000030615	transmembrane protein 126A	-4.116	0.0000	0.0000
Tmem128	ENSMUSG00000067365	transmembrane protein 128	-1.564	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem129	ENSMUSG00000019295	transmembrane protein 129	-2.904	0.0000	0.0000
Tmem140	ENSMUSG00000057137	transmembrane protein 140	-1.852	0.0003	0.0010
Tmem143	ENSMUSG00000002781	transmembrane protein 143	-2.172	0.0000	0.0000
Tmem144	ENSMUSG00000027956	transmembrane protein 144	-2.376	0.0000	0.0000
Tmem14a	ENSMUSG00000025933	transmembrane protein 14A	-1.923	0.0007	0.0023
Tmem154	ENSMUSG00000056498	transmembrane protein 154	-1.646	0.0047	0.0124
Tmem17	ENSMUSG00000049904	transmembrane protein 17	-1.549	0.0237	0.0508
Tmem175	ENSMUSG00000013495	transmembrane protein 175	-2.379	0.0000	0.0000
Tmem176a	ENSMUSG00000023367	transmembrane protein 176A	-1.502	0.0107	0.0255
Tmem176b	ENSMUSG00000029810	transmembrane protein 176B	-2.531	0.0000	0.0000
Tmem177	ENSMUSG00000036975	transmembrane protein 177	-1.538	0.0000	0.0000
Tmem179b	ENSMUSG00000118346	transmembrane protein 179B	-2.175	0.0000	0.0000
Tmem184b	ENSMUSG00000009035	transmembrane protein 184b	-2.351	0.0000	0.0000
Tmem198	ENSMUSG00000051703	transmembrane protein 198	-2.304	0.0394	0.0788
Tmem204	ENSMUSG00000024168	transmembrane protein 204	-1.947	0.0000	0.0000
Tmem205	ENSMUSG00000040883	transmembrane protein 205	-2.133	0.0000	0.0000
Tmem208	ENSMUSG00000014856	transmembrane protein 208	-2.929	0.0000	0.0000
Tmem216	ENSMUSG00000024667	transmembrane protein 216	-2.274	0.0000	0.0000
Tmem219	ENSMUSG00000060538	transmembrane protein 219	-1.733	0.0000	0.0000
Tmem221	ENSMUSG00000043664	transmembrane protein 221	-25.442	0.0058	0.0148
Tmem222	ENSMUSG00000028857	transmembrane protein 222	-1.737	0.0000	0.0000
Tmem223	ENSMUSG00000117924	transmembrane protein 223	-4.062	0.0000	0.0000
Tmem230	ENSMUSG00000027341	transmembrane protein 230	-1.988	0.0000	0.0001
Tmem241	ENSMUSG00000049411	transmembrane protein 241	-1.594	0.0001	0.0002
Tmem242	ENSMUSG00000004945	transmembrane protein 242	-2.194	0.0000	0.0000
Tmem25	ENSMUSG00000002032	transmembrane protein 25	-1.794	0.0008	0.0026
Tmem254	ENSMUSG00000072676	transmembrane protein 254	-1.592	0.0266	0.0562
Tmem255b	ENSMUSG00000038457	transmembrane protein 255B	-2.281	0.0013	0.0039
Tmem256	ENSMUSG00000070394	transmembrane protein 256	-1.841	0.0000	0.0000
Tmem258	ENSMUSG00000036372	transmembrane protein 258	-2.698	0.0000	0.0000
Tmem266	ENSMUSG00000032313	transmembrane protein 266	-1.547	0.0098	0.0237

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem35b	ENSMUSG00000070737	transmembrane protein 35B	-2.373	0.0011	0.0033
Tmem37	ENSMUSG00000050777	transmembrane protein 37	-6.581	0.0000	0.0000
Tmem41a	ENSMUSG00000022856	transmembrane protein 41a	-1.693	0.0051	0.0133
Tmem41b	ENSMUSG00000047554	transmembrane protein 41B	-1.812	0.0000	0.0000
Tmem41b-ps	ENSMUSG00000096647	transmembrane protein 41B, pseudogene	-3.194	0.0482	0.0937
Tmem42	ENSMUSG00000066233	transmembrane protein 42	-1.522	0.0009	0.0028
Tmem45a	ENSMUSG00000022754	transmembrane protein 45a	-1.788	0.0017	0.0051
Tmem52	ENSMUSG00000023153	transmembrane protein 52	-4.560	0.0000	0.0002
Tmem53	ENSMUSG00000048772	transmembrane protein 53	-1.721	0.0000	0.0000
Tmem59	ENSMUSG00000028618	transmembrane protein 59	-1.776	0.0000	0.0000
Tmem60	ENSMUSG00000045435	transmembrane protein 60	-2.102	0.0000	0.0000
Tmem63a	ENSMUSG00000026519	transmembrane protein 63a	-1.571	0.0000	0.0000
Tmem79	ENSMUSG00000001420	transmembrane protein 79	-2.584	0.0000	0.0001
Tmem81	ENSMUSG00000048174	transmembrane protein 81	-1.654	0.0070	0.0176
Tmem86a	ENSMUSG00000010307	transmembrane protein 86A	-3.127	0.0000	0.0000
Tmem88	ENSMUSG00000045377	transmembrane protein 88	-2.933	0.0000	0.0000
Tmem9	ENSMUSG00000026411	transmembrane protein 9	-1.652	0.0000	0.0001
Tmem94	ENSMUSG00000020747	transmembrane protein 94	-2.020	0.0000	0.0000
Tmem97	ENSMUSG00000037278	transmembrane protein 97	-1.686	0.0011	0.0033
Tmem98	ENSMUSG00000035413	transmembrane protein 98	-1.698	0.0003	0.0011
Tmod4	ENSMUSG00000005628	tropomodulin 4	-1.717	0.0001	0.0004
Tmprss4	ENSMUSG00000032091	transmembrane protease, serine 4	-2.002	0.0155	0.0351
Tmprss5	ENSMUSG00000032268	transmembrane protease, serine 5 (spinesin)	-8.577	0.0057	0.0146
Tmsb10	ENSMUSG00000079523	thymosin, beta 10	-1.921	0.0004	0.0014
Tmub2	ENSMUSG00000034757	transmembrane and ubiquitin-like domain containing 2	-1.610	0.0000	0.0000
Tnfaip8l1	ENSMUSG00000044469	tumor necrosis factor, alpha-induced protein 8-like 1	-2.433	0.0000	0.0000
Tnfaip8l2	ENSMUSG00000013707	tumor necrosis factor, alpha-induced protein 8-like 2	-4.787	0.0000	0.0000
Tnfrsf10b	ENSMUSG00000022074	tumor necrosis factor receptor superfamily, member 10b	-1.548	0.0077	0.0190
Tnfrsf11b	ENSMUSG00000063727	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	-5.673	0.0211	0.0461
Tnfrsf12a	ENSMUSG00000023905	tumor necrosis factor receptor superfamily, member 12a	-2.360	0.0000	0.0000
Tnfrsf1a	ENSMUSG00000030341	tumor necrosis factor receptor superfamily, member 1a	-2.167	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tnfrsf23	ENSMUSG00000037613	tumor necrosis factor receptor superfamily, member 23	-1.790	0.0017	0.0050
Tnfrsf26	ENSMUSG00000045362	tumor necrosis factor receptor superfamily, member 26	-2.280	0.0047	0.0123
Tnfrsf8	ENSMUSG00000028602	tumor necrosis factor receptor superfamily, member 8	-10.259	0.0222	0.0482
Tnfsf13b	ENSMUSG00000031497	tumor necrosis factor (ligand) superfamily, member 13b	-1.960	0.0106	0.0253
Tnfsf9	ENSMUSG00000035678	tumor necrosis factor (ligand) superfamily, member 9	-2.791	0.0246	0.0526
Tnfsfm13	ENSMUSG00000018752	tumor necrosis factor (ligand) superfamily, membrane-bound member 13	-3.644	0.0380	0.0764
Tnip3	ENSMUSG00000044162	TNFAIP3 interacting protein 3	-1.745	0.0474	0.0923
Tnxb	ENSMUSG00000033327	tenascin XB	-1.870	0.0000	0.0000
Togaram2	ENSMUSG00000045761	TOG array regulator of axonemal microtubules 2	-2.659	0.0000	0.0000
Tom1	ENSMUSG00000042870	target of myb1 trafficking protein	-3.127	0.0000	0.0000
Tomm5	ENSMUSG00000078713	translocase of outer mitochondrial membrane 5	-1.634	0.0000	0.0000
Tor2a	ENSMUSG00000009563	torsin family 2, member A	-2.284	0.0000	0.0000
Tor4a	ENSMUSG00000059555	torsin family 4, member A	-1.615	0.0001	0.0003
Tpcn1	ENSMUSG00000032741	two pore channel 1	-1.595	0.0000	0.0000
Tpd52l1	ENSMUSG00000000296	tumor protein D52-like 1	-1.597	0.0037	0.0099
Tpgs1	ENSMUSG00000020308	tubulin polyglutamylase complex subunit 1	-3.370	0.0000	0.0000
Tpk1	ENSMUSG00000029735	thiamine pyrophosphokinase	-2.314	0.0000	0.0001
Tpp1	ENSMUSG00000030894	tripeptidyl peptidase I	-2.172	0.0000	0.0000
Tpra1	ENSMUSG00000002871	transmembrane protein, adipocyte asscociated 1	-2.569	0.0000	0.0000
Tpst2	ENSMUSG00000029344	protein-tyrosine sulfotransferase 2	-1.782	0.0000	0.0000
Traf3ip2	ENSMUSG00000019842	TRAF3 interacting protein 2	-1.557	0.0004	0.0014
Traf5	ENSMUSG00000026637	TNF receptor-associated factor 5	-1.587	0.0009	0.0027
Traf7	ENSMUSG00000052752	TNF receptor-associated factor 7	-2.762	0.0000	0.0000
Trappc12	ENSMUSG00000020628	trafficking protein particle complex 12	-1.701	0.0000	0.0000
Trappc4	ENSMUSG00000032112	trafficking protein particle complex 4	-2.067	0.0000	0.0000
Trappc9	ENSMUSG00000047921	trafficking protein particle complex 9	-2.375	0.0000	0.0000
Trf	ENSMUSG00000032554	transferrin	-1.946	0.0000	0.0000
Triap1	ENSMUSG00000029535	TP53 regulated inhibitor of apoptosis 1	-2.030	0.0000	0.0000
Trib3	ENSMUSG00000032715	tribbles pseudokinase 3	-1.871	0.0003	0.0011
Tril	ENSMUSG00000043496	TLR4 interactor with leucine-rich repeats	-1.587	0.0001	0.0005
Trim32	ENSMUSG00000051675	tripartite motif-containing 32	-1.841	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Trim46	ENSMUSG00000042766	tripartite motif-containing 46	-2.635	0.0003	0.0009
Trim65	ENSMUSG00000054517	tripartite motif-containing 65	-1.766	0.0000	0.0000
Triqk	ENSMUSG00000055963	triple QxxK/R motif containing	-2.079	0.0000	0.0000
Trmt1	ENSMUSG00000001909	tRNA methyltransferase 1	-1.930	0.0000	0.0000
Trmt112	ENSMUSG00000038812	tRNA methyltransferase 11-2	-1.717	0.0000	0.0000
Trmt112-ps2	ENSMUSG00000070572	tRNA methyltransferase 11-2, pseudogene 2	-32.846	0.0001	0.0004
Tro	ENSMUSG00000025272	trophinin	-2.110	0.0468	0.0914
Troap	ENSMUSG00000032783	trophinin associated protein	-2.805	0.0243	0.0520
Trp53i13	ENSMUSG00000044328	transformation related protein 53 inducible protein 13	-1.775	0.0007	0.0021
Trpm4	ENSMUSG00000038260	transient receptor potential cation channel, subfamily M, member 4	-1.746	0.0000	0.0000
Trpt1	ENSMUSG00000047656	tRNA phosphotransferase 1	-3.361	0.0000	0.0000
Trpv4	ENSMUSG00000014158	transient receptor potential cation channel, subfamily V, member 4	-2.268	0.0003	0.0009
Trrap	ENSMUSG00000045482	transformation/transcription domain-associated protein	-1.855	0.0000	0.0000
Trub2	ENSMUSG00000039826	TruB pseudouridine (psi) synthase family member 2	-2.42691345	0.0000	0.0000
Tsacc	ENSMUSG00000010538	TSSK6 activating co-chaperone	-2.31796615	0.0154	0.0350
Tsc2	ENSMUSG00000002496	TSC complex subunit 2	-1.83262662	0.0000	0.0000
Tsen15	ENSMUSG00000014980	tRNA splicing endonuclease subunit 15	-1.79902138	0.0000	0.0000
Tsen2	ENSMUSG00000042389	tRNA splicing endonuclease subunit 2	-1.54244247	0.0004	0.0014
Tsku	ENSMUSG00000049580	tsukushi, small leucine rich proteoglycan	-1.6103917	0.0060	0.0151
Tspan10	ENSMUSG00000039691	tetraspanin 10	-6.63838958	0.0045	0.0118
Tspan11	ENSMUSG00000030351	tetraspanin 11	-2.48743674	0.0019	0.0055
Tspan4	ENSMUSG00000025511	tetraspanin 4	-2.16597765	0.0000	0.0000
Tspo	ENSMUSG00000041736	translocator protein	-4.99878005	0.0000	0.0000
Tspyl3	ENSMUSG00000074671	TSPY-like 3	-1.95089096	0.0006	0.0018
Tst	ENSMUSG00000044986	thiosulfate sulfurtransferase, mitochondrial	-2.00228416	0.0000	0.0000
Ttc13	ENSMUSG00000037300	tetratricopeptide repeat domain 13	-1.52070324	0.0000	0.0001
Ttc28	ENSMUSG00000033209	tetratricopeptide repeat domain 28	-1.7212105	0.0000	0.0000
Ttc30a2	ENSMUSG00000075272	tetratricopeptide repeat domain 30A2	-3.04586139	0.0136	0.0314
Ttc32	ENSMUSG00000066637	tetratricopeptide repeat domain 32	-2.0816982	0.0000	0.0000
Ttc38	ENSMUSG00000035944	tetratricopeptide repeat domain 38	-2.40427661	0.0000	0.0000
Ttc39a	ENSMUSG00000028555	tetratricopeptide repeat domain 39A	-2.0651832	0.0233	0.0501

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ttc7	ENSMUSG00000036918	tetratricopeptide repeat domain 7	-1.94579523	0.0000	0.0000
Ttc7b	ENSMUSG00000033530	tetratricopeptide repeat domain 7B	-1.58007558	0.0000	0.0000
Ttll1	ENSMUSG00000022442	tubulin tyrosine ligase-like 1	-3.10158888	0.0000	0.0000
Ttll12	ENSMUSG00000016757	tubulin tyrosine ligase-like family, member 12	-1.52433328	0.0001	0.0002
Ttpa	ENSMUSG00000073988	tocopherol (alpha) transfer protein	-2.72817555	0.0210	0.0460
Ttr	ENSMUSG00000061808	transthyretin	-4.88725231	0.0475	0.0926
Tuba3b	ENSMUSG00000067338	tubulin, alpha 3B	-41.5034417	0.0001	0.0003
Tubg1	ENSMUSG00000035198	tubulin, gamma 1	-3.03672575	0.0000	0.0000
Tubg2	ENSMUSG00000045007	tubulin, gamma 2	-1.60970521	0.0262	0.0554
Tubgcp2	ENSMUSG00000025474	tubulin, gamma complex associated protein 2	-1.7759422	0.0000	0.0000
Tubgcp4	ENSMUSG00000027263	tubulin, gamma complex associated protein 4	-1.799875	0.0000	0.0000
Tvp23a	ENSMUSG00000050908	trans-golgi network vesicle protein 23A	-3.35492875	0.0010	0.0030
Twf2	ENSMUSG00000023277	twinfilin actin binding protein 2	-3.7482746	0.0000	0.0000
Tyk2	ENSMUSG00000032175	tyrosine kinase 2	-2.13417759	0.0000	0.0000
Tyro3	ENSMUSG00000027298	TYRO3 protein tyrosine kinase 3	-1.78275783	0.0005	0.0016
Tyrobp	ENSMUSG00000030579	TYRO protein tyrosine kinase binding protein	-1.94637123	0.0015	0.0045
Uba7	ENSMUSG00000032596	ubiquitin-like modifier activating enzyme 7	-1.68191891	0.0109	0.0260
Ubac2	ENSMUSG00000041765	ubiquitin associated domain containing 2	-1.50745752	0.0000	0.0000
Ubald1	ENSMUSG00000039568	UBA-like domain containing 1	-1.58064159	0.0002	0.0008
Ubb-ps	ENSMUSG00000044285	ubiquitin B, pseudogene	-3.17330938	0.0000	0.0000
Ubc	ENSMUSG00000008348	ubiquitin C	-5.52799399	0.0000	0.0000
Ube2a	ENSMUSG00000016308	ubiquitin-conjugating enzyme E2A	-1.72864422	0.0000	0.0000
Ube2c	ENSMUSG00000001403	ubiquitin-conjugating enzyme E2C	-2.02991434	0.0003	0.0009
Ube2d-ps	ENSMUSG00000083844	ubiquitin-conjugating enzyme E2D, pseudogene	-2.15169646	0.0000	0.0000
Ube2l3	ENSMUSG00000038965	ubiquitin-conjugating enzyme E2L 3	-1.62917784	0.0000	0.0000
Ube2t	ENSMUSG00000026429	ubiquitin-conjugating enzyme E2T	-2.06087656	0.0000	0.0001
Ube4bos1	ENSMUSG00000085819	ubiquitination factor E4B, opposite strand 1	-2.11744035	0.0370	0.0747
Ubiad1	ENSMUSG00000047719	UbiA prenyltransferase domain containing 1	-1.54550391	0.0001	0.0003
Ubl7	ENSMUSG00000055720	ubiquitin-like 7 (bone marrow stromal cell-derived)	-2.05312366	0.0000	0.0000
Ubox5	ENSMUSG00000027300	U box domain containing 5	-1.98088122	0.0000	0.0000
Ubtd1	ENSMUSG00000025171	ubiquitin domain containing 1	-1.85022356	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ubxn6	ENSMUSG00000019578	UBX domain protein 6	-2.00935734	0.0000	0.0000
Uchl1	ENSMUSG00000029223	ubiquitin carboxy-terminal hydrolase L1	-2.06093588	0.0003	0.0011
Uchl4	ENSMUSG00000035337	ubiquitin carboxyl-terminal esterase L4	-6.01404772	0.0000	0.0000
Uck1	ENSMUSG00000002550	uridine-cytidine kinase 1	-2.44618844	0.0000	0.0000
Uckl1	ENSMUSG00000089917	uridine-cytidine kinase 1-like 1	-2.5853145	0.0000	0.0000
Ugt1a6a	ENSMUSG00000054545	UDP glucuronosyltransferase 1 family, polypeptide A6A	-15.919324	0.0112	0.0265
Ugt1a6b	ENSMUSG00000090145	UDP glucuronosyltransferase 1 family, polypeptide A6B	-2.24598452	0.0343	0.0700
Unc93b1	ENSMUSG00000036908	unc-93 homolog B1, TLR signaling regulator	-2.4770779	0.0000	0.0000
Upb1	ENSMUSG00000033427	ureidopropionase, beta	-7.69434968	0.0000	0.0000
Upk1b	ENSMUSG00000049436	uroplakin 1B	-7.4689151	0.0023	0.0065
Upk2	ENSMUSG00000041523	uroplakin 2	-4.30869141	0.0340	0.0695
Upk3b	ENSMUSG00000042985	uroplakin 3B	-34.4464748	0.0001	0.0003
Upp1	ENSMUSG00000020407	uridine phosphorylase 1	-2.15512256	0.0000	0.0002
Uqcc2	ENSMUSG00000024208	ubiquinol-cytochrome c reductase complex assembly factor 2	-3.35413735	0.0000	0.0000
Uqcr10	ENSMUSG00000059534	ubiquinol-cytochrome c reductase, complex III subunit X	-1.84225943	0.0000	0.0000
Uqcr11	ENSMUSG00000020163	ubiquinol-cytochrome c reductase, complex III subunit XI	-4.34277453	0.0000	0.0000
Urah	ENSMUSG00000025481	urate (5-hydroxyiso-) hydrolase	-3.30601104	0.0232	0.0499
Urb1	ENSMUSG00000039929	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	-1.70642113	0.0000	0.0000
Urod	ENSMUSG00000028684	uroporphyrinogen decarboxylase	-1.85331779	0.0000	0.0000
Use1	ENSMUSG00000002395	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	-1.72136416	0.0000	0.0000
Usf1	ENSMUSG00000026641	upstream transcription factor 1	-1.6074262	0.0000	0.0000
Usp18	ENSMUSG00000030107	ubiquitin specific peptidase 18	-1.68173674	0.0190	0.0419
Usp22	ENSMUSG00000042506	ubiquitin specific peptidase 22	-1.94346141	0.0000	0.0000
Uxt	ENSMUSG00000001134	ubiquitously expressed prefoldin like chaperone	-1.578667	0.0000	0.0000
Vasn	ENSMUSG00000039646	vasorin	-1.67542262	0.0004	0.0014
Vdr	ENSMUSG00000022479	vitamin D (1,25-dihydroxyvitamin D3) receptor	-1.98917756	0.0350	0.0713
Vegfc	ENSMUSG00000031520	vascular endothelial growth factor C	-1.54570651	0.0012	0.0037
Vegfd	ENSMUSG00000031380	vascular endothelial growth factor D	-1.93604481	0.0011	0.0034
Vipr2	ENSMUSG00000011171	vasoactive intestinal peptide receptor 2	-1.5519992	0.0424	0.0840
Vkorc1	ENSMUSG00000096145	vitamin K epoxide reductase complex, subunit 1	-2.59383788	0.0014	0.0041
Vma21-ps	ENSMUSG00000061619	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae), pseudogene	-25.6002436	0.0007	0.0022

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Vmac	ENSMUSG00000054723	vimentin-type intermediate filament associated coiled-coil protein	-2.11118258	0.0000	0.0000
Vnn1	ENSMUSG00000037440	vanin 1	-5.51085555	0.0184	0.0409
Vps11	ENSMUSG00000032127	VPS11, CORVET/HOPS core subunit	-1.54549015	0.0008	0.0025
Vps29	ENSMUSG00000029462	VPS29 retromer complex component	-1.5536933	0.0000	0.0000
Vps35l	ENSMUSG00000030982	VPS35 endosomal protein sorting factor like	-2.26806848	0.0000	0.0000
Vps37b	ENSMUSG00000066278	vacuolar protein sorting 37B	-1.54481428	0.0000	0.0002
Vps51	ENSMUSG00000024797	VPS51 GARP complex subunit	-1.86769867	0.0000	0.0000
Vps9d1	ENSMUSG00000001062	VPS9 domain containing 1	-1.70067332	0.0000	0.0000
Vrk3	ENSMUSG00000002205	vaccinia related kinase 3	-2.16055124	0.0000	0.0000
Vtn	ENSMUSG00000017344	vitronectin	-2.89124016	0.0000	0.0000
Vwa3a	ENSMUSG00000030889	von Willebrand factor A domain containing 3A	-1.83416733	0.0004	0.0014
Vwa5a	ENSMUSG00000023186	von Willebrand factor A domain containing 5A	-1.99217413	0.0000	0.0000
Vwa7	ENSMUSG00000007030	von Willebrand factor A domain containing 7	-1.57754774	0.0000	0.0000
Was	ENSMUSG00000031165	Wiskott-Aldrich syndrome	-2.03724976	0.0006	0.0019
Washc3	ENSMUSG00000020056	WASH complex subunit 3	-1.63892025	0.0000	0.0000
Washc5	ENSMUSG00000022350	WASH complex subunit 5	-1.83182355	0.0000	0.0000
Wbp2	ENSMUSG00000034341	WW domain binding protein 2	-2.48215266	0.0000	0.0000
Wdfy4	ENSMUSG00000051506	WD repeat and FYVE domain containing 4	-1.84560863	0.0015	0.0044
Wdr18	ENSMUSG00000035754	WD repeat domain 18	-2.15691569	0.0000	0.0000
Wdr19	ENSMUSG00000037890	WD repeat domain 19	-1.80712089	0.0008	0.0026
Wdr24	ENSMUSG00000025737	WD repeat domain 24	-1.89618957	0.0000	0.0000
Wdr45	ENSMUSG00000039382	WD repeat domain 45	-2.17587987	0.0000	0.0001
Wdr54	ENSMUSG00000030032	WD repeat domain 54	-2.24575851	0.0084	0.0205
Wdr6	ENSMUSG00000066357	WD repeat domain 6	-1.95487016	0.0000	0.0000
Wdr70	ENSMUSG00000039828	WD repeat domain 70	-1.50840391	0.0004	0.0012
Wdr73	ENSMUSG00000025722	WD repeat domain 73	-1.85911766	0.0000	0.0000
Wdr74	ENSMUSG00000042729	WD repeat domain 74	-2.38266899	0.0000	0.0000
Wdr83os	ENSMUSG00000059355	WD repeat domain 83 opposite strand	-2.12746112	0.0000	0.0000
Wdr86	ENSMUSG00000055235	WD repeat domain 86	-5.2604795	0.0004	0.0012
Wdr90	ENSMUSG00000073434	WD repeat domain 90	-2.23839285	0.0000	0.0001
Wdr91	ENSMUSG00000058486	WD repeat domain 91	-1.88207747	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Wfdc1	ENSMUSG00000023336	WAP four-disulfide core domain 1	-3.49376761	0.0000	0.0000
Wfdc2	ENSMUSG00000017723	WAP four-disulfide core domain 2	-27.894755	0.0074	0.0183
Wfikkn1	ENSMUSG00000071192	WAP, FS, Ig, KU, and NTR-containing protein 1	-10.3804463	0.0208	0.0456
Wif1	ENSMUSG00000020218	Wnt inhibitory factor 1	-1.73319556	0.0012	0.0036
Wipf3	ENSMUSG00000086040	WAS/WASL interacting protein family, member 3	-1.72436526	0.0000	0.0000
Wrap53	ENSMUSG00000041346	WD repeat containing, antisense to Trp53	-1.57945657	0.0000	0.0000
Wrap73	ENSMUSG00000029029	WD repeat containing, antisense to Trp73	-2.28935268	0.0000	0.0000
Wscd1	ENSMUSG00000020811	WSC domain containing 1	-1.85726531	0.0001	0.0004
Wwp2	ENSMUSG00000031930	WW domain containing E3 ubiquitin protein ligase 2	-1.63738525	0.0000	0.0000
Xaf1	ENSMUSG00000040483	XIAP associated factor 1	-1.71635731	0.0039	0.0105
Xirp1	ENSMUSG00000079243	xin actin-binding repeat containing 1	-1.9191001	0.0000	0.0000
Xlr4a	ENSMUSG00000079845	X-linked lymphocyte-regulated 4A	-33.7692312	0.0343	0.0700
Xpnpep1	ENSMUSG00000025027	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-2.14188843	0.0000	0.0000
Xpnpep2	ENSMUSG00000037005	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	-10.7031304	0.0004	0.0013
Xrcc1	ENSMUSG00000051768	X-ray repair complementing defective repair in Chinese hamster cells 1	-1.60567964	0.0000	0.0000
Xrcc3	ENSMUSG00000021287	X-ray repair complementing defective repair in Chinese hamster cells 3	-1.8702479	0.0445	0.0874
Ydjc	ENSMUSG00000041774	YdjC homolog (bacterial)	-2.80463259	0.0000	0.0001
Yeats2	ENSMUSG00000041215	YEATS domain containing 2	-1.52168521	0.0019	0.0055
Yif1a	ENSMUSG00000024875	Yip1 interacting factor homolog A (S. cerevisiae)	-2.2680719	0.0000	0.0000
Yif1b	ENSMUSG00000030588	Yip1 interacting factor homolog B (S. cerevisiae)	-3.85695737	0.0000	0.0000
Yipf1	ENSMUSG00000057375	Yip1 domain family, member 1	-1.85173245	0.0000	0.0000
Yipf7	ENSMUSG00000029158	Yip1 domain family, member 7	-1.93591492	0.0000	0.0000
Yjefn3	ENSMUSG00000048967	YjeF N-terminal domain containing 3	-1.73117374	0.0011	0.0035
Yju2	ENSMUSG00000003208	YJU2 splicing factor	-1.50614646	0.0001	0.0003
Zbed5-ps	ENSMUSG00000110424	zinc finger, BED type containing 5, pseudogene	-1.86108657	0.0161	0.0363
Zbtb3	ENSMUSG00000071661	zinc finger and BTB domain containing 3	-1.6993721	0.0018	0.0052
Zbtb45	ENSMUSG00000049600	zinc finger and BTB domain containing 45	-2.25582318	0.0000	0.0000
Zbtb48	ENSMUSG00000028952	zinc finger and BTB domain containing 48	-1.72766686	0.0001	0.0002
Zc2hc1c	ENSMUSG00000045064	zinc finger, C2HC-type containing 1C	-1.54937131	0.0391	0.0783
Zc3h3	ENSMUSG00000075600	zinc finger CCCH type containing 3	-3.3067722	0.0000	0.0001
Zc3hc1	ENSMUSG00000039130	zinc finger, C3HC type 1	-1.51565652	0.0000	0.0000

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zdhhc12	ENSMUSG00000015335	zinc finger, DHHC domain containing 12	-4.22543412	0.0000	0.0000
Zdhhc16	ENSMUSG00000025157	zinc finger, DHHC domain containing 16	-1.73308187	0.0000	0.0000
Zdhhc24	ENSMUSG00000006463	zinc finger, DHHC domain containing 24	-1.5231179	0.0001	0.0004
Zdhhc4	ENSMUSG00000001844	zinc finger, DHHC domain containing 4	-1.74701493	0.0000	0.0000
Zdhhc8	ENSMUSG00000060166	zinc finger, DHHC domain containing 8	-1.62244371	0.0000	0.0000
Zer1	ENSMUSG00000039686	zyg-11 related, cell cycle regulator	-1.85091707	0.0000	0.0000
Zfand2a	ENSMUSG00000053581	zinc finger, AN1-type domain 2A	-1.69325086	0.0000	0.0000
Zfand2b	ENSMUSG00000026197	zinc finger, AN1 type domain 2B	-1.90333811	0.0000	0.0000
Zfat	ENSMUSG00000022335	zinc finger and AT hook domain containing	-1.6237571	0.0004	0.0014
Zfp119a	ENSMUSG00000057835	zinc finger protein 119a	-1.93517444	0.0000	0.0000
Zfp128	ENSMUSG00000060397	zinc finger protein 128	-1.67918767	0.0006	0.0021
Zfp142	ENSMUSG00000026135	zinc finger protein 142	-1.60081739	0.0000	0.0000
Zfp174	ENSMUSG00000054939	zinc finger protein 174	-2.09726444	0.0000	0.0000
Zfp185	ENSMUSG00000031351	zinc finger protein 185	-2.34095454	0.0101	0.0243
Zfp2	ENSMUSG00000049321	zinc finger protein 2	-1.69480161	0.0000	0.0001
Zfp213	ENSMUSG00000071256	zinc finger protein 213	-1.8384027	0.0000	0.0001
Zfp263	ENSMUSG00000022529	zinc finger protein 263	-1.55670637	0.0000	0.0000
Zfp276	ENSMUSG00000001065	zinc finger protein (C2H2 type) 276	-1.94568228	0.0000	0.0000
Zfp277	ENSMUSG00000055917	zinc finger protein 277	-2.12653845	0.0000	0.0000
Zfp296	ENSMUSG00000011267	zinc finger protein 296	-3.06954383	0.0015	0.0044
Zfp324	ENSMUSG00000004500	zinc finger protein 324	-1.83483691	0.0000	0.0001
Zfp335	ENSMUSG00000039834	zinc finger protein 335	-1.82540202	0.0000	0.0000
Zfp346	ENSMUSG00000021481	zinc finger protein 346	-1.65013902	0.0000	0.0000
Zfp358	ENSMUSG00000047264	zinc finger protein 358	-1.68609445	0.0000	0.0000
Zfp36l1-ps	ENSMUSG00000080942	zinc finger protein 36, C3H type-like 1, pseudogene	-20.1000866	0.0000	0.0000
Zfp41	ENSMUSG00000047003	zinc finger protein 41	-1.83143113	0.0003	0.0012
Zfp410	ENSMUSG00000042472	zinc finger protein 410	-1.51404305	0.0203	0.0446
Zfp414	ENSMUSG00000073423	zinc finger protein 414	-2.25368539	0.0000	0.0000
Zfp418	ENSMUSG00000034538	zinc finger protein 418	-1.52078304	0.0448	0.0880
Zfp446	ENSMUSG00000033961	zinc finger protein 446	-2.29847231	0.0000	0.0000
Zfp455	ENSMUSG00000051037	zinc finger protein 455	-1.60304685	0.0106	0.0252

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp456	ENSMUSG00000078995	zinc finger protein 456	-2.06462625	0.0112	0.0266
Zfp458	ENSMUSG00000055480	zinc finger protein 458	-1.6522269	0.0479	0.0931
Zfp469	ENSMUSG00000043903	zinc finger protein 469	-2.06904928	0.0000	0.0000
Zfp51	ENSMUSG00000023892	zinc finger protein 51	-1.909091	0.0000	0.0000
Zfp511	ENSMUSG00000025470	zinc finger protein 511	-2.02395591	0.0000	0.0000
Zfp524	ENSMUSG00000051184	zinc finger protein 524	-2.80931994	0.0000	0.0000
Zfp536	ENSMUSG00000043456	zinc finger protein 536	-1.54211569	0.0092	0.0223
Zfp619	ENSMUSG00000068959	zinc finger protein 619	-1.70331022	0.0001	0.0005
Zfp637	ENSMUSG00000059689	zinc finger protein 637	-2.57126135	0.0000	0.0000
Zfp64	ENSMUSG00000027551	zinc finger protein 64	-1.76590035	0.0000	0.0000
Zfp647	ENSMUSG00000054967	zinc finger protein 647	-4.73025741	0.0000	0.0000
Zfp653	ENSMUSG00000038895	zinc finger protein 653	-2.48880042	0.0000	0.0001
Zfp658	ENSMUSG00000056592	zinc finger protein 658	-1.74972354	0.0315	0.0651
Zfp672	ENSMUSG00000049755	zinc finger protein 672	-2.07970494	0.0000	0.0000
Zfp688	ENSMUSG00000045251	zinc finger protein 688	-1.69015734	0.0008	0.0025
Zfp706	ENSMUSG00000062397	zinc finger protein 706	-1.57910898	0.0002	0.0005
Zfp707	ENSMUSG00000034429	zinc finger protein 707	-1.75214826	0.0001	0.0004
Zfp709	ENSMUSG00000056019	zinc finger protein 709	-1.5711442	0.0003	0.0011
Zfp712	ENSMUSG00000090641	zinc finger protein 712	-3.27306034	0.0000	0.0000
Zfp719	ENSMUSG00000030469	zinc finger protein 719	-1.7093512	0.0001	0.0005
Zfp729b	ENSMUSG00000058093	zinc finger protein 729b	-2.07306616	0.0000	0.0000
Zfp748	ENSMUSG00000095432	zinc finger protein 748	-2.21092284	0.0000	0.0000
Zfp781	ENSMUSG00000096718	zinc finger protein 781	-4.60538972	0.0228	0.0493
Zfp788	ENSMUSG00000074165	zinc finger protein 788	-1.60066552	0.0000	0.0001
Zfp808	ENSMUSG00000074867	zinc finger protein 808	-5.08415984	0.0000	0.0000
Zfp810	ENSMUSG00000066829	zinc finger protein 810	-1.51613918	0.0000	0.0000
Zfp85	ENSMUSG00000058331	zinc finger protein 85	-1.62532432	0.0024	0.0068
Zfp862-ps	ENSMUSG00000107476	zinc finger protein 862, pseudogene	-1.51722067	0.0000	0.0000
Zfp868	ENSMUSG00000060427	zinc finger protein 868	-1.52524574	0.0000	0.0001
Zfp87	ENSMUSG00000097333	zinc finger protein 87	-1.84350382	0.0000	0.0000
Zfp873	ENSMUSG00000061371	zinc finger protein 873	-1.64959888	0.0025	0.0071

• **Table S1: Differentially expressed transcripts in mG4H-ON compared to Con-ON**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp874a	ENSMUSG00000069206	zinc finger protein 874a	-1.68342142	0.0006	0.0018
Zfp874b	ENSMUSG00000059839	zinc finger protein 874b	-1.65921772	0.0003	0.0010
Zfp9	ENSMUSG00000072623	zinc finger protein 9	-1.8939723	0.0000	0.0000
Zfp954	ENSMUSG00000062116	zinc finger protein 954	-2.21125099	0.0000	0.0000
Zfp956	ENSMUSG00000045466	zinc finger protein 956	-1.79504966	0.0010	0.0031
Zfp958	ENSMUSG00000058748	zinc finger protein 958	-2.0989543	0.0000	0.0000
Zfp964	ENSMUSG00000091764	zinc finger protein 964	-1.62601563	0.0062	0.0156
Zfp97	ENSMUSG00000095990	zinc finger protein 97	-4.2692082	0.0000	0.0000
Zfp971	ENSMUSG00000074519	zinc finger protein 971	-1.78049241	0.0000	0.0000
Zfp975	ENSMUSG00000069727	zinc finger protein 975	-1.5749701	0.0053	0.0138
Zfp977	ENSMUSG00000092335	zinc finger protein 977	-8.39923237	0.0001	0.0003
Zfp983	ENSMUSG00000035868	zinc finger protein 983	-1.9948797	0.0047	0.0123
Zfpl1	ENSMUSG00000024792	zinc finger like protein 1	-1.77180633	0.0000	0.0000
Zfyve19	ENSMUSG00000068580	zinc finger, FYVE domain containing 19	-2.42167038	0.0000	0.0000
Zfyve21	ENSMUSG00000021286	zinc finger, FYVE domain containing 21	-2.63688181	0.0000	0.0000
Zfyve26	ENSMUSG00000066440	zinc finger, FYVE domain containing 26	-1.93496346	0.0000	0.0000
Zkscan17	ENSMUSG00000020472	zinc finger with KRAB and SCAN domains 17	-2.38045092	0.0000	0.0000
Zkscan5	ENSMUSG00000055991	zinc finger with KRAB and SCAN domains 5	-1.60062712	0.0002	0.0008
Zmat5	ENSMUSG00000009076	zinc finger, matrin type 5	-1.58924793	0.0000	0.0000
Zmiz1os1	ENSMUSG00000087535	Zmiz1 opposite strand 1	-2.97987828	0.0110	0.0261
Zmiz2	ENSMUSG00000041164	zinc finger, MIZ-type containing 2	-1.544475	0.0000	0.0000
Zmym3	ENSMUSG00000031310	zinc finger, MYM-type 3	-1.50929409	0.0000	0.0000
Znhit1	ENSMUSG00000059518	zinc finger, HIT domain containing 1	-1.60518842	0.0000	0.0000
Znhit2	ENSMUSG00000075227	zinc finger, HIT domain containing 2	-2.55512051	0.0000	0.0000
Znhit3	ENSMUSG00000020526	zinc finger, HIT type 3	-1.98883941	0.0000	0.0000
Zp2	ENSMUSG00000030911	zona pellucida glycoprotein 2	-2.78362105	0.0042	0.0110
Zswim1	ENSMUSG00000017764	zinc finger SWIM-type containing 1	-2.56890141	0.0000	0.0000
Zswim3	ENSMUSG00000045822	zinc finger SWIM-type containing 3	-1.5303502	0.0227	0.0491
Zswim7	ENSMUSG00000014243	zinc finger SWIM-type containing 7	-1.88850493	0.0000	0.0000
Zwint	ENSMUSG00000019923	ZW10 interactor	-1.71233275	0.0000	0.0000
	ENSMUSG00000095041		-1.51834691	0.0072	0.0180

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610009L18Rik	ENSMUSG00000043644	RIKEN cDNA 0610009L18 gene	4.378	0.0000	0.0000
1110004F10Rik	ENSMUSG00000030663	RIKEN cDNA 1110004F10 gene	1.658	0.0000	0.0000
1110018N20Rik	ENSMUSG00000085151	RIKEN cDNA 1110018N20 gene	2.370	0.0000	0.0000
1110032F04Rik	ENSMUSG00000046999	RIKEN cDNA 1110032F04 gene	4.323	0.0003	0.0011
1110038F14Rik	ENSMUSG00000063236	RIKEN cDNA 1110038F14 gene	1.848	0.0000	0.0000
1110065P20Rik	ENSMUSG00000078570	RIKEN cDNA 1110065P20 gene	1.612	0.0447	0.0941
1190005I06Rik	ENSMUSG00000043687	RIKEN cDNA 1190005I06 gene	5.736	0.0000	0.0000
1300002E11Rik	ENSMUSG00000097290	RIKEN cDNA 1300002E11 gene	2.146	0.0000	0.0000
1500011B03Rik	ENSMUSG00000072694	RIKEN cDNA 1500011B03 gene	1.576	0.0060	0.0168
1600014C23Rik	ENSMUSG00000094690	RIKEN cDNA 1600014C23 gene	4.303	0.0001	0.0006
1700018L02Rik	ENSMUSG00000100075	RIKEN cDNA 1700018L02 gene	1.791	0.0397	0.0855
1700034H15Rik	ENSMUSG00000055833	RIKEN cDNA 1700034H15 gene	3.746	0.0000	0.0000
1700048O20Rik	ENSMUSG00000043773	RIKEN cDNA 1700048O20 gene	2.572	0.0168	0.0411
1700063J08Rik	ENSMUSG00000117080	RIKEN cDNA 1700063J08 gene	3.062	0.0400	0.0861
1700081N11Rik	ENSMUSG00000113209	RIKEN cDNA 1700081N11 gene	2.585	0.0005	0.0017
1700084E18Rik	ENSMUSG00000100747	RIKEN cDNA 1700084E18 gene	3.881	0.0000	0.0000
1700095B10Rik	ENSMUSG00000098230	RIKEN cDNA 1700095B10 gene	30.945	0.0001	0.0002
1700119I11Rik	ENSMUSG00000082488	RIKEN cDNA 1700119I11 gene	5.654	0.0357	0.0781
1810009A15Rik	ENSMUSG00000071653	RIKEN cDNA 1810009A15 gene	5.807	0.0426	0.0906
1810019N24Rik	ENSMUSG00000097115	RIKEN cDNA 1810019N24 gene	2.310	0.0477	0.0995
1810034E14Rik	ENSMUSG00000097101	RIKEN cDNA 1810034E14 gene	1.501	0.0179	0.0435
1810037I17Rik	ENSMUSG00000054091	RIKEN cDNA 1810037I17 gene	1.769	0.0000	0.0000
1810049J17Rik	ENSMUSG00000097221	RIKEN cDNA 1810049J17 gene	59.315	0.0000	0.0000
1810073O08Rik	ENSMUSG00000117442	RIKEN cDNA 1810073O08 gene	2.295	0.0135	0.0341
2010001A14Rik	ENSMUSG00000087165	RIKEN cDNA 2010001A14 gene	5.474	0.0000	0.0000
2300009A05Rik	ENSMUSG00000032403	RIKEN cDNA 2300009A05 gene	2.070	0.0000	0.0001
2310001H17Rik	ENSMUSG00000097354	RIKEN cDNA 2310001H17 gene	1.655	0.0179	0.0434
2310009B15Rik	ENSMUSG00000079283	RIKEN cDNA 2310009B15 gene	1.778	0.0000	0.0000
2310010J17Rik	ENSMUSG00000097162	RIKEN cDNA 2310010J17 gene	2.980	0.0000	0.0000
2310014F06Rik	ENSMUSG00000085945	RIKEN cDNA 2310014F06 gene	2.237	0.0056	0.0157
2310061I04Rik	ENSMUSG00000050705	RIKEN cDNA 2310061I04 gene	2.311	0.0026	0.0081

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
2410004B18Rik	ENSMUSG00000036873	RIKEN cDNA 2410004B18 gene	1.557	0.0065	0.0180
2410022M11Rik	ENSMUSG00000100017	RIKEN cDNA 2410022M11 gene	2.692	0.0001	0.0005
2510039O18Rik	ENSMUSG00000044496	RIKEN cDNA 2510039O18 gene	1.736	0.0005	0.0018
2610037D02Rik	ENSMUSG00000097536	RIKEN cDNA 2610037D02 gene	2.051	0.0120	0.0307
2610306M01Rik	ENSMUSG00000100164	RIKEN cDNA 2610306M01 gene	2.124	0.0000	0.0000
2810002D19Rik	ENSMUSG00000045464	RIKEN cDNA 2810002D19 gene	2.284	0.0001	0.0003
2810021J22Rik	ENSMUSG00000020491	RIKEN cDNA 2810021J22 gene	1.586	0.0041	0.0120
2810405F17Rik	ENSMUSG00000101493	RIKEN cDNA 2810405F17 gene	2.166	0.0473	0.0988
2900005J15Rik	ENSMUSG00000043833	RIKEN cDNA 2900005J15 gene	4.676	0.0001	0.0002
2900089D17Rik	ENSMUSG00000087484	RIKEN cDNA 2900089D17 gene	2.583	0.0000	0.0001
3110021N24Rik	ENSMUSG00000094958	RIKEN cDNA 3110021N24 gene	10.525	0.0000	0.0000
3110040N11Rik	ENSMUSG00000025102	RIKEN cDNA 3110040N11 gene	1.944	0.0000	0.0000
3110082I17Rik	ENSMUSG00000053553	RIKEN cDNA 3110082I17 gene	2.094	0.0000	0.0000
4833403J16Rik	ENSMUSG00000107481	RIKEN cDNA 4833403J16 gene	2.119	0.0002	0.0010
4833438C02Rik	ENSMUSG00000118087	RIKEN cDNA 4833438C02 gene	2.014	0.0009	0.0031
4921504A21Rik	ENSMUSG00000097626	RIKEN cDNA 4921504A21 gene	2.147	0.0000	0.0000
4921524J17Rik	ENSMUSG00000036934	RIKEN cDNA 4921524J17 gene	1.705	0.0000	0.0000
4921531C22Rik	ENSMUSG00000085704	RIKEN cDNA 4921531C22 gene	1.804	0.0051	0.0146
4930412F12Rik	ENSMUSG00000110289	RIKEN cDNA 4930412F12 gene	2.785	0.0100	0.0262
4930500M09Rik	ENSMUSG00000044306	RIKEN cDNA 4930500M09 gene	19.383	0.0062	0.0172
4930507D05Rik	ENSMUSG00000097129	RIKEN cDNA 4930507D05 gene	4.256	0.0001	0.0003
4930526A20Rik	ENSMUSG00000085521	RIKEN cDNA 4930526A20 gene	12.011	0.0000	0.0000
4930577N17Rik	ENSMUSG00000087440	RIKEN cDNA 4930577N17 gene	8.191	0.0000	0.0000
4930597O21Rik	ENSMUSG00000053442	RIKEN cDNA 4930597O21 gene	18.762	0.0389	0.0842
4931403E22Rik	ENSMUSG00000093772	RIKEN cDNA 4931403E22 gene	12.952	0.0000	0.0000
4931440P22Rik	ENSMUSG00000074580	RIKEN cDNA 4931440P22 gene	7.419	0.0000	0.0000
4933412E12Rik	ENSMUSG00000112627	RIKEN cDNA 4933412E12 gene	2.101	0.0004	0.0013
4933415A04Rik	ENSMUSG00000045877	RIKEN cDNA 4933415A04 gene	6.148	0.0000	0.0001
4933421O10Rik	ENSMUSG00000085037	RIKEN cDNA 4933421O10 gene	2.097	0.0000	0.0001
4933427D14Rik	ENSMUSG00000107877	RIKEN cDNA 4933427D14 gene	3.771	0.0006	0.0023
4933431K14Rik	ENSMUSG00000103715	RIKEN cDNA 4933431K14 gene	1.580	0.0037	0.0111

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
5033417F24Rik	ENSMUSG00000097251	RIKEN cDNA 5033417F24 gene	1.713	0.0140	0.0351
5330439K02Rik	ENSMUSG00000097827	RIKEN cDNA 5330439K02 gene	5.432	0.0000	0.0000
5730409E04Rik	ENSMUSG00000073755	RIKEN cDNA 5730409E04Rik gene	1.953	0.0000	0.0000
5730480H06Rik	ENSMUSG00000029089	RIKEN cDNA 5730480H06 gene	1.753	0.0000	0.0001
5830454E08Rik	ENSMUSG00000052658	RIKEN cDNA 5830454E08 gene	2.782	0.0001	0.0006
6330562C20Rik	ENSMUSG00000093424	RIKEN cDNA 6330562C20 gene	2.356	0.0051	0.0146
6430573P05Rik	ENSMUSG00000102545	RIKEN cDNA 6430573P05 gene	3.034	0.0000	0.0000
6430710C18Rik	ENSMUSG00000085427	RIKEN cDNA 6430710C18 gene	1.682	0.0466	0.0977
6530402F18Rik	ENSMUSG00000079499	RIKEN cDNA 6530402F18 gene	3.561	0.0000	0.0000
8030453O22Rik	ENSMUSG00000085058	RIKEN cDNA 8030453O22 gene	2.449	0.0450	0.0947
9030407P20Rik	ENSMUSG00000097343	RIKEN cDNA 9030407P20 gene	1.706	0.0092	0.0244
9130017K11Rik	ENSMUSG00000055134	RIKEN cDNA 9130017K11 gene	2.759	0.0049	0.0141
9130230N09Rik	ENSMUSG00000092626	RIKEN cDNA 9130230N09 gene	3.302	0.0153	0.0380
9130401M01Rik	ENSMUSG00000101892	RIKEN cDNA 9130401M01 gene	1.815	0.0000	0.0000
9330160F10Rik	ENSMUSG00000072809	RIKEN cDNA 9330160F10 gene	2.007	0.0097	0.0256
9330162012Rik	ENSMUSG00000086448	cDNA RIKEN 9330162012 gene	2.328	0.0002	0.0008
9330162G02Rik	ENSMUSG00000109536	RIKEN cDNA 9330162G02 gene	1.897	0.0015	0.0051
9430062P05Rik	ENSMUSG00000104263	RIKEN cDNA 9430062P05 gene	2.341	0.0088	0.0235
A330041J22Rik	ENSMUSG00000087466	RIKEN cDNA A330041J22 gene	5.935	0.0000	0.0000
A430027H14Rik	ENSMUSG00000104507	RIKEN cDNA A430027H14 gene	6.618	0.0007	0.0026
A530058N18Rik	ENSMUSG00000092201	RIKEN cDNA A530058N18 gene	2.092	0.0216	0.0509
A530072M11Rik	ENSMUSG00000085112	RIKEN cDNA gene A530072M11	2.199	0.0233	0.0544
A630019I02Rik	ENSMUSG00000114968	RIKEN cDNA A630019I02 gene	5.917	0.0000	0.0001
A830035O19Rik	ENSMUSG00000111329	RIKEN cDNA A830035O19 gene	2.498	0.0001	0.0004
A930015D03Rik	ENSMUSG00000092368	RIKEN cDNA A930015D03 gene	2.409	0.0000	0.0000
A930016O22Rik	ENSMUSG00000040705	RIKEN cDNA A930016O22 gene	5.082	0.0000	0.0000
A930018P22Rik	ENSMUSG00000032671	RIKEN cDNA A930018P22 gene	6.698	0.0002	0.0009
A930035D04Rik	ENSMUSG00000052241	RIKEN cDNA A930035D04 gene	5.402	0.0000	0.0000
AA414768	ENSMUSG00000083307	expressed sequence AA414768	1.924	0.0136	0.0344
Aatf	ENSMUSG00000018697	apoptosis antagonizing transcription factor	1.933	0.0000	0.0000
Abcc3	ENSMUSG00000020865	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	1.516	0.0397	0.0855

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Abcf1	ENSMUSG00000038762	ATP-binding cassette, sub-family F (GCN20), member 1	2.050	0.0000	0.0000
Abhd11os	ENSMUSG00000085042	abhydrolase domain containing 11, opposite strand	3.701	0.0111	0.0287
Abhd17a	ENSMUSG00000003346	abhydrolase domain containing 17A	1.512	0.0263	0.0604
Abhd17b	ENSMUSG00000047368	abhydrolase domain containing 17B	1.615	0.0000	0.0002
Abl2	ENSMUSG00000026596	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	1.595	0.0000	0.0001
Abracl	ENSMUSG00000078453	ABRA C-terminal like	1.779	0.0000	0.0000
Acbd3	ENSMUSG00000026499	acyl-Coenzyme A binding domain containing 3	3.341	0.0000	0.0000
Acbd6	ENSMUSG00000033701	acyl-Coenzyme A binding domain containing 6	1.886	0.0384	0.0831
Acin1	ENSMUSG00000022185	apoptotic chromatin condensation inducer 1	2.055	0.0000	0.0000
Ackr4	ENSMUSG00000079355	atypical chemokine receptor 4	1.829	0.0116	0.0297
Acot4	ENSMUSG00000052392	acyl-CoA thioesterase 4	1.530	0.0331	0.0731
Acsm5	ENSMUSG00000030972	acyl-CoA synthetase medium-chain family member 5	2.140	0.0000	0.0001
Actr3-ps	ENSMUSG00000082319	actin related protein 3, pseudogene	2.212	0.0000	0.0000
Acvr1b	ENSMUSG00000000532	activin A receptor, type 1B	1.810	0.0000	0.0000
Acvr2b	ENSMUSG00000061393	activin receptor IIB	1.861	0.0000	0.0000
Adam23	ENSMUSG00000025964	a disintegrin and metallopeptidase domain 23	1.735	0.0000	0.0000
Adamts19	ENSMUSG00000053441	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19	2.066	0.0025	0.0079
Adamts8	ENSMUSG00000031994	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8	2.357	0.0279	0.0636
Adat2	ENSMUSG00000019808	adenosine deaminase, tRNA-specific 2	2.590	0.0000	0.0000
Adgrb2	ENSMUSG00000028782	adhesion G protein-coupled receptor B2	2.242	0.0014	0.0045
Adgrl1	ENSMUSG00000013033	adhesion G protein-coupled receptor L1	1.508	0.0001	0.0004
Adipor1	ENSMUSG00000026457	adiponectin receptor 1	1.660	0.0000	0.0000
Adnp	ENSMUSG00000051149	activity-dependent neuroprotective protein	23.217	0.0000	0.0000
Adra1d	ENSMUSG00000027335	adrenergic receptor, alpha 1d	2.544	0.0000	0.0001
Adra2c	ENSMUSG00000045318	adrenergic receptor, alpha 2c	4.541	0.0002	0.0007
Adrb1	ENSMUSG00000035283	adrenergic receptor, beta 1	2.727	0.0000	0.0000
Adssl1	ENSMUSG00000011148	adenylosuccinate synthetase like 1	1.781	0.0000	0.0000
Aebp2	ENSMUSG00000030232	AE binding protein 2	2.580	0.0000	0.0000
Aga	ENSMUSG00000031521	aspartylglucosaminidase	1.946	0.0000	0.0000
Agap3	ENSMUSG00000023353	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	2.481	0.0000	0.0000
Agbl5	ENSMUSG00000029165	ATP/GTP binding protein-like 5	1.634	0.0000	0.0002

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Agpat4	ENSMUSG00000023827	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	1.553	0.0001	0.0003
Agpat5	ENSMUSG00000031467	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.554	0.0000	0.0000
Agtpbp1	ENSMUSG00000021557	ATP/GTP binding protein 1	1.807	0.0000	0.0000
Ahcyl1	ENSMUSG00000027893	S-adenosylhomocysteine hydrolase-like 1	1.851	0.0000	0.0000
Ahcyl2	ENSMUSG00000029772	S-adenosylhomocysteine hydrolase-like 2	1.752	0.0000	0.0000
Ahsa2	ENSMUSG00000020288	AHA1, activator of heat shock protein ATPase 2	1.663	0.0000	0.0000
AI662270	ENSMUSG00000087107	expressed sequence AI662270	2.284	0.0206	0.0490
Aif1	ENSMUSG00000024397	allograft inflammatory factor 1	2.395	0.0024	0.0075
Aif1l	ENSMUSG00000001864	allograft inflammatory factor 1-like	1.958	0.0000	0.0002
Aifm1	ENSMUSG00000036932	apoptosis-inducing factor, mitochondrion-associated 1	2.051	0.0000	0.0000
Ak6	ENSMUSG00000078941	adenylate kinase 6	1.997	0.0000	0.0000
Akap7	ENSMUSG00000039166	A kinase (PRKA) anchor protein 7	1.943	0.0000	0.0000
Akap8	ENSMUSG00000024045	A kinase (PRKA) anchor protein 8	2.122	0.0000	0.0000
Akap9	ENSMUSG00000040407	A kinase (PRKA) anchor protein (yotiao) 9	1.551	0.0001	0.0005
Akirin2	ENSMUSG00000028291	akirin 2	2.208	0.0000	0.0000
Akr1c13	ENSMUSG00000021213	aldo-keto reductase family 1, member C13	2.043	0.0082	0.0220
Aktip	ENSMUSG00000031667	AKT interacting protein	1.500	0.0000	0.0000
Aldoa	ENSMUSG00000114515	aldolase A, fructose-bisphosphate	3.355	0.0078	0.0211
Aldoart1	ENSMUSG00000059343	aldolase 1 A, retrogene 1	8.125	0.0000	0.0000
Alk	ENSMUSG00000055471	anaplastic lymphoma kinase	9.753	0.0128	0.0325
Alox8	ENSMUSG00000020891	arachidonate 8-lipoxygenase	7.373	0.0266	0.0609
Als2	ENSMUSG00000026024	alsin Rho guanine nucleotide exchange factor	1.561	0.0000	0.0000
Alyref	ENSMUSG00000025134	Aly/REF export factor	6.399	0.0000	0.0000
Alyref2	ENSMUSG00000060244	Aly/REF export factor 2	1.828	0.0007	0.0027
Amy1	ENSMUSG00000074264	amylase 1, salivary	1.550	0.0170	0.0416
Anapc13	ENSMUSG00000035048	anaphase promoting complex subunit 13	4.278	0.0000	0.0000
Anapc15	ENSMUSG00000030649	anaphase promoting complex C subunit 15	1.939	0.0000	0.0000
Ank1	ENSMUSG00000031543	ankyrin 1, erythroid	1.867	0.0000	0.0000
Ankhd1	ENSMUSG00000024483	ankyrin repeat and KH domain containing 1	1.537	0.0000	0.0001
Ankle1	ENSMUSG00000046295	ankyrin repeat and LEM domain containing 1	3.333	0.0195	0.0467
Ankrd1	ENSMUSG00000024803	ankyrin repeat domain 1 (cardiac muscle)	1.755	0.0066	0.0182

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ankrd11	ENSMUSG00000035569	ankyrin repeat domain 11	1.611	0.0000	0.0000
Ankrd13a	ENSMUSG00000041870	ankyrin repeat domain 13a	1.650	0.0000	0.0000
Ankrd35	ENSMUSG00000038354	ankyrin repeat domain 35	2.480	0.0017	0.0056
Ankrd40	ENSMUSG00000020864	ankyrin repeat domain 40	2.204	0.0000	0.0000
Ankrd63	ENSMUSG00000078137	ankyrin repeat domain 63	2.012	0.0058	0.0164
Anks1b	ENSMUSG00000058589	ankyrin repeat and sterile alpha motif domain containing 1B	2.046	0.0245	0.0568
Ano8	ENSMUSG00000034863	anoctamin 8	3.821	0.0000	0.0000
Anp32a	ENSMUSG00000032249	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	2.455	0.0000	0.0000
Anp32b	ENSMUSG00000028333	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	7.115	0.0000	0.0000
Anp32b-ps1	ENSMUSG00000081792	Bacidic (leucine-rich) nuclear phosphoprotein 32 family, member B, pseudogene 1	10.362	0.0014	0.0047
Anp32e	ENSMUSG00000015749	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	2.359	0.0000	0.0000
Anxa5	ENSMUSG00000027712	annexin A5	1.943	0.0000	0.0000
Anxa8	ENSMUSG00000021950	annexin A8	2.855	0.0442	0.0932
Ap1ar	ENSMUSG00000074238	adaptor-related protein complex 1 associated regulatory protein	1.516	0.0001	0.0003
Ap3b1	ENSMUSG00000021686	adaptor-related protein complex 3, beta 1 subunit	2.057	0.0000	0.0000
Ap3s1	ENSMUSG00000024480	adaptor-related protein complex 3, sigma 1 subunit	3.656	0.0000	0.0000
Apip	ENSMUSG00000010911	APAF1 interacting protein	1.538	0.0000	0.0000
Aplf	ENSMUSG00000030051	aprataxin and PNKP like factor	1.742	0.0000	0.0000
Aplp1	ENSMUSG00000006651	amyloid beta (A4) precursor-like protein 1	1.795	0.0000	0.0001
Aplp2	ENSMUSG00000031996	amyloid beta (A4) precursor-like protein 2	1.589	0.0000	0.0000
Apobr	ENSMUSG00000042759	apolipoprotein B receptor	2.660	0.0001	0.0003
Apoe	ENSMUSG00000002985	apolipoprotein E	1.707	0.0001	0.0004
Apol10b	ENSMUSG00000050014	apolipoprotein L 10B	2.174	0.0016	0.0052
Apol8	ENSMUSG00000056656	apolipoprotein L 8	3.937	0.0378	0.0821
Apold1	ENSMUSG00000090698	apolipoprotein L domain containing 1	1.543	0.0099	0.0262
Apoo-ps	ENSMUSG00000049233	apolipoprotein O, pseudogene	1.787	0.0003	0.0011
App	ENSMUSG00000022892	amyloid beta (A4) precursor protein	1.699	0.0000	0.0000
Aptx	ENSMUSG00000028411	aprataxin	1.551	0.0000	0.0000
Arf3	ENSMUSG00000051853	ADP-ribosylation factor 3	2.301	0.0000	0.0000
Arf5	ENSMUSG00000020440	ADP-ribosylation factor 5	2.569	0.0000	0.0000
Arf6	ENSMUSG00000044147	ADP-ribosylation factor 6	3.558	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Arglu1	ENSMUSG00000040459	arginine and glutamate rich 1	2.781	0.0000	0.0000
Arhgap11a	ENSMUSG00000041219	Rho GTPase activating protein 11A	2.287	0.0000	0.0000
Arhgap19	ENSMUSG00000025154	Rho GTPase activating protein 19	1.620	0.0001	0.0006
Arhgap22	ENSMUSG00000063506	Rho GTPase activating protein 22	1.793	0.0104	0.0271
Arhgap23	ENSMUSG00000049807	Rho GTPase activating protein 23	2.810	0.0000	0.0000
Arhgap30	ENSMUSG00000048865	Rho GTPase activating protein 30	2.269	0.0000	0.0000
Arhgap44	ENSMUSG00000033389	Rho GTPase activating protein 44	1.630	0.0000	0.0002
Arhgef9	ENSMUSG00000025656	CDC42 guanine nucleotide exchange factor (GEF) 9	1.614	0.0000	0.0000
Arid4a	ENSMUSG00000048118	AT rich interactive domain 4A (RBP1-like)	1.928	0.0000	0.0000
Arid4b	ENSMUSG00000039219	AT rich interactive domain 4B (RBP1-like)	1.731	0.0000	0.0000
Arih1	ENSMUSG00000025234	ariadne RBR E3 ubiquitin protein ligase 1	1.515	0.0000	0.0000
Arl1	ENSMUSG00000060904	ADP-ribosylation factor-like 1	2.048	0.0000	0.0000
Arl10	ENSMUSG00000025870	ADP-ribosylation factor-like 10	2.564	0.0000	0.0001
Arl2bp	ENSMUSG00000031776	ADP-ribosylation factor-like 2 binding protein	1.611	0.0000	0.0000
Arl4a	ENSMUSG00000047446	ADP-ribosylation factor-like 4A	2.173	0.0000	0.0002
Arl4c	ENSMUSG00000049866	ADP-ribosylation factor-like 4C	2.010	0.0000	0.0000
Arl4d	ENSMUSG00000034936	ADP-ribosylation factor-like 4D	1.822	0.0000	0.0001
Arl6ip4	ENSMUSG00000029404	ADP-ribosylation factor-like 6 interacting protein 4	1.895	0.0000	0.0000
Arl6ip5	ENSMUSG00000035199	ADP-ribosylation factor-like 6 interacting protein 5	1.553	0.0000	0.0000
Arl6ip6	ENSMUSG00000026960	ADP-ribosylation factor-like 6 interacting protein 6	1.627	0.0000	0.0000
Arl8a	ENSMUSG00000026426	ADP-ribosylation factor-like 8A	2.852	0.0000	0.0000
Armcx6	ENSMUSG00000050394	armadillo repeat containing, X-linked 6	2.005	0.0012	0.0041
Arnt	ENSMUSG00000015522	aryl hydrocarbon receptor nuclear translocator	1.572	0.0000	0.0000
Arpc2	ENSMUSG00000006304	actin related protein 2/3 complex, subunit 2	1.524	0.0000	0.0000
Arpc5l	ENSMUSG00000026755	actin related protein 2/3 complex, subunit 5-like	1.532	0.0000	0.0000
Arpp19	ENSMUSG00000007656	cAMP-regulated phosphoprotein 19	2.036	0.0000	0.0000
Ascc2	ENSMUSG00000020412	activating signal cointegrator 1 complex subunit 2	1.550	0.0000	0.0000
Asf1a	ENSMUSG00000019857	anti-silencing function 1A histone chaperone	2.678	0.0000	0.0000
Ash2l	ENSMUSG00000031575	ASH2 like histone lysine methyltransferase complex subunit	2.362	0.0000	0.0000
Asph	ENSMUSG00000028207	aspartate-beta-hydroxylase	1.732	0.0000	0.0000
Asprv1	ENSMUSG00000033508	aspartic peptidase, retroviral-like 1	32.090	0.0021	0.0067

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Asrgl1	ENSMUSG00000024654	asparaginase like 1	1.820	0.0000	0.0000
Atad1	ENSMUSG00000013662	ATPase family, AAA domain containing 1	1.819	0.0000	0.0000
Atad2	ENSMUSG00000022360	ATPase family, AAA domain containing 2	1.510	0.0114	0.0294
Atad2b	ENSMUSG00000052812	ATPase family, AAA domain containing 2B	1.506	0.0000	0.0000
Atad3a	ENSMUSG00000029036	ATPase family, AAA domain containing 3A	1.929	0.0000	0.0000
Atf1	ENSMUSG00000023027	activating transcription factor 1	1.892	0.0000	0.0000
Atf2	ENSMUSG00000027104	activating transcription factor 2	1.525	0.0000	0.0000
Atf5	ENSMUSG00000038539	activating transcription factor 5	2.308	0.0002	0.0009
Atg10	ENSMUSG00000021619	autophagy related 10	1.561	0.0000	0.0000
Atg3	ENSMUSG00000022663	autophagy related 3	3.644	0.0000	0.0000
Atn1	ENSMUSG00000004263	atrophin 1	5.929	0.0000	0.0000
Atp1b3	ENSMUSG00000032412	ATPase, Na+/K+ transporting, beta 3 polypeptide	1.789	0.0000	0.0000
Atp2a2	ENSMUSG00000029467	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	2.011	0.0000	0.0000
Atp6v0d2	ENSMUSG00000028238	ATPase, H+ transporting, lysosomal V0 subunit D2	4.124	0.0035	0.0105
Atp6v1g1	ENSMUSG00000039105	ATPase, H+ transporting, lysosomal V1 subunit G1	1.773	0.0000	0.0000
Atp6v1g2	ENSMUSG00000024403	ATPase, H+ transporting, lysosomal V1 subunit G2	1.592	0.0023	0.0073
Atp8b5	ENSMUSG00000028457	ATPase, class I, type 8B, member 5	3.463	0.0109	0.0284
Atxn7	ENSMUSG00000021738	ataxin 7	1.531	0.0000	0.0000
Atxn7l3	ENSMUSG00000059995	ataxin 7-like 3	1.585	0.0001	0.0003
AV099323	ENSMUSG00000087377	expressed sequence AV099323	3.006	0.0265	0.0607
AV356131	ENSMUSG00000108461	expressed sequence AV356131	2.320	0.0304	0.0682
Aven	ENSMUSG00000003604	apoptosis, caspase activation inhibitor	5.515	0.0000	0.0000
AW046200	ENSMUSG00000110419	expressed sequence AW046200	4.242	0.0000	0.0001
Axin1	ENSMUSG00000024182	axin 1	1.662	0.0001	0.0005
Axin2	ENSMUSG00000000142	axin 2	2.143	0.0000	0.0000
Azin2	ENSMUSG00000028789	antizyme inhibitor 2	1.617	0.0018	0.0057
B130046B21Rik	ENSMUSG00000097414	RIKEN cDNA B130046B21 gene	4.685	0.0027	0.0084
B230216N24Rik	ENSMUSG00000089706	RIKEN cDNA B230216N24 gene	2.491	0.0103	0.0269
B230217O12Rik	ENSMUSG00000097785	RIKEN cDNA B230217O12 gene	2.971	0.0079	0.0213
B230317F23Rik	ENSMUSG00000045746	RIKEN cDNA B230317F23 gene	7.002	0.0073	0.0200
B230322F03Rik	ENSMUSG00000097509	RIKEN cDNA B230322F03 gene	2.189	0.0069	0.0189

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
B230377A18Rik	ENSMUSG00000104195	RIKEN cDNA B230377A18 gene	7.030	0.0000	0.0000
B330016D10Rik	ENSMUSG00000048406	RIKEN cDNA B330016D10 gene	2.347	0.0000	0.0000
B3gat3	ENSMUSG00000071649	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	1.533	0.0000	0.0000
B3gnt2	ENSMUSG00000051650	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	10.456	0.0000	0.0000
B430319G15Rik	ENSMUSG00000103622	RIKEN cDNA B430319G15 gene	1.938	0.0159	0.0393
B4galt2	ENSMUSG00000028541	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 2	3.918	0.0000	0.0000
B630019K06Rik	ENSMUSG00000052364	RIKEN cDNA B630019K06 gene	1.845	0.0046	0.0134
B930095G15Rik	ENSMUSG00000085133	RIKEN cDNA B930095G15 gene	1.584	0.0005	0.0018
Bag1	ENSMUSG00000028416	BCL2-associated athanogene 1	2.375	0.0000	0.0000
Basp1	ENSMUSG00000045763	brain abundant, membrane attached signal protein 1	7.375	0.0000	0.0000
Baz1b	ENSMUSG00000002748	bromodomain adjacent to zinc finger domain, 1B	2.147	0.0000	0.0000
Bbc3	ENSMUSG00000002083	BCL2 binding component 3	6.174	0.0000	0.0000
Bbof1	ENSMUSG00000057265	basal body orientation factor 1	1.864	0.0000	0.0001
BC002189	ENSMUSG00000104465	cDNA sequence BC002189	2.347	0.0235	0.0549
BC005624	ENSMUSG00000026851	cDNA sequence BC005624	2.465	0.0000	0.0000
BC051226	ENSMUSG00000092564	cDNA sequence BC051226	2.120	0.0037	0.0110
Bcas2	ENSMUSG00000005687	BCAS2 pre-mRNA processing factor	1.572	0.0000	0.0000
Bccip	ENSMUSG00000030983	BRCA2 and CDKN1A interacting protein	2.747	0.0000	0.0000
Bcl2a1b	ENSMUSG00000089929	B cell leukemia/lymphoma 2 related protein A1b	10.910	0.0198	0.0473
Bcl2l2	ENSMUSG00000089682	BCL2-like 2	2.116	0.0000	0.0000
Bcl3	ENSMUSG00000053175	B cell leukemia/lymphoma 3	4.117	0.0000	0.0000
Bcl7c	ENSMUSG00000030814	B cell CLL/lymphoma 7C	5.583	0.0000	0.0000
Bdp1	ENSMUSG00000049658	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	1.609	0.0000	0.0000
Bean1	ENSMUSG00000031872	brain expressed, associated with Nedd4, 1	1.834	0.0050	0.0145
Becn1	ENSMUSG00000035086	beclin 1, autophagy related	1.955	0.0000	0.0000
Bend4	ENSMUSG00000092060	BEN domain containing 4	1.555	0.0003	0.0010
Bend5	ENSMUSG00000028545	BEN domain containing 5	1.786	0.0000	0.0000
Bex1	ENSMUSG00000050071	brain expressed X-linked 1	3.048	0.0000	0.0000
Bex4	ENSMUSG00000047844	brain expressed X-linked 4	7.887	0.0009	0.0033
Bhlhe22	ENSMUSG00000025128	basic helix-loop-helix family, member e22	2.367	0.0176	0.0429
Bhlhe41	ENSMUSG00000030256	basic helix-loop-helix family, member e41	1.785	0.0035	0.0105

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Bicd2	ENSMUSG00000037933	BICD cargo adaptor 2	1.688	0.0000	0.0000
Bloc1s4	ENSMUSG00000060708	biogenesis of lysosomal organelles complex-1, subunit 4, cappuccino	2.658	0.0000	0.0000
Bmp6	ENSMUSG00000039004	bone morphogenetic protein 6	1.658	0.0102	0.0267
Bms1	ENSMUSG00000030138	BMS1, ribosome biogenesis factor	2.654	0.0000	0.0000
Bmx	ENSMUSG00000031377	BMX non-receptor tyrosine kinase	2.023	0.0000	0.0001
Bnip2	ENSMUSG00000011958	BCL2/adenovirus E1B interacting protein 2	1.679	0.0000	0.0000
Bod1	ENSMUSG00000044502	biorientation of chromosomes in cell division 1	1.572	0.0000	0.0000
Bod1l	ENSMUSG00000061755	biorientation of chromosomes in cell division 1-like	1.797	0.0000	0.0000
Bod1-ps	ENSMUSG00000116936	biorientation of chromosomes in cell division 1, pseudogene	1.734	0.0001	0.0005
Borcs6	ENSMUSG00000045176	BLOC-1 related complex subunit 6	2.273	0.0011	0.0037
Brd7	ENSMUSG00000031660	bromodomain containing 7	1.856	0.0000	0.0000
Brd8	ENSMUSG00000003778	bromodomain containing 8	1.513	0.0000	0.0000
Brd9	ENSMUSG00000057649	bromodomain containing 9	1.714	0.0000	0.0000
Brf1	ENSMUSG00000011158	BRF1, RNA polymerase III transcription initiation factor 90 kDa subunit	1.752	0.0000	0.0000
Bri3	ENSMUSG00000047843	brain protein I3	9.261	0.0000	0.0000
Brsk1	ENSMUSG00000035390	BR serine/threonine kinase 1	2.181	0.0000	0.0000
Btbd1	ENSMUSG00000025103	BTB (POZ) domain containing 1	2.063	0.0000	0.0000
Btf3	ENSMUSG00000021660	basic transcription factor 3	1.688	0.0000	0.0000
Btf3l4	ENSMUSG00000028568	basic transcription factor 3-like 4	2.172	0.0000	0.0000
Btg1	ENSMUSG00000036478	BTG anti-proliferation factor 1	4.591	0.0000	0.0000
Btg3	ENSMUSG00000022863	BTG anti-proliferation factor 3	2.861	0.0000	0.0000
Bud13	ENSMUSG00000032077	BUD13 homolog	1.784	0.0000	0.0000
C030037D09Rik	ENSMUSG00000087574	RIKEN cDNA C030037D09 gene	1.691	0.0000	0.0000
C130046K22Rik	ENSMUSG00000085154	RIKEN cDNA C130046K22 gene	1.791	0.0305	0.0683
C130074G19Rik	ENSMUSG00000039349	RIKEN cDNA C130074G19 gene	2.178	0.0000	0.0000
C1galt1c1	ENSMUSG00000048970	C1GALT1-specific chaperone 1	1.546	0.0000	0.0002
C1qb	ENSMUSG00000036905	complement component 1, q subcomponent, beta polypeptide	1.620	0.0028	0.0087
C1qc	ENSMUSG00000036896	complement component 1, q subcomponent, C chain	3.933	0.0008	0.0030
C1ql3	ENSMUSG00000049630	C1q-like 3	3.409	0.0081	0.0218
C1qtnf9	ENSMUSG00000071347	C1q and tumor necrosis factor related protein 9	1.713	0.0001	0.0004
C1rb	ENSMUSG00000098470	complement component 1, r subcomponent B	3.491	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
C230013L11Rik	ENSMUSG00000117171	RIKEN cDNA C230013L11 gene	3.591	0.0000	0.0000
C230034O21Rik	ENSMUSG00000086181	RIKEN cDNA C230034O21 gene	3.180	0.0159	0.0394
C230062I16Rik	ENSMUSG00000063623	RIKEN cDNA C230062I16 gene	1.658	0.0053	0.0152
C230096K16Rik	ENSMUSG00000106205	RIKEN cDNA C230096K16 gene	3.904	0.0000	0.0000
C330011M18Rik	ENSMUSG00000056753	RIKEN cDNA C330011M18 gene	1.887	0.0000	0.0000
C430014B12Rik	ENSMUSG00000097564	RIKEN cDNA C430014B12 gene	2.410	0.0120	0.0307
C430049B03Rik	ENSMUSG00000087365	RIKEN cDNA C430049B03 gene	2.343	0.0085	0.0229
C5ar1	ENSMUSG00000049130	complement component 5a receptor 1	2.972	0.0000	0.0000
C630043F03Rik	ENSMUSG00000084910	RIKEN cDNA C630043F03 gene	2.072	0.0025	0.0077
Caap1	ENSMUSG00000028578	caspase activity and apoptosis inhibitor 1	1.795	0.0000	0.0000
Cab39	ENSMUSG00000036707	calcium binding protein 39	1.870	0.0000	0.0000
Cables1	ENSMUSG00000040957	CDK5 and Abl enzyme substrate 1	1.972	0.0000	0.0000
Cables2	ENSMUSG00000038990	CDK5 and Abl enzyme substrate 2	1.688	0.0000	0.0000
Cacfd1	ENSMUSG00000015488	calcium channel flower domain containing 1	1.952	0.0000	0.0000
Cacna2d2	ENSMUSG00000010066	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.849	0.0029	0.0088
Cacng7	ENSMUSG00000069806	calcium channel, voltage-dependent, gamma subunit 7	3.068	0.0000	0.0000
Cadm1	ENSMUSG00000032076	cell adhesion molecule 1	1.857	0.0000	0.0000
Cald1	ENSMUSG00000029761	caldesmon 1	1.944	0.0000	0.0000
Calm2	ENSMUSG00000036438	calmodulin 2	1.872	0.0000	0.0000
Calm3	ENSMUSG00000019370	calmodulin 3	2.237	0.0000	0.0000
Calr	ENSMUSG00000003814	calreticulin	1.893	0.0000	0.0000
Camk1	ENSMUSG00000030272	calcium/calmodulin-dependent protein kinase I	2.598	0.0000	0.0000
Camk2n1	ENSMUSG00000046447	calcium/calmodulin-dependent protein kinase II inhibitor 1	5.034	0.0000	0.0000
Camk2n2	ENSMUSG00000051146	calcium/calmodulin-dependent protein kinase II inhibitor 2	3.813	0.0000	0.0000
Camk4	ENSMUSG00000038128	calcium/calmodulin-dependent protein kinase IV	4.605	0.0393	0.0849
Canx	ENSMUSG00000020368	calnexin	1.715	0.0000	0.0000
Caprin1	ENSMUSG00000027184	cell cycle associated protein 1	1.796	0.0000	0.0000
Carnmt1	ENSMUSG00000024726	carnosine N-methyltransferase 1	2.890	0.0000	0.0000
Casc3	ENSMUSG00000078676	cancer susceptibility candidate 3	1.779	0.0000	0.0000
Casz1	ENSMUSG00000028977	castor zinc finger 1	1.681	0.0000	0.0000
Cavin1	ENSMUSG00000004044	caveolae associated 1	2.375	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cbfb	ENSMUSG00000031885	core binding factor beta	2.388	0.0000	0.0000
Cbx1	ENSMUSG00000018666	chromobox 1	2.429	0.0000	0.0000
Cbx3	ENSMUSG00000029836	chromobox 3	2.491	0.0000	0.0000
Ccar1	ENSMUSG00000020074	cell division cycle and apoptosis regulator 1	2.232	0.0000	0.0000
Ccdc102a	ENSMUSG00000063605	coiled-coil domain containing 102A	1.680	0.0000	0.0000
Ccdc112	ENSMUSG00000071855	coiled-coil domain containing 112	1.868	0.0038	0.0112
Ccdc117	ENSMUSG00000020482	coiled-coil domain containing 117	2.062	0.0000	0.0000
Ccdc12	ENSMUSG00000019659	coiled-coil domain containing 12	2.180	0.0000	0.0000
Ccdc122	ENSMUSG00000034795	coiled-coil domain containing 122	2.999	0.0000	0.0000
Ccdc124	ENSMUSG00000007721	coiled-coil domain containing 124	2.866	0.0000	0.0000
Ccdc142os	ENSMUSG00000087578	coiled-coil domain containing 142, opposite strand	1.680	0.0264	0.0607
Ccdc146	ENSMUSG00000064280	coiled-coil domain containing 146	1.942	0.0000	0.0000
Ccdc149	ENSMUSG00000045790	coiled-coil domain containing 149	1.594	0.0016	0.0053
Ccdc160	ENSMUSG00000073207	coiled-coil domain containing 160	2.078	0.0352	0.0773
Ccdc173	ENSMUSG00000070883	coiled-coil domain containing 173	3.273	0.0000	0.0000
Ccdc174	ENSMUSG00000034083	coiled-coil domain containing 174	2.147	0.0000	0.0000
Ccdc181	ENSMUSG00000026578	coiled-coil domain containing 181	2.324	0.0000	0.0000
Ccdc191	ENSMUSG00000022701	coiled-coil domain containing 191	2.428	0.0000	0.0000
Ccdc25	ENSMUSG00000022035	coiled-coil domain containing 25	2.051	0.0000	0.0000
Ccdc28a	ENSMUSG00000059554	coiled-coil domain containing 28A	1.575	0.0002	0.0007
Ccdc28b	ENSMUSG00000028795	coiled coil domain containing 28B	1.834	0.0000	0.0000
Ccdc34	ENSMUSG00000027160	coiled-coil domain containing 34	4.215	0.0000	0.0000
Ccdc47	ENSMUSG00000078622	coiled-coil domain containing 47	2.273	0.0000	0.0000
Ccdc62	ENSMUSG00000061882	coiled-coil domain containing 62	1.637	0.0330	0.0731
Ccdc66	ENSMUSG00000046753	coiled-coil domain containing 66	1.518	0.0001	0.0003
Ccdc71l	ENSMUSG00000090946	coiled-coil domain containing 71 like	2.375	0.0000	0.0000
Ccdc80	ENSMUSG00000022665	coiled-coil domain containing 80	1.666	0.0012	0.0039
Ccdc82	ENSMUSG00000079084	coiled-coil domain containing 82	1.729	0.0000	0.0000
Ccdc85c	ENSMUSG00000084883	coiled-coil domain containing 85C	1.998	0.0000	0.0000
Ccdc88b	ENSMUSG00000047810	coiled-coil domain containing 88B	2.025	0.0055	0.0155
Ccdc9	ENSMUSG00000041375	coiled-coil domain containing 9	2.423	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ccdc91	ENSMUSG00000030301	coiled-coil domain containing 91	2.300	0.0000	0.0000
Ccdc96	ENSMUSG00000050677	coiled-coil domain containing 96	2.030	0.0005	0.0017
Cchcr1	ENSMUSG00000040312	coiled-coil alpha-helical rod protein 1	2.394	0.0000	0.0000
Ccl6	ENSMUSG00000018927	chemokine (C-C motif) ligand 6	1.715	0.0133	0.0336
Ccm2l	ENSMUSG00000027474	cerebral cavernous malformation 2-like	1.706	0.0002	0.0007
Ccnd1	ENSMUSG00000070348	cyclin D1	1.907	0.0005	0.0018
Ccng2	ENSMUSG00000029385	cyclin G2	2.275	0.0000	0.0000
Ccni	ENSMUSG00000063015	cyclin I	2.044	0.0000	0.0000
Ccnj	ENSMUSG00000025010	cyclin J	2.144	0.0000	0.0000
Ccnjl	ENSMUSG00000044707	cyclin J-like	1.532	0.0168	0.0412
Ccnt1	ENSMUSG00000011960	cyclin T1	1.602	0.0000	0.0000
Ccs	ENSMUSG00000034108	copper chaperone for superoxide dismutase	1.946	0.0000	0.0000
Ccsap	ENSMUSG00000031971	centriole, cilia and spindle associated protein	2.308	0.0002	0.0007
Ccz1	ENSMUSG00000029617	CCZ1 vacuolar protein trafficking and biogenesis associated	2.296	0.0000	0.0000
Cd163	ENSMUSG00000008845	CD163 antigen	1.910	0.0057	0.0160
Cd248	ENSMUSG00000056481	CD248 antigen, endosialin	1.725	0.0154	0.0384
Cd2bp2	ENSMUSG00000042502	CD2 cytoplasmic tail binding protein 2	1.582	0.0000	0.0000
Cd300a	ENSMUSG00000034652	CD300A molecule	1.982	0.0016	0.0052
Cd300e	ENSMUSG00000048498	CD300E molecule	3.525	0.0185	0.0447
Cd3e	ENSMUSG00000032093	CD3 antigen, epsilon polypeptide	3.726	0.0000	0.0001
Cd63	ENSMUSG00000025351	CD63 antigen	1.831	0.0000	0.0000
Cd72	ENSMUSG00000028459	CD72 antigen	3.465	0.0033	0.0101
Cd79b	ENSMUSG00000040592	CD79B antigen	2.062	0.0285	0.0646
Cd9	ENSMUSG00000030342	CD9 antigen	1.711	0.0000	0.0001
Cdc25a	ENSMUSG00000032477	cell division cycle 25A	1.605	0.0000	0.0000
Cdc26	ENSMUSG00000066149	cell division cycle 26	1.802	0.0000	0.0000
Cdc34	ENSMUSG00000020307	cell division cycle 34	1.646	0.0000	0.0000
Cdc37	ENSMUSG00000019471	cell division cycle 37	2.291	0.0000	0.0000
Cdh24	ENSMUSG00000059674	cadherin-like 24	2.998	0.0171	0.0417
Cdk11b	ENSMUSG00000029062	cyclin-dependent kinase 11B	2.619	0.0000	0.0000
Cdk13	ENSMUSG00000041297	cyclin-dependent kinase 13	1.537	0.0002	0.0007

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cdk18	ENSMUSG00000026437	cyclin-dependent kinase 18	1.675	0.0000	0.0000
Cdk2ap1	ENSMUSG00000029394	CDK2 (cyclin-dependent kinase 2)-associated protein 1	1.741	0.0021	0.0067
Cdk5rap3	ENSMUSG00000018669	CDK5 regulatory subunit associated protein 3	2.090	0.0000	0.0000
Cdk8	ENSMUSG00000029635	cyclin-dependent kinase 8	1.912	0.0000	0.0000
Cdkn1c	ENSMUSG00000037664	cyclin-dependent kinase inhibitor 1C (P57)	3.382	0.0000	0.0000
Cdkn2c	ENSMUSG00000028551	cyclin dependent kinase inhibitor 2C	1.792	0.0000	0.0000
Cdnf	ENSMUSG00000039496	cerebral dopamine neurotrophic factor	1.886	0.0000	0.0000
Cdr2	ENSMUSG00000030878	cerebellar degeneration-related 2	2.386	0.0000	0.0000
Cdr2l	ENSMUSG00000050910	cerebellar degeneration-related protein 2-like	2.398	0.0000	0.0000
Cds1	ENSMUSG00000029330	CDP-diacylglycerol synthase 1	2.363	0.0000	0.0000
Cdv3	ENSMUSG00000032803	carnitine deficiency-associated gene expressed in ventricle 3	3.299	0.0000	0.0000
Cdv3-ps	ENSMUSG00000090389	Cdv3 retrotransposed pseudogene	3.863	0.0066	0.0182
Cdyl	ENSMUSG00000059288	chromodomain protein, Y chromosome-like	1.810	0.0000	0.0000
Cebpa	ENSMUSG00000034957	CCAAT/enhancer binding protein (C/EBP), alpha	4.284	0.0000	0.0000
Cebpb	ENSMUSG00000056501	CCAAT/enhancer binding protein (C/EBP), beta	9.906	0.0000	0.0000
Cebpg	ENSMUSG00000056216	CCAAT/enhancer binding protein (C/EBP), gamma	1.526	0.0000	0.0000
Celf4	ENSMUSG00000024268	CUGBP, Elav-like family member 4	3.031	0.0115	0.0295
Cenpb	ENSMUSG00000068267	centromere protein B	1.795	0.0000	0.0000
Cenps	ENSMUSG00000073705	centromere protein S	2.497	0.0001	0.0006
Cenpv	ENSMUSG00000018509	centromere protein V	2.859	0.0000	0.0000
Cep131	ENSMUSG00000039781	centrosomal protein 131	1.577	0.0032	0.0097
Cep164	ENSMUSG00000043987	centrosomal protein 164	1.637	0.0000	0.0000
Cep250	ENSMUSG00000038241	centrosomal protein 250	1.776	0.0000	0.0000
Cep63	ENSMUSG00000032534	centrosomal protein 63	2.477	0.0000	0.0000
Cep83	ENSMUSG00000020024	centrosomal protein 83	1.688	0.0000	0.0000
Cep89	ENSMUSG00000023072	centrosomal protein 89	2.038	0.0000	0.0000
Cep97	ENSMUSG00000022604	centrosomal protein 97	2.138	0.0000	0.0000
Cerkl	ENSMUSG00000075256	ceramide kinase-like	1.943	0.0161	0.0398
Cetn3	ENSMUSG00000021537	centrin 3	3.684	0.0000	0.0000
Cetn4	ENSMUSG00000045031	centrin 4	2.011	0.0372	0.0810
Cfap298	ENSMUSG00000022972	cilia and flagella associate protien 298	2.366	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cfap36	ENSMUSG00000020462	cilia and flagella associated protein 36	1.977	0.0000	0.0000
Cfap45	ENSMUSG00000026546	cilia and flagella associated protein 45	2.018	0.0374	0.0813
Cfap53	ENSMUSG00000035394	cilia and flagella associated protein 53	6.971	0.0334	0.0738
Cfdp1	ENSMUSG00000031954	craniofacial development protein 1	2.671	0.0000	0.0000
Cflar	ENSMUSG00000026031	CASP8 and FADD-like apoptosis regulator	1.585	0.0000	0.0000
Cgnl1	ENSMUSG00000032232	cingulin-like 1	1.677	0.0000	0.0000
Cgref1	ENSMUSG00000029161	cell growth regulator with EF hand domain 1	3.042	0.0002	0.0007
Chaf1a	ENSMUSG00000002835	chromatin assembly factor 1, subunit A (p150)	2.938	0.0000	0.0000
Chaserr	ENSMUSG00000101970	CHD2 adjacent suppressive regulatory RNA	2.780	0.0000	0.0000
Chchd4	ENSMUSG00000034203	coiled-coil-helix-coiled-coil-helix domain containing 4	1.617	0.0000	0.0000
Chd1	ENSMUSG00000023852	chromodomain helicase DNA binding protein 1	1.795	0.0000	0.0000
Chd2	ENSMUSG00000078671	chromodomain helicase DNA binding protein 2	1.705	0.0000	0.0000
Chd3	ENSMUSG00000018474	chromodomain helicase DNA binding protein 3	1.599	0.0000	0.0000
Chd4	ENSMUSG00000063870	chromodomain helicase DNA binding protein 4	1.826	0.0000	0.0000
Chgb	ENSMUSG00000027350	chromogranin B	4.769	0.0000	0.0000
Chic2	ENSMUSG00000029229	cysteine-rich hydrophobic domain 2	4.662	0.0000	0.0000
Chmp2a	ENSMUSG00000033916	charged multivesicular body protein 2A	1.658	0.0000	0.0000
Chmp3	ENSMUSG00000053119	charged multivesicular body protein 3	1.930	0.0000	0.0000
Chmp4b	ENSMUSG00000038467	charged multivesicular body protein 4B	2.340	0.0000	0.0000
Chmp4c	ENSMUSG00000027536	charged multivesicular body protein 4C	1.610	0.0000	0.0000
Chmp7	ENSMUSG00000034190	charged multivesicular body protein 7	2.404	0.0000	0.0000
Chst14	ENSMUSG00000074916	carbohydrate sulfotransferase 14	1.888	0.0000	0.0000
Chst2	ENSMUSG00000033350	carbohydrate sulfotransferase 2	2.726	0.0000	0.0000
Chsy1	ENSMUSG00000032640	chondroitin sulfate synthase 1	2.180	0.0000	0.0000
Chsy3	ENSMUSG00000058152	chondroitin sulfate synthase 3	2.655	0.0058	0.0164
Chtf18	ENSMUSG00000019214	CTF18, chromosome transmission fidelity factor 18	1.771	0.0057	0.0162
Chuk	ENSMUSG00000025199	conserved helix-loop-helix ubiquitous kinase	1.537	0.0000	0.0000
Cib2	ENSMUSG00000037493	calcium and integrin binding family member 2	2.560	0.0003	0.0013
Cideb	ENSMUSG00000022219	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	1.727	0.0082	0.0220
Cir1	ENSMUSG00000041777	corepressor interacting with RBPJ, 1	2.275	0.0000	0.0001
Cirbp	ENSMUSG00000045193	cold inducible RNA binding protein	1.960	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Cited2	ENSMUSG00000039910	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1.731	0.0092	0.0244
Cited4	ENSMUSG00000070803	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	3.045	0.0022	0.0071
Ckap4	ENSMUSG00000046841	cytoskeleton-associated protein 4	2.065	0.0000	0.0000
Clasrp	ENSMUSG00000061028	CLK4-associating serine/arginine rich protein	1.775	0.0003	0.0013
Clec4d	ENSMUSG00000030144	C-type lectin domain family 4, member d	3.668	0.0428	0.0909
Clint1	ENSMUSG00000006169	clathrin interactor 1	1.747	0.0000	0.0000
Clk1	ENSMUSG00000026034	CDC-like kinase 1	1.524	0.0259	0.0596
Clmp	ENSMUSG00000032024	CXADR-like membrane protein	1.622	0.0003	0.0011
Clptm1	ENSMUSG00000002981	cleft lip and palate associated transmembrane protein 1	1.892	0.0000	0.0002
Clstn1	ENSMUSG00000039953	calsyntenin 1	1.518	0.0000	0.0000
Cltb	ENSMUSG00000047547	clathrin, light polypeptide (Lcb)	2.522	0.0000	0.0000
Cluap1	ENSMUSG00000014232	clusterin associated protein 1	1.864	0.0000	0.0000
Cmas	ENSMUSG00000030282	cytidine monophospho-N-acetylneuraminic acid synthetase	2.992	0.0000	0.0000
Cmpk1	ENSMUSG00000028719	cytidine monophosphate (UMP-CMP) kinase 1	1.584	0.0000	0.0000
Cmtm6	ENSMUSG00000032434	CKLF-like MARVEL transmembrane domain containing 6	1.558	0.0000	0.0000
Cnot11	ENSMUSG00000003135	CCR4-NOT transcription complex, subunit 11	1.912	0.0000	0.0000
Cnpy4	ENSMUSG00000036968	canopy FGF signaling regulator 4	1.861	0.0000	0.0000
Cntf	ENSMUSG00000079415	ciliary neurotrophic factor	11.432	0.0006	0.0023
Col11a1	ENSMUSG00000027966	collagen, type XI, alpha 1	5.413	0.0164	0.0403
Col13a1	ENSMUSG00000058806	collagen, type XIII, alpha 1	2.516	0.0015	0.0051
Commd1	ENSMUSG00000051355	COMM domain containing 1	1.780	0.0000	0.0000
Coprs	ENSMUSG00000031458	coordinator of PRMT5, differentiation stimulator	1.684	0.0004	0.0014
Copz2	ENSMUSG00000018672	coatomer protein complex, subunit zeta 2	3.727	0.0000	0.0000
Coq10a	ENSMUSG00000039914	coenzyme Q10A	1.695	0.0000	0.0000
Cox11	ENSMUSG00000020544	cytochrome c oxidase assembly protein 11, copper chaperone	2.378	0.0000	0.0000
Cox20	ENSMUSG00000026500	cytochrome c oxidase assembly protein 20	1.574	0.0000	0.0000
Cox7c	ENSMUSG00000017778	cytochrome c oxidase subunit 7C	2.500	0.0000	0.0000
Cpe	ENSMUSG00000037852	carboxypeptidase E	1.687	0.0000	0.0000
Cpeb2	ENSMUSG00000039782	cytoplasmic polyadenylation element binding protein 2	2.180	0.0000	0.0000
Cpne2	ENSMUSG00000034361	copine II	1.753	0.0027	0.0085
Cpox	ENSMUSG00000022742	coproporphyrinogen oxidase	2.341	0.0000	0.0000

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Cpsf4	ENSMUSG00000029625	cleavage and polyadenylation specific factor 4	1.604	0.0012	0.0039
Cracr2b	ENSMUSG00000048200	calcium release activated channel regulator 2B	1.902	0.0000	0.0000
Creb3	ENSMUSG00000028466	cAMP responsive element binding protein 3	2.772	0.0000	0.0000
Creb3l1	ENSMUSG00000027230	cAMP responsive element binding protein 3-like 1	1.746	0.0004	0.0013
Crebzf	ENSMUSG00000051451	CREB/ATF bZIP transcription factor	3.154	0.0000	0.0000
Creld2	ENSMUSG00000023272	cysteine-rich with EGF-like domains 2	1.570	0.0000	0.0001
Crim1	ENSMUSG00000024074	cysteine rich transmembrane BMP regulator 1 (chordin like)	1.551	0.0000	0.0000
Crlf1	ENSMUSG00000007888	cytokine receptor-like factor 1	4.690	0.0013	0.0045
Crls1	ENSMUSG00000027357	cardiolipin synthase 1	2.049	0.0000	0.0000
Crnkl1	ENSMUSG00000001767	crooked neck pre-mRNA splicing factor 1	1.571	0.0000	0.0000
Csde1	ENSMUSG00000068823	cold shock domain containing E1, RNA binding	1.894	0.0000	0.0000
Csk	ENSMUSG00000032312	c-src tyrosine kinase	2.224	0.0000	0.0000
Csnk1e	ENSMUSG00000022433	casein kinase 1, epsilon	1.613	0.0003	0.0013
Csnk1g2	ENSMUSG00000003345	casein kinase 1, gamma 2	1.736	0.0000	0.0000
Csnk1g3	ENSMUSG00000073563	casein kinase 1, gamma 3	1.994	0.0000	0.0000
Csnk2a1	ENSMUSG00000074698	casein kinase 2, alpha 1 polypeptide	2.181	0.0000	0.0000
Cspp1	ENSMUSG00000056763	centrosome and spindle pole associated protein 1	1.828	0.0000	0.0000
Csrp2	ENSMUSG00000020186	cysteine and glycine-rich protein 2	2.065	0.0000	0.0000
Ctcf	ENSMUSG00000005698	CCCTC-binding factor	1.530	0.0000	0.0000
Ctdnep1	ENSMUSG00000018559	CTD nuclear envelope phosphatase 1	1.611	0.0003	0.0012
Ctdp1	ENSMUSG00000033323	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	1.863	0.0000	0.0000
Ctdsp1	ENSMUSG00000026176	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	1.676	0.0000	0.0000
Ctdsp2	ENSMUSG00000078429	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	1.602	0.0004	0.0016
Cthrc1	ENSMUSG00000054196	collagen triple helix repeat containing 1	3.735	0.0041	0.0121
Ctnnbip1	ENSMUSG00000028988	catenin beta interacting protein 1	1.543	0.0001	0.0005
Ctnnbl1	ENSMUSG00000027649	catenin, beta like 1	1.832	0.0000	0.0000
Ctnnd1	ENSMUSG00000034101	catenin (cadherin associated protein), delta 1	2.843	0.0000	0.0000
Ctss	ENSMUSG00000038642	cathepsin S	1.665	0.0037	0.0111
Cul4a	ENSMUSG00000031446	cullin 4A	1.934	0.0000	0.0000
Cutal	ENSMUSG00000026870	cutA divalent cation tolerance homolog-like	2.182	0.0001	0.0004
Cutc	ENSMUSG00000025193	cutC copper transporter	2.218	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cwc15	ENSMUSG00000004096	CWC15 spliceosome-associated protein	2.136	0.0000	0.0000
Cwc25	ENSMUSG00000018541	CWC25 spliceosome-associated protein	1.532	0.0000	0.0000
Cwc27	ENSMUSG00000021715	CWC27 spliceosome-associated protein	3.434	0.0000	0.0000
Cyb5d1	ENSMUSG00000044795	cytochrome b5 domain containing 1	1.816	0.0000	0.0000
Cyb5r4	ENSMUSG00000032872	cytochrome b5 reductase 4	2.181	0.0000	0.0000
Cyhr1	ENSMUSG00000053929	cysteine and histidine rich 1	1.774	0.0000	0.0000
Cyp51	ENSMUSG00000001467	cytochrome P450, family 51	1.770	0.0000	0.0000
Cyrib	ENSMUSG00000022378	CYFIP related Rac1 interactor B	1.964	0.0000	0.0000
Cys1	ENSMUSG00000062563	cystin 1	4.652	0.0000	0.0000
Cyth2	ENSMUSG00000003269	cytohesin 2	2.030	0.0001	0.0003
D330050I16Rik	ENSMUSG00000117959	RIKEN cDNA D330050I16 gene	6.731	0.0000	0.0000
D630033A02Rik	ENSMUSG00000112237	RIKEN cDNA D630033A02 gene	3.023	0.0010	0.0033
D830035M03Rik	ENSMUSG00000111828	RIKEN cDNA D830035M03 gene	1.909	0.0065	0.0179
D830050J10Rik	ENSMUSG00000107994	RIKEN cDNA D830050J10 gene	2.919	0.0000	0.0001
D8Ertd738e	ENSMUSG00000019362	DNA segment, Chr 8, ERATO Doi 738, expressed	1.836	0.0000	0.0000
Dact1	ENSMUSG00000044548	dishevelled-binding antagonist of beta-catenin 1	1.792	0.0007	0.0025
Dact3	ENSMUSG00000078794	dishevelled-binding antagonist of beta-catenin 3	5.233	0.0000	0.0000
Dazap1	ENSMUSG00000069565	DAZ associated protein 1	2.442	0.0000	0.0000
Dbf4	ENSMUSG00000002297	DBF4 zinc finger	1.832	0.0029	0.0088
Dbn1	ENSMUSG00000034675	drebrin 1	2.172	0.0000	0.0000
Dbndd2	ENSMUSG00000017734	dysbindin (dystrobrevin binding protein 1) domain containing 2	1.817	0.0000	0.0000
Dbp	ENSMUSG00000059824	D site albumin promoter binding protein	2.196	0.0316	0.0705
Dcaf13	ENSMUSG00000022300	DDB1 and CUL4 associated factor 13	1.517	0.0000	0.0000
Dctn5	ENSMUSG00000030868	dynactin 5	1.597	0.0000	0.0000
Dcun1d5	ENSMUSG00000032002	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	4.412	0.0000	0.0000
Ddc	ENSMUSG00000020182	dopa decarboxylase	2.703	0.0000	0.0000
Ddrgk1	ENSMUSG00000068290	DDRGK domain containing 1	2.249	0.0000	0.0000
Ddx10	ENSMUSG00000053289	DEAD box helicase 10	2.302	0.0000	0.0000
Ddx19b	ENSMUSG00000033658	DEAD box helicase 19b	1.666	0.0000	0.0000
Ddx23	ENSMUSG00000003360	DEAD box helicase 23	1.654	0.0000	0.0000
Ddx27	ENSMUSG00000017999	DEAD box helicase 27	2.273	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ddx3x	ENSMUSG00000000787	DEAD box helicase 3, X-linked	2.202	0.0000	0.0000
Ddx42	ENSMUSG00000020705	DEAD box helicase 42	1.629	0.0000	0.0000
Ddx43	ENSMUSG00000070291	DEAD box helicase 43	2.104	0.0252	0.0583
Ddx46	ENSMUSG00000021500	DEAD box helicase 46	2.096	0.0000	0.0000
Ddx55	ENSMUSG00000029389	DEAD box helicase 55	2.065	0.0000	0.0000
Deaf1	ENSMUSG00000058886	DEAF1, transcription factor	1.753	0.0007	0.0026
Decr1	ENSMUSG00000028223	2,4-dienoyl CoA reductase 1, mitochondrial	1.620	0.0000	0.0000
Dek	ENSMUSG00000021377	DEK proto-oncogene (DNA binding)	1.892	0.0000	0.0000
Denr	ENSMUSG00000023106	density-regulated protein	2.302	0.0000	0.0000
Dexi	ENSMUSG00000038055	dexamethasone-induced transcript	3.765	0.0000	0.0000
Dhdh	ENSMUSG00000011382	dihydrodiol dehydrogenase (dimeric)	2.388	0.0000	0.0000
Dhrs4	ENSMUSG00000022210	dehydrogenase/reductase (SDR family) member 4	2.189	0.0000	0.0000
Dhrs7	ENSMUSG00000021094	dehydrogenase/reductase (SDR family) member 7	1.861	0.0000	0.0000
Dhx16	ENSMUSG00000024422	DEAH (Asp-Glu-Ala-His) box polypeptide 16	1.642	0.0000	0.0000
Dhx38	ENSMUSG00000037993	DEAH (Asp-Glu-Ala-His) box polypeptide 38	1.581	0.0000	0.0000
Diaph1	ENSMUSG00000024456	diaphanous related formin 1	1.626	0.0000	0.0000
Dmrt2	ENSMUSG00000048138	doublesex and mab-3 related transcription factor 2	18.899	0.0120	0.0308
Dmrta2	ENSMUSG00000047143	doublesex and mab-3 related transcription factor like family A2	5.962	0.0013	0.0044
Dmwd	ENSMUSG00000030410	dystrophia myotonica-containing WD repeat motif	1.504	0.0001	0.0003
Dnaja4	ENSMUSG00000032285	DnaJ heat shock protein family (Hsp40) member A4	2.728	0.0000	0.0000
Dnajb11	ENSMUSG00000004460	DnaJ heat shock protein family (Hsp40) member B11	3.122	0.0000	0.0000
Dnajb2	ENSMUSG00000026203	DnaJ heat shock protein family (Hsp40) member B2	2.141	0.0000	0.0000
Dnajb6	ENSMUSG00000029131	DnaJ heat shock protein family (Hsp40) member B6	2.375	0.0000	0.0000
Dnajb6-ps	ENSMUSG00000091905	DnaJ heat shock protein family (Hsp40) member B6, pseudogene	4.277	0.0025	0.0078
Dnajc11	ENSMUSG00000039768	DnaJ heat shock protein family (Hsp40) member C11	1.811	0.0000	0.0000
Dnajc14	ENSMUSG00000025354	DnaJ heat shock protein family (Hsp40) member C14	1.857	0.0000	0.0000
Dnajc17	ENSMUSG00000034278	DnaJ heat shock protein family (Hsp40) member C17	1.566	0.0013	0.0043
Dnajc2	ENSMUSG00000029014	DnaJ heat shock protein family (Hsp40) member C2	2.219	0.0000	0.0000
Dnajc21	ENSMUSG00000044224	DnaJ heat shock protein family (Hsp40) member C21	4.789	0.0000	0.0000
Dnajc25	ENSMUSG00000070972	DnaJ heat shock protein family (Hsp40) member C25	2.058	0.0000	0.0000
Dnajc8	ENSMUSG00000054405	DnaJ heat shock protein family (Hsp40) member C8	3.255	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dnlz	ENSMUSG00000075467	DNL-type zinc finger	2.616	0.0000	0.0000
Dnm1	ENSMUSG00000026825	dynamin 1	2.112	0.0000	0.0000
Dnmt3b	ENSMUSG00000027478	DNA methyltransferase 3B	1.688	0.0131	0.0331
Dnttip1	ENSMUSG00000017299	deoxynucleotidyltransferase, terminal, interacting protein 1	2.680	0.0000	0.0000
Doc2g	ENSMUSG00000024871	double C2, gamma	1.570	0.0000	0.0000
Dok5	ENSMUSG00000027560	docking protein 5	1.864	0.0045	0.0132
Donson	ENSMUSG00000022960	downstream neighbor of SON	1.784	0.0010	0.0036
Dpcd	ENSMUSG00000041035	deleted in primary ciliary dyskinesia	3.297	0.0000	0.0000
Dpy30	ENSMUSG00000024067	dpy-30, histone methyltransferase complex regulatory subunit	1.634	0.0000	0.0000
Dpysl2	ENSMUSG00000022048	dihydropyrimidinase-like 2	1.576	0.0000	0.0000
Dpysl3	ENSMUSG00000024501	dihydropyrimidinase-like 3	1.635	0.0121	0.0310
Drap1	ENSMUSG00000024914	Dr1 associated protein 1 (negative cofactor 2 alpha)	4.289	0.0000	0.0000
Dtnbp1	ENSMUSG00000057531	dystrobrevin binding protein 1	1.549	0.0000	0.0001
Dusp18	ENSMUSG00000047205	dual specificity phosphatase 18	1.596	0.0037	0.0110
Dusp26	ENSMUSG00000039661	dual specificity phosphatase 26 (putative)	2.391	0.0000	0.0002
Dusp27	ENSMUSG00000026564	dual specificity phosphatase 27 (putative)	2.534	0.0000	0.0000
Dusp7	ENSMUSG00000053716	dual specificity phosphatase 7	1.662	0.0000	0.0000
Dusp8	ENSMUSG00000037887	dual specificity phosphatase 8	1.511	0.0272	0.0621
Dync1li2	ENSMUSG00000035770	dynein, cytoplasmic 1 light intermediate chain 2	2.284	0.0000	0.0000
Dync2i1	ENSMUSG00000042050	dynein 2 intermediate chain 1	1.877	0.0000	0.0000
Dynll2	ENSMUSG00000020483	dynein light chain LC8-type 2	2.391	0.0000	0.0000
Dynlt2b	ENSMUSG00000014075	dynein light chain Tctex-type 2B	1.969	0.0000	0.0000
Dynlt3	ENSMUSG00000031176	dynein light chain Tctex-type 3	1.733	0.0000	0.0000
E130102H24Rik	ENSMUSG00000086782	RIKEN cDNA E130102H24 gene	1.878	0.0176	0.0427
E130201H02Rik	ENSMUSG00000044141	RIKEN cDNA E130201H02 gene	39.282	0.0002	0.0007
E130208F15Rik	ENSMUSG00000074210	RIKEN cDNA E130208F15 gene	2.672	0.0001	0.0004
E2f1	ENSMUSG00000027490	E2F transcription factor 1	2.678	0.0000	0.0002
E2f4	ENSMUSG00000014859	E2F transcription factor 4	1.828	0.0000	0.0000
E330034L11Rik	ENSMUSG00000106383	RIKEN cDNA E330034L11 gene	1.931	0.0007	0.0025
Ebag9	ENSMUSG00000022339	estrogen receptor-binding fragment-associated gene 9	3.322	0.0000	0.0000
Ebf1	ENSMUSG00000057098	early B cell factor 1	1.627	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Echdc1	ENSMUSG00000019883	enoyl Coenzyme A hydratase domain containing 1	1.731	0.0000	0.0000
Edem3	ENSMUSG00000043019	ER degradation enhancer, mannosidase alpha-like 3	1.748	0.0000	0.0000
Eea1	ENSMUSG00000036499	early endosome antigen 1	1.717	0.0000	0.0000
Eed	ENSMUSG00000030619	embryonic ectoderm development	1.567	0.0000	0.0000
Efcab2	ENSMUSG00000026495	EF-hand calcium binding domain 2	2.129	0.0000	0.0000
Efcab9	ENSMUSG00000044056	EF-hand calcium binding domain 9	3.805	0.0442	0.0933
Efhd1	ENSMUSG00000026255	EF hand domain containing 1	1.836	0.0001	0.0006
Efhd2	ENSMUSG00000040659	EF hand domain containing 2	1.623	0.0112	0.0289
Efna2	ENSMUSG00000003070	ephrin A2	1.897	0.0024	0.0074
Efnb2	ENSMUSG00000001300	ephrin B2	1.744	0.0000	0.0000
Egln1	ENSMUSG00000031987	egl-9 family hypoxia-inducible factor 1	1.523	0.0000	0.0000
Egln2	ENSMUSG00000058709	egl-9 family hypoxia-inducible factor 2	1.705	0.0010	0.0036
Ehbp1	ENSMUSG00000042302	EH domain binding protein 1	1.858	0.0000	0.0000
Ehbp1l1	ENSMUSG00000024937	EH domain binding protein 1-like 1	1.623	0.0000	0.0000
Ei24	ENSMUSG00000062762	etoposide induced 2.4 mRNA	1.900	0.0000	0.0000
Eid1	ENSMUSG00000091337	EP300 interacting inhibitor of differentiation 1	2.946	0.0000	0.0000
Eid2	ENSMUSG00000046058	EP300 interacting inhibitor of differentiation 2	4.807	0.0000	0.0000
Eid2b	ENSMUSG00000070705	EP300 interacting inhibitor of differentiation 2B	1.621	0.0095	0.0251
Eif1a	ENSMUSG00000057561	eukaryotic translation initiation factor 1A	1.690	0.0000	0.0000
Eif1ad	ENSMUSG00000024841	eukaryotic translation initiation factor 1A domain containing	2.107	0.0000	0.0000
Eif2b5	ENSMUSG00000003235	eukaryotic translation initiation factor 2B, subunit 5 epsilon	1.633	0.0000	0.0000
Eif3a	ENSMUSG00000024991	eukaryotic translation initiation factor 3, subunit A	3.676	0.0000	0.0000
Eif3b	ENSMUSG00000056076	eukaryotic translation initiation factor 3, subunit B	2.655	0.0000	0.0000
Eif3f	ENSMUSG00000031029	eukaryotic translation initiation factor 3, subunit F	1.689	0.0089	0.0238
Eif3j1	ENSMUSG00000027236	eukaryotic translation initiation factor 3, subunit J1	4.060	0.0000	0.0000
Eif3j2	ENSMUSG00000043424	eukaryotic translation initiation factor 3, subunit J2	2.326	0.0000	0.0000
Eif4b	ENSMUSG00000058655	eukaryotic translation initiation factor 4B	1.608	0.0000	0.0000
Eif4e	ENSMUSG00000028156	eukaryotic translation initiation factor 4E	1.610	0.0001	0.0004
Eif4e2	ENSMUSG00000026254	eukaryotic translation initiation factor 4E member 2	1.852	0.0000	0.0000
Eif4g1	ENSMUSG00000045983	eukaryotic translation initiation factor 4, gamma 1	2.133	0.0000	0.0000
Eif5b	ENSMUSG00000026083	eukaryotic translation initiation factor 5B	2.657	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Eipr1	ENSMUSG00000036613	EARP complex and GARP complex interacting protein 1	1.501	0.0000	0.0000
Elac1	ENSMUSG00000036941	elaC ribonuclease Z 1	1.502	0.0000	0.0000
Eldr	ENSMUSG00000087060	Egfr long non-coding downstream RNA	2.840	0.0035	0.0105
Ell2	ENSMUSG00000001542	elongation factor for RNA polymerase II 2	1.766	0.0006	0.0023
Eln	ENSMUSG00000029675	elastin	3.014	0.0000	0.0000
Eloc	ENSMUSG00000079658	elongin C	1.828	0.0000	0.0000
Emc10	ENSMUSG00000008140	ER membrane protein complex subunit 10	2.357	0.0000	0.0000
Enah	ENSMUSG00000022995	ENAH actin regulator	1.558	0.0000	0.0002
Endog	ENSMUSG00000015337	endonuclease G	2.080	0.0008	0.0028
Engase	ENSMUSG00000033857	endo-beta-N-acetylglucosaminidase	3.239	0.0000	0.0000
Enho	ENSMUSG00000028445	energy homeostasis associated	3.233	0.0000	0.0000
Entr1	ENSMUSG00000026927	endosome associated trafficking regulator 1	1.529	0.0000	0.0000
Eny2	ENSMUSG00000022338	ENY2 transcription and export complex 2 subunit	1.662	0.0000	0.0000
Epb41l2	ENSMUSG00000019978	erythrocyte membrane protein band 4.1 like 2	1.549	0.0000	0.0000
Epb41l4b	ENSMUSG00000028434	erythrocyte membrane protein band 4.1 like 4b	1.677	0.0025	0.0079
Epha7	ENSMUSG00000028289	Eph receptor A7	1.596	0.0008	0.0029
Ephb3	ENSMUSG00000005958	Eph receptor B3	1.719	0.0018	0.0059
Epop	ENSMUSG00000043439	elongin BC and polycomb repressive complex 2 associated protein	4.076	0.0015	0.0051
Erf	ENSMUSG00000040857	Ets2 repressor factor	1.766	0.0000	0.0001
Erh	ENSMUSG00000021131	ERH mRNA splicing and mitosis factor	3.269	0.0000	0.0000
Eri3	ENSMUSG00000033423	exoribonuclease 3	1.672	0.0033	0.0101
Erich3	ENSMUSG00000078161	glutamate rich 3	3.288	0.0000	0.0002
Erlec1	ENSMUSG00000020311	endoplasmic reticulum lectin 1	1.718	0.0000	0.0000
Esf1	ENSMUSG00000045624	ESF1 nucleolar pre-rRNA processing protein homolog	1.945	0.0000	0.0000
Esm1	ENSMUSG00000042379	endothelial cell-specific molecule 1	2.166	0.0013	0.0043
Espn	ENSMUSG00000028943	espin	2.066	0.0000	0.0000
Esrra	ENSMUSG00000024955	estrogen related receptor, alpha	2.154	0.0000	0.0000
Etfb	ENSMUSG00000004610	electron transferring flavoprotein, beta polypeptide	1.796	0.0000	0.0000
Eva1b	ENSMUSG00000050212	eva-1 homolog B (C. elegans)	1.936	0.0045	0.0132
Evl	ENSMUSG00000021262	Ena-vasodilator stimulated phosphoprotein	2.521	0.0000	0.0000
Ewsr1	ENSMUSG00000009079	Ewing sarcoma breakpoint region 1	2.408	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Exd1	ENSMUSG00000048647	exonuclease 3'-5' domain containing 1	1.586	0.0116	0.0299
Exo5	ENSMUSG00000028629	exonuclease 5	1.611	0.0001	0.0005
Exosc2	ENSMUSG00000039356	exosome component 2	2.115	0.0000	0.0000
Exosc3	ENSMUSG00000028322	exosome component 3	2.372	0.0000	0.0000
Exosc7	ENSMUSG00000025785	exosome component 7	2.449	0.0000	0.0000
Exosc9	ENSMUSG00000027714	exosome component 9	2.190	0.0000	0.0000
Faap20	ENSMUSG00000073684	Fanconi anemia core complex associated protein 20	1.582	0.0054	0.0154
Fabp4	ENSMUSG00000062515	fatty acid binding protein 4, adipocyte	2.214	0.0000	0.0000
Fabp5	ENSMUSG00000027533	fatty acid binding protein 5, epidermal	2.113	0.0000	0.0000
Fabp7	ENSMUSG00000019874	fatty acid binding protein 7, brain	3.130	0.0000	0.0000
Fads3	ENSMUSG00000024664	fatty acid desaturase 3	1.556	0.0008	0.0028
Fahd1	ENSMUSG00000045316	fumarylacetoacetate hydrolase domain containing 1	2.446	0.0000	0.0000
Faim	ENSMUSG00000032463	Fas apoptotic inhibitory molecule	2.076	0.0000	0.0000
Faim2	ENSMUSG00000023011	Fas apoptotic inhibitory molecule 2	7.468	0.0472	0.0986
Fam104a	ENSMUSG00000041629	family with sequence similarity 104, member A	1.762	0.0027	0.0085
Fam110d	ENSMUSG00000050105	family with sequence similarity 110, member D	1.811	0.0079	0.0215
Fam122a	ENSMUSG00000074922	family with sequence similarity 122, member A	4.400	0.0000	0.0000
Fam131b	ENSMUSG00000029861	family with sequence similarity 131, member B	2.288	0.0021	0.0066
Fam131c	ENSMUSG00000006218	family with sequence similarity 131, member C	1.602	0.0012	0.0040
Fam133b	ENSMUSG00000058503	family with sequence similarity 133, member B	2.016	0.0000	0.0000
Fam149b	ENSMUSG00000039599	family with sequence similarity 149, member B	2.303	0.0000	0.0000
Fam167b	ENSMUSG00000050493	family with sequence similarity 167, member B	2.360	0.0209	0.0496
Fam171a2	ENSMUSG00000034685	family with sequence similarity 171, member A2	3.548	0.0000	0.0000
Fam174a	ENSMUSG00000051185	family with sequence similarity 174, member A	1.501	0.0050	0.0144
Fam174c	ENSMUSG00000035595	family with sequence similarity 174, member C	1.530	0.0286	0.0648
Fam184a	ENSMUSG00000019856	family with sequence similarity 184, member A	1.593	0.0480	0.0999
Fam193a	ENSMUSG00000037210	family with sequence homology 193, member A	1.776	0.0000	0.0000
Fam204a	ENSMUSG00000057858	family with sequence similarity 204, member A	2.639	0.0000	0.0000
Fam219a	ENSMUSG00000028439	family with sequence similarity 219, member A	1.540	0.0000	0.0000
Fam219b	ENSMUSG00000032305	family with sequence similarity 219, member B	1.675	0.0030	0.0091
Fam241a	ENSMUSG00000050549	family with sequence similarity 241, member A	4.792	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fam32a	ENSMUSG00000003039	family with sequence similarity 32, member A	1.587	0.0000	0.0000
Fam3c	ENSMUSG00000029672	FAM3 metabolism regulating signaling molecule C	3.074	0.0000	0.0000
Fam50a	ENSMUSG00000001962	family with sequence similarity 50, member A	2.725	0.0000	0.0000
Fam53c	ENSMUSG00000034300	family with sequence similarity 53, member C	1.870	0.0000	0.0000
Fam76b	ENSMUSG00000037808	family with sequence similarity 76, member B	1.734	0.0000	0.0001
Fam89a	ENSMUSG00000043068	family with sequence similarity 89, member A	2.162	0.0008	0.0030
Fam8a1	ENSMUSG00000069237	family with sequence similarity 8, member A1	2.136	0.0000	0.0000
Faxc	ENSMUSG00000028246	failed axon connections homolog	1.946	0.0094	0.0249
Fbl	ENSMUSG00000046865	fibrillarin	2.501	0.0000	0.0000
Fbrs	ENSMUSG00000042423	fibrosin	1.557	0.0051	0.0147
Fbxl14	ENSMUSG00000030019	F-box and leucine-rich repeat protein 14	3.132	0.0000	0.0000
Fbxl19	ENSMUSG00000030811	F-box and leucine-rich repeat protein 19	2.191	0.0000	0.0002
Fbxl3	ENSMUSG00000022124	F-box and leucine-rich repeat protein 3	1.665	0.0002	0.0007
Fbxo28	ENSMUSG00000047539	F-box protein 28	1.553	0.0000	0.0000
Fbxo4	ENSMUSG00000022184	F-box protein 4	1.525	0.0042	0.0124
Fbxo45	ENSMUSG00000035764	F-box protein 45	2.019	0.0000	0.0000
Fbxw11	ENSMUSG00000020271	F-box and WD-40 domain protein 11	1.582	0.0000	0.0000
Fbxw4	ENSMUSG00000040913	F-box and WD-40 domain protein 4	1.964	0.0000	0.0000
Fbxw8	ENSMUSG00000032867	F-box and WD-40 domain protein 8	1.534	0.0009	0.0032
Fer	ENSMUSG00000000127	fer (fms/fps related) protein kinase	1.524	0.0000	0.0000
Fgf16	ENSMUSG00000031230	fibroblast growth factor 16	2.822	0.0000	0.0000
Fgf20	ENSMUSG00000031603	fibroblast growth factor 20	10.071	0.0000	0.0000
Fgf7	ENSMUSG00000027208	fibroblast growth factor 7	1.767	0.0104	0.0272
Fgf9	ENSMUSG00000021974	fibroblast growth factor 9	1.639	0.0000	0.0002
Fgfbp3	ENSMUSG00000047632	fibroblast growth factor binding protein 3	2.329	0.0000	0.0000
Fhip2b	ENSMUSG00000022095	FHF complex subunit HOOK interacting protein 2B	2.603	0.0000	0.0000
Fignl2	ENSMUSG00000095440	fidgetin-like 2	2.152	0.0002	0.0008
Filip1	ENSMUSG00000034898	filamin A interacting protein 1	1.875	0.0000	0.0000
Fip1l1	ENSMUSG00000029227	FIP1 like 1 (S. cerevisiae)	1.676	0.0000	0.0000
Firre	ENSMUSG00000085396	functional intergenic repeating RNA element	1.745	0.0180	0.0435
Fkbp1a	ENSMUSG00000032966	FK506 binding protein 1a	1.865	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fkbp1b	ENSMUSG00000020635	FK506 binding protein 1b	4.826	0.0000	0.0000
Fkbp2	ENSMUSG00000056629	FK506 binding protein 2	4.473	0.0000	0.0000
Fkbp4	ENSMUSG00000030357	FK506 binding protein 4	1.506	0.0003	0.0010
Fkbp8	ENSMUSG00000019428	FK506 binding protein 8	1.949	0.0000	0.0000
Fkbp9	ENSMUSG00000029781	FK506 binding protein 9	1.815	0.0000	0.0000
Fkbpl	ENSMUSG00000033739	FK506 binding protein-like	2.598	0.0000	0.0000
Flvcr1	ENSMUSG00000066595	feline leukemia virus subgroup C cellular receptor 1	1.631	0.0000	0.0000
Fmnl2	ENSMUSG00000036053	formin-like 2	1.653	0.0000	0.0000
Fn3krp	ENSMUSG00000039253	fructosamine 3 kinase related protein	1.721	0.0000	0.0000
Fnbp1l	ENSMUSG00000039735	formin binding protein 1-like	1.694	0.0000	0.0000
Fndc4	ENSMUSG00000038552	fibronectin type III domain containing 4	2.205	0.0000	0.0001
Fndc5	ENSMUSG00000001334	fibronectin type III domain containing 5	1.602	0.0000	0.0000
Fnta	ENSMUSG00000015994	farnesyltransferase, CAAX box, alpha	2.182	0.0000	0.0000
Foxc1	ENSMUSG00000050295	forkhead box C1	3.916	0.0000	0.0000
Foxd1	ENSMUSG00000078302	forkhead box D1	4.643	0.0465	0.0975
Foxd2	ENSMUSG00000055210	forkhead box D2	3.548	0.0000	0.0000
Foxd3	ENSMUSG00000067261	forkhead box D3	4.341	0.0000	0.0002
Foxf1	ENSMUSG00000042812	forkhead box F1	2.310	0.0122	0.0312
Foxk2	ENSMUSG00000039275	forkhead box K2	1.509	0.0000	0.0000
Foxo4	ENSMUSG00000042903	forkhead box O4	1.628	0.0000	0.0000
Foxo6	ENSMUSG00000052135	forkhead box O6	4.380	0.0000	0.0001
Foxp4	ENSMUSG00000023991	forkhead box P4	2.362	0.0000	0.0000
Foxq1	ENSMUSG00000038415	forkhead box Q1	5.715	0.0019	0.0062
Fra10ac1	ENSMUSG00000054237	FRA10AC1 homolog (human)	2.464	0.0000	0.0000
Frat1	ENSMUSG00000067199	frequently rearranged in advanced T cell lymphomas	2.631	0.0000	0.0000
Frat2	ENSMUSG00000047604	frequently rearranged in advanced T cell lymphomas 2	4.685	0.0000	0.0000
Frg1	ENSMUSG00000031590	FSHD region gene 1	1.684	0.0000	0.0000
Ftsj3	ENSMUSG00000020706	FtsJ RNA methyltransferase homolog 3 (E. coli)	2.141	0.0000	0.0000
Fubp1	ENSMUSG00000028034	far upstream element (FUSE) binding protein 1	2.185	0.0000	0.0000
Fubp3	ENSMUSG00000026843	far upstream element (FUSE) binding protein 3	2.411	0.0000	0.0000
Fv1	ENSMUSG00000070583	Friend virus susceptibility 1	2.901	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fxr2	ENSMUSG00000018765	FMR1 autosomal homolog 2	2.130	0.0000	0.0000
Fyb	ENSMUSG00000022148	FYN binding protein	2.252	0.0000	0.0001
Fyn	ENSMUSG00000019843	Fyn proto-oncogene	3.018	0.0000	0.0000
Fzd1	ENSMUSG00000044674	frizzled class receptor 1	2.176	0.0000	0.0001
Fzd2	ENSMUSG00000050288	frizzled class receptor 2	2.400	0.0000	0.0000
Fzd6	ENSMUSG00000022297	frizzled class receptor 6	1.871	0.0000	0.0000
Fzd7	ENSMUSG00000041075	frizzled class receptor 7	1.753	0.0000	0.0001
Fzd8	ENSMUSG00000036904	frizzled class receptor 8	1.641	0.0018	0.0058
G430095P16Rik	ENSMUSG00000074203	RIKEN cDNA G430095P16 gene	3.287	0.0319	0.0710
Gadd45a	ENSMUSG00000036390	growth arrest and DNA-damage-inducible 45 alpha	2.312	0.0000	0.0000
Galnt1	ENSMUSG00000000420	polypeptide N-acetylgalactosaminyltransferase 1	1.813	0.0000	0.0000
Galnt2	ENSMUSG00000089704	polypeptide N-acetylgalactosaminyltransferase 2	36.401	0.0000	0.0000
Galnt3	ENSMUSG00000026994	polypeptide N-acetylgalactosaminyltransferase 3	3.592	0.0400	0.0861
Gar1	ENSMUSG00000028010	GAR1 ribonucleoprotein	1.867	0.0000	0.0000
Gart	ENSMUSG00000022962	phosphoribosylglycinamide formyltransferase	1.501	0.0000	0.0000
Gas1	ENSMUSG00000052957	growth arrest specific 1	2.155	0.0001	0.0002
Gas2l1	ENSMUSG00000034201	growth arrest-specific 2 like 1	1.615	0.0175	0.0425
Gas5	ENSMUSG00000053332	growth arrest specific 5	2.694	0.0000	0.0000
Gas7	ENSMUSG00000033066	growth arrest specific 7	1.686	0.0009	0.0030
Gas8	ENSMUSG00000040220	growth arrest specific 8	3.059	0.0000	0.0000
Gata6	ENSMUSG00000005836	GATA binding protein 6	1.664	0.0002	0.0007
Gatad1	ENSMUSG00000007415	GATA zinc finger domain containing 1	1.909	0.0000	0.0000
Gatad2a	ENSMUSG00000036180	GATA zinc finger domain containing 2A	1.541	0.0000	0.0000
Gatad2b	ENSMUSG00000042390	GATA zinc finger domain containing 2B	1.532	0.0012	0.0041
Gbp2	ENSMUSG00000028270	guanylate binding protein 2	1.509	0.0061	0.0170
Gbp3	ENSMUSG00000028268	guanylate binding protein 3	2.015	0.0010	0.0034
Gbp8	ENSMUSG00000034438	guanylate-binding protein 8	3.031	0.0295	0.0666
Gcfc2	ENSMUSG00000035125	GC-rich sequence DNA binding factor 2	1.539	0.0180	0.0437
Gch1	ENSMUSG00000037580	GTP cyclohydrolase 1	1.965	0.0000	0.0000
Gclc	ENSMUSG00000032350	glutamate-cysteine ligase, catalytic subunit	1.840	0.0001	0.0005
Gcnt2	ENSMUSG00000021360	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.702	0.0092	0.0245

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gcsh	ENSMUSG00000034424	glycine cleavage system protein H (aminomethyl carrier)	1.865	0.0000	0.0000
Gdf11	ENSMUSG00000025352	growth differentiation factor 11	2.161	0.0000	0.0000
Gdf6	ENSMUSG00000051279	growth differentiation factor 6	2.388	0.0006	0.0022
Gemin2	ENSMUSG00000060121	gem nuclear organelle associated protein 2	1.628	0.0000	0.0000
Gemin6	ENSMUSG00000055760	gem nuclear organelle associated protein 6	1.600	0.0002	0.0007
Gfra2	ENSMUSG00000022103	glial cell line derived neurotrophic factor family receptor alpha 2	2.128	0.0000	0.0002
Ggct	ENSMUSG00000002797	gamma-glutamyl cyclotransferase	2.078	0.0000	0.0000
Gid4	ENSMUSG00000018415	GID complex subunit 4, VID24 homolog	1.582	0.0000	0.0000
Gigyf2	ENSMUSG00000048000	GRB10 interacting GYF protein 2	1.663	0.0000	0.0000
Gimap1os	ENSMUSG00000044867	GTPase, IMAP family member 1, opposite strand	7.161	0.0005	0.0018
Gimap4	ENSMUSG00000054435	GTPase, IMAP family member 4	1.956	0.0000	0.0001
Gimap8	ENSMUSG00000064262	GTPase, IMAP family member 8	1.502	0.0000	0.0001
Ginm1	ENSMUSG00000040006	glycoprotein integral membrane 1	1.676	0.0000	0.0000
Gins2	ENSMUSG00000031821	GINS complex subunit 2 (Psf2 homolog)	1.574	0.0327	0.0724
Gja1	ENSMUSG00000050953	gap junction protein, alpha 1	1.606	0.0000	0.0000
Gjc1	ENSMUSG00000034520	gap junction protein, gamma 1	1.898	0.0000	0.0000
Gkap1	ENSMUSG00000021552	G kinase anchoring protein 1	2.408	0.0000	0.0000
Glcci1	ENSMUSG00000029638	glucocorticoid induced transcript 1	11.828	0.0000	0.0000
Glp2r	ENSMUSG00000049928	glucagon-like peptide 2 receptor	1.997	0.0367	0.0800
Glrx5	ENSMUSG00000021102	glutaredoxin 5	4.300	0.0000	0.0000
Gm10043	ENSMUSG00000109793	predicted pseudogene 10043	3.191	0.0437	0.0924
Gm10052	ENSMUSG00000058922	predicted pseudogene 10052	19.262	0.0000	0.0000
Gm10060	ENSMUSG00000110669	predicted gene 10060	2.977	0.0002	0.0010
Gm10080	ENSMUSG00000060467	predicted gene 10080	4.530	0.0278	0.0633
Gm10086	ENSMUSG00000060730	predicted pseudogene 10086	5.276	0.0001	0.0003
Gm10095	ENSMUSG00000113555	predicted gene 10095	1.598	0.0040	0.0118
Gm10125	ENSMUSG00000063087	predicted gene 10125	1.795	0.0261	0.0601
Gm10138	ENSMUSG00000100954	predicted gene 10138	1.724	0.0007	0.0025
Gm10209	ENSMUSG00000108080	predicted gene 10209	4.461	0.0001	0.0003
Gm10222	ENSMUSG00000067736	predicted gene 10222	2.570	0.0014	0.0046
Gm10232	ENSMUSG00000068141	predicted pseudogene 10232	3.111	0.0001	0.0004

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm10244	ENSMUSG00000068601	predicted gene 10244	6.824	0.0000	0.0001
Gm10254	ENSMUSG00000069011	predicted gene 10254	2.874	0.0105	0.0274
Gm10293	ENSMUSG00000070490	predicted pseudogene 10293	2.027	0.0001	0.0006
Gm10356	ENSMUSG00000072387	predicted gene 10356	4.507	0.0421	0.0898
Gm10371	ENSMUSG00000072589	predicted gene 10371	10.062	0.0000	0.0001
Gm10524	ENSMUSG00000097141	predicted gene 10524	2.362	0.0000	0.0000
Gm10575	ENSMUSG00000073787	predicted gene 10575	1.682	0.0028	0.0087
Gm10638	ENSMUSG00000074178	predicted gene 10638	9.048	0.0000	0.0000
Gm10642	ENSMUSG00000074213	predicted gene 10642	3.641	0.0004	0.0015
Gm10657	ENSMUSG00000103486	predicted gene 10657	5.875	0.0053	0.0151
Gm10705	ENSMUSG00000074506	predicted gene 10705	7.705	0.0000	0.0000
Gm10762	ENSMUSG00000074807	predicted gene 10762	3.142	0.0000	0.0000
Gm10925	ENSMUSG00000100862	predicted gene 10925	19.369	0.0000	0.0000
Gm10941	ENSMUSG00000078444	predicted gene 10941	7.014	0.0193	0.0463
Gm11175	ENSMUSG00000080058	predicted gene 11175	14.925	0.0000	0.0000
Gm11223	ENSMUSG00000046341	predicted gene 11223	3.805	0.0008	0.0029
Gm11407	ENSMUSG00000082179	predicted gene 11407	2.197	0.0166	0.0407
Gm11423	ENSMUSG00000085175	predicted gene 11423	1.658	0.0467	0.0977
Gm11478	ENSMUSG00000083992	predicted gene 11478	2.506	0.0000	0.0000
Gm11488	ENSMUSG00000081871	predicted gene 11488	4.541	0.0416	0.0888
Gm11560	ENSMUSG00000086688	predicted gene 11560	4.010	0.0000	0.0000
Gm11638	ENSMUSG00000086487	predicted gene 11638	6.096	0.0213	0.0504
Gm11642	ENSMUSG00000086794	predicted gene 11642	2.889	0.0000	0.0000
Gm11696	ENSMUSG00000056687	predicted gene 11696	2.714	0.0000	0.0000
Gm11732	ENSMUSG00000085336	predicted gene 11732	1.974	0.0003	0.0013
Gm11748	ENSMUSG00000087036	predicted gene 11748	77.664	0.0000	0.0000
Gm11756	ENSMUSG00000093962	predicted gene 11756	2.590	0.0198	0.0473
Gm11821	ENSMUSG00000081884	predicted gene 11821	5.701	0.0019	0.0061
Gm11940	ENSMUSG00000087692	predicted gene 11940	1.754	0.0030	0.0091
Gm11973	ENSMUSG00000086839	predicted gene 11973	4.377	0.0004	0.0016
Gm12100	ENSMUSG00000087474	predicted gene 12100	5.938	0.0014	0.0047

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm12129	ENSMUSG00000082587	predicted gene 12129	64.561	0.0000	0.0001
Gm12138	ENSMUSG00000082087	predicted gene 12138	6.830	0.0000	0.0000
Gm12183	ENSMUSG00000082454	predicted gene 12183	1.673	0.0134	0.0339
Gm12184	ENSMUSG00000078154	predicted gene 12184	2.878	0.0000	0.0000
Gm12191	ENSMUSG00000083061	predicted gene 12191	2.999	0.0001	0.0005
Gm12312	ENSMUSG00000082145	predicted gene 12312	2.707	0.0000	0.0000
Gm12346	ENSMUSG00000083899	predicted gene 12346	1.994	0.0155	0.0385
Gm12430	ENSMUSG00000081152	predicted gene 12430	7.243	0.0445	0.0938
Gm12444	ENSMUSG00000082194	predicted gene 12444	5.064	0.0288	0.0651
Gm12473	ENSMUSG00000086043	predicted gene 12473	23.508	0.0155	0.0385
Gm12669	ENSMUSG00000100863	predicted gene 12669	1.527	0.0092	0.0244
Gm12688	ENSMUSG00000086096	predicted gene 12688	7.059	0.0044	0.0128
Gm12693	ENSMUSG00000083179	predicted gene 12693	13.481	0.0000	0.0000
Gm12844	ENSMUSG00000084260	predicted gene 12844	2.372	0.0314	0.0701
Gm12905	ENSMUSG00000085875	predicted gene 12905	3.509	0.0004	0.0013
Gm12966	ENSMUSG00000070729	predicted gene 12966	4.610	0.0000	0.0000
Gm12992	ENSMUSG00000085667	predicted gene 12992	3.191	0.0000	0.0000
Gm12999	ENSMUSG00000087352	predicted gene 12999	2.504	0.0002	0.0010
Gm13161	ENSMUSG00000082248	predicted gene 13161	29.590	0.0000	0.0000
Gm13162	ENSMUSG00000082779	predicted pseudogene 13162	70.205	0.0002	0.0007
Gm13243	ENSMUSG00000094417	predicted gene 13243	66.554	0.0000	0.0000
Gm13339	ENSMUSG00000082884	predicted gene 13339	3.357	0.0000	0.0001
Gm13341	ENSMUSG00000083863	predicted gene 13341	1.762	0.0001	0.0006
Gm13369	ENSMUSG00000083796	predicted gene 13369	7.424	0.0356	0.0779
Gm13430	ENSMUSG00000083101	predicted gene 13430	41.024	0.0100	0.0262
Gm13453	ENSMUSG00000083240	predicted gene 13453	4.070	0.0000	0.0000
Gm13528	ENSMUSG00000085087	predicted gene 13528	1.781	0.0297	0.0668
Gm13577	ENSMUSG00000082127	predicted gene 13577	10.708	0.0000	0.0000
Gm13594	ENSMUSG00000086881	predicted gene 13594	17.730	0.0000	0.0000
Gm13601	ENSMUSG00000087467	predicted gene 13601	12.916	0.0131	0.0332
Gm13620	ENSMUSG00000086603	predicted gene 13620	3.958	0.0050	0.0145

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm13657	ENSMUSG00000086813	predicted gene 13657	2.264	0.0032	0.0097
Gm13712	ENSMUSG00000082534	predicted gene 13712	3.938	0.0000	0.0000
Gm13736	ENSMUSG00000082908	predicted gene 13736	1.536	0.0000	0.0000
Gm13886	ENSMUSG00000083856	predicted gene 13886	3.659	0.0115	0.0297
Gm13889	ENSMUSG00000087006	predicted gene 13889	2.268	0.0001	0.0003
Gm14057	ENSMUSG00000089662	predicted gene 14057	1.988	0.0068	0.0188
Gm14221	ENSMUSG00000078956	predicted gene 14221	4.319	0.0000	0.0000
Gm14398	ENSMUSG00000083993	predicted gene 14398	6.161	0.0001	0.0005
Gm14703	ENSMUSG00000087644	predicted gene 14703	1.695	0.0158	0.0391
Gm14964	ENSMUSG00000052188	predicted gene 14964	2.532	0.0000	0.0000
Gm15163	ENSMUSG00000085711	predicted gene 15163	3.763	0.0000	0.0000
Gm15270	ENSMUSG00000087400	predicted gene 15270	1.820	0.0002	0.0009
Gm15285	ENSMUSG00000081277	predicted gene 15285	4.189	0.0000	0.0000
Gm15327	ENSMUSG00000085204	predicted gene 15327	3.063	0.0147	0.0367
Gm15387	ENSMUSG00000082585	predicted gene 15387	5.041	0.0271	0.0620
Gm15441	ENSMUSG00000074398	predicted gene 15441	4.381	0.0000	0.0000
Gm15445	ENSMUSG00000085311	predicted gene 15445	9.674	0.0046	0.0134
Gm15500	ENSMUSG00000086583	predicted pseudogene 15500	1.855	0.0010	0.0034
Gm15542	ENSMUSG00000083396	predicted gene 15542	5.530	0.0000	0.0000
Gm15609	ENSMUSG00000086602	predicted gene 15609	18.971	0.0000	0.0000
Gm15610	ENSMUSG00000078183	predicted gene 15610	2.176	0.0000	0.0000
Gm15706	ENSMUSG00000086013	predicted gene 15706	2.201	0.0029	0.0089
Gm15793	ENSMUSG00000082769	predicted gene 15793	6.117	0.0402	0.0864
Gm15801	ENSMUSG00000096592	predicted gene 15801	27.027	0.0000	0.0000
Gm15853	ENSMUSG00000103400	predicted gene 15853	1.858	0.0099	0.0262
Gm15860	ENSMUSG00000087336	predicted gene 15860	3.038	0.0000	0.0001
Gm15906	ENSMUSG00000087416	predicted gene 15906	139.414	0.0000	0.0000
Gm15934	ENSMUSG00000090088	predicted gene 15934	2.174	0.0211	0.0499
Gm15952	ENSMUSG00000085655	predicted gene 15952	6.338	0.0004	0.0015
Gm16089	ENSMUSG00000081228	predicted gene 16089	3.548	0.0000	0.0000
Gm16124	ENSMUSG00000086914	predicted gene 16124	3.589	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm16136	ENSMUSG00000089804	predicted gene 16136	2.362	0.0006	0.0021
Gm16140	ENSMUSG00000084085	predicted gene 16140	3.023	0.0138	0.0347
Gm16409	ENSMUSG00000075581	predicted gene 16409	10.399	0.0004	0.0015
Gm16437	ENSMUSG00000024761	predicted pseudogene 16437	2.570	0.0009	0.0032
Gm16701	ENSMUSG00000097823	predicted gene, 16701	2.563	0.0013	0.0043
Gm16754	ENSMUSG00000097439	predicted gene, 16754	10.359	0.0465	0.0973
Gm16845	ENSMUSG00000096981	predicted gene, 16845	2.524	0.0422	0.0899
Gm16861	ENSMUSG00000097397	predicted gene, 16861	7.249	0.0004	0.0017
Gm16933	ENSMUSG00000086289	predicted gene, 16933	17.416	0.0055	0.0156
Gm17082	ENSMUSG00000090674	predicted gene 17082	8.816	0.0212	0.0501
Gm17092	ENSMUSG00000091623	predicted gene 17092	9.212	0.0000	0.0000
Gm17110	ENSMUSG00000090779	predicted gene 17110	21.889	0.0000	0.0000
Gm17251	ENSMUSG00000090952	predicted gene, 17251	2.320	0.0001	0.0004
Gm17334	ENSMUSG00000091191	predicted gene, 17334	2.754	0.0407	0.0872
Gm17349	ENSMUSG00000091604	predicted gene, 17349	4.630	0.0192	0.0462
Gm17382	ENSMUSG00000078838	predicted gene, 17382	2.487	0.0389	0.0841
Gm17396	ENSMUSG00000079669	predicted gene, 17396	2.253	0.0068	0.0187
Gm17428	ENSMUSG00000090889	predicted gene, 17428	5.256	0.0000	0.0000
Gm17484	ENSMUSG00000091514	predicted gene, 17484	2.198	0.0396	0.0854
Gm17606	ENSMUSG00000091306	predicted gene, 17606	7.852	0.0429	0.0912
Gm17661	ENSMUSG00000091037	predicted gene, 17661	20.880	0.0000	0.0000
Gm18860	ENSMUSG00000110569	predicted gene, 18860	1.870	0.0000	0.0000
Gm18911	ENSMUSG00000116438	predicted gene, 18911	21.572	0.0000	0.0000
Gm19221	ENSMUSG00000113491	predicted gene, 19221	5.864	0.0143	0.0360
Gm19426	ENSMUSG00000097187	predicted gene, 19426	1.686	0.0137	0.0345
Gm19557	ENSMUSG00000097990	predicted gene, 19557	3.195	0.0000	0.0002
Gm2000	ENSMUSG00000078193	predicted gene 2000	1.797	0.0000	0.0000
Gm20033	ENSMUSG00000097640	predicted gene, 20033	5.641	0.0000	0.0000
Gm20036	ENSMUSG00000093579	predicted gene, 20036	1.840	0.0290	0.0655
Gm20045	ENSMUSG00000103983	predicted gene, 20045	2.024	0.0239	0.0556
Gm20091	ENSMUSG00000094249	predicted gene, 20091	6.381	0.0010	0.0035

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm20125	ENSMUSG00000101969	predicted gene, 20125	5.286	0.0339	0.0747
Gm20186	ENSMUSG00000106874	predicted gene, 20186	2.714	0.0003	0.0011
Gm20300	ENSMUSG00000111080	predicted gene, 20300	1.616	0.0000	0.0000
Gm20379	ENSMUSG00000100622	predicted gene, 20379	34.131	0.0003	0.0013
Gm20400	ENSMUSG00000092500	predicted gene 20400	5.807	0.0057	0.0161
Gm20421	ENSMUSG00000092483	predicted gene 20421	6.508	0.0003	0.0013
Gm20457	ENSMUSG00000092187	predicted gene 20457	2.019	0.0000	0.0000
Gm20522	ENSMUSG00000092241	predicted gene 20522	2.183	0.0020	0.0064
Gm20544	ENSMUSG00000092569	predicted gene 20544	2.651	0.0000	0.0000
Gm2058	ENSMUSG00000074903	predicted gene 2058	3.027	0.0000	0.0000
Gm20721	ENSMUSG00000090625	predicted gene, 20721	22.563	0.0000	0.0000
Gm21399	ENSMUSG00000094530	predicted gene, 21399	2.811	0.0000	0.0000
Gm21596	ENSMUSG00000096006	predicted gene, 21596	9.080	0.0000	0.0000
Gm21926	ENSMUSG00000116995	predicted gene, 21926	1.847	0.0000	0.0001
Gm22009	ENSMUSG00000089417	predicted gene, 22009	2.942	0.0000	0.0000
Gm2223	ENSMUSG00000079297	predicted pseudogene 2223	1.882	0.0310	0.0692
Gm22953	ENSMUSG00000080374	predicted gene, 22953	3.898	0.0129	0.0329
Gm2296	ENSMUSG00000118653	predicted gene 2296	13.855	0.0000	0.0000
Gm2308	ENSMUSG00000092257	predicted gene 2308	2.055	0.0006	0.0020
Gm23119	ENSMUSG00000089235	predicted gene, 23119	3.218	0.0179	0.0434
Gm24045	ENSMUSG00000065047	predicted gene, 24045	5.279	0.0171	0.0418
Gm2415	ENSMUSG00000086119	predicted gene 2415	1.530	0.0161	0.0398
Gm26558	ENSMUSG00000097025	predicted gene, 26558	6.810	0.0027	0.0083
Gm26586	ENSMUSG00000097472	predicted gene, 26586	7.847	0.0395	0.0851
Gm26631	ENSMUSG00000097445	predicted gene, 26631	12.095	0.0006	0.0023
Gm26704	ENSMUSG00000097875	predicted gene, 26704	2.352	0.0392	0.0847
Gm26881	ENSMUSG00000096974	predicted gene, 26881	1.757	0.0000	0.0001
Gm26910	ENSMUSG00000097835	predicted gene, 26910	2.509	0.0002	0.0006
Gm2710	ENSMUSG00000060128	predicted gene 2710	42.607	0.0005	0.0019
Gm27184	ENSMUSG00000098447	predicted gene 27184	4.897	0.0161	0.0398
Gm28035	ENSMUSG00000099041	predicted gene, 28035	12.667	0.0045	0.0131

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm2830	ENSMUSG00000086567	predicted gene 2830	2.695	0.0000	0.0000
Gm28424	ENSMUSG00000101037	predicted gene 28424	2.474	0.0446	0.0939
Gm28437	ENSMUSG00000101111	predicted gene 28437	6.568	0.0000	0.0000
Gm28439	ENSMUSG00000100131	predicted gene 28439	4.453	0.0000	0.0000
Gm28529	ENSMUSG00000101320	predicted gene 28529	3.711	0.0000	0.0000
Gm28661	ENSMUSG00000102070	predicted gene 28661	2.867	0.0000	0.0000
Gm29216	ENSMUSG00000101249	predicted gene 29216	16.994	0.0000	0.0000
Gm29246	ENSMUSG00000102062	predicted gene 29246	4.627	0.0000	0.0002
Gm29346	ENSMUSG00000101386	predicted gene 29346	3.179	0.0045	0.0131
Gm2962	ENSMUSG00000089838	predicted pseudogene 2962	4.732	0.0000	0.0000
Gm29629	ENSMUSG00000099874	predicted gene 29629	31.965	0.0000	0.0000
Gm29675	ENSMUSG00000113515	predicted gene, 29675	2.321	0.0295	0.0666
Gm29686	ENSMUSG00000116725	predicted gene, 29686	2.613	0.0114	0.0294
Gm30025	ENSMUSG00000112278	predicted gene, 30025	2.073	0.0020	0.0063
Gm30873	ENSMUSG00000109341	predicted gene, 30873	2.332	0.0297	0.0669
Gm31166	ENSMUSG00000109695	predicted gene, 31166	4.335	0.0000	0.0000
Gm32282	ENSMUSG00000117648	predicted gene, 32282	2.606	0.0003	0.0010
Gm32699	ENSMUSG00000113528	predicted gene, 32699	1.828	0.0299	0.0672
Gm34220	ENSMUSG00000114045	predicted gene, 34220	6.073	0.0000	0.0000
Gm35558	ENSMUSG00000113662	predicted gene, 35558	2.494	0.0001	0.0006
Gm36033	ENSMUSG00000111058	predicted gene, 36033	7.233	0.0019	0.0062
Gm3625	ENSMUSG00000118449	predicted gene 3625	2.017	0.0000	0.0000
Gm36827	ENSMUSG00000112327	predicted gene, 36827	1.753	0.0002	0.0007
Gm37116	ENSMUSG00000103574	predicted gene, 37116	4.471	0.0000	0.0000
Gm37123	ENSMUSG00000103039	predicted gene, 37123	2.518	0.0029	0.0090
Gm3716	ENSMUSG00000105402	predicted gene 3716	1.732	0.0244	0.0566
Gm37194	ENSMUSG00000102189	predicted gene, 37194	47.504	0.0000	0.0000
Gm37201	ENSMUSG00000103658	predicted gene, 37201	7.264	0.0000	0.0000
Gm37376	ENSMUSG00000102349	predicted gene, 37376	8.898	0.0264	0.0606
Gm37563	ENSMUSG00000104040	predicted gene, 37563	16.950	0.0114	0.0294
Gm37694	ENSMUSG00000102562	predicted gene, 37694	2.291	0.0051	0.0146

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm37711	ENSMUSG00000102796	predicted gene, 37711	3.583	0.0234	0.0546
Gm37786	ENSMUSG00000102632	predicted gene, 37786	3.403	0.0192	0.0461
Gm3788	ENSMUSG00000094392	predicted gene 3788	13.231	0.0005	0.0020
Gm37969	ENSMUSG00000102577	predicted gene, 37969	10.783	0.0133	0.0338
Gm39302	ENSMUSG00000111172	predicted gene, 39302	3.733	0.0000	0.0002
Gm40466	ENSMUSG00000110649	predicted gene, 40466	1.877	0.0030	0.0093
Gm4076	ENSMUSG00000096449	predicted gene 4076	2.056	0.0000	0.0001
Gm41144	ENSMUSG00000115846	predicted gene, 41144	7.163	0.0021	0.0067
Gm41381	ENSMUSG00000118456	predicted gene, 41381	3.607	0.0000	0.0000
Gm41505	ENSMUSG00000116641	predicted gene, 41505	3.937	0.0001	0.0003
Gm41760	ENSMUSG00000117992	predicted gene, 41760	2.381	0.0000	0.0000
Gm4202	ENSMUSG00000091421	predicted gene 4202	1.789	0.0048	0.0140
Gm42462	ENSMUSG00000104728	predicted gene 42462	4.131	0.0084	0.0226
Gm42517	ENSMUSG00000105867	predicted gene 42517	3.713	0.0000	0.0000
Gm42547	ENSMUSG00000106990	predicted gene 42547	1.582	0.0056	0.0159
Gm42596	ENSMUSG00000105482	predicted gene 42596	26.542	0.0002	0.0009
Gm42922	ENSMUSG00000104605	predicted gene 42922	4.213	0.0007	0.0027
Gm42984	ENSMUSG00000104784	predicted gene 42984	6.999	0.0000	0.0000
Gm43011	ENSMUSG00000106475	predicted gene 43011	1.847	0.0459	0.0964
Gm43034	ENSMUSG00000106662	predicted gene 43034	1.549	0.0234	0.0546
Gm43062	ENSMUSG00000104671	predicted gene 43062	7.159	0.0033	0.0101
Gm43075	ENSMUSG00000105004	predicted gene 43075	2.978	0.0158	0.0392
Gm43196	ENSMUSG00000107017	predicted gene 43196	3.191	0.0052	0.0149
Gm43324	ENSMUSG00000105487	predicted gene 43324	8.302	0.0004	0.0015
Gm43361	ENSMUSG00000106375	predicted gene 43361	4.129	0.0011	0.0039
Gm43481	ENSMUSG00000107000	predicted gene 43481	2.476	0.0021	0.0066
Gm43500	ENSMUSG00000107296	predicted gene 43500	7.794	0.0212	0.0502
Gm43568	ENSMUSG00000106365	predicted gene 43568	4.894	0.0304	0.0682
Gm43573	ENSMUSG00000104786	predicted gene 43573	4.529	0.0000	0.0001
Gm4366	ENSMUSG00000107383	predicted gene 4366	2.215	0.0000	0.0000
Gm43712	ENSMUSG00000104649	predicted gene 43712	3.598	0.0180	0.0435

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm44136	ENSMUSG00000107524	predicted gene, 44136	5.330	0.0192	0.0462
Gm44250	ENSMUSG00000107881	predicted gene, 44250	1.578	0.0000	0.0000
Gm44421	ENSMUSG00000107451	predicted gene, 44421	2.392	0.0000	0.0001
Gm44423	ENSMUSG00000108064	predicted gene, 44423	2.942	0.0173	0.0421
Gm44731	ENSMUSG00000108190	predicted gene 44731	6.447	0.0000	0.0002
Gm44732	ENSMUSG00000108934	predicted gene 44732	17.750	0.0000	0.0000
Gm44837	ENSMUSG00000108723	predicted gene 44837	18.931	0.0178	0.0433
Gm44899	ENSMUSG00000109008	predicted gene 44899	4.202	0.0000	0.0000
Gm44950	ENSMUSG00000108350	predicted gene 44950	1.626	0.0001	0.0005
Gm45074	ENSMUSG00000109568	predicted gene 45074	13.572	0.0098	0.0259
Gm4524	ENSMUSG00000090257	predicted gene 4524	2.415	0.0023	0.0072
Gm45246	ENSMUSG00000109645	predicted gene 45246	2.904	0.0001	0.0003
Gm45250	ENSMUSG00000110317	predicted gene 45250	2.583	0.0027	0.0084
Gm45371	ENSMUSG00000109954	predicted gene 45371	21.774	0.0095	0.0252
Gm45380	ENSMUSG00000110360	predicted gene 45380	1.973	0.0006	0.0021
Gm45494	ENSMUSG00000110161	predicted gene 45494	2.803	0.0000	0.0000
Gm45897	ENSMUSG00000110676	predicted gene 45897	2.838	0.0177	0.0431
Gm4617	ENSMUSG00000096544	predicted pseudogene 4617	4.446	0.0000	0.0000
Gm4673	ENSMUSG00000097750	predicted gene 4673	3.467	0.0000	0.0000
Gm47155	ENSMUSG00000114019	predicted gene, 47155	2.424	0.0000	0.0000
Gm47205	ENSMUSG00000111312	predicted gene, 47205	8.142	0.0013	0.0042
Gm47210	ENSMUSG00000113647	predicted gene, 47210	5.019	0.0004	0.0014
Gm4734	ENSMUSG00000106208	predicted gene 4734	9.000	0.0058	0.0164
Gm4754	ENSMUSG00000106895	predicted gene 4754	3.629	0.0313	0.0699
Gm47766	ENSMUSG00000112336	predicted gene, 47766	19.770	0.0000	0.0000
Gm47863	ENSMUSG00000113165	predicted gene, 47863	1.739	0.0031	0.0096
Gm4811	ENSMUSG00000113263	predicted gene 4811	2.297	0.0016	0.0051
Gm48226	ENSMUSG00000112302	predicted gene, 48226	2.073	0.0000	0.0000
Gm48295	ENSMUSG00000114309	predicted gene, 48295	1.907	0.0419	0.0894
Gm4835	ENSMUSG00000043223	predicted pseudogene 4835	4.914	0.0001	0.0002
Gm4853	ENSMUSG00000081473	predicted pseudogene 4853	2.609	0.0009	0.0032

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm48604	ENSMUSG00000111291	predicted gene, 48604	1.543	0.0107	0.0279
Gm48607	ENSMUSG00000113735	predicted gene, 48607	2.098	0.0322	0.0717
Gm48623	ENSMUSG00000112941	predicted gene, 48623	2.548	0.0369	0.0804
Gm4864	ENSMUSG00000112003	predicted gene 4864	1.928	0.0076	0.0207
Gm48667	ENSMUSG00000113964	predicted gene, 48667	66.637	0.0000	0.0001
Gm48705	ENSMUSG00000114834	predicted gene, 48705	15.316	0.0130	0.0329
Gm48768	ENSMUSG00000112346	predicted gene, 48768	2.404	0.0000	0.0001
Gm48933	ENSMUSG00000115003	predicted gene, 48933	12.583	0.0000	0.0000
Gm4895	ENSMUSG00000044268	predicted gene 4895	3.423	0.0002	0.0009
Gm49041	ENSMUSG00000115026	predicted gene, 49041	1.936	0.0074	0.0202
Gm49130	ENSMUSG00000115234	predicted gene, 49130	7.674	0.0000	0.0000
Gm49207	ENSMUSG00000115497	predicted gene, 49207	6.477	0.0130	0.0330
Gm4925	ENSMUSG00000069540	predicted gene 4925	2.647	0.0117	0.0300
Gm49284	ENSMUSG00000114995	predicted gene, 49284	1.617	0.0049	0.0142
Gm49330	ENSMUSG00000113234	predicted gene, 49330	10.568	0.0077	0.0210
Gm49492	ENSMUSG00000116180	predicted gene, 49492	1.737	0.0000	0.0000
Gm49540	ENSMUSG00000116272	predicted gene, 49540	3.219	0.0001	0.0005
Gm49544	ENSMUSG00000116262	predicted gene, 49544	40.185	0.0000	0.0000
Gm49727	ENSMUSG00000116836	predicted gene, 49727	3.289	0.0175	0.0427
Gm49741	ENSMUSG00000116571	predicted gene, 49741	4.563	0.0000	0.0000
Gm49768	ENSMUSG00000115220	predicted gene, 49768	2.311	0.0000	0.0001
Gm49864	ENSMUSG00000117255	predicted gene, 49864	18.030	0.0000	0.0000
Gm49883	ENSMUSG00000117113	predicted gene, 49883	2.312	0.0009	0.0031
Gm49894	ENSMUSG00000117069	predicted gene, 49894	7.495	0.0010	0.0034
Gm50069	ENSMUSG00000117634	predicted gene, 50069	2.508	0.0011	0.0037
Gm50144	ENSMUSG00000118184	predicted gene, 50144	3.534	0.0000	0.0000
Gm50163	ENSMUSG00000118030	predicted gene, 50163	6.528	0.0306	0.0685
Gm50240	ENSMUSG00000117725	predicted gene, 50240	2.031	0.0000	0.0000
Gm50251	ENSMUSG00000117839	predicted gene, 50251	3.824	0.0168	0.0412
Gm50253	ENSMUSG00000117819	predicted gene, 50253	5.430	0.0000	0.0000
Gm50464	ENSMUSG00000118487	predicted gene, 50464	4.666	0.0148	0.0370

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5216	ENSMUSG00000116398	predicted gene 5216	30.594	0.0000	0.0000
Gm527	ENSMUSG00000047227	predicted gene 527	2.271	0.0000	0.0000
Gm53012	ENSMUSG00000118504	predicted gene, 53012	2.266	0.0002	0.0007
Gm53023	ENSMUSG00000118572	predicted gene, 53023	10.307	0.0000	0.0000
Gm5422	ENSMUSG00000039684	predicted pseudogene 5422	3.602	0.0000	0.0000
Gm5469	ENSMUSG00000116083	predicted gene 5469	4.669	0.0019	0.0062
Gm55094	ENSMUSG00002075524	predicted gene, 55094	6.773	0.0024	0.0075
Gm55118	ENSMUSG00002076173	predicted gene, 55118	42.138	0.0000	0.0000
Gm5512	ENSMUSG00000112693	predicted gene 5512	30.352	0.0000	0.0000
Gm5526	ENSMUSG00000084817	predicted pseudogene 5526	3.147	0.0413	0.0884
Gm55276	ENSMUSG00002075551	predicted gene, 55276	3.260	0.0048	0.0140
Gm5550	ENSMUSG00000106419	predicted gene 5550	44.942	0.0007	0.0025
Gm55594	ENSMUSG00000095562	predicted gene, 55594	3.293	0.0011	0.0038
Gm55632	ENSMUSG00002075486	predicted gene, 55632	50.703	0.0000	0.0000
Gm5577	ENSMUSG00000084950	predicted gene 5577	5.060	0.0281	0.0639
Gm55936	ENSMUSG00002075188	predicted gene, 55936	15.760	0.0000	0.0001
Gm55944	ENSMUSG00002076463	predicted gene, 55944	20.293	0.0000	0.0000
Gm5602	ENSMUSG00000086108	predicted gene 5602	2.064	0.0027	0.0084
Gm5611	ENSMUSG00000090602	predicted gene 5611	4.975	0.0064	0.0178
Gm56171	ENSMUSG00002075501	predicted gene, 56171	22.337	0.0000	0.0000
Gm5620	ENSMUSG00000056904	predicted gene 5620	3.213	0.0022	0.0068
Gm56228	ENSMUSG00002075075	predicted gene, 56228	3.960	0.0000	0.0000
Gm56257	ENSMUSG00002075231	predicted gene, 56257	16.681	0.0000	0.0000
Gm56478	ENSMUSG00002076074	predicted gene, 56478	4.154	0.0000	0.0000
Gm5778	ENSMUSG00000091825	predicted gene 5778	2.368	0.0115	0.0296
Gm5805	ENSMUSG00000061848	predicted gene 5805	12.301	0.0000	0.0000
Gm5819	ENSMUSG00000092097	predicted gene 5819	9.822	0.0041	0.0122
Gm5828	ENSMUSG00000091020	predicted gene 5828	3.143	0.0000	0.0001
Gm5898	ENSMUSG00000081788	predicted gene 5898	6.314	0.0000	0.0000
Gm5904	ENSMUSG00000109894	predicted gene 5904	4.288	0.0231	0.0540
Gm5909	ENSMUSG00000082491	predicted gene 5909	1.722	0.0214	0.0505

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5921	ENSMUSG00000074034	predicted gene 5921	3.672	0.0029	0.0090
Gm6139	ENSMUSG00000057244	predicted gene 6139	3.688	0.0103	0.0269
Gm6204	ENSMUSG00000105879	predicted gene 6204	11.773	0.0000	0.0000
Gm6254	ENSMUSG00000066538	predicted gene 6254	5.716	0.0049	0.0140
Gm6277	ENSMUSG00000097440	predicted gene 6277	1.768	0.0159	0.0394
Gm6363	ENSMUSG00000114993	predicted gene 6363	5.022	0.0123	0.0313
Gm6433	ENSMUSG00000083382	predicted gene 6433	3.552	0.0241	0.0560
Gm6444	ENSMUSG00000080836	predicted gene 6444	1.837	0.0374	0.0813
Gm6445	ENSMUSG00000100141	predicted gene 6445	24.611	0.0000	0.0000
Gm6457	ENSMUSG00000053740	predicted pseudogene 6457	3.387	0.0446	0.0939
Gm6477	ENSMUSG00000111877	predicted gene 6477	4.045	0.0010	0.0034
Gm6556	ENSMUSG00000097806	predicted gene 6556	4.387	0.0009	0.0033
Gm6579	ENSMUSG00000109565	predicted gene 6579	9.820	0.0290	0.0656
Gm6682	ENSMUSG00000091269	predicted gene 6682	2.520	0.0022	0.0068
Gm6685	ENSMUSG00000032889	predicted pseudogene 6685	1.644	0.0368	0.0802
Gm6728	ENSMUSG00000091408	predicted gene 6728	2.325	0.0001	0.0006
Gm6877	ENSMUSG00000083557	predicted pseudogene 6877	19.908	0.0003	0.0011
Gm6916	ENSMUSG00000108608	predicted pseudogene 6916	3.004	0.0000	0.0000
Gm6974	ENSMUSG00000117673	predicted gene 6974	23.221	0.0011	0.0038
Gm7198	ENSMUSG00000112395	predicted gene 7198	36.495	0.0421	0.0897
Gm7292	ENSMUSG00000104222	predicted gene 7292	3.302	0.0000	0.0000
Gm7334	ENSMUSG00000044645	predicted gene 7334	4.270	0.0014	0.0048
Gm7335	ENSMUSG00000067189	predicted gene 7335	5.174	0.0370	0.0806
Gm7390	ENSMUSG00000110644	predicted gene 7390	11.337	0.0000	0.0000
Gm7466	ENSMUSG00000117359	predicted gene 7466	2.385	0.0249	0.0576
Gm7467	ENSMUSG00000098449	predicted gene 7467	7.779	0.0000	0.0000
Gm7591	ENSMUSG00000114349	predicted gene 7591	2.798	0.0001	0.0004
Gm7666	ENSMUSG00000067547	predicted pseudogene 7666	1.960	0.0000	0.0000
Gm7729	ENSMUSG00000046636	predicted gene 7729	7.060	0.0000	0.0000
Gm7803	ENSMUSG00000083754	predicted gene 7803	5.320	0.0432	0.0916
Gm7809	ENSMUSG00000099397	predicted gene 7809	4.487	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm7887	ENSMUSG00000044211	predicted gene 7887	2.289	0.0000	0.0000
Gm7895	ENSMUSG00000100347	predicted gene 7895	3.329	0.0002	0.0009
Gm7984	ENSMUSG00000049891	predicted gene 7984	2.356	0.0000	0.0001
Gm8066	ENSMUSG00000106237	predicted gene 8066	8.575	0.0000	0.0000
Gm8098	ENSMUSG00000073073	predicted gene 8098	3.455	0.0002	0.0007
Gm8116	ENSMUSG00000059422	predicted gene 8116	4.582	0.0000	0.0000
Gm8130	ENSMUSG00000116637	predicted gene 8130	3.265	0.0009	0.0031
Gm8451	ENSMUSG00000099471	predicted gene 8451	9.720	0.0000	0.0000
Gm8518	ENSMUSG00000115312	predicted gene 8518	2.342	0.0058	0.0163
Gm8546	ENSMUSG00000094463	predicted gene 8546	2.642	0.0191	0.0459
Gm8643	ENSMUSG00000102809	predicted gene 8643	5.367	0.0080	0.0217
Gm8717	ENSMUSG00000117935	predicted gene 8717	4.438	0.0030	0.0091
Gm8806	ENSMUSG00000083367	predicted gene 8806	3.706	0.0122	0.0311
Gm8826	ENSMUSG00000102268	predicted gene 8826	14.982	0.0020	0.0063
Gm8991	ENSMUSG00000059179	predicted pseudogene 8991	18.517	0.0010	0.0033
Gm9118	ENSMUSG00000112825	predicted gene 9118	3.811	0.0345	0.0759
Gm9162	ENSMUSG00000098044	predicted gene 9162	16.368	0.0000	0.0000
Gm9202	ENSMUSG00000114066	predicted gene 9202	3.222	0.0100	0.0264
Gm9276	ENSMUSG00000118377	predicted gene 9276	3.889	0.0251	0.0581
Gm9316	ENSMUSG00000117262	predicted gene 9316	4.383	0.0001	0.0005
Gm9358	ENSMUSG00000098199	predicted gene 9358	6.735	0.0000	0.0000
Gm9392	ENSMUSG00000087298	predicted pseudogene 9392	9.831	0.0000	0.0000
Gm9431	ENSMUSG00000083468	predicted gene 9431	17.179	0.0001	0.0004
Gm9442	ENSMUSG00000104241	predicted gene 9442	3.049	0.0228	0.0535
Gm9755	ENSMUSG00000030735	predicted pseudogene 9755	1.934	0.0079	0.0213
Gm9761	ENSMUSG00000034437	predicted gene 9761	1.771	0.0220	0.0518
Gm9800	ENSMUSG00000045799	predicted gene 9800	13.698	0.0000	0.0000
Gm9812	ENSMUSG00000046747	predicted gene 9812	6.820	0.0000	0.0000
Gm9828	ENSMUSG00000048603	predicted gene 9828	2.064	0.0284	0.0644
Gm9847	ENSMUSG00000050974	predicted pseudogene 9847	2.031	0.0009	0.0032
Gm9856	ENSMUSG00000110945	predicted gene 9856	2.993	0.0001	0.0006

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm9870	ENSMUSG00000052154	predicted gene 9870	1.909	0.0025	0.0078
Gm9905	ENSMUSG00000053358	predicted gene 9905	3.135	0.0000	0.0000
Gm9939	ENSMUSG00000054247	predicted gene 9939	1.993	0.0020	0.0063
Gm9959	ENSMUSG00000054957	predicted gene 9959	24.038	0.0219	0.0515
Gmfg	ENSMUSG00000060791	glia maturation factor, gamma	1.966	0.0001	0.0006
Gmpr2	ENSMUSG00000002326	guanosine monophosphate reductase 2	1.886	0.0000	0.0000
Gnai2	ENSMUSG00000032562	guanine nucleotide binding protein (G protein), alpha inhibiting 2	1.557	0.0000	0.0000
Gngt2	ENSMUSG00000038811	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	2.170	0.0000	0.0000
Gnl1	ENSMUSG00000024429	guanine nucleotide binding protein-like 1	2.143	0.0000	0.0000
Gnl3	ENSMUSG00000042354	guanine nucleotide binding protein-like 3 (nucleolar)	1.532	0.0000	0.0002
Golga2	ENSMUSG00000002546	golgi autoantigen, golgin subfamily a, 2	1.578	0.0000	0.0000
Golga4	ENSMUSG00000038708	golgi autoantigen, golgin subfamily a, 4	2.591	0.0000	0.0000
Golim4	ENSMUSG00000034109	golgi integral membrane protein 4	1.982	0.0000	0.0000
Golph3	ENSMUSG00000022200	golgi phosphoprotein 3	2.138	0.0000	0.0000
Gon7	ENSMUSG00000091931	GON7 subunit of KEOPS complex	1.570	0.0053	0.0151
Gopc	ENSMUSG00000019861	golgi associated PDZ and coiled-coil motif containing	1.530	0.0000	0.0000
Gpatch11	ENSMUSG00000050668	G patch domain containing 11	2.016	0.0000	0.0000
Gpatch3	ENSMUSG00000028850	G patch domain containing 3	3.001	0.0000	0.0000
Gpatch4	ENSMUSG00000028069	G patch domain containing 4	5.863	0.0000	0.0000
Gpc1	ENSMUSG00000034220	glypican 1	1.560	0.0000	0.0000
Gpc3	ENSMUSG00000055653	glypican 3	2.145	0.0003	0.0013
Gpc4	ENSMUSG00000031119	glypican 4	1.735	0.0000	0.0000
Gpr141	ENSMUSG00000053101	G protein-coupled receptor 141	3.877	0.0215	0.0508
Gpr27	ENSMUSG00000072875	G protein-coupled receptor 27	3.282	0.0000	0.0000
Gpr63	ENSMUSG00000040372	G protein-coupled receptor 63	2.404	0.0118	0.0303
Gps2	ENSMUSG00000023170	G protein pathway suppressor 2	2.873	0.0000	0.0000
Gpsm3	ENSMUSG00000034786	G-protein signalling modulator 3 (AGS3-like, C. elegans)	1.540	0.0027	0.0085
Gpx4-ps2	ENSMUSG00000110841	glutathione peroxidase 4, pseudogene 2	1.892	0.0000	0.0000
Grap2	ENSMUSG00000042351	GRB2-related adaptor protein 2	2.109	0.0239	0.0556
Grik5	ENSMUSG00000003378	glutamate receptor, ionotropic, kainate 5 (gamma 2)	2.374	0.0000	0.0000
Grin2d	ENSMUSG00000002771	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	2.943	0.0001	0.0003

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gripap1	ENSMUSG00000031153	GRIP1 associated protein 1	1.534	0.0000	0.0000
Grk3	ENSMUSG00000042249	G protein-coupled receptor kinase 3	1.520	0.0001	0.0004
Grsf1	ENSMUSG00000044221	G-rich RNA sequence binding factor 1	1.569	0.0000	0.0000
Gsg1l	ENSMUSG00000046182	GSG1-like	1.701	0.0002	0.0008
Gsk3a	ENSMUSG00000057177	glycogen synthase kinase 3 alpha	1.697	0.0000	0.0000
Gsr	ENSMUSG00000031584	glutathione reductase	2.423	0.0000	0.0000
Gsta4	ENSMUSG00000032348	glutathione S-transferase, alpha 4	1.872	0.0000	0.0000
Gstp-ps	ENSMUSG00000103653	glutathione S-transferase, pi, pseudogene	2.866	0.0000	0.0000
Gtf2a1	ENSMUSG00000020962	general transcription factor II A, 1	2.114	0.0000	0.0000
Gtf2e1	ENSMUSG00000022828	general transcription factor II E, polypeptide 1 (alpha subunit)	1.614	0.0000	0.0000
Gtf2f1	ENSMUSG00000002658	general transcription factor IIF, polypeptide 1	2.895	0.0000	0.0000
Gtf2h3	ENSMUSG00000029387	general transcription factor IIH, polypeptide 3	1.798	0.0000	0.0002
Gtf3c6	ENSMUSG00000019837	general transcription factor IIIC, polypeptide 6, alpha	2.753	0.0000	0.0000
Gtpbp4	ENSMUSG00000021149	GTP binding protein 4	1.721	0.0000	0.0000
Guf1	ENSMUSG00000029208	GUF1 homolog, GTPase	1.593	0.0000	0.0000
Gxylt1	ENSMUSG00000036197	glucoside xylosyltransferase 1	1.787	0.0000	0.0000
Gzmm	ENSMUSG00000054206	granzyme M (lymphocyte met-ase 1)	1.581	0.0016	0.0054
H19	ENSMUSG00000000031	H19, imprinted maternally expressed transcript	1.808	0.0026	0.0081
H1f10	ENSMUSG00000044927	H1.10 linker histone	8.300	0.0000	0.0000
H1f2	ENSMUSG00000036181	H1.2 linker histone, cluster member	1.516	0.0006	0.0023
H2aw	ENSMUSG00000078851	H2A.W histone	3.975	0.0000	0.0000
H2-Bl	ENSMUSG00000073406	histocompatibility 2, blastocyst	3.731	0.0000	0.0000
H2-DMb1	ENSMUSG00000079547	histocompatibility 2, class II, locus Mb1	2.163	0.0389	0.0841
H2-M5	ENSMUSG00000024459	histocompatibility 2, M region locus 5	5.840	0.0130	0.0329
H2-Q1	ENSMUSG00000079507	histocompatibility 2, Q region locus 1	3.246	0.0000	0.0001
H2-Q6	ENSMUSG00000073409	histocompatibility 2, Q region locus 6	2.881	0.0124	0.0316
H2-T10	ENSMUSG00000079491	histocompatibility 2, T region locus 10	1.503	0.0056	0.0159
H2-T-ps	ENSMUSG00000073405	histocompatibility 2, T region locus, pseudogene	1.529	0.0175	0.0425
Habp4	ENSMUSG00000021476	hyaluronic acid binding protein 4	1.674	0.0000	0.0000
Hand2	ENSMUSG00000038193	heart and neural crest derivatives expressed 2	4.303	0.0000	0.0000
Hars	ENSMUSG00000001380	histidyl-tRNA synthetase	1.579	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Haus3	ENSMUSG00000079555	HAUS augmin-like complex, subunit 3	1.561	0.0002	0.0009
Hax1	ENSMUSG00000027944	HCLS1 associated X-1	1.597	0.0000	0.0000
Hccs	ENSMUSG00000031352	holocytochrome c synthetase	2.365	0.0000	0.0000
Hcls1	ENSMUSG00000022831	hematopoietic cell specific Lyn substrate 1	2.748	0.0000	0.0000
Hcn2	ENSMUSG00000020331	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	3.828	0.0000	0.0000
Hdac2	ENSMUSG00000019777	histone deacetylase 2	3.842	0.0000	0.0000
Hdac7	ENSMUSG00000022475	histone deacetylase 7	1.642	0.0000	0.0000
Hdgf	ENSMUSG00000004897	heparin binding growth factor	2.062	0.0000	0.0000
Hdgfl3	ENSMUSG00000025104	HDGF like 3	1.987	0.0000	0.0000
Hdnr	ENSMUSG00000097910	Hand2 downstream lncRNA	1.829	0.0001	0.0004
Herc2	ENSMUSG00000030451	HECT and RLD domain containing E3 ubiquitin protein ligase 2	1.526	0.0000	0.0001
Hes1	ENSMUSG00000022528	hes family bHLH transcription factor 1	1.797	0.0042	0.0124
Hes7	ENSMUSG00000023781	hes family bHLH transcription factor 7	10.463	0.0370	0.0805
Hey2	ENSMUSG00000019789	hairy/enhancer-of-split related with YRPW motif 2	1.780	0.0033	0.0099
Hic1	ENSMUSG00000043099	hypermethylated in cancer 1	3.430	0.0000	0.0000
Hirip3	ENSMUSG00000042606	HIRA interacting protein 3	3.375	0.0000	0.0000
Hjv	ENSMUSG00000038403	hemojuvelin BMP co-receptor	2.386	0.0000	0.0000
Hk1	ENSMUSG00000037012	hexokinase 1	1.921	0.0000	0.0000
Hmga1	ENSMUSG00000046711	high mobility group AT-hook 1	6.605	0.0000	0.0000
Hmga1b	ENSMUSG00000078249	high mobility group AT-hook 1B	3.879	0.0000	0.0000
Hmgb1	ENSMUSG00000066551	high mobility group box 1	1.779	0.0000	0.0000
Hmgb1-ps7	ENSMUSG00000092281	high-mobility group high mobility group box 1, pseudogene 7	16.069	0.0000	0.0000
Hmgb3	ENSMUSG00000015217	high mobility group box 3	2.511	0.0000	0.0000
Hmgcs1	ENSMUSG00000093930	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1.514	0.0000	0.0000
Hmgn1	ENSMUSG00000040681	high mobility group nucleosomal binding domain 1	1.625	0.0000	0.0000
Hmgn3	ENSMUSG00000066456	high mobility group nucleosomal binding domain 3	3.346	0.0000	0.0000
Hmgn5	ENSMUSG00000031245	high-mobility group nucleosome binding domain 5	8.351	0.0000	0.0000
Hnrnpa0	ENSMUSG00000007836	heterogeneous nuclear ribonucleoprotein A0	3.001	0.0000	0.0000
Hnrnpa1	ENSMUSG00000046434	heterogeneous nuclear ribonucleoprotein A1	2.221	0.0000	0.0000
Hnrnpa1l2-ps2	ENSMUSG00000021927	heterogeneous nuclear ribonucleoprotein A1-like 2, pseudogene 2	18.153	0.0000	0.0000
Hnrnpa2b1	ENSMUSG00000004980	heterogeneous nuclear ribonucleoprotein A2/B1	2.298	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hnrnpa3	ENSMUSG00000059005	heterogeneous nuclear ribonucleoprotein A3	4.092	0.0000	0.0000
Hnrnpab	ENSMUSG00000020358	heterogeneous nuclear ribonucleoprotein A/B	4.851	0.0000	0.0000
Hnrnpc	ENSMUSG00000060373	heterogeneous nuclear ribonucleoprotein C	1.708	0.0000	0.0000
Hnrnpd	ENSMUSG00000000568	heterogeneous nuclear ribonucleoprotein D	3.084	0.0000	0.0000
Hnrnpdl	ENSMUSG00000029328	heterogeneous nuclear ribonucleoprotein D-like	1.888	0.0000	0.0000
Hnrnph1	ENSMUSG00000007850	heterogeneous nuclear ribonucleoprotein H1	2.921	0.0000	0.0000
Hnrnph2	ENSMUSG00000045427	heterogeneous nuclear ribonucleoprotein H2	2.244	0.0000	0.0000
Hnrnph3	ENSMUSG00000020069	heterogeneous nuclear ribonucleoprotein H3	2.684	0.0000	0.0000
Hnrnpk	ENSMUSG00000021546	heterogeneous nuclear ribonucleoprotein K	1.666	0.0000	0.0000
Hnrnpl	ENSMUSG00000015165	heterogeneous nuclear ribonucleoprotein L	1.913	0.0000	0.0000
Hnrnpll	ENSMUSG00000024095	heterogeneous nuclear ribonucleoprotein L-like	1.985	0.0000	0.0000
Hnrnpm	ENSMUSG00000059208	heterogeneous nuclear ribonucleoprotein M	3.128	0.0000	0.0000
Hnrnpr	ENSMUSG00000066037	heterogeneous nuclear ribonucleoprotein R	2.463	0.0000	0.0000
Hnrnpu	ENSMUSG00000039630	heterogeneous nuclear ribonucleoprotein U	2.273	0.0000	0.0000
Hnrnpul1	ENSMUSG00000040725	heterogeneous nuclear ribonucleoprotein U-like 1	2.855	0.0000	0.0000
Hnrnpul2	ENSMUSG00000071659	heterogeneous nuclear ribonucleoprotein U-like 2	2.924	0.0000	0.0000
Homer2	ENSMUSG00000025813	homer scaffolding protein 2	1.660	0.0000	0.0000
Hoxa3	ENSMUSG00000079560	homeobox A3	1.978	0.0043	0.0127
Hoxa4	ENSMUSG00000000942	homeobox A4	8.845	0.0000	0.0000
Hoxb3os	ENSMUSG00000084844	homeobox B3 and homeobox B2, opposite strand	2.047	0.0066	0.0182
Hoxb4	ENSMUSG00000038692	homeobox B4	1.956	0.0030	0.0093
Hoxd8	ENSMUSG00000027102	homeobox D8	3.664	0.0000	0.0000
Hoxd9	ENSMUSG00000043342	homeobox D9	6.922	0.0000	0.0001
Hpf1	ENSMUSG00000038005	histone PARylation factor 1	1.679	0.0000	0.0000
Hras	ENSMUSG00000025499	Harvey rat sarcoma virus oncogene	3.071	0.0000	0.0000
Hrc	ENSMUSG00000038239	histidine rich calcium binding protein	2.449	0.0000	0.0000
Hs3st3a1	ENSMUSG00000047759	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	3.148	0.0000	0.0000
Hs3st3b1	ENSMUSG00000070407	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	1.514	0.0158	0.0391
Hsbp1l1	ENSMUSG00000078963	heat shock factor binding protein 1-like 1	1.637	0.0187	0.0451
Hscb	ENSMUSG00000043510	HscB iron-sulfur cluster co-chaperone	1.509	0.0000	0.0000
Hsd17b4	ENSMUSG00000024507	hydroxysteroid (17-beta) dehydrogenase 4	2.073	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hsd3b7	ENSMUSG00000042289	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	3.226	0.0022	0.0069
Hsdl2	ENSMUSG00000028383	hydroxysteroid dehydrogenase like 2	2.132	0.0000	0.0000
Hsp90aa1	ENSMUSG00000021270	heat shock protein 90, alpha (cytosolic), class A member 1	1.514	0.0002	0.0009
Hsp90ab1	ENSMUSG00000023944	heat shock protein 90 alpha (cytosolic), class B member 1	2.304	0.0000	0.0000
Hsp90b1	ENSMUSG00000020048	heat shock protein 90, beta (Grp94), member 1	1.863	0.0000	0.0000
Hspa4	ENSMUSG00000020361	heat shock protein 4	2.291	0.0000	0.0000
Hspa9	ENSMUSG00000024359	heat shock protein 9	1.796	0.0000	0.0000
Hspd1	ENSMUSG00000025980	heat shock protein 1 (chaperonin)	2.113	0.0000	0.0000
Hspd1-ps3	ENSMUSG00000058809	heat shock protein 1 (chaperonin), pseudogene 3	1.615	0.0381	0.0826
Hspe1	ENSMUSG00000073676	heat shock protein 1 (chaperonin 10)	1.930	0.0000	0.0000
Hspe1-rs1	ENSMUSG00000117621	heat shock protein 1 (chaperonin 10), related sequence 1	2.857	0.0000	0.0000
Hsph1	ENSMUSG00000029657	heat shock 105kDa/110kDa protein 1	1.820	0.0000	0.0000
Htatsf1	ENSMUSG00000067873	HIV TAT specific factor 1	2.924	0.0000	0.0000
Hyi	ENSMUSG00000006395	hydroxypyruvate isomerase (putative)	1.517	0.0263	0.0604
Hypk	ENSMUSG00000027245	huntingtin interacting protein K	2.682	0.0000	0.0000
Ier5	ENSMUSG00000056708	immediate early response 5	3.068	0.0000	0.0000
Ier5l	ENSMUSG00000089762	immediate early response 5-like	2.349	0.0006	0.0022
Iffo2	ENSMUSG00000041025	intermediate filament family orphan 2	1.673	0.0000	0.0000
Ifi204	ENSMUSG00000073489	interferon activated gene 204	1.753	0.0015	0.0048
Ifit3	ENSMUSG00000074896	interferon-induced protein with tetratricopeptide repeats 3	1.909	0.0009	0.0030
Ifrd1	ENSMUSG00000001627	interferon-related developmental regulator 1	2.229	0.0003	0.0011
Ift172	ENSMUSG00000038564	intraflagellar transport 172	1.565	0.0000	0.0000
Ift57	ENSMUSG00000032965	intraflagellar transport 57	1.981	0.0000	0.0001
Igf2	ENSMUSG00000048583	insulin-like growth factor 2	1.745	0.0180	0.0435
Igfbp7	ENSMUSG00000036256	insulin-like growth factor binding protein 7	1.931	0.0001	0.0002
Ighj1	ENSMUSG00000076621	immunoglobulin heavy joining 1	5.444	0.0055	0.0155
Igsf11	ENSMUSG00000022790	immunoglobulin superfamily, member 11	1.557	0.0198	0.0473
Ik	ENSMUSG00000024474	IK cytokine	2.281	0.0000	0.0000
Il17d	ENSMUSG00000050222	interleukin 17D	2.903	0.0000	0.0001
Il1rl1	ENSMUSG00000026069	interleukin 1 receptor-like 1	2.344	0.0198	0.0473
Ildr2	ENSMUSG00000040612	immunoglobulin-like domain containing receptor 2	2.224	0.0297	0.0668

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ilk	ENSMUSG00000030890	integrin linked kinase	1.506	0.0000	0.0000
Ilkap	ENSMUSG00000026309	integrin-linked kinase-associated serine/threonine phosphatase 2C	1.549	0.0000	0.0000
Ilrun	ENSMUSG00000056692	inflammation and lipid regulator with UBA-like and NBR1-like domains	1.904	0.0000	0.0000
Inafm2	ENSMUSG00000074918	InaF motif containing 2	3.385	0.0000	0.0000
Incenp	ENSMUSG00000024660	inner centromere protein	2.337	0.0000	0.0000
Ing1	ENSMUSG00000045969	inhibitor of growth family, member 1	1.559	0.0002	0.0009
Ing5	ENSMUSG00000026283	inhibitor of growth family, member 5	1.622	0.0000	0.0000
Inhba	ENSMUSG00000041324	inhibin beta-A	2.074	0.0005	0.0019
Inhbb	ENSMUSG00000037035	inhibin beta-B	2.419	0.0000	0.0000
Ino80b	ENSMUSG00000030034	INO80 complex subunit B	3.906	0.0000	0.0000
Ino80dos	ENSMUSG00000084799	INO80 complex subunit D, opposite strand	2.681	0.0000	0.0000
Inpp5a	ENSMUSG00000025477	inositol polyphosphate-5-phosphatase A	1.841	0.0000	0.0000
Ipo8	ENSMUSG00000040029	importin 8	1.608	0.0000	0.0000
Ipp	ENSMUSG00000028696	IAP promoted placental gene	1.527	0.0000	0.0000
Iqcg	ENSMUSG00000035578	IQ motif containing G	2.711	0.0012	0.0039
Iqsec2	ENSMUSG00000041115	IQ motif and Sec7 domain 2	1.854	0.0000	0.0000
Irak4	ENSMUSG00000059883	interleukin-1 receptor-associated kinase 4	1.818	0.0000	0.0000
Irf2bp1	ENSMUSG00000044030	interferon regulatory factor 2 binding protein 1	1.674	0.0000	0.0001
Irf2bp2	ENSMUSG00000051495	interferon regulatory factor 2 binding protein 2	2.302	0.0000	0.0000
Irf7	ENSMUSG00000025498	interferon regulatory factor 7	1.689	0.0316	0.0704
Irx1	ENSMUSG00000060969	Iroquois homeobox 1	2.147	0.0014	0.0048
Irx3	ENSMUSG00000031734	Iroquois related homeobox 3	4.665	0.0000	0.0000
Irx3os	ENSMUSG00000046413	iroquois homeobox 3, opposite strand	3.200	0.0004	0.0017
Irx5	ENSMUSG00000031737	Iroquois homeobox 5	2.087	0.0000	0.0001
Iscu	ENSMUSG00000025825	iron-sulfur cluster assembly enzyme	2.947	0.0000	0.0000
Ism1	ENSMUSG00000074766	isthmin 1, angiogenesis inhibitor	2.257	0.0116	0.0299
Itgam	ENSMUSG00000030786	integrin alpha M	3.037	0.0000	0.0000
Itgb1	ENSMUSG00000025809	integrin beta 1 (fibronectin receptor beta)	1.904	0.0000	0.0000
Itgb3	ENSMUSG00000020689	integrin beta 3	2.014	0.0056	0.0158
Itgbl1	ENSMUSG00000032925	integrin, beta-like 1	3.627	0.0000	0.0000
Itpka	ENSMUSG00000027296	inositol 1,4,5-trisphosphate 3-kinase A	2.377	0.0004	0.0017

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Itpripl2	ENSMUSG00000095115	inositol 1,4,5-triphosphate receptor interacting protein-like 2	2.000	0.0000	0.0000
Itsn1	ENSMUSG00000022957	intersectin 1 (SH3 domain protein 1A)	1.960	0.0000	0.0000
Iws1	ENSMUSG00000024384	IWS1, SUPT6 interacting protein	1.829	0.0000	0.0000
Jdp2	ENSMUSG00000034271	Jun dimerization protein 2	1.792	0.0010	0.0033
Jph2	ENSMUSG00000017817	junctophilin 2	2.242	0.0000	0.0001
Jund	ENSMUSG00000071076	jun D proto-oncogene	9.349	0.0000	0.0000
Junos	ENSMUSG00000087366	jun proto-oncogene, opposite strand	4.197	0.0000	0.0000
K230015D01Rik	ENSMUSG00000110630	RIKEN cDNA K230015D01 gene	1.916	0.0131	0.0331
Kansl2	ENSMUSG00000022992	KAT8 regulatory NSL complex subunit 2	1.920	0.0000	0.0001
Kantr	ENSMUSG00000087403	Kdm5c adjacent non-coding transcript	1.781	0.0001	0.0005
Kazald1	ENSMUSG00000025213	Kazal-type serine peptidase inhibitor domain 1	2.053	0.0001	0.0003
Kazn	ENSMUSG00000040606	kazrin, periplakin interacting protein	1.783	0.0000	0.0000
Kbtbd11	ENSMUSG00000055675	kelch repeat and BTB (POZ) domain containing 11	1.624	0.0007	0.0026
Kcmf1	ENSMUSG00000055239	potassium channel modulatory factor 1	1.982	0.0000	0.0000
Kcna1	ENSMUSG00000047976	potassium voltage-gated channel, shaker-related subfamily, member 1	1.550	0.0188	0.0452
Kcnab1	ENSMUSG00000027827	potassium voltage-gated channel, shaker-related subfamily, beta member 1	1.583	0.0027	0.0083
Kcnab3	ENSMUSG00000018470	potassium voltage-gated channel, shaker-related subfamily, beta member 3	2.544	0.0021	0.0067
Kcnc3	ENSMUSG00000062785	potassium voltage gated channel, Shaw-related subfamily, member 3	1.694	0.0000	0.0002
Kcnd3os	ENSMUSG00000074346	potassium voltage-gated channel, Shal-related family, member 3, opposite strand	2.239	0.0027	0.0083
Kcng2	ENSMUSG00000059852	potassium voltage-gated channel, subfamily G, member 2	2.029	0.0000	0.0000
Kcnip2	ENSMUSG00000025221	Kv channel-interacting protein 2	1.785	0.0000	0.0000
Kcnj12	ENSMUSG00000042529	potassium inwardly-rectifying channel, subfamily J, member 12	1.970	0.0000	0.0001
Kcnk2	ENSMUSG00000037624	potassium channel, subfamily K, member 2	2.117	0.0000	0.0000
Kcnk3	ENSMUSG00000049265	potassium channel, subfamily K, member 3	1.590	0.0000	0.0000
Kcnmb4	ENSMUSG00000054934	potassium large conductance calcium-activated channel, subfamily M, beta member 4	4.689	0.0114	0.0293
Kctd1	ENSMUSG00000036225	potassium channel tetramerisation domain containing 1	1.573	0.0003	0.0010
Kctd15	ENSMUSG00000030499	potassium channel tetramerisation domain containing 15	1.680	0.0216	0.0510
Kctd18	ENSMUSG00000054770	potassium channel tetramerisation domain containing 18	1.562	0.0000	0.0001
Kctd2	ENSMUSG00000016940	potassium channel tetramerisation domain containing 2	3.250	0.0000	0.0000
Kctd3	ENSMUSG00000026608	potassium channel tetramerisation domain containing 3	1.901	0.0000	0.0000
Kctd6	ENSMUSG00000021752	potassium channel tetramerisation domain containing 6	1.738	0.0000	0.0002

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kctd9	ENSMUSG00000034327	potassium channel tetramerisation domain containing 9	1.757	0.0000	0.0000
Kdm1a	ENSMUSG00000036940	lysine (K)-specific demethylase 1A	2.441	0.0000	0.0000
Kdm6b	ENSMUSG00000018476	KDM1 lysine (K)-specific demethylase 6B	1.617	0.0052	0.0149
Kdr	ENSMUSG00000062960	kinase insert domain protein receptor	1.559	0.0002	0.0008
Khdrbs1	ENSMUSG00000028790	KH domain containing, RNA binding, signal transduction associated 1	1.679	0.0001	0.0006
Khdrbs3	ENSMUSG00000022332	KH domain containing, RNA binding, signal transduction associated 3	1.709	0.0000	0.0000
Khsrp	ENSMUSG00000007670	KH-type splicing regulatory protein	3.464	0.0000	0.0000
Kif1c	ENSMUSG00000020821	kinesin family member 1C	1.965	0.0000	0.0000
Kif21a	ENSMUSG00000022629	kinesin family member 21A	1.537	0.0000	0.0000
Kif2a	ENSMUSG00000021693	kinesin family member 2A	1.570	0.0000	0.0000
Kif3a	ENSMUSG00000018395	kinesin family member 3A	2.244	0.0000	0.0000
Kif5a	ENSMUSG00000074657	kinesin family member 5A	1.527	0.0164	0.0403
Kifbp	ENSMUSG00000036955	kinesin family binding protein	1.538	0.0000	0.0000
Kin	ENSMUSG00000037262	Kin17 DNA and RNA binding protein	1.607	0.0000	0.0002
Klc1	ENSMUSG00000021288	kinesin light chain 1	1.566	0.0000	0.0000
Klf16	ENSMUSG00000035397	Kruppel-like factor 16	1.801	0.0000	0.0001
Klf2	ENSMUSG00000055148	Kruppel-like factor 2 (lung)	2.331	0.0000	0.0000
Klf3	ENSMUSG00000029178	Kruppel-like factor 3 (basic)	1.598	0.0000	0.0000
Klf4	ENSMUSG00000003032	Kruppel-like factor 4 (gut)	1.815	0.0000	0.0000
Klhdc2	ENSMUSG00000020978	kelch domain containing 2	2.010	0.0000	0.0000
Klhdc4	ENSMUSG00000040263	kelch domain containing 4	2.616	0.0000	0.0000
Klhdc8b	ENSMUSG00000032609	kelch domain containing 8B	1.951	0.0000	0.0000
Klhl17	ENSMUSG00002076083	kelch-like 17	1.710	0.0000	0.0000
Klhl2	ENSMUSG00000031605	kelch-like 2, Mayven	1.606	0.0047	0.0137
Klhl8	ENSMUSG00000029312	kelch-like 8	1.596	0.0000	0.0000
Kmt2b	ENSMUSG00000006307	lysine (K)-specific methyltransferase 2B	1.540	0.0001	0.0003
Kpna2	ENSMUSG00000018362	karyopherin (importin) alpha 2	1.567	0.0001	0.0002
Kpnb1	ENSMUSG00000001440	karyopherin (importin) beta 1	1.504	0.0000	0.0000
Kras	ENSMUSG00000030265	Kirsten rat sarcoma viral oncogene homolog	1.761	0.0000	0.0000
Krcc1	ENSMUSG00000053012	lysine-rich coiled-coil 1	1.775	0.0000	0.0000
Lacc1	ENSMUSG00000044350	laccase domain containing 1	1.727	0.0001	0.0004

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lactb	ENSMUSG00000032370	lactamase, beta	2.178	0.0000	0.0000
Lamtor2	ENSMUSG00000028062	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	1.567	0.0000	0.0000
Lamtor3	ENSMUSG00000091512	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3	1.598	0.0000	0.0000
Larp1	ENSMUSG00000037331	La ribonucleoprotein domain family, member 1	1.594	0.0000	0.0000
Larp1b	ENSMUSG00000025762	La ribonucleoprotein domain family, member 1B	2.498	0.0000	0.0000
Larp6	ENSMUSG00000034839	La ribonucleoprotein domain family, member 6	1.553	0.0391	0.0845
Las1l	ENSMUSG00000057421	LAS1-like (S. cerevisiae)	1.577	0.0000	0.0000
Lat	ENSMUSG00000030742	linker for activation of T cells	2.845	0.0131	0.0333
Lat2	ENSMUSG00000040751	linker for activation of T cells family, member 2	2.037	0.0009	0.0032
Lbhd1	ENSMUSG00000096740	LBH domain containing 1	1.684	0.0046	0.0134
Ldhb	ENSMUSG00000030246	lactate dehydrogenase B	1.860	0.0000	0.0000
Lemd2	ENSMUSG00000044857	LEM domain containing 2	3.005	0.0000	0.0000
Lemd3	ENSMUSG00000048661	LEM domain containing 3	2.233	0.0000	0.0000
Leng1	ENSMUSG00000078813	leukocyte receptor cluster (LRC) member 1	3.011	0.0000	0.0000
Leng8	ENSMUSG00000035545	leukocyte receptor cluster (LRC) member 8	2.014	0.0003	0.0010
Leo1	ENSMUSG00000042487	Leo1, Paf1/RNA polymerase II complex component	1.956	0.0000	0.0000
Lhfpl4	ENSMUSG00000042873	lipoma HMGIC fusion partner-like protein 4	3.300	0.0000	0.0000
Lig4	ENSMUSG00000049717	ligase IV, DNA, ATP-dependent	1.573	0.0000	0.0000
Limd2	ENSMUSG00000040699	LIM domain containing 2	2.184	0.0000	0.0002
Lin7a	ENSMUSG00000019906	lin-7 homolog A, crumbs cell polarity complex component	2.542	0.0002	0.0010
Lipo4	ENSMUSG00000079344	lipase, member O4	1.570	0.0152	0.0378
Lix1l	ENSMUSG00000049288	Lix1-like	1.508	0.0000	0.0000
Llph-ps1	ENSMUSG00000081459	LLP homolog, pseudogene 1	85.398	0.0000	0.0000
Llph-ps2	ENSMUSG00000083364	LLP homolog, pseudogene 2	11.986	0.0000	0.0000
Lmcd1	ENSMUSG00000057604	LIM and cysteine-rich domains 1	1.748	0.0000	0.0000
Lmln	ENSMUSG00000022802	leishmanolysin-like (metallopeptidase M8 family)	1.735	0.0001	0.0003
Lmnb1	ENSMUSG00000024590	lamin B1	1.765	0.0009	0.0032
Lmo2	ENSMUSG00000032698	LIM domain only 2	2.727	0.0000	0.0000
Lmod1	ENSMUSG00000048096	leiomodin 1 (smooth muscle)	3.452	0.0000	0.0000
Lmod2	ENSMUSG00000029683	leiomodin 2 (cardiac)	2.498	0.0000	0.0000
Lmod3	ENSMUSG00000044086	leiomodin 3 (fetal)	2.096	0.0017	0.0055

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lncob1	ENSMUSG00000092381	lncRNA osteoblastogenesis associated 1	5.823	0.0004	0.0017
Lonp1	ENSMUSG00000041168	lon peptidase 1, mitochondrial	2.152	0.0000	0.0000
Lonrf1	ENSMUSG00000039633	LON peptidase N-terminal domain and ring finger 1	2.506	0.0000	0.0000
Lpar1	ENSMUSG00000038668	lysophosphatidic acid receptor 1	2.308	0.0000	0.0000
Lpcat1	ENSMUSG00000021608	lysophosphatidylcholine acyltransferase 1	1.636	0.0000	0.0000
Lpcat4	ENSMUSG00000027134	lysophosphatidylcholine acyltransferase 4	3.405	0.0000	0.0000
Lrch1	ENSMUSG00000068015	leucine-rich repeats and calponin homology (CH) domain containing 1	1.651	0.0002	0.0007
Lrfn1	ENSMUSG00000030600	leucine rich repeat and fibronectin type III domain containing 1	4.002	0.0000	0.0000
Lrfn4	ENSMUSG00000045045	leucine rich repeat and fibronectin type III domain containing 4	2.158	0.0002	0.0007
Lrrc38	ENSMUSG00000028584	leucine rich repeat containing 38	5.500	0.0217	0.0511
Lrrc47	ENSMUSG00000029028	leucine rich repeat containing 47	4.025	0.0000	0.0000
Lrrc75a	ENSMUSG00000046417	leucine rich repeat containing 75A	1.550	0.0032	0.0098
Lrrc8a	ENSMUSG00000007476	leucine rich repeat containing 8A VRAC subunit A	1.751	0.0022	0.0069
Lsg1	ENSMUSG00000022538	large 60S subunit nuclear export GTPase 1	1.672	0.0000	0.0000
Lsm11	ENSMUSG00000044847	U7 snRNP-specific Sm-like protein LSM11	1.510	0.0003	0.0013
Lsm14a	ENSMUSG00000066568	LSM14A mRNA processing body assembly factor	1.584	0.0000	0.0000
Lsm6	ENSMUSG00000031683	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated	2.803	0.0000	0.0000
Lsm8	ENSMUSG00000044155	LSM8 homolog, U6 small nuclear RNA associated	2.176	0.0000	0.0000
Lsmem1	ENSMUSG00000071342	leucine-rich single-pass membrane protein 1	1.827	0.0378	0.0821
Lsp1	ENSMUSG00000018819	lymphocyte specific 1	1.617	0.0000	0.0000
Ltbp1	ENSMUSG00000001870	latent transforming growth factor beta binding protein 1	1.522	0.0000	0.0000
Ltv1	ENSMUSG00000019814	LTV1 ribosome biogenesis factor	1.925	0.0000	0.0000
Luc7l2	ENSMUSG00000029823	LUC7-like 2 (S. cerevisiae)	1.885	0.0000	0.0000
Luc7l3	ENSMUSG00000020863	LUC7-like 3 (S. cerevisiae)	2.258	0.0000	0.0000
Ly75	ENSMUSG00000026980	lymphocyte antigen 75	1.506	0.0060	0.0169
Lyar	ENSMUSG00000067367	Ly1 antibody reactive clone	1.946	0.0000	0.0000
Lzts3	ENSMUSG00000037703	leucine zipper, putative tumor suppressor family member 3	1.585	0.0010	0.0034
Maco1	ENSMUSG00000028826	macoilin 1	2.101	0.0000	0.0000
Macrod1	ENSMUSG00000036278	mono-ADP ribosylhydrolase 1	2.225	0.0000	0.0000
Macrod2	ENSMUSG00000068205	mono-ADP ribosylhydrolase 2	2.142	0.0000	0.0000
Macroh2a1	ENSMUSG00000015937	macroH2A.1 histone	1.523	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mad1l1	ENSMUSG00000029554	MAD1 mitotic arrest deficient 1-like 1	2.107	0.0000	0.0000
Madd	ENSMUSG00000040687	MAP-kinase activating death domain	1.540	0.0000	0.0000
Maf	ENSMUSG00000055435	avian musculoaponeurotic fibrosarcoma oncogene homolog	2.444	0.0000	0.0000
Mafa	ENSMUSG00000047591	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (avian)	6.488	0.0000	0.0000
Mafk	ENSMUSG00000018143	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	1.684	0.0245	0.0568
Magohb	ENSMUSG00000030188	mago homolog B, exon junction complex core component	1.697	0.0005	0.0018
Mak16	ENSMUSG00000031578	MAK16 homolog	1.984	0.0000	0.0000
Malat1	ENSMUSG00000092341	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	2.989	0.0031	0.0094
Malsu1	ENSMUSG00000029815	mitochondrial assembly of ribosomal large subunit 1	2.078	0.0000	0.0000
Manf	ENSMUSG00000032575	mesencephalic astrocyte-derived neurotrophic factor	2.013	0.0000	0.0000
Map1lc3a	ENSMUSG00000027602	microtubule-associated protein 1 light chain 3 alpha	2.320	0.0000	0.0001
Map2k2	ENSMUSG00000035027	mitogen-activated protein kinase kinase 2	1.816	0.0030	0.0091
Map2k7	ENSMUSG00000002948	mitogen-activated protein kinase kinase 7	1.963	0.0000	0.0000
Map3k10	ENSMUSG00000040390	mitogen-activated protein kinase kinase kinase 10	3.112	0.0000	0.0000
Map3k5	ENSMUSG00000071369	mitogen-activated protein kinase kinase kinase 5	1.779	0.0000	0.0000
Map4	ENSMUSG00000032479	microtubule-associated protein 4	1.561	0.0000	0.0000
Map4k4	ENSMUSG00000026074	mitogen-activated protein kinase kinase kinase kinase 4	2.265	0.0000	0.0000
Map7	ENSMUSG00000019996	microtubule-associated protein 7	2.061	0.0000	0.0000
Map7d1	ENSMUSG00000028849	MAP7 domain containing 1	2.416	0.0000	0.0000
Map7d2	ENSMUSG00000041020	MAP7 domain containing 2	2.861	0.0000	0.0000
Mapk1ip1l	ENSMUSG00000021840	mitogen-activated protein kinase 1 interacting protein 1-like	1.775	0.0000	0.0000
Mapkapk2	ENSMUSG00000016528	MAP kinase-activated protein kinase 2	1.511	0.0000	0.0001
Mapkapk5	ENSMUSG00000029454	MAP kinase-activated protein kinase 5	13.052	0.0000	0.0000
Marchf1	ENSMUSG00000036469	membrane associated ring-CH-type finger 1	1.929	0.0022	0.0069
Marchf11	ENSMUSG00000022269	membrane associated ring-CH-type finger 11	4.900	0.0000	0.0000
Marchf2	ENSMUSG00000079557	membrane associated ring-CH-type finger 2	1.780	0.0000	0.0000
Marchf5	ENSMUSG00000023307	membrane associated ring-CH-type finger 5	2.498	0.0000	0.0000
Marchf8	ENSMUSG00000025702	membrane associated ring-CH-type finger 8	1.579	0.0000	0.0000
Marchf9	ENSMUSG00000040502	membrane associated ring-CH-type finger 9	5.288	0.0000	0.0000
Marcks	ENSMUSG00000069662	myristoylated alanine rich protein kinase C substrate	3.896	0.0000	0.0000
Marcksl1	ENSMUSG00000047945	MARCKS-like 1	1.730	0.0080	0.0216

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mark2	ENSMUSG00000024969	MAP/microtubule affinity regulating kinase 2	1.539	0.0000	0.0000
Mark3	ENSMUSG00000007411	MAP/microtubule affinity regulating kinase 3	1.655	0.0000	0.0000
Mark4	ENSMUSG00000030397	MAP/microtubule affinity regulating kinase 4	1.956	0.0013	0.0043
Max	ENSMUSG00000059436	Max protein	1.655	0.0000	0.0002
Maz	ENSMUSG00000030678	MYC-associated zinc finger protein (purine-binding transcription factor)	2.476	0.0000	0.0000
Mb	ENSMUSG00000018893	myoglobin	1.684	0.0000	0.0000
Mbd2	ENSMUSG00000024513	methyl-CpG binding domain protein 2	3.427	0.0000	0.0000
Mbd3	ENSMUSG00000035478	methyl-CpG binding domain protein 3	1.571	0.0001	0.0006
Mcat	ENSMUSG00000048755	malonyl CoA:ACP acyltransferase (mitochondrial)	1.659	0.0000	0.0000
Mcf2l	ENSMUSG00000031442	mcf.2 transforming sequence-like	1.644	0.0337	0.0744
Mcl1	ENSMUSG00000038612	myeloid cell leukemia sequence 1	2.192	0.0000	0.0000
Mcm9	ENSMUSG00000058298	minichromosome maintenance 9 homologous recombination repair factor	1.593	0.0003	0.0011
Mdfic	ENSMUSG00000041390	MyoD family inhibitor domain containing	1.914	0.0000	0.0000
Mdga2	ENSMUSG00000034912	MAM domain containing glycosylphosphatidylinositol anchor 2	1.833	0.0345	0.0759
Mdn1	ENSMUSG00000058006	midasin AAA ATPase 1	1.557	0.0000	0.0000
Mecomos	ENSMUSG00000085702	MDS1 and EVI1 complex locus, opposite strand	7.913	0.0000	0.0002
Med16	ENSMUSG00000013833	mediator complex subunit 16	1.759	0.0000	0.0000
Med30	ENSMUSG00000038622	mediator complex subunit 30	2.557	0.0000	0.0000
Med4	ENSMUSG00000022109	mediator complex subunit 4	1.661	0.0000	0.0000
Medag	ENSMUSG00000029659	mesenteric estrogen dependent adipogenesis	2.955	0.0000	0.0000
Meig1	ENSMUSG00000026650	meiosis expressed gene 1	1.985	0.0000	0.0000
Meis1	ENSMUSG00000020160	Meis homeobox 1	1.713	0.0000	0.0000
Meox1	ENSMUSG00000001493	mesenchyme homeobox 1	2.534	0.0024	0.0074
Mepce	ENSMUSG00000029726	methylphosphate capping enzyme	1.641	0.0000	0.0000
Mesd	ENSMUSG00000038503	mesoderm development LRP chaperone	1.635	0.0000	0.0000
Metap2	ENSMUSG00000036112	methionine aminopeptidase 2	1.867	0.0000	0.0000
Metrnl	ENSMUSG00000039208	meteorin, glial cell differentiation regulator-like	2.060	0.0000	0.0000
Mettl14	ENSMUSG00000028114	methyltransferase like 14	1.896	0.0000	0.0000
Mettl5	ENSMUSG00000051730	methyltransferase like 5	2.982	0.0000	0.0000
Mettl6	ENSMUSG00000021891	methyltransferase like 6	1.635	0.0000	0.0000
Mex3a	ENSMUSG00000074480	mex3 RNA binding family member A	1.711	0.0220	0.0517

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mex3d	ENSMUSG00000048696	mex3 RNA binding family member D	1.952	0.0000	0.0001
Mfn1	ENSMUSG00000027668	mitofusin 1	1.896	0.0000	0.0000
Mfsd1	ENSMUSG00000027775	major facilitator superfamily domain containing 1	1.897	0.0000	0.0000
Mfsd12	ENSMUSG00000034854	major facilitator superfamily domain containing 12	1.843	0.0000	0.0000
Mfsd6	ENSMUSG00000041439	major facilitator superfamily domain containing 6	1.649	0.0000	0.0000
Mgat4b	ENSMUSG00000036620	mannoside acetylglucosaminyltransferase 4, isoenzyme B	2.219	0.0000	0.0001
Mhrt	ENSMUSG00000097652	myosin heavy chain associated RNA transcript	3.082	0.0000	0.0000
Mia3	ENSMUSG00000056050	MIA SH3 domain ER export factor 3	1.599	0.0000	0.0000
Mib1	ENSMUSG00000024294	MIB E3 ubiquitin protein ligase 1	1.721	0.0000	0.0000
Mib2	ENSMUSG00000029060	mindbomb E3 ubiquitin protein ligase 2	1.645	0.0000	0.0000
Micos13	ENSMUSG00000049760	mitochondrial contact site and cristae organizing system subunit 13	1.815	0.0000	0.0000
Micu2	ENSMUSG00000021973	mitochondrial calcium uptake 2	1.667	0.0000	0.0000
Midn	ENSMUSG00000035621	midnolin	1.880	0.0006	0.0021
Mios	ENSMUSG00000042447	meiosis regulator for oocyte development	2.295	0.0000	0.0000
Mipep	ENSMUSG00000021993	mitochondrial intermediate peptidase	1.632	0.0000	0.0000
Mipol1	ENSMUSG00000047022	mirror-image polydactyly 1	1.552	0.0012	0.0042
Mir1943	ENSMUSG00000088901	microRNA 1943	8.044	0.0323	0.0719
Mir208a	ENSMUSG00000065432	microRNA 208a	3.829	0.0318	0.0708
Mir7052	ENSMUSG00000098661	microRNA 7052	5.611	0.0334	0.0738
Mir762	ENSMUSG00000076454	microRNA 762	25.813	0.0000	0.0000
Mir8091	ENSMUSG00000098286	microRNA 8091	4.921	0.0001	0.0002
Mkrn1	ENSMUSG00000029922	makorin, ring finger protein, 1	2.954	0.0000	0.0000
Mlec	ENSMUSG00000048578	malectin	1.594	0.0000	0.0000
Mllt6	ENSMUSG00000038437	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6	1.540	0.0000	0.0000
Mlycd	ENSMUSG00000074064	malonyl-CoA decarboxylase	1.655	0.0003	0.0010
Mmab	ENSMUSG00000029575	methylmalonic aciduria (cobalamin deficiency) cblB type homolog (human)	1.686	0.0000	0.0000
Mmadhc	ENSMUSG00000026766	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	1.502	0.0000	0.0000
Mmp14	ENSMUSG00000000957	matrix metallopeptidase 14 (membrane-inserted)	1.851	0.0001	0.0004
Mmp3	ENSMUSG00000043613	matrix metallopeptidase 3	2.734	0.0127	0.0323
Mnat1	ENSMUSG00000021103	menage a trois 1	1.805	0.0000	0.0000
Mnd1	ENSMUSG00000033752	meiotic nuclear divisions 1	2.101	0.0049	0.0141

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mocs3	ENSMUSG00000074576	molybdenum cofactor synthesis 3	1.681	0.0153	0.0380
Mon1b	ENSMUSG00000078908	MON1 homolog B, secretory traffciking associated	1.625	0.0000	0.0000
Morf4l1	ENSMUSG00000062270	mortality factor 4 like 1	1.692	0.0000	0.0000
Morrbid	ENSMUSG00000074813	myeloid RNA regulator of BCL2L11 induced cell death	1.870	0.0000	0.0001
Mospd3	ENSMUSG00000037221	motile sperm domain containing 3	6.173	0.0000	0.0000
Mpdz	ENSMUSG00000028402	multiple PDZ domain crumbs cell polarity complex component	1.527	0.0000	0.0000
Mpeg1	ENSMUSG00000046805	macrophage expressed gene 1	1.823	0.0005	0.0019
Mphosph10	ENSMUSG00000030521	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	1.561	0.0000	0.0001
Mphosph6	ENSMUSG00000031843	M phase phosphoprotein 6	2.414	0.0000	0.0000
Mphosph8	ENSMUSG00000079184	M-phase phosphoprotein 8	1.720	0.0000	0.0000
Mplkip	ENSMUSG00000012429	M-phase specific PLK1 intereacting protein	2.884	0.0000	0.0000
Mpnd	ENSMUSG00000003199	MPN domain containing	2.548	0.0000	0.0000
Mpzl3	ENSMUSG00000070305	myelin protein zero-like 3	1.528	0.0002	0.0006
Mras	ENSMUSG00000032470	muscle and microspikes RAS	1.614	0.0000	0.0000
Mreg	ENSMUSG00000039395	melanoregulin	2.409	0.0000	0.0000
Mrfap1	ENSMUSG00000055302	Morf4 family associated protein 1	1.864	0.0000	0.0000
Mrgbp	ENSMUSG00000027569	MRG/MORF4L binding protein	2.314	0.0000	0.0000
Mrln	ENSMUSG00000019933	myoregulin	1.717	0.0480	0.0999
Mrpl16	ENSMUSG00000024683	mitochondrial ribosomal protein L16	1.726	0.0000	0.0000
Mrpl18	ENSMUSG00000057388	mitochondrial ribosomal protein L18	1.545	0.0000	0.0000
Mrpl43	ENSMUSG00000025208	mitochondrial ribosomal protein L43	2.135	0.0000	0.0000
Mrpl50	ENSMUSG00000044018	mitochondrial ribosomal protein L50	1.554	0.0000	0.0000
Mrpl9	ENSMUSG00000028140	mitochondrial ribosomal protein L9	2.115	0.0000	0.0000
Mrps25	ENSMUSG00000014551	mitochondrial ribosomal protein S25	1.643	0.0000	0.0000
Mrps5	ENSMUSG00000027374	mitochondrial ribosomal protein S5	2.447	0.0000	0.0000
Msantd3	ENSMUSG00000039693	Myb/SANT-like DNA-binding domain containing 3	2.495	0.0000	0.0000
Msi1	ENSMUSG00000054256	musashi RNA-binding protein 1	3.345	0.0000	0.0000
Msl1	ENSMUSG00000052915	male specific lethal 1	2.245	0.0000	0.0000
Msl3	ENSMUSG00000031358	MSL complex subunit 3	1.929	0.0012	0.0039
Msx2	ENSMUSG00000021469	msh homeobox 2	3.723	0.0325	0.0721
Mt3	ENSMUSG00000031760	metallothionein 3	1.883	0.0103	0.0269

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
mt-Atp6	ENSMUSG00000064357	mitochondrially encoded ATP synthase 6	119.215	0.0000	0.0000
mt-Atp8	ENSMUSG00000064356	mitochondrially encoded ATP synthase 8	682.269	0.0000	0.0000
Mtch1	ENSMUSG00000024012	mitochondrial carrier 1	2.324	0.0000	0.0000
Mtcl1	ENSMUSG00000052105	microtubule crosslinking factor 1	2.565	0.0000	0.0000
mt-Co2	ENSMUSG00000064354	mitochondrially encoded cytochrome c oxidase II	48.709	0.0000	0.0000
mt-Co3	ENSMUSG00000064358	mitochondrially encoded cytochrome c oxidase III	13.444	0.0000	0.0001
Mthfd1l	ENSMUSG00000040675	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1.755	0.0341	0.0751
Mthfd2	ENSMUSG00000005667	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	1.756	0.0052	0.0149
Mthfd2l	ENSMUSG00000029376	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	2.214	0.0000	0.0000
Mtif2	ENSMUSG00000020459	mitochondrial translational initiation factor 2	1.781	0.0000	0.0000
mt-Nd4l	ENSMUSG00000065947	mitochondrially encoded NADH dehydrogenase 4L	101.439	0.0000	0.0000
mt-Nd6	ENSMUSG00000064368	mitochondrially encoded NADH dehydrogenase 6	6.376	0.0000	0.0000
Mtres1	ENSMUSG00000019797	mitochondrial transcription rescue factor 1	2.590	0.0000	0.0000
Mtrf1l	ENSMUSG00000019774	mitochondrial translational release factor 1-like	2.112	0.0000	0.0000
Mtss2	ENSMUSG00000033763	MTSS I-BAR domain containing 2	1.795	0.0000	0.0000
Mtx3	ENSMUSG00000021704	metaxin 3	1.609	0.0087	0.0233
Mvp	ENSMUSG00000030681	major vault protein	1.752	0.0000	0.0000
Mxra7	ENSMUSG00000020814	matrix-remodelling associated 7	4.029	0.0000	0.0000
Myadm	ENSMUSG00000068566	myeloid-associated differentiation marker	2.091	0.0000	0.0000
Mycl	ENSMUSG00000028654	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived	3.212	0.0004	0.0015
Myef2	ENSMUSG00000027201	myelin basic protein expression factor 2, repressor	2.241	0.0000	0.0000
Myef2l	ENSMUSG00000049230	myelin expression factor 2 like	7.681	0.0000	0.0000
Myh10	ENSMUSG00000020900	myosin, heavy polypeptide 10, non-muscle	1.962	0.0000	0.0000
Myh11	ENSMUSG00000018830	myosin, heavy polypeptide 11, smooth muscle	1.962	0.0000	0.0000
Myh14	ENSMUSG00000030739	myosin, heavy polypeptide 14	1.899	0.0000	0.0000
Myh6	ENSMUSG00000040752	myosin, heavy polypeptide 6, cardiac muscle, alpha	1.928	0.0000	0.0000
Myh7	ENSMUSG00000053093	myosin, heavy polypeptide 7, cardiac muscle, beta	1.559	0.0035	0.0107
Myh7b	ENSMUSG00000074652	myosin, heavy chain 7B, cardiac muscle, beta	1.866	0.0006	0.0021
Myh9	ENSMUSG00000022443	myosin, heavy polypeptide 9, non-muscle	2.165	0.0000	0.0000
Myl12b	ENSMUSG00000034868	myosin, light chain 12B, regulatory	1.856	0.0002	0.0009

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mylk	ENSMUSG00000022836	myosin, light polypeptide kinase	1.594	0.0000	0.0001
Mylk4	ENSMUSG00000044951	myosin light chain kinase family, member 4	1.610	0.0054	0.0154
Myo18b	ENSMUSG00000072720	myosin XVIIIb	1.786	0.0000	0.0000
Myo1e	ENSMUSG00000032220	myosin IE	1.580	0.0000	0.0000
Mypop	ENSMUSG00000048481	Myb-related transcription factor, partner of profilin	2.004	0.0022	0.0070
Myzap	ENSMUSG00000041361	myocardial zonula adherens protein	1.700	0.0000	0.0000
N4bp2os	ENSMUSG00000106978	NEDD4 binding protein 2, opposite strand	8.252	0.0000	0.0000
Naa30	ENSMUSG00000036282	N(alpha)-acetyltransferase 30, NatC catalytic subunit	2.467	0.0000	0.0000
Naa50	ENSMUSG00000022698	N(alpha)-acetyltransferase 50, NatE catalytic subunit	1.850	0.0000	0.0000
Nab2	ENSMUSG00000025402	Ngfi-A binding protein 2	1.676	0.0002	0.0008
Nabp1	ENSMUSG00000026107	nucleic acid binding protein 1	1.569	0.0004	0.0016
Nacc1	ENSMUSG00000001910	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	1.604	0.0000	0.0000
Naf1	ENSMUSG00000014907	nuclear assembly factor 1 ribonucleoprotein	2.301	0.0001	0.0002
Naif1	ENSMUSG00000039164	nuclear apoptosis inducing factor 1	1.805	0.0000	0.0000
Nanos3	ENSMUSG00000056155	nanos C2HC-type zinc finger 3	3.138	0.0011	0.0037
Nasp	ENSMUSG00000028693	nuclear autoantigenic sperm protein (histone-binding)	3.104	0.0000	0.0000
Nat10	ENSMUSG00000027185	N-acetyltransferase 10	1.609	0.0000	0.0000
Nat14	ENSMUSG00000035285	N-acetyltransferase 14	1.877	0.0003	0.0011
Nat8l	ENSMUSG00000048142	N-acetyltransferase 8-like	2.526	0.0000	0.0001
Nbl1	ENSMUSG00000041120	NBL1, DAN family BMP antagonist	1.954	0.0009	0.0030
Ncbp1	ENSMUSG00000028330	nuclear cap binding protein subunit 1	1.570	0.0000	0.0000
Ncbp3	ENSMUSG00000020783	nuclear cap binding subunit 3	1.604	0.0000	0.0000
Ncf2	ENSMUSG00000026480	neutrophil cytosolic factor 2	1.609	0.0037	0.0112
Nck2	ENSMUSG00000066877	non-catalytic region of tyrosine kinase adaptor protein 2	1.945	0.0000	0.0000
Ncl	ENSMUSG00000026234	nucleolin	2.591	0.0000	0.0000
Ncoa5	ENSMUSG00000039804	nuclear receptor coactivator 5	1.998	0.0000	0.0000
Ndfip2	ENSMUSG00000053253	Nedd4 family interacting protein 2	2.515	0.0000	0.0000
Ndufa12	ENSMUSG00000020022	NADH:ubiquinone oxidoreductase subunit A12	1.699	0.0000	0.0000
Ndufa5	ENSMUSG00000023089	NADH:ubiquinone oxidoreductase subunit A5	2.953	0.0000	0.0000
Ndufa9	ENSMUSG00000000399	NADH:ubiquinone oxidoreductase subunit A9	1.902	0.0000	0.0000
Ndufaf2	ENSMUSG00000068184	NADH:ubiquinone oxidoreductase complex assembly factor 2	1.571	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ndufaf6	ENSMUSG00000050323	NADH:ubiquinone oxidoreductase complex assembly factor 6	2.398	0.0000	0.0000
Ndufb10	ENSMUSG00000040048	NADH:ubiquinone oxidoreductase subunit B10	1.841	0.0000	0.0000
Ndufb3	ENSMUSG00000026032	NADH:ubiquinone oxidoreductase subunit B3	1.754	0.0000	0.0000
Ndufb9	ENSMUSG00000022354	NADH:ubiquinone oxidoreductase subunit B9	1.809	0.0000	0.0000
Ndufs6b	ENSMUSG00000083820	NADH:ubiquinone oxidoreductase subunit S6B	7.135	0.0000	0.0000
Neat1	ENSMUSG00000092274	nuclear paraspeckle assembly transcript 1 (non-protein coding)	2.035	0.0454	0.0955
Nedd8	ENSMUSG00000010376	neural precursor cell expressed, developmentally down-regulated gene 8	2.086	0.0000	0.0000
Nefl	ENSMUSG00000022055	neurofilament, light polypeptide	10.169	0.0448	0.0943
Nek2	ENSMUSG00000026622	NIMA (never in mitosis gene a)-related expressed kinase 2	1.843	0.0211	0.0500
Nek7	ENSMUSG00000026393	NIMA (never in mitosis gene a)-related expressed kinase 7	1.862	0.0000	0.0000
Nemf	ENSMUSG00000020982	nuclear export mediator factor	1.914	0.0000	0.0000
Nes	ENSMUSG00000004891	nestin	1.829	0.0008	0.0030
Net1	ENSMUSG00000021215	neuroepithelial cell transforming gene 1	2.046	0.0000	0.0000
Nexn	ENSMUSG00000039103	nexilin	3.138	0.0000	0.0000
Nfe2l1	ENSMUSG00000038615	nuclear factor, erythroid derived 2,-like 1	1.710	0.0000	0.0000
Nfix	ENSMUSG00000001911	nuclear factor I/X	2.155	0.0000	0.0000
Nfxl1	ENSMUSG00000072889	nuclear transcription factor, X-box binding-like 1	1.989	0.0000	0.0000
Nfyb	ENSMUSG00000020248	nuclear transcription factor-Y beta	2.803	0.0000	0.0000
Nkain1	ENSMUSG00000078532	Na+/K+ transporting ATPase interacting 1	1.869	0.0020	0.0063
Nkapd1	ENSMUSG00000059820	NKAP domain containing 1	1.549	0.0000	0.0000
Nkiras1	ENSMUSG00000021772	NFKB inhibitor interacting Ras-like protein 1	1.969	0.0000	0.0000
Nlgn2	ENSMUSG00000051790	neuroligin 2	1.980	0.0000	0.0000
Nlgn3	ENSMUSG00000031302	neuroligin 3	2.516	0.0248	0.0573
Noc2l	ENSMUSG00000095567	NOC2 like nucleolar associated transcriptional repressor	2.101	0.0000	0.0000
Noc3l	ENSMUSG00000024999	NOC3 like DNA replication regulator	1.757	0.0000	0.0000
Nog	ENSMUSG00000048616	noggin	5.154	0.0044	0.0128
Nol7	ENSMUSG00000063200	nucleolar protein 7	2.061	0.0001	0.0002
Nol8	ENSMUSG00000021392	nucleolar protein 8	1.510	0.0000	0.0000
Nono	ENSMUSG00000031311	non-POU-domain-containing, octamer binding protein	2.238	0.0000	0.0000
Nop14	ENSMUSG00000036693	NOP14 nucleolar protein	1.756	0.0000	0.0000
Nop2	ENSMUSG00000038279	NOP2 nucleolar protein	1.582	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nop58	ENSMUSG00000026020	NOP58 ribonucleoprotein	1.846	0.0000	0.0000
Nop9	ENSMUSG00000019297	NOP9 nucleolar protein	1.777	0.0000	0.0000
Norad	ENSMUSG00000102869	non-coding RNA activated by DNA damage	2.406	0.0000	0.0000
Notumos	ENSMUSG00000053613	notum palmitoleoyl-protein carboxylesterase, opposite strand	7.005	0.0013	0.0043
Nova2	ENSMUSG00000030411	NOVA alternative splicing regulator 2	2.115	0.0000	0.0000
Noxred1	ENSMUSG00000072919	NADP+ dependent oxidoreductase domain containing 1	3.282	0.0156	0.0387
Npc2	ENSMUSG00000021242	NPC intracellular cholesterol transporter 2	1.614	0.0000	0.0000
Nphp1	ENSMUSG00000027378	nephronophthisis 1 (juvenile) homolog (human)	2.174	0.0000	0.0000
Npm1	ENSMUSG00000057113	nucleophosmin 1	2.907	0.0000	0.0000
Npnt	ENSMUSG00000040998	nephronectin	2.024	0.0176	0.0428
Nr2f1	ENSMUSG00000069171	nuclear receptor subfamily 2, group F, member 1	3.045	0.0000	0.0000
Nr2f2	ENSMUSG00000030551	nuclear receptor subfamily 2, group F, member 2	2.537	0.0000	0.0000
Nr2f6	ENSMUSG00000002393	nuclear receptor subfamily 2, group F, member 6	2.632	0.0000	0.0002
Nr4a2	ENSMUSG00000026826	nuclear receptor subfamily 4, group A, member 2	2.670	0.0002	0.0008
Nrarp	ENSMUSG00000078202	Notch-regulated ankyrin repeat protein	1.913	0.0000	0.0002
Nrd1	ENSMUSG00000053510	nardilysin, N-arginine dibasic convertase, NRD convertase 1	2.142	0.0000	0.0000
Nrgn	ENSMUSG00000053310	neurogranin	8.592	0.0000	0.0000
Nrn1	ENSMUSG00000039114	neuritin 1	2.002	0.0112	0.0291
Nrtn	ENSMUSG00000039481	neurturin	8.582	0.0000	0.0000
Nsa2	ENSMUSG00000060739	NSA2 ribosome biogenesis homolog	3.005	0.0000	0.0000
Nsa2-ps1	ENSMUSG00000118353	NSA2 ribosome biogenesis homolog, pseudogene 1	3.005	0.0107	0.0280
Nsmce3	ENSMUSG00000070520	NSE3 homolog, SMC5-SMC6 complex component	2.081	0.0000	0.0000
Nsmce4a	ENSMUSG00000040331	NSE4 homolog A, SMC5-SMC6 complex component	2.392	0.0000	0.0000
Nsrp1	ENSMUSG00000037958	nuclear speckle regulatory protein 1	4.004	0.0000	0.0000
Ntn4	ENSMUSG00000020019	netrin 4	2.001	0.0000	0.0000
Ntng2	ENSMUSG00000035513	netrin G2	1.511	0.0219	0.0516
Nucb1	ENSMUSG00000030824	nucleobindin 1	1.861	0.0000	0.0000
Nucb2	ENSMUSG00000030659	nucleobindin 2	2.016	0.0000	0.0000
Nucks1	ENSMUSG00000026434	nuclear casein kinase and cyclin-dependent kinase substrate 1	1.914	0.0000	0.0000
Nudc	ENSMUSG00000028851	nudC nuclear distribution protein	3.182	0.0000	0.0000
Nudc-ps1	ENSMUSG00000110331	nuclear distribution gene C homolog (Aspergillus), pseudogene 1	2.102	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nudt13	ENSMUSG00000021809	nudix (nucleoside diphosphate linked moiety X)-type motif 13	1.563	0.0000	0.0000
Nudt3	ENSMUSG00000024213	nudix (nucleotide diphosphate linked moiety X)-type motif 3	2.466	0.0000	0.0000
Nudt4	ENSMUSG00000020029	nudix (nucleoside diphosphate linked moiety X)-type motif 4	2.498	0.0000	0.0000
Nudt6	ENSMUSG00000050174	nudix (nucleoside diphosphate linked moiety X)-type motif 6	3.557	0.0000	0.0000
Nudt9	ENSMUSG00000029310	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2.160	0.0000	0.0000
Numbl	ENSMUSG00000063160	numb-like	1.583	0.0057	0.0162
Nup107	ENSMUSG00000052798	nucleoporin 107	1.624	0.0000	0.0000
Nutf2-ps1	ENSMUSG00000071497	nuclear transport factor 2, pseudogene 1	20.547	0.0000	0.0000
Nxn	ENSMUSG00000020844	nucleoredoxin	1.741	0.0001	0.0005
Nyap1	ENSMUSG00000045348	neuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 1	2.135	0.0000	0.0000
Oaf	ENSMUSG00000032014	out at first homolog	1.614	0.0169	0.0414
Oas3	ENSMUSG00000032661	2'-5' oligoadenylate synthetase 3	4.099	0.0249	0.0577
Obi1	ENSMUSG00000022120	ORC ubiquitin ligase 1	1.618	0.0002	0.0006
Ociad2	ENSMUSG00000029153	OCIA domain containing 2	1.760	0.0000	0.0000
Odaph	ENSMUSG00000096035	odontogenesis associated phosphoprotein	2.052	0.0344	0.0757
Odc1	ENSMUSG00000011179	ornithine decarboxylase, structural 1	1.907	0.0000	0.0000
Ogfrl1	ENSMUSG00000026158	opioid growth factor receptor-like 1	2.500	0.0000	0.0000
Olfm1	ENSMUSG00000026833	olfactomedin 1	2.481	0.0000	0.0000
Optn	ENSMUSG00000026672	optineurin	1.508	0.0002	0.0006
Orai1	ENSMUSG00000049686	ORAI calcium release-activated calcium modulator 1	3.550	0.0000	0.0000
Os9	ENSMUSG00000040462	amplified in osteosarcoma	1.628	0.0000	0.0000
Osbpl10	ENSMUSG00000040875	oxysterol binding protein-like 10	2.045	0.0000	0.0000
Otud1	ENSMUSG00000043415	OTU domain containing 1	2.305	0.0000	0.0000
Otud3	ENSMUSG00000041161	OTU domain containing 3	1.843	0.0000	0.0001
Otud6b	ENSMUSG00000040550	OTU domain containing 6B	1.834	0.0000	0.0000
Otud7b	ENSMUSG00000038495	OTU domain containing 7B	1.889	0.0000	0.0000
Otulin	ENSMUSG00000046034	OTU deubiquitinase with linear linkage specificity	3.128	0.0000	0.0000
Otulinl	ENSMUSG00000056069	OTU deubiquitinase with linear linkage specificity like	2.404	0.0000	0.0000
Oxsr1	ENSMUSG00000036737	oxidative-stress responsive 1	1.746	0.0000	0.0000
P3h3	ENSMUSG00000023191	prolyl 3-hydroxylase 3	1.756	0.0031	0.0094
Pabpc4	ENSMUSG00000011257	poly(A) binding protein, cytoplasmic 4	1.560	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pabpn1	ENSMUSG00000022194	poly(A) binding protein, nuclear 1	20.333	0.0000	0.0000
Pacsin3	ENSMUSG00000027257	protein kinase C and casein kinase substrate in neurons 3	1.921	0.0000	0.0000
Paf1	ENSMUSG00000003437	Paf1, RNA polymerase II complex component	2.835	0.0000	0.0000
Paip1	ENSMUSG00000025451	polyadenylate binding protein-interacting protein 1	2.722	0.0000	0.0000
Palm3	ENSMUSG00000047986	paralemmin 3	5.170	0.0000	0.0000
Pals2	ENSMUSG00000038388	protein associated with LIN7 2, MAGUK family member	1.856	0.0000	0.0000
Pan3	ENSMUSG00000029647	PAN3 poly(A) specific ribonuclease subunit	1.605	0.0000	0.0001
Pank1	ENSMUSG00000033610	pantothenate kinase 1	1.597	0.0000	0.0000
Pank2	ENSMUSG00000037514	pantothenate kinase 2	2.234	0.0000	0.0000
Paqr3	ENSMUSG00000055725	progestin and adipoQ receptor family member III	3.594	0.0000	0.0000
Paqr4	ENSMUSG00000023909	progestin and adipoQ receptor family member IV	2.702	0.0000	0.0000
Paqr9	ENSMUSG00000064225	progestin and adipoQ receptor family member IX	1.670	0.0002	0.0007
Pard3	ENSMUSG00000025812	par-3 family cell polarity regulator	1.866	0.0000	0.0000
Pard6b	ENSMUSG00000044641	par-6 family cell polarity regulator beta	2.079	0.0000	0.0000
Parn	ENSMUSG00000022685	poly(A)-specific ribonuclease (deadenylation nuclease)	1.620	0.0000	0.0000
Parp2	ENSMUSG00000036023	poly (ADP-ribose) polymerase family, member 2	1.514	0.0001	0.0003
Pawr	ENSMUSG00000035873	PRKC, apoptosis, WT1, regulator	4.358	0.0000	0.0000
Paxbp1	ENSMUSG00000022974	PAX3 and PAX7 binding protein 1	1.891	0.0000	0.0000
Pbdc1	ENSMUSG00000031226	polysaccharide biosynthesis domain containing 1	2.683	0.0000	0.0000
Pbx2	ENSMUSG00000034673	pre B cell leukemia homeobox 2	1.969	0.0000	0.0000
Pcbd2	ENSMUSG00000021496	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	6.620	0.0000	0.0000
Pcdh20	ENSMUSG00000050505	protocadherin 20	3.010	0.0195	0.0467
Pcdhb16	ENSMUSG00000047910	protocadherin beta 16	2.130	0.0000	0.0002
Pcdhb2	ENSMUSG00000051599	protocadherin beta 2	2.757	0.0226	0.0529
Pcdhb20	ENSMUSG00000046191	protocadherin beta 20	1.674	0.0001	0.0006
Pcf11	ENSMUSG00000041328	PCF11 cleavage and polyadenylation factor subunit	1.816	0.0000	0.0000
Pcgf3	ENSMUSG00000033623	polycomb group ring finger 3	1.747	0.0000	0.0000
Pcgf6	ENSMUSG00000025050	polycomb group ring finger 6	2.005	0.0000	0.0000
Pcm1	ENSMUSG00000031592	pericentriolar material 1	1.609	0.0000	0.0000
Pcnt	ENSMUSG00000001151	pericentrin (kendrin)	1.526	0.0008	0.0028

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pdap1	ENSMUSG00000029623	PDGFA associated protein 1	2.847	0.0000	0.0000
Pdcd4	ENSMUSG00000024975	programmed cell death 4	2.676	0.0000	0.0000
Pdcd5	ENSMUSG00000030417	programmed cell death 5	2.590	0.0000	0.0000
Pdcd7	ENSMUSG00000041837	programmed cell death 7	4.013	0.0000	0.0000
Pdcl	ENSMUSG00000009030	phosducin-like	1.527	0.0000	0.0000
Pdcl3	ENSMUSG00000026078	phosducin-like 3	2.557	0.0000	0.0000
Pde3b	ENSMUSG00000030671	phosphodiesterase 3B, cGMP-inhibited	1.865	0.0040	0.0119
Pde6d	ENSMUSG00000026239	phosphodiesterase 6D, cGMP-specific, rod, delta	1.686	0.0000	0.0002
Pdgfb	ENSMUSG00000000489	platelet derived growth factor, B polypeptide	1.906	0.0000	0.0000
Pdha1	ENSMUSG00000031299	pyruvate dehydrogenase E1 alpha 1	1.512	0.0000	0.0000
Pdhb	ENSMUSG00000021748	pyruvate dehydrogenase (lipoamide) beta	1.569	0.0000	0.0000
Pdia6	ENSMUSG00000020571	protein disulfide isomerase associated 6	1.766	0.0000	0.0000
Pdlim2	ENSMUSG00000022090	PDZ and LIM domain 2	1.755	0.0001	0.0004
Pdrg1	ENSMUSG00000027472	p53 and DNA damage regulated 1	1.508	0.0000	0.0000
Pdxp	ENSMUSG00000116165	pyridoxal (pyridoxine, vitamin B6) phosphatase	2.808	0.0327	0.0725
Pdzd11	ENSMUSG00000015668	PDZ domain containing 11	1.626	0.0000	0.0000
Pdzrn4	ENSMUSG00000036218	PDZ domain containing RING finger 4	2.311	0.0075	0.0206
Peg12	ENSMUSG00000070526	paternally expressed 12	1.971	0.0057	0.0161
Peg3	ENSMUSG00000002265	paternally expressed 3	1.533	0.0103	0.0269
Peli3	ENSMUSG00000024901	pellino 3	1.708	0.0000	0.0000
Pet100	ENSMUSG00000087687	PET100 homolog	2.278	0.0000	0.0000
Pex16	ENSMUSG00000027222	peroxisomal biogenesis factor 16	1.504	0.0003	0.0010
Pfdn2	ENSMUSG00000006412	prefoldin 2	3.294	0.0000	0.0000
Pfdn6	ENSMUSG00000024309	prefoldin subunit 6	2.082	0.0000	0.0000
Pfn4	ENSMUSG00000020639	profilin family, member 4	1.577	0.0165	0.0406
Pgrmc2	ENSMUSG00000049940	progesterone receptor membrane component 2	2.345	0.0000	0.0000
Phactr3	ENSMUSG00000027525	phosphatase and actin regulator 3	2.297	0.0015	0.0048
Phc2	ENSMUSG00000028796	polyhomeotic 2	1.988	0.0000	0.0000
Pheta2	ENSMUSG00000049687	PH domain containing endocytic trafficking adaptor 2	1.786	0.0031	0.0096
Phf1	ENSMUSG00000024193	PHD finger protein 1	1.921	0.0000	0.0000
Phf10	ENSMUSG00000023883	PHD finger protein 10	1.902	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Phf13	ENSMUSG00000047777	PHD finger protein 13	2.527	0.0000	0.0000
Phf21a	ENSMUSG00000058318	PHD finger protein 21A	1.536	0.0000	0.0000
Phf21b	ENSMUSG00000016624	PHD finger protein 21B	1.616	0.0172	0.0420
Phlda3	ENSMUSG00000041801	pleckstrin homology like domain, family A, member 3	1.732	0.0121	0.0310
Phldb3	ENSMUSG00000074277	pleckstrin homology like domain, family B, member 3	2.676	0.0076	0.0206
Phospho1	ENSMUSG00000050860	phosphatase, orphan 1	8.823	0.0000	0.0000
Phox2a	ENSMUSG00000007946	paired-like homeobox 2a	2.469	0.0071	0.0194
Phtf1	ENSMUSG00000058388	putative homeodomain transcription factor 1	2.133	0.0000	0.0000
Pi4k2b	ENSMUSG00000029186	phosphatidylinositol 4-kinase type 2 beta	1.598	0.0232	0.0541
Pick1	ENSMUSG00000068206	protein interacting with C kinase 1	1.679	0.0001	0.0004
Piezo2	ENSMUSG00000041482	piezo-type mechanosensitive ion channel component 2	2.249	0.0253	0.0583
Pilra	ENSMUSG00000046245	paired immunoglobin-like type 2 receptor alpha	2.493	0.0016	0.0053
Pin4	ENSMUSG00000079480	peptidyl-prolyl cis/trans isomerase, NIMA-interacting, 4 (parvulin)	4.904	0.0000	0.0000
Pip4k2b	ENSMUSG00000018547	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	1.733	0.0000	0.0000
Pip4p1	ENSMUSG00000035953	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 1	1.653	0.0018	0.0060
Pitpna	ENSMUSG00000017781	phosphatidylinositol transfer protein, alpha	2.794	0.0000	0.0000
Pitpnb	ENSMUSG00000050017	phosphatidylinositol transfer protein, beta	1.831	0.0000	0.0000
Pitx3	ENSMUSG00000025229	paired-like homeodomain transcription factor 3	4.276	0.0002	0.0009
Pkd2	ENSMUSG00000034462	polycystin 2, transient receptor potential cation channel	2.106	0.0000	0.0000
Pkdcc	ENSMUSG00000024247	protein kinase domain containing, cytoplasmic	2.081	0.0000	0.0000
Pkm	ENSMUSG00000032294	pyruvate kinase, muscle	2.524	0.0000	0.0000
Pkp2	ENSMUSG00000041957	plakophilin 2	1.512	0.0023	0.0072
Pla2g12a	ENSMUSG00000027999	phospholipase A2, group XIIA	3.535	0.0000	0.0000
Plcl1	ENSMUSG00000038349	phospholipase C-like 1	1.724	0.0000	0.0001
Plekha1	ENSMUSG00000040268	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	1.683	0.0000	0.0000
Plekha3	ENSMUSG00000002733	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	1.863	0.0000	0.0000
Plekha8	ENSMUSG00000005225	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	1.564	0.0000	0.0000
Plekhd1	ENSMUSG00000066438	pleckstrin homology domain containing, family D (with coiled-coil domains) member 1	3.320	0.0364	0.0795
Plekhh3	ENSMUSG00000035172	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	1.788	0.0020	0.0065
Plekhj1	ENSMUSG00000035278	pleckstrin homology domain containing, family J member 1	2.564	0.0000	0.0000
Plet1os	ENSMUSG00000101304	placenta expressed transcript 1, opposite strand	1.759	0.0000	0.0001

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Plod2	ENSMUSG00000032374	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1.530	0.0000	0.0002
Plpp6	ENSMUSG00000040105	phospholipid phosphatase 6	1.752	0.0000	0.0000
Plppr2	ENSMUSG00000040563	phospholipid phosphatase related 2	2.226	0.0000	0.0001
Pm20d2	ENSMUSG00000054659	peptidase M20 domain containing 2	1.565	0.0212	0.0500
Pmepa1	ENSMUSG00000038400	prostate transmembrane protein, androgen induced 1	1.563	0.0000	0.0000
Pmvk	ENSMUSG00000027952	phosphomevalonate kinase	1.778	0.0000	0.0000
Pnisr	ENSMUSG00000028248	PNN interacting serine/arginine-rich	2.067	0.0000	0.0000
Pnma8b	ENSMUSG00000070802	PNMA family member 8B	1.915	0.0000	0.0000
Pnn	ENSMUSG00000020994	pinin	3.805	0.0000	0.0000
Pnrc1	ENSMUSG00000040128	proline-rich nuclear receptor coactivator 1	2.101	0.0003	0.0012
Polr1c	ENSMUSG00000067148	polymerase (RNA) I polypeptide C	1.692	0.0000	0.0000
Polr1has	ENSMUSG00000036214	RNA polymerase I subunit H, antisense	1.692	0.0000	0.0000
Polr2a	ENSMUSG00000005198	polymerase (RNA) II (DNA directed) polypeptide A	1.602	0.0000	0.0001
Polr2m	ENSMUSG00000032199	polymerase (RNA) II (DNA directed) polypeptide M	1.543	0.0000	0.0000
Polr3d	ENSMUSG00000000776	polymerase (RNA) III (DNA directed) polypeptide D	1.560	0.0000	0.0000
Polr3g	ENSMUSG00000035834	polymerase (RNA) III (DNA directed) polypeptide G	1.879	0.0000	0.0000
Polr3gl	ENSMUSG00000028104	polymerase (RNA) III (DNA directed) polypeptide G like	2.332	0.0000	0.0000
Pou2f2	ENSMUSG00000008496	POU domain, class 2, transcription factor 2	2.107	0.0173	0.0421
Pou3f1	ENSMUSG00000090125	POU domain, class 3, transcription factor 1	5.884	0.0000	0.0000
Ppat	ENSMUSG00000029246	phosphoribosyl pyrophosphate amidotransferase	1.545	0.0000	0.0000
Ppfia3	ENSMUSG00000003863	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	3.470	0.0146	0.0366
Ppfibp1	ENSMUSG00000016487	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.075	0.0000	0.0000
Ppid	ENSMUSG00000027804	peptidylprolyl isomerase D (cyclophilin D)	2.027	0.0000	0.0000
Ppig	ENSMUSG00000042133	peptidyl-prolyl isomerase G (cyclophilin G)	3.267	0.0000	0.0000
Ppih	ENSMUSG00000060288	peptidyl prolyl isomerase H	1.500	0.0000	0.0002
Ppil3	ENSMUSG00000026035	peptidylprolyl isomerase (cyclophilin)-like 3	2.183	0.0000	0.0000
Ppil4	ENSMUSG00000015757	peptidylprolyl isomerase (cyclophilin)-like 4	1.880	0.0000	0.0000
Ppl	ENSMUSG00000039457	periplakin	1.714	0.0013	0.0044
Ppm1a	ENSMUSG00000021096	protein phosphatase 1A, magnesium dependent, alpha isoform	2.553	0.0000	0.0000
Ppm1b	ENSMUSG00000061130	protein phosphatase 1B, magnesium dependent, beta isoform	3.146	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ppm1g	ENSMUSG00000029147	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	2.106	0.0000	0.0000
Ppm1m	ENSMUSG00000020253	protein phosphatase 1M	1.542	0.0000	0.0000
Ppp1cb	ENSMUSG00000014956	protein phosphatase 1 catalytic subunit beta	1.705	0.0000	0.0000
Ppp1cc	ENSMUSG00000004455	protein phosphatase 1 catalytic subunit gamma	1.741	0.0000	0.0000
Ppp1r11	ENSMUSG00000036398	protein phosphatase 1, regulatory inhibitor subunit 11	2.592	0.0000	0.0000
Ppp1r12a	ENSMUSG00000019907	protein phosphatase 1, regulatory subunit 12A	1.697	0.0000	0.0000
Ppp1r14a	ENSMUSG00000037166	protein phosphatase 1, regulatory inhibitor subunit 14A	1.894	0.0124	0.0315
Ppp1r14b	ENSMUSG00000056612	protein phosphatase 1, regulatory inhibitor subunit 14B	4.526	0.0000	0.0000
Ppp1r18	ENSMUSG00000034595	protein phosphatase 1, regulatory subunit 18	1.693	0.0000	0.0000
Ppp1r18os	ENSMUSG00000087443	protein phosphatase 1, regulatory subunit 18, opposite strand	3.232	0.0432	0.0916
Ppp1r1a	ENSMUSG00000022490	protein phosphatase 1, regulatory inhibitor subunit 1A	1.718	0.0156	0.0386
Ppp1r2-ps4	ENSMUSG00000059237	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 4	2.521	0.0164	0.0403
Ppp1r35	ENSMUSG00000029725	protein phosphatase 1, regulatory subunit 35	3.962	0.0000	0.0000
Ppp1r37	ENSMUSG00000051403	protein phosphatase 1, regulatory subunit 37	1.753	0.0000	0.0000
Ppp1r3f	ENSMUSG00000039556	protein phosphatase 1, regulatory subunit 3F	4.459	0.0000	0.0000
Ppp1r9b	ENSMUSG00000038976	protein phosphatase 1, regulatory subunit 9B	3.945	0.0000	0.0000
Ppp2ca	ENSMUSG00000020349	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	1.716	0.0000	0.0000
Ppp2r5a	ENSMUSG00000026626	protein phosphatase 2, regulatory subunit B', alpha	1.995	0.0000	0.0000
Ppp3cc	ENSMUSG00000022092	protein phosphatase 3, catalytic subunit, gamma isoform	2.009	0.0000	0.0000
Ppp4c	ENSMUSG00000030697	protein phosphatase 4, catalytic subunit	2.414	0.0000	0.0000
Ppp4r1l-ps	ENSMUSG00000055897	protein phosphatase 4, regulatory subunit 1-like, pseudogene	1.716	0.0002	0.0007
Ppp4r3a	ENSMUSG00000041846	protein phosphatase 4 regulatory subunit 3A	1.592	0.0000	0.0000
Ppp6r1	ENSMUSG00000052296	protein phosphatase 6, regulatory subunit 1	1.713	0.0000	0.0000
Ppwd1	ENSMUSG00000021713	peptidylprolyl isomerase domain and WD repeat containing 1	1.640	0.0000	0.0000
Prcd	ENSMUSG00000075410	photoreceptor disc component	2.423	0.0001	0.0006
Prdm10	ENSMUSG00000042496	PR domain containing 10	1.579	0.0000	0.0000
Prdm6	ENSMUSG00000069378	PR domain containing 6	6.608	0.0048	0.0140
Prdm8	ENSMUSG00000035456	PR domain containing 8	6.438	0.0000	0.0000
Prdx5	ENSMUSG00000024953	peroxiredoxin 5	1.774	0.0000	0.0000
Prkar1a	ENSMUSG00000020612	protein kinase, cAMP dependent regulatory, type I, alpha	1.529	0.0000	0.0000
Prkci	ENSMUSG00000037643	protein kinase C, iota	1.764	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Prkg1	ENSMUSG00000052920	protein kinase, cGMP-dependent, type I	1.574	0.0000	0.0000
Prkrip1	ENSMUSG00000039737	Prkr interacting protein 1 (IL11 inducible)	1.618	0.0000	0.0000
Prmt6	ENSMUSG00000049300	protein arginine N-methyltransferase 6	1.505	0.0000	0.0002
Prmt9	ENSMUSG00000037134	protein arginine methyltransferase 9	2.208	0.0000	0.0000
Procr	ENSMUSG00000027611	protein C receptor, endothelial	2.750	0.0000	0.0000
Prpf18	ENSMUSG00000039449	pre-mRNA processing factor 18	1.523	0.0000	0.0000
Prpf3	ENSMUSG00000015748	pre-mRNA processing factor 3	2.072	0.0000	0.0000
Prpf31	ENSMUSG00000008373	pre-mRNA processing factor 31	2.615	0.0000	0.0000
Prpf38b	ENSMUSG00000027881	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	2.927	0.0000	0.0000
Prpf40b	ENSMUSG00000023007	pre-mRNA processing factor 40B	1.677	0.0000	0.0000
Prpf6	ENSMUSG00000002455	pre-mRNA splicing factor 6	1.639	0.0000	0.0000
Prph	ENSMUSG00000023484	peripherin	5.139	0.0067	0.0186
Prr13	ENSMUSG00000023048	proline rich 13	1.568	0.0000	0.0000
Prr15	ENSMUSG00000045725	proline rich 15	2.097	0.0125	0.0318
Prr18	ENSMUSG00000055945	proline rich 18	2.850	0.0265	0.0607
Prr3	ENSMUSG00000038500	proline-rich polypeptide 3	1.742	0.0004	0.0016
Prr33	ENSMUSG00000043795	proline rich 33	1.724	0.0003	0.0011
Prr5	ENSMUSG00000036106	proline rich 5 (renal)	2.577	0.0000	0.0000
Prr7	ENSMUSG00000034686	proline rich 7 (synaptic)	2.566	0.0223	0.0523
Prrx2	ENSMUSG00000039476	paired related homeobox 2	8.978	0.0000	0.0000
Prx	ENSMUSG00000053198	periaxin	1.608	0.0439	0.0928
Psip1	ENSMUSG00000028484	PC4 and SFRS1 interacting protein 1	2.502	0.0000	0.0000
Psma5	ENSMUSG00000068749	proteasome subunit alpha 5	1.572	0.0000	0.0000
Psmb7	ENSMUSG00000026750	proteasome (prosome, macropain) subunit, beta type 7	1.972	0.0000	0.0000
Psmc3	ENSMUSG00000002102	proteasome (prosome, macropain) 26S subunit, ATPase 3	1.613	0.0000	0.0000
Psmd10	ENSMUSG00000031429	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	1.660	0.0000	0.0000
Psmd14	ENSMUSG00000026914	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	2.217	0.0000	0.0000
Psmd7	ENSMUSG00000039067	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.592	0.0001	0.0004
Psme2b	ENSMUSG00000078153	protease (prosome, macropain) activator subunit 2B	1.511	0.0100	0.0262
Pstpip1	ENSMUSG00000032322	proline-serine-threonine phosphatase-interacting protein 1	1.924	0.0041	0.0121
Pten	ENSMUSG00000013663	phosphatase and tensin homolog	1.580	0.0001	0.0006

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ptges2	ENSMUSG00000026820	prostaglandin E synthase 2	1.684	0.0000	0.0000
Ptges3	ENSMUSG00000071072	prostaglandin E synthase 3	2.224	0.0000	0.0000
Ptges3-ps	ENSMUSG00000040078	prostaglandin E synthase 3, pseudogene	1.787	0.0209	0.0495
Ptgr2	ENSMUSG00000072946	prostaglandin reductase 2	1.612	0.0000	0.0000
Ptma	ENSMUSG00000026238	prothymosin alpha	6.791	0.0000	0.0000
Ptma-ps2	ENSMUSG00000084274	prothymosin alpha, pseudogene 2	11.122	0.0000	0.0000
Ptms	ENSMUSG00000030122	parathymosin	4.979	0.0000	0.0000
Ptp4a3	ENSMUSG00000059895	protein tyrosine phosphatase 4a3	1.598	0.0001	0.0005
Ptpdc1	ENSMUSG00000038042	protein tyrosine phosphatase domain containing 1	1.509	0.0000	0.0002
Ptpn11	ENSMUSG00000043733	protein tyrosine phosphatase, non-receptor type 11	1.573	0.0004	0.0016
Ptpra	ENSMUSG00000027303	protein tyrosine phosphatase, receptor type, A	1.795	0.0000	0.0000
Ptprc	ENSMUSG00000026395	protein tyrosine phosphatase, receptor type, C	1.744	0.0109	0.0284
Ptx3	ENSMUSG00000027832	pentraxin related gene	3.786	0.0006	0.0023
Pum3	ENSMUSG00000041360	pumilio RNA-binding family member 3	1.650	0.0000	0.0000
Pura	ENSMUSG00000043991	purine rich element binding protein A	1.552	0.0000	0.0000
Purb	ENSMUSG00000094483	purine rich element binding protein B	1.621	0.0000	0.0000
Pwwp2a	ENSMUSG00000044950	PWWP domain containing 2A	2.041	0.0000	0.0000
Pxdc1	ENSMUSG00000021411	PX domain containing 1	2.978	0.0000	0.0000
Pygo1	ENSMUSG00000034910	pygopus 1	1.670	0.0000	0.0000
Pygo2	ENSMUSG00000047824	pygopus 2	1.628	0.0000	0.0001
Pym1	ENSMUSG00000064030	PYM homolog 1, exon junction complex associated factor	1.719	0.0000	0.0001
Qki	ENSMUSG00000062078	quaking, KH domain containing RNA binding	1.832	0.0000	0.0000
R3hcc1	ENSMUSG00000034194	R3H domain and coiled-coil containing 1	3.088	0.0000	0.0000
R3hdm4	ENSMUSG00000035781	R3H domain containing 4	2.096	0.0000	0.0000
Rab10os	ENSMUSG00000079179	RAB10, member RAS oncogene family, opposite strand	1.644	0.0003	0.0010
Rab11fip1	ENSMUSG00000031488	RAB11 family interacting protein 1 (class I)	2.266	0.0121	0.0309
Rab12	ENSMUSG00000023460	RAB12, member RAS oncogene family	1.646	0.0000	0.0000
Rab18	ENSMUSG00000073639	RAB18, member RAS oncogene family	2.232	0.0000	0.0000
Rab21	ENSMUSG00000020132	RAB21, member RAS oncogene family	1.844	0.0000	0.0000
Rab22a	ENSMUSG00000027519	RAB22A, member RAS oncogene family	2.120	0.0000	0.0000
Rab24	ENSMUSG00000034789	RAB24, member RAS oncogene family	1.800	0.0034	0.0103

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rab27a	ENSMUSG00000032202	RAB27A, member RAS oncogene family	1.605	0.0063	0.0176
Rab28	ENSMUSG00000029128	RAB28, member RAS oncogene family	2.654	0.0000	0.0000
Rab2a	ENSMUSG00000047187	RAB2A, member RAS oncogene family	1.950	0.0000	0.0000
Rab43	ENSMUSG00000030055	RAB43, member RAS oncogene family	5.662	0.0000	0.0000
Rab5a	ENSMUSG00000017831	RAB5A, member RAS oncogene family	1.563	0.0001	0.0004
Rab5if	ENSMUSG00000027637	RAB5 interacting factor	3.088	0.0000	0.0000
Rab6b	ENSMUSG00000032549	RAB6B, member RAS oncogene family	2.287	0.0190	0.0456
Rab8a	ENSMUSG00000003037	RAB8A, member RAS oncogene family	2.994	0.0000	0.0000
Rab9b	ENSMUSG00000043463	RAB9B, member RAS oncogene family	2.408	0.0121	0.0311
Rabl3	ENSMUSG00000022827	RAB, member RAS oncogene family-like 3	1.570	0.0000	0.0000
Rabl6	ENSMUSG00000015087	RAB, member RAS oncogene family-like 6	1.512	0.0000	0.0000
Rac1	ENSMUSG00000001847	Rac family small GTPase 1	1.546	0.0000	0.0000
Rad23b	ENSMUSG00000028426	RAD23 homolog B, nucleotide excision repair protein	1.763	0.0000	0.0000
Rad51c	ENSMUSG00000007646	RAD51 paralog C	1.547	0.0172	0.0420
Rala	ENSMUSG00000008859	v-ral simian leukemia viral oncogene A (ras related)	1.794	0.0000	0.0000
Ramac	ENSMUSG00000038646	RNA guanine-7 methyltransferase activating subunit	1.939	0.0000	0.0000
Ranbp1	ENSMUSG00000005732	RAN binding protein 1	2.235	0.0000	0.0000
Ranbp9	ENSMUSG00000038546	RAN binding protein 9	1.708	0.0060	0.0168
Rangrf	ENSMUSG00000032892	RAN guanine nucleotide release factor	1.902	0.0000	0.0000
Rap1a	ENSMUSG00000068798	RAS-related protein 1a	2.228	0.0000	0.0000
Rap1b	ENSMUSG00000052681	RAS related protein 1b	1.851	0.0000	0.0000
Rap2b	ENSMUSG00000036894	RAP2B, member of RAS oncogene family	2.328	0.0000	0.0000
Rars	ENSMUSG00000018848	arginyl-tRNA synthetase	1.518	0.0000	0.0000
Rasgef1a	ENSMUSG00000030134	RasGEF domain family, member 1A	1.882	0.0055	0.0157
Rasl10b	ENSMUSG00000020684	RAS-like, family 10, member B	2.111	0.0000	0.0000
Rassf10	ENSMUSG00000098132	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	1.893	0.0000	0.0000
Rassf3	ENSMUSG00000025795	Ras association (RalGDS/AF-6) domain family member 3	2.081	0.0000	0.0000
Rassf8	ENSMUSG00000030259	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	1.517	0.0000	0.0000
Rbm15b	ENSMUSG00000074102	RNA binding motif protein 15B	1.619	0.0000	0.0000
Rbm17	ENSMUSG00000037197	RNA binding motif protein 17	4.039	0.0000	0.0000
Rbm24	ENSMUSG00000038132	RNA binding motif protein 24	2.437	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rbm25	ENSMUSG00000010608	RNA binding motif protein 25	3.017	0.0000	0.0000
Rbm3	ENSMUSG00000031167	RNA binding motif (RNP1, RRM) protein 3	1.979	0.0000	0.0000
Rbm33	ENSMUSG00000048271	RNA binding motif protein 33	1.708	0.0017	0.0054
Rbm45	ENSMUSG00000042369	RNA binding motif protein 45	1.917	0.0000	0.0000
Rbm5	ENSMUSG00000032580	RNA binding motif protein 5	1.616	0.0000	0.0001
Rbm6	ENSMUSG00000032582	RNA binding motif protein 6	1.679	0.0000	0.0000
Rbm8a	ENSMUSG00000038374	RNA binding motif protein 8a	2.288	0.0000	0.0000
Rbp1	ENSMUSG00000046402	retinol binding protein 1, cellular	1.878	0.0000	0.0001
Rbpj-ps3	ENSMUSG00000079575	recombination signal binding protein for immunoglobulin kappa J region, pseudogene 3	1.980	0.0000	0.0000
Rbpms	ENSMUSG00000031586	RNA binding protein gene with multiple splicing	3.197	0.0000	0.0000
Rcan2	ENSMUSG00000039601	regulator of calcineurin 2	1.699	0.0000	0.0000
Rcc2	ENSMUSG00000040945	regulator of chromosome condensation 2	1.694	0.0000	0.0000
Rcn1	ENSMUSG00000005973	reticulocalbin 1	1.851	0.0000	0.0000
Rcn3	ENSMUSG00000019539	reticulocalbin 3, EF-hand calcium binding domain	1.622	0.0027	0.0084
Rcor2	ENSMUSG00000024968	REST corepressor 2	1.829	0.0000	0.0001
Rdh10	ENSMUSG00000025921	retinol dehydrogenase 10 (all-trans)	1.560	0.0000	0.0000
Rell1	ENSMUSG00000047881	RELT-like 1	1.722	0.0000	0.0000
Renbp	ENSMUSG00000031387	renin binding protein	2.424	0.0000	0.0000
Rest	ENSMUSG00000029249	RE1-silencing transcription factor	1.772	0.0000	0.0000
Rexo4	ENSMUSG00000052406	REX4, 3'-5' exonuclease	1.657	0.0000	0.0000
Rflnb	ENSMUSG00000020846	refilin B	1.961	0.0000	0.0000
Rfxap	ENSMUSG00000036615	regulatory factor X-associated protein	5.052	0.0000	0.0000
Rhbdl1	ENSMUSG00000025735	rhomboid like 1	14.849	0.0013	0.0044
Rhbdl3	ENSMUSG00000017692	rhomboid like 3	3.447	0.0000	0.0000
Rheb	ENSMUSG00000028945	Ras homolog enriched in brain	2.066	0.0000	0.0000
Rhoa	ENSMUSG00000007815	ras homolog family member A	1.885	0.0000	0.0000
Rhot2	ENSMUSG00000025733	ras homolog family member T2	1.894	0.0000	0.0000
Rhox5	ENSMUSG00000095180	reproductive homeobox 5	2.088	0.0004	0.0017
Ribc1	ENSMUSG00000025257	RIB43A domain with coiled-coils 1	2.623	0.0009	0.0032
Rida	ENSMUSG00000022323	reactive intermediate imine deaminase A homolog	1.789	0.0000	0.0000
Rilpl1	ENSMUSG00000029392	Rab interacting lysosomal protein-like 1	1.870	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rilpl2	ENSMUSG00000029401	Rab interacting lysosomal protein-like 2	1.694	0.0000	0.0000
Rims4	ENSMUSG00000035226	regulating synaptic membrane exocytosis 4	1.707	0.0110	0.0285
Ring1	ENSMUSG00000024325	ring finger protein 1	1.745	0.0017	0.0056
Ripk1	ENSMUSG00000021408	receptor (TNFRSF)-interacting serine-threonine kinase 1	1.507	0.0000	0.0001
Rnf10	ENSMUSG00000041740	ring finger protein 10	1.748	0.0013	0.0045
Rnf103	ENSMUSG00000052656	ring finger protein 103	2.344	0.0000	0.0000
Rnf11	ENSMUSG00000028557	ring finger protein 11	1.702	0.0000	0.0000
Rnf113a2	ENSMUSG00000098134	ring finger protein 113A2	2.405	0.0000	0.0000
Rnf125	ENSMUSG00000033107	ring finger protein 125	1.729	0.0011	0.0036
Rnf146	ENSMUSG00000038876	ring finger protein 146	1.640	0.0000	0.0000
Rnf149	ENSMUSG00000048234	ring finger protein 149	2.379	0.0000	0.0000
Rnf166	ENSMUSG00000014470	ring finger protein 166	1.693	0.0000	0.0000
Rnf19b	ENSMUSG00000028793	ring finger protein 19B	2.483	0.0000	0.0000
Rnf20	ENSMUSG00000028309	ring finger protein 20	1.820	0.0000	0.0000
Rnf214	ENSMUSG00000042790	ring finger protein 214	1.694	0.0000	0.0000
Rnf217	ENSMUSG00000063760	ring finger protein 217	1.624	0.0000	0.0000
Rnf220	ENSMUSG00000028677	ring finger protein 220	2.612	0.0000	0.0000
Rnf40	ENSMUSG00000030816	ring finger protein 40	1.521	0.0000	0.0000
Rnps1	ENSMUSG00000034681	RNA binding protein with serine rich domain 1	2.949	0.0000	0.0000
Robo1	ENSMUSG00000022883	roundabout guidance receptor 1	1.730	0.0042	0.0124
Robo2	ENSMUSG00000052516	roundabout guidance receptor 2	2.125	0.0021	0.0067
Rock1	ENSMUSG00000024290	Rho-associated coiled-coil containing protein kinase 1	1.857	0.0000	0.0000
Rock2	ENSMUSG00000020580	Rho-associated coiled-coil containing protein kinase 2	1.561	0.0000	0.0000
Rp9	ENSMUSG00000032239	retinitis pigmentosa 9 (human)	2.272	0.0000	0.0000
Rpain	ENSMUSG00000018449	RPA interacting protein	1.509	0.0001	0.0004
Rpia	ENSMUSG00000053604	ribose 5-phosphate isomerase A	1.707	0.0023	0.0074
Rpl11	ENSMUSG00000059291	ribosomal protein L11	2.809	0.0000	0.0000
Rpl14-ps1	ENSMUSG00000046721	ribosomal protein L14, pseudogene 1	1.588	0.0000	0.0001
Rpl15-ps6	ENSMUSG00000057262	ribosomal protein L15, pseudogene 6	6.326	0.0002	0.0010
Rpl30-ps11	ENSMUSG00000081461	ribosomal protein L30, pseudogene 11	3.829	0.0152	0.0379
Rpl5	ENSMUSG00000058558	ribosomal protein L5	2.219	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpl5-ps2	ENSMUSG00000082064	ribisomal protein L5, pseudogene 2	3.616	0.0000	0.0000
Rpl9	ENSMUSG00000047215	ribosomal protein L9	1.857	0.0000	0.0000
Rpl9-ps7	ENSMUSG00000047965	ribosomal protein L9, pseudogene 7	4.230	0.0000	0.0000
Rps12-ps4	ENSMUSG00000109509	ribosomal protein S12, pseudogene 4	5.876	0.0161	0.0398
Rps14	ENSMUSG00000024608	ribosomal protein S14	2.095	0.0000	0.0000
Rps15a-ps6	ENSMUSG00000083022	ribosomal protein S15A, pseudogene 6	2.737	0.0396	0.0853
Rps18	ENSMUSG00000008668	ribosomal protein S18	2.280	0.0000	0.0000
Rps2	ENSMUSG00000044533	ribosomal protein S2	1.992	0.0063	0.0175
Rps23-ps1	ENSMUSG00000100755	ribosomal protein S23, pseudogene 1	1.957	0.0018	0.0060
Rps2-ps10	ENSMUSG00000091957	ribosomal protein S2, pseudogene 10	4.730	0.0000	0.0000
Rps2-ps13	ENSMUSG00000081684	ribosomal protein S2, pseudogene 13	3.848	0.0020	0.0063
Rps2-ps8	ENSMUSG00000118161	ribosomal protein S2, pseudogene 8	2.903	0.0447	0.0941
Rps3	ENSMUSG00000030744	ribosomal protein S3	1.846	0.0000	0.0000
Rps6	ENSMUSG00000028495	ribosomal protein S6	1.556	0.0000	0.0000
Rps6kb1	ENSMUSG00000020516	ribosomal protein S6 kinase, polypeptide 1	1.657	0.0000	0.0000
Rps6-ps3	ENSMUSG00000082465	ribosomal protein S6, pseudogene 3	4.280	0.0233	0.0543
Rps6-ps4	ENSMUSG00000081406	ribosomal protein S6, pseudogene 4	2.797	0.0035	0.0106
Rras	ENSMUSG00000038387	related RAS viral (r-ras) oncogene	2.260	0.0000	0.0000
Rras2	ENSMUSG00000055723	related RAS viral (r-ras) oncogene 2	1.960	0.0000	0.0000
Rrbp1	ENSMUSG00000027422	ribosome binding protein 1	1.824	0.0000	0.0000
Rrp1	ENSMUSG00000061032	ribosomal RNA processing 1	2.393	0.0000	0.0000
Rrp15	ENSMUSG00000001305	ribosomal RNA processing 15 homolog	2.433	0.0000	0.0000
Rrp7a	ENSMUSG00000018040	ribosomal RNA processing 7 homolog A	1.586	0.0000	0.0000
Rrp9	ENSMUSG00000041506	ribosomal RNA processing 9, U3 small nucleolar RNA binding protein	2.210	0.0000	0.0000
Rsad2	ENSMUSG00000020641	radical S-adenosyl methionine domain containing 2	1.508	0.0000	0.0002
Rsf1	ENSMUSG00000035623	remodeling and spacing factor 1	1.521	0.0001	0.0005
Rsl24d1	ENSMUSG00000032215	ribosomal L24 domain containing 1	2.577	0.0000	0.0000
Rsph3a	ENSMUSG00000073471	radial spoke 3A homolog (Chlamydomonas)	1.637	0.0000	0.0000
Rsph3b	ENSMUSG00000023806	radial spoke 3B homolog (Chlamydomonas)	1.724	0.0014	0.0046
Rsrc2	ENSMUSG00000029422	arginine/serine-rich coiled-coil 2	1.809	0.0000	0.0000
Rsu1	ENSMUSG00000026727	Ras suppressor protein 1	1.504	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rtcb	ENSMUSG00000001783	RNA 2',3'-cyclic phosphate and 5'-OH ligase	1.937	0.0000	0.0000
Rtf2	ENSMUSG00000027502	replication termination factor 2	1.541	0.0000	0.0000
Rtn4	ENSMUSG00000020458	reticulon 4	2.148	0.0000	0.0000
Rtn4ip1	ENSMUSG00000019864	reticulon 4 interacting protein 1	1.997	0.0000	0.0000
Rtn4r	ENSMUSG00000043811	reticulon 4 receptor	3.138	0.0171	0.0417
Rtn4rl2	ENSMUSG00000050896	reticulon 4 receptor-like 2	2.342	0.0405	0.0869
Rufy1	ENSMUSG00000020375	RUN and FYVE domain containing 1	2.811	0.0000	0.0000
Rufy3	ENSMUSG00000029291	RUN and FYVE domain containing 3	1.563	0.0001	0.0005
Runx2	ENSMUSG00000039153	runt related transcription factor 2	1.800	0.0005	0.0019
Runx3	ENSMUSG00000070691	runt related transcription factor 3	2.080	0.0071	0.0194
Ruvbl1	ENSMUSG00000030079	RuvB-like protein 1	1.933	0.0000	0.0000
Rwdd3	ENSMUSG00000028133	RWD domain containing 3	1.532	0.0115	0.0296
Rwdd4a	ENSMUSG00000031568	RWD domain containing 4A	1.553	0.0000	0.0000
S1pr5	ENSMUSG00000045087	sphingosine-1-phosphate receptor 5	2.044	0.0002	0.0009
Safb	ENSMUSG00000071054	scaffold attachment factor B	2.313	0.0000	0.0000
Safb2	ENSMUSG00000042625	scaffold attachment factor B2	1.777	0.0000	0.0000
Sall4	ENSMUSG00000027547	spalt like transcription factor 4	1.728	0.0100	0.0264
Samd1	ENSMUSG00000079003	sterile alpha motif domain containing 1	3.265	0.0000	0.0000
Samd4	ENSMUSG00000021838	sterile alpha motif domain containing 4	1.531	0.0000	0.0000
Sap18	ENSMUSG00000021963	Sin3-associated polypeptide 18	1.694	0.0000	0.0000
Sap18b	ENSMUSG00000061104	Sin3-associated polypeptide 18B	3.846	0.0000	0.0000
Sap30	ENSMUSG00000031609	sin3 associated polypeptide	3.869	0.0000	0.0000
Sap30l	ENSMUSG00000020519	SAP30-like	10.074	0.0000	0.0000
Sarnp	ENSMUSG00000078427	SAP domain containing ribonucleoprotein	2.005	0.0000	0.0000
Sars	ENSMUSG00000068739	seryl-aminoacyl-tRNA synthetase	1.962	0.0000	0.0000
Sart1	ENSMUSG00000039148	squamous cell carcinoma antigen recognized by T cells 1	3.149	0.0000	0.0000
Sart3	ENSMUSG00000018974	squamous cell carcinoma antigen recognized by T cells 3	2.079	0.0000	0.0000
Satb1	ENSMUSG00000023927	special AT-rich sequence binding protein 1	1.753	0.0000	0.0000
Sbds	ENSMUSG00000025337	SBDS ribosome maturation factor	2.018	0.0000	0.0000
Sbk2	ENSMUSG00000030433	SH3-binding domain kinase family, member 2	2.289	0.0000	0.0000
Sbsn	ENSMUSG00000046056	suprabasin	2.307	0.0213	0.0504

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Scaf4	ENSMUSG00000022983	SR-related CTD-associated factor 4	1.972	0.0000	0.0000
Scamp1	ENSMUSG00000021687	secretory carrier membrane protein 1	1.548	0.0000	0.0000
Scand1	ENSMUSG00000046229	SCAN domain-containing 1	6.347	0.0000	0.0001
Scarf2	ENSMUSG00000012017	scavenger receptor class F, member 2	2.699	0.0000	0.0000
Schip1	ENSMUSG00000027777	schwannomin interacting protein 1	1.938	0.0000	0.0000
Scml4	ENSMUSG00000044770	Scm polycomb group protein like 4	1.936	0.0304	0.0682
Scn1b	ENSMUSG00000019194	sodium channel, voltage-gated, type I, beta	1.834	0.0000	0.0001
Scn2b	ENSMUSG00000070304	sodium channel, voltage-gated, type II, beta	2.345	0.0019	0.0060
Scx	ENSMUSG00000034161	scleraxis	5.703	0.0000	0.0000
Sdc4	ENSMUSG00000017009	syndecan 4	2.263	0.0000	0.0000
Sdccag8	ENSMUSG00000026504	serologically defined colon cancer antigen 8	1.678	0.0000	0.0000
Sdf2l1	ENSMUSG00000022769	stromal cell-derived factor 2-like 1	1.810	0.0031	0.0095
Sdha	ENSMUSG00000021577	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.573	0.0000	0.0000
Sdhaf1	ENSMUSG00000074211	succinate dehydrogenase complex assembly factor 1	2.172	0.0000	0.0000
Sdsl	ENSMUSG00000029596	serine dehydratase-like	1.689	0.0000	0.0000
Sec11a	ENSMUSG00000025724	SEC11 homolog A, signal peptidase complex subunit	1.689	0.0000	0.0000
Sec11c	ENSMUSG00000024516	SEC11 homolog C, signal peptidase complex subunit	1.550	0.0000	0.0000
Sec22c	ENSMUSG00000061536	SEC22 homolog C, vesicle trafficking protein	1.848	0.0000	0.0000
Sec62	ENSMUSG00000027706	SEC62 homolog (S. cerevisiae)	2.250	0.0000	0.0000
Sec63	ENSMUSG00000019802	SEC63-like (S. cerevisiae)	1.842	0.0000	0.0000
Secisbp2l	ENSMUSG00000035093	SECIS binding protein 2-like	1.857	0.0000	0.0000
Sem1	ENSMUSG00000042541	SEM1, 26S proteasome complex subunit	2.098	0.0000	0.0000
Sema6b	ENSMUSG00000001227	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	3.853	0.0000	0.0000
Sema6c	ENSMUSG00000038777	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	1.983	0.0018	0.0058
Septin10	ENSMUSG00000019917	septin 10	2.131	0.0000	0.0000
Septin3	ENSMUSG00000022456	septin 3	1.992	0.0036	0.0109
Septin7	ENSMUSG00000001833	septin 7	2.205	0.0000	0.0000
Serbp1	ENSMUSG00000036371	serpine1 mRNA binding protein 1	2.602	0.0000	0.0000
Serpinb1c	ENSMUSG00000079049	serine (or cysteine) peptidase inhibitor, clade B, member 1c	6.650	0.0059	0.0166
Sertad4	ENSMUSG00000016262	SERTA domain containing 4	1.680	0.0042	0.0124
Set	ENSMUSG00000054766	SET nuclear oncogene	3.109	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Setd1b	ENSMUSG00000038384	SET domain containing 1B	1.536	0.0001	0.0004
Setd3	ENSMUSG00000056770	SET domain containing 3	1.791	0.0000	0.0000
Setd6	ENSMUSG00000031671	SET domain containing 6	2.861	0.0000	0.0000
Sf3a1	ENSMUSG00000002129	splicing factor 3a, subunit 1	1.979	0.0000	0.0000
Sf3a3	ENSMUSG00000028902	splicing factor 3a, subunit 3	1.619	0.0000	0.0000
Sf3b2	ENSMUSG00000024853	splicing factor 3b, subunit 2	2.037	0.0000	0.0000
Sfpq	ENSMUSG00000028820	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	2.999	0.0000	0.0000
Sfr1	ENSMUSG00000025066	SWI5 dependent recombination repair 1	2.482	0.0000	0.0000
Sfrp5	ENSMUSG00000018822	secreted frizzled-related sequence protein 5	1.970	0.0157	0.0389
Sfswap	ENSMUSG00000029439	splicing factor SWAP	2.067	0.0000	0.0000
Sgpp1	ENSMUSG00000021054	sphingosine-1-phosphate phosphatase 1	1.602	0.0001	0.0005
Sh3bgr	ENSMUSG00000040666	SH3-binding domain glutamic acid-rich protein	2.006	0.0000	0.0000
Sh3gl3	ENSMUSG00000030638	SH3-domain GRB2-like 3	3.065	0.0000	0.0001
Sh3pxd2a	ENSMUSG00000053617	SH3 and PX domains 2A	1.577	0.0000	0.0000
Shank1	ENSMUSG00000038738	SH3 and multiple ankyrin repeat domains 1	1.763	0.0119	0.0307
Shc2	ENSMUSG00000020312	SHC (Src homology 2 domain containing) transforming protein 2	1.585	0.0014	0.0047
Shc3	ENSMUSG00000021448	src homology 2 domain-containing transforming protein C3	1.978	0.0113	0.0292
Shf	ENSMUSG00000033256	Src homology 2 domain containing F	2.922	0.0000	0.0000
Shisa2	ENSMUSG00000044461	shisa family member 2	1.751	0.0228	0.0535
Shisa4	ENSMUSG00000041889	shisa family member 4	1.822	0.0026	0.0082
Shoc2	ENSMUSG00000024976	Shoc2, leucine rich repeat scaffold protein	1.652	0.0000	0.0000
Shtn1	ENSMUSG00000041362	shootin 1	1.949	0.0000	0.0000
Siah1a	ENSMUSG00000036840	siah E3 ubiquitin protein ligase 1A	1.916	0.0000	0.0000
Siah2	ENSMUSG00000036432	siah E3 ubiquitin protein ligase 2	2.636	0.0000	0.0000
Siglece	ENSMUSG00000030474	sialic acid binding Ig-like lectin E	1.938	0.0163	0.0401
Sinhcaf	ENSMUSG00000039985	SIN3-HDAC complex associated factor	2.010	0.0008	0.0027
Six1	ENSMUSG00000051367	sine oculis-related homeobox 1	1.792	0.0344	0.0756
Skap2	ENSMUSG00000059182	src family associated phosphoprotein 2	1.853	0.0000	0.0000
Sla	ENSMUSG00000022372	src-like adaptor	1.885	0.0014	0.0046
Slbp	ENSMUSG00000004642	stem-loop binding protein	1.507	0.0001	0.0002
Slc12a2	ENSMUSG00000024597	solute carrier family 12, member 2	1.556	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc16a11	ENSMUSG00000040938	solute carrier family 16 (monocarboxylic acid transporters), member 11	3.357	0.0041	0.0122
Slc17a7	ENSMUSG00000070570	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	1.930	0.0000	0.0000
Slc22a3	ENSMUSG00000023828	solute carrier family 22 (organic cation transporter), member 3	1.559	0.0379	0.0822
Slc24a1	ENSMUSG00000034452	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	1.663	0.0260	0.0598
Slc24a3	ENSMUSG00000063873	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	1.756	0.0000	0.0000
Slc25a15	ENSMUSG00000031482	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	1.527	0.0000	0.0000
Slc25a38	ENSMUSG00000032519	solute carrier family 25, member 38	1.995	0.0000	0.0000
Slc28a2b	ENSMUSG00000079071	solute carrier family 28 member 2b	1.569	0.0002	0.0007
Slc35a2	ENSMUSG00000031156	solute carrier family 35 (UDP-galactose transporter), member A2	1.663	0.0000	0.0000
Slc35a3	ENSMUSG00000027957	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	1.795	0.0000	0.0000
Slc35d1	ENSMUSG00000028521	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	1.589	0.0000	0.0000
Slc38a1	ENSMUSG00000023169	solute carrier family 38, member 1	1.551	0.0212	0.0500
Slc49a4	ENSMUSG00000022848	solute carrier family 49 member 4	1.879	0.0000	0.0001
Slc4a1ap	ENSMUSG00000029141	solute carrier family 4 (anion exchanger), member 1, adaptor protein	2.040	0.0000	0.0000
Slc6a8	ENSMUSG00000019558	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	2.196	0.0000	0.0000
Slc8a2	ENSMUSG00000030376	solute carrier family 8 (sodium/calcium exchanger), member 2	1.558	0.0272	0.0621
Slco5a1	ENSMUSG00000025938	solute carrier organic anion transporter family, member 5A1	1.652	0.0000	0.0000
Slfn1	ENSMUSG00000078763	schlafen 1	2.886	0.0296	0.0668
Slk	ENSMUSG00000025060	STE20-like kinase	1.668	0.0000	0.0000
Slmap	ENSMUSG00000021870	sarcolemma associated protein	1.698	0.0000	0.0000
Sltm	ENSMUSG00000032212	SAFB-like, transcription modulator	1.884	0.0000	0.0001
Smad1	ENSMUSG00000031681	SMAD family member 1	1.706	0.0000	0.0000
Smad4	ENSMUSG00000024515	SMAD family member 4	1.982	0.0000	0.0000
Smad6	ENSMUSG00000036867	SMAD family member 6	2.847	0.0000	0.0000
Smad7	ENSMUSG00000025880	SMAD family member 7	3.717	0.0000	0.0000
Smagp	ENSMUSG00000053559	small cell adhesion glycoprotein	2.814	0.0000	0.0000
Smap1	ENSMUSG00000026155	small ArfGAP 1	1.629	0.0001	0.0003
Smap2	ENSMUSG00000032870	small ArfGAP 2	1.842	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Smarca2	ENSMUSG00000024921	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	2.623	0.0000	0.0000
Smarca4	ENSMUSG00000032187	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	1.541	0.0000	0.0000
Smarca5	ENSMUSG00000031715	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	1.784	0.0000	0.0000
Smarcc2	ENSMUSG00000025369	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	2.176	0.0000	0.0000
Smarcd3	ENSMUSG00000028949	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	4.032	0.0000	0.0000
Smarce1	ENSMUSG00000037935	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	1.686	0.0000	0.0000
Smc1a	ENSMUSG00000041133	structural maintenance of chromosomes 1A	1.991	0.0000	0.0000
Smc3	ENSMUSG00000024974	structural maintenance of chromosomes 3	2.061	0.0000	0.0000
Smc6	ENSMUSG00000020608	structural maintenance of chromosomes 6	1.759	0.0000	0.0000
Smco4	ENSMUSG00000058173	single-pass membrane protein with coiled-coil domains 4	2.436	0.0000	0.0000
Smim10l1	ENSMUSG00000072704	small integral membrane protein 10 like 1	1.759	0.0000	0.0000
Smim13	ENSMUSG00000091264	small integral membrane protein 13	1.510	0.0000	0.0001
Smim36	ENSMUSG00000110344	small integral membrane protein 36	1.513	0.0000	0.0000
Smndc1	ENSMUSG00000025024	survival motor neuron domain containing 1	1.914	0.0000	0.0000
Smox	ENSMUSG00000027333	spermine oxidase	1.512	0.0006	0.0021
Smtnl1	ENSMUSG00000027077	smoothelin-like 1	10.468	0.0002	0.0008
Snapc5	ENSMUSG00000032398	small nuclear RNA activating complex, polypeptide 5	1.761	0.0000	0.0000
Snca	ENSMUSG00000025889	synuclein, alpha	3.615	0.0001	0.0002
Sncg	ENSMUSG00000023064	synuclein, gamma	1.521	0.0000	0.0001
Snhg3	ENSMUSG00000085241	small nucleolar RNA host gene 3	2.160	0.0000	0.0000
Snhg4	ENSMUSG00000117869	small nucleolar RNA host gene 4	1.727	0.0049	0.0143
Snhg5	ENSMUSG00000097195	small nucleolar RNA host gene 5	1.814	0.0254	0.0585
Snhg8	ENSMUSG00000104960	small nucleolar RNA host gene 8	1.502	0.0029	0.0089
Snora73b	ENSMUSG00000065353	small nucleolar RNA, H/ACA box 73b	4.676	0.0000	0.0000
Snord55	ENSMUSG00000092680	small nucleolar RNA, C/D box 55	7.366	0.0084	0.0227
Snord73b	ENSMUSG00000064390	small nucleolar RNA, C/D box U73B	3.852	0.0455	0.0956
Snrnp27	ENSMUSG00000001158	small nuclear ribonucleoprotein 27 (U4/U6.U5)	2.037	0.0000	0.0000
Snrnp35	ENSMUSG00000029402	small nuclear ribonucleoprotein 35 (U11/U12)	1.830	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Snrnp48	ENSMUSG00000021431	small nuclear ribonucleoprotein 48 (U11/U12)	3.172	0.0000	0.0000
Snrnp70	ENSMUSG00000063511	small nuclear ribonucleoprotein 70 (U1)	1.863	0.0000	0.0000
Snrpd1	ENSMUSG00000002477	small nuclear ribonucleoprotein D1	1.546	0.0004	0.0014
Snw1	ENSMUSG00000021039	SNW domain containing 1	1.887	0.0000	0.0000
Snx12	ENSMUSG00000046032	sorting nexin 12	1.661	0.0000	0.0000
Snx2	ENSMUSG00000034484	sorting nexin 2	1.664	0.0000	0.0000
Snx7	ENSMUSG00000028007	sorting nexin 7	2.083	0.0000	0.0000
Snx9	ENSMUSG00000002365	sorting nexin 9	1.566	0.0000	0.0001
Sobp	ENSMUSG00000038248	sine oculis binding protein	2.258	0.0000	0.0000
Socs6	ENSMUSG00000056153	suppressor of cytokine signaling 6	1.651	0.0000	0.0000
Socs7	ENSMUSG00000038485	suppressor of cytokine signaling 7	2.125	0.0000	0.0000
Sost	ENSMUSG00000001494	sclerostin	3.303	0.0019	0.0060
Sox10	ENSMUSG00000033006	SRY (sex determining region Y)-box 10	2.410	0.0018	0.0060
Sox12	ENSMUSG00000051817	SRY (sex determining region Y)-box 12	5.623	0.0000	0.0000
Sox4	ENSMUSG00000076431	SRY (sex determining region Y)-box 4	2.531	0.0000	0.0000
Sp110	ENSMUSG00000070034	Sp110 nuclear body protein	2.078	0.0000	0.0001
Spa17	ENSMUSG00000001948	sperm autoantigenic protein 17	1.835	0.0001	0.0003
Spaca6	ENSMUSG00000080316	sperm acrosome associated 6	1.939	0.0199	0.0475
Spag6	ENSMUSG00000037708	sperm associated antigen 6	6.670	0.0224	0.0526
Spata48	ENSMUSG00000020191	spermatogenesis associated 48	3.963	0.0000	0.0000
Spata5	ENSMUSG00000027722	spermatogenesis associated 5	1.844	0.0000	0.0000
Spats2	ENSMUSG00000051934	spermatogenesis associated, serine-rich 2	1.521	0.0000	0.0001
Spcs2	ENSMUSG00000035227	signal peptidase complex subunit 2 homolog (S. cerevisiae)	2.098	0.0000	0.0000
Spg7	ENSMUSG00000000738	SPG7, paraplegin matrix AAA peptidase subunit	2.168	0.0000	0.0000
Spin2c	ENSMUSG00000046550	spindlin family, member 2C	4.264	0.0048	0.0140
Spindoc	ENSMUSG00000024970	spindlin interactor and repressor of chromatin binding	1.573	0.0001	0.0005
Spn	ENSMUSG00000051457	sialophorin	3.242	0.0000	0.0000
Spop	ENSMUSG00000057522	speckle-type BTB/POZ protein	2.301	0.0000	0.0000
Spopl	ENSMUSG00000026771	speckle-type BTB/POZ protein-like	1.880	0.0000	0.0000
Sppl3	ENSMUSG00000029550	signal peptide peptidase 3	1.855	0.0000	0.0000
Spred2	ENSMUSG00000045671	sprouty-related EVH1 domain containing 2	1.931	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Spred3	ENSMUSG00000037239	sprouty-related EVH1 domain containing 3	2.140	0.0256	0.0590
Spring1	ENSMUSG00000032840	SREBF pathway regulator in golgi 1	1.570	0.0000	0.0000
Spry1	ENSMUSG00000037211	sprouty RTK signaling antagonist 1	1.625	0.0003	0.0013
Spta1	ENSMUSG00000026532	spectrin alpha, erythrocytic 1	1.913	0.0000	0.0000
Srek1	ENSMUSG00000032621	splicing regulatory glutamine/lysine-rich protein 1	2.018	0.0000	0.0000
Srf	ENSMUSG00000015605	serum response factor	3.943	0.0000	0.0000
Srfbp1	ENSMUSG00000024528	serum response factor binding protein 1	1.817	0.0000	0.0000
Srgap3	ENSMUSG00000030257	SLIT-ROBO Rho GTPase activating protein 3	1.998	0.0017	0.0057
Srp14	ENSMUSG00000009549	signal recognition particle 14	1.867	0.0000	0.0000
Srp54a	ENSMUSG00000073079	signal recognition particle 54A	2.052	0.0000	0.0000
Srp54c	ENSMUSG00000079108	signal recognition particle 54C	2.602	0.0000	0.0000
Srrd	ENSMUSG00000029346	SRR1 domain containing	3.416	0.0000	0.0000
Srrm4	ENSMUSG00000063919	serine/arginine repetitive matrix 4	1.639	0.0000	0.0001
Srrt	ENSMUSG00000037364	serrate RNA effector molecule homolog (Arabidopsis)	2.726	0.0000	0.0000
Srsf1	ENSMUSG00000018379	serine and arginine-rich splicing factor 1	2.687	0.0000	0.0000
Srsf11	ENSMUSG00000055436	serine and arginine-rich splicing factor 11	2.013	0.0000	0.0000
Srsf2	ENSMUSG00000034120	serine and arginine-rich splicing factor 2	1.981	0.0000	0.0000
Srsf5	ENSMUSG00000021134	serine and arginine-rich splicing factor 5	2.186	0.0000	0.0000
Srsf9	ENSMUSG00000029538	serine and arginine-rich splicing factor 9	2.504	0.0000	0.0000
Ss18l1	ENSMUSG00000039086	SS18, nBAF chromatin remodeling complex subunit like 1	1.739	0.0000	0.0000
Ssb	ENSMUSG00000068882	Sjogren syndrome antigen B	1.986	0.0000	0.0000
Ssbp1	ENSMUSG00000029911	single-stranded DNA binding protein 1	2.494	0.0000	0.0000
Ssbp3	ENSMUSG00000061887	single-stranded DNA binding protein 3	2.369	0.0000	0.0000
Ssbp4	ENSMUSG00000070003	single stranded DNA binding protein 4	3.119	0.0000	0.0000
Ssc5d	ENSMUSG00000035279	scavenger receptor cysteine rich family, 5 domains	1.654	0.0051	0.0147
Ssrp1	ENSMUSG00000027067	structure specific recognition protein 1	1.681	0.0000	0.0000
Ssx2ip	ENSMUSG00000036825	synovial sarcoma, X 2 interacting protein	1.644	0.0000	0.0000
St13	ENSMUSG00000022403	suppression of tumorigenicity 13	1.767	0.0000	0.0000
St3gal5	ENSMUSG00000056091	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	2.284	0.0000	0.0000
Stard5	ENSMUSG00000046027	StAR-related lipid transfer (START) domain containing 5	1.749	0.0000	0.0002
Stbd1	ENSMUSG00000047963	starch binding domain 1	2.584	0.0007	0.0025

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Stc2	ENSMUSG00000020303	stanniocalcin 2	1.934	0.0000	0.0000
Stim2	ENSMUSG00000039156	stromal interaction molecule 2	2.069	0.0000	0.0000
Stk10	ENSMUSG00000020272	serine/threonine kinase 10	1.602	0.0001	0.0004
Stk11	ENSMUSG00000003068	serine/threonine kinase 11	1.775	0.0000	0.0000
Stk24	ENSMUSG00000063410	serine/threonine kinase 24	1.806	0.0000	0.0000
Stk32c	ENSMUSG00000015981	serine/threonine kinase 32C	1.538	0.0286	0.0649
Stk39	ENSMUSG00000027030	serine/threonine kinase 39	1.768	0.0000	0.0000
Stk40	ENSMUSG00000042608	serine/threonine kinase 40	1.833	0.0000	0.0000
Stmn1	ENSMUSG00000028832	stathmin 1	2.212	0.0000	0.0000
Strbp	ENSMUSG00000026915	spermatid perinuclear RNA binding protein	1.840	0.0000	0.0000
Strn3	ENSMUSG00000020954	striatin, calmodulin binding protein 3	3.119	0.0000	0.0000
Stt3b	ENSMUSG00000032437	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	2.339	0.0000	0.0000
Stx11	ENSMUSG00000039232	syntaxin 11	1.534	0.0242	0.0561
Stx1a	ENSMUSG00000007207	syntaxin 1A (brain)	1.692	0.0297	0.0669
Stx1b	ENSMUSG00000030806	syntaxin 1B	2.557	0.0003	0.0012
Stx4a	ENSMUSG00000030805	syntaxin 4A (placental)	1.702	0.0000	0.0000
Suds3	ENSMUSG00000066900	suppressor of defective silencing 3 homolog (S. cerevisiae)	2.788	0.0000	0.0000
Sumf1	ENSMUSG00000030101	sulfatase modifying factor 1	1.567	0.0000	0.0000
Sumo1	ENSMUSG00000026021	small ubiquitin-like modifier 1	2.312	0.0000	0.0000
Sun2	ENSMUSG00000042524	Sad1 and UNC84 domain containing 2	1.506	0.0076	0.0208
Suox	ENSMUSG00000049858	sulfite oxidase	2.007	0.0000	0.0000
Supt16	ENSMUSG00000035726	SPT16, facilitates chromatin remodeling subunit	1.766	0.0000	0.0000
Supt5	ENSMUSG00000003435	suppressor of Ty 5, DSIF elongation factor subunit	1.591	0.0000	0.0000
Supt6	ENSMUSG00000002052	SPT6, histone chaperone and transcription elongation factor	1.574	0.0000	0.0000
Suv39h2	ENSMUSG00000026646	suppressor of variegation 3-9 2	1.897	0.0072	0.0198
Suz12	ENSMUSG00000017548	SUZ12 polycomb repressive complex 2 subunit	1.512	0.0000	0.0000
Svbp	ENSMUSG00000028643	small vasohibin binding protein	1.722	0.0087	0.0232
Swap70	ENSMUSG00000031015	SWA-70 protein	1.845	0.0000	0.0000
Syf2	ENSMUSG00000028821	SYF2 homolog, RNA splicing factor (S. cerevisiae)	2.613	0.0000	0.0000
Sync	ENSMUSG00000001333	syncoilin	1.714	0.0000	0.0000
Synj2bp	ENSMUSG00000090935	synaptojanin 2 binding protein	1.550	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Synm	ENSMUSG00000030554	synemin, intermediate filament protein	1.719	0.0000	0.0000
Synpo2	ENSMUSG00000050315	synaptopodin 2	1.569	0.0000	0.0000
Syp	ENSMUSG00000031144	synaptophysin	3.404	0.0000	0.0000
Szrd1	ENSMUSG00000040842	SUZ RNA binding domain containing 1	1.502	0.0000	0.0000
Taf10	ENSMUSG00000043866	TATA-box binding protein associated factor 10	5.721	0.0000	0.0000
Taf12	ENSMUSG00000028899	TATA-box binding protein associated factor 12	1.758	0.0000	0.0000
Taf13	ENSMUSG00000048100	TATA-box binding protein associated factor 13	1.958	0.0000	0.0000
Taf15	ENSMUSG00000020680	TATA-box binding protein associated factor 15	4.053	0.0000	0.0000
Taf1a	ENSMUSG00000072258	TATA-box binding protein associated factor, RNA polymerase I, A	1.786	0.0000	0.0000
Taf3	ENSMUSG00000025782	TATA-box binding protein associated factor 3	2.238	0.0000	0.0000
Taf4	ENSMUSG00000039117	TATA-box binding protein associated factor 4	1.817	0.0000	0.0000
Taf5	ENSMUSG00000025049	TATA-box binding protein associated factor 5	3.104	0.0000	0.0000
Tagln	ENSMUSG00000032085	transgelin	1.917	0.0003	0.0011
Tamalin	ENSMUSG00000000531	trafficking regulator and scaffold protein tamalin	2.719	0.0000	0.0000
Taok3	ENSMUSG00000061288	TAO kinase 3	1.578	0.0002	0.0007
Tardbp	ENSMUSG00000041459	TAR DNA binding protein	1.653	0.0000	0.0000
Tbc1d12	ENSMUSG00000048720	TBC1D12: TBC1 domain family, member 12	1.766	0.0000	0.0000
Tbc1d20	ENSMUSG00000027465	TBC1 domain family, member 20	2.211	0.0000	0.0000
Tbcc	ENSMUSG00000036430	tubulin-specific chaperone C	2.634	0.0000	0.0000
Tbcel	ENSMUSG00000037287	tubulin folding cofactor E-like	2.277	0.0000	0.0000
Tbkbp1	ENSMUSG00000038517	TBK1 binding protein 1	1.717	0.0031	0.0094
Tbx1	ENSMUSG00000009097	T-box 1	2.402	0.0016	0.0054
Tbx15	ENSMUSG00000027868	T-box 15	2.236	0.0073	0.0198
Tbx2	ENSMUSG00000000093	T-box 2	2.996	0.0000	0.0000
Tbx3	ENSMUSG00000018604	T-box 3	1.991	0.0000	0.0000
Tcea1-ps1	ENSMUSG00000067869	transcription elongation factor A (SII) 1, pseudogene 1	2.092	0.0055	0.0157
Tceal1	ENSMUSG00000049536	transcription elongation factor A (SII)-like 1	1.765	0.0000	0.0002
Tceal3	ENSMUSG00000044550	transcription elongation factor A (SII)-like 3	7.220	0.0003	0.0013
Tceal9	ENSMUSG00000042712	transcription elongation factor A like 9	1.623	0.0000	0.0000
Tcerg1	ENSMUSG00000024498	transcription elongation regulator 1 (CA150)	1.972	0.0000	0.0000
Tcf15	ENSMUSG00000068079	transcription factor 15	3.840	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tcf3	ENSMUSG00000020167	transcription factor 3	1.580	0.0007	0.0025
Tcf7l1	ENSMUSG00000055799	transcription factor 7 like 1 (T cell specific, HMG box)	1.656	0.0000	0.0000
Tchp	ENSMUSG00000002486	trichoplein, keratin filament binding	2.764	0.0000	0.0000
Tcp11l1	ENSMUSG00000027175	t-complex 11 like 1	2.578	0.0000	0.0000
Tcte2	ENSMUSG00000038347	t-complex-associated testis expressed 2	2.275	0.0055	0.0155
Tdp2	ENSMUSG00000035958	tyrosyl-DNA phosphodiesterase 2	1.675	0.0000	0.0000
Tead2	ENSMUSG00000030796	TEA domain family member 2	1.773	0.0012	0.0041
Tead3	ENSMUSG00000002249	TEA domain family member 3	1.970	0.0000	0.0001
Tent4a	ENSMUSG00000034575	terminal nucleotidyltransferase 4A	2.008	0.0000	0.0000
Tent4b	ENSMUSG00000036779	terminal nucleotidyltransferase 4B	2.797	0.0000	0.0000
Terf1	ENSMUSG00000025925	telomeric repeat binding factor 1	2.508	0.0000	0.0000
Tesc	ENSMUSG00000029359	tescalcin	3.161	0.0000	0.0000
Tesk1	ENSMUSG00000028458	testis specific protein kinase 1	2.148	0.0000	0.0000
Tex9	ENSMUSG00000090626	testis expressed gene 9	2.018	0.0021	0.0067
Tfam	ENSMUSG00000003923	transcription factor A, mitochondrial	1.689	0.0000	0.0000
Tfap2a	ENSMUSG00000021359	transcription factor AP-2, alpha	4.015	0.0040	0.0119
Tfap2e	ENSMUSG00000042477	transcription factor AP-2, epsilon	8.652	0.0069	0.0190
Tfdp1	ENSMUSG00000038482	transcription factor Dp 1	2.215	0.0000	0.0000
Tfpt	ENSMUSG00000006335	TCF3 (E2A) fusion partner	2.557	0.0000	0.0000
Tgfb1	ENSMUSG00000002603	transforming growth factor, beta 1	2.165	0.0000	0.0000
Tgfb3	ENSMUSG00000021253	transforming growth factor, beta 3	1.751	0.0000	0.0001
Thap12	ENSMUSG00000030753	THAP domain containing 12	1.526	0.0000	0.0000
Thbs4	ENSMUSG00000021702	thrombospondin 4	2.282	0.0454	0.0955
Thg1l	ENSMUSG00000011254	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	1.999	0.0000	0.0000
Thoc2	ENSMUSG00000037475	THO complex 2	1.519	0.0000	0.0000
Thoc2l	ENSMUSG00000097392	THO complex subunit 2-like	1.959	0.0000	0.0000
Thra	ENSMUSG00000058756	thyroid hormone receptor alpha	2.186	0.0000	0.0000
Thumpd1	ENSMUSG00000030942	THUMP domain containing 1	3.095	0.0000	0.0000
Tigd5	ENSMUSG00000103906	tigger transposable element derived 5	1.552	0.0045	0.0132
Timd4	ENSMUSG00000055546	T cell immunoglobulin and mucin domain containing 4	1.811	0.0423	0.0901
Timeless	ENSMUSG00000039994	timeless circadian clock 1	2.513	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Timm10	ENSMUSG00000027076	translocase of inner mitochondrial membrane 10	2.008	0.0000	0.0000
Timm29	ENSMUSG00000048429	translocase of inner mitochondrial membrane 29	2.018	0.0000	0.0000
Timm44	ENSMUSG00000002949	translocase of inner mitochondrial membrane 44	1.945	0.0000	0.0000
Timm8b	ENSMUSG00000039016	translocase of inner mitochondrial membrane 8B	1.657	0.0000	0.0000
Timmdc1	ENSMUSG00000002846	translocase of inner mitochondrial membrane domain containing 1	1.745	0.0000	0.0000
Timp2	ENSMUSG00000017466	tissue inhibitor of metalloproteinase 2	1.780	0.0000	0.0000
Tle1	ENSMUSG00000008305	transducin-like enhancer of split 1	2.306	0.0000	0.0000
Tle5	ENSMUSG00000054452	TLE family member 5, transcriptional modulator	3.920	0.0000	0.0000
Tlk2	ENSMUSG00000020694	tousled-like kinase 2 (Arabidopsis)	1.727	0.0000	0.0000
Tm6sf1	ENSMUSG00000038623	transmembrane 6 superfamily member 1	2.477	0.0000	0.0000
Tm9sf3	ENSMUSG00000025016	transmembrane 9 superfamily member 3	1.939	0.0000	0.0000
Tma7	ENSMUSG00000091537	translational machinery associated 7	1.516	0.0000	0.0000
Tma7-ps	ENSMUSG00000059058	translational machinery associated 7 homolog (S. cerevisiae), pseudogene	2.908	0.0000	0.0000
Tmbim6	ENSMUSG00000023010	transmembrane BAX inhibitor motif containing 6	1.590	0.0000	0.0000
Tmc7	ENSMUSG00000042246	transmembrane channel-like gene family 7	1.545	0.0000	0.0002
Tmco6	ENSMUSG00000006850	transmembrane and coiled-coil domains 6	1.706	0.0007	0.0025
Tmed9	ENSMUSG00000058569	transmembrane p24 trafficking protein 9	1.663	0.0000	0.0000
Tmem101	ENSMUSG00000020921	transmembrane protein 101	3.932	0.0000	0.0000
Tmem127	ENSMUSG00000034850	transmembrane protein 127	1.843	0.0000	0.0000
Tmem150a	ENSMUSG00000055912	transmembrane protein 150A	2.382	0.0000	0.0000
Tmem158	ENSMUSG00000054871	transmembrane protein 158	4.780	0.0000	0.0000
Tmem160	ENSMUSG00000019158	transmembrane protein 160	4.627	0.0000	0.0000
Tmem164	ENSMUSG00000047045	transmembrane protein 164	1.691	0.0007	0.0026
Tmem165	ENSMUSG00000029234	transmembrane protein 165	2.693	0.0000	0.0000
Tmem179	ENSMUSG00000054013	transmembrane protein 179	2.073	0.0222	0.0521
Tmem181b-ps	ENSMUSG00000096780	transmembrane protein 181B, pseudogene	12.338	0.0000	0.0002
Tmem192	ENSMUSG00000025521	transmembrane protein 192	2.153	0.0000	0.0000
Tmem196	ENSMUSG00000048004	transmembrane protein 196	2.028	0.0001	0.0006
Tmem200b	ENSMUSG00000070720	transmembrane protein 200B	1.868	0.0247	0.0571
Tmem240	ENSMUSG00000084845	transmembrane protein 240	2.216	0.0202	0.0480
Tmem243	ENSMUSG00000079659	transmembrane protein 243, mitochondrial	2.004	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem248	ENSMUSG00000053094	transmembrane protein 248	1.655	0.0000	0.0000
Tmem251	ENSMUSG00000046675	transmembrane protein 251	1.922	0.0000	0.0000
Tmem259	ENSMUSG00000013858	transmembrane protein 259	1.771	0.0003	0.0011
Tmem38b	ENSMUSG00000028420	transmembrane protein 38B	1.729	0.0009	0.0033
Tmem51os1	ENSMUSG00000073728	Tmem51 opposite strand 1	2.238	0.0041	0.0123
Tmem64	ENSMUSG00000043252	transmembrane protein 64	1.536	0.0000	0.0000
Tmem65	ENSMUSG00000062373	transmembrane protein 65	2.070	0.0000	0.0000
Tmf1	ENSMUSG00000030059	TATA element modulatory factor 1	1.538	0.0001	0.0005
Tmpo	ENSMUSG00000019961	thymopoietin	1.563	0.0000	0.0000
Tmx1	ENSMUSG00000021072	thioredoxin-related transmembrane protein 1	1.642	0.0000	0.0000
Tnfrsf11a	ENSMUSG00000026321	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	1.990	0.0015	0.0049
Tnip2	ENSMUSG00000059866	TNFAIP3 interacting protein 2	2.350	0.0000	0.0000
Tnks1bp1	ENSMUSG00000033955	tankyrase 1 binding protein 1	1.647	0.0000	0.0000
Tnnc1	ENSMUSG00000091898	troponin C, cardiac/slow skeletal	2.369	0.0000	0.0000
Tnni3	ENSMUSG00000035458	troponin I, cardiac 3	1.639	0.0000	0.0000
Tnnt1	ENSMUSG00000064179	troponin T1, skeletal, slow	1.529	0.0001	0.0004
Tnnt2	ENSMUSG00000026414	troponin T2, cardiac	4.134	0.0000	0.0000
Tnnt3	ENSMUSG00000061723	troponin T3, skeletal, fast	2.748	0.0068	0.0188
Tnrc18	ENSMUSG00000039477	trinucleotide repeat containing 18	1.719	0.0000	0.0000
Tnrc6c	ENSMUSG00000025571	trinucleotide repeat containing 6C	2.335	0.0000	0.0000
Tom1l1	ENSMUSG00000020541	target of myb1-like 1 (chicken)	1.545	0.0000	0.0000
Tomm70a	ENSMUSG00000022752	translocase of outer mitochondrial membrane 70A	1.574	0.0000	0.0000
Top1	ENSMUSG00000070544	topoisomerase (DNA) I	2.055	0.0000	0.0000
Tox2	ENSMUSG00000074607	TOX high mobility group box family member 2	2.643	0.0000	0.0000
Tox3	ENSMUSG00000043668	TOX high mobility group box family member 3	1.767	0.0000	0.0001
Tpbg	ENSMUSG00000035274	trophoblast glycoprotein	2.570	0.0007	0.0026
Tpm1	ENSMUSG00000032366	tropomyosin 1, alpha	1.696	0.0000	0.0000
Tpm2	ENSMUSG00000028464	tropomyosin 2, beta	1.864	0.0000	0.0000
Tpm3	ENSMUSG00000027940	tropomyosin 3, gamma	2.411	0.0000	0.0000
Tpm3-rs7	ENSMUSG00000058126	tropomyosin 3, related sequence 7	4.861	0.0000	0.0000
Tpm4	ENSMUSG00000031799	tropomyosin 4	1.504	0.0007	0.0026

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tpr	ENSMUSG00000006005	translocated promoter region, nuclear basket protein	1.706	0.0000	0.0000
Tpt1	ENSMUSG00000060126	tumor protein, translationally-controlled 1	1.844	0.0000	0.0000
Traf3ip1	ENSMUSG00000034292	TRAF3 interacting protein 1	2.765	0.0000	0.0000
Trak1	ENSMUSG00000032536	trafficking protein, kinesin binding 1	1.551	0.0000	0.0000
Trappc3	ENSMUSG00000028847	trafficking protein particle complex 3	2.019	0.0000	0.0000
Trappc6b	ENSMUSG00000020993	trafficking protein particle complex 6B	2.980	0.0000	0.0000
Trim21	ENSMUSG00000030966	tripartite motif-containing 21	1.912	0.0000	0.0000
Trim27	ENSMUSG00000021326	tripartite motif-containing 27	1.972	0.0000	0.0000
Trim44	ENSMUSG00000027189	tripartite motif-containing 44	1.620	0.0000	0.0000
Trim45	ENSMUSG00000033233	tripartite motif-containing 45	1.725	0.0001	0.0002
Trim54	ENSMUSG00000062077	tripartite motif-containing 54	1.772	0.0000	0.0001
Trim68	ENSMUSG00000073968	tripartite motif-containing 68	1.504	0.0000	0.0000
Trim72	ENSMUSG00000042828	tripartite motif-containing 72	2.685	0.0000	0.0000
Trim8	ENSMUSG00000025034	tripartite motif-containing 8	3.317	0.0000	0.0000
Triobp	ENSMUSG00000033088	TRIO and F-actin binding protein	1.635	0.0000	0.0000
Trip10	ENSMUSG00000019487	thyroid hormone receptor interactor 10	1.563	0.0007	0.0025
Trip13	ENSMUSG00000021569	thyroid hormone receptor interactor 13	2.296	0.0062	0.0173
Trir	ENSMUSG00000041203	telomerase RNA component interacting RNase	13.891	0.0000	0.0000
Trmt10a	ENSMUSG00000004127	tRNA methyltransferase 10A	1.898	0.0000	0.0000
Trmt6	ENSMUSG00000037376	tRNA methyltransferase 6	1.565	0.0000	0.0000
Trnp1	ENSMUSG00000056596	TMF1-regulated nuclear protein 1	3.235	0.0020	0.0065
Trp53bp2	ENSMUSG00000026510	transformation related protein 53 binding protein 2	1.938	0.0000	0.0000
Trp53rkb	ENSMUSG00000042854	transformation related protein 53 regulating kinase B	2.052	0.0000	0.0000
Trub1	ENSMUSG00000025086	TruB pseudouridine (psi) synthase family member 1	2.185	0.0000	0.0000
Tsc22d2	ENSMUSG00000027806	TSC22 domain family, member 2	1.956	0.0000	0.0000
Tsen34	ENSMUSG00000035585	tRNA splicing endonuclease subunit 34	2.900	0.0000	0.0000
Tslp	ENSMUSG00000024379	thymic stromal lymphopoietin	2.914	0.0000	0.0000
Tsnax	ENSMUSG00000056820	translin-associated factor X	1.752	0.0000	0.0000
Tspan17	ENSMUSG00000025875	tetraspanin 17	3.125	0.0000	0.0000
Tspan33	ENSMUSG00000001763	tetraspanin 33	1.502	0.0159	0.0393
Tspan5	ENSMUSG00000028152	tetraspanin 5	2.313	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tspyl2	ENSMUSG00000041096	TSPY-like 2	2.337	0.0000	0.0000
Tsr2	ENSMUSG00000025264	TSR2 20S rRNA accumulation	1.693	0.0000	0.0000
Tstd3	ENSMUSG00000028251	thiosulfate sulfurtransferase (rhodanese)-like domain containing 3	1.556	0.0001	0.0002
Ttc1	ENSMUSG00000041278	tetratricopeptide repeat domain 1	1.679	0.0000	0.0000
Ttc39aos1	ENSMUSG00000085873	Ttc39a opposite strand RNA 1	2.272	0.0155	0.0385
Ttc39c	ENSMUSG00000024424	tetratricopeptide repeat domain 39C	1.563	0.0006	0.0023
Ttc5	ENSMUSG00000006288	tetratricopeptide repeat domain 5	1.557	0.0000	0.0000
Ttc9	ENSMUSG00000042734	tetratricopeptide repeat domain 9	2.329	0.0005	0.0017
Ttll11	ENSMUSG00000026885	tubulin tyrosine ligase-like family, member 11	2.860	0.0000	0.0000
Ttyh1	ENSMUSG00000030428	tweety family member 1	2.358	0.0332	0.0734
Tuba1a	ENSMUSG00000072235	tubulin, alpha 1A	1.644	0.0072	0.0196
Tuba1b	ENSMUSG00000023004	tubulin, alpha 1B	1.682	0.0076	0.0208
Tubb2a	ENSMUSG00000058672	tubulin, beta 2A class IIA	1.681	0.0000	0.0001
Tubb4b-ps1	ENSMUSG00000095159	tubulin, beta 4B class IVB, pseudogene 1	19.289	0.0000	0.0000
Tusc1	ENSMUSG00000054000	tumor suppressor candidate 1	4.873	0.0000	0.0000
Tut7	ENSMUSG00000035248	terminal uridylyl transferase 7	1.659	0.0000	0.0000
Tvp23b	ENSMUSG00000014177	trans-golgi network vesicle protein 23B	1.730	0.0000	0.0000
Twist1	ENSMUSG00000035799	twist basic helix-loop-helix transcription factor 1	3.708	0.0000	0.0000
Twist2	ENSMUSG00000007805	twist basic helix-loop-helix transcription factor 2	4.247	0.0000	0.0001
Txnrd1	ENSMUSG00000020250	thioredoxin reductase 1	1.547	0.0033	0.0100
U2af1	ENSMUSG00000061613	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	1.695	0.0000	0.0000
U2surp	ENSMUSG00000032407	U2 snRNP-associated SURP domain containing	1.621	0.0000	0.0000
Uaca	ENSMUSG00000034485	uveal autoantigen with coiled-coil domains and ankyrin repeats	1.590	0.0000	0.0000
Uba3	ENSMUSG00000030061	ubiquitin-like modifier activating enzyme 3	1.812	0.0000	0.0000
Uba5	ENSMUSG00000032557	ubiquitin-like modifier activating enzyme 5	1.635	0.0000	0.0000
Uba52	ENSMUSG00000090137	ubiquitin A-52 residue ribosomal protein fusion product 1	14.280	0.0000	0.0000
Ube2d3	ENSMUSG00000078578	ubiquitin-conjugating enzyme E2D 3	1.879	0.0000	0.0000
Ube2e2	ENSMUSG00000058317	ubiquitin-conjugating enzyme E2E 2	1.676	0.0000	0.0000
Ube2g2	ENSMUSG00000009293	ubiquitin-conjugating enzyme E2G 2	1.984	0.0000	0.0000
Ube2h	ENSMUSG00000039159	ubiquitin-conjugating enzyme E2H	3.120	0.0000	0.0000
Ube2j2	ENSMUSG00000023286	ubiquitin-conjugating enzyme E2J 2	2.208	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ube2k	ENSMUSG00000029203	ubiquitin-conjugating enzyme E2K	1.804	0.0000	0.0000
Ube2m	ENSMUSG00000005575	ubiquitin-conjugating enzyme E2M	3.185	0.0000	0.0000
Ube2q1	ENSMUSG00000042572	ubiquitin-conjugating enzyme E2Q family member 1	3.404	0.0000	0.0000
Ube2q2	ENSMUSG00000032307	ubiquitin-conjugating enzyme E2Q family member 2	1.790	0.0000	0.0000
Ube2r2	ENSMUSG00000036241	ubiquitin-conjugating enzyme E2R 2	4.190	0.0000	0.0000
Ube2s	ENSMUSG00000060860	ubiquitin-conjugating enzyme E2S	7.399	0.0000	0.0000
Ube2v2	ENSMUSG00000022674	ubiquitin-conjugating enzyme E2 variant 2	1.690	0.0006	0.0020
Ubfd1	ENSMUSG00000030870	ubiquitin family domain containing 1	1.703	0.0002	0.0007
Ubtd2	ENSMUSG00000044949	ubiquitin domain containing 2	2.264	0.0000	0.0000
Ubtf	ENSMUSG00000020923	upstream binding transcription factor, RNA polymerase I	2.665	0.0000	0.0000
Ubxn1	ENSMUSG00000071655	UBX domain protein 1	2.522	0.0000	0.0000
Uck2	ENSMUSG00000026558	uridine-cytidine kinase 2	1.534	0.0065	0.0180
Ugcg	ENSMUSG00000028381	UDP-glucose ceramide glucosyltransferase	1.689	0.0000	0.0000
Ugt1a7c	ENSMUSG00000090124	UDP glucuronosyltransferase 1 family, polypeptide A7C	2.685	0.0008	0.0029
Uhrf2	ENSMUSG00000024817	ubiquitin-like, containing PHD and RING finger domains 2	1.594	0.0011	0.0036
Uimc1	ENSMUSG00000025878	ubiquitin interaction motif containing 1	2.465	0.0000	0.0000
Unc119	ENSMUSG00000002058	unc-119 lipid binding chaperone	3.776	0.0000	0.0000
Upf1	ENSMUSG00000058301	UPF1 regulator of nonsense transcripts homolog (yeast)	2.141	0.0000	0.0000
Upf2	ENSMUSG00000043241	UPF2 regulator of nonsense transcripts homolog (yeast)	2.158	0.0000	0.0000
Upf3a	ENSMUSG00000038398	UPF3 regulator of nonsense transcripts homolog A (yeast)	3.360	0.0000	0.0000
Upf3b	ENSMUSG00000036572	UPF3 regulator of nonsense transcripts homolog B (yeast)	2.254	0.0000	0.0000
Upp2	ENSMUSG00000026839	uridine phosphorylase 2	6.343	0.0000	0.0000
Uqcrb	ENSMUSG00000021520	ubiquinol-cytochrome c reductase binding protein	2.075	0.0000	0.0000
Urm1	ENSMUSG00000069020	ubiquitin related modifier 1	1.766	0.0000	0.0000
Usb1	ENSMUSG00000031792	U6 snRNA biogenesis 1	1.515	0.0000	0.0000
Usf2	ENSMUSG00000058239	upstream transcription factor 2	1.946	0.0000	0.0001
Ush1c	ENSMUSG00000030838	USH1 protein network component harmonin	1.824	0.0053	0.0152
Usp1	ENSMUSG00000028560	ubiquitin specific peptidase 1	1.611	0.0000	0.0001
Usp12	ENSMUSG00000029640	ubiquitin specific peptidase 12	1.603	0.0000	0.0000
Usp2	ENSMUSG00000032010	ubiquitin specific peptidase 2	1.743	0.0011	0.0038
Usp27x	ENSMUSG00000046269	ubiquitin specific peptidase 27, X chromosome	2.548	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Usp31	ENSMUSG00000063317	ubiquitin specific peptidase 31	1.558	0.0000	0.0000
Utp14b	ENSMUSG00000079470	UTP14B small subunit processome component	2.804	0.0000	0.0001
Utp18	ENSMUSG00000054079	UTP18 small subunit processome component	3.322	0.0000	0.0000
Utp3	ENSMUSG00000070697	UTP3 small subunit processome component	2.930	0.0000	0.0000
Vamp1	ENSMUSG00000030337	vesicle-associated membrane protein 1	1.692	0.0000	0.0000
Vamp2	ENSMUSG00000020894	vesicle-associated membrane protein 2	2.047	0.0000	0.0000
Vamp8	ENSMUSG00000050732	vesicle-associated membrane protein 8	3.076	0.0000	0.0000
Vangl2	ENSMUSG00000026556	VANGL planar cell polarity 2	1.570	0.0001	0.0003
Vapb	ENSMUSG00000054455	vesicle-associated membrane protein, associated protein B and C	2.360	0.0000	0.0000
Vcp	ENSMUSG00000028452	valosin containing protein	1.957	0.0000	0.0000
Vdac1	ENSMUSG00000020402	voltage-dependent anion channel 1	1.731	0.0000	0.0000
Vdac3-ps1	ENSMUSG00000075053	voltage-dependent anion channel 3, pseudogene 1	3.213	0.0000	0.0000
Vegfa	ENSMUSG00000023951	vascular endothelial growth factor A	1.852	0.0004	0.0014
Vegfb	ENSMUSG00000024962	vascular endothelial growth factor B	2.044	0.0000	0.0000
Vil1	ENSMUSG00000026175	villin 1	1.845	0.0331	0.0731
Vopp1	ENSMUSG00000037788	vesicular, overexpressed in cancer, prosurvival protein 1	1.641	0.0000	0.0001
Vps37d	ENSMUSG00000043614	vacuolar protein sorting 37D	1.776	0.0151	0.0376
Vps72	ENSMUSG00000008958	vacuolar protein sorting 72	1.559	0.0000	0.0000
Vstm2b	ENSMUSG00000039257	V-set and transmembrane domain containing 2B	4.233	0.0055	0.0156
Vwc2	ENSMUSG00000050830	von Willebrand factor C domain containing 2	3.323	0.0000	0.0000
Wapl	ENSMUSG00000041408	WAPL cohesin release factor	1.729	0.0000	0.0000
Wasf3	ENSMUSG00000029636	WASP family, member 3	1.857	0.0002	0.0009
Wbp11	ENSMUSG00000030216	WW domain binding protein 11	1.662	0.0000	0.0000
Wbp4	ENSMUSG00000022023	WW domain binding protein 4	1.662	0.0000	0.0000
Wdr26	ENSMUSG00000038733	WD repeat domain 26	1.628	0.0003	0.0012
Wdr43	ENSMUSG00000041057	WD repeat domain 43	1.738	0.0000	0.0000
Whamm	ENSMUSG00000045795	WAS protein homolog associated with actin, golgi membranes and microtubules	1.539	0.0311	0.0694
Whrn	ENSMUSG00000039137	whirlin	1.680	0.0044	0.0128
Wnt5a	ENSMUSG00000021994	wingless-type MMTV integration site family, member 5A	1.942	0.0000	0.0002
Wnt5b	ENSMUSG00000030170	wingless-type MMTV integration site family, member 5B	1.775	0.0046	0.0134
Wnt9a	ENSMUSG00000000126	wingless-type MMTV integration site family, member 9A	1.565	0.0002	0.0008

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Wsb1	ENSMUSG00000017677	WD repeat and SOCS box-containing 1	1.616	0.0000	0.0001
Wtap	ENSMUSG00000060475	WT1 associating protein	2.974	0.0000	0.0000
Wtip	ENSMUSG00000036459	WT1 interacting protein	2.940	0.0000	0.0000
Xirp2	ENSMUSG00000027022	xin actin-binding repeat containing 2	1.642	0.0022	0.0069
Xkr6	ENSMUSG00000035067	X-linked Kx blood group related 6	2.047	0.0003	0.0011
Xkr8	ENSMUSG00000037752	X-linked Kx blood group related 8	1.877	0.0000	0.0000
Xndc1	ENSMUSG00000099481	Xrcc1 N-terminal domain containing 1	2.242	0.0007	0.0024
Xpa	ENSMUSG00000028329	xeroderma pigmentosum, complementation group A	2.632	0.0000	0.0000
Ybx1	ENSMUSG00000028639	Y box protein 1	4.452	0.0000	0.0000
Ybx2	ENSMUSG00000018554	Y box protein 2	2.319	0.0000	0.0002
Ybx3	ENSMUSG00000030189	Y box protein 3	4.168	0.0000	0.0000
Yeats4	ENSMUSG00000020171	YEATS domain containing 4	1.588	0.0002	0.0007
Ykt6	ENSMUSG00000002741	YKT6 v-SNARE homolog (S. cerevisiae)	1.732	0.0000	0.0000
Ylpm1	ENSMUSG00000021244	YLP motif containing 1	1.623	0.0000	0.0000
Ypel3	ENSMUSG00000042675	yippee like 3	4.769	0.0000	0.0000
Ythdc1	ENSMUSG00000035851	YTH domain containing 1	2.120	0.0000	0.0000
Ythdf1	ENSMUSG00000038848	YTH N6-methyladenosine RNA binding protein 1	1.906	0.0000	0.0000
Ywhae	ENSMUSG00000020849	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2.641	0.0000	0.0000
Ywhah	ENSMUSG00000018965	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	2.703	0.0000	0.0000
Ywhaz	ENSMUSG00000022285	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	2.077	0.0000	0.0000
Yy1	ENSMUSG00000021264	YY1 transcription factor	2.420	0.0000	0.0000
Zbtb11os1	ENSMUSG00000102101	zinc finger and BTB domain containing 11, opposite strand 1	3.046	0.0000	0.0000
Zbtb12	ENSMUSG00000049823	zinc finger and BTB domain containing 12	1.912	0.0000	0.0000
Zbtb18	ENSMUSG00000063659	zinc finger and BTB domain containing 18	1.543	0.0000	0.0000
Zbtb42	ENSMUSG00000037638	zinc finger and BTB domain containing 42	1.719	0.0000	0.0000
Zbtb44	ENSMUSG00000047412	zinc finger and BTB domain containing 44	1.578	0.0002	0.0010
Zbtb7a	ENSMUSG00000035011	zinc finger and BTB domain containing 7a	2.316	0.0000	0.0000
Zbtb7c	ENSMUSG00000044646	zinc finger and BTB domain containing 7C	1.810	0.0028	0.0086
Zc3h12d	ENSMUSG00000039981	zinc finger CCCH type containing 12D	2.843	0.0014	0.0047

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zc3h13	ENSMUSG00000022000	zinc finger CCCH type containing 13	2.226	0.0000	0.0000
Zc3h15	ENSMUSG00000027091	zinc finger CCCH-type containing 15	2.287	0.0000	0.0000
Zc3h18	ENSMUSG00000017478	zinc finger CCCH-type containing 18	1.755	0.0000	0.0000
Zc3h6	ENSMUSG00000042851	zinc finger CCCH type containing 6	1.715	0.0001	0.0005
Zcchc10	ENSMUSG00000018239	zinc finger, CCHC domain containing 10	1.787	0.0003	0.0013
Zcchc17	ENSMUSG00000028772	zinc finger, CCHC domain containing 17	1.834	0.0000	0.0000
Zcchc2	ENSMUSG00000038866	zinc finger, CCHC domain containing 2	1.712	0.0000	0.0000
Zcchc3	ENSMUSG00000074682	zinc finger, CCHC domain containing 3	1.621	0.0059	0.0167
Zcrb1	ENSMUSG00000022635	zinc finger CCHC-type and RNA binding motif 1	2.657	0.0000	0.0000
Zdhhc14	ENSMUSG00000034265	zinc finger, DHHC domain containing 14	1.659	0.0003	0.0012
Zdhhc2	ENSMUSG00000039470	zinc finger, DHHC domain containing 2	1.847	0.0000	0.0001
Zeb2os	ENSMUSG00000052248	zinc finger E-box binding homeobox 2, opposite strand	3.784	0.0000	0.0000
Zfas1	ENSMUSG00000074578	zinc finger, NFX1-type containing 1, antisense RNA 1	3.351	0.0000	0.0000
Zfhx3	ENSMUSG00000038872	zinc finger homeobox 3	1.558	0.0000	0.0000
Zfp207	ENSMUSG00000017421	zinc finger protein 207	2.097	0.0000	0.0000
Zfp251	ENSMUSG00000022526	zinc finger protein 251	1.604	0.0000	0.0000
Zfp316	ENSMUSG00000046658	zinc finger protein 316	1.643	0.0000	0.0000
Zfp330	ENSMUSG00000031711	zinc finger protein 330	2.498	0.0000	0.0000
Zfp335os	ENSMUSG00000085436	zinc finger protein 335, opposite strand	3.073	0.0000	0.0000
Zfp362	ENSMUSG00000028799	zinc finger protein 362	2.110	0.0000	0.0000
Zfp369	ENSMUSG00000021514	zinc finger protein 369	1.612	0.0000	0.0000
Zfp36l2	ENSMUSG00000045817	zinc finger protein 36, C3H type-like 2	2.073	0.0000	0.0002
Zfp385a	ENSMUSG00000000552	zinc finger protein 385A	1.595	0.0001	0.0006
Zfp385c	ENSMUSG00000014198	zinc finger protein 385C	2.279	0.0243	0.0563
Zfp451	ENSMUSG00000042197	zinc finger protein 451	1.513	0.0000	0.0000
Zfp462	ENSMUSG00000060206	zinc finger protein 462	1.518	0.0001	0.0004
Zfp513	ENSMUSG00000043059	zinc finger protein 513	2.651	0.0000	0.0000
Zfp593	ENSMUSG00000028840	zinc finger protein 593	2.724	0.0005	0.0019
Zfp622	ENSMUSG00000052253	zinc finger protein 622	3.705	0.0000	0.0000
Zfp628	ENSMUSG00000074406	zinc finger protein 628	1.649	0.0045	0.0132
Zfp667	ENSMUSG00000054893	zinc finger protein 667	1.674	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp697	ENSMUSG00000050064	zinc finger protein 697	1.577	0.0129	0.0328
Zfp703	ENSMUSG00000085795	zinc finger protein 703	1.560	0.0279	0.0636
Zfp710	ENSMUSG00000048897	zinc finger protein 710	1.621	0.0000	0.0000
Zfp740	ENSMUSG00000046897	zinc finger protein 740	1.676	0.0000	0.0000
Zfp787	ENSMUSG00000046792	zinc finger protein 787	1.574	0.0001	0.0005
Zfp821	ENSMUSG00000031728	zinc finger protein 821	2.526	0.0000	0.0000
Zfp827	ENSMUSG00000071064	zinc finger protein 827	1.936	0.0000	0.0000
Zfp830	ENSMUSG00000046010	zinc finger protein 830	2.601	0.0000	0.0000
Zfp839	ENSMUSG00000021271	zinc finger protein 839	2.828	0.0000	0.0000
Zfp84	ENSMUSG00000046185	zinc finger protein 84	1.685	0.0000	0.0000
Zfp938	ENSMUSG00000062931	zinc finger protein 938	3.496	0.0000	0.0000
Zfp982	ENSMUSG00000078496	zinc finger protein 982	1.651	0.0006	0.0022
Zfpm1	ENSMUSG00000049577	zinc finger protein, multitype 1	3.046	0.0000	0.0000
Zfr2	ENSMUSG00000034949	zinc finger RNA binding protein 2	1.580	0.0031	0.0094
Zfta	ENSMUSG00000053080	zinc finger translocation associated	2.276	0.0000	0.0000
Zhx2	ENSMUSG00000071757	zinc fingers and homeoboxes 2	1.563	0.0000	0.0000
Zmat2	ENSMUSG00000001383	zinc finger, matrin type 2	3.127	0.0000	0.0000
Zmynd19	ENSMUSG00000026974	zinc finger, MYND domain containing 19	2.200	0.0000	0.0000
Znhit6	ENSMUSG00000074182	zinc finger, HIT type 6	2.346	0.0000	0.0000
Znrf1	ENSMUSG00000033545	zinc and ring finger 1	2.085	0.0000	0.0000
Znrf2	ENSMUSG00000058446	zinc and ring finger 2	2.297	0.0000	0.0000
Zpbp	ENSMUSG00000020193	zona pellucida binding protein	2.376	0.0012	0.0041
Zranb1	ENSMUSG00000030967	zinc finger, RAN-binding domain containing 1	1.515	0.0081	0.0218
Zranb2	ENSMUSG00000028180	zinc finger, RAN-binding domain containing 2	1.772	0.0000	0.0000
Zrsr1	ENSMUSG00000044068	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	1.974	0.0000	0.0000
Zrsr2	ENSMUSG00000031370	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	3.084	0.0000	0.0000
Zscan29	ENSMUSG00000050619	zinc finger SCAN domains 29	1.724	0.0000	0.0000
Zswim4	ENSMUSG00000035671	zinc finger SWIM-type containing 4	1.860	0.0001	0.0004
Zswim9	ENSMUSG00000070814	zinc finger SWIM-type containing 9	2.309	0.0000	0.0000
Zxdc	ENSMUSG00000034430	ZXD family zinc finger C	1.522	0.0206	0.0489
	ENSMUSG00000095742		14.771	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610012G03Rik	ENSMUSG00000107002	RIKEN cDNA 0610012G03 gene	-2.224	0.0000	0.0000
1010001B22Rik	ENSMUSG00000097863	RIKEN cDNA 1010001B22 gene	-5.163	0.0000	0.0002
1110002O04Rik	ENSMUSG00000102531	RIKEN cDNA 1110002O04 gene	-4.813	0.0178	0.0432
1110019D14Rik	ENSMUSG00000097616	RIKEN cDNA 1110019D14 gene	-8.030	0.0000	0.0001
1110032A03Rik	ENSMUSG00000037971	RIKEN cDNA 1110032A03 gene	-1.675	0.0000	0.0000
1110038B12Rik	ENSMUSG00000092203	RIKEN cDNA 1110038B12 gene	-2.307	0.0019	0.0062
1190007I07Rik	ENSMUSG00000063320	RIKEN cDNA 1190007I07 gene	-2.834	0.0000	0.0000
1500004A13Rik	ENSMUSG00000098912	RIKEN cDNA 1500004A13 gene	-2.918	0.0403	0.0865
1500026H17Rik	ENSMUSG00000097383	RIKEN cDNA 1500026H17 gene	-2.804	0.0062	0.0173
1600020E01Rik	ENSMUSG00000097048	RIKEN cDNA 1600020E01 gene	-1.606	0.0251	0.0580
1700001O22Rik	ENSMUSG00000044320	RIKEN cDNA 1700001O22 gene	-2.248	0.0051	0.0148
1700008O03Rik	ENSMUSG00000008028	RIKEN cDNA 1700008O03 gene	-16.430	0.0146	0.0365
1700017B05Rik	ENSMUSG00000032300	RIKEN cDNA 1700017B05 gene	-1.609	0.0052	0.0148
1700022N22Rik	ENSMUSG00000097523	RIKEN cDNA 1700022N22 gene	-17.537	0.0063	0.0176
1700037H04Rik	ENSMUSG00000027327	RIKEN cDNA 1700037H04 gene	-1.633	0.0009	0.0031
1700066B19Rik	ENSMUSG00000073598	RIKEN cDNA 1700066B19 gene	-8.651	0.0409	0.0875
1700088E04Rik	ENSMUSG00000033029	RIKEN cDNA 1700088E04 gene	-3.275	0.0000	0.0000
1700101I11Rik	ENSMUSG00000097675	RIKEN cDNA 1700101I11 gene	-2.136	0.0002	0.0006
1700120C14Rik	ENSMUSG00000100599	RIKEN cDNA 1700120C14 gene	-2.204	0.0000	0.0000
1810010H24Rik	ENSMUSG00000078607	RIKEN cDNA 1810010H24 gene	-1.851	0.0155	0.0384
1810019D21Rik	ENSMUSG00000086390	RIKEN cDNA 1810019D21 gene	-3.813	0.0312	0.0696
1810021B22Rik	ENSMUSG00000087331	RIKEN cDNA 1810021B22 gene	-1.700	0.0014	0.0045
1810024B03Rik	ENSMUSG00000044145	RIKEN cDNA 1810024B03 gene	-2.154	0.0221	0.0519
1810044D09Rik	ENSMUSG00000100680	RIKEN cDNA 1810044D09 gene	-1.659	0.0225	0.0528
1810055G02Rik	ENSMUSG00000035372	RIKEN cDNA 1810055G02 gene	-1.597	0.0014	0.0047
1810058I24Rik	ENSMUSG00000073155	RIKEN cDNA 1810058I24 gene	-2.328	0.0000	0.0000
2010001K21Rik	ENSMUSG00000051606	RIKEN cDNA 2010001K21 gene	-1.526	0.0042	0.0123
2210408I21Rik	ENSMUSG00000071252	RIKEN cDNA 2210408I21 gene	-1.731	0.0000	0.0000
2310001K24Rik	ENSMUSG00000053353	RIKEN cDNA 2310001K24 gene	-4.452	0.0019	0.0062
2310002D06Rik	ENSMUSG00000112701	RIKEN cDNA 2310002D06 gene	-19.718	0.0001	0.0004
2310011J03Rik	ENSMUSG00000020133	RIKEN cDNA 2310011J03 gene	-1.649	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
2310016G11Rik	ENSMUSG00000070574	RIKEN cDNA 2310016G11 gene	-2.688	0.0001	0.0005
2310020H05Rik	ENSMUSG00000100410	RIKEN cDNA 2310020H05 gene	-1.679	0.0178	0.0432
2310022A10Rik	ENSMUSG00000049643	RIKEN cDNA 2310022A10 gene	-1.589	0.0000	0.0000
2310039H08Rik	ENSMUSG00000062619	RIKEN cDNA 2310039H08 gene	-2.888	0.0000	0.0000
2410002F23Rik	ENSMUSG00000045411	RIKEN cDNA 2410002F23 gene	-1.551	0.0036	0.0108
2500002B13Rik	ENSMUSG00000096917	RIKEN cDNA 2500002B13 gene	-1.554	0.0003	0.0010
2510002D24Rik	ENSMUSG00000071632	RIKEN cDNA 2510002D24 gene	-1.525	0.0000	0.0001
2510016D11Rik	ENSMUSG00000106825	RIKEN cDNA 2510016D11 gene	-3.698	0.0040	0.0118
2610306O10Rik	ENSMUSG00000108614	RIKEN cDNA 2610306O10 gene	-3.345	0.0408	0.0875
2700046G09Rik	ENSMUSG00000097787	RIKEN cDNA 2700046G09 gene	-2.078	0.0004	0.0015
2810403D21Rik	ENSMUSG00000086629	RIKEN cDNA 2810403D21 gene	-1.864	0.0052	0.0149
2900009J06Rik	ENSMUSG00000102014	RIKEN cDNA 2900009J06 gene	-2.111	0.0311	0.0694
3110009E18Rik	ENSMUSG00000026388	RIKEN cDNA 3110009E18 gene	-3.243	0.0000	0.0001
3110070M22Rik	ENSMUSG00000074635	RIKEN cDNA 3110070M22 gene	-2.095	0.0119	0.0304
3222401L13Rik	ENSMUSG00000073590	RIKEN cDNA 3222401L13 gene	-1.511	0.0095	0.0252
3300002I08Rik	ENSMUSG00000063364	RIKEN cDNA 3300002I08 gene	-15.706	0.0004	0.0016
4631405J19Rik	ENSMUSG00000075027	RIKEN cDNA 4631405J19 gene	-1.630	0.0002	0.0006
4833408A19Rik	ENSMUSG00000118132	RIKEN cDNA 4833408A19 gene	-1.930	0.0125	0.0319
4833419F23Rik	ENSMUSG00000117401	RIKEN cDNA 4833419F23 gene	-2.085	0.0395	0.0853
4833445I07Rik	ENSMUSG00000103103	RIKEN cDNA 4833445I07 gene	-4.375	0.0151	0.0377
4921507P07Rik	ENSMUSG00000029828	RIKEN cDNA 4921507P07 gene	-3.466	0.0020	0.0065
4921536K21Rik	ENSMUSG00000020434	RIKEN cDNA 4921536K21 gene	-2.426	0.0008	0.0028
4930431P22Rik	ENSMUSG00000115709	RIKEN cDNA 4930431P22 gene	-8.272	0.0377	0.0819
4930466K18Rik	ENSMUSG00000112332	RIKEN cDNA 4930466K18 gene	-2.305	0.0204	0.0485
4930506C21Rik	ENSMUSG00000087478	RIKEN cDNA 4930506C21 gene	-14.961	0.0074	0.0203
4930522L14Rik	ENSMUSG00000072762	RIKEN cDNA 4930522L14 gene	-2.047	0.0106	0.0276
4930523C07Rik	ENSMUSG00000090394	RIKEN cDNA 4930523C07 gene	-1.533	0.0002	0.0008
4930525G20Rik	ENSMUSG00000097276	RIKEN cDNA 4930525G20 gene	-12.451	0.0160	0.0396
4930581F22Rik	ENSMUSG00000070315	RIKEN cDNA 4930581F22 gene	-1.567	0.0288	0.0651
4930592C13Rik	ENSMUSG00000105834	RIKEN cDNA 4930592C13 gene	-8.770	0.0329	0.0728
4933406P04Rik	ENSMUSG00000069713	RIKEN cDNA 4933406P04 gene	-3.434	0.0003	0.0013

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
4933434E20Rik	ENSMUSG00000027942	RIKEN cDNA 4933434E20 gene	-1.885	0.0000	0.0000
4933440J02Rik	ENSMUSG00000097082	RIKEN cDNA 4933440J02 gene	-17.586	0.0066	0.0183
5033430I15Rik	ENSMUSG00000038152	RIKEN cDNA 5033430I15 gene	-2.755	0.0000	0.0000
5430403G16Rik	ENSMUSG00000072763	RIKEN cDNA 5430403G16 gene	-1.947	0.0118	0.0302
5530601H04Rik	ENSMUSG00000087174	RIKEN cDNA 5530601H04 gene	-1.741	0.0015	0.0049
5830432E09Rik	ENSMUSG00000097471	RIKEN cDNA 5830432E09 gene	-1.968	0.0472	0.0986
5830448L01Rik	ENSMUSG00000115007	RIKEN cDNA 5830448L01 gene	-2.065	0.0223	0.0524
5930430L01Rik	ENSMUSG00000106951	RIKEN cDNA 5930430L01 gene	-1.790	0.0000	0.0000
6030443J06Rik	ENSMUSG00000097207	RIKEN cDNA 6030443J06 gene	-2.564	0.0012	0.0040
6330549D23Rik	ENSMUSG00000045327	RIKEN cDNA 6330549D23 gene	-6.216	0.0011	0.0037
6430584L05Rik	ENSMUSG00000108228	RIKEN cDNA 6430584L05 gene	-3.499	0.0083	0.0224
6720489N17Rik	ENSMUSG00000072066	RIKEN cDNA 6720489N17 gene	-3.423	0.0000	0.0002
8430437L04Rik	ENSMUSG00000085252	RIKEN cDNA 8430437L04 gene	-11.618	0.0266	0.0610
9130604C24Rik	ENSMUSG00000105851	RIKEN cDNA 9130604C24 gene	-5.683	0.0010	0.0035
9330020H09Rik	ENSMUSG00000091050	RIKEN cDNA 9330020H09 gene	-4.574	0.0000	0.0001
9430015G10Rik	ENSMUSG00000059939	RIKEN cDNA 9430015G10 gene	-1.754	0.0019	0.0062
9430091E24Rik	ENSMUSG00000084808	RIKEN cDNA 9430091E24 gene	-3.777	0.0094	0.0249
9530026P05Rik	ENSMUSG00000097462	RIKEN cDNA 9530026P05 gene	-1.760	0.0348	0.0765
9630013D21Rik	ENSMUSG00000059027	RIKEN cDNA 9630013D21 gene	-2.534	0.0003	0.0010
9930111J21Rik1	ENSMUSG00000069893	RIKEN cDNA 9930111J21 gene 1	-2.323	0.0000	0.0001
9930111J21Rik2	ENSMUSG00000069892	RIKEN cDNA 9930111J21 gene 2	-1.695	0.0004	0.0016
A230009B12Rik	ENSMUSG00000089633	RIKEN cDNA A230009B12 gene	-15.725	0.0020	0.0065
A230065N10Rik	ENSMUSG00000092071	RIKEN cDNA A230065N10 gene	-3.213	0.0066	0.0182
A430005L14Rik	ENSMUSG00000047613	RIKEN cDNA A430005L14 gene	-1.587	0.0000	0.0000
A530016L24Rik	ENSMUSG00000043122	RIKEN cDNA A530016L24 gene	-1.859	0.0000	0.0001
A630076J17Rik	ENSMUSG00000094613	RIKEN cDNA A630076J17 gene	-16.275	0.0106	0.0276
A730011C13Rik	ENSMUSG00000084846	RIKEN cDNA A730011C13 gene	-4.771	0.0012	0.0040
A730020M07Rik	ENSMUSG00000044522	RIKEN cDNA A730020M07 gene	-2.241	0.0001	0.0004
A930004D18Rik	ENSMUSG00000054057	RIKEN cDNA A930004D18 gene	-1.631	0.0125	0.0318
A930007I19Rik	ENSMUSG00000097855	RIKEN cDNA A930007I19 gene	-2.414	0.0476	0.0993
A930012L18Rik	ENSMUSG00000097610	RIKEN cDNA A930012L18 gene	-12.521	0.0110	0.0285

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
A930024E05Rik	ENSMUSG00000056735	RIKEN cDNA A930024E05 gene	-2.940	0.0475	0.0991
AA986860	ENSMUSG00000042510	expressed sequence AA986860	-1.927	0.0142	0.0356
Abca2	ENSMUSG00000026944	ATP-binding cassette, sub-family A (ABC1), member 2	-1.578	0.0000	0.0001
Abca3	ENSMUSG00000024130	ATP-binding cassette, sub-family A (ABC1), member 3	-1.838	0.0000	0.0000
Abca7	ENSMUSG00000035722	ATP-binding cassette, sub-family A (ABC1), member 7	-1.540	0.0111	0.0289
Abcb8	ENSMUSG00000028973	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-1.842	0.0000	0.0000
Abcb9	ENSMUSG00000029408	ATP-binding cassette, sub-family B (MDR/TAP), member 9	-1.880	0.0000	0.0001
Abcc8	ENSMUSG00000040136	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-2.145	0.0000	0.0000
Abcd1	ENSMUSG00000031378	ATP-binding cassette, sub-family D (ALD), member 1	-1.715	0.0000	0.0000
Abhd14b	ENSMUSG00000042073	abhydrolase domain containing 14b	-2.461	0.0000	0.0000
Abhd18	ENSMUSG00000037818	abhydrolase domain containing 18	-1.549	0.0000	0.0001
Abhd4	ENSMUSG00000040997	abhydrolase domain containing 4	-2.581	0.0000	0.0000
Abhd8	ENSMUSG00000007950	abhydrolase domain containing 8	-2.166	0.0000	0.0000
Abi3	ENSMUSG00000018381	ABI family member 3	-1.821	0.0000	0.0000
Abitram	ENSMUSG00000038827	actin binding transcription modulator	-1.626	0.0003	0.0012
Acad10	ENSMUSG00000029456	acyl-Coenzyme A dehydrogenase family, member 10	-2.377	0.0000	0.0000
Acad11	ENSMUSG00000090150	acyl-Coenzyme A dehydrogenase family, member 11	-1.518	0.0000	0.0000
Acad12	ENSMUSG00000042647	acyl-Coenzyme A dehydrogenase family, member 12	-1.562	0.0000	0.0000
Acad9	ENSMUSG00000027710	acyl-Coenzyme A dehydrogenase family, member 9	-1.747	0.0000	0.0000
Acads	ENSMUSG00000029545	acyl-Coenzyme A dehydrogenase, short chain	-2.492	0.0000	0.0000
Acd	ENSMUSG00000038000	adrenocortical dysplasia	-1.621	0.0000	0.0001
Ace	ENSMUSG00000020681	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	-1.744	0.0007	0.0025
Ache	ENSMUSG00000023328	acetylcholinesterase	-1.943	0.0001	0.0004
Ackr3	ENSMUSG00000044337	atypical chemokine receptor 3	-1.917	0.0000	0.0000
Acod1	ENSMUSG00000022126	aconitate decarboxylase 1	-13.828	0.0182	0.0441
Acot2	ENSMUSG00000021226	acyl-CoA thioesterase 2	-1.794	0.0001	0.0003
Acot8	ENSMUSG00000017307	acyl-CoA thioesterase 8	-1.936	0.0000	0.0000
Acox2	ENSMUSG00000021751	acyl-Coenzyme A oxidase 2, branched chain	-18.657	0.0079	0.0213
Acp1	ENSMUSG00000044573	acid phosphatase 1, soluble	-1.950	0.0000	0.0000
Acp2	ENSMUSG00000002103	acid phosphatase 2, lysosomal	-1.926	0.0000	0.0000
Acp5	ENSMUSG00000001348	acid phosphatase 5, tartrate resistant	-2.238	0.0215	0.0508

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Acsbg1	ENSMUSG00000032281	acyl-CoA synthetase bubblegum family member 1	-3.763	0.0081	0.0218
Acss3	ENSMUSG00000035948	acyl-CoA synthetase short-chain family member 3	-1.592	0.0128	0.0325
Acta2	ENSMUSG00000035783	actin alpha 2, smooth muscle, aorta	-1.622	0.0006	0.0023
Actc1	ENSMUSG00000068614	actin, alpha, cardiac muscle 1	-1.982	0.0000	0.0000
Actg1	ENSMUSG00000062825	actin, gamma, cytoplasmic 1	-2.036	0.0000	0.0000
Acy3	ENSMUSG00000024866	aspartoacylase (aminoacylase) 3	-3.054	0.0000	0.0000
Ada	ENSMUSG00000017697	adenosine deaminase	-2.304	0.0152	0.0379
Adal	ENSMUSG00000027259	adenosine deaminase-like	-1.863	0.0000	0.0000
Adam15	ENSMUSG00000028041	a disintegrin and metallopeptidase domain 15 (metargidin)	-1.580	0.0000	0.0000
Adamtsl4	ENSMUSG00000015850	ADAMTS-like 4	-1.683	0.0002	0.0007
Adamtsl5	ENSMUSG00000043822	ADAMTS-like 5	-1.845	0.0000	0.0000
Adar	ENSMUSG00000027951	adenosine deaminase, RNA-specific	-1.542	0.0000	0.0002
Adck1	ENSMUSG00000021044	aarF domain containing kinase 1	-1.807	0.0000	0.0000
Adck5	ENSMUSG00000022550	aarF domain containing kinase 5	-1.707	0.0083	0.0224
Adcy4	ENSMUSG00000022220	adenylate cyclase 4	-1.571	0.0006	0.0021
Adgre5	ENSMUSG00000002885	adhesion G protein-coupled receptor E5	-1.581	0.0000	0.0000
Adgrg1	ENSMUSG00000031785	adhesion G protein-coupled receptor G1	-1.729	0.0134	0.0338
Adgrg3	ENSMUSG00000060470	adhesion G protein-coupled receptor G3	-2.303	0.0026	0.0082
Adrm1	ENSMUSG00000039041	adhesion regulating molecule 1	-1.500	0.0008	0.0027
Adsl	ENSMUSG00000022407	adenylosuccinate lyase	-2.038	0.0000	0.0000
Afmid	ENSMUSG00000017718	arylformamidase	-2.085	0.0034	0.0102
Agmo	ENSMUSG00000050103	alkylglycerol monooxygenase	-2.221	0.0005	0.0017
Agt	ENSMUSG00000031980	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-2.346	0.0140	0.0351
Ahcy	ENSMUSG00000027597	S-adenosylhomocysteine hydrolase	-2.407	0.0000	0.0000
AI467606	ENSMUSG00000045165	expressed sequence AI467606	-1.869	0.0062	0.0174
AI661453	ENSMUSG00000034382	expressed sequence AI661453	-2.231	0.0108	0.0282
AI838599	ENSMUSG00000085180	expressed sequence AI838599	-8.703	0.0023	0.0074
Airn	ENSMUSG00000078247	antisense Igf2r RNA	-1.757	0.0002	0.0007
AK157302	ENSMUSG00000078139	cDNA sequence AK157302	-2.553	0.0000	0.0000
Ak3	ENSMUSG00000024782	adenylate kinase 3	-1.942	0.0000	0.0000
Ak3l2-ps	ENSMUSG00000081957	adenylate kinase 3-like 2, pseudogene	-15.806	0.0000	0.0001

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Akna	ENSMUSG00000039158	AT-hook transcription factor	-1.750	0.0000	0.0001
Akr1b10	ENSMUSG00000061758	aldo-keto reductase family 1, member B10 (aldose reductase)	-1.676	0.0000	0.0000
Akr7a5	ENSMUSG00000028743	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	-2.538	0.0000	0.0000
Alad	ENSMUSG00000028393	aminolevulinate, delta-, dehydratase	-2.682	0.0000	0.0000
Aldh18a1	ENSMUSG00000025007	aldehyde dehydrogenase 18 family, member A1	-1.577	0.0073	0.0201
Alg1	ENSMUSG00000039427	asparagine-linked glycosylation 1 (beta-1,4-mannosyltransferase)	-1.732	0.0000	0.0000
Alg12	ENSMUSG00000035845	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase)	-2.119	0.0000	0.0000
Alg8	ENSMUSG00000035704	asparagine-linked glycosylation 8 (alpha-1,3-glucosyltransferase)	-1.867	0.0003	0.0013
Alg9	ENSMUSG00000032059	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase)	-1.541	0.0001	0.0005
Alkal2	ENSMUSG00000054204	ALK and LTK ligand 2	-3.293	0.0099	0.0261
Alkbh6	ENSMUSG00000042831	alkB homolog 6	-2.023	0.0000	0.0000
Alkbh7	ENSMUSG00000002661	alkB homolog 7	-2.823	0.0000	0.0000
Alox5ap	ENSMUSG00000060063	arachidonate 5-lipoxygenase activating protein	-2.252	0.0000	0.0002
Amdhd2	ENSMUSG00000036820	amidohydrolase domain containing 2	-1.565	0.0029	0.0089
Amigo3	ENSMUSG00000032593	adhesion molecule with Ig like domain 3	-2.911	0.0026	0.0080
Anapc16	ENSMUSG00000020107	anaphase promoting complex subunit 16	-1.741	0.0001	0.0003
Ang	ENSMUSG00000072115	angiogenin, ribonuclease, RNase A family, 5	-2.504	0.0175	0.0425
Angel1	ENSMUSG00000021257	angel homolog 1	-1.542	0.0001	0.0002
Angptl2	ENSMUSG00000004105	angiopoietin-like 2	-1.565	0.0011	0.0038
Angptl4	ENSMUSG00000002289	angiopoietin-like 4	-2.312	0.0323	0.0718
Angptl6	ENSMUSG00000038742	angiopoietin-like 6	-1.779	0.0002	0.0007
Ankrd10	ENSMUSG00000031508	ankyrin repeat domain 10	-1.566	0.0000	0.0000
Ankrd23	ENSMUSG00000067653	ankyrin repeat domain 23	-2.707	0.0000	0.0000
Ankrd39	ENSMUSG00000079610	ankyrin repeat domain 39	-1.613	0.0011	0.0037
Ankrd46	ENSMUSG00000048307	ankyrin repeat domain 46	-1.511	0.0000	0.0000
Ankrd54	ENSMUSG00000033055	ankyrin repeat domain 54	-1.745	0.0009	0.0032
Aoah	ENSMUSG00000021322	acyloxyacyl hydrolase	-2.538	0.0163	0.0401
Aopep	ENSMUSG00000021458	aminopeptidase O	-1.601	0.0000	0.0000
Ap1b1	ENSMUSG00000009090	adaptor protein complex AP-1, beta 1 subunit	-1.546	0.0000	0.0000
Ap2a1	ENSMUSG00000060279	adaptor-related protein complex 2, alpha 1 subunit	-1.811	0.0000	0.0000
Ap2m1-ps	ENSMUSG00000081272	adaptor-related protein complex 2, mu 1 subunit, pseudogene	-1.837	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ap5b1	ENSMUSG00000049562	adaptor-related protein complex 5, beta 1 subunit	-2.407	0.0000	0.0000
Ap5m1	ENSMUSG00000036291	adaptor-related protein complex 5, mu 1 subunit	-1.996	0.0000	0.0000
Ap5z1	ENSMUSG00000039623	adaptor-related protein complex 5, zeta 1 subunit	-1.633	0.0000	0.0001
Apba3	ENSMUSG00000004931	amyloid beta (A4) precursor protein-binding, family A, member 3	-1.846	0.0000	0.0000
Apc2	ENSMUSG00000020135	APC regulator of WNT signaling pathway 2	-1.999	0.0005	0.0020
Apeh	ENSMUSG00000032590	acylpeptide hydrolase	-1.919	0.0000	0.0000
Aph1b	ENSMUSG00000032375	aph1 homolog B, gamma secretase subunit	-2.120	0.0000	0.0000
Aph1c	ENSMUSG00000053040	aph1 homolog C, gamma secretase subunit	-1.651	0.0286	0.0649
Apobec1	ENSMUSG00000040613	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	-1.513	0.0034	0.0101
Aprt	ENSMUSG00000006589	adenine phosphoribosyl transferase	-1.661	0.0000	0.0000
Aqp1	ENSMUSG00000004655	aquaporin 1	-1.740	0.0159	0.0394
Arfip1	ENSMUSG00000074513	ADP-ribosylation factor interacting protein 1	-2.137	0.0000	0.0000
Arhgap1	ENSMUSG00000027247	Rho GTPase activating protein 1	-1.984	0.0000	0.0000
Arhgap27	ENSMUSG00000034255	Rho GTPase activating protein 27	-1.929	0.0035	0.0106
Arhgap28	ENSMUSG00000024043	Rho GTPase activating protein 28	-1.713	0.0006	0.0023
Arhgdia	ENSMUSG00000025132	Rho GDP dissociation inhibitor (GDI) alpha	-1.649	0.0000	0.0000
Arl11	ENSMUSG00000043157	ADP-ribosylation factor-like 11	-2.170	0.0343	0.0755
Arl15	ENSMUSG00000042348	ADP-ribosylation factor-like 15	-1.757	0.0000	0.0000
Arl2	ENSMUSG00000024944	ADP-ribosylation factor-like 2	-1.549	0.0000	0.0000
Arl5c	ENSMUSG00000038352	ADP-ribosylation factor-like 5C	-1.669	0.0176	0.0428
Arl6	ENSMUSG00000022722	ADP-ribosylation factor-like 6	-1.598	0.0001	0.0006
Armc6	ENSMUSG00000002343	armadillo repeat containing 6	-1.845	0.0000	0.0000
Arntl2	ENSMUSG00000040187	aryl hydrocarbon receptor nuclear translocator-like 2	-6.734	0.0245	0.0567
Arpc3	ENSMUSG00000029465	actin related protein 2/3 complex, subunit 3	-2.022	0.0000	0.0000
Arrdc1	ENSMUSG00000026972	arrestin domain containing 1	-1.560	0.0168	0.0411
Arsa	ENSMUSG00000022620	arylsulfatase A	-1.593	0.0000	0.0000
Arsg	ENSMUSG00000020604	arylsulfatase G	-2.050	0.0001	0.0004
Arsk	ENSMUSG00000021592	arylsulfatase K	-2.263	0.0000	0.0000
Art1	ENSMUSG00000030996	ADP-ribosyltransferase 1	-1.568	0.0000	0.0002
Art4	ENSMUSG00000030217	ADP-ribosyltransferase 4	-2.363	0.0000	0.0002
Asb11	ENSMUSG00000031382	ankyrin repeat and SOCS box-containing 11	-1.524	0.0012	0.0040

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Asb12	ENSMUSG00000031204	ankyrin repeat and SOCS box-containing 12	-1.517	0.0002	0.0009
Asb14	ENSMUSG00000021898	ankyrin repeat and SOCS box-containing 14	-2.066	0.0000	0.0000
Asb18	ENSMUSG00000067081	ankyrin repeat and SOCS box-containing 18	-1.787	0.0000	0.0000
Asb2	ENSMUSG00000021200	ankyrin repeat and SOCS box-containing 2	-1.518	0.0000	0.0002
Asb5	ENSMUSG00000031519	ankyrin repeat and SOCs box-containing 5	-1.641	0.0097	0.0257
Asb6	ENSMUSG00000039483	ankyrin repeat and SOCS box-containing 6	-1.816	0.0000	0.0000
Ascc1	ENSMUSG00000044475	activating signal cointegrator 1 complex subunit 1	-1.872	0.0000	0.0001
Asf1b	ENSMUSG00000005470	anti-silencing function 1B histone chaperone	-2.339	0.0002	0.0008
Asl	ENSMUSG00000025533	argininosuccinate lyase	-2.011	0.0000	0.0002
Asns	ENSMUSG00000029752	asparagine synthetase	-1.559	0.0456	0.0958
Asnsd1	ENSMUSG00000026095	asparagine synthetase domain containing 1	-2.263	0.0000	0.0000
Aspa	ENSMUSG00000020774	aspartoacylase	-2.264	0.0003	0.0013
Aspg	ENSMUSG00000037686	asparaginase	-3.418	0.0366	0.0798
Asxl3	ENSMUSG00000045215	ASXL transcriptional regulator 3	-1.652	0.0170	0.0415
Atat1	ENSMUSG00000024426	alpha tubulin acetyltransferase 1	-1.505	0.0110	0.0286
Atf1-ps	ENSMUSG00000080968	activating transcription factor 1, pseudogene	-6.682	0.0055	0.0155
Atg2a	ENSMUSG00000024773	autophagy related 2A	-2.117	0.0000	0.0000
Atg9a	ENSMUSG00000033124	autophagy related 9A	-2.308	0.0000	0.0000
Atox1	ENSMUSG00000018585	antioxidant 1 copper chaperone	-3.545	0.0000	0.0000
Atp10d	ENSMUSG00000046808	ATPase, class V, type 10D	-1.583	0.0020	0.0065
Atp5d	ENSMUSG00000003072	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-3.150	0.0000	0.0000
Atp5g2	ENSMUSG00000062683	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	-3.936	0.0000	0.0000
Atp5l	ENSMUSG00000038717	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	-5.764	0.0000	0.0000
Atp5mpl	ENSMUSG00000021290	ATP synthase membrane subunit 6.8PL	-1.539	0.0000	0.0000
Atp5o	ENSMUSG00000022956	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-2.515	0.0000	0.0000
Atp6v0c	ENSMUSG00000024121	ATPase, H+ transporting, lysosomal V0 subunit C	-4.689	0.0000	0.0000
Atp6v0c-ps2	ENSMUSG00000080242	ATPase, H+ transporting, lysosomal V0 subunit C, pseudogene 2	-7.059	0.0000	0.0000
Atp6v0d1	ENSMUSG00000013160	ATPase, H+ transporting, lysosomal V0 subunit D1	-2.713	0.0000	0.0000
Atp6v0e	ENSMUSG00000015575	ATPase, H+ transporting, lysosomal V0 subunit E	-1.644	0.0000	0.0000
Atp6v0e2	ENSMUSG00000039347	ATPase, H+ transporting, lysosomal V0 subunit E2	-1.910	0.0000	0.0000
Atp6v1b2	ENSMUSG00000006273	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.712	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Atp6v1f	ENSMUSG00000004285	ATPase, H+ transporting, lysosomal V1 subunit F	-1.575	0.0000	0.0000
Atpsckmt	ENSMUSG00000039065	ATP synthase C subunit lysine N-methyltransferase	-1.548	0.0001	0.0004
Atraid	ENSMUSG00000013622	all-trans retinoic acid induced differentiation factor	-1.592	0.0000	0.0000
Atrip	ENSMUSG00000025646	ATR interacting protein	-1.954	0.0000	0.0000
Atxn7l2	ENSMUSG00000048997	ataxin 7-like 2	-2.053	0.0006	0.0020
AU021092	ENSMUSG00000051669	expressed sequence AU021092	-2.422	0.0000	0.0000
AU041133	ENSMUSG00000078435	expressed sequence AU041133	-1.680	0.0478	0.0996
Aurka	ENSMUSG00000027496	aurora kinase A	-2.535	0.0006	0.0023
Aurkaip1	ENSMUSG00000065990	aurora kinase A interacting protein 1	-1.841	0.0000	0.0000
Avl9	ENSMUSG00000029787	AVL9 cell migration associated	-1.559	0.0000	0.0000
Avpi1	ENSMUSG00000018821	arginine vasopressin-induced 1	-1.662	0.0000	0.0000
AW112010	ENSMUSG00000075010	expressed sequence AW112010	-2.958	0.0000	0.0000
B2m	ENSMUSG00000060802	beta-2 microglobulin	-2.016	0.0000	0.0000
B3galt4	ENSMUSG00000067370	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	-3.008	0.0000	0.0000
B3galt6	ENSMUSG00000050796	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	-3.238	0.0000	0.0000
B3gntl1	ENSMUSG00000046605	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	-1.876	0.0016	0.0053
B9d2	ENSMUSG00000063439	B9 protein domain 2	-2.860	0.0000	0.0000
Bace2	ENSMUSG00000040605	beta-site APP-cleaving enzyme 2	-1.639	0.0017	0.0055
Baiap3	ENSMUSG00000047507	BAI1-associated protein 3	-2.510	0.0159	0.0394
Bak1	ENSMUSG00000057789	BCL2-antagonist/killer 1	-2.354	0.0000	0.0000
Bambi-ps1	ENSMUSG00000081219	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus laevis)	-3.127	0.0000	0.0002
Banf2os	ENSMUSG00000086384	barrier to autointegration factor 2, opposite strand	-2.908	0.0002	0.0007
Bax	ENSMUSG00000003873	BCL2-associated X protein	-1.586	0.0008	0.0028
BB218582	ENSMUSG00000085218	expressed sequence BB218582	-1.909	0.0006	0.0023
Bbip1	ENSMUSG00000084957	BBSome interacting protein 1	-1.595	0.0000	0.0000
Bbs4	ENSMUSG00000025235	Bardet-Biedl syndrome 4 (human)	-2.262	0.0000	0.0000
BC002059	ENSMUSG00000060149	cDNA sequence BC002059	-1.967	0.0000	0.0000
BC004004	ENSMUSG00000052712	cDNA sequence BC004004	-1.921	0.0000	0.0000
BC024063	ENSMUSG00000112160	cDNA sequence BC024063	-1.859	0.0177	0.0431
BC028528	ENSMUSG00000038543	cDNA sequence BC028528	-1.582	0.0005	0.0020
BC029722	ENSMUSG00000074649	cDNA sequence BC029722	-1.649	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Bcam	ENSMUSG00000002980	basal cell adhesion molecule	-1.774	0.0000	0.0000
Bche	ENSMUSG00000027792	butyrylcholinesterase	-1.732	0.0000	0.0000
Bckdha	ENSMUSG00000060376	branched chain ketoacid dehydrogenase E1, alpha polypeptide	-1.849	0.0000	0.0000
Bckdhb	ENSMUSG00000032263	branched chain ketoacid dehydrogenase E1, beta polypeptide	-1.634	0.0007	0.0023
Bckdk	ENSMUSG00000030802	branched chain ketoacid dehydrogenase kinase	-1.844	0.0000	0.0000
Bdh2	ENSMUSG00000028167	3-hydroxybutyrate dehydrogenase, type 2	-3.075	0.0438	0.0926
Best3	ENSMUSG00000020169	bestrophin 3	-1.999	0.0002	0.0008
Bfsp2	ENSMUSG00000032556	beaded filament structural protein 2, phakinin	-2.389	0.0198	0.0473
Bicra	ENSMUSG00000070808	BRD4 interacting chromatin remodeling complex associated protein	-1.602	0.0001	0.0003
Bicral	ENSMUSG00000036568	BRD4 interacting chromatin remodeling complex associated protein like	-1.616	0.0000	0.0000
Bid	ENSMUSG00000004446	BH3 interacting domain death agonist	-2.026	0.0091	0.0243
Bik	ENSMUSG00000016758	BCL2-interacting killer	-1.513	0.0120	0.0307
Blnk	ENSMUSG00000061132	B cell linker	-2.110	0.0000	0.0002
Bloc1s1	ENSMUSG00000090247	biogenesis of lysosomal organelles complex-1, subunit 1	-2.370	0.0000	0.0001
Bloc1s6	ENSMUSG00000005804	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin	-1.726	0.0000	0.0000
Blvrb	ENSMUSG00000040466	biliverdin reductase B (flavin reductase (NADPH))	-2.236	0.0000	0.0000
Bmp10	ENSMUSG00000030046	bone morphogenetic protein 10	-83.565	0.0011	0.0039
Bmp2	ENSMUSG00000027358	bone morphogenetic protein 2	-1.615	0.0122	0.0312
Bmp7	ENSMUSG00000008999	bone morphogenetic protein 7	-2.308	0.0000	0.0001
Bmyc	ENSMUSG00000049086	brain expressed myelocytomatosis oncogene	-1.560	0.0000	0.0000
Bnip1	ENSMUSG00000024191	BCL2/adenovirus E1B interacting protein 1	-1.948	0.0000	0.0000
Boc	ENSMUSG00000022687	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein	-1.887	0.0000	0.0000
Bok	ENSMUSG00000026278	BCL2-related ovarian killer	-2.647	0.0000	0.0001
Bola1	ENSMUSG00000015943	bolA-like 1 (E. coli)	-2.389	0.0000	0.0000
Bop1	ENSMUSG00000022557	block of proliferation 1	-1.506	0.0000	0.0000
Borcs8	ENSMUSG00000002345	BLOC-1 related complex subunit 8	-1.518	0.0004	0.0015
Brca1	ENSMUSG00000017146	breast cancer 1, early onset	-2.358	0.0324	0.0719
Brd3os	ENSMUSG00000109946	bromodomain containing 3, opposite strand	-1.837	0.0048	0.0138
Brf2	ENSMUSG00000031487	BRF2, RNA polymerase III transcription initiation factor 50kDa subunit	-1.669	0.0000	0.0000
Brinp2	ENSMUSG00000004031	bone morphogenic protein/retinoic acid inducible neural-specific 2	-19.441	0.0017	0.0055
Brk1	ENSMUSG00000033940	BRICK1, SCAR/WAVE actin-nucleating complex subunit	-1.614	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Brme1	ENSMUSG00000008129	break repair meiotic recombinase recruitment factor 1	-5.323	0.0022	0.0070
Bscl2	ENSMUSG00000071657	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	-1.685	0.0000	0.0002
Bst2	ENSMUSG00000046718	bone marrow stromal cell antigen 2	-1.856	0.0000	0.0002
Btbd3	ENSMUSG00000062098	BTB (POZ) domain containing 3	-1.767	0.0000	0.0000
Btbd6	ENSMUSG00000002803	BTB (POZ) domain containing 6	-2.754	0.0000	0.0000
Btd	ENSMUSG00000021900	biotinidase	-1.931	0.0000	0.0000
Btf3l4b	ENSMUSG00000114133	basic transcription factor 3 like 4B	-2.134	0.0001	0.0005
C030013G03Rik	ENSMUSG00000117314	RIKEN cDNA C030013G03 gene	-4.969	0.0071	0.0194
C1qtnf12	ENSMUSG00000023571	C1q and tumor necrosis factor related 12	-2.585	0.0000	0.0000
C1qtnf6	ENSMUSG00000022440	C1q and tumor necrosis factor related protein 6	-1.711	0.0007	0.0024
C2cd3	ENSMUSG00000047248	C2 calcium-dependent domain containing 3	-1.891	0.0000	0.0000
C87436	ENSMUSG00000046679	expressed sequence C87436	-2.205	0.0000	0.0000
Cab39l	ENSMUSG00000021981	calcium binding protein 39-like	-1.578	0.0118	0.0302
Cabin1	ENSMUSG00000020196	calcineurin binding protein 1	-1.706	0.0000	0.0000
Cacna1s	ENSMUSG00000026407	calcium channel, voltage-dependent, L type, alpha 1S subunit	-1.836	0.0002	0.0007
Calhm2	ENSMUSG00000033033	calcium homeostasis modulator family member 2	-1.794	0.0000	0.0001
Calhm5	ENSMUSG00000049872	calcium homeostasis modulator family member 5	-1.665	0.0168	0.0411
Camk1g	ENSMUSG00000016179	calcium/calmodulin-dependent protein kinase I gamma	-6.808	0.0467	0.0977
Cand2	ENSMUSG00000030319	cullin-associated and neddylation-dissociated 2 (putative)	-1.863	0.0000	0.0000
Capn3	ENSMUSG00000079110	calpain 3	-1.883	0.0151	0.0376
Capns1	ENSMUSG00000001794	calpain, small subunit 1	-1.937	0.0000	0.0000
Car15	ENSMUSG00000090236	carbonic anhydrase 15	-24.890	0.0007	0.0025
Car3	ENSMUSG00000027559	carbonic anhydrase 3	-2.688	0.0446	0.0939
Car7	ENSMUSG00000031883	carbonic anhydrase 7	-2.482	0.0000	0.0000
Carm1	ENSMUSG00000032185	coactivator-associated arginine methyltransferase 1	-1.582	0.0000	0.0000
Carmil3	ENSMUSG00000022211	capping protein regulator and myosin 1 linker 3	-1.519	0.0218	0.0514
Caskin2	ENSMUSG00000034471	CASK-interacting protein 2	-2.487	0.0000	0.0000
Cass4	ENSMUSG00000074570	Cas scaffolding protein family member 4	-2.613	0.0443	0.0934
Cat	ENSMUSG00000027187	catalase	-1.536	0.0024	0.0075
Catsperg1	ENSMUSG00000049676	cation channel sperm associated auxiliary subunit gamma 1	-3.821	0.0218	0.0513
Cav1	ENSMUSG00000007655	caveolin 1, caveolae protein	-1.662	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cav2	ENSMUSG00000000058	caveolin 2	-2.125	0.0000	0.0000
Cbln1	ENSMUSG00000031654	cerebellin 1 precursor protein	-2.975	0.0385	0.0833
Ccdc103	ENSMUSG00000020930	coiled-coil domain containing 103	-4.949	0.0282	0.0641
Ccdc107	ENSMUSG00000028461	coiled-coil domain containing 107	-2.311	0.0000	0.0000
Ccdc116	ENSMUSG00000022768	coiled-coil domain containing 116	-11.607	0.0152	0.0379
Ccdc130	ENSMUSG00000004994	coiled-coil domain containing 130	-1.614	0.0001	0.0005
Ccdc134	ENSMUSG00000068114	coiled-coil domain containing 134	-1.533	0.0004	0.0015
Ccdc159	ENSMUSG00000006241	coiled-coil domain containing 159	-1.888	0.0001	0.0003
Ccdc162	ENSMUSG00000075225	coiled-coil domain containing 162	-8.413	0.0203	0.0483
Ccdc166	ENSMUSG00000098176	coiled-coil domain containing 166	-3.689	0.0000	0.0000
Ccdc17	ENSMUSG00000034035	coiled-coil domain containing 17	-2.478	0.0016	0.0052
Ccdc22	ENSMUSG00000031143	coiled-coil domain containing 22	-3.898	0.0043	0.0126
Ccdc40	ENSMUSG00000039963	coiled-coil domain containing 40	-28.732	0.0007	0.0024
Ccdc69	ENSMUSG00000049588	coiled-coil domain containing 69	-1.905	0.0089	0.0237
Ccdc73	ENSMUSG00000045106	coiled-coil domain containing 73	-5.224	0.0000	0.0000
Ccdc86	ENSMUSG00000024732	coiled-coil domain containing 86	-2.258	0.0000	0.0000
Ccdc90b	ENSMUSG00000030613	coiled-coil domain containing 90B	-1.700	0.0000	0.0000
Ccnq	ENSMUSG00000049489	cyclin Q	-1.719	0.0000	0.0000
Ccr1	ENSMUSG00000025804	chemokine (C-C motif) receptor 1	-2.260	0.0196	0.0469
Ccrl2	ENSMUSG00000043953	chemokine (C-C motif) receptor-like 2	-1.885	0.0002	0.0008
Cd109	ENSMUSG00000046186	CD109 antigen	-2.388	0.0000	0.0002
Cd14	ENSMUSG00000051439	CD14 antigen	-1.871	0.0002	0.0008
Cd151	ENSMUSG00000025510	CD151 antigen	-2.107	0.0000	0.0000
Cd207	ENSMUSG00000034783	CD207 antigen	-22.672	0.0118	0.0304
Cd209b	ENSMUSG00000065987	CD209b antigen	-34.175	0.0001	0.0006
Cd300ld	ENSMUSG00000034641	CD300 molecule like family member d	-1.763	0.0086	0.0231
Cd302	ENSMUSG00000060703	CD302 antigen	-1.983	0.0000	0.0000
Cd320	ENSMUSG00000002308	CD320 antigen	-2.011	0.0000	0.0000
Cd40	ENSMUSG00000017652	CD40 antigen	-2.644	0.0000	0.0000
Cd48	ENSMUSG00000015355	CD48 antigen	-2.276	0.0085	0.0229
Cd59b	ENSMUSG00000068686	CD59b antigen	-2.052	0.0001	0.0002

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cd7	ENSMUSG00000025163	CD7 antigen	-14.279	0.0076	0.0207
Cd74	ENSMUSG00000024610	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-1.657	0.0244	0.0566
Cd83	ENSMUSG00000015396	CD83 antigen	-1.950	0.0022	0.0070
Cda	ENSMUSG00000028755	cytidine deaminase	-2.462	0.0165	0.0405
Cdc42ep2	ENSMUSG00000045664	CDC42 effector protein (Rho GTPase binding) 2	-1.820	0.0000	0.0000
Cdca5	ENSMUSG00000024791	cell division cycle associated 5	-4.009	0.0262	0.0601
Cdcp3	ENSMUSG00000006204	CUB domain containing protein 3	-1.557	0.0272	0.0621
Cdh13	ENSMUSG00000031841	cadherin 13	-1.507	0.0000	0.0000
Cdh15	ENSMUSG00000031962	cadherin 15	-8.765	0.0351	0.0771
Cdh16	ENSMUSG00000031881	cadherin 16	-2.183	0.0000	0.0000
Cdh23	ENSMUSG00000012819	cadherin 23 (otocadherin)	-2.176	0.0000	0.0000
Cdip1	ENSMUSG00000004071	cell death inducing Trp53 target 1	-1.556	0.0000	0.0000
Cdipt	ENSMUSG00000030682	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	-1.680	0.0000	0.0000
Cdk1	ENSMUSG00000019942	cyclin-dependent kinase 1	-2.146	0.0188	0.0453
Cdk2ap2	ENSMUSG00000024856	CDK2-associated protein 2	-2.256	0.0000	0.0000
Cdk4	ENSMUSG00000006728	cyclin-dependent kinase 4	-1.996	0.0000	0.0000
Cdkl1	ENSMUSG00000020990	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-1.591	0.0037	0.0111
Cdpf1	ENSMUSG00000064284	cysteine rich, DPF motif domain containing 1	-2.177	0.0000	0.0000
Cdt1	ENSMUSG00000006585	chromatin licensing and DNA replication factor 1	-1.702	0.0245	0.0569
Ceacam2	ENSMUSG00000054385	carcinoembryonic antigen-related cell adhesion molecule 2	-4.196	0.0241	0.0560
Cela1	ENSMUSG00000023031	chymotrypsin-like elastase family, member 1	-2.493	0.0090	0.0240
Celsr1	ENSMUSG00000016028	cadherin, EGF LAG seven-pass G-type receptor 1	-1.656	0.0053	0.0152
Cenpa	ENSMUSG00000029177	centromere protein A	-1.663	0.0001	0.0004
Cenpn	ENSMUSG00000031756	centromere protein N	-5.248	0.0000	0.0001
Cenpt	ENSMUSG00000036672	centromere protein T	-1.832	0.0275	0.0627
Cenpw	ENSMUSG00000075266	centromere protein W	-2.559	0.0185	0.0448
Cenpx	ENSMUSG00000025144	centromere protein X	-2.206	0.0000	0.0000
Cep295	ENSMUSG00000046111	centrosomal protein 295	-1.575	0.0002	0.0007
Cep72	ENSMUSG00000021572	centrosomal protein 72	-2.000	0.0393	0.0848
Cep83os	ENSMUSG00000097164	centrosomal protein 83, opposite strand	-1.664	0.0020	0.0063

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cept1	ENSMUSG00000040774	choline/ethanolaminephosphotransferase 1	-1.920	0.0000	0.0000
Cerox1	ENSMUSG00000091475	cytoplasmic endogenous regulator of oxidative phosphorylation 1	-2.050	0.0330	0.0731
Ces1f	ENSMUSG00000031725	carboxylesterase 1F	-17.783	0.0037	0.0111
Ces2e	ENSMUSG00000031886	carboxylesterase 2E	-1.904	0.0324	0.0720
Cfap126	ENSMUSG00000026649	cilia and flagella associated protein 126	-1.774	0.0197	0.0471
Cfap20	ENSMUSG00000031796	cilia and flagella associated protein 20	-1.663	0.0000	0.0001
Cfap418	ENSMUSG00000059482	cilia and flagella associated protein 418	-1.679	0.0008	0.0029
Cfap54	ENSMUSG00000020014	cilia and flagella associated protein 54	-2.605	0.0000	0.0000
Chchd1	ENSMUSG00000063787	coiled-coil-helix-coiled-coil-helix domain containing 1	-3.161	0.0000	0.0000
Chchd10	ENSMUSG00000049422	coiled-coil-helix-coiled-coil-helix domain containing 10	-2.644	0.0107	0.0279
Chchd2	ENSMUSG00000070493	coiled-coil-helix-coiled-coil-helix domain containing 2	-1.737	0.0000	0.0000
Chchd2-ps	ENSMUSG00000094320	coiled-coil-helix-coiled-coil-helix domain containing 2, pseudogene	-6.611	0.0010	0.0034
Chchd5	ENSMUSG00000037938	coiled-coil-helix-coiled-coil-helix domain containing 5	-1.813	0.0000	0.0000
Chic1	ENSMUSG00000031327	cysteine-rich hydrophobic domain 1	-1.684	0.0422	0.0899
Chka	ENSMUSG00000024843	choline kinase alpha	-1.720	0.0472	0.0987
Chpf2	ENSMUSG00000038181	chondroitin polymerizing factor 2	-1.646	0.0041	0.0121
Chrd	ENSMUSG00000006958	chordin	-1.788	0.0091	0.0242
Chrdl2	ENSMUSG00000030732	chordin-like 2	-16.640	0.0037	0.0110
Chst12	ENSMUSG00000036599	carbohydrate sulfotransferase 12	-1.846	0.0000	0.0000
Chst7	ENSMUSG00000037347	carbohydrate (N-acetylglucosamino) sulfotransferase 7	-2.507	0.0000	0.0000
Churc1	ENSMUSG00000090258	churchill domain containing 1	-2.741	0.0000	0.0000
Ciao3	ENSMUSG00000002280	cytosolic iron-sulfur assembly component 3	-1.992	0.0000	0.0000
Cib1	ENSMUSG00000030538	calcium and integrin binding 1 (calmyrin)	-1.895	0.0000	0.0000
Cidea	ENSMUSG00000024526	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	-1.735	0.0000	0.0000
Cidec	ENSMUSG00000030278	cell death-inducing DFFA-like effector c	-7.910	0.0003	0.0010
Ciita	ENSMUSG00000022504	class II transactivator	-2.500	0.0211	0.0499
Cipc	ENSMUSG00000034157	CLOCK interacting protein, circadian	-1.802	0.0001	0.0006
Cisd3	ENSMUSG00000078695	CDGSH iron sulfur domain 3	-1.578	0.0000	0.0000
Cish	ENSMUSG00000032578	cytokine inducible SH2-containing protein	-1.914	0.0012	0.0039
Ckb	ENSMUSG00000001270	creatine kinase, brain	-3.712	0.0000	0.0000
Cklf	ENSMUSG00000054400	chemokine-like factor	-1.661	0.0195	0.0468

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DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ckm	ENSMUSG00000030399	creatine kinase, muscle	-1.597	0.0000	0.0000
Cks1b	ENSMUSG00000028044	CDC28 protein kinase 1b	-1.726	0.0050	0.0145
Clca2	ENSMUSG00000036960	chloride channel accessory 2	-19.023	0.0015	0.0050
Clcn7	ENSMUSG00000036636	chloride channel, voltage-sensitive 7	-1.693	0.0000	0.0000
Cldn12	ENSMUSG00000046798	claudin 12	-1.697	0.0000	0.0000
Cldn34c1	ENSMUSG00000079450	claudin 34C1	-2.625	0.0171	0.0419
Cldn5	ENSMUSG00000041378	claudin 5	-1.814	0.0000	0.0002
Clec18a	ENSMUSG00000033633	C-type lectin domain family 18, member A	-2.370	0.0193	0.0463
Clec2d	ENSMUSG00000030157	C-type lectin domain family 2, member d	-3.666	0.0000	0.0000
Clec3b	ENSMUSG00000025784	C-type lectin domain family 3, member b	-2.707	0.0000	0.0000
Clec4a3	ENSMUSG00000043832	C-type lectin domain family 4, member a3	-2.244	0.0036	0.0108
Clec4e	ENSMUSG00000030142	C-type lectin domain family 4, member e	-10.228	0.0478	0.0996
Clic1	ENSMUSG00000007041	chloride intracellular channel 1	-2.163	0.0000	0.0000
Cln5	ENSMUSG00000022125	ceroid-lipofuscinosis, neuronal 5	-1.648	0.0000	0.0000
Clstn3	ENSMUSG00000008153	calsyntenin 3	-2.912	0.0460	0.0964
Cmtm3	ENSMUSG00000031875	CKLF-like MARVEL transmembrane domain containing 3	-2.296	0.0000	0.0000
Cmtm5	ENSMUSG00000040759	CKLF-like MARVEL transmembrane domain containing 5	-4.478	0.0229	0.0535
Cmtm7	ENSMUSG00000032436	CKLF-like MARVEL transmembrane domain containing 7	-2.440	0.0199	0.0475
Cmtr1	ENSMUSG00000024019	cap methyltransferase 1	-1.839	0.0000	0.0000
Cmtr2	ENSMUSG00000046441	cap methyltransferase 2	-1.515	0.0012	0.0040
Cnep1r1	ENSMUSG00000036810	CTD nuclear envelope phosphatase 1 regulatory subunit 1	-1.931	0.0000	0.0000
Cnih1	ENSMUSG00000015759	cornichon family AMPA receptor auxiliary protein 1	-1.724	0.0000	0.0000
Cnksr1	ENSMUSG00000028841	connector enhancer of kinase suppressor of Ras 1	-2.256	0.0142	0.0356
Cnn3	ENSMUSG00000053931	calponin 3, acidic	-1.826	0.0000	0.0000
Cntnap1	ENSMUSG00000017167	contactin associated protein-like 1	-1.688	0.0165	0.0406
Coa3	ENSMUSG00000017188	cytochrome C oxidase assembly factor 3	-2.063	0.0000	0.0000
Coa6	ENSMUSG00000051671	cytochrome c oxidase assembly factor 6	-2.029	0.0000	0.0000
Cog8	ENSMUSG00000031916	component of oligomeric golgi complex 8	-2.271	0.0000	0.0000
Col4a5	ENSMUSG00000031274	collagen, type IV, alpha 5	-1.670	0.0000	0.0000
Colec12	ENSMUSG00000036103	collectin sub-family member 12	-1.517	0.0000	0.0001
Commd2	ENSMUSG00000036513	COMM domain containing 2	-1.664	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Commd4	ENSMUSG00000032299	COMM domain containing 4	-3.290	0.0000	0.0000
Commd9	ENSMUSG00000027163	COMM domain containing 9	-2.170	0.0000	0.0000
Comt	ENSMUSG00000000326	catechol-O-methyltransferase	-2.037	0.0000	0.0000
Comtd1	ENSMUSG00000021773	catechol-O-methyltransferase domain containing 1	-2.569	0.0000	0.0000
Cope	ENSMUSG00000055681	coatomer protein complex, subunit epsilon	-2.403	0.0000	0.0000
Cops3	ENSMUSG00000019373	COP9 signalosome subunit 3	-1.862	0.0000	0.0000
Cops6	ENSMUSG00000019494	COP9 signalosome subunit 6	-1.644	0.0000	0.0000
Cops7a	ENSMUSG00000030127	COP9 signalosome subunit 7A	-2.014	0.0000	0.0000
Coq4	ENSMUSG00000026798	coenzyme Q4	-2.223	0.0000	0.0000
Coq6	ENSMUSG00000021235	coenzyme Q6 monooxygenase	-1.647	0.0000	0.0000
Coq8a	ENSMUSG00000026489	coenzyme Q8A	-1.598	0.0001	0.0002
Coq9	ENSMUSG00000031782	coenzyme Q9	-1.661	0.0000	0.0000
Coro1b	ENSMUSG00000024835	coronin, actin binding protein 1B	-2.283	0.0000	0.0000
Cox14	ENSMUSG00000023020	cytochrome c oxidase assembly protein 14	-1.633	0.0000	0.0000
Cox16	ENSMUSG00000091803	cytochrome c oxidase assembly protein 16	-4.890	0.0000	0.0000
Cox18	ENSMUSG00000035505	cytochrome c oxidase assembly protein 18	-1.809	0.0000	0.0000
Cox4i2	ENSMUSG00000009876	cytochrome c oxidase subunit 4I2	-1.962	0.0000	0.0000
Cox6a1	ENSMUSG00000041697	cytochrome c oxidase subunit 6A1	-1.727	0.0000	0.0000
Cox6a2	ENSMUSG00000030785	cytochrome c oxidase subunit 6A2	-3.933	0.0000	0.0000
Cox6b1	ENSMUSG00000036751	cytochrome c oxidase, subunit 6B1	-2.343	0.0000	0.0000
Cox6c2	ENSMUSG00000066491	cytochrome c oxidase subunit 6C2	-2.899	0.0017	0.0056
Cox7a1	ENSMUSG00000074218	cytochrome c oxidase subunit 7A1	-2.638	0.0000	0.0000
Cox7a2	ENSMUSG00000032330	cytochrome c oxidase subunit 7A2	-3.474	0.0000	0.0000
Cox7a2l	ENSMUSG00000024248	cytochrome c oxidase subunit 7A2 like	-1.980	0.0000	0.0000
Cox7b	ENSMUSG00000031231	cytochrome c oxidase subunit 7B	-1.980	0.0000	0.0000
Cox7b2	ENSMUSG00000049387	cytochrome c oxidase subunit 7B2	-4.617	0.0023	0.0072
Cox8a	ENSMUSG00000035885	cytochrome c oxidase subunit 8A	-3.414	0.0000	0.0000
Cpm	ENSMUSG00000020183	carboxypeptidase M	-1.632	0.0046	0.0134
Cpt1b	ENSMUSG00000078937	carnitine palmitoyltransferase 1b, muscle	-3.678	0.0000	0.0000
Cpt1c	ENSMUSG00000007783	carnitine palmitoyltransferase 1c	-2.203	0.0001	0.0005
Cpt2	ENSMUSG00000028607	carnitine palmitoyltransferase 2	-1.870	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cpxm1	ENSMUSG00000027408	carboxypeptidase X 1 (M14 family)	-3.736	0.0000	0.0000
Crat	ENSMUSG00000026853	carnitine acetyltransferase	-2.068	0.0000	0.0000
Crb2	ENSMUSG00000035403	crumbs family member 2	-10.609	0.0354	0.0775
Creb3l4	ENSMUSG00000027938	cAMP responsive element binding protein 3-like 4	-4.657	0.0036	0.0107
Crip2	ENSMUSG00000006356	cysteine rich protein 2	-1.633	0.0000	0.0000
Crlf2	ENSMUSG00000033467	cytokine receptor-like factor 2	-3.208	0.0000	0.0000
Crtc1	ENSMUSG00000003575	CREB regulated transcription coactivator 1	-1.644	0.0000	0.0000
Cryab	ENSMUSG00000032060	crystallin, alpha B	-1.553	0.0000	0.0000
Crybb1	ENSMUSG00000029343	crystallin, beta B1	-2.416	0.0000	0.0001
Cs	ENSMUSG00000005683	citrate synthase	-1.749	0.0000	0.0000
Csdc2	ENSMUSG00000042109	cold shock domain containing C2, RNA binding	-1.516	0.0217	0.0511
Cse1l	ENSMUSG00000002718	chromosome segregation 1-like (S. cerevisiae)	-1.593	0.0000	0.0000
Csf1r	ENSMUSG00000024621	colony stimulating factor 1 receptor	-1.566	0.0011	0.0038
Csf2rb2	ENSMUSG00000071714	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	-2.845	0.0015	0.0050
Csnk2a1-ps3	ENSMUSG00000101523	casein kinase 2, alpha 1 polypeptide, pseudogene 3	-1.644	0.0145	0.0364
Csnk2b	ENSMUSG00000024387	casein kinase 2, beta polypeptide	-2.686	0.0000	0.0000
Cspg4	ENSMUSG00000032911	chondroitin sulfate proteoglycan 4	-1.712	0.0000	0.0000
Cst6	ENSMUSG00000024846	cystatin E/M	-3.941	0.0000	0.0000
Cstf1	ENSMUSG00000027498	cleavage stimulation factor, 3' pre-RNA, subunit 1	-1.762	0.0000	0.0000
Cstf2	ENSMUSG00000031256	cleavage stimulation factor, 3' pre-RNA subunit 2	-1.510	0.0006	0.0021
Cstpp1	ENSMUSG00000040591	centriolar satellite-associated tubulin polyglutamylase complex regulator 1	-1.722	0.0000	0.0001
Ctbp2	ENSMUSG00000030970	C-terminal binding protein 2	-1.701	0.0000	0.0000
Ctc1	ENSMUSG00000020898	CTS telomere maintenance complex component 1	-1.787	0.0000	0.0000
Ctsa	ENSMUSG00000017760	cathepsin A	-1.512	0.0000	0.0000
Ctsb	ENSMUSG00000021939	cathepsin B	-1.707	0.0000	0.0000
Ctsd	ENSMUSG00000007891	cathepsin D	-3.353	0.0000	0.0000
Ctsh	ENSMUSG00000032359	cathepsin H	-1.541	0.0046	0.0134
Ctso	ENSMUSG00000028015	cathepsin O	-1.683	0.0000	0.0000
Cttnbp2	ENSMUSG00000000416	cortactin binding protein 2	-1.538	0.0463	0.0971
Ctu2	ENSMUSG00000049482	cytosolic thiouridylase subunit 2	-1.745	0.0000	0.0000
Cul2	ENSMUSG00000024231	cullin 2	-1.518	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cuta	ENSMUSG00000024194	cutA divalent cation tolerance homolog	-1.578	0.0000	0.0000
Cuzd1	ENSMUSG00000040205	CUB and zona pellucida-like domains 1	-2.666	0.0001	0.0005
Cx3cl1	ENSMUSG00000031778	chemokine (C-X3-C motif) ligand 1	-1.680	0.0020	0.0064
Cxcr6	ENSMUSG00000048521	chemokine (C-X-C motif) receptor 6	-18.578	0.0021	0.0067
Cyb561d2	ENSMUSG00000037190	cytochrome b-561 domain containing 2	-2.235	0.0000	0.0000
Cyb5a	ENSMUSG00000024646	cytochrome b5 type A (microsomal)	-2.608	0.0000	0.0000
Cyb5r1	ENSMUSG00000026456	cytochrome b5 reductase 1	-1.611	0.0000	0.0000
Cyp1a1	ENSMUSG00000032315	cytochrome P450, family 1, subfamily a, polypeptide 1	-14.849	0.0052	0.0149
Cyp27a1	ENSMUSG00000026170	cytochrome P450, family 27, subfamily a, polypeptide 1	-2.108	0.0001	0.0003
Cyp2ab1	ENSMUSG00000022818	cytochrome P450, family 2, subfamily ab, polypeptide 1	-7.010	0.0153	0.0381
Cyp2d22	ENSMUSG00000061740	cytochrome P450, family 2, subfamily d, polypeptide 22	-1.705	0.0000	0.0001
Cyp4f14	ENSMUSG00000024292	cytochrome P450, family 4, subfamily f, polypeptide 14	-8.461	0.0295	0.0666
Cyp4f16	ENSMUSG00000048440	cytochrome P450, family 4, subfamily f, polypeptide 16	-2.024	0.0000	0.0000
Cyp4f18	ENSMUSG00000003484	cytochrome P450, family 4, subfamily f, polypeptide 18	-9.303	0.0186	0.0449
Cystm1	ENSMUSG00000046727	cysteine-rich transmembrane module containing 1	-2.324	0.0000	0.0000
Cytl1	ENSMUSG00000062329	cytokine-like 1	-2.342	0.0001	0.0005
D330023K18Rik	ENSMUSG00000087269	RIKEN cDNA D330023K18 gene	-3.721	0.0000	0.0000
D430040D24Rik	ENSMUSG00000087589	RIKEN cDNA D430040D24 gene	-1.608	0.0021	0.0067
D630003M21Rik	ENSMUSG00000037813	RIKEN cDNA D630003M21 gene	-1.943	0.0000	0.0000
D630024D03Rik	ENSMUSG00000085772	RIKEN cDNA D630024D03 gene	-28.991	0.0001	0.0005
D630036H23Rik	ENSMUSG00000091007	RIKEN cDNA D630036H23 gene	-11.217	0.0023	0.0073
D830005E20Rik	ENSMUSG00000112707	RIKEN cDNA D830005E20 gene	-1.511	0.0005	0.0017
D930030I03Rik	ENSMUSG00000097576	RIKEN cDNA D930030I03 gene	-11.469	0.0248	0.0574
Dad1	ENSMUSG00000022174	defender against cell death 1	-3.838	0.0000	0.0000
Dap	ENSMUSG00000039168	death-associated protein	-2.263	0.0000	0.0000
Dapp1	ENSMUSG00000028159	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	-1.622	0.0029	0.0088
Dbil5	ENSMUSG00000038057	diazepam binding inhibitor-like 5	-3.312	0.0289	0.0654
Dcaf15	ENSMUSG00000037103	DDB1 and CUL4 associated factor 15	-1.701	0.0000	0.0000
Dcaf4	ENSMUSG00000021222	DDB1 and CUL4 associated factor 4	-1.731	0.0001	0.0005
Dcakd	ENSMUSG00000020935	dephospho-CoA kinase domain containing	-2.513	0.0000	0.0000
Dclre1c	ENSMUSG00000026648	DNA cross-link repair 1C	-1.588	0.0074	0.0203

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Dcn	ENSMUSG00000019929	decorin	-2.346	0.0000	0.0000
Dcp1b	ENSMUSG00000041477	decapping mRNA 1B	-1.737	0.0008	0.0028
Dctn4	ENSMUSG00000024603	dynactin 4	-1.575	0.0000	0.0000
Dctpp1	ENSMUSG00000042462	dCTP pyrophosphatase 1	-1.808	0.0000	0.0000
Dcxr	ENSMUSG00000039450	dicarbonyl L-xylulose reductase	-3.418	0.0000	0.0000
Dda1	ENSMUSG00000074247	DET1 and DDB1 associated 1	-2.270	0.0000	0.0000
Ddost	ENSMUSG00000028757	dolichyl-di-phosphooligosaccharide-protein glycotransferase	-1.567	0.0000	0.0000
Ddx28	ENSMUSG00000045538	DEAD box helicase 28	-2.146	0.0000	0.0000
Ddx39b	ENSMUSG00000019432	DEAD box helicase 39b	-1.681	0.0000	0.0000
Ddx56	ENSMUSG00000004393	DEAD box helicase 56	-1.975	0.0000	0.0000
Defb42	ENSMUSG00000054763	defensin beta 42	-4.738	0.0059	0.0165
Degs1	ENSMUSG00000038633	delta(4)-desaturase, sphingolipid 1	-1.564	0.0000	0.0000
Dele1	ENSMUSG00000024442	DAP3 binding cell death enhancer 1	-2.701	0.0000	0.0000
Dennd10	ENSMUSG00000024993	DENN domain containing 10	-1.525	0.0000	0.0000
Dennd6b	ENSMUSG00000015377	DENN/MADD domain containing 6B	-1.980	0.0000	0.0000
Derl1	ENSMUSG00000022365	Der1-like domain family, member 1	-1.536	0.0000	0.0000
Dgkeos	ENSMUSG00000063109	diacylglycerol kinase, epsilon, opposite strand	-2.046	0.0425	0.0904
Dgkz	ENSMUSG00000040479	diacylglycerol kinase zeta	-1.787	0.0000	0.0000
Dguok	ENSMUSG00000014554	deoxyguanosine kinase	-2.003	0.0000	0.0000
Dhcr7	ENSMUSG00000058454	7-dehydrocholesterol reductase	-1.655	0.0005	0.0018
Dhodh	ENSMUSG00000031730	dihydroorotate dehydrogenase	-1.700	0.0000	0.0000
Dhrs11	ENSMUSG00000034449	dehydrogenase/reductase (SDR family) member 11	-1.732	0.0000	0.0000
Dhrs13	ENSMUSG00000020834	dehydrogenase/reductase (SDR family) member 13	-1.831	0.0000	0.0000
Dhrs7b	ENSMUSG00000042569	dehydrogenase/reductase (SDR family) member 7B	-1.986	0.0000	0.0000
Dhx30	ENSMUSG00000032480	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-1.625	0.0000	0.0000
Dhx32	ENSMUSG00000030986	DEAH (Asp-Glu-Ala-His) box polypeptide 32	-1.633	0.0000	0.0000
Dhx34	ENSMUSG00000006019	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-1.664	0.0000	0.0000
Dhx35	ENSMUSG00000027655	DEAH (Asp-Glu-Ala-His) box polypeptide 35	-1.794	0.0000	0.0000
Dhx37	ENSMUSG00000029480	DEAH (Asp-Glu-Ala-His) box polypeptide 37	-1.849	0.0000	0.0000
Diablo	ENSMUSG00000029433	diablo, IAP-binding mitochondrial protein	-1.734	0.0002	0.0010
Dio3os	ENSMUSG00000113581	deiodinase, iodothyronine type III, opposite strand	-14.495	0.0105	0.0274

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dipk2b	ENSMUSG00000037358	divergent protein kinase domain 2B	-1.748	0.0000	0.0001
Disp3	ENSMUSG00000041544	dispatched RND transporter family member 3	-11.277	0.0311	0.0694
Dlk2	ENSMUSG00000047428	delta like non-canonical Notch ligand 2	-3.208	0.0408	0.0875
Dll4	ENSMUSG00000027314	delta like canonical Notch ligand 4	-1.976	0.0000	0.0000
Dmap1	ENSMUSG00000009640	DNA methyltransferase 1-associated protein 1	-1.562	0.0000	0.0000
Dnaaf2	ENSMUSG00000020973	dynein, axonemal assembly factor 2	-2.148	0.0087	0.0233
Dnajc15	ENSMUSG00000022013	DnaJ heat shock protein family (Hsp40) member C15	-2.575	0.0000	0.0000
Dnajc5b	ENSMUSG00000027606	DnaJ heat shock protein family (Hsp40) member C5 beta	-6.557	0.0280	0.0637
Dnase1l2	ENSMUSG00000024136	deoxyribonuclease 1-like 2	-8.389	0.0005	0.0019
Dnase2a	ENSMUSG00000003812	deoxyribonuclease II alpha	-1.511	0.0000	0.0000
Dnd1	ENSMUSG00000044595	DND microRNA-mediated repression inhibitor 1	-2.726	0.0005	0.0020
Dnpep	ENSMUSG00000026209	aspartyl aminopeptidase	-2.277	0.0000	0.0000
Dnph1	ENSMUSG00000040658	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	-1.710	0.0327	0.0725
Dohh	ENSMUSG00000078440	deoxyhypusine hydroxylase/monooxygenase	-1.530	0.0000	0.0001
Dok7	ENSMUSG00000044716	docking protein 7	-2.565	0.0000	0.0000
Dolpp1	ENSMUSG00000026856	dolichyl pyrophosphate phosphatase 1	-1.647	0.0000	0.0000
Dop1a	ENSMUSG00000034973	DOP1 leucine zipper like protein A	-1.848	0.0000	0.0000
Dop1b	ENSMUSG00000022946	DOP1 leucine zipper like protein B	-1.797	0.0000	0.0000
Dpagt1	ENSMUSG00000032123	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	-2.951	0.0000	0.0000
Dpep1	ENSMUSG00000019278	dipeptidase 1	-1.583	0.0060	0.0168
Dph1	ENSMUSG00000078789	diphthamide biosynthesis 1	-1.944	0.0000	0.0000
Dpm2	ENSMUSG00000026810	dolichol-phosphate (beta-D) mannosyltransferase 2	-2.982	0.0000	0.0000
Dpm3	ENSMUSG00000042737	dolichyl-phosphate mannosyltransferase polypeptide 3	-4.702	0.0000	0.0000
Dpp7	ENSMUSG00000026958	dipeptidylpeptidase 7	-2.635	0.0000	0.0000
Dpp9	ENSMUSG00000001229	dipeptidylpeptidase 9	-1.874	0.0000	0.0000
Dpysl4	ENSMUSG00000025478	dihydropyrimidinase-like 4	-1.613	0.0014	0.0047
Drg2	ENSMUSG00000020537	developmentally regulated GTP binding protein 2	-1.637	0.0000	0.0000
Dstn	ENSMUSG00000015932	destrin	-1.883	0.0000	0.0000
Dusp13	ENSMUSG00000021768	dual specificity phosphatase 13	-5.422	0.0251	0.0580
Dusp14	ENSMUSG00000018648	dual specificity phosphatase 14	-2.325	0.0420	0.0897

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dusp23	ENSMUSG00000026544	dual specificity phosphatase 23	-2.225	0.0000	0.0000
Dxo	ENSMUSG00000040482	decapping exoribonuclease	-2.955	0.0000	0.0000
Dync2i2	ENSMUSG00000039715	dynein 2 intermediate chain 2	-1.548	0.0122	0.0311
Dynll1	ENSMUSG00000009013	dynein light chain LC8-type 1	-1.610	0.0023	0.0074
Dynlt1a	ENSMUSG00000092074	dynein light chain Tctex-type 1A	-5.185	0.0041	0.0122
Dynlt1f	ENSMUSG00000095677	dynein light chain Tctex-type 1F	-2.883	0.0013	0.0043
E130215H24Rik	ENSMUSG00000087406	RIKEN cDNA E130215H24 gene	-4.740	0.0171	0.0417
E130310I04Rik	ENSMUSG00000116665	RIKEN cDNA E130310I04 gene	-2.000	0.0077	0.0209
E430024I08Rik	ENSMUSG00000112964	RIKEN cDNA E430024I08 gene	-1.808	0.0000	0.0000
Eaf2	ENSMUSG00000022838	ELL associated factor 2	-2.231	0.0025	0.0079
Ebi3	ENSMUSG00000003206	Epstein-Barr virus induced gene 3	-10.980	0.0005	0.0020
Ebpl	ENSMUSG00000021928	emopamil binding protein-like	-2.238	0.0021	0.0066
Ech1	ENSMUSG00000053898	enoyl coenzyme A hydratase 1, peroxisomal	-2.103	0.0000	0.0000
Echs1	ENSMUSG00000025465	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	-1.607	0.0000	0.0000
Edc3	ENSMUSG00000038957	enhancer of mRNA decapping 3	-1.519	0.0001	0.0002
Edc4	ENSMUSG00000036270	enhancer of mRNA decapping 4	-1.893	0.0000	0.0000
Eef1akmt1	ENSMUSG00000021951	EEF1A alpha lysine methyltransferase 1	-1.722	0.0000	0.0000
Eef1akmt4	ENSMUSG00000115219	EEF1A lysine methyltransferase 4	-3.699	0.0001	0.0006
Eef2kmt	ENSMUSG00000022544	eukaryotic elongation factor 2 lysine methyltransferase	-2.297	0.0000	0.0000
Eefsec	ENSMUSG00000033216	eukaryotic elongation factor, selenocysteine-tRNA-specific	-2.059	0.0000	0.0001
Efna1	ENSMUSG00000027954	ephrin A1	-2.118	0.0000	0.0000
Efr3a	ENSMUSG00000015002	EFR3 homolog A	-1.511	0.0000	0.0000
Efs	ENSMUSG00000022203	embryonal Fyn-associated substrate	-1.559	0.0031	0.0096
Eif1	ENSMUSG00000035530	eukaryotic translation initiation factor 1	-2.270	0.0000	0.0000
Eif2b3	ENSMUSG00000028683	eukaryotic translation initiation factor 2B, subunit 3	-1.760	0.0000	0.0000
Eif2d	ENSMUSG00000026427	eukaryotic translation initiation factor 2D	-1.817	0.0000	0.0000
Eif3h	ENSMUSG00000022312	eukaryotic translation initiation factor 3, subunit H	-1.738	0.0000	0.0000
Eif3i	ENSMUSG00000028798	eukaryotic translation initiation factor 3, subunit I	-2.894	0.0000	0.0000
Eif3k	ENSMUSG00000053565	eukaryotic translation initiation factor 3, subunit K	-1.955	0.0000	0.0000
Eif3l	ENSMUSG00000033047	eukaryotic translation initiation factor 3, subunit L	-1.802	0.0000	0.0000
Eif3m	ENSMUSG00000027170	eukaryotic translation initiation factor 3, subunit M	-1.790	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Eif3s6-ps2	ENSMUSG00000091697	eukaryotic translation initiation factor 3, subunit 6, pseudogene 2	-2.357	0.0001	0.0006
Eif3s6-ps4	ENSMUSG00000106885	eukaryotic translation initiation factor 3, subunit 6, pseudogene 4	-8.511	0.0338	0.0745
Eif4g2	ENSMUSG00000005610	eukaryotic translation initiation factor 4, gamma 2	-1.509	0.0000	0.0000
Eif5al3-ps	ENSMUSG00000043618	eukaryotic translation initiation factor 5A-like 3, pseudogene	-1.527	0.0002	0.0008
Elmo1	ENSMUSG00000041112	engulfment and cell motility 1	-1.822	0.0012	0.0041
Elmo2	ENSMUSG00000017670	engulfment and cell motility 2	-1.585	0.0000	0.0000
Elmo3	ENSMUSG00000014791	engulfment and cell motility 3	-1.886	0.0014	0.0047
Elmod3	ENSMUSG00000056698	ELMO/CED-12 domain containing 3	-2.123	0.0000	0.0000
Elob	ENSMUSG00000055839	elongin B	-2.571	0.0000	0.0000
Elobl	ENSMUSG00000057534	elongin B-like	-3.618	0.0155	0.0384
Elof1	ENSMUSG00000013822	ELF1 homolog, elongation factor 1	-2.183	0.0000	0.0000
Elovl1	ENSMUSG00000006390	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.657	0.0000	0.0000
Elovl4	ENSMUSG00000032262	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	-8.692	0.0376	0.0817
Elp4	ENSMUSG00000027167	elongator acetyltransferase complex subunit 4	-1.667	0.0000	0.0000
Emc6	ENSMUSG00000047260	ER membrane protein complex subunit 6	-1.847	0.0000	0.0000
Emcn	ENSMUSG00000054690	endomucin	-1.705	0.0000	0.0000
Emd	ENSMUSG00000001964	emerin	-1.641	0.0000	0.0000
Eme2	ENSMUSG00000073436	essential meiotic structure-specific endonuclease subunit 2	-1.788	0.0001	0.0005
Emid1	ENSMUSG00000034164	EMI domain containing 1	-1.684	0.0160	0.0395
Emp2	ENSMUSG00000022505	epithelial membrane protein 2	-1.610	0.0000	0.0000
Emp3	ENSMUSG00000040212	epithelial membrane protein 3	-4.186	0.0000	0.0000
Eng	ENSMUSG00000026814	endoglin	-2.054	0.0000	0.0000
Eno1	ENSMUSG00000063524	enolase 1, alpha non-neuron	-1.694	0.0000	0.0000
Eno1b	ENSMUSG00000059040	enolase 1B, retrotransposed	-3.883	0.0000	0.0000
Eno3	ENSMUSG00000060600	enolase 3, beta muscle	-1.586	0.0000	0.0000
Enox1	ENSMUSG00000022012	ecto-NOX disulfide-thiol exchanger 1	-1.770	0.0296	0.0667
Enpep	ENSMUSG00000028024	glutamyl aminopeptidase	-1.706	0.0000	0.0000
Enpp6	ENSMUSG00000038173	ectonucleotide pyrophosphatase/phosphodiesterase 6	-1.691	0.0000	0.0001
Entpd2	ENSMUSG00000015085	ectonucleoside triphosphate diphosphohydrolase 2	-3.529	0.0000	0.0000
Entpd6	ENSMUSG00000033068	ectonucleoside triphosphate diphosphohydrolase 6	-1.633	0.0000	0.0000
Eola1	ENSMUSG00000045237	endothelium and lymphocyte associated ASCH domain 1	-1.816	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Epcam	ENSMUSG00000045394	epithelial cell adhesion molecule	-11.474	0.0271	0.0620
Epdr1	ENSMUSG00000002808	ependymin related protein 1 (zebrafish)	-1.817	0.0003	0.0013
Epg5	ENSMUSG00000039840	ectopic P-granules autophagy protein 5 homolog (C. elegans)	-1.855	0.0000	0.0000
Ephx1	ENSMUSG00000038776	epoxide hydrolase 1, microsomal	-1.945	0.0000	0.0001
Ephx2	ENSMUSG00000022040	epoxide hydrolase 2, cytoplasmic	-2.033	0.0000	0.0000
Erap1	ENSMUSG00000021583	endoplasmic reticulum aminopeptidase 1	-1.530	0.0000	0.0000
Ercc1	ENSMUSG00000003549	excision repair cross-complementing rodent repair deficiency, complementation group 1	-1.912	0.0000	0.0000
Ercc2	ENSMUSG00000030400	excision repair cross-complementing rodent repair deficiency, complementation group 2	-2.253	0.0000	0.0000
Ermard	ENSMUSG00000036552	ER membrane associated RNA degradation	-1.880	0.0000	0.0000
Esd	ENSMUSG00000021996	esterase D/formylglutathione hydrolase	-1.657	0.0000	0.0000
Esrrb	ENSMUSG00000021255	estrogen related receptor, beta	-1.601	0.0000	0.0000
Ethe1	ENSMUSG00000064254	ethylmalonic encephalopathy 1	-4.026	0.0000	0.0000
Exoc3l4	ENSMUSG00000021280	exocyst complex component 3-like 4	-2.300	0.0001	0.0006
Exoc7	ENSMUSG00000020792	exocyst complex component 7	-1.500	0.0000	0.0000
Exosc5	ENSMUSG00000061286	exosome component 5	-1.653	0.0000	0.0000
Ext2	ENSMUSG00000027198	exostosin glycosyltransferase 2	-1.791	0.0001	0.0003
F2rl3	ENSMUSG00000050147	coagulation factor II (thrombin) receptor-like 3	-4.555	0.0001	0.0004
F8	ENSMUSG00000031196	coagulation factor VIII	-1.791	0.0001	0.0004
F8a	ENSMUSG00000078317	factor 8-associated gene A	-1.693	0.0000	0.0000
Faap100	ENSMUSG00000025384	Fanconi anemia core complex associated protein 100	-3.403	0.0000	0.0000
Faap24	ENSMUSG00000030493	Fanconi anemia core complex associated protein 24	-1.579	0.0324	0.0720
Fah	ENSMUSG00000030630	fumarylacetoacetate hydrolase	-2.158	0.0002	0.0009
Fam120b	ENSMUSG00000014763	family with sequence similarity 120, member B	-1.585	0.0000	0.0000
Fam13c	ENSMUSG00000043259	family with sequence similarity 13, member C	-1.513	0.0000	0.0000
Fam189b	ENSMUSG00000032657	family with sequence similarity 189, member B	-1.841	0.0000	0.0000
Fam205c	ENSMUSG00000050141	family with sequence similarity 205, member C	-3.731	0.0001	0.0003
Fam222b	ENSMUSG00000037750	family with sequence similarity 222, member B	-1.759	0.0000	0.0000
Fam228b	ENSMUSG00000050545	family with sequence similarity 228, member B	-2.076	0.0002	0.0008
Fam229b	ENSMUSG00000051736	family with sequence similarity 229, member B	-2.309	0.0000	0.0000
Fam234a	ENSMUSG00000024187	family with sequence similarity 234, member A	-2.048	0.0000	0.0000
Fam53b	ENSMUSG00000030956	family with sequence similarity 53, member B	-1.774	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fam72a	ENSMUSG00000055184	family with sequence similarity 72, member A	-1.836	0.0127	0.0322
Fan1	ENSMUSG00000033458	FANCD2/FANCI-associated nuclease 1	-1.515	0.0005	0.0019
Fancb	ENSMUSG00000047757	Fanconi anemia, complementation group B	-1.645	0.0086	0.0231
Fancg	ENSMUSG00000028453	Fanconi anemia, complementation group G	-1.902	0.0004	0.0015
Fanci	ENSMUSG00000039187	Fanconi anemia, complementation group I	-3.048	0.0405	0.0869
Fap	ENSMUSG00000000392	fibroblast activation protein	-1.671	0.0007	0.0024
Fars2	ENSMUSG00000021420	phenylalanine-tRNA synthetase 2 (mitochondrial)	-1.691	0.0000	0.0000
Farsb	ENSMUSG00000026245	phenylalanyl-tRNA synthetase, beta subunit	-2.279	0.0000	0.0000
Fasn	ENSMUSG00000025153	fatty acid synthase	-1.780	0.0001	0.0003
Fastkd1	ENSMUSG00000027086	FAST kinase domains 1	-1.760	0.0000	0.0000
Fastkd2	ENSMUSG00000025962	FAST kinase domains 2	-1.623	0.0000	0.0000
Fau	ENSMUSG00000038274	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	-1.943	0.0000	0.0000
Fbln2	ENSMUSG00000064080	fibulin 2	-1.570	0.0022	0.0069
Fbln5	ENSMUSG00000021186	fibulin 5	-1.593	0.0000	0.0000
Fbxl15	ENSMUSG00000025226	F-box and leucine-rich repeat protein 15	-5.591	0.0000	0.0000
Fbxl22	ENSMUSG00000050503	F-box and leucine-rich repeat protein 22	-2.111	0.0000	0.0001
Fbxl6	ENSMUSG00000022559	F-box and leucine-rich repeat protein 6	-2.086	0.0000	0.0000
Fbxo21	ENSMUSG00000032898	F-box protein 21	-1.576	0.0000	0.0000
Fbxo42	ENSMUSG00000028920	F-box protein 42	-1.551	0.0000	0.0002
Fbxo48	ENSMUSG00000044966	F-box protein 48	-20.121	0.0015	0.0051
Fbxo6	ENSMUSG00000055401	F-box protein 6	-1.683	0.0000	0.0000
Fbxo8	ENSMUSG00000038206	F-box protein 8	-1.675	0.0000	0.0000
Fcer1g	ENSMUSG00000058715	Fc receptor, IgE, high affinity I, gamma polypeptide	-2.872	0.0000	0.0000
Fcgr2b	ENSMUSG00000026656	Fc receptor, IgG, low affinity IIb	-1.847	0.0028	0.0086
Fcgr3	ENSMUSG00000059498	Fc receptor, IgG, low affinity III	-1.938	0.0004	0.0016
Fcna	ENSMUSG00000026938	ficolin A	-1.599	0.0146	0.0365
Fcsk	ENSMUSG00000033703	fucose kinase	-1.662	0.0001	0.0004
Fem1a	ENSMUSG00000043683	fem 1 homolog a	-1.764	0.0000	0.0000
Fgf10	ENSMUSG00000021732	fibroblast growth factor 10	-1.796	0.0096	0.0253
Fgf12	ENSMUSG00000022523	fibroblast growth factor 12	-3.586	0.0002	0.0009
Fgfr3	ENSMUSG00000054252	fibroblast growth factor receptor 3	-1.974	0.0001	0.0003

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fggy	ENSMUSG00000028573	FGGY carbohydrate kinase domain containing	-1.832	0.0008	0.0030
Fh1	ENSMUSG00000026526	fumarate hydratase 1	-1.740	0.0000	0.0000
Fhip1a	ENSMUSG00000051000	FHF complex subunit HOOK interacting protein 1A	-1.868	0.0000	0.0000
Fhl1	ENSMUSG00000023092	four and a half LIM domains 1	-1.583	0.0002	0.0006
Fhl2	ENSMUSG00000008136	four and a half LIM domains 2	-2.473	0.0000	0.0000
Ficd	ENSMUSG00000053334	FIC domain containing	-1.868	0.0000	0.0000
Fitm1	ENSMUSG00000022215	fat storage-inducing transmembrane protein 1	-3.736	0.0000	0.0000
Fiz1	ENSMUSG00000061374	Flt3 interacting zinc finger protein 1	-1.557	0.0038	0.0113
Fkbp10	ENSMUSG00000001555	FK506 binding protein 10	-1.914	0.0000	0.0000
Fkbp11	ENSMUSG00000003355	FK506 binding protein 11	-2.041	0.0003	0.0012
Flad1	ENSMUSG00000042642	flavin adenine dinucleotide synthetase 1	-1.525	0.0000	0.0000
Flnc	ENSMUSG00000068699	filamin C, gamma	-1.589	0.0000	0.0001
Flrt3	ENSMUSG00000051379	fibronectin leucine rich transmembrane protein 3	-2.327	0.0460	0.0966
Fmo4	ENSMUSG00000026692	flavin containing monooxygenase 4	-11.281	0.0259	0.0596
Fndc1	ENSMUSG00000071984	fibronectin type III domain containing 1	-1.639	0.0369	0.0803
Fndc10	ENSMUSG00000074738	fibronectin type III domain containing 10	-1.906	0.0004	0.0015
Fntb	ENSMUSG00000033373	farnesyltransferase, CAAX box, beta	-1.530	0.0000	0.0001
Focad	ENSMUSG00000038368	focadhesin	-2.047	0.0000	0.0000
Folr2	ENSMUSG00000032725	folate receptor 2 (fetal)	-2.362	0.0000	0.0000
Foxs1	ENSMUSG00000074676	forkhead box S1	-3.234	0.0000	0.0000
Fpgs	ENSMUSG00000009566	folylpolyglutamyl synthetase	-1.796	0.0002	0.0007
Frem2	ENSMUSG00000037016	Fras1 related extracellular matrix protein 2	-1.581	0.0098	0.0259
Frg2f1	ENSMUSG00000087385	FSHD region gene 2 family member 1	-2.004	0.0000	0.0000
Frmd5	ENSMUSG00000027238	FERM domain containing 5	-1.509	0.0030	0.0092
Frmd8	ENSMUSG00000024816	FERM domain containing 8	-2.072	0.0000	0.0000
Frmd8os	ENSMUSG00000043488	FERM domain containing 8, opposite strand	-5.305	0.0000	0.0000
Fscn2	ENSMUSG00000025380	fascin actin-bundling protein 2	-17.474	0.0070	0.0193
Fstl4	ENSMUSG00000036264	follistatin-like 4	-1.838	0.0099	0.0261
Ftl1	ENSMUSG00000050708	ferritin light polypeptide 1	-2.529	0.0000	0.0000
Fuom	ENSMUSG00000025466	fucose mutarotase	-1.635	0.0000	0.0000
Fxn	ENSMUSG00000059363	frataxin	-4.173	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fxyd1	ENSMUSG00000036570	FXYD domain-containing ion transport regulator 1	-2.057	0.0000	0.0000
Fxyd2	ENSMUSG00000059412	FXYD domain-containing ion transport regulator 2	-2.304	0.0002	0.0010
Fxyd5	ENSMUSG00000009687	FXYD domain-containing ion transport regulator 5	-1.591	0.0006	0.0023
Fxyd7	ENSMUSG00000036578	FXYD domain-containing ion transport regulator 7	-5.653	0.0148	0.0370
G0s2	ENSMUSG00000009633	G0/G1 switch gene 2	-3.445	0.0000	0.0000
G6pc3	ENSMUSG00000034793	glucose 6 phosphatase, catalytic, 3	-2.080	0.0000	0.0000
G6pdx	ENSMUSG00000031400	glucose-6-phosphate dehydrogenase X-linked	-1.536	0.0000	0.0000
Gaa	ENSMUSG00000025579	glucosidase, alpha, acid	-2.127	0.0000	0.0000
Gadd45g	ENSMUSG00000021453	growth arrest and DNA-damage-inducible 45 gamma	-1.614	0.0236	0.0550
Galns	ENSMUSG00000015027	galactosamine (N-acetyl)-6-sulfate sulfatase	-1.769	0.0000	0.0001
Galt	ENSMUSG00000036073	galactose-1-phosphate uridyl transferase	-2.017	0.0000	0.0000
Gamt	ENSMUSG00000020150	guanidinoacetate methyltransferase	-1.640	0.0143	0.0358
Ganab	ENSMUSG00000071650	alpha glucosidase 2 alpha neutral subunit	-1.814	0.0000	0.0000
Garre1	ENSMUSG00000066571	granule associated Rac and RHOG effector 1	-1.717	0.0000	0.0000
Gask1b	ENSMUSG00000027955	golgi associated kinase 1B	-1.769	0.0080	0.0216
Gatd3a	ENSMUSG00000053329	glutamine amidotransferase like class 1 domain containing 3A	-1.526	0.0000	0.0000
Gba	ENSMUSG00000028048	glucosidase, beta, acid	-1.525	0.0003	0.0010
Gchfr	ENSMUSG00000046814	GTP cyclohydrolase I feedback regulator	-1.522	0.0007	0.0025
Gcn1	ENSMUSG00000041638	GCN1 activator of EIF2AK4	-1.672	0.0000	0.0000
Gde1	ENSMUSG00000033917	glycerophosphodiester phosphodiesterase 1	-2.042	0.0000	0.0000
Gdf15	ENSMUSG00000038508	growth differentiation factor 15	-4.639	0.0000	0.0000
Gdnf	ENSMUSG00000022144	glial cell line derived neurotrophic factor	-3.418	0.0362	0.0790
Gdpd3	ENSMUSG00000030703	glycerophosphodiester phosphodiesterase domain containing 3	-1.657	0.0000	0.0000
Gdpgp1	ENSMUSG00000050973	GDP-D-glucose phosphorylase 1	-1.651	0.0004	0.0013
Gemin5	ENSMUSG00000037275	gem nuclear organelle associated protein 5	-1.955	0.0000	0.0000
Get3	ENSMUSG00000052456	guided entry of tail-anchored proteins factor 3, ATPase	-1.891	0.0000	0.0000
Gfer	ENSMUSG00000040888	growth factor, augmenter of liver regeneration	-1.697	0.0000	0.0000
Gfra3	ENSMUSG00000024366	glial cell line derived neurotrophic factor family receptor alpha 3	-2.439	0.0089	0.0237
Ggnbp1	ENSMUSG00000048731	gametogenetin binding protein 1	-1.892	0.0000	0.0000
Ggt5	ENSMUSG00000006344	gamma-glutamyltransferase 5	-2.165	0.0000	0.0000
Ggt7	ENSMUSG00000027603	gamma-glutamyltransferase 7	-1.925	0.0085	0.0228

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gipc1	ENSMUSG00000019433	GIPC PDZ domain containing family, member 1	-1.716	0.0000	0.0000
Git2	ENSMUSG00000041890	GIT ArfGAP 2	-1.625	0.0000	0.0000
Gkn3	ENSMUSG00000030048	gastrokine 3	-4.372	0.0345	0.0759
Glb1	ENSMUSG00000045594	galactosidase, beta 1	-1.776	0.0000	0.0000
Glb1l	ENSMUSG00000026200	galactosidase, beta 1-like	-1.501	0.0127	0.0324
Glis1	ENSMUSG00000034762	GLIS family zinc finger 1	-4.998	0.0266	0.0610
Glmp	ENSMUSG00000001418	glycosylated lysosomal membrane protein	-2.285	0.0000	0.0000
Glo1-ps	ENSMUSG00000075391	glyoxalase 1, pseudogene	-3.849	0.0000	0.0000
Glt8d2	ENSMUSG00000020251	glycosyltransferase 8 domain containing 2	-1.983	0.0153	0.0381
Gm10039	ENSMUSG00000091478	predicted pseudogene 10039	-2.147	0.0000	0.0000
Gm10053	ENSMUSG00000058927	predicted gene 10053	-2.137	0.0024	0.0076
Gm10059	ENSMUSG00000059064	predicted pseudogene 10059	-27.111	0.0006	0.0022
Gm10076	ENSMUSG00000060143	predicted gene 10076	-26.767	0.0000	0.0000
Gm10097	ENSMUSG00000096553	predicted gene 10097	-2.370	0.0331	0.0731
Gm10123	ENSMUSG00000062933	predicted pseudogene 10123	-6.576	0.0022	0.0071
Gm10131	ENSMUSG00000063412	predicted pseudogene 10131	-2.763	0.0347	0.0763
Gm10146	ENSMUSG00000064317	predicted gene 10146	-17.559	0.0041	0.0122
Gm10226	ENSMUSG00000067929	predicted gene 10226	-8.240	0.0000	0.0000
Gm10263	ENSMUSG00000066407	predicted gene 10263	-2.833	0.0000	0.0000
Gm10275	ENSMUSG00000069682	predicted pseudogene 10275	-3.617	0.0000	0.0000
Gm10288	ENSMUSG00000070343	predicted gene 10288	-4.753	0.0000	0.0000
Gm10291	ENSMUSG00000070443	predicted pseudogene 10291	-2.393	0.0016	0.0053
Gm10359	ENSMUSG00000094708	predicted gene 10359	-10.510	0.0034	0.0104
Gm10382	ENSMUSG00000072612	predicted gene 10382	-9.130	0.0138	0.0347
Gm10435	ENSMUSG00000072902	predicted gene 10435	-1.540	0.0220	0.0517
Gm10443	ENSMUSG00000072940	predicted pseudogene 10443	-2.142	0.0270	0.0617
Gm10509	ENSMUSG00000073448	predicted gene 10509	-4.921	0.0000	0.0001
Gm10557	ENSMUSG00000073647	predicted gene 10557	-1.716	0.0034	0.0101
Gm10570	ENSMUSG00000073752	predicted gene 10570	-1.556	0.0071	0.0195
Gm10605	ENSMUSG00000097974	predicted gene 10605	-3.207	0.0216	0.0510
Gm10608	ENSMUSG00000111197	predicted gene 10608	-25.535	0.0020	0.0064

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm10736	ENSMUSG00000096842	predicted gene 10736	-81.090	0.0000	0.0000
Gm10790	ENSMUSG00000113856	predicted gene 10790	-29.305	0.0003	0.0012
Gm10819	ENSMUSG00000075268	predicted gene 10819	-3.469	0.0015	0.0050
Gm10863	ENSMUSG00000075555	predicted gene 10863	-6.316	0.0256	0.0589
Gm11451	ENSMUSG00000083567	predicted gene 11451	-2.985	0.0009	0.0030
Gm11470	ENSMUSG00000082665	predicted gene 11470	-13.759	0.0095	0.0251
Gm11512	ENSMUSG00000081043	predicted gene 11512	-2.068	0.0079	0.0214
Gm11517	ENSMUSG00000081249	predicted gene 11517	-5.168	0.0033	0.0099
Gm11658	ENSMUSG00000081524	predicted gene 11658	-6.681	0.0054	0.0153
Gm11702	ENSMUSG00000084277	predicted gene 11702	-33.761	0.0000	0.0002
Gm11730	ENSMUSG00000087057	predicted gene 11730	-2.513	0.0173	0.0422
Gm11734	ENSMUSG00000085419	predicted gene 11734	-1.723	0.0101	0.0265
Gm11808	ENSMUSG00000068240	predicted gene 11808	-4.199	0.0000	0.0000
Gm11816	ENSMUSG00000086233	predicted gene 11816	-2.694	0.0004	0.0016
Gm11868	ENSMUSG00000050550	predicted gene 11868	-1.892	0.0000	0.0000
Gm11942	ENSMUSG00000094344	predicted gene 11942	-2.153	0.0000	0.0000
Gm11953	ENSMUSG00000082816	predicted gene 11953	-3.104	0.0001	0.0006
Gm11960	ENSMUSG00000081974	predicted gene 11960	-6.693	0.0000	0.0000
Gm11993	ENSMUSG00000101841	predicted gene 11993	-11.380	0.0121	0.0310
Gm12167	ENSMUSG00000085853	predicted gene 12167	-4.067	0.0000	0.0000
Gm12182	ENSMUSG00000083460	predicted gene 12182	-4.879	0.0003	0.0012
Gm12224	ENSMUSG00000085888	predicted gene 12224	-1.939	0.0188	0.0453
Gm12250	ENSMUSG00000082292	predicted gene 12250	-3.074	0.0007	0.0024
Gm12319	ENSMUSG00000087523	predicted gene 12319	-2.725	0.0000	0.0000
Gm12337	ENSMUSG00000084224	predicted gene 12337	-3.184	0.0287	0.0650
Gm12350	ENSMUSG00000095588	predicted gene 12350	-4.177	0.0017	0.0056
Gm12416	ENSMUSG00000083044	predicted gene 12416	-2.002	0.0058	0.0162
Gm12426	ENSMUSG00000087500	predicted gene 12426	-12.926	0.0059	0.0166
Gm12439	ENSMUSG00000080850	predicted gene 12439	-1.913	0.0000	0.0000
Gm12454	ENSMUSG00000087142	predicted gene 12454	-3.172	0.0324	0.0719
Gm12519	ENSMUSG00000085643	predicted gene 12519	-1.672	0.0269	0.0616

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm12537	ENSMUSG00000095042	predicted gene 12537	-3.240	0.0017	0.0056
Gm12592	ENSMUSG00000053263	predicted gene 12592	-2.715	0.0072	0.0197
Gm12655	ENSMUSG00000087128	predicted gene 12655	-1.843	0.0000	0.0002
Gm12727	ENSMUSG00000082768	predicted gene 12727	-16.001	0.0119	0.0304
Gm12751	ENSMUSG00000062554	predicted gene 12751	-4.063	0.0000	0.0000
Gm12791	ENSMUSG00000081121	predicted gene 12791	-4.084	0.0274	0.0625
Gm12864	ENSMUSG00000082143	predicted gene 12864	-17.689	0.0038	0.0114
Gm12925	ENSMUSG00000087307	predicted gene 12925	-2.420	0.0208	0.0493
Gm12963	ENSMUSG00000085517	predicted gene 12963	-4.192	0.0178	0.0432
Gm13090	ENSMUSG00000078491	predicted gene 13090	-6.840	0.0022	0.0069
Gm13092	ENSMUSG00000085787	predicted gene 13092	-6.026	0.0000	0.0000
Gm13192	ENSMUSG00000069188	predicted gene 13192	-24.231	0.0007	0.0026
Gm13215	ENSMUSG00000081394	predicted gene 13215	-23.964	0.0007	0.0025
Gm13292	ENSMUSG00000082424	predicted gene 13292	-3.163	0.0184	0.0445
Gm13324	ENSMUSG00000085100	predicted gene 13324	-7.136	0.0305	0.0684
Gm13410	ENSMUSG00000083116	predicted gene 13410	-7.104	0.0007	0.0026
Gm13563	ENSMUSG00000085767	predicted gene 13563	-3.832	0.0005	0.0019
Gm13707	ENSMUSG00000085768	predicted gene 13707	-9.724	0.0275	0.0627
Gm13919	ENSMUSG00000085417	predicted gene 13919	-12.262	0.0273	0.0624
Gm14022	ENSMUSG00000087151	predicted gene 14022	-2.994	0.0007	0.0024
Gm14026	ENSMUSG00000082274	predicted gene 14026	-1.785	0.0405	0.0868
Gm14048	ENSMUSG00000080989	predicted gene 14048	-2.832	0.0350	0.0768
Gm14097	ENSMUSG00000084839	predicted gene 14097	-1.865	0.0025	0.0079
Gm14117	ENSMUSG00000042938	predicted gene 14117	-3.360	0.0003	0.0013
Gm14122	ENSMUSG00000083964	predicted gene 14122	-5.056	0.0039	0.0116
Gm14130	ENSMUSG00000081494	predicted gene 14130	-6.508	0.0000	0.0000
Gm14165	ENSMUSG00000081434	predicted gene 14165	-10.972	0.0000	0.0000
Gm14269	ENSMUSG00000084067	predicted gene 14269	-3.116	0.0271	0.0620
Gm14292	ENSMUSG00000061897	predicted gene 14292	-3.467	0.0000	0.0000
Gm14303	ENSMUSG00000081344	predicted gene 14303	-1.976	0.0022	0.0069
Gm14321	ENSMUSG00000084797	predicted gene 14321	-21.854	0.0021	0.0066

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm14327	ENSMUSG00000074521	predicted gene 14327	-3.191	0.0001	0.0003
Gm14403	ENSMUSG00000094786	predicted gene 14403	-1.855	0.0000	0.0000
Gm14539	ENSMUSG00000084830	predicted gene 14539	-2.111	0.0000	0.0000
Gm14902	ENSMUSG00000086736	predicted gene 14902	-25.174	0.0003	0.0010
Gm15191	ENSMUSG00000082778	predicted gene 15191	-2.225	0.0054	0.0154
Gm15361	ENSMUSG00000083283	predicted pseudogene 15361	-2.316	0.0000	0.0001
Gm15420	ENSMUSG00000087387	predicted gene 15420	-3.026	0.0034	0.0102
Gm15446	ENSMUSG00000090015	predicted gene 15446	-2.251	0.0000	0.0001
Gm15499	ENSMUSG00000086722	predicted gene 15499	-14.999	0.0084	0.0226
Gm15545	ENSMUSG00000087138	predicted gene 15545	-1.575	0.0399	0.0858
Gm15564	ENSMUSG00000086324	predicted gene 15564	-4376.174	0.0000	0.0000
Gm15608	ENSMUSG00000112110	predicted gene 15608	-14.553	0.0066	0.0182
Gm15626	ENSMUSG00000081822	predicted gene 15626	-4.139	0.0121	0.0309
Gm15651	ENSMUSG00000089663	predicted gene 15651	-2.194	0.0445	0.0938
Gm15703	ENSMUSG00000083890	predicted gene 15703	-6.871	0.0322	0.0717
Gm15753	ENSMUSG00000082088	predicted gene 15753	-16.178	0.0048	0.0140
Gm15832	ENSMUSG00000085894	predicted gene 15832	-5.145	0.0273	0.0624
Gm15879	ENSMUSG00000084790	predicted gene 15879	-2.376	0.0258	0.0595
Gm15932	ENSMUSG00000086341	predicted gene 15932	-3.467	0.0194	0.0465
Gm15950	ENSMUSG00000089818	predicted gene 15950	-20.142	0.0040	0.0119
Gm15972	ENSMUSG00000086287	predicted gene 15972	-4.091	0.0000	0.0000
Gm16177	ENSMUSG00000082484	predicted gene 16177	-4.626	0.0001	0.0003
Gm16253	ENSMUSG00000087610	predicted gene 16253	-1.610	0.0008	0.0029
Gm16378	ENSMUSG00000095762	predicted gene 16378	-3.205	0.0000	0.0000
Gm16380	ENSMUSG00000059830	predicted pseudogene 16380	-2.004	0.0073	0.0200
Gm16418	ENSMUSG00000084093	predicted pseudogene 16418	-2.184	0.0267	0.0612
Gm16534	ENSMUSG00000090157	predicted gene 16534	-2.246	0.0002	0.0008
Gm16574	ENSMUSG00000089769	predicted gene 16574	-2.053	0.0301	0.0676
Gm1673	ENSMUSG00000070858	predicted gene 1673	-4.207	0.0002	0.0009
Gm16793	ENSMUSG00000097357	predicted gene, 16793	-2.236	0.0001	0.0005
Gm17017	ENSMUSG00000090246	predicted gene 17017	-23.713	0.0004	0.0016

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm17068	ENSMUSG00000078528	predicted gene 17068	-2.358	0.0305	0.0684
Gm17354	ENSMUSG00000091985	predicted gene, 17354	-1.732	0.0273	0.0624
Gm17511	ENSMUSG00000090460	predicted gene, 17511	-12.223	0.0000	0.0000
Gm17799	ENSMUSG00000097945	predicted gene, 17799	-5.725	0.0047	0.0137
Gm18095	ENSMUSG00000115856	predicted gene, 18095	-3.171	0.0057	0.0160
Gm18194	ENSMUSG00000109724	predicted gene, 18194	-4.670	0.0425	0.0904
Gm18234	ENSMUSG00000116926	predicted gene, 18234	-3.404	0.0000	0.0000
Gm18283	ENSMUSG00000115920	predicted gene, 18283	-6.244	0.0401	0.0862
Gm18537	ENSMUSG00000108484	predicted gene, 18537	-25.390	0.0005	0.0018
Gm18734	ENSMUSG00000092438	predicted gene, 18734	-48.652	0.0000	0.0001
Gm18736	ENSMUSG00000117300	predicted gene, 18736	-2.272	0.0000	0.0000
Gm18943	ENSMUSG00000109472	predicted gene, 18943	-15.273	0.0066	0.0184
Gm19052	ENSMUSG00000117492	predicted gene, 19052	-8.906	0.0406	0.0871
Gm19412	ENSMUSG00000101438	predicted gene, 19412	-6.720	0.0466	0.0976
Gm1943	ENSMUSG00000110528	predicted gene 1943	-32.630	0.0002	0.0007
Gm19503	ENSMUSG00000100551	predicted gene, 19503	-3.802	0.0471	0.0984
Gm19605	ENSMUSG00000113585	predicted gene, 19605	-1.957	0.0050	0.0145
Gm19689	ENSMUSG00000117399	predicted gene, 19689	-15.226	0.0063	0.0175
Gm19810	ENSMUSG00000111897	predicted gene, 19810	-18.145	0.0049	0.0143
Gm20490	ENSMUSG00000092596	predicted gene 20490	-3.707	0.0008	0.0029
Gm20559	ENSMUSG00000106734	predicted gene, 20559	-1.850	0.0261	0.0601
Gm20604	ENSMUSG00000041716	predicted gene 20604	-2.677	0.0000	0.0000
Gm20619	ENSMUSG00000093482	predicted gene 20619	-2.170	0.0002	0.0008
Gm20667	ENSMUSG00000093726	predicted gene 20667	-13.892	0.0062	0.0173
Gm20685	ENSMUSG00000093380	predicted gene 20685	-14.058	0.0332	0.0733
Gm20707	ENSMUSG00000093594	predicted gene 20707	-2.793	0.0111	0.0287
Gm20939	ENSMUSG00000095193	predicted gene, 20939	-3.090	0.0122	0.0312
Gm21811	ENSMUSG00000096401	predicted gene, 21811	-2.157	0.0310	0.0692
Gm2199	ENSMUSG00000083829	predicted gene 2199	-9.105	0.0207	0.0491
Gm23297	ENSMUSG00000065118	predicted gene, 23297	-17.737	0.0043	0.0126
Gm2383	ENSMUSG00000097628	predicted gene 2383	-2.965	0.0264	0.0606

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm2445	ENSMUSG00000098113	predicted gene 2445	-3.585	0.0000	0.0002
Gm24474	ENSMUSG00000114005	predicted gene, 24474	-1.723	0.0092	0.0245
Gm25135	ENSMUSG00000064582	predicted gene, 25135	-9.750	0.0436	0.0922
Gm2573	ENSMUSG00000115017	predicted gene 2573	-5.730	0.0000	0.0002
Gm25788	ENSMUSG00000064655	predicted gene, 25788	-16.104	0.0067	0.0186
Gm2614	ENSMUSG00000113113	predicted gene 2614	-6.469	0.0014	0.0046
Gm26397	ENSMUSG00000065637	predicted gene, 26397	-12.849	0.0135	0.0341
Gm26493	ENSMUSG00000065089	predicted gene, 26493	-18.785	0.0046	0.0134
Gm26569	ENSMUSG00000097313	predicted gene, 26569	-35.211	0.0002	0.0008
Gm26620	ENSMUSG00000096968	predicted gene, 26620	-2.780	0.0186	0.0448
Gm26621	ENSMUSG00000096967	predicted gene, 26621	-2.265	0.0296	0.0667
Gm26795	ENSMUSG00000097776	predicted gene, 26795	-1.633	0.0184	0.0444
Gm27030	ENSMUSG00000098221	predicted gene, 27030	-26.729	0.0004	0.0013
Gm27045	ENSMUSG00000098211	predicted gene, 27045	-3.376	0.0131	0.0332
Gm27232	ENSMUSG00000098573	predicted gene 27232	-8.587	0.0112	0.0290
Gm28231	ENSMUSG00000100782	predicted gene 28231	-2.923	0.0046	0.0135
Gm28386	ENSMUSG00000101849	predicted gene 28386	-19.321	0.0027	0.0085
Gm28438	ENSMUSG00000101939	predicted gene 28438	-3.014	0.0000	0.0000
Gm28455	ENSMUSG00000100490	predicted gene 28455	-14.148	0.0091	0.0241
Gm28578	ENSMUSG00000100417	predicted gene 28578	-6.824	0.0018	0.0060
Gm28610	ENSMUSG00000100685	predicted gene 28610	-15.608	0.0244	0.0567
Gm28723	ENSMUSG00000101028	predicted gene 28723	-2.068	0.0268	0.0615
Gm28874	ENSMUSG00000100813	predicted gene 28874	-8.925	0.0299	0.0673
Gm28932	ENSMUSG00000101445	predicted gene 28932	-11.758	0.0120	0.0307
Gm2897	ENSMUSG00000079410	predicted gene 2897	-16.551	0.0133	0.0336
Gm29427	ENSMUSG00000101904	predicted gene 29427	-9.725	0.0382	0.0829
Gm29460	ENSMUSG00000099686	predicted gene 29460	-9.888	0.0408	0.0875
Gm29668	ENSMUSG00000099835	predicted gene 29668	-3.099	0.0000	0.0000
Gm30292	ENSMUSG00000104109	predicted gene, 30292	-11.301	0.0172	0.0421
Gm30373	ENSMUSG00000111758	predicted gene, 30373	-2.019	0.0030	0.0092
Gm30382	ENSMUSG00000106515	predicted gene, 30382	-3.809	0.0155	0.0384

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm30970	ENSMUSG00000115637	predicted gene, 30970	-7.294	0.0000	0.0000
Gm30984	ENSMUSG00000117361	predicted gene, 30984	-29.777	0.0005	0.0020
Gm31105	ENSMUSG00000109587	predicted gene, 31105	-1.605	0.0087	0.0234
Gm31663	ENSMUSG00000108994	predicted gene, 31663	-1.912	0.0001	0.0003
Gm31812	ENSMUSG00000109599	predicted gene, 31812	-5.181	0.0010	0.0034
Gm32031	ENSMUSG00000109118	predicted gene, 32031	-3.538	0.0002	0.0008
Gm3226	ENSMUSG00000114547	predicted gene 3226	-3.337	0.0017	0.0057
Gm32352	ENSMUSG00000110453	predicted gene, 32352	-2.521	0.0002	0.0009
Gm32369	ENSMUSG00000112950	predicted gene, 32369	-17.569	0.0110	0.0286
Gm32591	ENSMUSG00000108015	predicted gene, 32591	-2.480	0.0081	0.0219
Gm33024	ENSMUSG00000107682	predicted gene, 33024	-2.421	0.0438	0.0926
Gm33104	ENSMUSG00000110902	predicted gene, 33104	-7.075	0.0300	0.0674
Gm3325	ENSMUSG00000113836	predicted gene 3325	-9.182	0.0000	0.0000
Gm33424	ENSMUSG00000113101	predicted gene, 33424	-1.522	0.0162	0.0400
Gm33543	ENSMUSG00000110353	predicted gene, 33543	-1.559	0.0421	0.0898
Gm3375	ENSMUSG00000107470	predicted gene 3375	-2.694	0.0000	0.0000
Gm33940	ENSMUSG00000109733	predicted gene, 33940	-4.679	0.0426	0.0906
Gm34121	ENSMUSG00000108659	predicted gene, 34121	-11.410	0.0120	0.0308
Gm34276	ENSMUSG00000113977	predicted gene, 34276	-22.424	0.0026	0.0082
Gm3435	ENSMUSG00000116895	predicted gene 3435	-23.863	0.0010	0.0034
Gm3436	ENSMUSG00000096160	predicted pseudogene 3436	-12.753	0.0116	0.0298
Gm34655	ENSMUSG00000110863	predicted gene, 34655	-3.029	0.0032	0.0096
Gm34934	ENSMUSG00000115100	predicted gene, 34934	-2.162	0.0000	0.0000
Gm35167	ENSMUSG00000115680	predicted gene, 35167	-14.951	0.0055	0.0156
Gm35290	ENSMUSG00000117263	predicted gene, 35290	-1.869	0.0225	0.0527
Gm3534	ENSMUSG00000098192	predicted pseudogene 3534	-2.397	0.0175	0.0426
Gm35438	ENSMUSG00000118209	predicted gene, 35438	-16.653	0.0029	0.0089
Gm3555	ENSMUSG00000089791	predicted pseudogene 3555	-1.621	0.0436	0.0924
Gm35638	ENSMUSG00000113188	predicted gene, 35638	-3.857	0.0046	0.0133
Gm3604	ENSMUSG00000094942	predicted gene 3604	-2.442	0.0120	0.0307
Gm36173	ENSMUSG00000112835	predicted gene, 36173	-11.186	0.0177	0.0431

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm36235	ENSMUSG00000113930	predicted gene, 36235	-10.165	0.0309	0.0690
Gm36298	ENSMUSG00000114172	predicted gene, 36298	-2.315	0.0259	0.0596
Gm3646	ENSMUSG00000091937	predicted gene 3646	-1.505	0.0469	0.0980
Gm36569	ENSMUSG00000102191	predicted gene, 36569	-23.952	0.0012	0.0040
Gm36684	ENSMUSG00000117278	predicted gene, 36684	-1.800	0.0031	0.0095
Gm3671	ENSMUSG00000098232	predicted gene 3671	-2.131	0.0183	0.0443
Gm36738	ENSMUSG00000116097	predicted gene, 36738	-28.224	0.0003	0.0013
Gm3699	ENSMUSG00000094955	predicted gene 3699	-8.354	0.0000	0.0001
Gm37254	ENSMUSG00000104394	predicted gene, 37254	-2.281	0.0024	0.0076
Gm37486	ENSMUSG00000104126	predicted gene, 37486	-7.898	0.0343	0.0755
Gm3756	ENSMUSG00000091639	predicted gene 3756	-3.299	0.0281	0.0639
Gm37986	ENSMUSG00000104212	predicted gene, 37986	-15.004	0.0048	0.0140
Gm3809	ENSMUSG00000097935	predicted gene 3809	-3.752	0.0328	0.0727
Gm3815	ENSMUSG00000118088	predicted gene 3815	-3.740	0.0475	0.0991
Gm38228	ENSMUSG00000103945	predicted gene, 38228	-5.999	0.0373	0.0810
Gm39168	ENSMUSG00000110179	predicted gene, 39168	-6.434	0.0105	0.0273
Gm39469	ENSMUSG00000110834	predicted gene, 39469	-1.548	0.0114	0.0295
Gm4045	ENSMUSG00000108231	predicted gene 4045	-4.914	0.0000	0.0000
Gm41341	ENSMUSG00000069996	predicted gene, 41341	-2.160	0.0052	0.0149
Gm4149	ENSMUSG00000074800	predicted pseudogene 4149	-28.134	0.0003	0.0013
Gm4217	ENSMUSG00000097954	predicted gene 4217	-1.605	0.0378	0.0821
Gm42528	ENSMUSG00000107134	predicted gene 42528	-2.099	0.0011	0.0038
Gm42688	ENSMUSG00000079511	predicted gene 42688	-2.135	0.0262	0.0602
Gm42732	ENSMUSG00000107331	predicted gene 42732	-1.558	0.0010	0.0034
Gm4287	ENSMUSG00000092552	predicted gene 4287	-14.358	0.0418	0.0892
Gm42879	ENSMUSG00000106590	predicted gene 42879	-20.286	0.0014	0.0048
Gm43081	ENSMUSG00000106103	predicted gene 43081	-21.661	0.0041	0.0122
Gm43101	ENSMUSG00000106754	predicted gene 43101	-19.051	0.0051	0.0147
Gm43185	ENSMUSG00000104621	predicted gene 43185	-2.041	0.0034	0.0103
Gm43197	ENSMUSG00000107215	predicted gene 43197	-2.461	0.0139	0.0351
Gm43247	ENSMUSG00000105406	predicted gene 43247	-6.238	0.0007	0.0025

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm43327	ENSMUSG00000105695	predicted gene 43327	-6.477	0.0321	0.0715
Gm4335	ENSMUSG00000097989	predicted gene 4335	-2.298	0.0174	0.0425
Gm4353	ENSMUSG00000091900	predicted gene 4353	-2.598	0.0020	0.0064
Gm43598	ENSMUSG00000106927	predicted gene 43598	-15.129	0.0104	0.0272
Gm43667	ENSMUSG00000105135	predicted gene 43667	-1.796	0.0097	0.0256
Gm43682	ENSMUSG00000107019	predicted gene 43682	-2.231	0.0017	0.0055
Gm43693	ENSMUSG00000105929	predicted gene 43693	-23.067	0.0019	0.0062
Gm43814	ENSMUSG00000104654	predicted gene 43814	-3.817	0.0102	0.0267
Gm43823	ENSMUSG00000106224	predicted gene 43823	-2.402	0.0067	0.0184
Gm4419	ENSMUSG00000097055	predicted gene 4419	-24.069	0.0002	0.0010
Gm44220	ENSMUSG00000107655	predicted gene, 44220	-1.668	0.0198	0.0474
Gm44386	ENSMUSG00000107689	predicted gene, 44386	-2.633	0.0000	0.0000
Gm44623	ENSMUSG00000108883	predicted gene 44623	-12.454	0.0104	0.0272
Gm44717	ENSMUSG00000109029	predicted gene 44717	-13.074	0.0089	0.0237
Gm44878	ENSMUSG00000108477	predicted gene 44878	-10.250	0.0282	0.0641
Gm44929	ENSMUSG00000109009	predicted gene 44929	-11.291	0.0206	0.0489
Gm45114	ENSMUSG00000109136	predicted gene 45114	-5.127	0.0083	0.0224
Gm45137	ENSMUSG00000109206	predicted gene 45137	-2.355	0.0438	0.0927
Gm4518	ENSMUSG00000098123	predicted gene 4518	-4.332	0.0002	0.0010
Gm45187	ENSMUSG00000109130	predicted gene 45187	-11.197	0.0161	0.0398
Gm45353	ENSMUSG00000109957	predicted gene 45353	-5.133	0.0097	0.0255
Gm45378	ENSMUSG00000110326	predicted gene 45378	-14.829	0.0259	0.0595
Gm45552	ENSMUSG00000110279	predicted gene 45552	-2.031	0.0040	0.0118
Gm45871	ENSMUSG00000110277	predicted gene 45871	-2.552	0.0000	0.0000
Gm45889	ENSMUSG00000109936	predicted gene 45889	-3.732	0.0184	0.0444
Gm4596	ENSMUSG00000082394	predicted gene 4596	-3.718	0.0347	0.0763
Gm4609	ENSMUSG00000078592	predicted gene 4609	-4.022	0.0056	0.0159
Gm46620	ENSMUSG00000118012	predicted gene, 46620	-1.573	0.0063	0.0175
Gm47021	ENSMUSG00000113036	predicted gene, 47021	-14.232	0.0043	0.0128
Gm47108	ENSMUSG00000111000	predicted gene, 47108	-2.544	0.0173	0.0422
Gm47232	ENSMUSG00000111656	predicted gene, 47232	-11.682	0.0303	0.0679

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm47547	ENSMUSG00000114196	predicted gene, 47547	-3.929	0.0000	0.0000
Gm47604	ENSMUSG00000110946	predicted gene, 47604	-5.828	0.0011	0.0039
Gm47794	ENSMUSG00000114907	predicted gene, 47794	-9.641	0.0184	0.0445
Gm47826	ENSMUSG00000113650	predicted gene, 47826	-13.930	0.0226	0.0529
Gm47962	ENSMUSG00000111583	predicted gene, 47962	-20.502	0.0030	0.0093
Gm47976	ENSMUSG00000112300	predicted gene, 47976	-3.454	0.0361	0.0788
Gm4800	ENSMUSG00000111759	predicted gene 4800	-3.912	0.0325	0.0721
Gm4804	ENSMUSG00000098158	predicted gene 4804	-14.323	0.0035	0.0105
Gm48069	ENSMUSG00000111547	predicted gene, 48069	-1.741	0.0353	0.0774
Gm4815	ENSMUSG00000114733	predicted gene 4815	-8.272	0.0001	0.0004
Gm48357	ENSMUSG00000114524	predicted gene, 48357	-14.271	0.0241	0.0561
Gm4840	ENSMUSG00000118282	predicted gene 4840	-2.750	0.0165	0.0405
Gm48483	ENSMUSG00000111318	predicted gene, 48483	-2.081	0.0168	0.0413
Gm48496	ENSMUSG00000112969	predicted gene, 48496	-4.547	0.0000	0.0002
Gm48630	ENSMUSG00000113682	predicted gene, 48630	-3.784	0.0163	0.0401
Gm4875	ENSMUSG00000082791	predicted gene 4875	-2.092	0.0388	0.0839
Gm48796	ENSMUSG00000111390	predicted gene, 48796	-4.126	0.0405	0.0869
Gm4890	ENSMUSG00000097174	predicted gene 4890	-14.392	0.0038	0.0114
Gm48931	ENSMUSG00000115458	predicted gene, 48931	-3.915	0.0000	0.0001
Gm49024	ENSMUSG00000115575	predicted gene, 49024	-6.111	0.0000	0.0000
Gm49120	ENSMUSG00000115636	predicted gene, 49120	-7.745	0.0162	0.0400
Gm49326	ENSMUSG00000113294	predicted gene, 49326	-4.519	0.0350	0.0768
Gm49331	ENSMUSG00000114025	predicted gene, 49331	-4.660	0.0000	0.0000
Gm49338	ENSMUSG00000111128	predicted gene, 49338	-2.260	0.0000	0.0000
Gm4935	ENSMUSG00000113405	predicted gene 4935	-2.550	0.0410	0.0877
Gm49390	ENSMUSG00000114898	predicted gene, 49390	-2.217	0.0006	0.0021
Gm49395	ENSMUSG00000114470	predicted gene, 49395	-15.456	0.0068	0.0187
Gm49477	ENSMUSG00000116066	predicted gene, 49477	-1.891	0.0001	0.0004
Gm49486	ENSMUSG00000116121	predicted gene, 49486	-2.669	0.0474	0.0988
Gm49494	ENSMUSG00000116518	predicted gene, 49494	-2.438	0.0475	0.0991
Gm49539	ENSMUSG00000116004	predicted gene, 49539	-6.799	0.0288	0.0651

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm49980	ENSMUSG00000117465	predicted gene, 49980	-9.920	0.0199	0.0475
Gm50020	ENSMUSG00000117444	predicted gene, 50020	-11.963	0.0206	0.0490
Gm50114	ENSMUSG00000117692	predicted gene, 50114	-1.507	0.0109	0.0283
Gm50145	ENSMUSG00000117731	predicted gene, 50145	-3.960	0.0001	0.0004
Gm50402	ENSMUSG00000118159	predicted gene, 50402	-18.991	0.0024	0.0076
Gm50415	ENSMUSG00000118387	predicted gene, 50415	-5.616	0.0027	0.0083
Gm50455	ENSMUSG00000118071	predicted gene, 50455	-2.526	0.0469	0.0981
Gm5075	ENSMUSG00000105944	predicted gene 5075	-8.903	0.0379	0.0822
Gm5105	ENSMUSG00000049349	predicted gene 5105	-2.654	0.0003	0.0013
Gm5131	ENSMUSG00000110715	predicted gene 5131	-2.078	0.0000	0.0000
Gm5141	ENSMUSG00000091183	predicted gene 5141	-2.558	0.0099	0.0260
Gm5165	ENSMUSG00000116802	predicted gene 5165	-3.206	0.0000	0.0000
Gm5187	ENSMUSG00000082362	predicted gene 5187	-6.979	0.0183	0.0443
Gm5276	ENSMUSG00000105452	predicted gene 5276	-5.723	0.0001	0.0004
Gm52948	ENSMUSG00000118521	predicted gene, 52948	-7.905	0.0107	0.0278
Gm5421	ENSMUSG00000097245	predicted gene 5421	-2.098	0.0020	0.0065
Gm5425	ENSMUSG00000111875	predicted gene 5425	-2.867	0.0169	0.0413
Gm5430	ENSMUSG00000098180	predicted gene 5430	-4.020	0.0002	0.0008
Gm5436	ENSMUSG00000042962	predicted pseudogene 5436	-2.950	0.0000	0.0000
Gm54867	ENSMUSG00002075795	predicted gene, 54867	-12.539	0.0000	0.0000
Gm5503	ENSMUSG00000117730	predicted gene 5503	-6.254	0.0000	0.0000
Gm5507	ENSMUSG00000069376	predicted gene 5507	-2.345	0.0121	0.0310
Gm55073	ENSMUSG00002075637	predicted gene, 55073	-43.849	0.0001	0.0006
Gm5510	ENSMUSG00000083458	predicted pseudogene 5510	-17.688	0.0066	0.0183
Gm5523	ENSMUSG00000097711	predicted pseudogene 5523	-2.251	0.0042	0.0124
Gm55371	ENSMUSG00002074854	predicted gene, 55371	-21.764	0.0026	0.0081
Gm5540	ENSMUSG00000048916	predicted pseudogene 5540	-2.137	0.0359	0.0784
Gm5560	ENSMUSG00000067161	predicted pseudogene 5560	-3.280	0.0038	0.0112
Gm5566	ENSMUSG00000080002	predicted pseudogene 5566	-4.065	0.0001	0.0002
Gm5578	ENSMUSG00000029633	predicted pseudogene 5578	-3.457	0.0232	0.0542
Gm5617	ENSMUSG00000042293	predicted gene 5617	-2.926	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5621	ENSMUSG00000101597	predicted gene 5621	-29.193	0.0002	0.0008
Gm5687	ENSMUSG00000080866	predicted gene 5687	-4.609	0.0052	0.0148
Gm5693	ENSMUSG00000117793	predicted gene 5693	-2.234	0.0055	0.0157
Gm5737	ENSMUSG00000109392	predicted gene 5737	-4.120	0.0183	0.0443
Gm5791	ENSMUSG00000113753	predicted gene 5791	-7.747	0.0467	0.0977
Gm5823	ENSMUSG00000117813	predicted gene 5823	-4.382	0.0000	0.0000
Gm5824	ENSMUSG00000118241	predicted gene 5824	-19.354	0.0012	0.0041
Gm5841	ENSMUSG00000103921	predicted gene 5841	-12.395	0.0024	0.0075
Gm5855	ENSMUSG00000105558	predicted gene 5855	-2.411	0.0016	0.0053
Gm5865	ENSMUSG00000104923	predicted gene 5865	-15.202	0.0005	0.0020
Gm5874	ENSMUSG00000071568	predicted gene 5874	-13.560	0.0000	0.0000
Gm5884	ENSMUSG00000037827	predicted pseudogene 5884	-3.883	0.0000	0.0000
Gm5900	ENSMUSG00000094685	predicted pseudogene 5900	-1.876	0.0000	0.0001
Gm5913	ENSMUSG00000081111	predicted gene 5913	-6.689	0.0001	0.0005
Gm5920	ENSMUSG00000100839	predicted gene 5920	-11.628	0.0180	0.0435
Gm6054	ENSMUSG00000057157	predicted gene 6054	-9.916	0.0284	0.0643
Gm6055	ENSMUSG00000062081	predicted gene 6055	-2.478	0.0003	0.0010
Gm6206	ENSMUSG00000048949	predicted pseudogene 6206	-1.750	0.0000	0.0000
Gm6278	ENSMUSG00000116972	predicted gene 6278	-39.758	0.0000	0.0000
Gm6316	ENSMUSG00000078370	predicted pseudogene 6316	-2.530	0.0001	0.0004
Gm6322	ENSMUSG00000082018	predicted gene 6322	-9.257	0.0086	0.0230
Gm6368	ENSMUSG00000080775	predicted gene 6368	-4.883	0.0000	0.0000
Gm6402	ENSMUSG00000117962	predicted pseudogene 6402	-6.663	0.0232	0.0542
Gm6419	ENSMUSG00000072407	predicted gene 6419	-17.834	0.0002	0.0008
Gm6475	ENSMUSG00000116838	predicted gene 6475	-4.292	0.0219	0.0516
Gm6493	ENSMUSG00000090021	predicted gene 6493	-10.489	0.0158	0.0391
Gm6505	ENSMUSG00000070522	predicted pseudogene 6505	-3.201	0.0000	0.0000
Gm6517	ENSMUSG00000082420	predicted gene 6517	-14.839	0.0000	0.0000
Gm6542	ENSMUSG00000085172	predicted gene 6542	-1.929	0.0313	0.0698
Gm6552	ENSMUSG00000117458	predicted gene 6552	-3.471	0.0035	0.0105
Gm6644	ENSMUSG00000100309	predicted gene 6644	-7.246	0.0004	0.0016

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm6645	ENSMUSG00000083554	predicted gene 6645	-6.391	0.0001	0.0003
Gm6712	ENSMUSG00000072761	predicted gene 6712	-2.525	0.0001	0.0004
Gm6776	ENSMUSG00000047509	predicted pseudogene 6776	-10.168	0.0354	0.0776
Gm6967	ENSMUSG00000097937	predicted gene 6967	-8.321	0.0355	0.0778
Gm6988	ENSMUSG00000113198	predicted gene 6988	-12.599	0.0010	0.0035
Gm6997	ENSMUSG00000115539	predicted gene 6997	-9.065	0.0204	0.0485
Gm7027	ENSMUSG00000067121	predicted gene 7027	-3.438	0.0246	0.0571
Gm7114	ENSMUSG00000100481	predicted gene 7114	-8.471	0.0085	0.0229
Gm7251	ENSMUSG00000069236	predicted pseudogene 7251	-3.614	0.0030	0.0092
Gm7252	ENSMUSG00000114135	predicted gene 7252	-21.791	0.0017	0.0056
Gm7278	ENSMUSG00000080950	predicted gene 7278	-9.770	0.0166	0.0407
Gm7286	ENSMUSG00000098194	predicted gene 7286	-6.534	0.0009	0.0031
Gm7293	ENSMUSG00000111162	predicted gene 7293	-2.628	0.0225	0.0527
Gm7353	ENSMUSG00000055452	predicted pseudogene 7353	-3.277	0.0028	0.0087
Gm7367	ENSMUSG00000047370	predicted pseudogene 7367	-11.020	0.0091	0.0243
Gm7368	ENSMUSG00000110867	predicted gene 7368	-18.893	0.0046	0.0133
Gm7481	ENSMUSG00000098219	predicted gene 7481	-8.538	0.0354	0.0776
Gm7536	ENSMUSG00000057036	predicted gene 7536	-15.555	0.0000	0.0000
Gm7665	ENSMUSG00000063628	predicted pseudogene 7665	-5.623	0.0203	0.0483
Gm7741	ENSMUSG00000097713	predicted gene 7741	-16.227	0.0090	0.0240
Gm7808	ENSMUSG00000091460	predicted pseudogene 7808	-8.900	0.0112	0.0289
Gm7832	ENSMUSG00000106917	predicted gene 7832	-6.820	0.0000	0.0000
Gm7862	ENSMUSG00000046580	predicted gene 7862	-2.283	0.0345	0.0760
Gm8069	ENSMUSG00000105143	predicted pseudogene 8069	-20.097	0.0008	0.0029
Gm807	ENSMUSG00000097848	predicted gene 807	-10.076	0.0443	0.0934
Gm8075	ENSMUSG00000113321	predicted gene 8075	-5.625	0.0000	0.0000
Gm8121	ENSMUSG00000051116	predicted pseudogene 8121	-1.915	0.0000	0.0002
Gm8129	ENSMUSG00000059159	predicted pseudogene 8129	-5.703	0.0384	0.0831
Gm8188	ENSMUSG00000112163	predicted gene 8188	-3.072	0.0000	0.0001
Gm8189	ENSMUSG00000110298	predicted gene 8189	-1.622	0.0143	0.0358
Gm8210	ENSMUSG00000094497	predicted pseudogene 8210	-5.374	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm8216	ENSMUSG00000084303	predicted gene 8216	-13.755	0.0100	0.0262
Gm8242	ENSMUSG00000102827	predicted gene 8242	-3.393	0.0241	0.0560
Gm8330	ENSMUSG00000098048	predicted gene 8330	-4.810	0.0136	0.0344
Gm8349	ENSMUSG00000098208	predicted gene 8349	-2.135	0.0031	0.0094
Gm8494	ENSMUSG00000094090	predicted gene 8494	-2.155	0.0050	0.0144
Gm8539	ENSMUSG00000106294	predicted gene 8539	-16.396	0.0042	0.0124
Gm8566	ENSMUSG00000047905	predicted pseudogene 8566	-3.363	0.0296	0.0667
Gm8606	ENSMUSG00000083362	predicted gene 8606	-17.212	0.0080	0.0215
Gm8666	ENSMUSG00000048709	predicted gene 8666	-10.792	0.0006	0.0022
Gm8722	ENSMUSG00000081164	predicted gene 8722	-8.462	0.0376	0.0817
Gm8730	ENSMUSG00000063696	predicted pseudogene 8730	-10.364	0.0000	0.0000
Gm8741	ENSMUSG00000091655	predicted gene 8741	-30.523	0.0003	0.0013
Gm8756	ENSMUSG00000098238	predicted gene 8756	-1.769	0.0128	0.0325
Gm8864	ENSMUSG00000081892	predicted gene 8864	-3.194	0.0072	0.0197
Gm9008	ENSMUSG00000072476	predicted pseudogene 9008	-3.230	0.0000	0.0000
Gm9204	ENSMUSG00000110562	predicted gene 9204	-3.083	0.0358	0.0783
Gm9247	ENSMUSG00000115505	predicted gene 9247	-2.717	0.0138	0.0348
Gm9260	ENSMUSG00000106239	predicted gene 9260	-3.558	0.0096	0.0254
Gm9385	ENSMUSG00000080848	predicted pseudogene 9385	-4.711	0.0000	0.0000
Gm9616	ENSMUSG00000114003	predicted gene 9616	-1.962	0.0341	0.0752
Gm9625	ENSMUSG00000097906	predicted gene 9625	-5.247	0.0000	0.0000
Gm9790	ENSMUSG00000044330	predicted gene 9790	-5.876	0.0000	0.0000
Gm9843	ENSMUSG00000050299	predicted gene 9843	-2.861	0.0003	0.0011
Gm9892	ENSMUSG00000052825	predicted gene 9892	-3.048	0.0000	0.0001
Gm9895	ENSMUSG00000118038	predicted gene 9895	-3.596	0.0029	0.0089
Gm9903	ENSMUSG00000097271	predicted gene 9903	-2.063	0.0323	0.0719
Gm9951	ENSMUSG00000054618	predicted gene 9951	-12.588	0.0144	0.0361
Gm9967	ENSMUSG00000055323	predicted gene 9967	-7.229	0.0435	0.0922
Gmppa	ENSMUSG00000033021	GDP-mannose pyrophosphorylase A	-2.496	0.0000	0.0000
Gnat3	ENSMUSG00000028777	guanine nucleotide binding protein, alpha transducing 3	-1.758	0.0253	0.0584
Gng5	ENSMUSG00000068523	guanine nucleotide binding protein (G protein), gamma 5	-4.060	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gng7	ENSMUSG00000048240	guanine nucleotide binding protein (G protein), gamma 7	-1.912	0.0005	0.0017
Gnpda1	ENSMUSG00000052102	glucosamine-6-phosphate deaminase 1	-1.905	0.0000	0.0001
Golt1b	ENSMUSG00000030245	golgi transport 1B	-1.586	0.0001	0.0003
Gorasp1	ENSMUSG00000032513	golgi reassembly stacking protein 1	-2.099	0.0000	0.0000
Got2	ENSMUSG00000031672	glutamatic-oxaloacetic transaminase 2, mitochondrial	-1.646	0.0000	0.0000
Got2-ps1	ENSMUSG00000080935	glutamatic-oxaloacetic transaminase 2, mitochondrial, pseudogene 1	-1.534	0.0000	0.0000
Gpaa1	ENSMUSG00000022561	GPI anchor attachment protein 1	-2.863	0.0000	0.0000
Gpc6	ENSMUSG00000058571	glypican 6	-1.583	0.0023	0.0073
Gpd1l	ENSMUSG00000050627	glycerol-3-phosphate dehydrogenase 1-like	-1.656	0.0000	0.0000
Gper1	ENSMUSG00000053647	G protein-coupled estrogen receptor 1	-2.201	0.0002	0.0009
Gpihbp1	ENSMUSG00000022579	GPI-anchored HDL-binding protein 1	-1.603	0.0143	0.0360
Gpn2	ENSMUSG00000028848	GPN-loop GTPase 2	-2.051	0.0000	0.0000
Gpr132	ENSMUSG00000021298	G protein-coupled receptor 132	-8.481	0.0080	0.0217
Gpr135	ENSMUSG00000043398	G protein-coupled receptor 135	-2.384	0.0054	0.0154
Gpr137	ENSMUSG00000024958	G protein-coupled receptor 137	-1.731	0.0000	0.0000
Gpr137b-ps	ENSMUSG00000097715	G protein-coupled receptor 137B, pseudogene	-1.707	0.0002	0.0007
Gpr146	ENSMUSG00000044197	G protein-coupled receptor 146	-1.864	0.0000	0.0000
Gpr155	ENSMUSG00000041762	G protein-coupled receptor 155	-1.610	0.0001	0.0003
Gpr18	ENSMUSG00000050350	G protein-coupled receptor 18	-13.826	0.0167	0.0410
Gpr182	ENSMUSG00000058396	G protein-coupled receptor 182	-1.725	0.0002	0.0008
Gpr22	ENSMUSG00000044067	G protein-coupled receptor 22	-1.681	0.0003	0.0010
Gpr34	ENSMUSG00000040229	G protein-coupled receptor 34	-2.571	0.0007	0.0024
Gpr35	ENSMUSG00000026271	G protein-coupled receptor 35	-5.054	0.0007	0.0025
Gpr37l1	ENSMUSG00000026424	G protein-coupled receptor 37-like 1	-1.989	0.0394	0.0851
Gpr4	ENSMUSG00000044317	G protein-coupled receptor 4	-1.984	0.0000	0.0000
Gpr52	ENSMUSG00000118401	G protein-coupled receptor 52	-15.099	0.0065	0.0180
Gpr89	ENSMUSG00000028096	G protein-coupled receptor 89	-1.744	0.0000	0.0000
Gprc5c	ENSMUSG00000051043	G protein-coupled receptor, family C, group 5, member C	-1.998	0.0000	0.0000
Gps1	ENSMUSG00000025156	G protein pathway suppressor 1	-2.439	0.0000	0.0000
Gpsm1	ENSMUSG00000026930	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-1.909	0.0000	0.0000
Gpt2	ENSMUSG00000031700	glutamic pyruvate transaminase (alanine aminotransferase) 2	-1.502	0.0217	0.0511

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gpx3	ENSMUSG00000018339	glutathione peroxidase 3	-1.516	0.0027	0.0085
Gpx7	ENSMUSG00000028597	glutathione peroxidase 7	-2.175	0.0000	0.0000
Grin2a	ENSMUSG00000059003	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	-4.517	0.0214	0.0506
Grina	ENSMUSG00000022564	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	-1.667	0.0000	0.0000
Grpel1	ENSMUSG00000029198	GrpE-like 1, mitochondrial	-1.638	0.0000	0.0000
Grpel2	ENSMUSG00000024580	GrpE-like 2, mitochondrial	-1.632	0.0000	0.0000
Grtp1	ENSMUSG00000038515	GH regulated TBC protein 1	-1.606	0.0231	0.0541
Gsdma	ENSMUSG00000017204	gasdermin A	-5.754	0.0054	0.0154
Gstk1	ENSMUSG00000029864	glutathione S-transferase kappa 1	-1.804	0.0000	0.0000
Gstm1	ENSMUSG00000058135	glutathione S-transferase, mu 1	-1.713	0.0000	0.0000
Gstm2	ENSMUSG00000040562	glutathione S-transferase, mu 2	-2.066	0.0000	0.0000
Gstm2-ps1	ENSMUSG00000107369	glutathione S-transferase mu 2 (muscle), pseudogene 1	-5.967	0.0042	0.0125
Gsto1	ENSMUSG00000025068	glutathione S-transferase omega 1	-1.558	0.0000	0.0000
Gsto2	ENSMUSG00000025069	glutathione S-transferase omega 2	-1.812	0.0135	0.0342
Gstt1	ENSMUSG00000001663	glutathione S-transferase, theta 1	-1.872	0.0000	0.0000
Gstt2	ENSMUSG00000033318	glutathione S-transferase, theta 2	-1.644	0.0053	0.0151
Gtdc1	ENSMUSG00000036890	glycosyltransferase-like domain containing 1	-1.729	0.0000	0.0000
Gtf2h4	ENSMUSG00000001524	general transcription factor II H, polypeptide 4	-2.278	0.0000	0.0000
Gtf3a	ENSMUSG00000016503	general transcription factor III A	-1.828	0.0000	0.0000
Gtse1	ENSMUSG00000022385	G two S phase expressed protein 1	-5.193	0.0003	0.0011
Guk1	ENSMUSG00000020444	guanylate kinase 1	-2.103	0.0000	0.0000
Gvin1	ENSMUSG00000045868	GTPase, very large interferon inducible 1	-2.625	0.0154	0.0383
Gypc	ENSMUSG00000090523	glycophorin C	-1.708	0.0000	0.0000
H2-Ab1	ENSMUSG00000073421	histocompatibility 2, class II antigen A, beta 1	-1.887	0.0141	0.0355
H2af-ps2	ENSMUSG00000091383	H2A histone family, pseudogene 2	-6.281	0.0000	0.0000
H2ax	ENSMUSG00000049932	H2A.X variant histone	-2.186	0.0000	0.0002
H2bc3	ENSMUSG00000075031	H2B clustered histone 3	-4.378	0.0025	0.0079
H2bc4	ENSMUSG00000018102	H2B clustered histone 4	-3.552	0.0000	0.0000
H2-Ea	ENSMUSG00000036322	histocompatibility 2, class II antigen E alpha	-4.159	0.0099	0.0261
H2-T22	ENSMUSG00000056116	histocompatibility 2, T region locus 22	-2.874	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
H3c15	ENSMUSG00000081058	H3 clustered histone 15	-2.331	0.0061	0.0170
H3f3a-ps1	ENSMUSG00000082284	H3.3 histone A, pseudogene 1	-8.869	0.0059	0.0166
H4c4	ENSMUSG00000061482	H4 clustered histone 4	-20.150	0.0025	0.0079
H4c8	ENSMUSG00000060981	H4 clustered histone 8	-3.624	0.0000	0.0000
H4c9	ENSMUSG00000060639	H4 clustered histone 9	-1.504	0.0009	0.0031
Hacd2	ENSMUSG00000035376	3-hydroxyacyl-CoA dehydratase 2	-1.742	0.0000	0.0001
Hacl1	ENSMUSG00000021884	2-hydroxyacyl-CoA lyase 1	-2.295	0.0234	0.0546
Hadhb	ENSMUSG00000059447	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta	-2.188	0.0000	0.0000
Hadhb-ps	ENSMUSG00000063684	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta, pseudogene	-2.090	0.0000	0.0000
Hagh	ENSMUSG00000024158	hydroxyacyl glutathione hydrolase	-1.784	0.0000	0.0000
Has3	ENSMUSG00000031910	hyaluronan synthase 3	-2.143	0.0066	0.0182
Haus1	ENSMUSG00000041840	HAUS augmin-like complex, subunit 1	-1.541	0.0000	0.0000
Haus2	ENSMUSG00000027285	HAUS augmin-like complex, subunit 2	-1.535	0.0000	0.0001
Hba-a1	ENSMUSG00000069919	hemoglobin alpha, adult chain 1	-3.330	0.0000	0.0000
Hbb-bs	ENSMUSG00000052305	hemoglobin, beta adult s chain	-2.593	0.0000	0.0000
Hbb-bt	ENSMUSG00000073940	hemoglobin, beta adult t chain	-16.557	0.0000	0.0000
Hbp1	ENSMUSG00000002996	high mobility group box transcription factor 1	-1.551	0.0014	0.0048
Hcfc1r1	ENSMUSG00000023904	host cell factor C1 regulator 1 (XPO1-dependent)	-3.650	0.0000	0.0000
Hcst	ENSMUSG00000064109	hematopoietic cell signal transducer	-11.339	0.0169	0.0413
Hdac10	ENSMUSG00000062906	histone deacetylase 10	-1.780	0.0000	0.0001
Hdc	ENSMUSG00000027360	histidine decarboxylase	-2.421	0.0002	0.0006
Hddc2	ENSMUSG00000000295	HD domain containing 2	-2.094	0.0000	0.0000
Hebp2	ENSMUSG00000019853	heme binding protein 2	-1.671	0.0170	0.0415
Hectd4	ENSMUSG00000042744	HECT domain E3 ubiquitin protein ligase 4	-1.544	0.0000	0.0000
Hepacam2	ENSMUSG00000044156	HEPACAM family member 2	-4.905	0.0435	0.0922
Hes6	ENSMUSG00000067071	hairy and enhancer of split 6	-1.949	0.0093	0.0247
Hexdc	ENSMUSG00000039307	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	-1.906	0.0000	0.0000
Hexim2	ENSMUSG00000043372	hexamethylene bis-acetamide inducible 2	-2.416	0.0006	0.0021
Hfe	ENSMUSG00000006611	homeostatic iron regulator	-1.854	0.0000	0.0000
Hhatl	ENSMUSG00000032523	hedgehog acyltransferase-like	-2.262	0.0000	0.0000
Higd1b	ENSMUSG00000020928	HIG1 domain family, member 1B	-2.059	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Higd2a	ENSMUSG00000025868	HIG1 domain family, member 2A	-1.860	0.0000	0.0000
Hint2	ENSMUSG00000028470	histidine triad nucleotide binding protein 2	-1.898	0.0000	0.0000
Hmbs	ENSMUSG00000032126	hydroxymethylbilane synthase	-1.919	0.0000	0.0000
Hmcn2	ENSMUSG00000055632	hemicentin 2	-1.765	0.0002	0.0007
Hmgcl	ENSMUSG00000028672	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	-2.023	0.0000	0.0000
Hmgcs2	ENSMUSG00000027875	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	-1.608	0.0022	0.0070
Hmgn2-ps	ENSMUSG00000070713	high mobility group nucleosomal binding domain 2, pseudogene	-18.260	0.0013	0.0045
Hopx	ENSMUSG00000059325	HOP homeobox	-2.110	0.0000	0.0000
Hpcal1	ENSMUSG00000071379	hippocalcin-like 1	-1.835	0.0021	0.0068
Hpdl	ENSMUSG00000043155	4-hydroxyphenylpyruvate dioxygenase-like	-2.313	0.0000	0.0001
Hpgd	ENSMUSG00000031613	hydroxyprostaglandin dehydrogenase 15 (NAD)	-1.569	0.0017	0.0055
Hps1	ENSMUSG00000025188	HPS1, biogenesis of lysosomal organelles complex 3 subunit 1	-2.426	0.0001	0.0003
Hps4	ENSMUSG00000042328	HPS4, biogenesis of lysosomal organelles complex 3 subunit 2	-1.566	0.0000	0.0000
Hrct1	ENSMUSG00000071001	histidine rich carboxyl terminus 1	-1.853	0.0095	0.0251
Hs1bp3	ENSMUSG00000020605	HCLS1 binding protein 3	-1.527	0.0001	0.0003
Hsd11b1	ENSMUSG00000016194	hydroxysteroid 11-beta dehydrogenase 1	-1.562	0.0047	0.0136
Hsd17b10	ENSMUSG00000025260	hydroxysteroid (17-beta) dehydrogenase 10	-1.621	0.0000	0.0000
Hsf1	ENSMUSG00000022556	heat shock factor 1	-1.660	0.0000	0.0000
Hsf2	ENSMUSG00000019878	heat shock factor 2	-1.526	0.0000	0.0000
Hsf4	ENSMUSG00000033249	heat shock transcription factor 4	-2.117	0.0000	0.0001
Hspa1a	ENSMUSG00000091971	heat shock protein 1A	-3.094	0.0053	0.0152
Hspa1b	ENSMUSG00000090877	heat shock protein 1B	-4.458	0.0000	0.0002
Hspa8	ENSMUSG00000015656	heat shock protein 8	-1.740	0.0000	0.0000
Hspb1	ENSMUSG00000004951	heat shock protein 1	-3.589	0.0000	0.0000
Hspb11	ENSMUSG00000063172	heat shock protein family B (small), member 11	-2.474	0.0000	0.0000
Hspb3	ENSMUSG00000051456	heat shock protein 3	-2.514	0.0000	0.0000
Hspbp1	ENSMUSG00000063802	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	-1.934	0.0000	0.0000
Hspg2	ENSMUSG00000028763	perlecan (heparan sulfate proteoglycan 2)	-2.085	0.0000	0.0000
Htr2a	ENSMUSG00000034997	5-hydroxytryptamine (serotonin) receptor 2A	-1.666	0.0200	0.0477
Htra3	ENSMUSG00000029096	HtrA serine peptidase 3	-2.702	0.0000	0.0000
Htt	ENSMUSG00000029104	huntingtin	-1.504	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hyal2	ENSMUSG00000010047	hyaluronoglucosaminidase 2	-2.464	0.0000	0.0000
Iah1	ENSMUSG00000062054	isoamyl acetate-hydrolyzing esterase 1 homolog	-2.269	0.0000	0.0000
Icam2	ENSMUSG00000001029	intercellular adhesion molecule 2	-3.758	0.0000	0.0000
Id1	ENSMUSG00000042745	inhibitor of DNA binding 1, HLH protein	-4.877	0.0000	0.0000
Id3	ENSMUSG00000007872	inhibitor of DNA binding 3	-2.012	0.0000	0.0000
Ide	ENSMUSG00000056999	insulin degrading enzyme	-1.643	0.0000	0.0000
Idh3g	ENSMUSG00000002010	isocitrate dehydrogenase 3 (NAD+), gamma	-1.740	0.0000	0.0000
Idua	ENSMUSG00000033540	iduronidase, alpha-L	-1.568	0.0000	0.0000
Ier3	ENSMUSG00000003541	immediate early response 3	-2.618	0.0000	0.0000
Ifi203	ENSMUSG00000039997	interferon activated gene 203	-1.627	0.0017	0.0056
Ifi205	ENSMUSG00000054203	interferon activated gene 205	-1.657	0.0228	0.0535
Ifi27l2a	ENSMUSG00000079017	interferon, alpha-inducible protein 27 like 2A	-2.395	0.0004	0.0016
Ifi47	ENSMUSG00000078920	interferon gamma inducible protein 47	-1.772	0.0091	0.0241
Ifitm1	ENSMUSG00000025491	interferon induced transmembrane protein 1	-1.981	0.0091	0.0243
Ifngr2	ENSMUSG00000022965	interferon gamma receptor 2	-1.648	0.0004	0.0014
Ift27	ENSMUSG00000016637	intraflagellar transport 27	-1.697	0.0000	0.0000
Igsf6	ENSMUSG00000035004	immunoglobulin superfamily, member 6	-2.153	0.0015	0.0048
Il10ra	ENSMUSG00000032089	interleukin 10 receptor, alpha	-1.611	0.0236	0.0550
Il15	ENSMUSG00000031712	interleukin 15	-2.097	0.0000	0.0000
Il17rc	ENSMUSG00000030281	interleukin 17 receptor C	-2.664	0.0000	0.0000
Il18bp	ENSMUSG00000070427	interleukin 18 binding protein	-2.586	0.0000	0.0000
Il1rl2	ENSMUSG00000070942	interleukin 1 receptor-like 2	-1.849	0.0054	0.0154
Il27ra	ENSMUSG00000005465	interleukin 27 receptor, alpha	-1.581	0.0234	0.0546
Il2rb	ENSMUSG00000068227	interleukin 2 receptor, beta chain	-2.445	0.0043	0.0126
Il2rg	ENSMUSG00000031304	interleukin 2 receptor, gamma chain	-1.608	0.0080	0.0216
Il34	ENSMUSG00000031750	interleukin 34	-1.985	0.0000	0.0001
Il3ra	ENSMUSG00000068758	interleukin 3 receptor, alpha chain	-1.957	0.0005	0.0017
Impdh2	ENSMUSG00000062867	inosine monophosphate dehydrogenase 2	-1.599	0.0000	0.0000
Impdh2-ps	ENSMUSG00000071041	inosine monophosphate dehydrogenase 2, pseudogene	-4.530	0.0001	0.0003
Inpp5j	ENSMUSG00000034570	inositol polyphosphate 5-phosphatase J	-1.834	0.0004	0.0015
Inpp5k	ENSMUSG00000006127	inositol polyphosphate 5-phosphatase K	-1.598	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Insl6	ENSMUSG00000050957	insulin-like 6	-3.143	0.0111	0.0288
Ints12	ENSMUSG00000028016	integrator complex subunit 12	-1.575	0.0007	0.0024
Ints5	ENSMUSG00000071652	integrator complex subunit 5	-1.816	0.0000	0.0000
Ints9	ENSMUSG00000021975	integrator complex subunit 9	-1.738	0.0000	0.0000
Ipo13	ENSMUSG00000033365	importin 13	-1.794	0.0000	0.0000
Ipo4	ENSMUSG00000002319	importin 4	-2.740	0.0000	0.0000
Isca2	ENSMUSG00000021241	iron-sulfur cluster assembly 2	-1.556	0.0000	0.0000
Islr	ENSMUSG00000037206	immunoglobulin superfamily containing leucine-rich repeat	-1.970	0.0000	0.0001
Isyna1	ENSMUSG00000019139	myo-inositol 1-phosphate synthase A1	-3.131	0.0000	0.0000
Itga11	ENSMUSG00000032243	integrin alpha 11	-1.692	0.0074	0.0203
Itga3	ENSMUSG00000001507	integrin alpha 3	-1.716	0.0003	0.0013
Itga5	ENSMUSG00000000555	integrin alpha 5 (fibronectin receptor alpha)	-1.749	0.0000	0.0000
Itgb3bp	ENSMUSG00000028549	integrin beta 3 binding protein (beta3-endonexin)	-1.818	0.0001	0.0003
Itm2a	ENSMUSG00000031239	integral membrane protein 2A	-2.385	0.0000	0.0000
Itm2c	ENSMUSG00000026223	integral membrane protein 2C	-1.533	0.0000	0.0000
Ivd	ENSMUSG00000027332	isovaleryl coenzyme A dehydrogenase	-1.725	0.0000	0.0000
Izumo4	ENSMUSG00000055862	IZUMO family member 4	-2.855	0.0007	0.0024
Jagn1	ENSMUSG00000051256	jagunal homolog 1	-2.161	0.0000	0.0000
Jak3	ENSMUSG00000031805	Janus kinase 3	-1.581	0.0246	0.0569
Josd2	ENSMUSG00000038695	Josephin domain containing 2	-1.654	0.0000	0.0000
Jrk	ENSMUSG00000046380	jerky	-1.701	0.0000	0.0002
Jtb	ENSMUSG00000027937	jumping translocation breakpoint	-1.605	0.0000	0.0000
Kat8	ENSMUSG00000030801	K(lysine) acetyltransferase 8	-1.690	0.0000	0.0000
Katnb1	ENSMUSG00000031787	katanin p80 (WD40-containing) subunit B 1	-2.708	0.0000	0.0000
Kcnc2	ENSMUSG00000035681	potassium voltage gated channel, Shaw-related subfamily, member 2	-2.046	0.0326	0.0724
Kcnd1	ENSMUSG00000009731	potassium voltage-gated channel, Shal-related family, member 1	-2.980	0.0107	0.0279
Kcnip1	ENSMUSG00000053519	Kv channel-interacting protein 1	-15.109	0.0266	0.0610
Kcp	ENSMUSG00000059022	kielin/chordin-like protein	-1.640	0.0024	0.0074
Kctd21	ENSMUSG00000044952	potassium channel tetramerisation domain containing 21	-1.786	0.0000	0.0001
Kdelr1	ENSMUSG00000002778	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-1.946	0.0000	0.0000
Kdelr2	ENSMUSG00000079111	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	-1.838	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kdelr3	ENSMUSG00000010830	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	-2.232	0.0000	0.0001
Kics2	ENSMUSG00000053684	KICSTOR subunit 2	-1.513	0.0012	0.0041
Kif18a	ENSMUSG00000027115	kinesin family member 18A	-1.803	0.0431	0.0914
Kif26a	ENSMUSG00000021294	kinesin family member 26A	-2.039	0.0000	0.0000
Kif9	ENSMUSG00000032489	kinesin family member 9	-3.029	0.0194	0.0464
Kifc5b	ENSMUSG00000024301	kinesin family member C5B	-2.235	0.0182	0.0441
Klhl22	ENSMUSG00000022750	kelch-like 22	-1.595	0.0001	0.0003
Klhl26	ENSMUSG00000055707	kelch-like 26	-1.599	0.0000	0.0000
Klhl30	ENSMUSG00000026308	kelch-like 30	-1.848	0.0001	0.0002
Klhl40	ENSMUSG00000074001	kelch-like 40	-1.539	0.0070	0.0193
Klk10	ENSMUSG00000030693	kallikrein related-peptidase 10	-5.158	0.0005	0.0018
Klk14	ENSMUSG00000044737	kallikrein related-peptidase 14	-3.370	0.0028	0.0086
Klk8	ENSMUSG00000064023	kallikrein related-peptidase 8	-1.777	0.0002	0.0009
Klra8	ENSMUSG00000089727	killer cell lectin-like receptor, subfamily A, member 8	-11.376	0.0205	0.0488
Klra9	ENSMUSG00000033024	killer cell lectin-like receptor subfamily A, member 9	-2.537	0.0003	0.0012
Kptn	ENSMUSG00000006021	kaptin	-1.869	0.0000	0.0000
Krba1	ENSMUSG00000042810	KRAB-A domain containing 1	-1.828	0.0000	0.0000
Krt18	ENSMUSG00000023043	keratin 18	-1.729	0.0326	0.0724
Krtcap2	ENSMUSG00000042747	keratinocyte associated protein 2	-3.846	0.0000	0.0000
Kti12	ENSMUSG00000073775	KTI12 homolog, chromatin associated	-2.432	0.0000	0.0000
Kyat1	ENSMUSG00000039648	kynurenine aminotransferase 1	-1.660	0.0000	0.0000
Lage3	ENSMUSG00000015289	L antigen family, member 3	-2.065	0.0000	0.0000
Lama5	ENSMUSG00000015647	laminin, alpha 5	-2.133	0.0002	0.0008
Lamb2	ENSMUSG00000052911	laminin, beta 2	-1.652	0.0000	0.0000
Lamc3	ENSMUSG00000026840	laminin gamma 3	-2.221	0.0255	0.0588
Lancl1	ENSMUSG00000026000	LanC (bacterial lantibiotic synthetase component C)-like 1	-2.576	0.0000	0.0000
Lancl2	ENSMUSG00000062190	LanC (bacterial lantibiotic synthetase component C)-like 2	-1.553	0.0000	0.0000
Laptm4a	ENSMUSG00000020585	lysosomal-associated protein transmembrane 4A	-1.555	0.0000	0.0000
Laptm5	ENSMUSG00000028581	lysosomal-associated protein transmembrane 5	-1.523	0.0067	0.0185
Large1	ENSMUSG00000004383	LARGE xylosyl- and glucuronyltransferase 1	-1.549	0.0000	0.0000
Lars2	ENSMUSG00000035202	leucyl-tRNA synthetase, mitochondrial	-11.605	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lasp1	ENSMUSG00000038366	LIM and SH3 protein 1	-1.713	0.0000	0.0000
Lcmt2	ENSMUSG00000074890	leucine carboxyl methyltransferase 2	-1.743	0.0000	0.0000
Ldah	ENSMUSG00000037669	lipid droplet associated hydrolase	-1.887	0.0000	0.0000
Ldb3	ENSMUSG00000021798	LIM domain binding 3	-1.532	0.0000	0.0000
Ldhb-ps	ENSMUSG00000045104	lactate dehydrogenase B, pseudogene	-2.555	0.0000	0.0000
Ldlrad3	ENSMUSG00000048058	low density lipoprotein receptor class A domain containing 3	-1.554	0.0007	0.0025
Leat1	ENSMUSG00000109056	lncRNA Efnb2 associated transcript 1	-10.906	0.0165	0.0405
Limd1	ENSMUSG00000025239	LIM domains containing 1	-1.564	0.0080	0.0216
Lims1	ENSMUSG00000019920	LIM and senescent cell antigen-like domains 1	-1.566	0.0000	0.0000
Lingo4	ENSMUSG00000044505	leucine rich repeat and Ig domain containing 4	-3.289	0.0380	0.0824
Lipe	ENSMUSG00000003123	lipase, hormone sensitive	-1.549	0.0030	0.0092
Lipo2	ENSMUSG00000087303	lipase, member O2	-1.791	0.0004	0.0014
Lipo3	ENSMUSG00000024766	lipase, member O3	-2.216	0.0002	0.0007
Lipt2	ENSMUSG00000030725	lipoyl(octanoyl) transferase 2 (putative)	-1.689	0.0018	0.0059
Llgl1	ENSMUSG00000020536	LLGL1 scribble cell polarity complex component	-2.128	0.0000	0.0000
Lman1l	ENSMUSG00000056271	lectin, mannose-binding 1 like	-3.974	0.0002	0.0007
Lman2	ENSMUSG00000021484	lectin, mannose-binding 2	-1.508	0.0140	0.0353
Lmbr1l	ENSMUSG00000022999	limb region 1 like	-1.661	0.0158	0.0392
Lmf1	ENSMUSG00000002279	lipase maturation factor 1	-2.419	0.0000	0.0000
Lmf2	ENSMUSG00000022614	lipase maturation factor 2	-1.809	0.0000	0.0000
Lnx2	ENSMUSG00000016520	ligand of numb-protein X 2	-1.964	0.0001	0.0003
Loxl1	ENSMUSG00000032334	lysyl oxidase-like 1	-2.240	0.0004	0.0015
Lpar6	ENSMUSG00000033446	lysophosphatidic acid receptor 6	-1.990	0.0000	0.0000
Lpcat3	ENSMUSG00000004270	lysophosphatidylcholine acyltransferase 3	-1.927	0.0000	0.0000
Lrfn3	ENSMUSG00000036957	leucine rich repeat and fibronectin type III domain containing 3	-1.949	0.0077	0.0209
Lrp1	ENSMUSG00000040249	low density lipoprotein receptor-related protein 1	-1.533	0.0008	0.0029
Lrrc10	ENSMUSG00000060187	leucine rich repeat containing 10	-2.149	0.0137	0.0347
Lrrc24	ENSMUSG00000033707	leucine rich repeat containing 24	-2.580	0.0024	0.0074
Lrrc25	ENSMUSG00000049988	leucine rich repeat containing 25	-2.496	0.0001	0.0006
Lrrc28	ENSMUSG00000030556	leucine rich repeat containing 28	-1.782	0.0000	0.0000
Lrrc29	ENSMUSG00000041679	leucine rich repeat containing 29	-8.340	0.0002	0.0009

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lrrc30	ENSMUSG00000073375	leucine rich repeat containing 30	-3.040	0.0004	0.0013
Lrrc32	ENSMUSG00000090958	leucine rich repeat containing 32	-1.636	0.0019	0.0062
Lrrc49	ENSMUSG00000047766	leucine rich repeat containing 49	-1.748	0.0000	0.0001
Lrrc51	ENSMUSG00000064307	leucine rich repeat containing 51	-1.580	0.0249	0.0576
Lrrc56	ENSMUSG00000038637	leucine rich repeat containing 56	-2.006	0.0004	0.0015
Lrrc70	ENSMUSG00000118423	leucine rich repeat containing 70	-2.336	0.0034	0.0102
Lsm10	ENSMUSG00000050188	U7 snRNP-specific Sm-like protein LSM10	-2.953	0.0000	0.0000
Lsmem2	ENSMUSG00000103409	leucine-rich single-pass membrane protein 2	-1.506	0.0040	0.0118
Lta4h	ENSMUSG00000015889	leukotriene A4 hydrolase	-1.587	0.0000	0.0000
Ltb4r1	ENSMUSG00000046908	leukotriene B4 receptor 1	-3.992	0.0419	0.0894
Ltc4s	ENSMUSG00000020377	leukotriene C4 synthase	-2.970	0.0000	0.0002
Lum	ENSMUSG00000036446	lumican	-1.502	0.0257	0.0592
Lxn	ENSMUSG00000047557	latexin	-2.254	0.0001	0.0006
Ly6a	ENSMUSG00000075602	lymphocyte antigen 6 complex, locus A	-1.796	0.0000	0.0000
Ly6c1	ENSMUSG00000079018	lymphocyte antigen 6 complex, locus C1	-1.776	0.0000	0.0001
Ly6e	ENSMUSG00000022587	lymphocyte antigen 6 complex, locus E	-1.824	0.0000	0.0000
Ly6g6d	ENSMUSG00000073413	lymphocyte antigen 6 complex, locus G6D	-15.222	0.0050	0.0145
Ly86	ENSMUSG00000021423	lymphocyte antigen 86	-4.389	0.0000	0.0000
Ly96	ENSMUSG00000025779	lymphocyte antigen 96	-2.282	0.0001	0.0003
Lyl1	ENSMUSG00000034041	lymphoblastomic leukemia 1	-1.895	0.0010	0.0034
Lypd2	ENSMUSG00000022595	Ly6/Plaur domain containing 2	-2.500	0.0068	0.0188
Lypd8l	ENSMUSG00000037145	LY6/PLAUR domain containing 8 like	-2.798	0.0430	0.0913
Lypla1	ENSMUSG00000025903	lysophospholipase 1	-1.775	0.0001	0.0004
Lyrm1	ENSMUSG00000030922	LYR motif containing 1	-1.554	0.0028	0.0086
Lyrm2	ENSMUSG00000045854	LYR motif containing 2	-1.664	0.0000	0.0000
Lysmd2	ENSMUSG00000032184	LysM, putative peptidoglycan-binding, domain containing 2	-1.707	0.0013	0.0044
Lyz2	ENSMUSG00000069516	lysozyme 2	-1.608	0.0069	0.0189
Lztfl1	ENSMUSG00000025245	leucine zipper transcription factor-like 1	-1.539	0.0000	0.0000
Macroh2a2	ENSMUSG00000020086	macroH2A.2 histone	-1.792	0.0007	0.0025
Mad2l1bp	ENSMUSG00000034509	MAD2L1 binding protein	-1.506	0.0000	0.0000
Mad2l2	ENSMUSG00000029003	MAD2 mitotic arrest deficient-like 2	-1.763	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Maged1	ENSMUSG00000025151	MAGE family member D1	-2.088	0.0000	0.0000
Maged2	ENSMUSG00000025268	MAGE family member D2	-1.899	0.0000	0.0000
Maip1	ENSMUSG00000025971	matrix AAA peptidase interacting protein 1	-1.593	0.0000	0.0000
Mamdc4	ENSMUSG00000026941	MAM domain containing 4	-2.881	0.0056	0.0159
Maml2	ENSMUSG00000031925	mastermind like transcriptional coactivator 2	-1.532	0.0000	0.0002
Man2b2	ENSMUSG00000029119	mannosidase 2, alpha B2	-1.969	0.0000	0.0000
Manbal	ENSMUSG00000063019	mannosidase, beta A, lysosomal-like	-2.686	0.0000	0.0000
Manea	ENSMUSG00000040520	mannosidase, endo-alpha	-1.717	0.0000	0.0000
Map10	ENSMUSG00000050930	microtubule-associated protein 10	-1.657	0.0001	0.0003
Map1lc3b	ENSMUSG00000031812	microtubule-associated protein 1 light chain 3 beta	-2.009	0.0000	0.0000
Map1s	ENSMUSG00000019261	microtubule-associated protein 1S	-2.048	0.0000	0.0000
Map2k3os	ENSMUSG00000042549	mitogen-activated protein kinase kinase 3, opposite strand	-2.065	0.0009	0.0030
Map3k11	ENSMUSG00000004054	mitogen-activated protein kinase kinase kinase 11	-1.720	0.0005	0.0019
Map3k14	ENSMUSG00000020941	mitogen-activated protein kinase kinase kinase 14	-1.627	0.0002	0.0009
Mapk13	ENSMUSG00000004864	mitogen-activated protein kinase 13	-10.569	0.0023	0.0072
Mapk1ip1	ENSMUSG00000041775	mitogen-activated protein kinase 1 interacting protein 1	-1.947	0.0001	0.0002
Mapk3	ENSMUSG00000063065	mitogen-activated protein kinase 3	-2.060	0.0000	0.0000
Mapkapk3	ENSMUSG00000032577	mitogen-activated protein kinase-activated protein kinase 3	-1.532	0.0000	0.0000
Mast3	ENSMUSG00000031833	microtubule associated serine/threonine kinase 3	-1.502	0.0288	0.0652
Mavs	ENSMUSG00000037523	mitochondrial antiviral signaling protein	-1.954	0.0000	0.0000
Mbip	ENSMUSG00000021028	MAP3K12 binding inhibitory protein 1	-1.626	0.0000	0.0001
Mcfd2	ENSMUSG00000024150	multiple coagulation factor deficiency 2	-2.362	0.0000	0.0000
Mcm8	ENSMUSG00000027353	minichromosome maintenance 8 homologous recombination repair factor	-2.054	0.0000	0.0000
Mcrip2	ENSMUSG00000025732	MAPK regulated corepressor interacting protein 2	-1.667	0.0003	0.0013
Mcrs1	ENSMUSG00000037570	microspherule protein 1	-2.369	0.0000	0.0000
Mcts2	ENSMUSG00000042814	malignant T cell amplified sequence 2	-1.614	0.0000	0.0000
Mdh1	ENSMUSG00000020321	malate dehydrogenase 1, NAD (soluble)	-1.696	0.0000	0.0000
Mdh2	ENSMUSG00000019179	malate dehydrogenase 2, NAD (mitochondrial)	-2.469	0.0000	0.0000
Mdm4-ps	ENSMUSG00000081739	transformed mouse 3T3 cell double minute 4, pseudogene	-28.081	0.0007	0.0024
Mdp1	ENSMUSG00000002329	magnesium-dependent phosphatase 1	-1.726	0.0000	0.0000
Med10	ENSMUSG00000021598	mediator complex subunit 10	-1.655	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Med11	ENSMUSG00000018923	mediator complex subunit 11	-1.678	0.0000	0.0002
Med21	ENSMUSG00000030291	mediator complex subunit 21	-1.631	0.0000	0.0001
Med22	ENSMUSG00000015776	mediator complex subunit 22	-1.601	0.0000	0.0000
Med24	ENSMUSG00000017210	mediator complex subunit 24	-1.896	0.0000	0.0000
Med26	ENSMUSG00000045248	mediator complex subunit 26	-1.677	0.0000	0.0002
Med27	ENSMUSG00000026799	mediator complex subunit 27	-1.744	0.0000	0.0000
Med29	ENSMUSG00000003444	mediator complex subunit 29	-2.586	0.0000	0.0000
Med7	ENSMUSG00000020397	mediator complex subunit 7	-1.743	0.0000	0.0000
Mef2b	ENSMUSG00000079033	myocyte enhancer factor 2B	-3.768	0.0001	0.0004
Megf11	ENSMUSG00000036466	multiple EGF-like-domains 11	-8.940	0.0374	0.0813
Megf6	ENSMUSG00000057751	multiple EGF-like-domains 6	-1.954	0.0027	0.0084
Mest	ENSMUSG00000051855	mesoderm specific transcript	-2.761	0.0000	0.0000
Metrn	ENSMUSG00000002274	meteorin, glial cell differentiation regulator	-1.970	0.0000	0.0000
Mettl22	ENSMUSG00000039345	methyltransferase like 22	-2.428	0.0000	0.0000
Mettl23	ENSMUSG00000090266	methyltransferase like 23	-1.976	0.0000	0.0000
Mettl8	ENSMUSG00000041975	methyltransferase like 8	-1.674	0.0019	0.0061
Mfap1b	ENSMUSG00000048222	microfibrillar-associated protein 1B	-2.218	0.0000	0.0000
Mfap2	ENSMUSG00000060572	microfibrillar-associated protein 2	-1.729	0.0448	0.0943
Mfge8	ENSMUSG00000030605	milk fat globule EGF and factor V/VIII domain containing	-1.807	0.0000	0.0000
Mfsd10	ENSMUSG00000001082	major facilitator superfamily domain containing 10	-1.540	0.0001	0.0003
Mfsd11	ENSMUSG00000020818	major facilitator superfamily domain containing 11	-1.756	0.0000	0.0000
Mfsd14a	ENSMUSG00000089911	major facilitator superfamily domain containing 14A	-1.507	0.0000	0.0000
Mfsd14b	ENSMUSG00000038212	major facilitator superfamily domain containing 14B	-1.634	0.0000	0.0000
Mfsd3	ENSMUSG00000019080	major facilitator superfamily domain containing 3	-1.742	0.0018	0.0059
Mfsd4a	ENSMUSG00000059149	major facilitator superfamily domain containing 4A	-2.420	0.0000	0.0000
Mfsd4b1	ENSMUSG00000038522	major facilitator superfamily domain containing 4B1	-1.968	0.0002	0.0008
Mgat2	ENSMUSG00000043998	mannoside acetylglucosaminyltransferase 2	-1.606	0.0123	0.0314
Mgp	ENSMUSG00000030218	matrix Gla protein	-2.262	0.0000	0.0000
Mgrn1	ENSMUSG00000022517	mahogunin, ring finger 1	-1.522	0.0000	0.0000
Mgst1	ENSMUSG00000008540	microsomal glutathione S-transferase 1	-1.797	0.0026	0.0081
Mgst3	ENSMUSG00000026688	microsomal glutathione S-transferase 3	-2.645	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Micall2	ENSMUSG00000036718	MICAL-like 2	-1.981	0.0001	0.0003
Mif	ENSMUSG00000033307	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	-2.315	0.0000	0.0000
Mif4gd	ENSMUSG00000020743	MIF4G domain containing	-1.815	0.0000	0.0000
Miip	ENSMUSG00000029022	migration and invasion inhibitory protein	-1.714	0.0009	0.0033
Milr1	ENSMUSG00000040528	mast cell immunoglobulin like receptor 1	-4.309	0.0012	0.0041
Mindy1	ENSMUSG00000038712	MINDY lysine 48 deubiquitinase 1	-2.261	0.0000	0.0000
Mir133a-2	ENSMUSG00000065460	microRNA 133a-2	-25.440	0.0000	0.0001
Mir6240	ENSMUSG00000098343	microRNA 6240	-3.083	0.0448	0.0943
Mir703	ENSMUSG00000105814	microRNA 703	-4.400	0.0196	0.0469
Mir7-1	ENSMUSG00000065434	microRNA 7-1	-19.973	0.0020	0.0064
Mir7666	ENSMUSG00000098431	microRNA 7666	-22.794	0.0007	0.0025
Mis18bp1	ENSMUSG00000047534	MIS18 binding protein 1	-2.623	0.0188	0.0452
Mkks	ENSMUSG00000027274	McKusick-Kaufman syndrome	-1.999	0.0000	0.0000
Mkrn3	ENSMUSG00000070527	makorin, ring finger protein, 3	-2.670	0.0314	0.0701
Mlst8	ENSMUSG00000024142	MTOR associated protein, LST8 homolog (S. cerevisiae)	-1.617	0.0000	0.0001
Mlx	ENSMUSG00000017801	MAX-like protein X	-2.135	0.0000	0.0000
Mmachc	ENSMUSG00000028690	methylmalonic aciduria cblC type, with homocystinuria	-1.620	0.0000	0.0001
Mmp11	ENSMUSG00000000901	matrix metallopeptidase 11	-1.665	0.0002	0.0007
Mmp23	ENSMUSG00000029061	matrix metallopeptidase 23	-1.817	0.0057	0.0161
Mmp27	ENSMUSG00000070323	matrix metallopeptidase 27	-7.000	0.0195	0.0468
Mms19	ENSMUSG00000025159	MMS19 cytosolic iron-sulfur assembly component	-2.153	0.0000	0.0000
Mndal	ENSMUSG00000090272	myeloid nuclear differentiation antigen like	-2.215	0.0235	0.0547
Mob4	ENSMUSG00000025979	MOB family member 4, phocein	-1.627	0.0000	0.0000
Mocs1	ENSMUSG00000064120	molybdenum cofactor synthesis 1	-1.623	0.0181	0.0438
Mok	ENSMUSG00000056458	MOK protein kinase	-3.797	0.0051	0.0146
Mon1a	ENSMUSG00000032583	MON1 homolog A, secretory traffciking associated	-2.274	0.0000	0.0000
Morf4l1-ps1	ENSMUSG00000116875	mortality factor 4 like 1, pseudogene 1	-2.820	0.0001	0.0004
Mov10	ENSMUSG00000002227	Mov10 RISC complex RNA helicase	-1.531	0.0014	0.0046
Mpc1	ENSMUSG00000023861	mitochondrial pyruvate carrier 1	-2.783	0.0000	0.0000
Mpc1-ps	ENSMUSG00000091498	mitochondrial pyruvate carrier 1, pseudogene	-10.359	0.0000	0.0000
Mpdu1	ENSMUSG00000018761	mannose-P-dolichol utilization defect 1	-1.532	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mpst	ENSMUSG00000071711	mercaptopyruvate sulfurtransferase	-1.759	0.0000	0.0000
Mpv17	ENSMUSG00000107283	MpV17 mitochondrial inner membrane protein	-1.743	0.0000	0.0000
Mpv17l2	ENSMUSG00000035559	MPV17 mitochondrial membrane protein-like 2	-2.445	0.0000	0.0000
Mrap	ENSMUSG00000039956	melanocortin 2 receptor accessory protein	-1.834	0.0000	0.0000
Mrgpre	ENSMUSG00000048965	MAS-related GPR, member E	-1.871	0.0005	0.0020
Mrgprf	ENSMUSG00000031070	MAS-related GPR, member F	-2.875	0.0000	0.0000
Mrgprh	ENSMUSG00000059408	MAS-related GPR, member H	-1.685	0.0074	0.0203
Mrip-ps	ENSMUSG00000098404	Mom radiation induced polyposis, pseudogene	-2.504	0.0000	0.0000
Mroh1	ENSMUSG00000022558	maestro heat-like repeat family member 1	-1.743	0.0000	0.0000
Mrpl11	ENSMUSG00000024902	mitochondrial ribosomal protein L11	-1.536	0.0000	0.0000
Mrpl12	ENSMUSG00000039640	mitochondrial ribosomal protein L12	-2.036	0.0000	0.0000
Mrpl14	ENSMUSG00000023939	mitochondrial ribosomal protein L14	-2.776	0.0000	0.0000
Mrpl23	ENSMUSG00000037772	mitochondrial ribosomal protein L23	-2.183	0.0000	0.0000
Mrpl27	ENSMUSG00000024414	mitochondrial ribosomal protein L27	-1.709	0.0000	0.0000
Mrpl27-ps	ENSMUSG00000071867	mitochondrial ribosomal protein L27, pseudogene	-13.928	0.0097	0.0255
Mrpl3	ENSMUSG00000032563	mitochondrial ribosomal protein L3	-1.957	0.0000	0.0000
Mrpl30	ENSMUSG00000026087	mitochondrial ribosomal protein L30	-2.590	0.0000	0.0000
Mrpl34	ENSMUSG00000034880	mitochondrial ribosomal protein L34	-2.046	0.0000	0.0000
Mrpl36	ENSMUSG00000021607	mitochondrial ribosomal protein L36	-2.158	0.0000	0.0000
Mrpl4	ENSMUSG00000003299	mitochondrial ribosomal protein L4	-2.621	0.0000	0.0000
Mrpl52	ENSMUSG00000010406	mitochondrial ribosomal protein L52	-1.544	0.0000	0.0000
Mrpl54	ENSMUSG00000034932	mitochondrial ribosomal protein L54	-2.561	0.0000	0.0000
Mrpl57	ENSMUSG00000021967	mitochondrial ribosomal protein L57	-2.401	0.0000	0.0000
Mrps11	ENSMUSG00000030611	mitochondrial ribosomal protein S11	-1.697	0.0000	0.0000
Mrps12	ENSMUSG00000045948	mitochondrial ribosomal protein S12	-1.933	0.0000	0.0000
Mrps14	ENSMUSG00000058267	mitochondrial ribosomal protein S14	-1.923	0.0000	0.0000
Mrps16	ENSMUSG00000049960	mitochondrial ribosomal protein S16	-1.913	0.0000	0.0000
Mrps17	ENSMUSG00000034211	mitochondrial ribosomal protein S17	-1.554	0.0000	0.0000
Mrps18a	ENSMUSG00000023967	mitochondrial ribosomal protein S18A	-1.862	0.0000	0.0000
Mrps18b	ENSMUSG00000024436	mitochondrial ribosomal protein S18B	-2.420	0.0000	0.0000
Mrps24	ENSMUSG00000020477	mitochondrial ribosomal protein S24	-3.032	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mrps27	ENSMUSG00000041632	mitochondrial ribosomal protein S27	-1.776	0.0000	0.0000
Mrps28	ENSMUSG00000040269	mitochondrial ribosomal protein S28	-2.575	0.0000	0.0000
Mrps30	ENSMUSG00000021731	mitochondrial ribosomal protein S30	-2.201	0.0000	0.0000
Mrps36-ps1	ENSMUSG00000021631	mitichondrial ribosomal protein S36, pseudogene 1	-1.933	0.0357	0.0781
Mrps7	ENSMUSG00000046756	mitchondrial ribosomal protein S7	-1.546	0.0000	0.0000
Mrrf	ENSMUSG00000026887	mitochondrial ribosome recycling factor	-2.002	0.0000	0.0000
Mrtfb	ENSMUSG00000009569	myocardin related transcription factor B	-1.683	0.0000	0.0001
Ms4a6d	ENSMUSG00000024679	membrane-spanning 4-domains, subfamily A, member 6D	-4.102	0.0000	0.0000
Msh5	ENSMUSG00000007035	mutS homolog 5	-2.883	0.0356	0.0778
Msmo1	ENSMUSG00000031604	methylsterol monoxygenase 1	-1.542	0.0003	0.0012
Msra	ENSMUSG00000054733	methionine sulfoxide reductase A	-1.641	0.0000	0.0000
Msrb1	ENSMUSG00000075705	methionine sulfoxide reductase B1	-2.190	0.0000	0.0000
Msto1	ENSMUSG00000068922	misato 1, mitochondrial distribution and morphology regulator	-1.542	0.0004	0.0014
Msx1	ENSMUSG00000048450	msh homeobox 1	-2.152	0.0006	0.0021
Mterf3	ENSMUSG00000021519	mitochondrial transcription termination factor 3	-2.088	0.0000	0.0000
Mtg1	ENSMUSG00000039018	mitochondrial ribosome-associated GTPase 1	-1.713	0.0000	0.0000
Mthfr	ENSMUSG00000029009	methylenetetrahydrofolate reductase	-2.182	0.0000	0.0000
Mtln	ENSMUSG00000051319	mitoregulin	-3.164	0.0000	0.0000
Mtmr10	ENSMUSG00000030522	myotubularin related protein 10	-1.839	0.0003	0.0011
Mtmr11	ENSMUSG00000045934	myotubularin related protein 11	-1.575	0.0103	0.0271
Mtpap	ENSMUSG00000024234	mitochondrial poly(A) polymerase	-1.744	0.0000	0.0000
mt-Rnr1	ENSMUSG00000064337	mitochondrially encoded 12S rRNA	-2.577	0.0000	0.0000
mt-Rnr2	ENSMUSG00000064339	mitochondrially encoded 16S rRNA	-1.921	0.0000	0.0002
mt-Ta	ENSMUSG00000064347	mitochondrially encoded tRNA alanine	-8.326	0.0006	0.0022
mt-Ti	ENSMUSG00000064342	mitochondrially encoded tRNA isoleucine	-5.953	0.0000	0.0000
mt-Tl1	ENSMUSG00000064340	mitochondrially encoded tRNA leucine 1	-50.127	0.0000	0.0001
mt-Tm	ENSMUSG00000064344	mitochondrially encoded tRNA methionine	-19.101	0.0000	0.0000
mt-Tt	ENSMUSG00000064371	mitochondrially encoded tRNA threonine	-17.224	0.0000	0.0000
mt-Tw	ENSMUSG00000064346	mitochondrially encoded tRNA tryptophan	-3.158	0.0000	0.0000
mt-Ty	ENSMUSG00000064350	mitochondrially encoded tRNA tyrosine	-19.200	0.0020	0.0064
Mtx1	ENSMUSG00000064068	metaxin 1	-1.588	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Muc3a	ENSMUSG00000094840	mucin 3A, cell surface associated	-7.697	0.0015	0.0049
Mus81	ENSMUSG00000024906	MUS81 structure-specific endonuclease subunit	-2.045	0.0000	0.0000
Mutyh	ENSMUSG00000028687	mutY DNA glycosylase	-1.823	0.0239	0.0557
Myl12a	ENSMUSG00000024048	myosin, light chain 12A, regulatory, non-sarcomeric	-1.714	0.0000	0.0000
Myl2	ENSMUSG00000013936	myosin, light polypeptide 2, regulatory, cardiac, slow	-1.907	0.0000	0.0000
Myl6b	ENSMUSG00000039824	myosin, light polypeptide 6B	-1.749	0.0007	0.0026
Myl9	ENSMUSG00000067818	myosin, light polypeptide 9, regulatory	-2.072	0.0000	0.0000
Mylpf	ENSMUSG00000030672	myosin light chain, phosphorylatable, fast skeletal muscle	-3.339	0.0018	0.0059
Myo19	ENSMUSG00000020527	myosin XIX	-1.817	0.0051	0.0148
Myo7a	ENSMUSG00000030761	myosin VIIA	-1.500	0.0027	0.0083
Myo9b	ENSMUSG00000004677	myosin IXb	-1.612	0.0000	0.0000
Myot	ENSMUSG00000024471	myotilin	-2.026	0.0002	0.0008
Myoz2	ENSMUSG00000028116	myozenin 2	-1.898	0.0000	0.0000
Naa38	ENSMUSG00000059278	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	-2.567	0.0000	0.0000
Naa60	ENSMUSG00000005982	N(alpha)-acetyltransferase 60, NatF catalytic subunit	-2.073	0.0000	0.0000
Naa80	ENSMUSG00000079334	N(alpha)-acetyltransferase 80, NatH catalytic subunit	-2.006	0.0000	0.0000
Naaa	ENSMUSG00000029413	N-acylethanolamine acid amidase	-1.520	0.0004	0.0014
Nadk	ENSMUSG00000029063	NAD kinase	-1.676	0.0000	0.0000
Naga	ENSMUSG00000022453	N-acetyl galactosaminidase, alpha	-1.892	0.0000	0.0000
Naglu	ENSMUSG00000001751	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	-1.676	0.0007	0.0024
Naip2	ENSMUSG00000078945	NLR family, apoptosis inhibitory protein 2	-1.711	0.0027	0.0083
Napa	ENSMUSG00000006024	N-ethylmaleimide sensitive fusion protein attachment protein alpha	-2.468	0.0000	0.0000
Napsa	ENSMUSG00000002204	napsin A aspartic peptidase	-5.041	0.0057	0.0161
Nars2	ENSMUSG00000018995	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	-1.627	0.0000	0.0000
Nat8f1	ENSMUSG00000057103	N-acetyltransferase 8 (GCN5-related) family member 1	-1.871	0.0054	0.0154
Nat8f4	ENSMUSG00000068299	N-acetyltransferase 8 (GCN5-related) family member 4	-2.031	0.0018	0.0060
Natd1	ENSMUSG00000018931	N-acetyltransferase domain containing 1	-1.771	0.0000	0.0001
Naxd	ENSMUSG00000031505	NAD(P)HX dehydratase	-1.646	0.0000	0.0000
Nbdy	ENSMUSG00000086316	negative regulator of P-body association	-1.621	0.0000	0.0000
Nbeal2	ENSMUSG00000056724	neurobeachin-like 2	-1.763	0.0000	0.0000
Ncapd3	ENSMUSG00000035024	non-SMC condensin II complex, subunit D3	-1.668	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ncdn	ENSMUSG00000028833	neurochondrin	-1.606	0.0000	0.0000
Nckap5l	ENSMUSG00000023009	NCK-associated protein 5-like	-1.760	0.0000	0.0000
Nckipsd	ENSMUSG00000032598	NCK interacting protein with SH3 domain	-2.063	0.0000	0.0000
Ncln	ENSMUSG00000020238	nicalin	-3.322	0.0000	0.0000
Ncoa4-ps	ENSMUSG00000021908	nuclear receptor coactivator 4, pseudogene	-3.537	0.0018	0.0059
Ncstn	ENSMUSG00000003458	nicastrin	-1.532	0.0000	0.0000
Ndufa11	ENSMUSG00000002379	NADH:ubiquinone oxidoreductase subunit A11	-2.480	0.0000	0.0000
Ndufa12-ps	ENSMUSG00000080893	NADH:ubiquinone oxidoreductase subunit A12, pseudogene	-3.625	0.0000	0.0000
Ndufa3	ENSMUSG00000035674	NADH:ubiquinone oxidoreductase subunit A3	-2.215	0.0000	0.0000
Ndufa4l2	ENSMUSG00000040280	Ndufa4, mitochondrial complex associated like 2	-2.519	0.0000	0.0000
Ndufa7	ENSMUSG00000041881	NADH:ubiquinone oxidoreductase subunit A7	-2.416	0.0000	0.0000
Ndufab1-ps	ENSMUSG00000091989	NADH:ubiquinone oxidoreductase subunit AB1b	-3.668	0.0004	0.0016
Ndufaf3	ENSMUSG00000070283	NADH:ubiquinone oxidoreductase complex assembly factor 3	-1.654	0.0000	0.0000
Ndufaf8	ENSMUSG00000078572	NADH:ubiquinone oxidoreductase complex assembly factor 8	-1.804	0.0000	0.0000
Ndufb1	ENSMUSG00000113902	NADH:ubiquinone oxidoreductase subunit B1	-2.893	0.0000	0.0000
Ndufb11	ENSMUSG00000031059	NADH:ubiquinone oxidoreductase subunit B11	-2.332	0.0000	0.0000
Ndufb2	ENSMUSG00000002416	NADH:ubiquinone oxidoreductase subunit B2	-4.367	0.0000	0.0000
Ndufb5	ENSMUSG00000027673	NADH:ubiquinone oxidoreductase subunit B5	-2.516	0.0000	0.0000
Ndufb6	ENSMUSG00000071014	NADH:ubiquinone oxidoreductase subunit B6	-1.790	0.0000	0.0000
Ndufc1	ENSMUSG00000037152	NADH:ubiquinone oxidoreductase subunit C1	-1.595	0.0000	0.0000
Ndufs5	ENSMUSG00000028648	NADH:ubiquinone oxidoreductase core subunit S5	-5.076	0.0000	0.0000
Ndufs5-ps	ENSMUSG00000081824	NADH:ubiquinone oxidoreductase core subunit S5, pseudogene	-2.849	0.0000	0.0000
Ndufs7	ENSMUSG00000020153	NADH:ubiquinone oxidoreductase core subunit S7	-2.579	0.0000	0.0000
Ndufs8	ENSMUSG00000059734	NADH:ubiquinone oxidoreductase core subunit S8	-1.870	0.0000	0.0000
Neb	ENSMUSG00000026950	nebulin	-1.750	0.0152	0.0378
Necab1	ENSMUSG00000040536	N-terminal EF-hand calcium binding protein 1	-3.438	0.0005	0.0018
Necab3	ENSMUSG00000027489	N-terminal EF-hand calcium binding protein 3	-9.670	0.0075	0.0203
Nelfa	ENSMUSG00000029111	negative elongation factor complex member A, Whsc2	-1.558	0.0000	0.0000
Nepn	ENSMUSG00000038624	nephrocan	-1.666	0.0299	0.0673
Neurl1a	ENSMUSG00000006435	neuralized E3 ubiquitin protein ligase 1A	-1.543	0.0053	0.0152
Nfatc1	ENSMUSG00000033016	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1	-1.504	0.0005	0.0020

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nfe2l2	ENSMUSG00000015839	nuclear factor, erythroid derived 2, like 2	-1.510	0.0000	0.0000
Nfkbib	ENSMUSG00000030595	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta	-2.587	0.0000	0.0000
Nfs1	ENSMUSG00000027618	nitrogen fixation gene 1 (S. cerevisiae)	-2.258	0.0000	0.0000
Nfyc	ENSMUSG00000032897	nuclear transcription factor-Y gamma	-1.711	0.0000	0.0000
Nfyc-ps	ENSMUSG00000073233	nuclear transcription factor-Y gamma, pseudogene	-25.843	0.0002	0.0009
Ngf	ENSMUSG00000027859	nerve growth factor	-1.747	0.0006	0.0021
Nhej1	ENSMUSG00000026162	non-homologous end joining factor 1	-1.668	0.0000	0.0000
Nicn1	ENSMUSG00000032606	nicolin 1	-1.508	0.0000	0.0000
Nid2	ENSMUSG00000021806	nidogen 2	-1.854	0.0000	0.0000
Ninj1	ENSMUSG00000037966	ninjurin 1	-2.771	0.0000	0.0000
Nipsnap2	ENSMUSG00000029432	nipsnap homolog 2	-1.789	0.0000	0.0000
Nipsnap3b	ENSMUSG00000015247	nipsnap homolog 3B	-1.648	0.0000	0.0001
Nisch	ENSMUSG00000021910	nischarin	-1.751	0.0000	0.0000
Nit1	ENSMUSG00000013997	nitrilase 1	-1.509	0.0000	0.0000
Nit2	ENSMUSG00000022751	nitrilase family, member 2	-1.664	0.0000	0.0000
Nkiras2	ENSMUSG00000017837	NFKB inhibitor interacting Ras-like protein 2	-1.592	0.0000	0.0000
Nle1	ENSMUSG00000020692	notchless homolog 1	-1.583	0.0090	0.0241
Nlrc3	ENSMUSG00000049871	NLR family, CARD domain containing 3	-1.682	0.0085	0.0229
Nlrp1b	ENSMUSG00000070390	NLR family, pyrin domain containing 1B	-3.910	0.0152	0.0379
Nmb	ENSMUSG00000025723	neuromedin B	-2.245	0.0166	0.0407
Nmbr	ENSMUSG00000019865	neuromedin B receptor	-11.751	0.0096	0.0253
Nme2	ENSMUSG00000020857	NME/NM23 nucleoside diphosphate kinase 2	-3.330	0.0004	0.0014
Nme5	ENSMUSG00000035984	NME/NM23 family member 5	-1.577	0.0275	0.0628
Nmnat1	ENSMUSG00000028992	nicotinamide nucleotide adenylyltransferase 1	-1.533	0.0000	0.0001
Nmral1	ENSMUSG00000063445	NmrA-like family domain containing 1	-1.552	0.0187	0.0450
Nnmt	ENSMUSG00000032271	nicotinamide N-methyltransferase	-1.598	0.0305	0.0684
Noc4l	ENSMUSG00000033294	NOC4 like	-2.203	0.0000	0.0000
Nod1	ENSMUSG00000038058	nucleotide-binding oligomerization domain containing 1	-1.851	0.0000	0.0000
Nop10	ENSMUSG00000027133	NOP10 ribonucleoprotein	-1.869	0.0000	0.0000
Nos3	ENSMUSG00000028978	nitric oxide synthase 3, endothelial cell	-1.599	0.0000	0.0000
Nosip	ENSMUSG00000003421	nitric oxide synthase interacting protein	-1.705	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Notch1	ENSMUSG00000026923	notch 1	-1.509	0.0002	0.0007
Npdc1	ENSMUSG00000015094	neural proliferation, differentiation and control 1	-1.917	0.0000	0.0000
Npepl1	ENSMUSG00000039263	aminopeptidase-like 1	-1.601	0.0000	0.0000
Nphp4	ENSMUSG00000039577	nephronophthisis 4 (juvenile) homolog (human)	-2.302	0.0246	0.0571
Npm3	ENSMUSG00000056209	nucleoplasmin 3	-1.554	0.0010	0.0035
Npm3-ps1	ENSMUSG00000081669	nucleoplasmin 3, pseudogene 1	-1.942	0.0218	0.0514
Nprl2	ENSMUSG00000010057	NPR2 like, GATOR1 complex subunit	-3.775	0.0000	0.0000
Nprl3	ENSMUSG00000020289	nitrogen permease regulator-like 3	-1.827	0.0000	0.0000
Nqo1	ENSMUSG00000003849	NAD(P)H dehydrogenase, quinone 1	-1.500	0.0000	0.0000
Nr0b2	ENSMUSG00000037583	nuclear receptor subfamily 0, group B, member 2	-3.449	0.0000	0.0000
Nr1d1	ENSMUSG00000020889	nuclear receptor subfamily 1, group D, member 1	-1.638	0.0003	0.0012
Nr1h2	ENSMUSG00000060601	nuclear receptor subfamily 1, group H, member 2	-2.560	0.0000	0.0000
Nr4a1	ENSMUSG00000023034	nuclear receptor subfamily 4, group A, member 1	-1.742	0.0130	0.0330
Nradd	ENSMUSG00000032491	neurotrophin receptor associated death domain	-1.985	0.0458	0.0962
Nrbf2	ENSMUSG00000075000	nuclear receptor binding factor 2	-2.141	0.0001	0.0004
Nrm	ENSMUSG00000059791	nurim (nuclear envelope membrane protein)	-4.443	0.0000	0.0000
Nrros	ENSMUSG00000052384	negative regulator of reactive oxygen species	-2.118	0.0004	0.0015
Nsdhl	ENSMUSG00000031349	NAD(P) dependent steroid dehydrogenase-like	-2.097	0.0000	0.0000
Nsmf	ENSMUSG00000006476	NMDA receptor synaptonuclear signaling and neuronal migration factor	-1.666	0.0000	0.0000
Nsun5	ENSMUSG00000000916	NOL1/NOP2/Sun domain family, member 5	-2.189	0.0000	0.0000
Nt5c3b	ENSMUSG00000017176	5'-nucleotidase, cytosolic IIIB	-1.527	0.0000	0.0000
Nt5dc1	ENSMUSG00000039480	5'-nucleotidase domain containing 1	-1.565	0.0000	0.0001
Nt5e	ENSMUSG00000032420	5' nucleotidase, ecto	-1.524	0.0004	0.0015
Ntan1	ENSMUSG00000022681	N-terminal Asn amidase	-1.730	0.0000	0.0000
Ntf3	ENSMUSG00000049107	neurotrophin 3	-1.625	0.0005	0.0020
Ntmt1	ENSMUSG00000026857	N-terminal Xaa-Pro-Lys N-methyltransferase 1	-1.613	0.0000	0.0000
Ntsr2	ENSMUSG00000020591	neurotensin receptor 2	-1.756	0.0006	0.0021
Nudt11	ENSMUSG00000073295	nudix (nucleoside diphosphate linked moiety X)-type motif 11	-1.628	0.0104	0.0272
Nudt14	ENSMUSG00000002804	nudix (nucleoside diphosphate linked moiety X)-type motif 14	-1.990	0.0000	0.0000
Nudt15	ENSMUSG00000033405	nudix (nucleoside diphosphate linked moiety X)-type motif 15	-1.955	0.0021	0.0068
Nudt17	ENSMUSG00000028100	nudix (nucleoside diphosphate linked moiety X)-type motif 17	-2.197	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nudt19	ENSMUSG00000034875	nudix (nucleoside diphosphate linked moiety X)-type motif 19	-2.113	0.0000	0.0000
Nudt2	ENSMUSG00000028443	nudix (nucleoside diphosphate linked moiety X)-type motif 2	-3.005	0.0000	0.0000
Nudt22	ENSMUSG00000037349	nudix (nucleoside diphosphate linked moiety X)-type motif 22	-2.072	0.0000	0.0000
Nudt7	ENSMUSG00000031767	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-1.681	0.0000	0.0000
Nup133	ENSMUSG00000039509	nucleoporin 133	-1.638	0.0000	0.0000
Nup188	ENSMUSG00000052533	nucleoporin 188	-1.796	0.0000	0.0000
Nupr1l	ENSMUSG00000095789	nuclear protein transcriptional regulator 1 like	-3.208	0.0278	0.0634
Nusap1	ENSMUSG00000027306	nucleolar and spindle associated protein 1	-2.148	0.0101	0.0264
Nxpe3	ENSMUSG00000075033	neurexophilin and PC-esterase domain family, member 3	-1.809	0.0001	0.0006
Oas2	ENSMUSG00000032690	2'-5' oligoadenylate synthetase 2	-1.721	0.0477	0.0994
Oaz1	ENSMUSG00000035242	ornithine decarboxylase antizyme 1	-1.575	0.0000	0.0000
Oaz2-ps	ENSMUSG00000083610	ornithine decarboxylase antizyme 2, pseudogene	-3.306	0.0000	0.0000
Ocel1	ENSMUSG00000002396	occludin/ELL domain containing 1	-1.719	0.0182	0.0440
Odf3l1	ENSMUSG00000045620	outer dense fiber of sperm tails 3-like 1	-10.842	0.0148	0.0370
Ogdhl	ENSMUSG00000021913	oxoglutarate dehydrogenase-like	-1.613	0.0008	0.0029
Ogg1	ENSMUSG00000030271	8-oxoguanine DNA-glycosylase 1	-2.243	0.0000	0.0000
Ogn	ENSMUSG00000021390	osteoglycin	-1.786	0.0001	0.0003
Olfml1	ENSMUSG00000051041	olfactomedin-like 1	-1.554	0.0384	0.0832
Olfml2a	ENSMUSG00000046618	olfactomedin-like 2A	-1.529	0.0042	0.0123
Olfr78	ENSMUSG00000043366	olfactory receptor 78	-2.060	0.0116	0.0299
Onecut2	ENSMUSG00000045991	one cut domain, family member 2	-9.457	0.0442	0.0933
Optc	ENSMUSG00000010311	opticin	-11.618	0.0166	0.0406
Orc5	ENSMUSG00000029012	origin recognition complex, subunit 5	-2.025	0.0000	0.0000
Ormdl2	ENSMUSG00000025353	ORM1-like 2 (S. cerevisiae)	-2.104	0.0000	0.0000
Osbpl5	ENSMUSG00000037606	oxysterol binding protein-like 5	-1.650	0.0001	0.0003
Osgepl1	ENSMUSG00000026096	O-sialoglycoprotein endopeptidase-like 1	-2.542	0.0000	0.0000
Osgin1	ENSMUSG00000074063	oxidative stress induced growth inhibitor 1	-2.477	0.0011	0.0038
Osmr	ENSMUSG00000022146	oncostatin M receptor	-1.996	0.0000	0.0000
Osr1	ENSMUSG00000048387	odd-skipped related transcription factor 1	-2.079	0.0025	0.0077
Oxld1	ENSMUSG00000039670	oxidoreductase like domain containing 1	-1.587	0.0000	0.0000
P2ry10b	ENSMUSG00000054293	purinergic receptor P2Y, G-protein coupled 10B	-2.573	0.0012	0.0040

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
P2ry14	ENSMUSG00000036381	purinergic receptor P2Y, G-protein coupled, 14	-2.089	0.0000	0.0000
P2ry6	ENSMUSG00000048779	pyrimidinergic receptor P2Y, G-protein coupled, 6	-1.993	0.0025	0.0078
P3h1	ENSMUSG00000028641	prolyl 3-hydroxylase 1	-2.019	0.0000	0.0000
P4ha1	ENSMUSG00000019916	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	-1.506	0.0005	0.0019
P4htm	ENSMUSG00000006675	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	-1.871	0.0000	0.0000
Pacc1	ENSMUSG00000026627	proton activated chloride channel 1	-1.853	0.0000	0.0001
Padi3	ENSMUSG00000025328	peptidyl arginine deiminase, type III	-17.633	0.0090	0.0239
Pafah2	ENSMUSG00000037366	platelet-activating factor acetylhydrolase 2	-1.557	0.0003	0.0013
Pah	ENSMUSG00000020051	phenylalanine hydroxylase	-2.529	0.0001	0.0005
Pakap	ENSMUSG00000038729	paralemmin A kinase anchor protein	-8.507	0.0302	0.0678
Pam16	ENSMUSG00000014301	presequence translocase-asssociated motor 16	-2.996	0.0000	0.0000
Pank4	ENSMUSG00000029056	pantothenate kinase 4	-1.660	0.0000	0.0000
Pard6a	ENSMUSG00000005699	par-6 family cell polarity regulator alpha	-2.140	0.0000	0.0000
Parp16	ENSMUSG00000032392	poly (ADP-ribose) polymerase family, member 16	-1.887	0.0000	0.0000
Pars2	ENSMUSG00000043572	prolyl-tRNA synthetase (mitochondrial)(putative)	-1.697	0.0001	0.0004
Parvb	ENSMUSG00000022438	parvin, beta	-1.515	0.0000	0.0000
Patz1	ENSMUSG00000020453	POZ (BTB) and AT hook containing zinc finger 1	-1.550	0.0022	0.0069
Paxx	ENSMUSG00000047617	non-homologous end joining factor	-2.645	0.0000	0.0000
Pcdhb21	ENSMUSG00000044022	protocadherin beta 21	-2.036	0.0257	0.0592
Pcdhb6	ENSMUSG00000051678	protocadherin beta 6	-2.065	0.0398	0.0856
Pcdhga1	ENSMUSG00000103144	protocadherin gamma subfamily A, 1	-2.199	0.0055	0.0155
Pcdhga10	ENSMUSG00000102222	protocadherin gamma subfamily A, 10	-2.469	0.0000	0.0000
Pcdhga2	ENSMUSG00000103332	protocadherin gamma subfamily A, 2	-2.601	0.0000	0.0000
Pcdhga3	ENSMUSG00000104346	protocadherin gamma subfamily A, 3	-1.823	0.0049	0.0140
Pcdhga5	ENSMUSG00000103567	protocadherin gamma subfamily A, 5	-1.677	0.0039	0.0117
Pcdhga6	ENSMUSG00000103793	protocadherin gamma subfamily A, 6	-2.228	0.0220	0.0518
Pcdhga7	ENSMUSG00000103472	protocadherin gamma subfamily A, 7	-2.050	0.0000	0.0000
Pcdhga9	ENSMUSG00000102440	protocadherin gamma subfamily A, 9	-3.650	0.0050	0.0144
Pcdhgb2	ENSMUSG00000102748	protocadherin gamma subfamily B, 2	-1.626	0.0060	0.0168
Pcdhgb4	ENSMUSG00000103585	protocadherin gamma subfamily B, 4	-1.500	0.0278	0.0634

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pcdhgb7	ENSMUSG00000104063	protocadherin gamma subfamily B, 7	-1.626	0.0094	0.0249
Pcdhgc4	ENSMUSG00000023036	protocadherin gamma subfamily C, 4	-3.886	0.0063	0.0175
Pcgf1	ENSMUSG00000069678	polycomb group ring finger 1	-1.501	0.0016	0.0053
Pck1	ENSMUSG00000027513	phosphoenolpyruvate carboxykinase 1, cytosolic	-2.416	0.0335	0.0740
Pck2	ENSMUSG00000040618	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-1.520	0.0064	0.0177
Pcolce	ENSMUSG00000029718	procollagen C-endopeptidase enhancer protein	-1.739	0.0019	0.0062
Pcsk4	ENSMUSG00000020131	proprotein convertase subtilisin/kexin type 4	-1.883	0.0032	0.0098
Pdcd2	ENSMUSG00000014771	programmed cell death 2	-1.652	0.0012	0.0040
Pdcd6	ENSMUSG00000021576	programmed cell death 6	-1.509	0.0000	0.0000
Pde1b	ENSMUSG00000022489	phosphodiesterase 1B, Ca2+-calmodulin dependent	-1.569	0.0079	0.0215
Pdf	ENSMUSG00000078931	peptide deformylase (mitochondrial)	-5.652	0.0000	0.0000
Pdgfrb	ENSMUSG00000024620	platelet derived growth factor receptor, beta polypeptide	-1.741	0.0000	0.0000
Pdgfrl	ENSMUSG00000031595	platelet-derived growth factor receptor-like	-2.398	0.0002	0.0010
Pdia5	ENSMUSG00000022844	protein disulfide isomerase associated 5	-1.667	0.0103	0.0269
Pdk2	ENSMUSG00000038967	pyruvate dehydrogenase kinase, isoenzyme 2	-1.693	0.0000	0.0000
Pdk3	ENSMUSG00000035232	pyruvate dehydrogenase kinase, isoenzyme 3	-1.905	0.0012	0.0041
Pdlim1	ENSMUSG00000055044	PDZ and LIM domain 1 (elfin)	-1.765	0.0000	0.0000
Pdlim4	ENSMUSG00000020388	PDZ and LIM domain 4	-2.433	0.0000	0.0000
Pdlim7	ENSMUSG00000021493	PDZ and LIM domain 7	-1.675	0.0000	0.0000
Pear1	ENSMUSG00000028073	platelet endothelial aggregation receptor 1	-2.069	0.0000	0.0000
Pebp1	ENSMUSG00000032959	phosphatidylethanolamine binding protein 1	-1.755	0.0000	0.0000
Pef1	ENSMUSG00000028779	penta-EF hand domain containing 1	-1.903	0.0000	0.0000
Pemt	ENSMUSG00000000301	phosphatidylethanolamine N-methyltransferase	-5.229	0.0000	0.0000
Penk	ENSMUSG00000045573	preproenkephalin	-1.632	0.0029	0.0090
Pex10	ENSMUSG00000029047	peroxisomal biogenesis factor 10	-2.478	0.0000	0.0000
Pex2	ENSMUSG00000040374	peroxisomal biogenesis factor 2	-1.737	0.0000	0.0000
Pex3	ENSMUSG00000019809	peroxisomal biogenesis factor 3	-1.670	0.0000	0.0000
Pf4	ENSMUSG00000029373	platelet factor 4	-2.111	0.0067	0.0186
Pfkfb1	ENSMUSG00000025271	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	-1.862	0.0045	0.0131
Pfkfb4	ENSMUSG00000025648	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-1.917	0.0000	0.0000
Pgam1	ENSMUSG00000011752	phosphoglycerate mutase 1	-2.284	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pgam2	ENSMUSG00000020475	phosphoglycerate mutase 2	-1.786	0.0000	0.0000
Pgam5	ENSMUSG00000029500	phosphoglycerate mutase family member 5	-1.678	0.0000	0.0000
Pgap6	ENSMUSG00000024180	post-glycosylphosphatidylinositol attachment to proteins 6	-2.494	0.0000	0.0000
Pgls	ENSMUSG00000031807	6-phosphogluconolactonase	-4.524	0.0000	0.0000
Pgpep1l	ENSMUSG00000030553	pyroglutamyl-peptidase I-like	-30.796	0.0003	0.0013
Pgrmc1	ENSMUSG00000006373	progesterone receptor membrane component 1	-1.534	0.0000	0.0000
Pheta1	ENSMUSG00000044134	PH domain containing endocytic trafficking adaptor 1	-1.727	0.0000	0.0000
Phf7	ENSMUSG00000021902	PHD finger protein 7	-1.657	0.0016	0.0052
Phkg2	ENSMUSG00000030815	phosphorylase kinase, gamma 2 (testis)	-1.640	0.0002	0.0008
Pias3	ENSMUSG00000028101	protein inhibitor of activated STAT 3	-2.037	0.0000	0.0000
Pias4	ENSMUSG00000004934	protein inhibitor of activated STAT 4	-1.675	0.0003	0.0012
Pidd1	ENSMUSG00000025507	p53 induced death domain protein 1	-2.070	0.0105	0.0273
Pierce2	ENSMUSG00000086158	piercer of microtubule wall 2	-2.514	0.0000	0.0000
Pigb	ENSMUSG00000079469	phosphatidylinositol glycan anchor biosynthesis, class B	-2.156	0.0000	0.0000
Pigf	ENSMUSG00000024145	phosphatidylinositol glycan anchor biosynthesis, class F	-2.110	0.0001	0.0004
Pigo	ENSMUSG00000028454	phosphatidylinositol glycan anchor biosynthesis, class O	-2.125	0.0000	0.0000
Pigp	ENSMUSG00000022940	phosphatidylinositol glycan anchor biosynthesis, class P	-1.634	0.0000	0.0000
Pigq	ENSMUSG00000025728	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.615	0.0000	0.0000
Pigs	ENSMUSG00000041958	phosphatidylinositol glycan anchor biosynthesis, class S	-1.796	0.0000	0.0000
Pigt	ENSMUSG00000017721	phosphatidylinositol glycan anchor biosynthesis, class T	-1.940	0.0000	0.0000
Pigv	ENSMUSG00000043257	phosphatidylinositol glycan anchor biosynthesis, class V	-1.770	0.0000	0.0000
Pih1d1	ENSMUSG00000003423	PIH1 domain containing 1	-1.811	0.0000	0.0000
Pih1d2	ENSMUSG00000000167	PIH1 domain containing 2	-3.174	0.0208	0.0493
Pik3cg	ENSMUSG00000020573	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma	-1.880	0.0160	0.0396
Pik3r6	ENSMUSG00000046207	phosphoinositide-3-kinase regulatory subunit 5	-1.709	0.0001	0.0005
Pilrb1	ENSMUSG00000066684	paired immunoglobin-like type 2 receptor beta 1	-8.660	0.0212	0.0501
Pin1	ENSMUSG00000032171	peptidyl-prolyl cis/trans isomerase, NIMA-interacting 1	-1.875	0.0000	0.0000
Pip4p2	ENSMUSG00000028221	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 2	-1.798	0.0000	0.0000
Pip5k1b	ENSMUSG00000024867	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-2.008	0.0000	0.0000
Pira12	ENSMUSG00000074417	paired-Ig-like receptor A12	-7.611	0.0000	0.0002
Pitpnm1	ENSMUSG00000024851	phosphatidylinositol transfer protein, membrane-associated 1	-2.070	0.0000	0.0000

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Piwil2	ENSMUSG00000033644	piwi-like RNA-mediated gene silencing 2	-1.818	0.0413	0.0882
Pkd1	ENSMUSG00000032855	polycystin 1, transient receptor potential channel interacting	-1.619	0.0000	0.0000
Pkmyt1	ENSMUSG00000023908	protein kinase, membrane associated tyrosine/threonine 1	-2.056	0.0380	0.0825
Pla1a	ENSMUSG00000002847	phospholipase A1 member A	-1.556	0.0008	0.0027
Pla2g4e	ENSMUSG00000050211	phospholipase A2, group IVE	-1.815	0.0113	0.0291
Pla2g6	ENSMUSG00000042632	phospholipase A2, group VI	-1.565	0.0000	0.0001
Plag1	ENSMUSG00000003282	pleiomorphic adenoma gene 1	-1.540	0.0162	0.0399
Platr25	ENSMUSG00000074863	pluripotency associated transcript 25	-3.084	0.0000	0.0000
Plb1	ENSMUSG00000029134	phospholipase B1	-1.934	0.0135	0.0341
Plbd1	ENSMUSG00000030214	phospholipase B domain containing 1	-1.523	0.0001	0.0002
Plcd1	ENSMUSG00000010660	phospholipase C, delta 1	-1.662	0.0000	0.0000
Pld3	ENSMUSG00000003363	phospholipase D family, member 3	-2.689	0.0000	0.0000
Pld4	ENSMUSG00000052160	phospholipase D family, member 4	-1.855	0.0002	0.0007
Plekhg1	ENSMUSG00000040624	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	-1.548	0.0024	0.0074
Plekhg2	ENSMUSG00000037552	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	-1.823	0.0000	0.0000
Plekhm1	ENSMUSG00000034247	pleckstrin homology domain containing, family M (with RUN domain) member 1	-1.616	0.0009	0.0032
Plekho1	ENSMUSG00000015745	pleckstrin homology domain containing, family O member 1	-2.294	0.0000	0.0000
Plet1	ENSMUSG00000032068	placenta expressed transcript 1	-3.063	0.0061	0.0171
Plin4	ENSMUSG00000002831	perilipin 4	-1.769	0.0098	0.0259
Plin5	ENSMUSG00000011305	perilipin 5	-1.654	0.0013	0.0044
Plk5	ENSMUSG00000035486	polo like kinase 5	-2.007	0.0008	0.0029
Pllp	ENSMUSG00000031775	plasma membrane proteolipid	-2.963	0.0176	0.0428
Pln	ENSMUSG00000038583	phospholamban	-1.741	0.0000	0.0000
Plod1	ENSMUSG00000019055	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-1.506	0.0000	0.0000
Plp2	ENSMUSG00000031146	proteolipid protein 2	-2.360	0.0000	0.0000
Plpbp	ENSMUSG00000031485	pyridoxal phosphate binding protein	-2.191	0.0000	0.0000
Plpp1	ENSMUSG00000021759	phospholipid phosphatase 1	-1.846	0.0000	0.0000
Plpp2	ENSMUSG00000052151	phospholipid phosphatase 2	-1.754	0.0101	0.0266
Plpp5	ENSMUSG00000031570	phospholipid phosphatase 5	-1.805	0.0000	0.0000
Plpp7	ENSMUSG00000051373	phospholipid phosphatase 7 (inactive)	-1.632	0.0000	0.0000
Plscr2	ENSMUSG00000032372	phospholipid scramblase 2	-1.544	0.0000	0.0002

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DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pltp	ENSMUSG00000017754	phospholipid transfer protein	-2.426	0.0000	0.0000
Plxnb2	ENSMUSG00000036606	plexin B2	-1.871	0.0000	0.0000
Plxnb3	ENSMUSG00000031385	plexin B3	-1.707	0.0001	0.0004
Plxnd1	ENSMUSG00000030123	plexin D1	-1.845	0.0000	0.0000
Pmf1	ENSMUSG00000028066	polyamine-modulated factor 1	-1.984	0.0000	0.0000
Pnck	ENSMUSG00000002012	pregnancy upregulated non-ubiquitously expressed CaM kinase	-1.620	0.0000	0.0001
Pnkd	ENSMUSG00000026179	paroxysmal nonkinesiogenic dyskinesia	-1.671	0.0000	0.0000
Pnp	ENSMUSG00000115338	purine-nucleoside phosphorylase	-1.809	0.0013	0.0045
Pnpla3	ENSMUSG00000041653	patatin-like phospholipase domain containing 3	-5.260	0.0003	0.0011
Pnpo	ENSMUSG00000018659	pyridoxine 5'-phosphate oxidase	-2.138	0.0000	0.0000
Poc1a	ENSMUSG00000023345	POC1 centriolar protein A	-1.648	0.0055	0.0157
Pola2	ENSMUSG00000024833	polymerase (DNA directed), alpha 2	-2.549	0.0000	0.0000
Pold1	ENSMUSG00000038644	polymerase (DNA directed), delta 1, catalytic subunit	-1.524	0.0000	0.0002
Pold2	ENSMUSG00000020471	polymerase (DNA directed), delta 2, regulatory subunit	-1.813	0.0000	0.0000
Pold4	ENSMUSG00000024854	polymerase (DNA-directed), delta 4	-2.591	0.0000	0.0000
Pole	ENSMUSG00000007080	polymerase (DNA directed), epsilon	-1.751	0.0065	0.0180
Polg2	ENSMUSG00000020718	polymerase (DNA directed), gamma 2, accessory subunit	-1.616	0.0012	0.0041
Polm	ENSMUSG00000020474	polymerase (DNA directed), mu	-3.136	0.0000	0.0000
Poln	ENSMUSG00000045102	DNA polymerase N	-1.833	0.0157	0.0389
Polr1b	ENSMUSG00000027395	polymerase (RNA) I polypeptide B	-2.074	0.0000	0.0000
Polr1d	ENSMUSG00000029642	polymerase (RNA) I polypeptide D	-2.236	0.0000	0.0000
Polr2c	ENSMUSG00000031783	polymerase (RNA) II (DNA directed) polypeptide C	-2.561	0.0000	0.0000
Polr2d	ENSMUSG00000024258	polymerase (RNA) II (DNA directed) polypeptide D	-1.854	0.0000	0.0000
Polr2e	ENSMUSG00000004667	polymerase (RNA) II (DNA directed) polypeptide E	-1.888	0.0000	0.0000
Polr2i	ENSMUSG00000019738	polymerase (RNA) II (DNA directed) polypeptide I	-2.064	0.0000	0.0000
Polr2l	ENSMUSG00000038489	polymerase (RNA) II (DNA directed) polypeptide L	-2.141	0.0000	0.0000
Pon1	ENSMUSG00000002588	paraoxonase 1	-27.553	0.0027	0.0085
Pop4	ENSMUSG00000030423	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	-2.399	0.0000	0.0000
Pop7	ENSMUSG00000029715	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	-2.275	0.0000	0.0000
Ppcdc	ENSMUSG00000063849	phosphopantothenoylcysteine decarboxylase	-1.612	0.0001	0.0005
Ppia	ENSMUSG00000071866	peptidylprolyl isomerase A	-1.651	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ppif	ENSMUSG00000021868	peptidylprolyl isomerase F (cyclophilin F)	-1.674	0.0000	0.0000
Ppil2	ENSMUSG00000022771	peptidylprolyl isomerase (cyclophilin)-like 2	-1.778	0.0000	0.0000
Ppp1r27	ENSMUSG00000025129	protein phosphatase 1, regulatory subunit 27	-12.300	0.0090	0.0239
Ppp2r3d	ENSMUSG00000093803	protein phosphatase 2 (formerly 2A), regulatory subunit B", delta	-1.961	0.0000	0.0000
Pqlc3	ENSMUSG00000045679	PQ loop repeat containing	-2.553	0.0020	0.0063
Praf2	ENSMUSG00000031149	PRA1 domain family 2	-4.008	0.0000	0.0000
Prdm5	ENSMUSG00000029913	PR domain containing 5	-1.572	0.0018	0.0057
Prdx2	ENSMUSG00000005161	peroxiredoxin 2	-2.506	0.0000	0.0000
Prdx2-ps1	ENSMUSG00000082431	peroxiredoxin 2, pseudogene 1	-10.469	0.0000	0.0000
Prdx4	ENSMUSG00000025289	peroxiredoxin 4	-1.818	0.0000	0.0000
Prickle3	ENSMUSG00000031145	prickle planar cell polarity protein 3	-1.795	0.0009	0.0032
Prkab1	ENSMUSG00000029513	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-1.564	0.0020	0.0065
Prkag3	ENSMUSG00000006542	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	-1.690	0.0099	0.0261
Prkcz	ENSMUSG00000029053	protein kinase C, zeta	-1.609	0.0005	0.0020
Prkd2	ENSMUSG00000041187	protein kinase D2	-1.676	0.0003	0.0013
Prkra	ENSMUSG00000002731	protein kinase, interferon inducible double stranded RNA dependent activator	-1.711	0.0000	0.0000
Prnp	ENSMUSG00000079037	prion protein	-1.656	0.0000	0.0000
Proscos	ENSMUSG00000091154	proline synthetase co-transcribed, opposite strand	-1.833	0.0003	0.0010
Proser2	ENSMUSG00000045319	proline and serine rich 2	-1.959	0.0238	0.0555
Proser3	ENSMUSG00000036864	proline and serine rich 3	-2.562	0.0000	0.0000
Prpf8	ENSMUSG00000020850	pre-mRNA processing factor 8	-1.538	0.0000	0.0000
Prpsap1	ENSMUSG00000015869	phosphoribosyl pyrophosphate synthetase-associated protein 1	-1.892	0.0000	0.0000
Prpsap2	ENSMUSG00000020528	phosphoribosyl pyrophosphate synthetase-associated protein 2	-1.830	0.0003	0.0012
Prr14	ENSMUSG00000030822	proline rich 14	-1.837	0.0002	0.0008
Prrg2	ENSMUSG00000007837	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	-1.665	0.0001	0.0003
Prss36	ENSMUSG00000070371	protease, serine 36	-2.052	0.0000	0.0000
Prss45	ENSMUSG00000047257	protease, serine 45	-18.073	0.0089	0.0238
Psenen	ENSMUSG00000036835	presenilin enhancer gamma secretase subunit	-2.924	0.0000	0.0000
Psenen-ps	ENSMUSG00000056412	presenilin enhancer gamma secretase subunit, pseudogene	-19.097	0.0015	0.0049
Pskh1	ENSMUSG00000048310	protein serine kinase H1	-1.528	0.0001	0.0003
Psmb3	ENSMUSG00000069744	proteasome (prosome, macropain) subunit, beta type 3	-1.703	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Psmd5	ENSMUSG00000026869	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-1.606	0.0000	0.0000
Psmd8	ENSMUSG00000030591	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	-1.550	0.0000	0.0000
Psmf1	ENSMUSG00000032869	proteasome (prosome, macropain) inhibitor subunit 1	-2.015	0.0000	0.0000
Psmg2	ENSMUSG00000024537	proteasome (prosome, macropain) assembly chaperone 2	-2.341	0.0000	0.0000
Psmg3	ENSMUSG00000029551	proteasome (prosome, macropain) assembly chaperone 3	-2.236	0.0000	0.0001
Ptbp1	ENSMUSG00000006498	polypyrimidine tract binding protein 1	-2.023	0.0000	0.0000
Ptcd1	ENSMUSG00000029624	pentatricopeptide repeat domain 1	-1.791	0.0001	0.0005
Ptdss2	ENSMUSG00000025495	phosphatidylserine synthase 2	-1.534	0.0133	0.0337
Ptger3	ENSMUSG00000040016	prostaglandin E receptor 3 (subtype EP3)	-2.749	0.0464	0.0973
Ptpn18	ENSMUSG00000026126	protein tyrosine phosphatase, non-receptor type 18	-3.200	0.0000	0.0000
Ptpn4	ENSMUSG00000026384	protein tyrosine phosphatase, non-receptor type 4	-1.618	0.0000	0.0000
Ptprn	ENSMUSG00000026204	protein tyrosine phosphatase, receptor type, N	-1.628	0.0185	0.0446
Ptpro	ENSMUSG00000030223	protein tyrosine phosphatase, receptor type, O	-1.657	0.0002	0.0008
Ptprv	ENSMUSG00000097993	protein tyrosine phosphatase, receptor type, V	-7.149	0.0007	0.0024
Ptrhd1	ENSMUSG00000096199	peptidyl-tRNA hydrolase domain containing 1	-1.760	0.0000	0.0000
Pvr	ENSMUSG00000040511	poliovirus receptor	-1.858	0.0000	0.0000
Pwp1	ENSMUSG00000001785	PWP1 homolog, endonuclein	-1.550	0.0000	0.0000
Pxdn	ENSMUSG00000020674	peroxidasin	-1.839	0.0000	0.0000
Pxmp4	ENSMUSG00000000876	peroxisomal membrane protein 4	-1.720	0.0000	0.0000
Pycrl	ENSMUSG00000022571	pyrroline-5-carboxylate reductase-like	-2.191	0.0000	0.0000
Pyroxd2	ENSMUSG00000060224	pyridine nucleotide-disulphide oxidoreductase domain 2	-2.631	0.0000	0.0000
Pyurf	ENSMUSG00000043162	Pigy upstream reading frame	-1.883	0.0000	0.0000
Pzp	ENSMUSG00000030359	PZP, alpha-2-macroglobulin like	-2.234	0.0245	0.0569
Qpct	ENSMUSG00000024084	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	-1.662	0.0009	0.0032
Rab11b-ps2	ENSMUSG00000095690	RAB11B, member RAS oncogene family, pseudogene 2	-2.483	0.0000	0.0000
Rab1b	ENSMUSG00000024870	RAB1B, member RAS oncogene family	-1.500	0.0000	0.0000
Rab20	ENSMUSG00000031504	RAB20, member RAS oncogene family	-1.672	0.0000	0.0000
Rab27b	ENSMUSG00000024511	RAB27B, member RAS oncogene family	-3.211	0.0046	0.0135
Rab36	ENSMUSG00000020175	RAB36, member RAS oncogene family	-1.991	0.0209	0.0496
Rab3a	ENSMUSG00000031840	RAB3A, member RAS oncogene family	-1.943	0.0000	0.0000
Rab3b	ENSMUSG00000003411	RAB3B, member RAS oncogene family	-1.963	0.0472	0.0986

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rab3il1	ENSMUSG00000024663	RAB3A interacting protein (rabin3)-like 1	-1.505	0.0448	0.0943
Rab42	ENSMUSG00000089687	RAB42, member RAS oncogene family	-2.304	0.0114	0.0295
Rab7-ps1	ENSMUSG00000111686	RAB7, member RAS oncogene family, pseudogene 1	-3.049	0.0184	0.0445
Rabac1	ENSMUSG00000003380	Rab acceptor 1 (prenylated)	-2.065	0.0000	0.0000
Rabggta	ENSMUSG00000040472	Rab geranylgeranyl transferase, a subunit	-2.043	0.0000	0.0000
Rabif	ENSMUSG00000042229	RAB interacting factor	-1.617	0.0178	0.0433
Rabl2	ENSMUSG00000022621	RAB, member RAS oncogene family-like 2	-2.109	0.0006	0.0023
Rack1	ENSMUSG00000020372	receptor for activated C kinase 1	-3.337	0.0000	0.0000
Rad9a	ENSMUSG00000024824	RAD9 checkpoint clamp component A	-1.627	0.0000	0.0001
Radil	ENSMUSG00000029576	Ras association and DIL domains	-1.589	0.0094	0.0248
Rae1	ENSMUSG00000027509	ribonucleic acid export 1	-2.195	0.0001	0.0003
Ralgapa1	ENSMUSG00000021027	Ral GTPase activating protein, alpha subunit 1	-1.584	0.0000	0.0000
Ralgds	ENSMUSG00000026821	ral guanine nucleotide dissociation stimulator	-1.621	0.0000	0.0000
Ramp3	ENSMUSG00000041046	receptor (calcitonin) activity modifying protein 3	-1.520	0.0029	0.0090
Rap1gapos	ENSMUSG00000087476	RAP1 GTPase activating protein, opposite strand	-3.287	0.0009	0.0033
Rapgef3os2	ENSMUSG00000087397	Rap guanine nucleotide exchange factor (GEF) 3, opposite strand 2	-2.865	0.0453	0.0953
Rapgef5	ENSMUSG00000041992	Rap guanine nucleotide exchange factor (GEF) 5	-1.552	0.0000	0.0000
Rara	ENSMUSG00000037992	retinoic acid receptor, alpha	-1.846	0.0000	0.0000
Rarres2	ENSMUSG00000009281	retinoic acid receptor responder (tazarotene induced) 2	-2.108	0.0000	0.0000
Rasl12	ENSMUSG00000041696	RAS-like, family 12	-2.628	0.0000	0.0000
Rasl2-9	ENSMUSG00000083649	RAS-like, family 2, locus 9	-1.652	0.0002	0.0007
Rbck1	ENSMUSG00000027466	RanBP-type and C3HC4-type zinc finger containing 1	-2.430	0.0000	0.0000
Rbfa	ENSMUSG00000024570	ribosome binding factor A	-1.504	0.0019	0.0062
Rbfaos	ENSMUSG00000118061	ribosome binding factor A, opposite strand	-2.702	0.0397	0.0856
Rbis	ENSMUSG00000078784	ribosomal biogenesis factor	-1.550	0.0002	0.0008
Rbks	ENSMUSG00000029136	ribokinase	-1.570	0.0293	0.0662
Rbm41	ENSMUSG00000031433	RNA binding motif protein 41	-1.556	0.0001	0.0004
Rbx1-ps	ENSMUSG00000049832	ring-box 1, pseudogene	-3.449	0.0005	0.0018
Rcc1	ENSMUSG00000028896	regulator of chromosome condensation 1	-1.531	0.0001	0.0004
Rce1	ENSMUSG00000024889	Ras converting CAAX endopeptidase 1	-1.803	0.0000	0.0000
Rcl1	ENSMUSG00000024785	RNA terminal phosphate cyclase-like 1	-1.667	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rdh13	ENSMUSG00000008435	retinol dehydrogenase 13 (all-trans and 9-cis)	-1.558	0.0000	0.0000
Rdm1	ENSMUSG00000010362	RAD52 motif 1	-1.636	0.0000	0.0000
Reep4	ENSMUSG00000033589	receptor accessory protein 4	-1.856	0.0026	0.0082
Reep6	ENSMUSG00000035504	receptor accessory protein 6	-1.780	0.0005	0.0017
Relb	ENSMUSG00000002983	avian reticuloendotheliosis viral (v-rel) oncogene related B	-1.507	0.0009	0.0032
Rem1	ENSMUSG00000000359	rad and gem related GTP binding protein 1	-1.582	0.0039	0.0116
Rer1	ENSMUSG00000029048	retention in endoplasmic reticulum sorting receptor 1	-1.886	0.0000	0.0000
Retsat	ENSMUSG00000056666	retinol saturase (all trans retinol 13,14 reductase)	-1.753	0.0000	0.0000
Rfc3	ENSMUSG00000033970	replication factor C (activator 1) 3	-1.956	0.0003	0.0011
Rfc5	ENSMUSG00000029363	replication factor C (activator 1) 5	-2.098	0.0000	0.0000
Rffl	ENSMUSG00000020696	ring finger and FYVE like domain containing protein	-1.662	0.0022	0.0071
Rfx2	ENSMUSG00000024206	regulatory factor X, 2 (influences HLA class II expression)	-1.879	0.0209	0.0496
Rgcc	ENSMUSG00000022018	regulator of cell cycle	-2.766	0.0000	0.0000
Rgl3	ENSMUSG00000040146	ral guanine nucleotide dissociation stimulator-like 3	-1.592	0.0000	0.0001
Rgs11	ENSMUSG00000024186	regulator of G-protein signaling 11	-2.831	0.0394	0.0851
Rgs18	ENSMUSG00000026357	regulator of G-protein signaling 18	-2.542	0.0076	0.0208
Rgs19	ENSMUSG00000002458	regulator of G-protein signaling 19	-1.726	0.0028	0.0086
Rgs3	ENSMUSG00000059810	regulator of G-protein signaling 3	-1.503	0.0000	0.0002
Rhbdd1	ENSMUSG00000026142	rhomboid domain containing 1	-1.543	0.0000	0.0000
Rhbdd2	ENSMUSG00000039917	rhomboid domain containing 2	-2.166	0.0000	0.0000
Rhbdd3	ENSMUSG00000034175	rhomboid domain containing 3	-2.490	0.0000	0.0000
Rhbdf2	ENSMUSG00000020806	rhomboid 5 homolog 2	-2.017	0.0000	0.0000
Rhd	ENSMUSG00000028825	Rh blood group, D antigen	-1.670	0.0001	0.0004
Rhebl1	ENSMUSG00000023755	Ras homolog enriched in brain like 1	-2.171	0.0016	0.0053
Rhod	ENSMUSG00000041845	ras homolog family member D	-3.370	0.0000	0.0000
Ric8a	ENSMUSG00000025485	RIC8 guanine nucleotide exchange factor A	-1.724	0.0000	0.0000
Ric8b	ENSMUSG00000035620	RIC8 guanine nucleotide exchange factor B	-1.551	0.0000	0.0000
Rilp	ENSMUSG00000038195	Rab interacting lysosomal protein	-1.821	0.0000	0.0000
Rimkla	ENSMUSG00000048899	ribosomal modification protein rimK-like family member A	-2.165	0.0075	0.0205
Rimoc1	ENSMUSG00000041935	RAB7A interacting MON1-CCZ1 complex subunit 1	-1.780	0.0000	0.0000
Rims2	ENSMUSG00000037386	regulating synaptic membrane exocytosis 2	-4.284	0.0203	0.0483

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rin1	ENSMUSG00000024883	Ras and Rab interactor 1	-1.897	0.0075	0.0203
Ripk3	ENSMUSG00000022221	receptor-interacting serine-threonine kinase 3	-1.570	0.0141	0.0355
Ripk4	ENSMUSG00000005251	receptor-interacting serine-threonine kinase 4	-3.562	0.0183	0.0442
Rita1	ENSMUSG00000029600	RBPJ interacting and tubulin associated 1	-1.545	0.0004	0.0016
Rmnd5b	ENSMUSG00000001054	required for meiotic nuclear division 5 homolog B	-2.793	0.0000	0.0000
Rn18s-rs5	ENSMUSG00000119584	18s RNA, related sequence 5	-2.184	0.0079	0.0214
Rn7sk	ENSMUSG00002076161	RNA, 7SK, nuclear	-2.056	0.0462	0.0969
Rnase4	ENSMUSG00000021876	ribonuclease, RNase A family 4	-1.671	0.0005	0.0018
Rnaseh2b	ENSMUSG00000021932	ribonuclease H2, subunit B	-1.530	0.0000	0.0000
Rnd1	ENSMUSG00000054855	Rho family GTPase 1	-1.650	0.0228	0.0534
Rnf122	ENSMUSG00000039328	ring finger protein 122	-1.747	0.0000	0.0000
Rnf123	ENSMUSG00000041528	ring finger protein 123	-1.504	0.0000	0.0000
Rnf13	ENSMUSG00000036503	ring finger protein 13	-1.712	0.0000	0.0000
Rnf135	ENSMUSG00000020707	ring finger protein 135	-1.593	0.0062	0.0173
Rnf138	ENSMUSG00000024317	ring finger protein 138	-1.756	0.0000	0.0000
Rnf180	ENSMUSG00000021720	ring finger protein 180	-2.303	0.0478	0.0996
Rnf181	ENSMUSG00000055850	ring finger protein 181	-1.913	0.0000	0.0000
Rnf208	ENSMUSG00000044628	ring finger protein 208	-2.753	0.0181	0.0438
Rnf225	ENSMUSG00000033967	ring finger protein 225	-4.349	0.0156	0.0387
Rnf25	ENSMUSG00000026171	ring finger protein 25	-2.548	0.0000	0.0000
Rnf32	ENSMUSG00000029130	ring finger protein 32	-15.184	0.0062	0.0173
Rnf39	ENSMUSG00000036492	ring finger protein 39	-7.675	0.0003	0.0012
Rnls	ENSMUSG00000071573	renalase, FAD-dependent amine oxidase	-1.689	0.0000	0.0000
Rnpep	ENSMUSG00000041926	arginyl aminopeptidase (aminopeptidase B)	-1.599	0.0000	0.0000
Robo4	ENSMUSG00000032125	roundabout guidance receptor 4	-1.524	0.0001	0.0003
Romo1	ENSMUSG00000067847	reactive oxygen species modulator 1	-2.063	0.0000	0.0000
Rph3al	ENSMUSG00000020847	rabphilin 3A-like (without C2 domains)	-1.874	0.0052	0.0149
Rpl10	ENSMUSG00000008682	ribosomal protein L10	-3.071	0.0000	0.0000
Rpl10a	ENSMUSG00000037805	ribosomal protein L10A	-2.518	0.0000	0.0000
Rpl10a-ps1	ENSMUSG00000084416	ribosomal protein L10A, pseudogene 1	-1.904	0.0103	0.0270
Rpl12	ENSMUSG00000038900	ribosomal protein L12	-2.534	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpl13	ENSMUSG00000000740	ribosomal protein L13	-4.407	0.0000	0.0000
Rpl18-ps1	ENSMUSG00000081382	ribosomal protein L18, pseudogene 1	-4.010	0.0173	0.0421
Rpl19-ps1	ENSMUSG00000064281	ribosomal protein L19, pseudogene 1	-5.638	0.0390	0.0844
Rpl19-ps11	ENSMUSG00000081094	ribosomal protein L19, pseudogene 11	-2.568	0.0000	0.0001
Rpl21-ps8	ENSMUSG00000061684	ribosomal protein L21, pseudogene 8	-9.268	0.0010	0.0033
Rpl22l1	ENSMUSG00000039221	ribosomal protein L22 like 1	-2.216	0.0000	0.0000
Rpl26	ENSMUSG00000060938	ribosomal protein L26	-4.663	0.0000	0.0000
Rpl27	ENSMUSG00000063316	ribosomal protein L27	-2.885	0.0000	0.0000
Rpl29	ENSMUSG00000048758	ribosomal protein L29	-2.386	0.0000	0.0000
Rpl3	ENSMUSG00000060036	ribosomal protein L3	-2.041	0.0000	0.0000
Rpl30	ENSMUSG00000058600	ribosomal protein L30	-1.634	0.0000	0.0000
Rpl31	ENSMUSG00000073702	ribosomal protein L31	-1.710	0.0000	0.0000
Rpl31-ps8	ENSMUSG00000067870	ribosomal protein L31, pseudogene 8	-2.127	0.0148	0.0370
Rpl32	ENSMUSG00000057841	ribosomal protein L32	-2.832	0.0000	0.0000
Rpl34	ENSMUSG00000062006	ribosomal protein L34	-2.724	0.0000	0.0000
Rpl34-ps1	ENSMUSG00000068396	ribosomal protein L34, pseudogene 1	-5.177	0.0000	0.0000
Rpl34-ps2	ENSMUSG00000061669	ribosomal protein L34, pseudogene 2	-33.605	0.0001	0.0006
Rpl35a	ENSMUSG00000060636	ribosomal protein L35A	-3.426	0.0000	0.0000
Rpl36	ENSMUSG00000057863	ribosomal protein L36	-4.184	0.0000	0.0000
Rpl36a	ENSMUSG00000079435	ribosomal protein L36A	-2.912	0.0000	0.0000
Rpl36-ps12	ENSMUSG00000091845	ribosomal protein L36, pseudogene 12	-9.458	0.0056	0.0158
Rpl37	ENSMUSG00000041841	ribosomal protein L37	-3.625	0.0000	0.0000
Rpl37a	ENSMUSG00000046330	ribosomal protein L37a	-2.760	0.0000	0.0000
Rpl38	ENSMUSG00000057322	ribosomal protein L38	-2.032	0.0000	0.0000
Rpl38-ps2	ENSMUSG00000080921	ribosomal protein L38, pseudogene 2	-8.825	0.0000	0.0000
Rpl39l	ENSMUSG00000039209	ribosomal protein L39-like	-12.938	0.0131	0.0332
Rpl3-ps1	ENSMUSG00000084349	ribosomal protein L3, pseudogene 1	-2.051	0.0000	0.0000
Rpl7	ENSMUSG00000043716	ribosomal protein L7	-1.571	0.0000	0.0000
Rpl8	ENSMUSG00000003970	ribosomal protein L8	-2.063	0.0000	0.0000
Rplp0	ENSMUSG00000067274	ribosomal protein, large, P0	-2.793	0.0000	0.0000
Rplp1	ENSMUSG00000007892	ribosomal protein, large, P1	-4.449	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpp21	ENSMUSG00000024446	ribonuclease P 21 subunit	-3.473	0.0000	0.0000
Rpp25l	ENSMUSG00000036114	ribonuclease P/MRP 25 subunit-like	-2.687	0.0000	0.0000
Rpp40	ENSMUSG00000021418	ribonuclease P 40 subunit	-2.681	0.0000	0.0000
Rprd1b	ENSMUSG00000027651	regulation of nuclear pre-mRNA domain containing 1B	-1.540	0.0000	0.0000
Rps10-ps1	ENSMUSG00000060438	ribosomal protein S10, pseudogene 1	-8.162	0.0000	0.0000
Rps10-ps2	ENSMUSG00000099764	ribosomal protein S10, pseudogene 2	-9.105	0.0007	0.0026
Rps11	ENSMUSG00000003429	ribosomal protein S11	-1.863	0.0000	0.0000
Rps12	ENSMUSG00000061983	ribosomal protein S12	-2.631	0.0000	0.0000
Rps12-ps1	ENSMUSG00000082746	ribosomal protein S12, pseudogene 1	-3.825	0.0096	0.0253
Rps13	ENSMUSG00000090862	ribosomal protein S13	-2.999	0.0000	0.0000
Rps13-ps2	ENSMUSG00000069972	ribosomal protein S13, pseudogene 2	-5.383	0.0000	0.0000
Rps15	ENSMUSG00000063457	ribosomal protein S15	-2.031	0.0000	0.0000
Rps15a	ENSMUSG00000008683	ribosomal protein S15A	-2.936	0.0000	0.0000
Rps15a-ps3	ENSMUSG00000084314	ribosomal protein S15A, pseudogene 3	-38.281	0.0000	0.0002
Rps15a-ps4	ENSMUSG00000083757	ribosomal protein S15A, pseudogene 4	-3.767	0.0362	0.0790
Rps18-ps3	ENSMUSG00000057657	ribosomal protein S18, pseudogene 3	-14.735	0.0038	0.0115
Rps18-ps5	ENSMUSG00000113061	ribosomal protein S18, pseudogene 5	-1.813	0.0001	0.0004
Rps19	ENSMUSG00000040952	ribosomal protein S19	-3.153	0.0000	0.0000
Rps19-ps3	ENSMUSG00000080059	ribosomal protein S19, pseudogene 3	-2.838	0.0020	0.0063
Rps19-ps6	ENSMUSG00000096942	ribosomal protein S19, pseudogene 6	-63.195	0.0000	0.0000
Rps21	ENSMUSG00000039001	ribosomal protein S21	-2.721	0.0000	0.0000
Rps24	ENSMUSG00000025290	ribosomal protein S24	-1.636	0.0000	0.0000
Rps24-ps3	ENSMUSG00000081049	ribosomal protein S24, pseudogene 3	-3.351	0.0000	0.0000
Rps25	ENSMUSG00000009927	ribosomal protein S25	-3.471	0.0000	0.0000
Rps27	ENSMUSG00000090733	ribosomal protein S27	-4.585	0.0000	0.0000
Rps27l	ENSMUSG00000036781	ribosomal protein S27-like	-2.101	0.0000	0.0000
Rps27rt	ENSMUSG00000050621	ribosomal protein S27, retrogene	-2.577	0.0097	0.0256
Rps28	ENSMUSG00000067288	ribosomal protein S28	-2.528	0.0000	0.0000
Rps29	ENSMUSG00000034892	ribosomal protein S29	-4.888	0.0000	0.0000
Rps3a3	ENSMUSG00000059751	ribosomal protein S3A3	-3.197	0.0275	0.0628
Rps4l	ENSMUSG00000063171	ribosomal protein S4-like	-2.136	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rps5	ENSMUSG00000012848	ribosomal protein S5	-2.199	0.0000	0.0000
Rps6ka6	ENSMUSG00000025665	ribosomal protein S6 kinase polypeptide 6	-4.664	0.0273	0.0624
Rps6kb2	ENSMUSG00000024830	ribosomal protein S6 kinase, polypeptide 2	-1.877	0.0000	0.0000
Rps6kl1	ENSMUSG00000019235	ribosomal protein S6 kinase-like 1	-1.632	0.0296	0.0668
Rps7-ps3	ENSMUSG00000095597	ribosomal protein S7, pseudogene 3	-9.195	0.0000	0.0000
Rpsa	ENSMUSG00000032518	ribosomal protein SA	-2.015	0.0000	0.0000
Rpsa-ps11	ENSMUSG00000082978	ribosomal protein SA, pseudogene 11	-3.749	0.0209	0.0495
Rpusd1	ENSMUSG00000041199	RNA pseudouridylate synthase domain containing 1	-2.207	0.0000	0.0000
Rpusd3	ENSMUSG00000051169	RNA pseudouridylate synthase domain containing 3	-1.978	0.0000	0.0000
Rrp1b	ENSMUSG00000058392	ribosomal RNA processing 1B	-1.752	0.0000	0.0000
Rrp36	ENSMUSG00000023971	ribosomal RNA processing 36	-1.862	0.0000	0.0000
Rsl1	ENSMUSG00000058900	regulator of sex limited protein 1	-1.775	0.0368	0.0802
Rsph9	ENSMUSG00000023966	radial spoke head 9 homolog (Chlamydomonas)	-2.983	0.0067	0.0186
Rtel1	ENSMUSG00000038685	regulator of telomere elongation helicase 1	-1.773	0.0003	0.0012
Rtl10	ENSMUSG00000086965	retrotransposon Gag like 10	-3.033	0.0170	0.0415
Rtl8a	ENSMUSG00000067925	retrotransposon Gag like 8A	-2.880	0.0000	0.0000
Rtl8b	ENSMUSG00000067924	retrotransposon Gag like 8B	-3.587	0.0000	0.0000
Rtl9	ENSMUSG00000085584	retrotransposon Gag like 9	-3.344	0.0145	0.0364
Rtn1	ENSMUSG00000021087	reticulon 1	-2.045	0.0013	0.0045
Rtp4	ENSMUSG00000033355	receptor transporter protein 4	-1.568	0.0211	0.0499
Rtraf	ENSMUSG00000021807	RNA transcription, translation and transport factor	-1.759	0.0000	0.0000
Rtraf-ps	ENSMUSG00000074479	RNA transcription, translation and transport factor, pseudogene	-2.255	0.0000	0.0000
S100a11	ENSMUSG00000027907	S100 calcium binding protein A11	-1.981	0.0002	0.0009
S100a13	ENSMUSG00000042312	S100 calcium binding protein A13	-2.420	0.0000	0.0000
S100a6	ENSMUSG00000001025	S100 calcium binding protein A6 (calcyclin)	-2.816	0.0000	0.0000
Sac3d1	ENSMUSG00000024790	SAC3 domain containing 1	-1.836	0.0113	0.0292
Samd10	ENSMUSG00000038605	sterile alpha motif domain containing 10	-1.655	0.0037	0.0110
Samd13	ENSMUSG00000048652	sterile alpha motif domain containing 13	-2.766	0.0029	0.0090
Sars2	ENSMUSG00000070699	seryl-aminoacyl-tRNA synthetase 2	-1.759	0.0000	0.0000
Sash3	ENSMUSG00000031101	SAM and SH3 domain containing 3	-2.099	0.0016	0.0054
Scamp2	ENSMUSG00000040188	secretory carrier membrane protein 2	-1.655	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Scamp3	ENSMUSG00000028049	secretory carrier membrane protein 3	-1.841	0.0000	0.0000
Scap	ENSMUSG00000032485	SREBF chaperone	-1.708	0.0000	0.0000
Scarf1	ENSMUSG00000038188	scavenger receptor class F, member 1	-1.577	0.0001	0.0005
Scgb1c1	ENSMUSG00000038801	secretoglobin, family 1C, member 1	-2.037	0.0086	0.0230
Scgb3a1	ENSMUSG00000064057	secretoglobin, family 3A, member 1	-36.517	0.0001	0.0002
Scmh1	ENSMUSG00000000085	sex comb on midleg homolog 1	-1.549	0.0000	0.0000
Scn4a	ENSMUSG00000001027	sodium channel, voltage-gated, type IV, alpha	-1.612	0.0050	0.0143
Sco2	ENSMUSG00000091780	SCO2 cytochrome c oxidase assembly protein	-4.932	0.0000	0.0000
Scp2-ps2	ENSMUSG00000058492	sterol carrier protein 2, pseudogene 2	-1.550	0.0081	0.0219
Scube2	ENSMUSG00000007279	signal peptide, CUB domain, EGF-like 2	-1.640	0.0015	0.0050
Sdcbp	ENSMUSG00000028249	syndecan binding protein	-1.558	0.0000	0.0000
Sdhaf2	ENSMUSG00000024668	succinate dehydrogenase complex assembly factor 2	-1.581	0.0000	0.0000
Sdhaf3	ENSMUSG00000042505	succinate dehydrogenase complex assembly factor 3	-1.541	0.0043	0.0126
Sdhaf4	ENSMUSG00000026154	succinate dehydrogenase complex assembly factor 4	-1.712	0.0000	0.0002
Sdhb	ENSMUSG00000009863	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-1.742	0.0000	0.0000
Sec22a	ENSMUSG00000034473	SEC22 homolog A, vesicle trafficking protein	-1.807	0.0000	0.0000
Sec61a1	ENSMUSG00000030082	Sec61 alpha 1 subunit (S. cerevisiae)	-1.607	0.0000	0.0000
Sec61g	ENSMUSG00000078974	SEC61, gamma subunit	-2.759	0.0000	0.0000
Selenbp1	ENSMUSG00000068874	selenium binding protein 1	-1.623	0.0021	0.0067
Selenoh	ENSMUSG00000076437	selenoprotein H	-1.991	0.0000	0.0000
Selenom	ENSMUSG00000075702	selenoprotein M	-1.796	0.0000	0.0000
Selenop	ENSMUSG00000064373	selenoprotein P	-1.756	0.0000	0.0000
Sema3a	ENSMUSG00000028883	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	-2.055	0.0009	0.0031
Sema4a	ENSMUSG00000028064	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	-3.490	0.0000	0.0000
Sema4b	ENSMUSG00000030539	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-1.652	0.0000	0.0000
Sema4c	ENSMUSG00000026121	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	-1.589	0.0000	0.0000
Sema4d	ENSMUSG00000021451	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	-1.551	0.0000	0.0000
Sema7a	ENSMUSG00000038264	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	-1.852	0.0001	0.0003
Serhl	ENSMUSG00000058586	serine hydrolase-like	-1.507	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Serpina3c	ENSMUSG00000066361	serine (or cysteine) peptidase inhibitor, clade A, member 3C	-2.422	0.0000	0.0001
Serpina3h	ENSMUSG00000041449	serine (or cysteine) peptidase inhibitor, clade A, member 3H	-5.269	0.0008	0.0027
Serpina3i	ENSMUSG00000079014	serine (or cysteine) peptidase inhibitor, clade A, member 3I	-12.502	0.0019	0.0061
Serpina3m	ENSMUSG00000079012	serine (or cysteine) peptidase inhibitor, clade A, member 3M	-13.830	0.0163	0.0402
Serpinb10	ENSMUSG00000092572	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	-14.083	0.0141	0.0355
Serpinb9	ENSMUSG00000045827	serine (or cysteine) peptidase inhibitor, clade B, member 9	-1.734	0.0000	0.0001
Serpinf1	ENSMUSG00000000753	serine (or cysteine) peptidase inhibitor, clade F, member 1	-1.678	0.0081	0.0218
Serping1	ENSMUSG00000023224	serine (or cysteine) peptidase inhibitor, clade G, member 1	-2.098	0.0000	0.0000
Sertad1	ENSMUSG00000008384	SERTA domain containing 1	-1.526	0.0010	0.0033
Sesn2	ENSMUSG00000028893	sestrin 2	-1.759	0.0011	0.0038
Sez6l2	ENSMUSG00000030683	seizure related 6 homolog like 2	-2.698	0.0000	0.0000
Sf3b4	ENSMUSG00000068856	splicing factor 3b, subunit 4	-2.074	0.0000	0.0000
Sf3b5	ENSMUSG00000078348	splicing factor 3b, subunit 5	-3.102	0.0000	0.0000
Sf3b6	ENSMUSG00000037361	splicing factor 3B, subunit 6	-2.247	0.0000	0.0000
Sft2d3	ENSMUSG00000044982	SFT2 domain containing 3	-1.944	0.0002	0.0009
Sgca	ENSMUSG00000001508	sarcoglycan, alpha (dystrophin-associated glycoprotein)	-2.607	0.0000	0.0000
Sgf29	ENSMUSG00000030714	SAGA complex associated factor 29	-1.745	0.0000	0.0000
Sgsm1	ENSMUSG00000042216	small G protein signaling modulator 1	-3.628	0.0003	0.0012
Sgsm3	ENSMUSG00000042303	small G protein signaling modulator 3	-2.169	0.0000	0.0000
Sh2b3	ENSMUSG00000042594	SH2B adaptor protein 3	-2.069	0.0003	0.0012
Sh2d3c	ENSMUSG00000059013	SH2 domain containing 3C	-1.959	0.0003	0.0013
Sh3bgrl3	ENSMUSG00000028843	SH3 domain binding glutamic acid-rich protein-like 3	-2.909	0.0000	0.0000
Sh3bp4	ENSMUSG00000036206	SH3-domain binding protein 4	-1.527	0.0015	0.0049
Sh3gl1	ENSMUSG00000003200	SH3-domain GRB2-like 1	-1.515	0.0000	0.0000
Sh3glb2	ENSMUSG00000026860	SH3-domain GRB2-like endophilin B2	-2.026	0.0000	0.0000
Sh3tc1	ENSMUSG00000036553	SH3 domain and tetratricopeptide repeats 1	-1.565	0.0028	0.0086
Sh3tc2	ENSMUSG00000045629	SH3 domain and tetratricopeptide repeats 2	-3.161	0.0000	0.0000
Shkbp1	ENSMUSG00000089832	Sh3kbp1 binding protein 1	-1.709	0.0000	0.0000
Shld1	ENSMUSG00000044991	shieldin complex subunit 1	-3.621	0.0003	0.0012
Shld3	ENSMUSG00000118537	shieldin complex subunit 3	-5.493	0.0003	0.0011
Sigirr	ENSMUSG00000025494	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	-1.730	0.0000	0.0001

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Siglech	ENSMUSG00000051504	sialic acid binding Ig-like lectin H	-21.264	0.0005	0.0018
Sik2	ENSMUSG00000037112	salt inducible kinase 2	-1.997	0.0000	0.0000
Skp2	ENSMUSG00000054115	S-phase kinase-associated protein 2	-1.683	0.0464	0.0973
Slamf9	ENSMUSG00000026548	SLAM family member 9	-2.651	0.0043	0.0126
Slc10a3	ENSMUSG00000032806	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	-2.911	0.0000	0.0000
Slc11a1	ENSMUSG00000026177	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	-1.707	0.0071	0.0195
Slc12a4	ENSMUSG00000017765	solute carrier family 12, member 4	-1.566	0.0000	0.0000
Slc13a3	ENSMUSG00000018459	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-4.643	0.0070	0.0193
Slc15a4	ENSMUSG00000029416	solute carrier family 15, member 4	-1.603	0.0033	0.0099
Slc16a12	ENSMUSG00000009378	solute carrier family 16 (monocarboxylic acid transporters), member 12	-2.707	0.0000	0.0000
Slc16a2	ENSMUSG00000033965	solute carrier family 16 (monocarboxylic acid transporters), member 2	-1.590	0.0011	0.0037
Slc16a3	ENSMUSG00000025161	solute carrier family 16 (monocarboxylic acid transporters), member 3	-2.026	0.0113	0.0291
Slc17a5	ENSMUSG00000049624	solute carrier family 17 (anion/sugar transporter), member 5	-1.563	0.0091	0.0243
Slc17a9	ENSMUSG00000023393	solute carrier family 17, member 9	-4.471	0.0311	0.0694
Slc19a1	ENSMUSG00000001436	solute carrier family 19 (folate transporter), member 1	-2.909	0.0000	0.0000
Slc22a18	ENSMUSG00000000154	solute carrier family 22 (organic cation transporter), member 18	-2.661	0.0178	0.0431
Slc22a21	ENSMUSG00000063652	solute carrier family 22 (organic cation transporter), member 21	-3.507	0.0004	0.0014
Slc22a5	ENSMUSG00000018900	solute carrier family 22 (organic cation transporter), member 5	-1.856	0.0000	0.0000
Slc23a4	ENSMUSG00000029847	solute carrier family 23 member 4	-21.495	0.0016	0.0052
Slc25a10	ENSMUSG00000025792	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	-2.321	0.0000	0.0000
Slc25a12	ENSMUSG00000027010	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	-1.612	0.0000	0.0000
Slc25a22	ENSMUSG00000019082	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	-1.673	0.0000	0.0001
Slc25a29	ENSMUSG00000021265	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	-2.728	0.0000	0.0000
Slc25a3	ENSMUSG00000061904	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	-2.008	0.0000	0.0000
Slc25a34	ENSMUSG00000040740	solute carrier family 25, member 34	-1.710	0.0000	0.0000
Slc25a42	ENSMUSG00000002346	solute carrier family 25, member 42	-1.584	0.0000	0.0000
Slc25a43	ENSMUSG00000037636	solute carrier family 25, member 43	-17.816	0.0028	0.0085
Slc26a11	ENSMUSG00000039908	solute carrier family 26, member 11	-2.054	0.0012	0.0041
Slc26a6	ENSMUSG00000023259	solute carrier family 26, member 6	-1.688	0.0000	0.0000
Slc29a1	ENSMUSG00000023942	solute carrier family 29 (nucleoside transporters), member 1	-1.973	0.0000	0.0000
Slc29a2	ENSMUSG00000024891	solute carrier family 29 (nucleoside transporters), member 2	-3.995	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc2a10	ENSMUSG00000027661	solute carrier family 2 (facilitated glucose transporter), member 10	-1.555	0.0192	0.0460
Slc2a12	ENSMUSG00000037490	solute carrier family 2 (facilitated glucose transporter), member 12	-2.056	0.0000	0.0000
Slc2a4	ENSMUSG00000018566	solute carrier family 2 (facilitated glucose transporter), member 4	-1.923	0.0000	0.0000
Slc2a8	ENSMUSG00000026791	solute carrier family 2, (facilitated glucose transporter), member 8	-2.772	0.0000	0.0000
Slc30a6	ENSMUSG00000024069	solute carrier family 30 (zinc transporter), member 6	-1.590	0.0000	0.0000
Slc31a2	ENSMUSG00000066152	solute carrier family 31, member 2	-2.208	0.0000	0.0000
Slc35a4	ENSMUSG00000033272	solute carrier family 35, member A4	-2.042	0.0000	0.0000
Slc35b1	ENSMUSG00000020873	solute carrier family 35, member B1	-1.601	0.0000	0.0000
Slc35c2	ENSMUSG00000017664	solute carrier family 35, member C2	-1.611	0.0000	0.0000
Slc35d2	ENSMUSG00000033114	solute carrier family 35, member D2	-2.768	0.0002	0.0008
Slc35e4	ENSMUSG00000048807	solute carrier family 35, member E4	-1.917	0.0028	0.0085
Slc35f6	ENSMUSG00000029175	solute carrier family 35, member F6	-1.583	0.0000	0.0000
Slc36a2	ENSMUSG00000020264	solute carrier family 36 (proton/amino acid symporter), member 2	-2.424	0.0000	0.0000
Slc37a1	ENSMUSG00000024036	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	-2.799	0.0000	0.0000
Slc38a11	ENSMUSG00000061171	solute carrier family 38, member 11	-1.632	0.0207	0.0492
Slc38a3	ENSMUSG00000010064	solute carrier family 38, member 3	-2.380	0.0000	0.0000
Slc38a7	ENSMUSG00000036534	solute carrier family 38, member 7	-1.773	0.0000	0.0000
Slc39a14	ENSMUSG00000022094	solute carrier family 39 (zinc transporter), member 14	-1.649	0.0000	0.0000
Slc39a3	ENSMUSG00000046822	solute carrier family 39 (zinc transporter), member 3	-1.788	0.0000	0.0000
Slc3a2	ENSMUSG00000010095	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	-1.642	0.0005	0.0017
Slc40a1	ENSMUSG00000025993	solute carrier family 40 (iron-regulated transporter), member 1	-1.848	0.0001	0.0003
Slc41a3	ENSMUSG00000030089	solute carrier family 41, member 3	-1.525	0.0000	0.0000
Slc46a1	ENSMUSG00000020829	solute carrier family 46, member 1	-3.379	0.0002	0.0009
Slc46a3	ENSMUSG00000029650	solute carrier family 46, member 3	-1.988	0.0000	0.0001
Slc48a1	ENSMUSG00000081534	solute carrier family 48 (heme transporter), member 1	-1.840	0.0000	0.0000
Slc4a11	ENSMUSG00000074796	solute carrier family 4, sodium bicarbonate transporter-like, member 11	-14.042	0.0070	0.0194
Slc50a1	ENSMUSG00000027953	solute carrier family 50 (sugar transporter), member 1	-3.083	0.0000	0.0000
Slc52a2	ENSMUSG00000022560	solute carrier protein 52, member 2	-1.563	0.0018	0.0059
Slc52a3	ENSMUSG00000027463	solute carrier protein family 52, member 3	-1.842	0.0046	0.0134
Slc66a1	ENSMUSG00000028744	solute carrier family 66 member 1	-2.304	0.0000	0.0000
Slc6a9	ENSMUSG00000028542	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-1.537	0.0410	0.0878

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc7a4	ENSMUSG00000022756	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	-2.278	0.0001	0.0004
Slc7a6	ENSMUSG00000031904	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-1.789	0.0000	0.0002
Slc9a8	ENSMUSG00000039463	solute carrier family 9 (sodium/hydrogen exchanger), member 8	-1.595	0.0000	0.0000
Smarcal1	ENSMUSG00000039354	SWI/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	-1.743	0.0000	0.0000
Smarcb1	ENSMUSG00000000902	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-1.775	0.0000	0.0000
Smco1	ENSMUSG00000046345	single-pass membrane protein with coiled-coil domains 1	-1.675	0.0001	0.0004
Smim15	ENSMUSG00000071180	small integral membrane protein 15	-1.835	0.0000	0.0000
Smim27	ENSMUSG00000028407	small integral membrane protein 27	-4.024	0.0000	0.0000
Smim5	ENSMUSG00000048442	small integral membrane protein 5	-2.185	0.0000	0.0002
Smim8	ENSMUSG00000028295	small integral membrane protein 8	-1.625	0.0000	0.0000
Smpd1	ENSMUSG00000037049	sphingomyelin phosphodiesterase 1, acid lysosomal	-1.759	0.0000	0.0000
Smpdl3a	ENSMUSG00000019872	sphingomyelin phosphodiesterase, acid-like 3A	-2.667	0.0000	0.0000
Smpx	ENSMUSG00000041476	small muscle protein, X-linked	-2.535	0.0000	0.0000
Sms-ps	ENSMUSG00000081752	spermine synthase, pseudogene	-2.970	0.0000	0.0000
Smtn	ENSMUSG00000020439	smoothelin	-1.698	0.0000	0.0000
Smyd4	ENSMUSG00000018809	SET and MYND domain containing 4	-1.629	0.0003	0.0013
Snai1	ENSMUSG00000042821	snail family zinc finger 1	-1.755	0.0211	0.0499
Snai2	ENSMUSG00000022676	snail family zinc finger 2	-2.073	0.0001	0.0005
Snai3	ENSMUSG00000006587	snail family zinc finger 3	-5.686	0.0000	0.0000
Snap47	ENSMUSG00000009894	synaptosomal-associated protein, 47	-2.151	0.0000	0.0000
Snapc2	ENSMUSG00000011837	small nuclear RNA activating complex, polypeptide 2	-2.112	0.0000	0.0000
Sned1	ENSMUSG00000047793	sushi, nidogen and EGF-like domains 1	-1.592	0.0025	0.0079
Snhg18	ENSMUSG00000096956	small nucleolar RNA host gene 18	-1.870	0.0000	0.0000
Snora17	ENSMUSG00000077192	small nucleolar RNA, H/ACA box 17	-10.088	0.0222	0.0522
Snrpb	ENSMUSG00000027404	small nuclear ribonucleoprotein B	-2.186	0.0000	0.0000
Snu13	ENSMUSG00000063480	SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5)	-1.555	0.0000	0.0000
Snx14	ENSMUSG00000032422	sorting nexin 14	-1.533	0.0000	0.0000
Snx17	ENSMUSG00000029146	sorting nexin 17	-1.502	0.0000	0.0000
Sorcs2	ENSMUSG00000029093	sortilin-related VPS10 domain containing receptor 2	-1.949	0.0019	0.0062
Sowaha	ENSMUSG00000044352	sosondowah ankyrin repeat domain family member A	-3.005	0.0415	0.0886

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sowahc	ENSMUSG00000098188	sosondowah ankyrin repeat domain family member C	-1.910	0.0001	0.0004
Sox18	ENSMUSG00000046470	SRY (sex determining region Y)-box 18	-3.484	0.0000	0.0000
Sp3os	ENSMUSG00000063714	trans-acting transcription factor 3, opposite strand	-1.861	0.0000	0.0001
Sp4	ENSMUSG00000025323	trans-acting transcription factor 4	-1.506	0.0094	0.0248
Spag8	ENSMUSG00000066196	sperm associated antigen 8	-13.872	0.0229	0.0536
Spata2	ENSMUSG00000047030	spermatogenesis associated 2	-1.745	0.0000	0.0000
Spata20	ENSMUSG00000020867	spermatogenesis associated 20	-2.440	0.0269	0.0615
Spata24	ENSMUSG00000024352	spermatogenesis associated 24	-1.772	0.0393	0.0849
Spata2l	ENSMUSG00000033594	spermatogenesis associated 2-like	-1.674	0.0045	0.0132
Spata6	ENSMUSG00000034401	spermatogenesis associated 6	-2.008	0.0000	0.0000
Spats1	ENSMUSG00000023935	spermatogenesis associated, serine-rich 1	-3.104	0.0009	0.0032
Spcs1	ENSMUSG00000021917	signal peptidase complex subunit 1 homolog (S. cerevisiae)	-1.585	0.0000	0.0000
Spic	ENSMUSG00000004359	Spi-C transcription factor (Spi-1/PU.1 related)	-9.150	0.0062	0.0174
Spink4	ENSMUSG00000028415	serine peptidase inhibitor, Kazal type 4	-22.451	0.0016	0.0052
Spns1	ENSMUSG00000030741	spinster homolog 1	-2.800	0.0000	0.0000
Spns3	ENSMUSG00000020798	spinster homolog 3	-9.670	0.0269	0.0616
Sppl2b	ENSMUSG00000035206	signal peptide peptidase like 2B	-2.137	0.0000	0.0000
Spr	ENSMUSG00000033735	sepiapterin reductase	-2.192	0.0000	0.0000
Sprn	ENSMUSG00000045733	shadow of prion protein	-2.068	0.0089	0.0238
Spr-ps1	ENSMUSG00000068303	sepiapterin reductase pseudogene 1	-6.293	0.0000	0.0000
Spryd4	ENSMUSG00000051346	SPRY domain containing 4	-1.886	0.0000	0.0000
Spsb1	ENSMUSG00000039911	splA/ryanodine receptor domain and SOCS box containing 1	-1.913	0.0010	0.0035
Spsb3	ENSMUSG00000024160	splA/ryanodine receptor domain and SOCS box containing 3	-1.558	0.0000	0.0000
Spsb4	ENSMUSG00000046997	splA/ryanodine receptor domain and SOCS box containing 4	-1.901	0.0005	0.0018
Sptssa	ENSMUSG00000044408	serine palmitoyltransferase, small subunit A	-1.650	0.0000	0.0002
Srd5a3	ENSMUSG00000029233	steroid 5 alpha-reductase 3	-2.489	0.0000	0.0000
Srebf1	ENSMUSG00000020538	sterol regulatory element binding transcription factor 1	-2.939	0.0000	0.0000
Srgn	ENSMUSG00000020077	serglycin	-1.523	0.0000	0.0000
Srms	ENSMUSG00000027579	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	-2.914	0.0142	0.0357
Srpx	ENSMUSG00000090084	sushi-repeat-containing protein	-2.666	0.0000	0.0000
Srr	ENSMUSG00000001323	serine racemase	-1.792	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ss18l2	ENSMUSG00000032526	SS18, nBAF chromatin remodeling complex subunit like 2	-2.420	0.0000	0.0000
Ssh3	ENSMUSG00000034616	slingshot protein phosphatase 3	-1.728	0.0012	0.0041
Ssna1	ENSMUSG00000026966	SS nuclear autoantigen 1	-2.648	0.0000	0.0000
Ssu2	ENSMUSG00000034387	ssu-2 homolog (C. elegans)	-1.874	0.0001	0.0002
St6galnac4	ENSMUSG00000079442	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	-2.123	0.0000	0.0000
St8sia2	ENSMUSG00000025789	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-17.933	0.0044	0.0128
St8sia4	ENSMUSG00000040710	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	-1.709	0.0003	0.0010
Stab1	ENSMUSG00000042286	stabilin 1	-1.662	0.0004	0.0015
Stap2	ENSMUSG00000038781	signal transducing adaptor family member 2	-1.543	0.0020	0.0064
Stard3	ENSMUSG00000018167	START domain containing 3	-1.519	0.0017	0.0057
Stard8	ENSMUSG00000031216	START domain containing 8	-1.866	0.0000	0.0000
Stat5a	ENSMUSG00000004043	signal transducer and activator of transcription 5A	-1.569	0.0002	0.0009
Sting1	ENSMUSG00000024349	stimulator of interferon response cGAMP interactor 1	-1.677	0.0048	0.0140
Stk11ip	ENSMUSG00000026213	serine/threonine kinase 11 interacting protein	-1.686	0.0016	0.0054
Stk19	ENSMUSG00000061207	serine/threonine kinase 19	-1.742	0.0001	0.0005
Stk25	ENSMUSG00000026277	serine/threonine kinase 25 (yeast)	-1.771	0.0000	0.0000
Stn1	ENSMUSG00000042694	STN1, CST complex subunit	-2.218	0.0000	0.0000
Stpg1	ENSMUSG00000028801	sperm tail PG rich repeat containing 1	-2.392	0.0298	0.0672
Stradb	ENSMUSG00000026027	STE20-related kinase adaptor beta	-1.639	0.0000	0.0000
Strip2	ENSMUSG00000039629	striatin interacting protein 2	-1.787	0.0000	0.0000
Strit1	ENSMUSG00000103476	small transmembrane regulator of ion transport 1	-2.706	0.0000	0.0000
Stx5a	ENSMUSG00000010110	syntaxin 5A	-1.635	0.0000	0.0002
Sufu	ENSMUSG00000025231	SUFU negative regulator of hedgehog signaling	-1.662	0.0000	0.0000
Sult1a1	ENSMUSG00000030711	sulfotransferase family 1A, phenol-preferring, member 1	-2.001	0.0355	0.0777
Sumf2	ENSMUSG00000025538	sulfatase modifying factor 2	-1.518	0.0000	0.0002
Sun1	ENSMUSG00000036817	Sad1 and UNC84 domain containing 1	-1.501	0.0000	0.0000
Sun3	ENSMUSG00000040985	Sad1 and UNC84 domain containing 3	-1.816	0.0007	0.0025
Supt4a	ENSMUSG00000020485	SPT4A, DSIF elongation factor subunit	-1.793	0.0000	0.0000
Susd3	ENSMUSG00000021384	sushi domain containing 3	-2.774	0.0367	0.0800
Suv39h1	ENSMUSG00000039231	suppressor of variegation 3-9 1	-2.379	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Swi5	ENSMUSG00000044627	SWI5 recombination repair homolog (yeast)	-1.682	0.0000	0.0000
Swsap1	ENSMUSG00000051238	SWIM type zinc finger 7 associated protein 1	-2.760	0.0000	0.0000
Swt1	ENSMUSG00000052748	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	-1.653	0.0000	0.0000
Syce2	ENSMUSG00000003824	synaptonemal complex central element protein 2	-3.555	0.0080	0.0217
Syngr2	ENSMUSG00000048277	synaptogyrin 2	-2.443	0.0000	0.0000
Syt17	ENSMUSG00000058420	synaptotagmin XVII	-1.582	0.0342	0.0752
Syt3	ENSMUSG00000030731	synaptotagmin III	-2.053	0.0001	0.0005
Syvn1	ENSMUSG00000024807	synovial apoptosis inhibitor 1, synoviolin	-1.817	0.0000	0.0000
Szt2	ENSMUSG00000033253	SZT2 subunit of KICSTOR complex	-1.739	0.0000	0.0000
Tab1	ENSMUSG00000022414	TGF-beta activated kinase 1/MAP3K7 binding protein 1	-2.017	0.0000	0.0000
Tada1	ENSMUSG00000026563	transcriptional adaptor 1	-2.188	0.0000	0.0000
Taf4b	ENSMUSG00000054321	TATA-box binding protein associated factor 4b	-1.731	0.0007	0.0025
Tafazzin	ENSMUSG00000009995	tafazzin, phospholipid-lysophospholipid transacylase	-1.570	0.0000	0.0000
Tagln2	ENSMUSG00000026547	transgelin 2	-1.725	0.0000	0.0000
Tamm41	ENSMUSG00000030316	TAM41 mitochondrial translocator assembly and maintenance homolog	-1.602	0.0018	0.0057
Tango2	ENSMUSG00000013539	transport and golgi organization 2	-2.139	0.0000	0.0000
Tbc1d10a	ENSMUSG00000034412	TBC1 domain family, member 10a	-2.033	0.0002	0.0007
Tbc1d17	ENSMUSG00000038520	TBC1 domain family, member 17	-1.535	0.0071	0.0195
Tbc1d2	ENSMUSG00000039813	TBC1 domain family, member 2	-2.905	0.0000	0.0000
Tbc1d22a	ENSMUSG00000051864	TBC1 domain family, member 22a	-2.076	0.0000	0.0000
Tbc1d25	ENSMUSG00000039201	TBC1 domain family, member 25	-1.558	0.0081	0.0219
Tbc1d5	ENSMUSG00000023923	TBC1 domain family, member 5	-1.627	0.0000	0.0000
Tbc1d7	ENSMUSG00000021368	TBC1 domain family, member 7	-1.606	0.0000	0.0000
Tbc1d8	ENSMUSG00000003134	TBC1 domain family, member 8	-1.737	0.0000	0.0000
Tbl3	ENSMUSG00000040688	transducin (beta)-like 3	-2.249	0.0000	0.0000
Tbxa2r	ENSMUSG00000034881	thromboxane A2 receptor	-2.347	0.0004	0.0016
Tcf19	ENSMUSG00000050410	transcription factor 19	-1.690	0.0151	0.0377
Tcirg1	ENSMUSG00000001750	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	-1.749	0.0031	0.0095
Tcn2	ENSMUSG00000020432	transcobalamin 2	-2.049	0.0000	0.0000
Tcp11l2	ENSMUSG00000020034	t-complex 11 (mouse) like 2	-2.064	0.0000	0.0001
Tcta	ENSMUSG00000039461	T cell leukemia translocation altered gene	-2.471	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tctn3	ENSMUSG00000025008	tectonic family member 3	-2.661	0.0000	0.0000
Tdp1	ENSMUSG00000021177	tyrosyl-DNA phosphodiesterase 1	-1.609	0.0000	0.0002
Tecpr1	ENSMUSG00000066621	tectonin beta-propeller repeat containing 1	-1.588	0.0000	0.0000
Tecr	ENSMUSG00000031708	trans-2,3-enoyl-CoA reductase	-1.543	0.0000	0.0000
Tecrl	ENSMUSG00000049537	trans-2,3-enoyl-CoA reductase-like	-2.955	0.0000	0.0000
Tedc2	ENSMUSG00000024118	tubulin epsilon and delta complex 2	-2.112	0.0139	0.0350
Tef	ENSMUSG00000022389	thyrotroph embryonic factor	-1.888	0.0005	0.0018
Ten1	ENSMUSG00000020778	TEN1 telomerase capping complex subunit	-1.509	0.0056	0.0159
Tepsin	ENSMUSG00000025377	TEPSIN, adaptor related protein complex 4 accessory protein	-1.740	0.0000	0.0000
Tex15	ENSMUSG00000009628	testis expressed gene 15	-25.034	0.0016	0.0052
Tfg	ENSMUSG00000022757	Trk-fused gene	-2.121	0.0000	0.0000
Tg	ENSMUSG00000053469	thyroglobulin	-1.945	0.0006	0.0022
Tgfb1i1	ENSMUSG00000030782	transforming growth factor beta 1 induced transcript 1	-1.995	0.0000	0.0000
Tgtp1	ENSMUSG00000078922	T cell specific GTPase 1	-2.939	0.0020	0.0063
Thap7	ENSMUSG00000022760	THAP domain containing 7	-2.590	0.0000	0.0000
Them4	ENSMUSG00000028145	thioesterase superfamily member 4	-1.735	0.0000	0.0001
Thnsl2	ENSMUSG00000054474	threonine synthase-like 2 (bacterial)	-1.573	0.0003	0.0013
Thop1	ENSMUSG00000004929	thimet oligopeptidase 1	-1.550	0.0000	0.0000
Ticam1	ENSMUSG00000047123	toll-like receptor adaptor molecule 1	-3.140	0.0000	0.0000
Timm13	ENSMUSG00000020219	translocase of inner mitochondrial membrane 13	-1.584	0.0000	0.0000
Timm50	ENSMUSG00000003438	translocase of inner mitochondrial membrane 50	-2.579	0.0000	0.0000
Timm9	ENSMUSG00000021079	translocase of inner mitochondrial membrane 9	-2.110	0.0000	0.0000
Tkt	ENSMUSG00000021957	transketolase	-2.431	0.0000	0.0000
Tlcd2	ENSMUSG00000038217	TLC domain containing 2	-1.715	0.0045	0.0132
Tlcd3a	ENSMUSG00000069808	TLC domain containing 3A	-2.344	0.0005	0.0020
Tle6	ENSMUSG00000034758	transducin-like enhancer of split 6	-2.043	0.0000	0.0000
Tlr13	ENSMUSG00000033777	toll-like receptor 13	-1.686	0.0260	0.0599
Tlr3	ENSMUSG00000031639	toll-like receptor 3	-1.593	0.0001	0.0003
Tlr4	ENSMUSG00000039005	toll-like receptor 4	-1.849	0.0003	0.0012
Tlr5	ENSMUSG00000079164	toll-like receptor 5	-2.571	0.0016	0.0054
Tm2d2	ENSMUSG00000031556	TM2 domain containing 2	-1.680	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tm2d3	ENSMUSG00000078681	TM2 domain containing 3	-1.705	0.0000	0.0000
Tm4sf1	ENSMUSG00000027800	transmembrane 4 superfamily member 1	-1.554	0.0001	0.0005
Tm9sf2	ENSMUSG00000025544	transmembrane 9 superfamily member 2	-1.564	0.0000	0.0000
Tmc5	ENSMUSG00000030650	transmembrane channel-like gene family 5	-2.203	0.0022	0.0069
Tmc6	ENSMUSG00000025572	transmembrane channel-like gene family 6	-1.701	0.0001	0.0005
Tmc8	ENSMUSG00000050106	transmembrane channel-like gene family 8	-1.832	0.0001	0.0003
Tmed1	ENSMUSG00000032180	transmembrane p24 trafficking protein 1	-1.730	0.0000	0.0000
Tmed10-ps	ENSMUSG00000114251	transmembrane p24 trafficking protein 10, pseudogene	-2.191	0.0000	0.0000
Tmed2b	ENSMUSG00000079884	transmembrane p24 trafficking protein 2B	-1.707	0.0437	0.0924
Tmed3	ENSMUSG00000032353	transmembrane p24 trafficking protein 3	-1.575	0.0000	0.0000
Tmed5	ENSMUSG00000063406	transmembrane p24 trafficking protein 5	-1.668	0.0000	0.0001
Tmem104	ENSMUSG00000045980	transmembrane protein 104	-1.723	0.0000	0.0000
Tmem108	ENSMUSG00000042757	transmembrane protein 108	-2.424	0.0000	0.0000
Tmem120a	ENSMUSG00000039886	transmembrane protein 120A	-2.798	0.0000	0.0000
Tmem120b	ENSMUSG00000054434	transmembrane protein 120B	-1.619	0.0001	0.0003
Tmem126a	ENSMUSG00000030615	transmembrane protein 126A	-4.094	0.0000	0.0000
Tmem128	ENSMUSG00000067365	transmembrane protein 128	-1.561	0.0000	0.0000
Tmem129	ENSMUSG00000019295	transmembrane protein 129	-2.736	0.0000	0.0000
Tmem140	ENSMUSG00000057137	transmembrane protein 140	-1.735	0.0012	0.0041
Tmem143	ENSMUSG00000002781	transmembrane protein 143	-1.834	0.0000	0.0000
Tmem144	ENSMUSG00000027956	transmembrane protein 144	-2.129	0.0000	0.0000
Tmem147os	ENSMUSG00000097320	transmembrane protein 147, opposite strand	-1.865	0.0242	0.0562
Tmem14a	ENSMUSG00000025933	transmembrane protein 14A	-1.880	0.0015	0.0048
Tmem154	ENSMUSG00000056498	transmembrane protein 154	-2.011	0.0001	0.0006
Tmem167	ENSMUSG00000012422	transmembrane protein 167	-1.614	0.0000	0.0000
Tmem175	ENSMUSG00000013495	transmembrane protein 175	-1.959	0.0000	0.0000
Tmem176b	ENSMUSG00000029810	transmembrane protein 176B	-1.567	0.0002	0.0010
Tmem177	ENSMUSG00000036975	transmembrane protein 177	-1.554	0.0000	0.0000
Tmem179b	ENSMUSG00000118346	transmembrane protein 179B	-1.798	0.0000	0.0000
Tmem184b	ENSMUSG00000009035	transmembrane protein 184b	-1.959	0.0000	0.0000
Tmem198b	ENSMUSG00000047090	transmembrane protein 198b	-1.546	0.0087	0.0234

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem203	ENSMUSG00000078201	transmembrane protein 203	-5.748	0.0000	0.0000
Tmem204	ENSMUSG00000024168	transmembrane protein 204	-1.786	0.0000	0.0000
Tmem205	ENSMUSG00000040883	transmembrane protein 205	-1.747	0.0000	0.0000
Tmem208	ENSMUSG00000014856	transmembrane protein 208	-3.169	0.0000	0.0000
Tmem216	ENSMUSG00000024667	transmembrane protein 216	-1.740	0.0000	0.0001
Tmem219	ENSMUSG00000060538	transmembrane protein 219	-1.627	0.0000	0.0001
Tmem223	ENSMUSG00000117924	transmembrane protein 223	-3.133	0.0000	0.0000
Tmem229b	ENSMUSG00000046157	transmembrane protein 229B	-1.731	0.0002	0.0009
Tmem230	ENSMUSG00000027341	transmembrane protein 230	-3.864	0.0000	0.0000
Tmem232	ENSMUSG00000045036	transmembrane protein 232	-5.752	0.0122	0.0311
Tmem241	ENSMUSG00000049411	transmembrane protein 241	-2.108	0.0000	0.0000
Tmem242	ENSMUSG00000004945	transmembrane protein 242	-2.069	0.0000	0.0000
Tmem25	ENSMUSG00000002032	transmembrane protein 25	-1.873	0.0003	0.0013
Tmem252	ENSMUSG00000048572	transmembrane protein 252	-21.208	0.0042	0.0123
Tmem254	ENSMUSG00000072676	transmembrane protein 254	-1.597	0.0279	0.0635
Tmem255a	ENSMUSG00000036502	transmembrane protein 255A	-2.353	0.0002	0.0007
Tmem258	ENSMUSG00000036372	transmembrane protein 258	-2.566	0.0000	0.0000
Tmem267	ENSMUSG00000074634	transmembrane protein 267	-1.698	0.0011	0.0039
Tmem30b	ENSMUSG00000034435	transmembrane protein 30B	-17.857	0.0027	0.0084
Tmem35b	ENSMUSG00000070737	transmembrane protein 35B	-2.008	0.0084	0.0225
Tmem37	ENSMUSG00000050777	transmembrane protein 37	-6.259	0.0000	0.0000
Tmem41a	ENSMUSG00000022856	transmembrane protein 41a	-1.851	0.0011	0.0039
Tmem41b	ENSMUSG00000047554	transmembrane protein 41B	-1.650	0.0000	0.0000
Tmem41b-ps	ENSMUSG00000096647	transmembrane protein 41B, pseudogene	-3.232	0.0355	0.0777
Tmem42	ENSMUSG00000066233	transmembrane protein 42	-1.654	0.0001	0.0004
Tmem45a	ENSMUSG00000022754	transmembrane protein 45a	-1.509	0.0278	0.0634
Tmem52	ENSMUSG00000023153	transmembrane protein 52	-2.623	0.0092	0.0245
Tmem53	ENSMUSG00000048772	transmembrane protein 53	-1.623	0.0000	0.0000
Tmem59	ENSMUSG00000028618	transmembrane protein 59	-1.730	0.0000	0.0000
Tmem60	ENSMUSG00000045435	transmembrane protein 60	-1.885	0.0000	0.0000
Tmem63a	ENSMUSG00000026519	transmembrane protein 63a	-1.530	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem70	ENSMUSG00000025940	transmembrane protein 70	-1.801	0.0000	0.0000
Tmem79	ENSMUSG00000001420	transmembrane protein 79	-3.214	0.0000	0.0000
Tmem81	ENSMUSG00000048174	transmembrane protein 81	-1.606	0.0126	0.0322
Tmem86a	ENSMUSG00000010307	transmembrane protein 86A	-2.317	0.0000	0.0000
Tmem88	ENSMUSG00000045377	transmembrane protein 88	-2.314	0.0000	0.0000
Tmem9	ENSMUSG00000026411	transmembrane protein 9	-1.512	0.0008	0.0028
Tmem94	ENSMUSG00000020747	transmembrane protein 94	-1.872	0.0000	0.0000
Tmem97	ENSMUSG00000037278	transmembrane protein 97	-2.001	0.0000	0.0001
Tmem98	ENSMUSG00000035413	transmembrane protein 98	-1.632	0.0009	0.0033
Tmsb10	ENSMUSG00000079523	thymosin, beta 10	-2.262	0.0000	0.0001
Tnfaip8l1	ENSMUSG00000044469	tumor necrosis factor, alpha-induced protein 8-like 1	-2.009	0.0000	0.0000
Tnfaip8l2	ENSMUSG00000013707	tumor necrosis factor, alpha-induced protein 8-like 2	-8.547	0.0000	0.0000
Tnfrsf12a	ENSMUSG00000023905	tumor necrosis factor receptor superfamily, member 12a	-2.473	0.0000	0.0000
Tnfrsf1a	ENSMUSG00000030341	tumor necrosis factor receptor superfamily, member 1a	-1.775	0.0000	0.0000
Tnfrsf26	ENSMUSG00000045362	tumor necrosis factor receptor superfamily, member 26	-3.162	0.0004	0.0015
Tnfrsf4	ENSMUSG00000029075	tumor necrosis factor receptor superfamily, member 4	-6.217	0.0477	0.0995
Tnfsf13	ENSMUSG00000089669	tumor necrosis factor (ligand) superfamily, member 13	-5.445	0.0037	0.0112
Tnfsf9	ENSMUSG00000035678	tumor necrosis factor (ligand) superfamily, member 9	-2.633	0.0379	0.0823
Tnxb	ENSMUSG00000033327	tenascin XB	-1.630	0.0000	0.0002
Tom1	ENSMUSG00000042870	target of myb1 trafficking protein	-2.487	0.0000	0.0000
Tomm40	ENSMUSG00000002984	translocase of outer mitochondrial membrane 40	-1.592	0.0001	0.0002
Tomm5	ENSMUSG00000078713	translocase of outer mitochondrial membrane 5	-1.604	0.0000	0.0000
Tomm6os	ENSMUSG00000084880	translocase of outer mitochondrial membrane 6, opposite strand	-4.246	0.0473	0.0988
Tor2a	ENSMUSG00000009563	torsin family 2, member A	-2.022	0.0000	0.0000
Tpd52l1	ENSMUSG00000000296	tumor protein D52-like 1	-1.640	0.0022	0.0070
Tpgs1	ENSMUSG00000020308	tubulin polyglutamylase complex subunit 1	-2.436	0.0000	0.0000
Tpk1	ENSMUSG00000029735	thiamine pyrophosphokinase	-1.687	0.0088	0.0235
Tpmt	ENSMUSG00000021376	thiopurine methyltransferase	-1.756	0.0000	0.0001
Tpp1	ENSMUSG00000030894	tripeptidyl peptidase I	-2.435	0.0000	0.0000
Tpra1	ENSMUSG00000002871	transmembrane protein, adipocyte asscociated 1	-2.160	0.0000	0.0000
Tpst2	ENSMUSG00000029344	protein-tyrosine sulfotransferase 2	-1.786	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Traf7	ENSMUSG00000052752	TNF receptor-associated factor 7	-2.656	0.0000	0.0000
Trappc12	ENSMUSG00000020628	trafficking protein particle complex 12	-1.672	0.0000	0.0000
Trappc2	ENSMUSG00000079317	trafficking protein particle complex 2	-1.698	0.0000	0.0000
Trappc4	ENSMUSG00000032112	trafficking protein particle complex 4	-2.229	0.0000	0.0000
Trappc9	ENSMUSG00000047921	trafficking protein particle complex 9	-1.969	0.0000	0.0000
Trem2	ENSMUSG00000023992	triggering receptor expressed on myeloid cells 2	-1.917	0.0361	0.0788
Triap1	ENSMUSG00000029535	TP53 regulated inhibitor of apoptosis 1	-1.902	0.0000	0.0000
Trib3	ENSMUSG00000032715	tribbles pseudokinase 3	-1.716	0.0020	0.0063
Trim28	ENSMUSG00000005566	tripartite motif-containing 28	-1.586	0.0000	0.0000
Trim32	ENSMUSG00000051675	tripartite motif-containing 32	-1.952	0.0000	0.0000
Trim46	ENSMUSG00000042766	tripartite motif-containing 46	-2.137	0.0047	0.0136
Trim65	ENSMUSG00000054517	tripartite motif-containing 65	-1.690	0.0000	0.0000
Trim9	ENSMUSG00000021071	tripartite motif-containing 9	-32.741	0.0001	0.0006
Triqk	ENSMUSG00000055963	triple QxxK/R motif containing	-2.334	0.0000	0.0000
Trmt112-ps2	ENSMUSG00000070572	tRNA methyltransferase 11-2, pseudogene 2	-3.114	0.0455	0.0955
Trp53i13	ENSMUSG00000044328	transformation related protein 53 inducible protein 13	-1.878	0.0002	0.0010
Trpt1	ENSMUSG00000047656	tRNA phosphotransferase 1	-2.268	0.0000	0.0000
Trpv1	ENSMUSG00000005952	transient receptor potential cation channel, subfamily V, member 1	-9.727	0.0244	0.0566
Trpv4	ENSMUSG00000014158	transient receptor potential cation channel, subfamily V, member 4	-1.812	0.0081	0.0220
Trrap	ENSMUSG00000045482	transformation/transcription domain-associated protein	-1.738	0.0000	0.0000
Trub2	ENSMUSG00000039826	TruB pseudouridine (psi) synthase family member 2	-2.188	0.0000	0.0000
Tsacc	ENSMUSG00000010538	TSSK6 activating co-chaperone	-2.513	0.0156	0.0386
Tsc2	ENSMUSG00000002496	TSC complex subunit 2	-1.555	0.0000	0.0000
Tsen15	ENSMUSG00000014980	tRNA splicing endonuclease subunit 15	-1.928	0.0000	0.0000
Tsen2	ENSMUSG00000042389	tRNA splicing endonuclease subunit 2	-1.525	0.0009	0.0030
Tsku	ENSMUSG00000049580	tsukushi, small leucine rich proteoglycan	-2.018	0.0002	0.0007
Tspan11	ENSMUSG00000030351	tetraspanin 11	-3.066	0.0003	0.0011
Tspan4	ENSMUSG00000025511	tetraspanin 4	-2.520	0.0000	0.0000
Tspan6	ENSMUSG00000067377	tetraspanin 6	-1.520	0.0020	0.0063
Tspo	ENSMUSG00000041736	translocator protein	-6.281	0.0000	0.0000
Tssk4	ENSMUSG00000007591	testis-specific serine kinase 4	-5.725	0.0432	0.0916

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ttc30a2	ENSMUSG00000075272	tetratricopeptide repeat domain 30A2	-3.848	0.0037	0.0110
Ttc32	ENSMUSG00000066637	tetratricopeptide repeat domain 32	-1.969	0.0000	0.0000
Ttc36	ENSMUSG00000039438	tetratricopeptide repeat domain 36	-16.480	0.0053	0.0152
Ttc38	ENSMUSG00000035944	tetratricopeptide repeat domain 38	-1.535	0.0001	0.0005
Ttc7b	ENSMUSG00000033530	tetratricopeptide repeat domain 7B	-1.671	0.0000	0.0000
Ttll1	ENSMUSG00000022442	tubulin tyrosine ligase-like 1	-2.796	0.0000	0.0000
Ttll3	ENSMUSG00000030276	tubulin tyrosine ligase-like family, member 3	-2.909	0.0094	0.0249
Ttyh2	ENSMUSG00000034714	tweety family member 2	-1.683	0.0062	0.0174
Tubg1	ENSMUSG00000035198	tubulin, gamma 1	-2.513	0.0000	0.0000
Tubgcp4	ENSMUSG00000027263	tubulin, gamma complex associated protein 4	-1.555	0.0000	0.0000
Twf2	ENSMUSG00000023277	twinfilin actin binding protein 2	-3.098	0.0000	0.0000
Txndc12	ENSMUSG00000028567	thioredoxin domain containing 12 (endoplasmic reticulum)	-1.530	0.0001	0.0005
Tyk2	ENSMUSG00000032175	tyrosine kinase 2	-1.617	0.0001	0.0003
Tyrobp	ENSMUSG00000030579	TYRO protein tyrosine kinase binding protein	-1.531	0.0437	0.0924
Ubald2	ENSMUSG00000050628	UBA-like domain containing 2	-1.956	0.0007	0.0026
Ubb-ps	ENSMUSG00000044285	ubiquitin B, pseudogene	-1.995	0.0000	0.0001
Ubc	ENSMUSG00000008348	ubiquitin C	-5.938	0.0000	0.0000
Ube2a	ENSMUSG00000016308	ubiquitin-conjugating enzyme E2A	-1.822	0.0000	0.0000
Ube2c	ENSMUSG00000001403	ubiquitin-conjugating enzyme E2C	-2.342	0.0001	0.0002
Ube2d-ps	ENSMUSG00000083844	ubiquitin-conjugating enzyme E2D, pseudogene	-2.002	0.0000	0.0000
Ube2l3	ENSMUSG00000038965	ubiquitin-conjugating enzyme E2L 3	-1.640	0.0000	0.0000
Ube2t	ENSMUSG00000026429	ubiquitin-conjugating enzyme E2T	-2.337	0.0000	0.0000
Ube2v1	ENSMUSG00000078923	ubiquitin-conjugating enzyme E2 variant 1	-7.135	0.0294	0.0664
Ube4bos1	ENSMUSG00000085819	ubiquitination factor E4B, opposite strand 1	-18.260	0.0002	0.0006
Ubiad1	ENSMUSG00000047719	UbiA prenyltransferase domain containing 1	-1.728	0.0000	0.0000
Ubl4a	ENSMUSG00000015290	ubiquitin-like 4A	-1.574	0.0000	0.0000
Ubl7	ENSMUSG00000055720	ubiquitin-like 7 (bone marrow stromal cell-derived)	-1.904	0.0000	0.0000
Ubox5	ENSMUSG00000027300	U box domain containing 5	-2.274	0.0000	0.0000
Ubtd1	ENSMUSG00000025171	ubiquitin domain containing 1	-2.109	0.0000	0.0000
Ubxn10	ENSMUSG00000043621	UBX domain protein 10	-1.656	0.0015	0.0051
Ubxn6	ENSMUSG00000019578	UBX domain protein 6	-1.649	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Uchl1	ENSMUSG00000029223	ubiquitin carboxy-terminal hydrolase L1	-1.710	0.0076	0.0208
Uchl4	ENSMUSG00000035337	ubiquitin carboxyl-terminal esterase L4	-7.485	0.0000	0.0000
Uck1	ENSMUSG00000002550	uridine-cytidine kinase 1	-2.774	0.0000	0.0000
Uckl1	ENSMUSG00000089917	uridine-cytidine kinase 1-like 1	-2.057	0.0000	0.0000
Ugt1a6b	ENSMUSG00000090145	UDP glucuronosyltransferase 1 family, polypeptide A6B	-2.406	0.0327	0.0725
Unc93b1	ENSMUSG00000036908	unc-93 homolog B1, TLR signaling regulator	-2.203	0.0000	0.0000
Unkl	ENSMUSG00000015127	unkempt family like zinc finger	-1.881	0.0046	0.0135
Upp1	ENSMUSG00000020407	uridine phosphorylase 1	-2.412	0.0000	0.0000
Uqcc2	ENSMUSG00000024208	ubiquinol-cytochrome c reductase complex assembly factor 2	-2.819	0.0000	0.0000
Uqcr10	ENSMUSG00000059534	ubiquinol-cytochrome c reductase, complex III subunit X	-1.815	0.0000	0.0000
Uqcr11	ENSMUSG00000020163	ubiquinol-cytochrome c reductase, complex III subunit XI	-3.632	0.0000	0.0000
Uqcrh-ps2	ENSMUSG00000081413	ubiquinol-cytochrome c reductase hinge protein, pseudogene 2	-31.572	0.0003	0.0010
Urb1	ENSMUSG00000039929	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	-1.718	0.0000	0.0000
Urod	ENSMUSG00000028684	uroporphyrinogen decarboxylase	-1.647	0.0000	0.0000
Usp22	ENSMUSG00000042506	ubiquitin specific peptidase 22	-2.248	0.0000	0.0000
Usp38	ENSMUSG00000038250	ubiquitin specific peptidase 38	-1.782	0.0000	0.0000
Uts2r	ENSMUSG00000039321	urotensin 2 receptor	-4.279	0.0102	0.0267
Uxt	ENSMUSG00000001134	ubiquitously expressed prefoldin like chaperone	-1.651	0.0000	0.0000
Vars	ENSMUSG00000007029	valyl-tRNA synthetase	-1.549	0.0028	0.0088
Vegfc	ENSMUSG00000031520	vascular endothelial growth factor C	-1.522	0.0019	0.0062
Vipr2	ENSMUSG00000011171	vasoactive intestinal peptide receptor 2	-1.786	0.0104	0.0271
Vkorc1	ENSMUSG00000096145	vitamin K epoxide reductase complex, subunit 1	-1.908	0.0202	0.0482
Vma21-ps	ENSMUSG00000061619	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae), pseudogene	-25.161	0.0007	0.0025
Vmac	ENSMUSG00000054723	vimentin-type intermediate filament associated coiled-coil protein	-1.711	0.0000	0.0000
Vnn1	ENSMUSG00000037440	vanin 1	-8.380	0.0104	0.0272
Vps35	ENSMUSG00000031696	VPS35 retromer complex component	-1.524	0.0000	0.0000
Vps35l	ENSMUSG00000030982	VPS35 endosomal protein sorting factor like	-1.901	0.0000	0.0000
Vps51	ENSMUSG00000024797	VPS51 GARP complex subunit	-1.566	0.0000	0.0000
Vrk3	ENSMUSG00000002205	vaccinia related kinase 3	-1.688	0.0000	0.0000
Vtn	ENSMUSG00000017344	vitronectin	-2.616	0.0000	0.0000
Vwa3a	ENSMUSG00000030889	von Willebrand factor A domain containing 3A	-1.832	0.0005	0.0019

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Vwa5a	ENSMUSG00000023186	von Willebrand factor A domain containing 5A	-1.986	0.0000	0.0000
Washc5	ENSMUSG00000022350	WASH complex subunit 5	-1.887	0.0000	0.0000
Wbp2	ENSMUSG00000034341	WW domain binding protein 2	-1.949	0.0000	0.0000
Wdfy2	ENSMUSG00000014547	WD repeat and FYVE domain containing 2	-1.632	0.0000	0.0000
Wdr18	ENSMUSG00000035754	WD repeat domain 18	-1.654	0.0000	0.0000
Wdr24	ENSMUSG00000025737	WD repeat domain 24	-1.572	0.0000	0.0000
Wdr45	ENSMUSG00000039382	WD repeat domain 45	-1.869	0.0004	0.0014
Wdr6	ENSMUSG00000066357	WD repeat domain 6	-1.539	0.0000	0.0000
Wdr74	ENSMUSG00000042729	WD repeat domain 74	-1.870	0.0000	0.0000
Wdr83os	ENSMUSG00000059355	WD repeat domain 83 opposite strand	-2.179	0.0000	0.0000
Wdr90	ENSMUSG00000073434	WD repeat domain 90	-1.593	0.0144	0.0361
Wdr91	ENSMUSG00000058486	WD repeat domain 91	-1.535	0.0010	0.0034
Wfdc1	ENSMUSG00000023336	WAP four-disulfide core domain 1	-2.881	0.0000	0.0000
Wfdc17	ENSMUSG00000069792	WAP four-disulfide core domain 17	-1.846	0.0032	0.0098
Wfdc2	ENSMUSG00000017723	WAP four-disulfide core domain 2	-15.434	0.0292	0.0660
Wipf3	ENSMUSG00000086040	WAS/WASL interacting protein family, member 3	-1.594	0.0000	0.0000
Wrap73	ENSMUSG00000029029	WD repeat containing, antisense to Trp73	-2.509	0.0000	0.0000
Wscd1	ENSMUSG00000020811	WSC domain containing 1	-1.606	0.0031	0.0095
Xbp1	ENSMUSG00000020484	X-box binding protein 1	-1.935	0.0000	0.0001
Xpnpep1	ENSMUSG00000025027	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-1.863	0.0000	0.0000
Ydjc	ENSMUSG00000041774	YdjC homolog (bacterial)	-3.714	0.0000	0.0000
Yeats2	ENSMUSG00000041215	YEATS domain containing 2	-1.852	0.0000	0.0000
Yif1a	ENSMUSG00000024875	Yip1 interacting factor homolog A (S. cerevisiae)	-2.144	0.0000	0.0000
Yif1b	ENSMUSG00000030588	Yip1 interacting factor homolog B (S. cerevisiae)	-2.486	0.0000	0.0000
Yipf1	ENSMUSG00000057375	Yip1 domain family, member 1	-1.794	0.0000	0.0000
Yipf7	ENSMUSG00000029158	Yip1 domain family, member 7	-1.919	0.0000	0.0000
Zbtb3	ENSMUSG00000071661	zinc finger and BTB domain containing 3	-2.368	0.0000	0.0001
Zbtb45	ENSMUSG00000049600	zinc finger and BTB domain containing 45	-2.339	0.0000	0.0000
Zc2hc1a	ENSMUSG00000043542	zinc finger, C2HC-type containing 1A	-1.668	0.0000	0.0000
Zc3h12b	ENSMUSG00000035045	zinc finger CCCH-type containing 12B	-2.940	0.0007	0.0024
Zc3h3	ENSMUSG00000075600	zinc finger CCCH type containing 3	-2.802	0.0002	0.0008

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zdhhc12	ENSMUSG00000015335	zinc finger, DHHC domain containing 12	-3.182	0.0000	0.0000
Zdhhc13	ENSMUSG00000030471	zinc finger, DHHC domain containing 13	-1.555	0.0000	0.0000
Zdhhc15	ENSMUSG00000033906	zinc finger, DHHC domain containing 15	-1.715	0.0350	0.0768
Zdhhc16	ENSMUSG00000025157	zinc finger, DHHC domain containing 16	-1.635	0.0000	0.0000
Zdhhc4	ENSMUSG00000001844	zinc finger, DHHC domain containing 4	-1.851	0.0000	0.0000
Zer1	ENSMUSG00000039686	zyg-11 related, cell cycle regulator	-1.635	0.0000	0.0000
Zfand2a	ENSMUSG00000053581	zinc finger, AN1-type domain 2A	-1.980	0.0000	0.0000
Zfand2b	ENSMUSG00000026197	zinc finger, AN1 type domain 2B	-1.699	0.0000	0.0001
Zfat	ENSMUSG00000022335	zinc finger and AT hook domain containing	-1.628	0.0005	0.0019
Zfp101	ENSMUSG00000055240	zinc finger protein 101	-1.559	0.0014	0.0048
Zfp119a	ENSMUSG00000057835	zinc finger protein 119a	-2.507	0.0000	0.0000
Zfp119b	ENSMUSG00000062101	zinc finger protein 119b	-1.707	0.0087	0.0234
Zfp128	ENSMUSG00000060397	zinc finger protein 128	-1.563	0.0036	0.0107
Zfp142	ENSMUSG00000026135	zinc finger protein 142	-1.595	0.0000	0.0000
Zfp174	ENSMUSG00000054939	zinc finger protein 174	-1.669	0.0001	0.0005
Zfp184	ENSMUSG00000006720	zinc finger protein 184 (Kruppel-like)	-5.473	0.0010	0.0035
Zfp2	ENSMUSG00000049321	zinc finger protein 2	-2.097	0.0000	0.0000
Zfp202	ENSMUSG00000025602	zinc finger protein 202	-1.540	0.0006	0.0021
Zfp213	ENSMUSG00000071256	zinc finger protein 213	-1.703	0.0003	0.0010
Zfp260	ENSMUSG00000049421	zinc finger protein 260	-1.681	0.0000	0.0000
Zfp276	ENSMUSG00000001065	zinc finger protein (C2H2 type) 276	-2.115	0.0000	0.0000
Zfp277	ENSMUSG00000055917	zinc finger protein 277	-2.092	0.0000	0.0000
Zfp324	ENSMUSG00000004500	zinc finger protein 324	-1.647	0.0005	0.0017
Zfp335	ENSMUSG00000039834	zinc finger protein 335	-1.859	0.0000	0.0000
Zfp346	ENSMUSG00000021481	zinc finger protein 346	-1.577	0.0000	0.0000
Zfp354a	ENSMUSG00000020364	zinc finger protein 354A	-1.679	0.0076	0.0206
Zfp36l1-ps	ENSMUSG00000080942	zinc finger protein 36, C3H type-like 1, pseudogene	-3.709	0.0028	0.0087
Zfp382	ENSMUSG00000074220	zinc finger protein 382	-4.814	0.0000	0.0002
Zfp40	ENSMUSG00000002617	zinc finger protein 40	-2.379	0.0000	0.0001
Zfp41	ENSMUSG00000047003	zinc finger protein 41	-1.657	0.0030	0.0093
Zfp414	ENSMUSG00000073423	zinc finger protein 414	-1.963	0.0000	0.0000

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp446	ENSMUSG00000033961	zinc finger protein 446	-1.844	0.0000	0.0000
Zfp455	ENSMUSG00000051037	zinc finger protein 455	-2.013	0.0003	0.0012
Zfp456	ENSMUSG00000078995	zinc finger protein 456	-2.208	0.0064	0.0178
Zfp459	ENSMUSG00000055560	zinc finger protein 459	-3.532	0.0003	0.0010
Zfp472	ENSMUSG00000053600	zinc finger protein 472	-2.095	0.0000	0.0000
Zfp51	ENSMUSG00000023892	zinc finger protein 51	-1.690	0.0000	0.0000
Zfp511	ENSMUSG00000025470	zinc finger protein 511	-2.062	0.0000	0.0000
Zfp536	ENSMUSG00000043456	zinc finger protein 536	-1.520	0.0125	0.0320
Zfp54	ENSMUSG00000023882	zinc finger protein 54	-2.086	0.0005	0.0019
Zfp558	ENSMUSG00000074500	zinc finger protein 558	-2.641	0.0025	0.0078
Zfp560	ENSMUSG00000045519	zinc finger protein 560	-1.644	0.0002	0.0007
Zfp574	ENSMUSG00000045252	zinc finger protein 574	-1.767	0.0035	0.0106
Zfp619	ENSMUSG00000068959	zinc finger protein 619	-1.607	0.0010	0.0036
Zfp623	ENSMUSG00000050846	zinc finger protein 623	-1.501	0.0004	0.0016
Zfp637	ENSMUSG00000059689	zinc finger protein 637	-2.189	0.0000	0.0000
Zfp64	ENSMUSG00000027551	zinc finger protein 64	-1.708	0.0000	0.0000
Zfp647	ENSMUSG00000054967	zinc finger protein 647	-3.292	0.0000	0.0002
Zfp652os	ENSMUSG00000086191	zinc finger protein 652, opposite strand	-13.376	0.0010	0.0036
Zfp653	ENSMUSG00000038895	zinc finger protein 653	-1.592	0.0231	0.0539
Zfp655	ENSMUSG00000007812	zinc finger protein 655	-1.662	0.0000	0.0000
Zfp658	ENSMUSG00000056592	zinc finger protein 658	-2.077	0.0086	0.0230
Zfp672	ENSMUSG00000049755	zinc finger protein 672	-2.150	0.0000	0.0000
Zfp677	ENSMUSG00000062743	zinc finger protein 677	-2.398	0.0029	0.0089
Zfp688	ENSMUSG00000045251	zinc finger protein 688	-1.644	0.0020	0.0064
Zfp7	ENSMUSG00000033669	zinc finger protein 7	-1.854	0.0249	0.0576
Zfp706	ENSMUSG00000062397	zinc finger protein 706	-2.062	0.0000	0.0000
Zfp709	ENSMUSG00000056019	zinc finger protein 709	-1.806	0.0000	0.0000
Zfp712	ENSMUSG00000090641	zinc finger protein 712	-1.635	0.0035	0.0106
Zfp715	ENSMUSG00000012640	zinc finger protein 715	-1.784	0.0000	0.0000
Zfp719	ENSMUSG00000030469	zinc finger protein 719	-1.879	0.0000	0.0000
Zfp72	ENSMUSG00000069184	zinc finger protein 72	-1.856	0.0012	0.0042

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp729b	ENSMUSG00000058093	zinc finger protein 729b	-2.380	0.0000	0.0000
Zfp748	ENSMUSG00000095432	zinc finger protein 748	-2.061	0.0000	0.0000
Zfp758	ENSMUSG00000044501	zinc finger protein 758	-1.809	0.0000	0.0000
Zfp759	ENSMUSG00000057396	zinc finger protein 759	-1.690	0.0020	0.0064
Zfp772	ENSMUSG00000066838	zinc finger protein 772	-1.613	0.0062	0.0174
Zfp781	ENSMUSG00000096718	zinc finger protein 781	-5.159	0.0265	0.0608
Zfp808	ENSMUSG00000074867	zinc finger protein 808	-4.112	0.0000	0.0000
Zfp810	ENSMUSG00000066829	zinc finger protein 810	-1.698	0.0000	0.0000
Zfp811	ENSMUSG00000055202	zinc finger protein 811	-18.866	0.0021	0.0068
Zfp820	ENSMUSG00000069743	zinc finger protein 820	-2.440	0.0009	0.0032
Zfp85	ENSMUSG00000058331	zinc finger protein 85	-1.996	0.0001	0.0005
Zfp853	ENSMUSG00000093910	zinc finger protein 853	-22.884	0.0009	0.0031
Zfp868	ENSMUSG00000060427	zinc finger protein 868	-1.614	0.0000	0.0000
Zfp873	ENSMUSG00000061371	zinc finger protein 873	-1.623	0.0042	0.0123
Zfp874a	ENSMUSG00000069206	zinc finger protein 874a	-1.797	0.0001	0.0005
Zfp874b	ENSMUSG00000059839	zinc finger protein 874b	-1.618	0.0006	0.0022
Zfp882	ENSMUSG00000089857	zinc finger protein 882	-2.052	0.0003	0.0011
Zfp9	ENSMUSG00000072623	zinc finger protein 9	-1.874	0.0000	0.0000
Zfp930	ENSMUSG00000059897	zinc finger protein 930	-2.238	0.0000	0.0000
Zfp931	ENSMUSG00000078861	zinc finger protein 931	-1.614	0.0133	0.0336
Zfp932	ENSMUSG00000066613	zinc finger protein 932	-1.801	0.0013	0.0043
Zfp934	ENSMUSG00000074865	zinc finger protein 934	-1.695	0.0082	0.0220
Zfp942	ENSMUSG00000071267	zinc finger protein 942	-1.742	0.0000	0.0000
Zfp944	ENSMUSG00000033972	zinc finger protein 944	-1.845	0.0000	0.0000
Zfp947	ENSMUSG00000063383	zinc finger protein 947	-3.063	0.0005	0.0018
Zfp948	ENSMUSG00000067931	zinc finger protein 948	-1.535	0.0052	0.0149
Zfp951	ENSMUSG00000072774	zinc finger protein 951	-2.355	0.0201	0.0478
Zfp954	ENSMUSG00000062116	zinc finger protein 954	-2.577	0.0000	0.0000
Zfp955a	ENSMUSG00000094441	zinc finger protein 955A	-1.659	0.0000	0.0000
Zfp958	ENSMUSG00000058748	zinc finger protein 958	-2.381	0.0000	0.0000
Zfp959	ENSMUSG00000003198	zinc finger protein 959	-1.829	0.0000	0.0001

• **Table S2: Differentially expressed transcripts in mG4H-OFF compared to Con-OFF**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp960	ENSMUSG00000096696	zinc finger protein 960	-13.131	0.0000	0.0002
Zfp97	ENSMUSG00000095990	zinc finger protein 97	-3.090	0.0001	0.0003
Zfp971	ENSMUSG00000074519	zinc finger protein 971	-1.888	0.0000	0.0000
Zfp975	ENSMUSG00000069727	zinc finger protein 975	-1.549	0.0090	0.0239
Zfp978	ENSMUSG00000078497	zinc finger protein 978	-27.426	0.0009	0.0032
Zfp979	ENSMUSG00000066000	zinc finger protein 979	-1.800	0.0003	0.0012
Zfp995	ENSMUSG00000078546	zinc finger protein 995	-2.199	0.0221	0.0519
Zfpl1	ENSMUSG00000024792	zinc finger like protein 1	-2.117	0.0000	0.0000
Zfyve19	ENSMUSG00000068580	zinc finger, FYVE domain containing 19	-2.297	0.0000	0.0000
Zfyve21	ENSMUSG00000021286	zinc finger, FYVE domain containing 21	-1.701	0.0003	0.0013
Zfyve26	ENSMUSG00000066440	zinc finger, FYVE domain containing 26	-1.878	0.0000	0.0000
Zkscan17	ENSMUSG00000020472	zinc finger with KRAB and SCAN domains 17	-2.025	0.0000	0.0001
Zkscan6	ENSMUSG00000018347	zinc finger with KRAB and SCAN domains 6	-1.516	0.0115	0.0296
Zmat4	ENSMUSG00000037492	zinc finger, matrin type 4	-3.201	0.0003	0.0012
Znhit2	ENSMUSG00000075227	zinc finger, HIT domain containing 2	-2.488	0.0000	0.0000
Zpr1	ENSMUSG00000032078	ZPR1 zinc finger	-1.592	0.0016	0.0054
Zscan30	ENSMUSG00000024274	zinc finger and SCAN domain containing 30	-2.988	0.0007	0.0026
Zswim1	ENSMUSG00000017764	zinc finger SWIM-type containing 1	-2.236	0.0000	0.0000
Zswim7	ENSMUSG00000014243	zinc finger SWIM-type containing 7	-2.047	0.0000	0.0000
Zwint	ENSMUSG00000019923	ZW10 interactor	-1.609	0.0000	0.0000
Zyg11a	ENSMUSG00000034645	zyg-11 family member A, cell cycle regulator	-15.509	0.0143	0.0360
	ENSMUSG00000095041		-1.553	0.0049	0.0142

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
1500009L16Rik	ENSMUSG00000087651	RIKEN cDNA 1500009L16 gene	1.666	0.0002	0.0006
1700001G17Rik	ENSMUSG00000103746	RIKEN cDNA 1700001G17 gene	3.576	0.0275	0.0580
1700008J07Rik	ENSMUSG00000101225	RIKEN cDNA 1700008J07 gene	1.513	0.0025	0.0071
1700034P13Rik	ENSMUSG00000097893	RIKEN cDNA 1700034P13 gene	4.363	0.0443	0.0871
1700040L08Rik	ENSMUSG00000107406	RIKEN cDNA 1700040L08 gene	27.172	0.0010	0.0032
1700052K11Rik	ENSMUSG00000099681	RIKEN cDNA 1700052K11 gene	1.592	0.0079	0.0196
1700056E22Rik	ENSMUSG00000044854	RIKEN cDNA 1700056E22 gene	3.228	0.0002	0.0007
1700096K18Rik	ENSMUSG00000101856	RIKEN cDNA 1700096K18 gene	1.531	0.0203	0.0446
1700105P06Rik	ENSMUSG00000099923	RIKEN cDNA 1700105P06 gene	4.930	0.0254	0.0541
2010007H06Rik	ENSMUSG00000044694	RIKEN cDNA 2010007H06 gene	1.952	0.0072	0.0179
2310015K22Rik	ENSMUSG00000101257	RIKEN cDNA 2310015K22 gene	2.377	0.0213	0.0464
2310016D23Rik	ENSMUSG00000085965	RIKEN cDNA 2310016D23 gene	3.064	0.0290	0.0606
2810457G06Rik	ENSMUSG00000115410	RIKEN cDNA 2810457G06 gene	5.018	0.0073	0.0181
3830403N18Rik	ENSMUSG00000031125	RIKEN cDNA 3830403N18 gene	1.802	0.0230	0.0497
3830408C21Rik	ENSMUSG00000071181	RIKEN cDNA 3830408C21 gene	1.624	0.0163	0.0367
4930578M01Rik	ENSMUSG00000097587	RIKEN cDNA 4930578M01 gene	1.956	0.0052	0.0134
4930589O11Rik	ENSMUSG00000107195	RIKEN cDNA 4930589O11 gene	2.410	0.0049	0.0127
4930590J08Rik	ENSMUSG00000034063	RIKEN cDNA 4930590J08 gene	2.139	0.0329	0.0675
4931428F04Rik	ENSMUSG00000014837	RIKEN cDNA 4931428F04 gene	1.541	0.0216	0.0471
4933440N22Rik	ENSMUSG00000042087	RIKEN cDNA 4933440N22 gene	2.372	0.0044	0.0117
5330438D12Rik	ENSMUSG00000052291	RIKEN cDNA 5330438D12 gene	1.995	0.0066	0.0167
5430414B19Rik	ENSMUSG00000114419	RIKEN cDNA 5430414B19 gene	3.102	0.0091	0.0220
5430416N02Rik	ENSMUSG00000097772	RIKEN cDNA 5430416N02 gene	2.712	0.0001	0.0005
5730414N17Rik	ENSMUSG00000116506	RIKEN cDNA 5730414N17 gene	2.354	0.0001	0.0005
5930420M18Rik	ENSMUSG00000107201	RIKEN cDNA 5930420M18 gene	1.903	0.0329	0.0677
6330418K02Rik	ENSMUSG00000085227	RIKEN cDNA 6330418K02 gene	1.842	0.0205	0.0450
6720427I07Rik	ENSMUSG00000097375	RIKEN cDNA 6720427I07 gene	1.800	0.0000	0.0000
6820431F20Rik	ENSMUSG00000071796	RIKEN cDNA 6820431F20 gene	1.836	0.0334	0.0685
9230111E07Rik	ENSMUSG00000087624	RIKEN cDNA 9230111E07 gene	9.302	0.0022	0.0063
9230116N13Rik	ENSMUSG00000097403	RIKEN cDNA 9230116N13 gene	1.663	0.0413	0.0822
9330121J05Rik	ENSMUSG00000103502	RIKEN cDNA 9330121J05 gene	15.129	0.0159	0.0360
9530085L11Rik	ENSMUSG00000107742	RIKEN cDNA 9530085L11 gene	2.367	0.0046	0.0119

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
9930021J03Rik	ENSMUSG00000046138	RIKEN cDNA 9930021J03 gene	1.649	0.0000	0.0000
A230072E10Rik	ENSMUSG00000084771	RIKEN cDNA A230072E10 gene	3.671	0.0388	0.0778
A530017D24Rik	ENSMUSG00000072847	RIKEN cDNA A530017D24 gene	1.634	0.0000	0.0000
A630072M18Rik	ENSMUSG00000101013	RIKEN cDNA A630072M18 gene	1.771	0.0000	0.0000
A930004J17Rik	ENSMUSG00000102602	RIKEN cDNA A930004J17 gene	1.810	0.0431	0.0852
AA465934	ENSMUSG00000093483	expressed sequence AA465934	1.954	0.0137	0.0315
AB124611	ENSMUSG00000057191	cDNA sequence AB124611	1.738	0.0314	0.0650
Abr	ENSMUSG00000017631	active BCR-related gene	1.553	0.0000	0.0000
Abra	ENSMUSG00000042895	actin-binding Rho activating protein	1.717	0.0136	0.0314
Acaca	ENSMUSG00000020532	acetyl-Coenzyme A carboxylase alpha	1.729	0.0000	0.0001
Acbd5	ENSMUSG00000026781	acyl-Coenzyme A binding domain containing 5	1.756	0.0000	0.0000
Acot1	ENSMUSG00000072949	acyl-CoA thioesterase 1	2.370	0.0000	0.0000
Acsl3	ENSMUSG00000032883	acyl-CoA synthetase long-chain family member 3	1.553	0.0000	0.0001
Acvr2a	ENSMUSG00000052155	activin receptor IIA	1.507	0.0000	0.0000
Adam1a	ENSMUSG00000072647	a disintegrin and metallopeptidase domain 1a	2.605	0.0046	0.0119
Adcy5	ENSMUSG00000022840	adenylate cyclase 5	1.571	0.0019	0.0054
Adss	ENSMUSG00000015961	adenylosuccinate synthetase, non muscle	1.898	0.0000	0.0000
Afg3l2	ENSMUSG00000024527	AFG3-like AAA ATPase 2	1.568	0.0000	0.0000
Akirin1	ENSMUSG00000023075	akirin 1	2.189	0.0000	0.0000
Akt3	ENSMUSG00000019699	thymoma viral proto-oncogene 3	1.537	0.0000	0.0000
Aldh5a1	ENSMUSG00000035936	aldhehyde dehydrogenase family 5, subfamily A1	1.573	0.0000	0.0000
Alkbh2	ENSMUSG00000044339	alkB homolog 2, alpha-ketoglutarate-dependent dioxygenase	2.018	0.0000	0.0000
Ammecr1	ENSMUSG00000042225	AMMECR nuclear protein 1	1.974	0.0000	0.0000
Angptl1	ENSMUSG00000033544	angiopoietin-like 1	1.555	0.0239	0.0512
Ankmy1	ENSMUSG00000034212	ankyrin repeat and MYND domain containing 1	9.800	0.0006	0.0020
Ankrd37	ENSMUSG00000050914	ankyrin repeat domain 37	2.033	0.0012	0.0036
Ap1g1	ENSMUSG00000031731	adaptor protein complex AP-1, gamma 1 subunit	1.535	0.0000	0.0000
Ap4s1	ENSMUSG00000020955	adaptor-related protein complex AP-4, sigma 1	2.122	0.0000	0.0000
Apba1	ENSMUSG00000024897	amyloid beta (A4) precursor protein binding, family A, member 1	1.770	0.0031	0.0084
Appbp2os	ENSMUSG00000085628	amyloid beta precursor protein (cytoplasmic tail) binding protein 2, opposite strand	5.475	0.0168	0.0377
Aqp4	ENSMUSG00000024411	aquaporin 4	1.651	0.0058	0.0147
Arhgdig	ENSMUSG00000073433	Rho GDP dissociation inhibitor (GDI) gamma	1.562	0.0414	0.0824

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Arid1a	ENSMUSG00000007880	AT rich interactive domain 1A (SWI-like)	1.592	0.0000	0.0001
Arl13b	ENSMUSG00000022911	ADP-ribosylation factor-like 13B	1.866	0.0000	0.0000
Arl5b	ENSMUSG00000017418	ADP-ribosylation factor-like 5B	1.545	0.0000	0.0000
Armc8	ENSMUSG00000032468	armadillo repeat containing 8	1.518	0.0000	0.0000
Armcx4	ENSMUSG00000049804	armadillo repeat containing, X-linked 4	2.551	0.0000	0.0000
Armh4	ENSMUSG00000036242	armadillo-like helical domain containing 4	1.590	0.0000	0.0000
Arrdc4	ENSMUSG00000042659	arrestin domain containing 4	2.146	0.0000	0.0000
Atp11b	ENSMUSG00000037400	ATPase, class VI, type 11B	2.024	0.0000	0.0000
Atp13a3	ENSMUSG00000022533	ATPase type 13A3	1.613	0.0000	0.0000
Atp1b1	ENSMUSG00000026576	ATPase, Na+/K+ transporting, beta 1 polypeptide	1.593	0.0000	0.0000
Atp23	ENSMUSG00000025436	ATP23 metallopeptidase and ATP synthase assembly factor homolog	1.541	0.0292	0.0609
Atrx	ENSMUSG00000031229	ATRX, chromatin remodeler	1.710	0.0000	0.0000
Azin1	ENSMUSG00000037458	antizyme inhibitor 1	1.721	0.0000	0.0000
B430219N15Rik	ENSMUSG00000085211	RIKEN cDNA B430219N15 gene	4.043	0.0003	0.0010
B430319F04Rik	ENSMUSG00000110062	RIKEN cDNA B430319F04 gene	3.483	0.0365	0.0738
B4galt1	ENSMUSG00000028413	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 1	1.509	0.0000	0.0000
B930094E09Rik	ENSMUSG00000092124	RIKEN cDNA B930094E09 gene	1.594	0.0120	0.0281
Baz1a	ENSMUSG00000035021	bromodomain adjacent to zinc finger domain 1A	1.734	0.0003	0.0009
Baz2b	ENSMUSG00000026987	bromodomain adjacent to zinc finger domain, 2B	1.514	0.0000	0.0000
Bbs5	ENSMUSG00000063145	Bardet-Biedl syndrome 5 (human)	1.578	0.0000	0.0001
Bbx	ENSMUSG00000022641	bobby sox HMG box containing	1.624	0.0000	0.0000
BC005537	ENSMUSG00000019132	cDNA sequence BC005537	1.568	0.0008	0.0025
Bcat1	ENSMUSG00000030268	branched chain aminotransferase 1, cytosolic	1.552	0.0256	0.0543
Bcl6b	ENSMUSG00000000317	B cell CLL/lymphoma 6, member B	1.723	0.0004	0.0013
Begain	ENSMUSG00000040867	brain-enriched guanylate kinase-associated	3.612	0.0106	0.0254
Bfsp1	ENSMUSG00000027420	beaded filament structural protein 1, in lens-CP94	1.977	0.0119	0.0280
Bmi1	ENSMUSG00000026739	Bmi1 polycomb ring finger oncogene	1.605	0.0000	0.0000
Bmpr1a	ENSMUSG00000021796	bone morphogenetic protein receptor, type 1A	1.642	0.0000	0.0000
Bmpr1b	ENSMUSG00000052430	bone morphogenetic protein receptor, type 1B	3.024	0.0000	0.0002
Bpnt1	ENSMUSG00000026617	3'(2'), 5'-bisphosphate nucleotidase 1	1.552	0.0010	0.0031
Bpnt2	ENSMUSG00000066324	3'(2'), 5'-bisphosphate nucleotidase 2	1.611	0.0000	0.0000
Btbd10	ENSMUSG00000038187	BTB (POZ) domain containing 10	1.621	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Btbd19	ENSMUSG00000073771	BTB (POZ) domain containing 19	1.772	0.0139	0.0319
Btla	ENSMUSG00000052013	B and T lymphocyte associated	2.178	0.0225	0.0488
Bub1b	ENSMUSG00000040084	BUB1B, mitotic checkpoint serine/threonine kinase	2.468	0.0008	0.0026
C030015A19Rik	ENSMUSG00000108181	RIKEN cDNA C030015A19 gene	1.645	0.0473	0.0923
C130080G10Rik	ENSMUSG00000092397	RIKEN cDNA C130080G10 gene	1.605	0.0003	0.0009
C2cd4b	ENSMUSG00000091956	C2 calcium-dependent domain containing 4B	2.258	0.0431	0.0851
C2cd4d	ENSMUSG00000091648	C2 calcium-dependent domain containing 4D	12.776	0.0015	0.0045
Cacul1	ENSMUSG00000033417	CDK2 associated, cullin domain 1	1.607	0.0000	0.0001
Cadm3	ENSMUSG00000005338	cell adhesion molecule 3	1.671	0.0427	0.0844
Cadps2	ENSMUSG00000017978	Ca2+-dependent activator protein for secretion 2	1.506	0.0387	0.0776
Camk2d	ENSMUSG00000053819	calcium/calmodulin-dependent protein kinase II, delta	1.618	0.0000	0.0000
Camkmt	ENSMUSG00000071037	calmodulin-lysine N-methyltransferase	2.150	0.0000	0.0002
Camsap2	ENSMUSG00000041570	calmodulin regulated spectrin-associated protein family, member 2	1.654	0.0000	0.0000
Casc1	ENSMUSG00000043541	cancer susceptibility candidate 1	2.636	0.0448	0.0879
Casq1	ENSMUSG00000007122	calsequestrin 1	1.516	0.0337	0.0690
Castor2	ENSMUSG00000015944	cytosolic arginine sensor for mTORC1 subunit 2	1.694	0.0033	0.0090
Cbx5	ENSMUSG00000009575	chromobox 5	1.632	0.0000	0.0000
Ccdc18	ENSMUSG00000056531	coiled-coil domain containing 18	2.735	0.0251	0.0535
Ccdc43	ENSMUSG00000020925	coiled-coil domain containing 43	1.525	0.0000	0.0000
Ccdc50	ENSMUSG00000038127	coiled-coil domain containing 50	1.570	0.0000	0.0000
Ccdc85b	ENSMUSG00000095098	coiled-coil domain containing 85B	3.463	0.0002	0.0006
Ccdc88a	ENSMUSG00000032740	coiled coil domain containing 88A	1.524	0.0000	0.0000
Ccnyl1	ENSMUSG00000070871	cyclin Y-like 1	1.578	0.0001	0.0005
Cd2	ENSMUSG00000027863	CD2 antigen	3.337	0.0040	0.0107
Cd209f	ENSMUSG00000051906	CD209f antigen	1.747	0.0518	0.0997
Cd44	ENSMUSG00000005087	CD44 antigen	1.688	0.0100	0.0241
Cdc37l1	ENSMUSG00000024780	cell division cycle 37-like 1	1.517	0.0214	0.0467
Cdk17	ENSMUSG00000020015	cyclin-dependent kinase 17	1.777	0.0000	0.0000
Cdkl3	ENSMUSG00000020389	cyclin-dependent kinase-like 3	1.630	0.0001	0.0002
Cebpd	ENSMUSG00000071637	CCAAT/enhancer binding protein (C/EBP), delta	3.492	0.0213	0.0465
Cebpz	ENSMUSG00000024081	CCAAT/enhancer binding protein zeta	1.602	0.0000	0.0000
Celf1	ENSMUSG00000005506	CUGBP, Elav-like family member 1	1.604	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cemip2	ENSMUSG00000024754	cell migration inducing hyaluronidase 2	1.685	0.0000	0.0000
Cenpe	ENSMUSG00000045328	centromere protein E	2.205	0.0023	0.0066
Cenpf	ENSMUSG00000026605	centromere protein F	1.671	0.0060	0.0153
Cenph	ENSMUSG00000045273	centromere protein H	2.640	0.0443	0.0872
Cep126	ENSMUSG00000040729	centrosomal protein 126	1.565	0.0015	0.0044
Cep170	ENSMUSG00000057335	centrosomal protein 170	1.522	0.0000	0.0000
Cep290	ENSMUSG00000019971	centrosomal protein 290	1.542	0.0000	0.0001
Cers3	ENSMUSG00000030510	ceramide synthase 3	2.081	0.0462	0.0904
Cgas	ENSMUSG00000032344	cyclic GMP-AMP synthase	1.730	0.0090	0.0219
Chmp5	ENSMUSG00000028419	charged multivesicular body protein 5	1.517	0.0000	0.0000
Chrna2	ENSMUSG00000022041	cholinergic receptor, nicotinic, alpha polypeptide 2 (neuronal)	2.468	0.0025	0.0071
Cldnd1	ENSMUSG00000022744	claudin domain containing 1	1.652	0.0000	0.0000
Clpx	ENSMUSG00000015357	caseinolytic mitochondrial matrix peptidase chaperone subunit	1.659	0.0004	0.0013
Clspn	ENSMUSG00000042489	claspin	2.281	0.0117	0.0275
Cmtm4	ENSMUSG00000096188	CKLF-like MARVEL transmembrane domain containing 4	1.666	0.0000	0.0000
Cnbd2	ENSMUSG00000038085	cyclic nucleotide binding domain containing 2	1.594	0.0166	0.0374
Cngb1	ENSMUSG00000031789	cyclic nucleotide gated channel beta 1	1.617	0.0069	0.0173
Cnih2	ENSMUSG00000024873	cornichon family AMPA receptor auxiliary protein 2	3.461	0.0504	0.0972
Cnnm2	ENSMUSG00000064105	cyclin M2	1.691	0.0002	0.0007
Cnot6l	ENSMUSG00000034724	CCR4-NOT transcription complex, subunit 6-like	1.580	0.0000	0.0000
Col20a1	ENSMUSG00000016356	collagen, type XX, alpha 1	1.794	0.0014	0.0042
Col7a1	ENSMUSG00000025650	collagen, type VII, alpha 1	2.364	0.0432	0.0853
Cop1	ENSMUSG00000040782	COP1, E3 ubiquitin ligase	1.813	0.0000	0.0000
Cox17	ENSMUSG00000046516	cytochrome c oxidase assembly protein 17, copper chaperone	2.264	0.0004	0.0012
Cpeb4	ENSMUSG00000020300	cytoplasmic polyadenylation element binding protein 4	1.631	0.0000	0.0000
Crispld1	ENSMUSG00000025776	cysteine-rich secretory protein LCCL domain containing 1	1.935	0.0000	0.0000
Crk	ENSMUSG00000017776	v-crk avian sarcoma virus CT10 oncogene homolog	1.651	0.0000	0.0000
Csrnp2	ENSMUSG00000044636	cysteine-serine-rich nuclear protein 2	1.637	0.0027	0.0075
Ctf1	ENSMUSG00000042340	cardiotrophin 1	1.548	0.0035	0.0095
Ctnnb1	ENSMUSG00000006932	catenin (cadherin associated protein), beta 1	1.549	0.0000	0.0000
Cul5	ENSMUSG00000032030	cullin 5	1.690	0.0000	0.0000
Cwf19l2	ENSMUSG00000025898	CWF19-like 2, cell cycle control (S. pombe)	1.792	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
D030034A15Rik	ENSMUSG00000111055	RIKEN cDNA D030034A15 gene	1.751	0.0226	0.0489
D030056L22Rik	ENSMUSG00000047044	RIKEN cDNA D030056L22 gene	2.139	0.0000	0.0000
D030062O11Rik	ENSMUSG00000103710	RIKEN cDNA D030062O11 gene	3.483	0.0144	0.0329
D7Bwg0826e	ENSMUSG00000109198	DNA segment, Chr 7, Brigham & Women's Genetics 0826 expressed	6.122	0.0226	0.0488
D830013O20Rik	ENSMUSG00000056359	RIKEN cDNA D830013O20 gene	1.665	0.0000	0.0001
D830036C21Rik	ENSMUSG00000108854	RIKEN cDNA D830036C21 gene	4.104	0.0010	0.0030
D930007J09Rik	ENSMUSG00000042874	RIKEN cDNA D930007J09 gene	2.837	0.0040	0.0106
Dcun1d1	ENSMUSG00000027708	DCN1, defective in cullin neddylation 1, domain containing 1 (S. cerevisiae)	2.014	0.0000	0.0000
Ddi2	ENSMUSG00000078515	DNA-damage inducible protein 2	1.717	0.0000	0.0000
Ddx21	ENSMUSG00000020075	DExD box helicase 21	1.601	0.0000	0.0000
Ddx3y	ENSMUSG00000069045	DEAD box helicase 3, Y-linked	1.885	0.0000	0.0000
Dennd6a	ENSMUSG00000040818	DENN/MADD domain containing 6A	1.556	0.0000	0.0000
Depdc1b	ENSMUSG00000021697	DEP domain containing 1B	2.438	0.0061	0.0154
Desi1	ENSMUSG00000022472	desumoylating isopeptidase 1	1.710	0.0027	0.0074
Desi2	ENSMUSG00000026502	desumoylating isopeptidase 2	1.660	0.0000	0.0000
Dgcr8	ENSMUSG00000022718	DGCR8, microprocessor complex subunit	1.549	0.0000	0.0000
Dhh	ENSMUSG00000023000	desert hedgehog	2.007	0.0343	0.0700
Dld	ENSMUSG00000020664	dihydrolipoamide dehydrogenase	1.613	0.0000	0.0000
Dleu2	ENSMUSG00000097589	deleted in lymphocytic leukemia, 2	1.812	0.0002	0.0008
Dnaja1	ENSMUSG00000028410	DnaJ heat shock protein family (Hsp40) member A1	1.547	0.0000	0.0000
Dnaja2	ENSMUSG00000031701	DnaJ heat shock protein family (Hsp40) member A2	1.624	0.0000	0.0000
Dnajb9	ENSMUSG00000014905	DnaJ heat shock protein family (Hsp40) member B9	1.842	0.0001	0.0003
Dnajc12	ENSMUSG00000036764	DnaJ heat shock protein family (Hsp40) member C12	1.654	0.0001	0.0002
Dnajc3	ENSMUSG00000022136	DnaJ heat shock protein family (Hsp40) member C3	1.661	0.0000	0.0001
Dnttip2	ENSMUSG00000039756	deoxynucleotidyltransferase, terminal, interacting protein 2	1.539	0.0156	0.0353
Dpf1	ENSMUSG00000030584	double PHD fingers 1	3.665	0.0239	0.0513
Dtwd2	ENSMUSG00000024505	DTW domain containing 2	2.372	0.0000	0.0000
Dusp6	ENSMUSG00000019960	dual specificity phosphatase 6	1.746	0.0000	0.0001
Dut	ENSMUSG00000027203	deoxyuridine triphosphatase	1.738	0.0000	0.0001
Dyrk1a	ENSMUSG00000022897	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1a	1.519	0.0000	0.0001
Dyrk1b	ENSMUSG00000002409	dual-specificity tyrosine-(Y)-phosphorylation regulated kinase 1b	1.516	0.0069	0.0173
E2f3	ENSMUSG00000016477	E2F transcription factor 3	1.716	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
E2f5	ENSMUSG00000027552	E2F transcription factor 5	1.599	0.0011	0.0034
Edn1	ENSMUSG00000021367	endothelin 1	1.571	0.0030	0.0083
Eef1akmt2	ENSMUSG00000030960	EEF1A lysine methyltransferase 2	1.520	0.0013	0.0039
Eef1b2	ENSMUSG00000025967	eukaryotic translation elongation factor 1 beta 2	1.580	0.0000	0.0000
Eef2-ps2	ENSMUSG00000082575	eukaryotic translation elongation factor 2, pseudogene 2	1.579	0.0328	0.0675
Efnb1	ENSMUSG00000031217	ephrin B1	1.699	0.0002	0.0006
Egr1	ENSMUSG00000038418	early growth response 1	2.301	0.0113	0.0267
Eif2s2	ENSMUSG00000074656	eukaryotic translation initiation factor 2, subunit 2 (beta)	1.560	0.0000	0.0000
Eif2s3x	ENSMUSG00000035150	eukaryotic translation initiation factor 2, subunit 3, structural gene X-linked	1.700	0.0000	0.0000
Eif3s6-ps1	ENSMUSG00000081629	eukaryotic translation initiation factor 3, subunit 6, pseudogene 1	2.428	0.0439	0.0866
Eif4a2	ENSMUSG00000022884	eukaryotic translation initiation factor 4A2	1.788	0.0000	0.0000
Enkur	ENSMUSG00000026679	enkurin, TRPC channel interacting protein	1.526	0.0151	0.0344
Epha8	ENSMUSG00000028661	Eph receptor A8	4.322	0.0351	0.0715
Etf1	ENSMUSG00000024360	eukaryotic translation termination factor 1	1.631	0.0000	0.0000
Etfa	ENSMUSG00000032314	electron transferring flavoprotein, alpha polypeptide	1.502	0.0000	0.0000
Etfdh	ENSMUSG00000027809	electron transferring flavoprotein, dehydrogenase	1.639	0.0000	0.0000
Etnk1	ENSMUSG00000030275	ethanolamine kinase 1	1.580	0.0000	0.0000
Exoc8	ENSMUSG00000074030	exocyst complex component 8	1.691	0.0000	0.0000
Ezh2	ENSMUSG00000029687	enhancer of zeste 2 polycomb repressive complex 2 subunit	2.326	0.0000	0.0000
F830016B08Rik	ENSMUSG00000090942	RIKEN cDNA F830016B08 gene	4.547	0.0000	0.0000
Fam149a	ENSMUSG00000070044	family with sequence similarity 149, member A	1.786	0.0004	0.0014
Fam161a	ENSMUSG00000049811	family with sequence similarity 161, member A	1.698	0.0026	0.0071
Fam181b	ENSMUSG00000051515	family with sequence similarity 181, member B	1.529	0.0439	0.0866
Fam199x	ENSMUSG00000042595	family with sequence similarity 199, X-linked	1.502	0.0000	0.0001
Fam216a	ENSMUSG00000029463	family with sequence similarity 216, member A	2.563	0.0000	0.0002
Fam78b	ENSMUSG00000060568	family with sequence similarity 78, member B	1.501	0.0019	0.0055
Fancf	ENSMUSG00000092118	Fanconi anemia, complementation group F	1.700	0.0149	0.0340
Fbxl17	ENSMUSG00000023965	F-box and leucine-rich repeat protein 17	1.588	0.0015	0.0044
Fbxo30	ENSMUSG00000047648	F-box protein 30	1.822	0.0001	0.0003
Fbxw7	ENSMUSG00000028086	F-box and WD-40 domain protein 7	1.714	0.0000	0.0000
Fdx2	ENSMUSG00000079677	ferredoxin 2	17.450	0.0488	0.0946
Fhad1	ENSMUSG00000051435	forkhead-associated (FHA) phosphopeptide binding domain 1	3.545	0.0113	0.0267

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fignl1	ENSMUSG00000035455	fidgetin-like 1	2.080	0.0123	0.0288
Fjx1	ENSMUSG00000075012	four jointed box 1	3.491	0.0049	0.0127
Fmr1	ENSMUSG00000000838	fragile X messenger ribonucleoprotein 1	1.517	0.0000	0.0001
Fosl2	ENSMUSG00000029135	fos-like antigen 2	1.542	0.0414	0.0824
Foxj3	ENSMUSG00000032998	forkhead box J3	1.745	0.0001	0.0002
Foxn3	ENSMUSG00000033713	forkhead box N3	1.509	0.0003	0.0011
Foxp1	ENSMUSG00000030067	forkhead box P1	1.523	0.0000	0.0001
Fst	ENSMUSG00000021765	follistatin	1.749	0.0175	0.0391
Fth1-ps	ENSMUSG00000084289	ferritin heavy polypeptide 1, pseudogene	3.424	0.0033	0.0091
Fxr1	ENSMUSG00000027680	FMR1 autosomal homolog 1	1.539	0.0000	0.0000
Fzd5	ENSMUSG00000045005	frizzled class receptor 5	1.595	0.0000	0.0000
Get4	ENSMUSG00000025858	golgi to ER traffic protein 4	1.664	0.0038	0.0100
Gid8	ENSMUSG00000027573	GID complex subunit 8	1.707	0.0000	0.0000
Gimap7	ENSMUSG00000043931	GTPase, IMAP family member 7	2.739	0.0379	0.0761
Gjc2	ENSMUSG00000043448	gap junction protein, gamma 2	2.752	0.0023	0.0066
Glce	ENSMUSG00000032252	glucuronyl C5-epimerase	1.531	0.0000	0.0002
Glrx2	ENSMUSG00000018196	glutaredoxin 2 (thioltransferase)	1.997	0.0000	0.0000
Gls	ENSMUSG00000026103	glutaminase	1.618	0.0000	0.0000
Gm10036	ENSMUSG00000058064	predicted gene 10036	2.196	0.0382	0.0768
Gm10069	ENSMUSG00000059659	predicted gene 10069	1.940	0.0001	0.0003
Gm10074	ENSMUSG00000101932	predicted gene 10074	5.211	0.0435	0.0858
Gm10167	ENSMUSG00000066554	predicted pseudogene 10167	1.972	0.0014	0.0041
Gm10366	ENSMUSG00000115767	predicted gene 10366	2.770	0.0024	0.0067
Gm10461	ENSMUSG00000107277	predicted gene 10461	1.826	0.0017	0.0051
Gm10817	ENSMUSG00000117710	predicted gene 10817	2.790	0.0271	0.0571
Gm11221	ENSMUSG00000082998	predicted gene 11221	6.253	0.0163	0.0367
Gm11581	ENSMUSG00000083355	predicted gene 11581	2.542	0.0147	0.0337
Gm11837	ENSMUSG00000086587	predicted gene 11837	2.478	0.0022	0.0063
Gm11847	ENSMUSG00000060989	predicted gene 11847	5.469	0.0081	0.0199
Gm12101	ENSMUSG00000083990	predicted gene 12101	3.291	0.0010	0.0030
Gm12295	ENSMUSG00000085162	predicted gene 12295	1.975	0.0000	0.0001
Gm12338	ENSMUSG00000081485	predicted gene 12338	1.754	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm12366	ENSMUSG00000082762	predicted gene 12366	3.908	0.0383	0.0770
Gm13091	ENSMUSG00000085213	predicted gene 13091	3.034	0.0102	0.0244
Gm13136	ENSMUSG00000081179	predicted gene 13136	2.953	0.0196	0.0433
Gm13179	ENSMUSG00000086018	predicted gene 13179	8.513	0.0317	0.0655
Gm13394	ENSMUSG00000083773	predicted gene 13394	1.527	0.0000	0.0000
Gm13421	ENSMUSG00000085929	predicted gene 13421	3.669	0.0139	0.0319
Gm14322	ENSMUSG00000078864	predicted gene 14322	2.367	0.0073	0.0182
Gm14890	ENSMUSG00000081209	predicted gene 14890	6.492	0.0011	0.0034
Gm15283	ENSMUSG00000087700	predicted gene 15283	1.602	0.0026	0.0071
Gm15419	ENSMUSG00000084783	predicted gene 15419	5.651	0.0122	0.0286
Gm15469	ENSMUSG00000107265	predicted gene 15469	3.990	0.0450	0.0883
Gm15543	ENSMUSG00000086863	predicted gene 15543	1.809	0.0012	0.0036
Gm15583	ENSMUSG00000080078	predicted gene 15583	2.118	0.0078	0.0192
Gm15728	ENSMUSG00000086075	predicted gene 15728	2.309	0.0204	0.0448
Gm15816	ENSMUSG00000086741	predicted gene 15816	3.288	0.0000	0.0000
Gm15856	ENSMUSG00000086527	predicted gene 15856	9.545	0.0008	0.0026
Gm15867	ENSMUSG00000089812	predicted gene 15867	5.828	0.0022	0.0062
Gm16576	ENSMUSG00000087543	predicted gene 16576	1.553	0.0001	0.0003
Gm17108	ENSMUSG00000091133	predicted gene 17108	10.843	0.0001	0.0003
Gm18588	ENSMUSG00000093402	predicted gene, 18588	1.801	0.0132	0.0307
Gm18706	ENSMUSG00000109882	predicted gene, 18706	3.401	0.0502	0.0968
Gm2027	ENSMUSG00000112795	predicted gene 2027	4.972	0.0137	0.0315
Gm20517	ENSMUSG00000023984	predicted gene 20517	2.730	0.0289	0.0604
Gm23969	ENSMUSG00000065258	predicted gene, 23969	26.854	0.0017	0.0050
Gm2451	ENSMUSG00000106574	predicted pseudogene 2451	3.982	0.0331	0.0679
Gm24616	ENSMUSG00000065208	predicted gene, 24616	15.563	0.0321	0.0662
Gm2619	ENSMUSG00000091199	predicted gene 2619	49.105	0.0004	0.0012
Gm26549	ENSMUSG00000097217	predicted gene, 26549	2.176	0.0119	0.0281
Gm26588	ENSMUSG00000097730	predicted gene, 26588	2.249	0.0156	0.0354
Gm26590	ENSMUSG00000097533	predicted gene, 26590	2.949	0.0425	0.0842
Gm26648	ENSMUSG00000097275	predicted gene, 26648	7.167	0.0032	0.0088
Gm26793	ENSMUSG00000096999	predicted gene, 26793	1.662	0.0516	0.0993

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm27151	ENSMUSG00000098739	predicted gene 27151	4.892	0.0499	0.0965
Gm28043	ENSMUSG00000098374	predicted gene, 28043	6.878	0.0004	0.0013
Gm28187	ENSMUSG00000099375	predicted gene 28187	7.245	0.0081	0.0199
Gm28523	ENSMUSG00000100707	predicted gene 28523	2.045	0.0012	0.0036
Gm29015	ENSMUSG00000101680	predicted gene 29015	1.946	0.0077	0.0191
Gm30698	ENSMUSG00000111090	predicted gene, 30698	4.337	0.0457	0.0895
Gm30735	ENSMUSG00000105168	predicted gene, 30735	3.034	0.0005	0.0016
Gm30934	ENSMUSG00000111082	predicted gene, 30934	2.230	0.0428	0.0846
Gm31659	ENSMUSG00000110489	predicted gene, 31659	1.620	0.0002	0.0006
Gm3200	ENSMUSG00000097388	predicted pseudogene 3200	1.807	0.0014	0.0042
Gm32391	ENSMUSG00000104011	predicted gene, 32391	1.558	0.0034	0.0092
Gm33023	ENSMUSG00000110652	predicted gene, 33023	1.919	0.0074	0.0183
Gm3411	ENSMUSG00000079396	predicted gene 3411	6.702	0.0362	0.0734
Gm3650	ENSMUSG00000097891	predicted gene 3650	1.832	0.0108	0.0257
Gm36989	ENSMUSG00000102496	predicted gene, 36989	3.360	0.0137	0.0316
Gm37083	ENSMUSG00000102852	predicted gene, 37083	6.392	0.0116	0.0274
Gm37120	ENSMUSG00000103966	predicted gene, 37120	8.710	0.0058	0.0147
Gm37309	ENSMUSG00000103046	predicted gene, 37309	3.108	0.0207	0.0454
Gm37415	ENSMUSG00000103864	predicted gene, 37415	5.504	0.0108	0.0257
Gm37499	ENSMUSG00000103901	predicted gene, 37499	1.919	0.0251	0.0535
Gm38190	ENSMUSG00000102302	predicted gene, 38190	2.881	0.0116	0.0274
Gm38393	ENSMUSG00000000948	predicted gene, 38393	2.682	0.0000	0.0000
Gm40477	ENSMUSG00000113940	predicted gene, 40477	2.361	0.0115	0.0272
Gm40841	ENSMUSG00000113216	predicted gene, 40841	2.328	0.0160	0.0361
Gm41717	ENSMUSG00000117919	predicted gene, 41717	1.659	0.0005	0.0018
Gm41757	ENSMUSG00000118163	predicted gene, 41757	7.538	0.0216	0.0470
Gm42432	ENSMUSG00000105962	predicted gene 42432	1.946	0.0046	0.0120
Gm42549	ENSMUSG00000107320	predicted gene 42549	3.197	0.0101	0.0242
Gm42636	ENSMUSG00000104682	predicted gene 42636	1.672	0.0276	0.0581
Gm42690	ENSMUSG00000106391	predicted gene 42690	3.136	0.0378	0.0761
Gm42734	ENSMUSG00000106999	predicted gene 42734	3.487	0.0014	0.0042
Gm42819	ENSMUSG00000105728	predicted gene 42819	3.269	0.0001	0.0004

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm42901	ENSMUSG00000104850	predicted gene 42901	1.796	0.0195	0.0430
Gm43457	ENSMUSG00000106678	predicted gene 43457	2.066	0.0291	0.0609
Gm43579	ENSMUSG00000107191	predicted gene 43579	10.975	0.0194	0.0428
Gm43808	ENSMUSG00000107086	predicted gene 43808	10.235	0.0008	0.0026
Gm43961	ENSMUSG00000107549	predicted gene, 43961	4.409	0.0422	0.0836
Gm44126	ENSMUSG00000107770	predicted gene, 44126	4.162	0.0237	0.0508
Gm44570	ENSMUSG00000109194	predicted gene 44570	5.751	0.0004	0.0014
Gm44616	ENSMUSG00000108701	predicted gene 44616	1.939	0.0231	0.0498
Gm4473	ENSMUSG00000086522	predicted gene 4473	3.397	0.0024	0.0066
Gm44954	ENSMUSG00000109205	predicted gene 44954	2.058	0.0084	0.0205
Gm45051	ENSMUSG00000108435	predicted gene 45051	2.122	0.0089	0.0217
Gm45112	ENSMUSG00000109304	predicted gene 45112	2.128	0.0095	0.0229
Gm45507	ENSMUSG00000109881	predicted gene 45507	59.209	0.0002	0.0007
Gm45527	ENSMUSG00000109618	predicted gene 45527	3.215	0.0181	0.0403
Gm45605	ENSMUSG00000109829	predicted gene 45605	1.837	0.0410	0.0817
Gm45760	ENSMUSG00000110711	predicted gene 45760	6.328	0.0100	0.0240
Gm45930	ENSMUSG00000113681	predicted gene, 45930	2.984	0.0356	0.0723
Gm46404	ENSMUSG00000113440	predicted gene, 46404	1.824	0.0001	0.0004
Gm47483	ENSMUSG00000111496	predicted gene, 47483	2.462	0.0237	0.0508
Gm47484	ENSMUSG00000113529	predicted gene, 47484	2.984	0.0002	0.0006
Gm47572	ENSMUSG00000112922	predicted gene, 47572	2.929	0.0000	0.0000
Gm47644	ENSMUSG00000112734	predicted gene, 47644	7.461	0.0000	0.0000
Gm4841	ENSMUSG00000068606	predicted gene 4841	33.154	0.0000	0.0000
Gm48488	ENSMUSG00000114433	predicted gene, 48488	2.982	0.0378	0.0761
Gm48878	ENSMUSG00000112794	predicted gene, 48878	1.865	0.0242	0.0519
Gm49227	ENSMUSG00000115469	predicted gene, 49227	9.079	0.0332	0.0681
Gm49336	ENSMUSG00000114797	predicted gene, 49336	1.594	0.0000	0.0000
Gm49759	ENSMUSG00000111394	predicted gene, 49759	1.917	0.0099	0.0238
Gm49774	ENSMUSG00000116657	predicted gene, 49774	2.987	0.0046	0.0121
Gm50107	ENSMUSG00000118239	predicted gene, 50107	2.019	0.0192	0.0425
Gm5112	ENSMUSG00000107868	predicted gene 5112	1.683	0.0156	0.0353
Gm5335	ENSMUSG00000098035	predicted gene 5335	2.548	0.0140	0.0322

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm56350	ENSMUSG00000103009	predicted gene, 56350	2.333	0.0001	0.0003
Gm5881	ENSMUSG00000107747	predicted gene 5881	7.284	0.0137	0.0316
Gm6123	ENSMUSG00000103922	predicted gene 6123	1.615	0.0295	0.0616
Gm6155	ENSMUSG00000068629	predicted pseudogene 6155	4.492	0.0028	0.0078
Gm6161	ENSMUSG00000081441	predicted gene 6161	5.043	0.0020	0.0057
Gm6392	ENSMUSG00000115503	predicted gene 6392	2.977	0.0226	0.0489
Gm6397	ENSMUSG00000089640	predicted gene 6397	13.166	0.0000	0.0002
Gm6430	ENSMUSG00000044757	predicted gene 6430	3.129	0.0101	0.0242
Gm6451	ENSMUSG00000084166	predicted gene 6451	2.148	0.0203	0.0446
Gm6467	ENSMUSG00000117327	predicted gene 6467	1.971	0.0124	0.0289
Gm6560	ENSMUSG00000104913	predicted gene 6560	1.608	0.0030	0.0083
Gm6598	ENSMUSG00000107143	predicted gene 6598	3.348	0.0194	0.0429
Gm6758	ENSMUSG00000081118	predicted gene 6758	6.338	0.0266	0.0562
Gm6793	ENSMUSG00000092086	predicted gene 6793	8.382	0.0002	0.0008
Gm6807	ENSMUSG00000057605	predicted gene 6807	2.186	0.0377	0.0758
Gm6863	ENSMUSG00000043483	predicted gene 6863	1.543	0.0362	0.0733
Gm7008	ENSMUSG00000035983	predicted gene 7008	2.005	0.0325	0.0669
Gm7224	ENSMUSG00000083623	predicted gene 7224	1.961	0.0219	0.0477
Gm7327	ENSMUSG00000050900	predicted gene 7327	2.086	0.0017	0.0050
Gm7432	ENSMUSG00000109610	predicted gene 7432	4.468	0.0154	0.0350
Gm7517	ENSMUSG00000115700	predicted gene 7517	2.723	0.0411	0.0817
Gm7859	ENSMUSG00000116089	predicted gene 7859	2.321	0.0016	0.0048
Gm8225	ENSMUSG00000068604	predicted gene 8225	2.975	0.0066	0.0167
Gm8228	ENSMUSG00000099779	predicted gene 8228	2.852	0.0231	0.0498
Gm8319	ENSMUSG00000108528	predicted gene 8319	4.595	0.0216	0.0470
Gm8797	ENSMUSG00000103034	predicted pseudogene 8797	3.774	0.0366	0.0739
Gm9104	ENSMUSG00000061242	predicted gene 9104	9.986	0.0029	0.0080
Gm9530	ENSMUSG00000096950	predicted gene 9530	4.048	0.0331	0.0679
Gm9887	ENSMUSG00000052673	predicted gene 9887	4.087	0.0000	0.0000
Gm9910	ENSMUSG00000103469	predicted gene 9910	2.992	0.0440	0.0867
Gm9988	ENSMUSG00000055968	predicted gene 9988	4.627	0.0230	0.0496
Gmfb	ENSMUSG00000062014	glia maturation factor, beta	1.668	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gnao1	ENSMUSG00000031748	guanine nucleotide binding protein, alpha O	1.645	0.0003	0.0010
Gnb1	ENSMUSG00000029064	guanine nucleotide binding protein (G protein), beta 1	1.549	0.0000	0.0000
Gng10	ENSMUSG00000038607	guanine nucleotide binding protein (G protein), gamma 10	4.396	0.0198	0.0437
Gng11	ENSMUSG00000032766	guanine nucleotide binding protein (G protein), gamma 11	1.592	0.0004	0.0013
Gpat3	ENSMUSG00000029314	glycerol-3-phosphate acyltransferase 3	1.640	0.0005	0.0016
Gpi-ps	ENSMUSG00000043192	glucose-6-phosphate isomerase, pseudogene	1.570	0.0251	0.0535
Gpr62	ENSMUSG00000091735	G protein-coupled receptor 62	4.437	0.0113	0.0268
Grik3	ENSMUSG00000001985	glutamate receptor, ionotropic, kainate 3	1.711	0.0351	0.0714
Gsk3b	ENSMUSG00000022812	glycogen synthase kinase 3 beta	1.644	0.0000	0.0000
Gspt1	ENSMUSG00000062203	G1 to S phase transition 1	1.597	0.0000	0.0000
Gspt2	ENSMUSG00000071723	G1 to S phase transition 2	1.938	0.0123	0.0287
Gtf2f2	ENSMUSG00000067995	general transcription factor IIF, polypeptide 2	1.507	0.0000	0.0000
Gvin2	ENSMUSG00000078606	GTPase, very large interferon inducible, family member 2	1.868	0.0078	0.0193
H2-Ke6	ENSMUSG00000073422	H2-K region expressed gene 6	6.860	0.0305	0.0634
H3f3a	ENSMUSG00000060743	H3.3 histone A	1.534	0.0000	0.0000
Hace1	ENSMUSG00000038822	HECT domain and ankyrin repeat containing, E3 ubiquitin protein ligase 1	1.674	0.0000	0.0000
Hcn4	ENSMUSG00000032338	hyperpolarization-activated, cyclic nucleotide-gated K+ 4	2.219	0.0000	0.0001
Heca	ENSMUSG00000039879	hdc homolog, cell cycle regulator	1.706	0.0001	0.0003
Herpud2	ENSMUSG00000008429	HERPUD family member 2	1.686	0.0002	0.0007
Hgsnat	ENSMUSG00000037260	heparan-alpha-glucosaminide N-acetyltransferase	1.563	0.0003	0.0011
Hlf	ENSMUSG00000003949	hepatic leukemia factor	1.514	0.0000	0.0000
Hmg20b	ENSMUSG00000020232	high mobility group 20B	2.095	0.0001	0.0003
Hmgb2	ENSMUSG00000054717	high mobility group box 2	1.742	0.0000	0.0000
Hnrnpf	ENSMUSG00000042079	heterogeneous nuclear ribonucleoprotein F	1.600	0.0000	0.0000
Homer1	ENSMUSG00000007617	homer scaffolding protein 1	1.723	0.0000	0.0000
Hook1	ENSMUSG00000028572	hook microtubule tethering protein 1	1.647	0.0000	0.0001
Hook3	ENSMUSG00000037234	hook microtubule tethering protein 3	1.521	0.0000	0.0000
Hoxa5	ENSMUSG00000038253	homeobox A5	2.280	0.0285	0.0597
Hoxb2	ENSMUSG00000075588	homeobox B2	2.142	0.0085	0.0209
Hpse	ENSMUSG00000035273	heparanase	1.598	0.0297	0.0618
Hspa14	ENSMUSG00000109865	heat shock protein 14	1.570	0.0000	0.0000
Hspa5	ENSMUSG00000026864	heat shock protein 5	1.569	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Htr7	ENSMUSG00000024798	5-hydroxytryptamine (serotonin) receptor 7	1.740	0.0152	0.0346
Ibtk	ENSMUSG00000035941	inhibitor of Bruton agammaglobulinemia tyrosine kinase	1.642	0.0000	0.0000
Ier2	ENSMUSG00000053560	immediate early response 2	1.922	0.0116	0.0274
Ifi202b	ENSMUSG00000026535	interferon activated gene 202B	1.555	0.0058	0.0149
Ifi35	ENSMUSG00000010358	interferon-induced protein 35	1.502	0.0000	0.0000
Ifit2	ENSMUSG00000045932	interferon-induced protein with tetratricopeptide repeats 2	1.570	0.0011	0.0033
Ifit3b	ENSMUSG00000062488	interferon-induced protein with tetratricopeptide repeats 3B	2.344	0.0001	0.0003
Ift80	ENSMUSG00000027778	intraflagellar transport 80	1.570	0.0001	0.0002
Iftap	ENSMUSG00000027165	intraflagellar transport associated protein	1.570	0.0000	0.0000
Igsf9b	ENSMUSG00000034275	immunoglobulin superfamily, member 9B	1.746	0.0034	0.0092
Igtp	ENSMUSG00000078853	interferon gamma induced GTPase	1.794	0.0103	0.0247
Iigp1	ENSMUSG00000054072	interferon inducible GTPase 1	2.084	0.0179	0.0398
Impa2	ENSMUSG00000024525	inositol monophosphatase 2	2.483	0.0000	0.0000
Inafm1	ENSMUSG00000091811	InaF motif containing 1	2.554	0.0000	0.0001
Ing2	ENSMUSG00000063049	inhibitor of growth family, member 2	1.957	0.0000	0.0001
Inka2	ENSMUSG00000048458	inka box actin regulator 2	1.637	0.0080	0.0196
Ints13	ENSMUSG00000040250	integrator complex subunit 13	1.553	0.0000	0.0000
Ints8	ENSMUSG00000040738	integrator complex subunit 8	1.527	0.0000	0.0000
Irak1bp1	ENSMUSG00000032251	interleukin-1 receptor-associated kinase 1 binding protein 1	1.717	0.0050	0.0130
Irgm2	ENSMUSG00000069874	immunity-related GTPase family M member 2	1.589	0.0108	0.0256
Irx2	ENSMUSG00000001504	Iroquois homeobox 2	2.947	0.0000	0.0001
Jakmip3	ENSMUSG00000056856	janus kinase and microtubule interacting protein 3	5.782	0.0326	0.0672
Jmjd7	ENSMUSG00000098789	jumonji domain containing 7	5.996	0.0346	0.0706
Jmy	ENSMUSG00000021690	junction-mediating and regulatory protein	1.734	0.0002	0.0008
Katnbl1	ENSMUSG00000027132	katanin p80 subunit B like 1	1.602	0.0001	0.0002
Kbtbd2	ENSMUSG00000059486	kelch repeat and BTB (POZ) domain containing 2	1.512	0.0000	0.0000
Kcna4	ENSMUSG00000042604	potassium voltage-gated channel, shaker-related subfamily, member 4	1.862	0.0273	0.0576
Kcnb1	ENSMUSG00000050556	potassium voltage gated channel, Shab-related subfamily, member 1	1.707	0.0000	0.0000
Kcng4	ENSMUSG00000045246	potassium voltage-gated channel, subfamily G, member 4	3.295	0.0067	0.0169
Kcnh2	ENSMUSG00000038319	potassium voltage-gated channel, subfamily H (eag-related), member 2	1.539	0.0250	0.0533
Kcnj10	ENSMUSG00000044708	potassium inwardly-rectifying channel, subfamily J, member 10	2.386	0.0154	0.0350
Kctd13	ENSMUSG00000030685	potassium channel tetramerisation domain containing 13	2.155	0.0006	0.0019

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kdm5d	ENSMUSG00000056673	lysine (K)-specific demethylase 5D	1.535	0.0000	0.0000
Kif14	ENSMUSG00000041498	kinesin family member 14	2.437	0.0022	0.0064
Kif20b	ENSMUSG00000024795	kinesin family member 20B	2.364	0.0001	0.0002
Klf10	ENSMUSG00000037465	Kruppel-like factor 10	2.045	0.0000	0.0000
Klf11	ENSMUSG00000020653	Kruppel-like factor 11	1.794	0.0000	0.0000
Klf5	ENSMUSG00000005148	Kruppel-like factor 5	2.749	0.0194	0.0429
Klhl12	ENSMUSG00000026455	kelch-like 12	1.636	0.0000	0.0000
Klhl20	ENSMUSG00000026705	kelch-like 20	1.653	0.0000	0.0000
Klhl31	ENSMUSG00000044938	kelch-like 31	1.668	0.0000	0.0000
Klhl9	ENSMUSG00000070923	kelch-like 9	1.583	0.0000	0.0000
Klrg2	ENSMUSG00000071537	killer cell lectin-like receptor subfamily G, member 2	2.194	0.0288	0.0603
Kmt5b	ENSMUSG00000045098	lysine methyltransferase 5B	1.542	0.0000	0.0000
Kpna4	ENSMUSG00000027782	karyopherin (importin) alpha 4	1.788	0.0000	0.0000
Ktn1	ENSMUSG00000021843	kinectin 1	1.537	0.0000	0.0000
Larp4b	ENSMUSG00000033499	La ribonucleoprotein domain family, member 4B	1.563	0.0000	0.0000
Lats2	ENSMUSG00000021959	large tumor suppressor 2	1.911	0.0000	0.0000
Lca5l	ENSMUSG00000045275	Leber congenital amaurosis 5-like	2.355	0.0000	0.0000
Ldlrad4	ENSMUSG00000024544	low density lipoprotein receptor class A domain containing 4	1.907	0.0000	0.0000
Lgals4	ENSMUSG00000053964	lectin, galactose binding, soluble 4	1.820	0.0130	0.0301
Lgi3	ENSMUSG00000033595	leucine-rich repeat LGI family, member 3	2.131	0.0000	0.0000
Lgr4	ENSMUSG00000050199	leucine-rich repeat-containing G protein-coupled receptor 4	1.523	0.0000	0.0000
Lhfp	ENSMUSG00000048332	lipoma HMGIC fusion partner	1.623	0.0000	0.0000
Lig1	ENSMUSG00000056394	ligase I, DNA, ATP-dependent	1.674	0.0003	0.0009
Lin7c	ENSMUSG00000027162	lin-7 homolog C, crumbs cell polarity complex component	1.706	0.0000	0.0000
Lingo1	ENSMUSG00000049556	leucine rich repeat and Ig domain containing 1	2.719	0.0050	0.0129
Lmtk3	ENSMUSG00000062044	lemur tyrosine kinase 3	10.326	0.0137	0.0316
Lpar4	ENSMUSG00000049929	lysophosphatidic acid receptor 4	1.748	0.0009	0.0029
Lrp6	ENSMUSG00000030201	low density lipoprotein receptor-related protein 6	1.601	0.0000	0.0000
Lrrc15	ENSMUSG00000052316	leucine rich repeat containing 15	12.936	0.0008	0.0026
Lrrc58	ENSMUSG00000034158	leucine rich repeat containing 58	1.537	0.0407	0.0812
Lrrfip1	ENSMUSG00000026305	leucine rich repeat (in FLII) interacting protein 1	1.531	0.0000	0.0000
Lrrfip2	ENSMUSG00000032497	leucine rich repeat (in FLII) interacting protein 2	1.541	0.0000	0.0001

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lsm3	ENSMUSG00000034192	LSM3 homolog, U6 small nuclear RNA and mRNA degradation associated	1.696	0.0001	0.0005
Lsm4	ENSMUSG00000031848	LSM4 homolog, U6 small nuclear RNA and mRNA degradation associated	2.029	0.0002	0.0008
Lsm5	ENSMUSG00000091625	LSM5 homolog, U6 small nuclear RNA and mRNA degradation associated	1.733	0.0001	0.0003
Ltb4r2	ENSMUSG00000040432	leukotriene B4 receptor 2	2.841	0.0141	0.0325
Lurap1l	ENSMUSG00000048706	leucine rich adaptor protein 1-like	1.574	0.0069	0.0173
Lyrm4	ENSMUSG00000046573	LYR motif containing 4	2.012	0.0000	0.0000
Macf1	ENSMUSG00000028649	microtubule-actin crosslinking factor 1	1.514	0.0000	0.0000
Maff	ENSMUSG00000042622	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein F (avian)	2.293	0.0369	0.0745
Map2k5	ENSMUSG00000058444	mitogen-activated protein kinase kinase 5	1.717	0.0002	0.0006
Mapk14	ENSMUSG00000053436	mitogen-activated protein kinase 14	1.538	0.0000	0.0000
Mapk9	ENSMUSG00000020366	mitogen-activated protein kinase 9	1.548	0.0000	0.0000
Mapre1	ENSMUSG00000027479	microtubule-associated protein, RP/EB family, member 1	1.520	0.0000	0.0000
Mat2a	ENSMUSG00000053907	methionine adenosyltransferase II, alpha	1.507	0.0000	0.0000
Mbd1	ENSMUSG00000024561	methyl-CpG binding domain protein 1	1.513	0.0283	0.0593
Mbtd1	ENSMUSG00000059474	mbt domain containing 1	1.757	0.0000	0.0000
Mbtps2	ENSMUSG00000046873	membrane-bound transcription factor peptidase, site 2	1.580	0.0000	0.0000
Mcur1	ENSMUSG00000021371	mitochondrial calcium uniporter regulator 1	1.546	0.0000	0.0001
Med13	ENSMUSG00000034297	mediator complex subunit 13	1.765	0.0000	0.0000
Mex3c	ENSMUSG00000037253	mex3 RNA binding family member C	1.803	0.0000	0.0000
Mir8116	ENSMUSG00000099145	microRNA 8116	4.576	0.0272	0.0573
Mlf2	ENSMUSG00000030120	myeloid leukemia factor 2	1.634	0.0005	0.0017
Mlkl	ENSMUSG00000012519	mixed lineage kinase domain-like	1.551	0.0007	0.0022
Mmd	ENSMUSG00000003948	monocyte to macrophage differentiation-associated	1.749	0.0006	0.0019
Mob1b	ENSMUSG00000006262	MOB kinase activator 1B	1.549	0.0000	0.0000
Mob3c	ENSMUSG00000028709	MOB kinase activator 3C	1.523	0.0002	0.0007
Mocs2	ENSMUSG00000015536	molybdenum cofactor synthesis 2	1.645	0.0000	0.0000
Morc4	ENSMUSG00000031434	microrchidia 4	1.500	0.0014	0.0043
Mrm1	ENSMUSG00000018405	mitochondrial rRNA methyltransferase 1	1.526	0.0002	0.0006
Mrps35	ENSMUSG00000040112	mitochondrial ribosomal protein S35	1.548	0.0000	0.0000
Mrto4	ENSMUSG00000028741	mRNA turnover 4, ribosome maturation factor	1.762	0.0001	0.0004
Msi2	ENSMUSG00000069769	musashi RNA-binding protein 2	1.606	0.0000	0.0000
Msl2	ENSMUSG00000066415	MSL complex subunit 2	1.685	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Msl3l2	ENSMUSG00000047669	MSL3 like 2	2.257	0.0061	0.0154
Msrb3	ENSMUSG00000051236	methionine sulfoxide reductase B3	1.820	0.0000	0.0000
Mtdh	ENSMUSG00000022255	metadherin	1.780	0.0000	0.0000
Mterf1a	ENSMUSG00000040429	mitochondrial transcription termination factor 1a	1.875	0.0001	0.0005
Mthfs	ENSMUSG00000066442	5, 10-methenyltetrahydrofolate synthetase	2.118	0.0247	0.0528
mt-Nd2	ENSMUSG00000064345	mitochondrially encoded NADH dehydrogenase 2	1.562	0.0000	0.0000
mt-Nd5	ENSMUSG00000064367	mitochondrially encoded NADH dehydrogenase 5	1.862	0.0000	0.0000
mt-Te	ENSMUSG00000064369	mitochondrially encoded tRNA glutamic acid	2.991	0.0003	0.0010
mt-Tq	ENSMUSG00000064343	mitochondrially encoded tRNA glutamine	3.651	0.0000	0.0000
Mtx2	ENSMUSG00000027099	metaxin 2	1.718	0.0000	0.0000
Mycbp	ENSMUSG00000028647	MYC binding protein	1.507	0.0000	0.0000
Naa15	ENSMUSG00000063273	N(alpha)-acetyltransferase 15, NatA auxiliary subunit	1.629	0.0000	0.0000
Nacc2	ENSMUSG00000026932	nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	1.511	0.0010	0.0030
Nadk2	ENSMUSG00000022253	NAD kinase 2, mitochondrial	1.589	0.0002	0.0008
Nap1l4	ENSMUSG00000059119	nucleosome assembly protein 1-like 4	1.504	0.0000	0.0000
Ncam2	ENSMUSG00000022762	neural cell adhesion molecule 2	18.665	0.0109	0.0259
Nck1	ENSMUSG00000032475	non-catalytic region of tyrosine kinase adaptor protein 1	1.574	0.0000	0.0000
Ncoa4	ENSMUSG00000056234	nuclear receptor coactivator 4	1.577	0.0000	0.0000
Ndc80	ENSMUSG00000024056	NDC80 kinetochore complex component	2.040	0.0300	0.0625
Nectin1	ENSMUSG00000032012	nectin cell adhesion molecule 1	1.528	0.0253	0.0538
Nenf	ENSMUSG00000037499	neuron derived neurotrophic factor	1.510	0.0372	0.0751
Nfatc2	ENSMUSG00000027544	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 2	1.934	0.0017	0.0050
Nfia	ENSMUSG00000028565	nuclear factor I/A	1.589	0.0000	0.0000
Nfkbiz	ENSMUSG00000035356	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, zeta	1.506	0.0192	0.0425
Nipa2	ENSMUSG00000030452	non imprinted in Prader-Willi/Angelman syndrome 2 homolog (human)	1.586	0.0000	0.0001
Nkd1	ENSMUSG00000031661	naked cuticle 1	2.384	0.0078	0.0192
Nkrf	ENSMUSG00000044149	NF-kappaB repressing factor	1.572	0.0003	0.0012
Nlrp5-ps	ENSMUSG00000041596	NLR family, pyrin domain containing 5, pseudogene	2.499	0.0263	0.0556
Nol10	ENSMUSG00000061458	nucleolar protein 10	1.590	0.0000	0.0000
Nom1	ENSMUSG00000001569	nucleolar protein with MIF4G domain 1	1.560	0.0000	0.0000
Nos1ap	ENSMUSG00000038473	nitric oxide synthase 1 (neuronal) adaptor protein	1.878	0.0043	0.0112
Npepps	ENSMUSG00000001441	aminopeptidase puromycin sensitive	1.570	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nr1d2	ENSMUSG00000021775	nuclear receptor subfamily 1, group D, member 2	1.558	0.0000	0.0000
Nrk	ENSMUSG00000052854	Nik related kinase	1.835	0.0097	0.0233
Nrp2	ENSMUSG00000025969	neuropilin 2	1.610	0.0005	0.0017
Nrxn2	ENSMUSG00000033768	neurexin II	2.645	0.0001	0.0004
Nsmce1	ENSMUSG00000030750	NSE1 homolog, SMC5-SMC6 complex component	1.575	0.0000	0.0000
Nsun2	ENSMUSG00000021595	NOL1/NOP2/Sun domain family member 2	1.625	0.0000	0.0000
Nt5c1a	ENSMUSG00000054958	5'-nucleotidase, cytosolic IA	1.740	0.0151	0.0343
Nuf2	ENSMUSG00000026683	NUF2, NDC80 kinetochore complex component	2.569	0.0234	0.0503
Nup50	ENSMUSG00000016619	nucleoporin 50	1.543	0.0000	0.0000
Nus1	ENSMUSG00000023068	NUS1 dehydrodolichyl diphosphate synthase subunit	1.600	0.0000	0.0000
Odad4	ENSMUSG00000006784	outer dynein arm complex subunit 4	23.190	0.0000	0.0000
Oga	ENSMUSG00000025220	O-GlcNAcase	1.545	0.0000	0.0001
Osbpl9	ENSMUSG00000028559	oxysterol binding protein-like 9	1.659	0.0000	0.0000
Otogl	ENSMUSG00000091455	otogelin-like	17.238	0.0075	0.0186
Otud4	ENSMUSG00000036990	OTU domain containing 4	1.746	0.0000	0.0000
Oxr1	ENSMUSG00000022307	oxidation resistance 1	1.722	0.0000	0.0000
P4ha3	ENSMUSG00000051048	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha polypeptide III	3.218	0.0434	0.0856
Pafah1b2	ENSMUSG00000003131	platelet-activating factor acetylhydrolase, isoform 1b, subunit 2	1.718	0.0000	0.0000
Parg	ENSMUSG00000021911	poly (ADP-ribose) glycohydrolase	1.600	0.0000	0.0000
Particl	ENSMUSG00000108591	promoter of Mat2a antisense radiation induced circulating long non-coding RNA	3.070	0.0000	0.0000
Patl1	ENSMUSG00000046139	protein associated with topoisomerase II homolog 1 (yeast)	1.532	0.0001	0.0002
Pcdhb22	ENSMUSG00000073591	protocadherin beta 22	1.521	0.0144	0.0330
Pcmt1	ENSMUSG00000019795	protein-L-isoaspartate (D-aspartate) O-methyltransferase 1	1.543	0.0000	0.0000
Pcmtd2	ENSMUSG00000027589	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2	1.608	0.0000	0.0000
Pcna	ENSMUSG00000027342	proliferating cell nuclear antigen	1.818	0.0000	0.0000
Pcnp	ENSMUSG00000071533	PEST proteolytic signal containing nuclear protein	1.513	0.0000	0.0000
Pcyox1l	ENSMUSG00000024579	prenylcysteine oxidase 1 like	1.657	0.0266	0.0563
Pcyt1b	ENSMUSG00000035246	phosphate cytidylyltransferase 1, choline, beta isoform	2.438	0.0320	0.0661
Pdcd5-ps	ENSMUSG00000102824	programmed cell death 5, pseudogene	1.713	0.0017	0.0050
Pdgfa	ENSMUSG00000025856	platelet derived growth factor, alpha	1.507	0.0004	0.0012
Pdk1	ENSMUSG00000006494	pyruvate dehydrogenase kinase, isoenzyme 1	1.521	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pdk4	ENSMUSG00000019577	pyruvate dehydrogenase kinase, isoenzyme 4	3.703	0.0001	0.0003
Pdzd4	ENSMUSG00000002006	PDZ domain containing 4	1.811	0.0001	0.0004
Pdzd9	ENSMUSG00000030887	PDZ domain containing 9	8.897	0.0043	0.0114
Peli1	ENSMUSG00000020134	pellino 1	1.746	0.0005	0.0015
Pex11a	ENSMUSG00000030545	peroxisomal biogenesis factor 11 alpha	1.509	0.0000	0.0000
Pex13	ENSMUSG00000020283	peroxisomal biogenesis factor 13	1.757	0.0003	0.0009
Pfdn4	ENSMUSG00000052033	prefoldin 4	1.548	0.0000	0.0001
Phf12	ENSMUSG00000037791	PHD finger protein 12	1.513	0.0009	0.0028
Phf14	ENSMUSG00000029629	PHD finger protein 14	1.605	0.0000	0.0000
Phf8	ENSMUSG00000041229	PHD finger protein 8	1.685	0.0000	0.0000
Pi15	ENSMUSG00000067780	peptidase inhibitor 15	1.574	0.0000	0.0001
Pikfyve	ENSMUSG00000025949	phosphoinositide kinase, FYVE type zinc finger containing	1.626	0.0000	0.0000
Pja2	ENSMUSG00000024083	praja ring finger ubiquitin ligase 2	1.519	0.0000	0.0000
Pkib	ENSMUSG00000019876	protein kinase inhibitor beta, cAMP dependent, testis specific	1.801	0.0182	0.0406
Plaa	ENSMUSG00000028577	phospholipase A2, activating protein	1.583	0.0000	0.0000
Plekhf2	ENSMUSG00000049969	pleckstrin homology domain containing, family F (with FYVE domain) member 2	1.860	0.0000	0.0001
Plin1	ENSMUSG00000030546	perilipin 1	3.828	0.0062	0.0156
Plk4	ENSMUSG00000025758	polo like kinase 4	1.572	0.0086	0.0211
Pole4	ENSMUSG00000030042	polymerase (DNA-directed), epsilon 4 (p12 subunit)	1.865	0.0031	0.0084
Ppargc1a	ENSMUSG00000029167	peroxisome proliferative activated receptor, gamma, coactivator 1 alpha	1.589	0.0000	0.0001
Ppm1e	ENSMUSG00000046442	protein phosphatase 1E (PP2C domain containing)	1.509	0.0135	0.0312
Ppme1	ENSMUSG00000030718	protein phosphatase methylesterase 1	1.527	0.0000	0.0000
Ppp1ccb	ENSMUSG00000100153	protein phosphatase 1 catalytic subunit gamma B	1.636	0.0491	0.0951
Ppp1r14c	ENSMUSG00000040653	protein phosphatase 1, regulatory inhibitor subunit 14C	1.512	0.0114	0.0268
Ppp1r1b	ENSMUSG00000061718	protein phosphatase 1, regulatory inhibitor subunit 1B	2.202	0.0036	0.0096
Ppp1r3b	ENSMUSG00000046794	protein phosphatase 1, regulatory subunit 3B	1.885	0.0004	0.0014
Ppp1r3e	ENSMUSG00000072494	protein phosphatase 1, regulatory subunit 3E	2.903	0.0038	0.0101
Ppp2r5e	ENSMUSG00000021051	protein phosphatase 2, regulatory subunit B', epsilon	1.586	0.0004	0.0012
Ppp3ca	ENSMUSG00000028161	protein phosphatase 3, catalytic subunit, alpha isoform	1.517	0.0000	0.0000
Ppp4r2	ENSMUSG00000052144	protein phosphatase 4, regulatory subunit 2	1.758	0.0000	0.0000
Prc1	ENSMUSG00000038943	protein regulator of cytokinesis 1	1.732	0.0269	0.0568
Prkag2	ENSMUSG00000028944	protein kinase, AMP-activated, gamma 2 non-catalytic subunit	1.808	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Prkar2b	ENSMUSG00000002997	protein kinase, cAMP dependent regulatory, type II beta	1.681	0.0141	0.0323
Prpf38a	ENSMUSG00000063800	PRP38 pre-mRNA processing factor 38 (yeast) domain containing A	1.564	0.0000	0.0000
Prpf40a	ENSMUSG00000061136	pre-mRNA processing factor 40A	1.617	0.0000	0.0000
Prpf4b	ENSMUSG00000021413	pre-mRNA processing factor 4B	1.514	0.0001	0.0003
Prrg3	ENSMUSG00000033361	proline rich Gla (G-carboxyglutamic acid) 3 (transmembrane)	1.565	0.0006	0.0020
Prrg4	ENSMUSG00000027171	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)	1.789	0.0175	0.0392
Psd	ENSMUSG00000037126	pleckstrin and Sec7 domain containing	2.400	0.0107	0.0255
Psma3	ENSMUSG00000060073	proteasome subunit alpha 3	1.529	0.0000	0.0000
Psma5-ps	ENSMUSG00000050490	proteasome subunit alpha 5, pseudogene	2.666	0.0181	0.0404
Pspc1	ENSMUSG00000021938	paraspeckle protein 1	1.538	0.0021	0.0059
Ptch1	ENSMUSG00000021466	patched 1	1.631	0.0007	0.0021
Ptger1	ENSMUSG00000019464	prostaglandin E receptor 1 (subtype EP1)	2.484	0.0068	0.0170
Ptgr1	ENSMUSG00000028378	prostaglandin reductase 1	1.545	0.0010	0.0029
Pth1r	ENSMUSG00000032492	parathyroid hormone 1 receptor	1.658	0.0025	0.0069
Ptov1	ENSMUSG00000038502	prostate tumor over expressed gene 1	1.606	0.0067	0.0169
Ptp4a1	ENSMUSG00000026064	protein tyrosine phosphatase 4a1	6.018	0.0003	0.0012
Ptp4a2	ENSMUSG00000028788	protein tyrosine phosphatase 4a2	1.686	0.0000	0.0000
Ptpn9	ENSMUSG00000032290	protein tyrosine phosphatase, non-receptor type 9	1.682	0.0005	0.0015
Ptprk	ENSMUSG00000019889	protein tyrosine phosphatase, receptor type, K	1.716	0.0000	0.0000
Rab11fip4	ENSMUSG00000017639	RAB11 family interacting protein 4 (class II)	4.229	0.0059	0.0150
Rab6a	ENSMUSG00000030704	RAB6A, member RAS oncogene family	1.776	0.0000	0.0000
Rabgap1l	ENSMUSG00000026721	RAB GTPase activating protein 1-like	1.679	0.0000	0.0000
Rabggtb	ENSMUSG00000038975	Rab geranylgeranyl transferase, b subunit	1.670	0.0000	0.0000
Rad50	ENSMUSG00000020380	RAD50 double strand break repair protein	1.567	0.0000	0.0000
Rad54l2	ENSMUSG00000040661	RAD54 like 2 (S. cerevisiae)	1.521	0.0000	0.0000
Rbfox2	ENSMUSG00000033565	RNA binding protein, fox-1 homolog (C. elegans) 2	1.567	0.0000	0.0000
Rbm39	ENSMUSG00000027620	RNA binding motif protein 39	1.605	0.0000	0.0000
Rbm4	ENSMUSG00000094936	RNA binding motif protein 4	1.886	0.0001	0.0005
Rbm47	ENSMUSG00000070780	RNA binding motif protein 47	1.874	0.0276	0.0580
Rbms1	ENSMUSG00000026970	RNA binding motif, single stranded interacting protein 1	1.580	0.0000	0.0000
Rc3h2	ENSMUSG00000075376	ring finger and CCCH-type zinc finger domains 2	1.558	0.0000	0.0000
Rcn2	ENSMUSG00000032320	reticulocalbin 2	1.523	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rdx	ENSMUSG00000032050	radixin	1.581	0.0000	0.0000
Rell2	ENSMUSG00000044024	RELT-like 2	3.097	0.0499	0.0965
Rev1	ENSMUSG00000026082	REV1, DNA directed polymerase	1.543	0.0069	0.0172
Rexo2	ENSMUSG00000032026	RNA exonuclease 2	1.516	0.0000	0.0000
Rfk	ENSMUSG00000024712	riboflavin kinase	2.024	0.0000	0.0000
Rgmb	ENSMUSG00000048027	repulsive guidance molecule family member B	1.565	0.0000	0.0000
Rgs16	ENSMUSG00000026475	regulator of G-protein signaling 16	1.714	0.0299	0.0622
Rgs7	ENSMUSG00000026527	regulator of G protein signaling 7	1.901	0.0013	0.0039
Rhox2h	ENSMUSG00000079627	reproductive homeobox 2H	5.269	0.0156	0.0354
Riox1	ENSMUSG00000046791	ribosomal oxygenase 1	2.040	0.0030	0.0083
Rnd3	ENSMUSG00000017144	Rho family GTPase 3	1.775	0.0000	0.0000
Rnf111	ENSMUSG00000032217	ring finger 111	1.640	0.0000	0.0000
Rnf152	ENSMUSG00000047496	ring finger protein 152	1.688	0.0000	0.0000
Rnf168	ENSMUSG00000014074	ring finger protein 168	1.749	0.0000	0.0000
Rnf187	ENSMUSG00000020496	ring finger protein 187	1.696	0.0001	0.0004
Rnf19a	ENSMUSG00000022280	ring finger protein 19A	1.515	0.0001	0.0002
Rnf227	ENSMUSG00000043419	ring finger protein 227	1.887	0.0301	0.0625
Rnf38	ENSMUSG00000035696	ring finger protein 38	1.573	0.0023	0.0066
Rora	ENSMUSG00000032238	RAR-related orphan receptor alpha	1.520	0.0240	0.0514
Rp1	ENSMUSG00000025900	retinitis pigmentosa 1 (human)	1.767	0.0149	0.0339
Rpf2	ENSMUSG00000038510	ribosome production factor 2 homolog	1.652	0.0000	0.0000
Rpl13a	ENSMUSG00000074129	ribosomal protein L13A	1.745	0.0000	0.0001
Rpl24	ENSMUSG00000098274	ribosomal protein L24	5.499	0.0202	0.0444
Rpl31-ps17	ENSMUSG00000072255	ribosomal protein L31, pseudogene 17	5.151	0.0212	0.0463
Rprml	ENSMUSG00000046215	reprimo-like	5.679	0.0010	0.0030
Rps18-ps4	ENSMUSG00000097346	ribosomal protein S18, pseudogene 4	5.804	0.0007	0.0022
Rps19bp1	ENSMUSG00000051518	ribosomal protein S19 binding protein 1	1.948	0.0100	0.0240
Rps2-ps11	ENSMUSG00000104280	ribosomal protein S2, pseudogene 11	5.221	0.0016	0.0048
Rps2-ps6	ENSMUSG00000095427	ribosomal protein S2, pseudogene 6	5.053	0.0069	0.0172
Rps7	ENSMUSG00000061477	ribosomal protein S7	1.555	0.0000	0.0000
Rpusd2	ENSMUSG00000027324	RNA pseudouridylate synthase domain containing 2	2.045	0.0000	0.0000
Rsbn1l	ENSMUSG00000039968	round spermatid basic protein 1-like	1.604	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rsph1	ENSMUSG00000024033	radial spoke head 1 homolog (Chlamydomonas)	1.767	0.0160	0.0362
Rtca	ENSMUSG00000000339	RNA 3'-terminal phosphate cyclase	1.564	0.0000	0.0000
Rtp3	ENSMUSG00000066319	receptor transporter protein 3	1.734	0.0001	0.0003
Satb2	ENSMUSG00000038331	special AT-rich sequence binding protein 2	2.040	0.0262	0.0555
Sbno1	ENSMUSG00000038095	strawberry notch 1	1.743	0.0000	0.0000
Scarna2	ENSMUSG00000088185	small Cajal body-specific RNA 2	9.050	0.0054	0.0139
Sclt1	ENSMUSG00000059834	sodium channel and clathrin linker 1	1.569	0.0002	0.0008
Sde2	ENSMUSG00000038806	SDE2 telomere maintenance homolog (S. pombe)	1.571	0.0000	0.0000
Selenoi	ENSMUSG00000075703	selenoprotein I	1.698	0.0000	0.0000
Selenot	ENSMUSG00000075700	selenoprotein T	1.808	0.0000	0.0000
Senp6	ENSMUSG00000034252	SUMO/sentrin specific peptidase 6	1.623	0.0000	0.0000
Serinc4	ENSMUSG00000046110	serine incorporator 4	3.692	0.0477	0.0928
Serpina1b	ENSMUSG00000071178	serine (or cysteine) preptidase inhibitor, clade A, member 1B	1.564	0.0423	0.0838
Setx	ENSMUSG00000043535	senataxin	1.511	0.0000	0.0000
Sf1	ENSMUSG00000024949	splicing factor 1	1.503	0.0000	0.0001
Shc4	ENSMUSG00000035109	SHC (Src homology 2 domain containing) family, member 4	1.868	0.0001	0.0004
Shox2	ENSMUSG00000027833	short stature homeobox 2	2.636	0.0225	0.0488
Shroom3	ENSMUSG00000029381	shroom family member 3	1.944	0.0002	0.0008
Six4	ENSMUSG00000034460	sine oculis-related homeobox 4	1.565	0.0018	0.0052
Skil	ENSMUSG00000027660	SKI-like	1.659	0.0000	0.0000
Slain1	ENSMUSG00000055717	SLAIN motif family, member 1	4.566	0.0249	0.0531
Slc16a1	ENSMUSG00000032902	solute carrier family 16 (monocarboxylic acid transporters), member 1	1.536	0.0001	0.0003
Slc16a10	ENSMUSG00000019838	solute carrier family 16 (monocarboxylic acid transporters), member 10	1.537	0.0009	0.0028
Slc25a32	ENSMUSG00000022299	solute carrier family 25, member 32	1.796	0.0000	0.0000
Slc29a4	ENSMUSG00000050822	solute carrier family 29 (nucleoside transporters), member 4	2.859	0.0024	0.0068
Slc30a1	ENSMUSG00000037434	solute carrier family 30 (zinc transporter), member 1	1.566	0.0000	0.0000
Slc30a5	ENSMUSG00000021629	solute carrier family 30 (zinc transporter), member 5	1.686	0.0000	0.0000
Slc35g1	ENSMUSG00000044026	solute carrier family 35, member G1	1.560	0.0042	0.0111
Slc5a1	ENSMUSG00000011034	solute carrier family 5 (sodium/glucose cotransporter), member 1	2.020	0.0018	0.0053
Slc7a6os	ENSMUSG00000033106	solute carrier family 7, member 6 opposite strand	1.504	0.0001	0.0005
Slc8a3	ENSMUSG00000079055	solute carrier family 8 (sodium/calcium exchanger), member 3	3.917	0.0239	0.0513
Slfn5	ENSMUSG00000054404	schlafen 5	1.625	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Smad2	ENSMUSG00000024563	SMAD family member 2	1.534	0.0000	0.0000
Smarca5-ps	ENSMUSG00000052912	SWI/SNF related, matrix associated, actin depenent ragulator of chromatin, subfamily a, member 5, pseudogene	2.606	0.0203	0.0446
Smc2	ENSMUSG00000028312	structural maintenance of chromosomes 2	1.653	0.0059	0.0150
Smc5	ENSMUSG00000024943	structural maintenance of chromosomes 5	1.716	0.0000	0.0000
Smim19	ENSMUSG00000031534	small integral membrane protein 19	1.798	0.0001	0.0003
Smkr-ps	ENSMUSG00000045709	smal lysine rich protein 1, pseudogene	5.414	0.0475	0.0925
Sms	ENSMUSG00000071708	spermine synthase	1.508	0.0000	0.0001
Snhg12	ENSMUSG00000086290	small nucleolar RNA host gene 12	1.603	0.0353	0.0718
Snhg14	ENSMUSG00000100826	small nucleolar RNA host gene 14	2.586	0.0005	0.0016
Snord104	ENSMUSG00000065126	small nucleolar RNA, C/D box 104	2.246	0.0076	0.0188
Snord72	ENSMUSG00000077737	small nucleolar RNA, C/D box 72	5.083	0.0004	0.0015
Snrpn	ENSMUSG00000102252	small nuclear ribonucleoprotein N	2.143	0.0000	0.0000
Snx18	ENSMUSG00000042364	sorting nexin 18	1.517	0.0012	0.0036
Snx4	ENSMUSG00000022808	sorting nexin 4	1.560	0.0000	0.0000
Soat1	ENSMUSG00000026600	sterol O-acyltransferase 1	1.516	0.0013	0.0039
Sox30	ENSMUSG00000040489	SRY (sex determining region Y)-box 30	3.479	0.0205	0.0450
Spata5l1	ENSMUSG00000118663	spermatogenesis associated 5-like 1	1.670	0.0031	0.0086
Spata6l	ENSMUSG00000064202	spermatogenesis associated 6 like	1.573	0.0000	0.0000
Speg	ENSMUSG00000026207	SPEG complex locus	1.572	0.0002	0.0007
Spi1	ENSMUSG00000002111	spleen focus forming virus (SFFV) proviral integration oncogene	2.041	0.0123	0.0287
Spin4	ENSMUSG00000071722	spindlin family, member 4	1.646	0.0336	0.0688
Sprtn	ENSMUSG00000031986	SprT-like N-terminal domain	1.637	0.0000	0.0000
Srcap	ENSMUSG00000053877	Snf2-related CREBBP activator protein	2.138	0.0000	0.0001
Srm	ENSMUSG00000006442	spermidine synthase	1.853	0.0033	0.0089
Srsf10	ENSMUSG00000028676	serine and arginine-rich splicing factor 10	1.533	0.0007	0.0021
Srsf4	ENSMUSG00000028911	serine and arginine-rich splicing factor 4	1.549	0.0000	0.0000
Srsf6	ENSMUSG00000016921	serine and arginine-rich splicing factor 6	1.546	0.0000	0.0000
Ssr3	ENSMUSG00000027828	signal sequence receptor, gamma	1.558	0.0000	0.0000
St3gal4	ENSMUSG00000032038	ST3 beta-galactoside alpha-2,3-sialyltransferase 4	1.593	0.0007	0.0021
Stard10	ENSMUSG00000030688	START domain containing 10	1.528	0.0000	0.0000
Steap4	ENSMUSG00000012428	STEAP family member 4	1.502	0.0021	0.0060

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Stx6	ENSMUSG00000026470	syntaxin 6	1.672	0.0022	0.0062
Suco	ENSMUSG00000040297	SUN domain containing ossification factor	1.569	0.0000	0.0000
Sugct	ENSMUSG00000055137	succinyl-CoA glutarate-CoA transferase	1.517	0.0142	0.0326
Syap1	ENSMUSG00000031357	synapse associated protein 1	2.093	0.0000	0.0000
Syde2	ENSMUSG00000036863	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)	1.675	0.0000	0.0001
Syn3	ENSMUSG00000059602	synapsin III	2.592	0.0226	0.0489
Syncrip	ENSMUSG00000032423	synaptotagmin binding, cytoplasmic RNA interacting protein	1.596	0.0000	0.0000
Syt7	ENSMUSG00000024743	synaptotagmin VII	1.694	0.0007	0.0023
Taf1	ENSMUSG00000031314	TATA-box binding protein associated factor 1	1.543	0.0000	0.0000
Tarsl2	ENSMUSG00000030515	threonyl-tRNA synthetase-like 2	1.802	0.0000	0.0000
Tbca	ENSMUSG00000042043	tubulin cofactor A	1.820	0.0000	0.0000
Tbk1	ENSMUSG00000020115	TANK-binding kinase 1	1.508	0.0001	0.0005
Tbpl1	ENSMUSG00000071359	TATA box binding protein-like 1	1.572	0.0000	0.0000
Tceal8	ENSMUSG00000051579	transcription elongation factor A (SII)-like 8	1.590	0.0000	0.0001
Tchh	ENSMUSG00000052415	trichohyalin	1.624	0.0013	0.0039
Tdg	ENSMUSG00000034674	thymine DNA glycosylase	2.833	0.0000	0.0002
Tdrkh	ENSMUSG00000041912	tudor and KH domain containing protein	1.605	0.0011	0.0032
Tes3-ps	ENSMUSG00000113255	testis derived transcript 3, pseudogene	1.592	0.0029	0.0080
Tex30	ENSMUSG00000026049	testis expressed 30	2.117	0.0000	0.0000
Tfec	ENSMUSG00000029553	transcription factor EC	2.494	0.0330	0.0678
Tgs1	ENSMUSG00000028233	trimethylguanosine synthase 1	1.521	0.0000	0.0000
Tlk1	ENSMUSG00000041997	tousled-like kinase 1	1.577	0.0000	0.0000
Tlnrd1	ENSMUSG00000070462	talin rod domain containing 1	2.550	0.0017	0.0050
Tmem138	ENSMUSG00000024666	transmembrane protein 138	1.755	0.0010	0.0031
Tmem170b	ENSMUSG00000087370	transmembrane protein 170B	1.579	0.0002	0.0007
Tmem201	ENSMUSG00000044700	transmembrane protein 201	1.519	0.0001	0.0004
Tmem250-ps	ENSMUSG00000087679	transmembrane protein 250, pseudogene	2.022	0.0003	0.0011
Tmem263	ENSMUSG00000060935	transmembrane protein 263	1.799	0.0000	0.0000
Tmem30a	ENSMUSG00000032328	transmembrane protein 30A	1.734	0.0000	0.0000
Tmem87a	ENSMUSG00000033808	transmembrane protein 87A	1.806	0.0000	0.0000
Tmx4	ENSMUSG00000034723	thioredoxin-related transmembrane protein 4	1.505	0.0000	0.0000
Tnfsf10	ENSMUSG00000039304	tumor necrosis factor (ligand) superfamily, member 10	1.516	0.0092	0.0222

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tnks2	ENSMUSG00000024811	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase 2	1.802	0.0000	0.0000
Tnrc6b	ENSMUSG00000047888	trinucleotide repeat containing 6b	1.502	0.0000	0.0000
Tob1	ENSMUSG00000037573	transducer of ErbB-2.1	1.774	0.0000	0.0000
Tomt	ENSMUSG00000078630	transmembrane O-methyltransferase	10.047	0.0019	0.0054
Top2a	ENSMUSG00000020914	topoisomerase (DNA) II alpha	1.869	0.0168	0.0377
Tox	ENSMUSG00000041272	thymocyte selection-associated high mobility group box	2.366	0.0000	0.0001
Trim34a	ENSMUSG00000056144	tripartite motif-containing 34A	1.947	0.0004	0.0013
Trim47	ENSMUSG00000020773	tripartite motif-containing 47	1.814	0.0061	0.0155
Trmt10c	ENSMUSG00000044763	tRNA methyltransferase 10C, mitochondrial RNase P subunit	1.507	0.0000	0.0000
Trnau1ap	ENSMUSG00000028898	tRNA selenocysteine 1 associated protein 1	1.685	0.0025	0.0070
Trp53rka	ENSMUSG00000039725	transformation related protein 53 regulating kinase A	1.845	0.0000	0.0000
Tspyl1	ENSMUSG00000047514	testis-specific protein, Y-encoded-like 1	1.507	0.0002	0.0007
Tsr1	ENSMUSG00000038335	TSR1 20S rRNA accumulation	1.644	0.0000	0.0000
Ttc30a1	ENSMUSG00000075271	tetratricopeptide repeat domain 30A1	1.623	0.0033	0.0089
Ttc33	ENSMUSG00000022151	tetratricopeptide repeat domain 33	1.687	0.0000	0.0000
Tubb1	ENSMUSG00000016255	tubulin, beta 1 class VI	3.052	0.0354	0.0719
Txnip	ENSMUSG00000038393	thioredoxin interacting protein	1.649	0.0005	0.0015
Ube2d1	ENSMUSG00000019927	ubiquitin-conjugating enzyme E2D 1	1.779	0.0000	0.0000
Ube2d2a	ENSMUSG00000091896	ubiquitin-conjugating enzyme E2D 2A	1.990	0.0000	0.0001
Ube2w	ENSMUSG00000025939	ubiquitin-conjugating enzyme E2W (putative)	1.649	0.0000	0.0000
Ubqln4	ENSMUSG00000008604	ubiquilin 4	1.742	0.0000	0.0001
Uchl5	ENSMUSG00000018189	ubiquitin carboxyl-terminal esterase L5	1.603	0.0000	0.0000
Ucp3	ENSMUSG00000032942	uncoupling protein 3 (mitochondrial, proton carrier)	1.631	0.0127	0.0296
Uhmk1	ENSMUSG00000026667	U2AF homology motif (UHM) kinase 1	1.609	0.0000	0.0000
Ulk4	ENSMUSG00000040936	unc-51-like kinase 4	5.500	0.0040	0.0107
Uri1	ENSMUSG00000030421	URI1, prefoldin-like chaperone	1.581	0.0000	0.0001
Usp47	ENSMUSG00000059263	ubiquitin specific peptidase 47	1.681	0.0000	0.0000
Ust	ENSMUSG00000047712	uronyl-2-sulfotransferase	1.527	0.0013	0.0038
Uvrag	ENSMUSG00000035354	UV radiation resistance associated gene	1.573	0.0128	0.0298
Vamp3	ENSMUSG00000028955	vesicle-associated membrane protein 3	1.606	0.0000	0.0000
Vamp4	ENSMUSG00000026696	vesicle-associated membrane protein 4	1.548	0.0000	0.0000
Vapa	ENSMUSG00000024091	vesicle-associated membrane protein, associated protein A	1.878	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Vhl	ENSMUSG00000033933	von Hippel-Lindau tumor suppressor	1.510	0.0000	0.0000
Vps45	ENSMUSG00000015747	vacuolar protein sorting 45	1.629	0.0000	0.0000
Vstm2l	ENSMUSG00000037843	V-set and transmembrane domain containing 2-like	4.707	0.0081	0.0200
Wdr31	ENSMUSG00000028391	WD repeat domain 31	2.151	0.0191	0.0422
Wrnip1	ENSMUSG00000021400	Werner helicase interacting protein 1	1.943	0.0000	0.0001
Xlr	ENSMUSG00000054626	X-linked lymphocyte-regulated	1.696	0.0051	0.0131
Xylt2	ENSMUSG00000020868	xylosyltransferase II	1.555	0.0338	0.0692
Yae1d1	ENSMUSG00000075054	Yae1 domain containing 1	1.536	0.0002	0.0008
Yap1	ENSMUSG00000053110	yes-associated protein 1	1.512	0.0000	0.0000
Yes1	ENSMUSG00000014932	YES proto-oncogene 1, Src family tyrosine kinase	1.611	0.0000	0.0000
Yipf4	ENSMUSG00000024072	Yip1 domain family, member 4	1.885	0.0000	0.0000
Yipf6	ENSMUSG00000047694	Yip1 domain family, member 6	1.677	0.0000	0.0000
Ypel5	ENSMUSG00000039770	yippee like 5	1.891	0.0000	0.0000
Yrdc	ENSMUSG00000028889	yrdC domain containing (E.coli)	1.821	0.0001	0.0005
Zadh2	ENSMUSG00000049090	zinc binding alcohol dehydrogenase, domain containing 2	1.535	0.0000	0.0000
Zbtb10	ENSMUSG00000069114	zinc finger and BTB domain containing 10	1.841	0.0000	0.0000
Zbtb41	ENSMUSG00000033964	zinc finger and BTB domain containing 41	1.783	0.0000	0.0000
Zbtb6	ENSMUSG00000066798	zinc finger and BTB domain containing 6	1.571	0.0000	0.0000
Zc3h11a	ENSMUSG00000102976	zinc finger CCCH type containing 11A	2.044	0.0000	0.0000
Zc3h8	ENSMUSG00000027387	zinc finger CCCH type containing 8	1.727	0.0000	0.0001
Zcwpw1	ENSMUSG00000037108	zinc finger, CW type with PWWP domain 1	2.253	0.0002	0.0007
Zdhhc7	ENSMUSG00000031823	zinc finger, DHHC domain containing 7	1.793	0.0000	0.0000
Zfand1	ENSMUSG00000039795	zinc finger, AN1-type domain 1	1.507	0.0009	0.0029
Zfand6	ENSMUSG00000030629	zinc finger, AN1-type domain 6	1.506	0.0000	0.0000
Zfp217	ENSMUSG00000052056	zinc finger protein 217	1.524	0.0000	0.0000
Zfp280b	ENSMUSG00000049764	zinc finger protein 280B	1.599	0.0000	0.0000
Zfp326	ENSMUSG00000029290	zinc finger protein 326	1.619	0.0000	0.0000
Zfp329	ENSMUSG00000057894	zinc finger protein 329	1.633	0.0030	0.0083
Zfp36l1	ENSMUSG00000021127	zinc finger protein 36, C3H type-like 1	1.512	0.0000	0.0000
Zfp445	ENSMUSG00000047036	zinc finger protein 445	1.533	0.0000	0.0001
Zfp579	ENSMUSG00000051550	zinc finger protein 579	1.948	0.0055	0.0141
Zfp641	ENSMUSG00000022987	zinc finger protein 641	1.547	0.0003	0.0009

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp870	ENSMUSG00000095325	zinc finger protein 870	1.564	0.0000	0.0000
Zfp991	ENSMUSG00000067916	zinc finger protein 991	1.653	0.0093	0.0226
Zgpat	ENSMUSG00000027582	zinc finger, CCCH-type with G patch domain	1.532	0.0046	0.0121
Zmynd11	ENSMUSG00000021156	zinc finger, MYND domain containing 11	1.547	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610005C13Rik	ENSMUSG00000109644	RIKEN cDNA 0610005C13 gene	-3.817	0.0470	0.0917
0610012D04Rik	ENSMUSG00000089755	RIKEN cDNA 0610012D04 gene	-4.077	0.0085	0.0209
0610025J13Rik	ENSMUSG00000046683	RIKEN cDNA 0610025J13 gene	-1.779	0.0223	0.0483
1110017D15Rik	ENSMUSG00000028441	RIKEN cDNA 1110017D15 gene	-8.878	0.0367	0.0742
1700003E16Rik	ENSMUSG00000030030	RIKEN cDNA 1700003E16 gene	-4.314	0.0144	0.0329
1700007L15Rik	ENSMUSG00000097318	RIKEN cDNA 1700007L15 gene	-2.294	0.0027	0.0076
1700102H20Rik	ENSMUSG00000116852	RIKEN cDNA 1700102H20 gene	-5.244	0.0047	0.0122
2210408F21Rik	ENSMUSG00000087380	RIKEN cDNA 2210408F21 gene	-1.586	0.0000	0.0000
2310015A16Rik	ENSMUSG00000117879	RIKEN cDNA 2310015A16 gene	-1.658	0.0000	0.0000
2310015D24Rik	ENSMUSG00000099411	RIKEN cDNA 2310015D24 gene	-2.284	0.0156	0.0355
2310039L15Rik	ENSMUSG00000100550	RIKEN cDNA 2310039L15 gene	-1.565	0.0411	0.0817
2410006H16Rik	ENSMUSG00000086841	RIKEN cDNA 2410006H16 gene	-2.017	0.0242	0.0519
2700038G22Rik	ENSMUSG00000097180	RIKEN cDNA 2700038G22 gene	-1.983	0.0061	0.0155
2700062C07Rik	ENSMUSG00000024273	RIKEN cDNA 2700062C07 gene	-2.643	0.0000	0.0000
2810039B14Rik	ENSMUSG00000099034	RIKEN cDNA 2810039B14 gene	-2.741	0.0067	0.0168
2810455O05Rik	ENSMUSG00000085030	RIKEN cDNA 2810455O05 gene	-13.210	0.0057	0.0146
3000002C10Rik	ENSMUSG00000070282	RIKEN cDNA 3000002C10 gene	-1.634	0.0399	0.0797
4930522O17Rik	ENSMUSG00000086947	RIKEN cDNA 4930522O17 gene	-2.576	0.0471	0.0918
4930547M16Rik	ENSMUSG00000097890	RIKEN cDNA 4930547M16 gene	-8.266	0.0223	0.0483
4931414P19Rik	ENSMUSG00000022179	RIKEN cDNA 4931414P19 gene	-1.960	0.0000	0.0000
4933404O12Rik	ENSMUSG00000097908	RIKEN cDNA 4933404O12 gene	-1.505	0.0502	0.0968
4933436F18Rik	ENSMUSG00000104380	RIKEN cDNA 4933436F18 gene	-8.164	0.0517	0.0996
5330411O13Rik	ENSMUSG00000108603	RIKEN cDNA 5330411O13 gene	-17.348	0.0080	0.0197
5430405H02Rik	ENSMUSG00000085741	RIKEN cDNA 5430405H02 gene	-1.720	0.0022	0.0061
5830405F06Rik	ENSMUSG00000103586	RIKEN cDNA 5830405F06 gene	-8.446	0.0307	0.0637
5830408C22Rik	ENSMUSG00000110148	RIKEN cDNA 5830408C22 gene	-2.471	0.0357	0.0725
9230114K14Rik	ENSMUSG00000097145	RIKEN cDNA 9230114K14 gene	-1.814	0.0001	0.0003
9330102E08Rik	ENSMUSG00000107879	RIKEN cDNA 9330102E08 gene	-1.559	0.0062	0.0158
9530020I12Rik	ENSMUSG00000112041	RIKEN cDNA 9530020I12 gene	-2.903	0.0350	0.0713
A130051J06Rik	ENSMUSG00000097643	RIKEN cDNA A130051J0 gene	-10.474	0.0316	0.0653
A330009N23Rik	ENSMUSG00000097915	RIKEN cDNA A330009N23 gene	-1.897	0.0161	0.0364

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
A430057M04Rik	ENSMUSG00000090564	RIKEN cDNA A430057M04 gene	-10.089	0.0389	0.0780
A530013C23Rik	ENSMUSG00000006462	RIKEN cDNA A530013C23 gene	-1.910	0.0231	0.0498
A630072L19Rik	ENSMUSG00000097160	RIKEN cDNA A630072L19 gene	-10.635	0.0085	0.0207
A930005H10Rik	ENSMUSG00000054426	RIKEN cDNA A930005H10 gene	-1.654	0.0000	0.0001
A930015P04Rik	ENSMUSG00000114526	RIKEN cDNA A930015P04 gene	-11.325	0.0473	0.0923
A930017K11Rik	ENSMUSG00000025727	RIKEN cDNA A930017K11 gene	-8.164	0.0054	0.0139
A930029G22Rik	ENSMUSG00000096988	RIKEN cDNA A930029G22 gene	-1.645	0.0516	0.0994
Aars2	ENSMUSG00000023938	alanyl-tRNA synthetase 2, mitochondrial	-1.895	0.0000	0.0000
Aass	ENSMUSG00000029695	aminoadipate-semialdehyde synthase	-2.759	0.0019	0.0055
Aatk	ENSMUSG00000025375	apoptosis-associated tyrosine kinase	-1.697	0.0001	0.0005
Abat	ENSMUSG00000057880	4-aminobutyrate aminotransferase	-6.029	0.0000	0.0000
Abcb6	ENSMUSG00000026198	ATP-binding cassette, sub-family B (MDR/TAP), member 6	-5.685	0.0004	0.0013
Abhd11	ENSMUSG00000040532	abhydrolase domain containing 11	-1.514	0.0000	0.0000
Abhd15	ENSMUSG00000000686	abhydrolase domain containing 15	-1.764	0.0336	0.0688
Abhd3	ENSMUSG00000002475	abhydrolase domain containing 3	-1.748	0.0002	0.0007
Acaa1a	ENSMUSG00000036138	acetyl-Coenzyme A acyltransferase 1A	-1.602	0.0000	0.0000
Accs	ENSMUSG00000040272	1-aminocyclopropane-1-carboxylate synthase (non-functional)	-1.690	0.0001	0.0004
Ackr2	ENSMUSG00000044534	atypical chemokine receptor 2	-1.572	0.0450	0.0883
Acr	ENSMUSG00000022622	acrosin prepropeptide	-6.176	0.0067	0.0167
Acta1	ENSMUSG00000031972	actin alpha 1, skeletal muscle	-1.743	0.0164	0.0369
Acy1	ENSMUSG00000023262	aminoacylase 1	-1.859	0.0000	0.0000
Adgre1	ENSMUSG00000004730	adhesion G protein-coupled receptor E1	-1.566	0.0083	0.0204
Adgrf3	ENSMUSG00000067642	adhesion G protein-coupled receptor F3	-12.967	0.0392	0.0784
Adhfe1	ENSMUSG00000025911	alcohol dehydrogenase, iron containing, 1	-1.788	0.0000	0.0000
Adig	ENSMUSG00000044405	adipogenin	-3.442	0.0009	0.0027
Adora2b	ENSMUSG00000018500	adenosine A2b receptor	-2.693	0.0125	0.0293
Aebp1	ENSMUSG00000020473	AE binding protein 1	-2.077	0.0003	0.0010
Agmat	ENSMUSG00000040706	agmatine ureohydrolase (agmatinase)	-3.224	0.0121	0.0284
Agpat1	ENSMUSG00000034254	1-acylglycerol-3-phosphate O-acyltransferase 1 (lysophosphatidic acid acyltransferase, alpha)	-1.817	0.0000	0.0000
Agpat2	ENSMUSG00000026922	1-acylglycerol-3-phosphate O-acyltransferase 2 (lysophosphatidic acid acyltransferase, beta)	-1.612	0.0000	0.0000
Ahrr	ENSMUSG00000021575	aryl-hydrocarbon receptor repressor	-1.647	0.0130	0.0302

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
AI413582	ENSMUSG00000062753	expressed sequence AI413582	-2.795	0.0000	0.0000
Aimp2	ENSMUSG00000029610	aminoacyl tRNA synthetase complex-interacting multifunctional protein 2	-1.537	0.0000	0.0000
Akip1	ENSMUSG00000031023	A kinase (PRKA) interacting protein 1	-1.567	0.0001	0.0002
Akr1b3	ENSMUSG00000001642	aldo-keto reductase family 1, member B3 (aldose reductase)	-1.545	0.0000	0.0000
Akr1b8	ENSMUSG00000029762	aldo-keto reductase family 1, member B8	-1.694	0.0001	0.0005
Akt2-ps	ENSMUSG00000084347	thymoma viral proto-oncogene 2, pseudogene	-2.957	0.0001	0.0003
Aldh16a1	ENSMUSG00000007833	aldehyde dehydrogenase 16 family, member A1	-1.630	0.0000	0.0000
Aldh1b1	ENSMUSG00000035561	aldehyde dehydrogenase 1 family, member B1	-1.611	0.0000	0.0000
Aldh1l1	ENSMUSG00000030088	aldehyde dehydrogenase 1 family, member L1	-2.318	0.0009	0.0027
Aldh3b3	ENSMUSG00000037263	aldehyde dehydrogenase 3 family, member B3	-3.691	0.0377	0.0759
Aldh4a1	ENSMUSG00000028737	aldehyde dehydrogenase 4 family, member A1	-1.700	0.0000	0.0000
Aldh6a1	ENSMUSG00000021238	aldehyde dehydrogenase family 6, subfamily A1	-1.604	0.0000	0.0000
Alg3	ENSMUSG00000033809	asparagine-linked glycosylation 3 (alpha-1,3-mannosyltransferase)	-1.662	0.0001	0.0002
Alkbh4	ENSMUSG00000039754	alkB homolog 4, lysine demethylase	-1.759	0.0004	0.0014
Als2cl	ENSMUSG00000044037	ALS2 C-terminal like	-1.573	0.0031	0.0085
Amd2	ENSMUSG00000063953	S-adenosylmethionine decarboxylase 2	-1.954	0.0075	0.0185
Amhr2	ENSMUSG00000023047	anti-Mullerian hormone type 2 receptor	-4.068	0.0046	0.0121
Amz2	ENSMUSG00000020610	archaelysin family metallopeptidase 2	-1.593	0.0000	0.0000
Angpt4	ENSMUSG00000027460	angiopoietin 4	-4.402	0.0313	0.0647
Angptl3	ENSMUSG00000028553	angiopoietin-like 3	-1.849	0.0231	0.0498
Ankrd55	ENSMUSG00000049985	ankyrin repeat domain 55	-4.088	0.0001	0.0005
Anpep	ENSMUSG00000039062	alanyl (membrane) aminopeptidase	-1.765	0.0003	0.0011
Ap1g2	ENSMUSG00000040701	adaptor protein complex AP-1, gamma 2 subunit	-1.714	0.0001	0.0002
Ap1m1	ENSMUSG00000003033	adaptor-related protein complex AP-1, mu subunit 1	-1.507	0.0000	0.0000
Ap2s1	ENSMUSG00000008036	adaptor-related protein complex 2, sigma 1 subunit	-1.690	0.0000	0.0000
Ap3s1-ps1	ENSMUSG00000085611	adaptor-related protein complex 3, sigma 1 subunit, pseudogene 1	-9.573	0.0206	0.0452
Aph1a	ENSMUSG00000015750	aph1 homolog A, gamma secretase subunit	-1.560	0.0000	0.0000
Apoc1	ENSMUSG00000040564	apolipoprotein C-I	-3.227	0.0329	0.0677
Aqp8	ENSMUSG00000030762	aquaporin 8	-2.154	0.0028	0.0076
Arap3	ENSMUSG00000024451	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 3	-1.508	0.0000	0.0000
Arc	ENSMUSG00000022602	activity regulated cytoskeletal-associated protein	-2.114	0.0168	0.0378

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Arhgap33	ENSMUSG00000036882	Rho GTPase activating protein 33	-1.905	0.0055	0.0141
Arhgap9	ENSMUSG00000040345	Rho GTPase activating protein 9	-2.271	0.0000	0.0000
Arhgef10	ENSMUSG00000071176	Rho guanine nucleotide exchange factor (GEF) 10	-1.629	0.0006	0.0018
Arhgef10l	ENSMUSG00000040964	Rho guanine nucleotide exchange factor (GEF) 10-like	-1.560	0.0000	0.0000
Arhgef16	ENSMUSG00000029032	Rho guanine nucleotide exchange factor (GEF) 16	-3.774	0.0004	0.0012
Arhgef40	ENSMUSG00000004562	Rho guanine nucleotide exchange factor (GEF) 40	-1.923	0.0000	0.0000
Armc2	ENSMUSG00000071324	armadillo repeat containing 2	-1.536	0.0136	0.0315
Armc5	ENSMUSG00000042178	armadillo repeat containing 5	-1.545	0.0000	0.0000
Armc9	ENSMUSG00000062590	armadillo repeat containing 9	-1.658	0.0001	0.0005
Arpc1b	ENSMUSG00000029622	actin related protein 2/3 complex, subunit 1B	-1.577	0.0000	0.0000
Arsb	ENSMUSG00000042082	arylsulfatase B	-1.866	0.0000	0.0000
Art3	ENSMUSG00000034842	ADP-ribosyltransferase 3	-1.646	0.0035	0.0095
Arv1	ENSMUSG00000031982	ARV1 homolog, fatty acid homeostasis modulator	-1.995	0.0000	0.0000
Atf6b	ENSMUSG00000015461	activating transcription factor 6 beta	-1.733	0.0000	0.0000
Atg4a-ps	ENSMUSG00000087119	autophagy related 4A, pseudogene	-2.439	0.0224	0.0486
Atg4d	ENSMUSG00000002820	autophagy related 4D, cysteine peptidase	-1.637	0.0000	0.0000
Atg7	ENSMUSG00000030314	autophagy related 7	-1.662	0.0000	0.0000
Atoh8	ENSMUSG00000037621	atonal bHLH transcription factor 8	-1.827	0.0123	0.0289
Atp10a	ENSMUSG00000025324	ATPase, class V, type 10A	-1.507	0.0218	0.0474
Atp13a1	ENSMUSG00000031862	ATPase type 13A1	-2.007	0.0000	0.0000
Atp1a3	ENSMUSG00000040907	ATPase, Na+/K+ transporting, alpha 3 polypeptide	-2.237	0.0187	0.0414
Atp5pb-ps	ENSMUSG00000044751	ATP synthase peripheral stalk-membrane subunit b, pseudogene	-1.573	0.0347	0.0708
Atp6ap1	ENSMUSG00000019087	ATPase, H+ transporting, lysosomal accessory protein 1	-1.591	0.0000	0.0000
Atxn10	ENSMUSG00000016541	ataxin 10	-1.620	0.0000	0.0000
Aunip	ENSMUSG00000078521	aurora kinase A and ninein interacting protein	-3.747	0.0137	0.0316
B230319C09Rik	ENSMUSG00000051844	RIKEN cDNA B230319C09 gene	-3.116	0.0247	0.0527
B3gnt9	ENSMUSG00000069920	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 9	-1.737	0.0028	0.0078
B4galt3	ENSMUSG00000052423	UDP-Gal:betaGlcNAc beta 1,4-galactosyltransferase, polypeptide 3	-1.629	0.0000	0.0000
Bag6	ENSMUSG00000024392	BCL2-associated athanogene 6	-1.529	0.0000	0.0000
Bahcc1	ENSMUSG00000039741	BAH domain and coiled-coil containing 1	-1.547	0.0000	0.0001
Baiap2	ENSMUSG00000025372	brain-specific angiogenesis inhibitor 1-associated protein 2	-3.222	0.0054	0.0138

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Baiap2l2	ENSMUSG00000018126	BAI1-associated protein 2-like 2	-17.551	0.0022	0.0062
Bbln	ENSMUSG00000039195	bublin coiled coil protein	-1.886	0.0000	0.0000
BC024978	ENSMUSG00000078786	cDNA sequence BC024978	-1.645	0.0000	0.0000
BC049352	ENSMUSG00000091996	cDNA sequence BC049352	-8.033	0.0375	0.0756
BC049762	ENSMUSG00000045942	cDNA sequence BC049762	-4.039	0.0208	0.0455
BC055324	ENSMUSG00000041406	cDNA sequence BC055324	-2.264	0.0031	0.0084
Bcar3	ENSMUSG00000028121	breast cancer anti-estrogen resistance 3	-1.648	0.0000	0.0001
Bcas3	ENSMUSG00000059439	BCAS3 microtubule associated cell migration factor	-1.903	0.0000	0.0000
Bcat2	ENSMUSG00000030826	branched chain aminotransferase 2, mitochondrial	-1.838	0.0000	0.0000
Bcl2l12	ENSMUSG00000003190	BCL2-like 12 (proline rich)	-1.788	0.0003	0.0010
Bdh1	ENSMUSG00000046598	3-hydroxybutyrate dehydrogenase, type 1	-3.671	0.0000	0.0000
Bdkrb2	ENSMUSG00000021070	bradykinin receptor, beta 2	-2.029	0.0000	0.0000
Best1	ENSMUSG00000037418	bestrophin 1	-3.640	0.0309	0.0641
Bgn	ENSMUSG00000031375	biglycan	-2.084	0.0000	0.0002
Bloc1s2	ENSMUSG00000057506	biogenesis of lysosomal organelles complex-1, subunit 2	-1.547	0.0003	0.0010
Bnc1	ENSMUSG00000025105	basonuclin 1	-22.445	0.0028	0.0077
Bnc2	ENSMUSG00000028487	basonuclin 2	-2.073	0.0176	0.0392
Borcs5	ENSMUSG00000042992	BLOC-1 related complex subunit 5	-1.584	0.0000	0.0000
Brat1	ENSMUSG00000000148	BRCA1-associated ATM activator 1	-1.736	0.0000	0.0000
Bst1	ENSMUSG00000029082	bone marrow stromal cell antigen 1	-9.558	0.0000	0.0000
Bud23	ENSMUSG00000005378	BUD23, rRNA methyltransferase and ribosome maturation factor	-1.811	0.0000	0.0000
C030006K11Rik	ENSMUSG00000116138	RIKEN cDNA C030006K11 gene	-1.729	0.0000	0.0000
C1qtnf2	ENSMUSG00000046491	C1q and tumor necrosis factor related protein 2	-2.346	0.0001	0.0005
C1ra	ENSMUSG00000055172	complement component 1, r subcomponent A	-1.685	0.0001	0.0003
C1s2	ENSMUSG00000079343	complement component 1, s subcomponent 2	-2.384	0.0000	0.0002
C2	ENSMUSG00000024371	complement component 2 (within H-2S)	-2.232	0.0468	0.0913
C77080	ENSMUSG00000050390	expressed sequence C77080	-1.704	0.0000	0.0001
C8g	ENSMUSG00000015083	complement component 8, gamma polypeptide	-3.691	0.0002	0.0007
Cacna1i	ENSMUSG00000022416	calcium channel, voltage-dependent, alpha 1I subunit	-17.754	0.0061	0.0156
Cacnb1	ENSMUSG00000020882	calcium channel, voltage-dependent, beta 1 subunit	-1.581	0.0000	0.0002
Cacng6	ENSMUSG00000078815	calcium channel, voltage-dependent, gamma subunit 6	-13.164	0.0111	0.0264

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Camkk1	ENSMUSG00000020785	calcium/calmodulin-dependent protein kinase kinase 1, alpha	-1.563	0.0295	0.0616
Capg	ENSMUSG00000056737	capping protein (actin filament), gelsolin-like	-1.620	0.0025	0.0069
Capn15	ENSMUSG00000037326	calpain 15	-1.673	0.0000	0.0001
Capn6	ENSMUSG00000067276	calpain 6	-4.622	0.0034	0.0093
Carns1	ENSMUSG00000075289	carnosine synthase 1	-1.843	0.0000	0.0001
Cbarp	ENSMUSG00000035640	calcium channel, voltage-dependent, beta subunit associated regulatory protein	-2.041	0.0004	0.0014
Cblc	ENSMUSG00000040525	Casitas B-lineage lymphoma c	-2.883	0.0140	0.0322
Cbr1	ENSMUSG00000051483	carbonyl reductase 1	-1.519	0.0000	0.0000
Cbs	ENSMUSG00000024039	cystathionine beta-synthase	-9.551	0.0358	0.0726
Cbx2	ENSMUSG00000025577	chromobox 2	-1.633	0.0004	0.0013
Ccdc106	ENSMUSG00000035228	coiled-coil domain containing 106	-10.328	0.0168	0.0378
Ccdc184	ENSMUSG00000029875	coiled-coil domain containing 184	-1.816	0.0291	0.0607
Ccdc68	ENSMUSG00000038903	coiled-coil domain containing 68	-2.133	0.0265	0.0559
Ccl12	ENSMUSG00000035352	chemokine (C-C motif) ligand 12	-5.028	0.0021	0.0060
Ccl21a	ENSMUSG00000094686	chemokine (C-C motif) ligand 21A (serine)	-2.821	0.0000	0.0001
Ccl24	ENSMUSG00000004814	chemokine (C-C motif) ligand 24	-2.638	0.0034	0.0092
Ccl5	ENSMUSG00000035042	chemokine (C-C motif) ligand 5	-2.671	0.0300	0.0624
Ccn4	ENSMUSG00000005124	cellular communication network factor 4	-1.880	0.0005	0.0016
Ccnd3	ENSMUSG00000034165	cyclin D3	-1.517	0.0000	0.0000
Cd180	ENSMUSG00000021624	CD180 antigen	-1.964	0.0272	0.0572
Cd247	ENSMUSG00000005763	CD247 antigen	-3.474	0.0010	0.0032
Cd27	ENSMUSG00000030336	CD27 antigen	-29.790	0.0003	0.0011
Cd300lb	ENSMUSG00000063193	CD300 molecule like family member B	-2.457	0.0194	0.0429
Cd34	ENSMUSG00000016494	CD34 antigen	-1.518	0.0000	0.0002
Cd46	ENSMUSG00000016493	CD46 antigen, complement regulatory protein	-1.750	0.0156	0.0353
Cd52	ENSMUSG00000000682	CD52 antigen	-3.257	0.0035	0.0096
Cd68	ENSMUSG00000018774	CD68 antigen	-1.786	0.0020	0.0057
Cd82	ENSMUSG00000027215	CD82 antigen	-1.664	0.0000	0.0001
Cdh3	ENSMUSG00000061048	cadherin 3	-6.154	0.0389	0.0779
Cdh4	ENSMUSG00000000305	cadherin 4	-3.064	0.0000	0.0000
Cdhr3	ENSMUSG00000035860	cadherin-related family member 3	-2.936	0.0356	0.0723

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cdin1	ENSMUSG00000040282	CDAN1 interacting nuclease 1	-1.764	0.0009	0.0027
Cdk20	ENSMUSG00000021483	cyclin-dependent kinase 20	-2.171	0.0002	0.0006
Cdsn	ENSMUSG00000039518	corneodesmosin	-2.778	0.0004	0.0012
Cers2	ENSMUSG00000015714	ceramide synthase 2	-1.551	0.0000	0.0000
Ces1e	ENSMUSG00000061959	carboxylesterase 1E	-2.666	0.0320	0.0661
Cfap300	ENSMUSG00000053070	cilia and flagella associated protein 300	-3.282	0.0001	0.0003
Cfap410	ENSMUSG00000020284	cilia and flagella associated protein 410	-2.156	0.0000	0.0000
Chac1	ENSMUSG00000027313	ChaC, cation transport regulator 1	-2.902	0.0342	0.0700
Chchd6	ENSMUSG00000030086	coiled-coil-helix-coiled-coil-helix domain containing 6	-1.508	0.0000	0.0001
Chrna1	ENSMUSG00000027107	cholinergic receptor, nicotinic, alpha polypeptide 1 (muscle)	-37.453	0.0008	0.0025
Cib3	ENSMUSG00000074240	calcium and integrin binding family member 3	-12.143	0.0001	0.0002
Clba1	ENSMUSG00000037594	clathrin binding box of aftiphilin containing 1	-1.865	0.0004	0.0014
Cldn10	ENSMUSG00000022132	claudin 10	-12.612	0.0498	0.0962
Cldn15	ENSMUSG00000001739	claudin 15	-3.144	0.0003	0.0009
Clec10a	ENSMUSG00000000318	C-type lectin domain family 10, member A	-1.704	0.0158	0.0358
Clec2e	ENSMUSG00000030155	C-type lectin domain family 2, member e	-4.498	0.0098	0.0237
Clec4a1	ENSMUSG00000049037	C-type lectin domain family 4, member a1	-1.681	0.0149	0.0340
Clec4f	ENSMUSG00000014542	C-type lectin domain family 4, member f	-14.337	0.0176	0.0392
Clic3	ENSMUSG00000015093	chloride intracellular channel 3	-15.986	0.0056	0.0144
Clpb	ENSMUSG00000001829	ClpB caseinolytic peptidase B	-1.524	0.0000	0.0000
Clpp	ENSMUSG00000002660	caseinolytic mitochondrial matrix peptidase proteolytic subunit	-1.767	0.0000	0.0000
Clu	ENSMUSG00000022037	clusterin	-1.890	0.0000	0.0000
Cmtm8	ENSMUSG00000041012	CKLF-like MARVEL transmembrane domain containing 8	-1.793	0.0000	0.0000
Cngb3	ENSMUSG00000056494	cyclic nucleotide gated channel beta 3	-2.028	0.0099	0.0237
Cnr2	ENSMUSG00000062585	cannabinoid receptor 2 (macrophage)	-1.640	0.0208	0.0455
Cntfr	ENSMUSG00000028444	ciliary neurotrophic factor receptor	-1.923	0.0006	0.0018
Coa8	ENSMUSG00000037787	cytochrome c oxidase assembly factor 8	-1.704	0.0000	0.0000
Coasy	ENSMUSG00000001755	Coenzyme A synthase	-1.624	0.0001	0.0002
Col4a6	ENSMUSG00000031273	collagen, type IV, alpha 6	-1.536	0.0258	0.0548
Col6a5	ENSMUSG00000091345	collagen, type VI, alpha 5	-5.942	0.0000	0.0001
Coq8b	ENSMUSG00000003762	coenzyme Q8B	-1.557	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Coro1a	ENSMUSG00000030707	coronin, actin binding protein 1A	-1.737	0.0124	0.0291
Coro6	ENSMUSG00000020836	coronin 6	-1.587	0.0000	0.0000
Cox10	ENSMUSG00000042148	heme A:farnesyltransferase cytochrome c oxidase assembly factor 10	-1.818	0.0000	0.0000
Cox8b	ENSMUSG00000025488	cytochrome c oxidase subunit 8B	-1.737	0.0000	0.0000
Cpa1	ENSMUSG00000054446	carboxypeptidase A1, pancreatic	-6.565	0.0423	0.0838
Cpped1	ENSMUSG00000065979	calcineurin-like phosphoesterase domain containing 1	-1.538	0.0000	0.0000
Cpsf1	ENSMUSG00000034022	cleavage and polyadenylation specific factor 1	-1.577	0.0000	0.0000
Cptp	ENSMUSG00000029073	ceramide-1-phosphate transfer protein	-1.772	0.0000	0.0001
Cpxm2	ENSMUSG00000030862	carboxypeptidase X 2 (M14 family)	-2.388	0.0000	0.0000
Cpz	ENSMUSG00000036596	carboxypeptidase Z	-3.829	0.0425	0.0842
Crb3	ENSMUSG00000044279	crumbs family member 3	-5.182	0.0015	0.0044
Crybb3	ENSMUSG00000029352	crystallin, beta B3	-2.638	0.0115	0.0272
Csf3r	ENSMUSG00000028859	colony stimulating factor 3 receptor (granulocyte)	-2.406	0.0073	0.0181
Csmd1	ENSMUSG00000060924	CUB and Sushi multiple domains 1	-2.699	0.0119	0.0280
Csrp3	ENSMUSG00000030470	cysteine and glycine-rich protein 3	-1.662	0.0000	0.0000
Cth	ENSMUSG00000028179	cystathionase (cystathionine gamma-lyase)	-2.639	0.0136	0.0314
Ctsf	ENSMUSG00000083282	cathepsin F	-1.514	0.0000	0.0000
Cubn	ENSMUSG00000026726	cubilin (intrinsic factor-cobalamin receptor)	-5.154	0.0005	0.0017
Cul9	ENSMUSG00000040327	cullin 9	-1.717	0.0000	0.0000
Cxcr5	ENSMUSG00000047880	chemokine (C-X-C motif) receptor 5	-6.627	0.0383	0.0770
Cyb561a3	ENSMUSG00000034445	cytochrome b561 family, member A3	-1.541	0.0000	0.0001
Cyba	ENSMUSG00000006519	cytochrome b-245, alpha polypeptide	-1.530	0.0001	0.0004
Cybrd1	ENSMUSG00000027015	cytochrome b reductase 1	-13.597	0.0002	0.0008
Cyfip2	ENSMUSG00000020340	cytoplasmic FMR1 interacting protein 2	-1.737	0.0001	0.0003
Cyp2j9	ENSMUSG00000015224	cytochrome P450, family 2, subfamily j, polypeptide 9	-1.837	0.0002	0.0007
Cyp2s1	ENSMUSG00000040703	cytochrome P450, family 2, subfamily s, polypeptide 1	-21.318	0.0000	0.0000
Cyp4f17	ENSMUSG00000091586	cytochrome P450, family 4, subfamily f, polypeptide 17	-1.599	0.0060	0.0152
Cyp7b1	ENSMUSG00000039519	cytochrome P450, family 7, subfamily b, polypeptide 1	-2.638	0.0109	0.0258
Cysltr1	ENSMUSG00000052821	cysteinyl leukotriene receptor 1	-1.501	0.0330	0.0677
D5Ertd605e	ENSMUSG00000106820	DNA segment, Chr 5, ERATO Doi 605, expressed	-21.435	0.0011	0.0032
D7Ertd443e	ENSMUSG00000030994	DNA segment, Chr 7, ERATO Doi 443, expressed	-1.941	0.0491	0.0950

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dalrd3	ENSMUSG00000019039	DALR anticodon binding domain containing 3	-2.338	0.0000	0.0000
Dbt	ENSMUSG00000000340	dihydrolipoamide branched chain transacylase E2	-1.543	0.0001	0.0005
Ddt	ENSMUSG00000001666	D-dopachrome tautomerase	-1.809	0.0000	0.0000
Ddx31	ENSMUSG00000026806	DEAD/H box helicase 31	-1.519	0.0000	0.0001
Dennd4b	ENSMUSG00000042404	DENN/MADD domain containing 4B	-1.506	0.0000	0.0000
Depdc7	ENSMUSG00000027173	DEP domain containing 7	-1.697	0.0121	0.0284
Depp1	ENSMUSG00000048489	DEPP1 autophagy regulator	-3.180	0.0037	0.0099
Dgki	ENSMUSG00000038665	diacylglycerol kinase, iota	-2.658	0.0122	0.0285
Dhrs1	ENSMUSG00000002332	dehydrogenase/reductase (SDR family) member 1	-1.538	0.0000	0.0000
Dhrs9	ENSMUSG00000027068	dehydrogenase/reductase (SDR family) member 9	-17.059	0.0080	0.0197
Disc1	ENSMUSG00000043051	disrupted in schizophrenia 1	-1.930	0.0135	0.0312
Dlec1	ENSMUSG00000038060	deleted in lung and esophageal cancer 1	-27.172	0.0012	0.0036
Dmac1	ENSMUSG00000028398	distal membrane arm assembly complex 1	-1.626	0.0000	0.0000
Dmkn	ENSMUSG00000060962	dermokine	-9.685	0.0166	0.0374
Dnaaf3	ENSMUSG00000055809	dynein, axonemal assembly factor 3	-1.593	0.0342	0.0699
Dnaaf8	ENSMUSG00000022543	dynein axonemal assembly factor 8	-1.822	0.0021	0.0060
Dnajc19-ps	ENSMUSG00000083854	DnaJ heat shock protein family (Hsp40) member C19, pseudogene	-4.446	0.0085	0.0208
Dnajc30	ENSMUSG00000061118	DnaJ heat shock protein family (Hsp40) member C30	-1.776	0.0000	0.0000
Dnal4	ENSMUSG00000022420	dynein, axonemal, light chain 4	-1.769	0.0000	0.0000
Dok1	ENSMUSG00000068335	docking protein 1	-1.612	0.0119	0.0280
Dok3	ENSMUSG00000035711	docking protein 3	-1.776	0.0341	0.0698
Dolk	ENSMUSG00000075419	dolichol kinase	-1.534	0.0000	0.0000
Dph2	ENSMUSG00000028540	DPH2 homolog	-2.336	0.0000	0.0000
Dpy19l3	ENSMUSG00000043671	dpy-19-like 3 (C. elegans)	-1.621	0.0006	0.0018
Drc3	ENSMUSG00000056598	dynein regulatory complex subunit 3	-1.640	0.0015	0.0043
Dus3l	ENSMUSG00000007603	dihydrouridine synthase 3-like (S. cerevisiae)	-1.845	0.0000	0.0000
Dynlt1c	ENSMUSG00000000579	dynein light chain Tctex-type 1C	-11.384	0.0007	0.0023
Dynlt1-ps1	ENSMUSG00000082691	dynein light chain Tctex-type 1, pseudogene 1	-11.850	0.0096	0.0231
E030042O20Rik	ENSMUSG00000087222	RIKEN cDNA E030042O20 gene	-1.791	0.0157	0.0356
E130317F20Rik	ENSMUSG00000091994	RIKEN cDNA E130317F20 gene	-1.956	0.0045	0.0118
E330011O21Rik	ENSMUSG00000109841	RIKEN cDNA E330011O21 gene	-1.519	0.0062	0.0158

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ear2	ENSMUSG00000072596	eosinophil-associated, ribonuclease A family, member 2	-11.412	0.0169	0.0379
Echdc2	ENSMUSG00000028601	enoyl Coenzyme A hydratase domain containing 2	-1.797	0.0000	0.0000
Ecm1	ENSMUSG00000028108	extracellular matrix protein 1	-1.761	0.0002	0.0007
Edf1	ENSMUSG00000015092	endothelial differentiation-related factor 1	-1.731	0.0000	0.0000
Eef2	ENSMUSG00000034994	eukaryotic translation elongation factor 2	-1.787	0.0000	0.0000
Efemp2	ENSMUSG00000024909	epidermal growth factor-containing fibulin-like extracellular matrix protein 2	-1.519	0.0120	0.0282
Efhc1	ENSMUSG00000041809	EF-hand domain (C-terminal) containing 1	-2.707	0.0056	0.0143
Efna4	ENSMUSG00000028040	ephrin A4	-3.291	0.0061	0.0155
Eftud2	ENSMUSG00000020929	elongation factor Tu GTP binding domain containing 2	-1.624	0.0000	0.0000
Ehd3	ENSMUSG00000024065	EH-domain containing 3	-1.550	0.0002	0.0006
Elp5	ENSMUSG00000018565	elongator acetyltransferase complex subunit 5	-1.806	0.0000	0.0000
Elp6	ENSMUSG00000054836	elongator acetyltransferase complex subunit 6	-1.665	0.0137	0.0316
Emc3	ENSMUSG00000030286	ER membrane protein complex subunit 3	-1.540	0.0000	0.0000
Emilin1	ENSMUSG00000029163	elastin microfibril interfacer 1	-1.627	0.0027	0.0076
Enkd1	ENSMUSG00000013155	enkurin domain containing 1	-1.996	0.0063	0.0159
Epb41l5	ENSMUSG00000026383	erythrocyte membrane protein band 4.1 like 5	-1.532	0.0028	0.0076
Ephb6	ENSMUSG00000029869	Eph receptor B6	-2.767	0.0016	0.0047
Ephx3	ENSMUSG00000037577	epoxide hydrolase 3	-2.320	0.0204	0.0448
Epn2	ENSMUSG00000001036	epsin 2	-1.663	0.0000	0.0000
Epn3	ENSMUSG00000010080	epsin 3	-2.928	0.0000	0.0000
Epor	ENSMUSG00000006235	erythropoietin receptor	-1.802	0.0198	0.0437
Eprn	ENSMUSG00000113346	ephemeron, early developmental lncRNA	-1.619	0.0331	0.0679
Eps15l1	ENSMUSG00000006276	epidermal growth factor receptor pathway substrate 15-like 1	-1.531	0.0000	0.0000
Ercc6l	ENSMUSG00000051220	excision repair cross-complementing rodent repair deficiency complementation group 6 like	-2.106	0.0033	0.0089
Espl1	ENSMUSG00000058290	extra spindle pole bodies 1, separase	-1.741	0.0302	0.0627
Espnl	ENSMUSG00000049515	espin-like	-11.408	0.0298	0.0620
Esrp2	ENSMUSG00000084128	epithelial splicing regulatory protein 2	-3.611	0.0017	0.0050
Eva1a	ENSMUSG00000035104	eva-1 homolog A (C. elegans)	-1.970	0.0014	0.0041
Eya4	ENSMUSG00000010461	EYA transcriptional coactivator and phosphatase 4	-3.001	0.0031	0.0085
F420014N23Rik	ENSMUSG00000097331	RIKEN cDNA F420014N23 gene	-18.965	0.0108	0.0258
Fabp3-ps1	ENSMUSG00000056366	fatty acid binding protein 3, muscle and heart, pseudogene 1	-1.689	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fads2	ENSMUSG00000024665	fatty acid desaturase 2	-1.698	0.0000	0.0000
Fads6	ENSMUSG00000044788	fatty acid desaturase domain family, member 6	-1.556	0.0001	0.0002
Fam110a	ENSMUSG00000027459	family with sequence similarity 110, member A	-2.253	0.0000	0.0000
Fam117a	ENSMUSG00000038893	family with sequence similarity 117, member A	-2.615	0.0000	0.0000
Fam186b	ENSMUSG00000078907	family with sequence similarity 186, member B	-14.402	0.0185	0.0411
Fam20a	ENSMUSG00000020614	FAM20A, golgi associated secretory pathway pseudokinase	-2.117	0.0000	0.0002
Fam221b	ENSMUSG00000043633	family with sequence similarity 221, member B	-4.093	0.0023	0.0064
Fam241b	ENSMUSG00000020083	family with sequence similarity 241, member B	-1.830	0.0005	0.0017
Fam83e	ENSMUSG00000054161	family with sequence similarity 83, member E	-10.468	0.0015	0.0044
Fam83h	ENSMUSG00000046761	family with sequence similarity 83, member H	-2.071	0.0065	0.0163
Fanca	ENSMUSG00000032815	Fanconi anemia, complementation group A	-3.032	0.0000	0.0000
Farp2	ENSMUSG00000034066	FERM, RhoGEF and pleckstrin domain protein 2	-1.648	0.0001	0.0005
Farsa	ENSMUSG00000003808	phenylalanyl-tRNA synthetase, alpha subunit	-1.558	0.0000	0.0000
Fastkd3	ENSMUSG00000021532	FAST kinase domains 3	-1.680	0.0001	0.0003
Fat2	ENSMUSG00000055333	FAT atypical cadherin 2	-4.412	0.0014	0.0041
Fbln1	ENSMUSG00000006369	fibulin 1	-1.733	0.0006	0.0019
Fbxl13	ENSMUSG00000048520	F-box and leucine-rich repeat protein 13	-5.833	0.0355	0.0722
Fbxl2	ENSMUSG00000032507	F-box and leucine-rich repeat protein 2	-3.071	0.0134	0.0311
Fbxo17	ENSMUSG00000030598	F-box protein 17	-1.678	0.0054	0.0140
Fbxo44	ENSMUSG00000029001	F-box protein 44	-2.106	0.0000	0.0000
Fbxw5	ENSMUSG00000015095	F-box and WD-40 domain protein 5	-1.633	0.0000	0.0000
Fbxw9	ENSMUSG00000008167	F-box and WD-40 domain protein 9	-1.606	0.0002	0.0005
Fcrls	ENSMUSG00000015852	Fc receptor-like S, scavenger receptor	-1.875	0.0232	0.0500
Fer1l5	ENSMUSG00000037432	fer-1-like 5 (C. elegans)	-9.498	0.0013	0.0039
Fermt3	ENSMUSG00000024965	fermitin family member 3	-1.615	0.0059	0.0151
Fetub	ENSMUSG00000022871	fetuin beta	-2.461	0.0107	0.0255
Fgd2	ENSMUSG00000024013	FYVE, RhoGEF and PH domain containing 2	-3.327	0.0008	0.0025
Fgfbp1	ENSMUSG00000048373	fibroblast growth factor binding protein 1	-10.331	0.0055	0.0141
Fhdc1	ENSMUSG00000041842	FH2 domain containing 1	-3.024	0.0008	0.0026
Fhod1	ENSMUSG00000014778	formin homology 2 domain containing 1	-1.634	0.0001	0.0004
Fkbp15	ENSMUSG00000066151	FK506 binding protein 15	-1.619	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Flt3l	ENSMUSG00000110206	FMS-like tyrosine kinase 3 ligand	-1.686	0.0370	0.0747
Fn1	ENSMUSG00000026193	fibronectin 1	-1.550	0.0025	0.0069
Frzb	ENSMUSG00000027004	frizzled-related protein	-1.545	0.0040	0.0106
Fstl3	ENSMUSG00000020325	follistatin-like 3	-2.208	0.0000	0.0000
Fut7	ENSMUSG00000036587	fucosyltransferase 7	-12.933	0.0247	0.0527
Fuz	ENSMUSG00000011658	fuzzy planar cell polarity protein	-1.677	0.0000	0.0000
Gabarap	ENSMUSG00000018567	gamma-aminobutyric acid receptor associated protein	-1.528	0.0000	0.0000
Gabrr1	ENSMUSG00000028280	gamma-aminobutyric acid (GABA) C receptor, subunit rho 1	-4.898	0.0215	0.0469
Gal3st2b	ENSMUSG00000093805	galactose-3-O-sulfotransferase 2B	-6.203	0.0000	0.0000
Gal3st3	ENSMUSG00000047658	galactose-3-O-sulfotransferase 3	-2.405	0.0108	0.0258
Galk1	ENSMUSG00000020766	galactokinase 1	-1.653	0.0000	0.0000
Galm	ENSMUSG00000035473	galactose mutarotase	-1.539	0.0000	0.0000
Galnt18	ENSMUSG00000038296	polypeptide N-acetylgalactosaminyltransferase 18	-1.640	0.0000	0.0000
Gbp6	ENSMUSG00000104713	guanylate binding protein 6	-10.988	0.0014	0.0042
Gbx2	ENSMUSG00000034486	gastrulation brain homeobox 2	-2.186	0.0146	0.0334
Gcat	ENSMUSG00000006378	glycine C-acetyltransferase (2-amino-3-ketobutyrate-coenzyme A ligase)	-1.940	0.0032	0.0086
Gcdh	ENSMUSG00000003809	glutaryl-Coenzyme A dehydrogenase	-1.831	0.0000	0.0000
Gemin6-ps	ENSMUSG00000071237	gem nuclear organelle associated protein 6, pseudogene	-6.579	0.0145	0.0332
Gimap1	ENSMUSG00000090019	GTPase, IMAP family member 1	-1.567	0.0063	0.0159
Gja4	ENSMUSG00000050234	gap junction protein, alpha 4	-1.874	0.0001	0.0003
Glb1l2	ENSMUSG00000036395	galactosidase, beta 1-like 2	-4.493	0.0166	0.0374
Glipr1	ENSMUSG00000056888	GLI pathogenesis-related 1 (glioma)	-3.527	0.0020	0.0059
Glis2	ENSMUSG00000014303	GLIS family zinc finger 2	-1.915	0.0000	0.0000
Gm10032	ENSMUSG00000057913	predicted gene 10032	-18.698	0.0091	0.0221
Gm10110	ENSMUSG00000062093	predicted gene 10110	-1.556	0.0000	0.0000
Gm10290	ENSMUSG00000105775	predicted pseudogene 10290	-2.892	0.0427	0.0844
Gm10353	ENSMUSG00000114220	predicted gene 10353	-2.160	0.0185	0.0412
Gm10499	ENSMUSG00000073403	predicted gene 10499	-2.768	0.0000	0.0002
Gm10644	ENSMUSG00000074219	predicted gene 10644	-2.138	0.0003	0.0010
Gm10766	ENSMUSG00000103957	predicted gene 10766	-6.861	0.0346	0.0706
Gm11346	ENSMUSG00000085603	predicted gene 11346	-7.208	0.0199	0.0439

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm11476	ENSMUSG00000085596	predicted gene 11476	-4.720	0.0380	0.0764
Gm11557	ENSMUSG00000082900	predicted gene 11557	-2.894	0.0036	0.0097
Gm11663	ENSMUSG00000082706	predicted gene 11663	-17.380	0.0117	0.0276
Gm11767	ENSMUSG00000085207	predicted gene 11767	-4.672	0.0488	0.0946
Gm11826	ENSMUSG00000083328	predicted gene 11826	-8.806	0.0217	0.0473
Gm11899	ENSMUSG00000087399	predicted gene 11899	-5.882	0.0088	0.0213
Gm11915	ENSMUSG00000086774	predicted gene 11915	-3.341	0.0383	0.0769
Gm11967	ENSMUSG00000084819	predicted gene 11967	-2.459	0.0001	0.0003
Gm11992	ENSMUSG00000040978	predicted gene 11992	-3.100	0.0004	0.0013
Gm12254	ENSMUSG00000085342	predicted gene 12254	-2.117	0.0285	0.0597
Gm12258	ENSMUSG00000072915	predicted gene 12258	-1.785	0.0329	0.0677
Gm12352	ENSMUSG00000084835	predicted gene 12352	-9.487	0.0260	0.0551
Gm12403	ENSMUSG00000082186	predicted gene 12403	-6.112	0.0038	0.0101
Gm12409	ENSMUSG00000085876	predicted gene 12409	-2.904	0.0303	0.0630
Gm12481	ENSMUSG00000043770	predicted gene 12481	-2.765	0.0000	0.0000
Gm12586	ENSMUSG00000084401	predicted gene 12586	-7.664	0.0333	0.0682
Gm12663	ENSMUSG00000101316	predicted gene 12663	-2.052	0.0000	0.0000
Gm12715	ENSMUSG00000059195	predicted gene 12715	-4.769	0.0119	0.0281
Gm12724	ENSMUSG00000086249	predicted gene 12724	-14.188	0.0079	0.0196
Gm12854	ENSMUSG00000078238	predicted gene 12854	-17.388	0.0003	0.0009
Gm12993	ENSMUSG00000082063	predicted gene 12993	-3.915	0.0487	0.0945
Gm12996	ENSMUSG00000086417	predicted gene 12996	-2.613	0.0004	0.0012
Gm13245	ENSMUSG00000081998	predicted gene 13245	-10.940	0.0161	0.0363
Gm13375	ENSMUSG00000075514	predicted gene 13375	-1.618	0.0000	0.0000
Gm13436	ENSMUSG00000083716	predicted gene 13436	-2.916	0.0000	0.0000
Gm13456	ENSMUSG00000082536	predicted gene 13456	-3.162	0.0001	0.0005
Gm13578	ENSMUSG00000084104	predicted gene 13578	-4.045	0.0217	0.0472
Gm13668	ENSMUSG00000083072	predicted gene 13668	-10.288	0.0124	0.0290
Gm13881	ENSMUSG00000084756	predicted gene 13881	-1.771	0.0072	0.0180
Gm14091	ENSMUSG00000086421	predicted gene 14091	-17.307	0.0078	0.0193
Gm14111	ENSMUSG00000080870	predicted gene 14111	-2.132	0.0482	0.0937

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm14121	ENSMUSG00000083325	predicted gene 14121	-2.384	0.0256	0.0545
Gm14270	ENSMUSG00000084013	predicted gene 14270	-4.289	0.0013	0.0038
Gm14286	ENSMUSG00000087445	predicted gene 14286	-3.956	0.0111	0.0262
Gm14494	ENSMUSG00000083097	predicted gene 14494	-1.874	0.0214	0.0467
Gm14546	ENSMUSG00000086762	predicted gene 14546	-3.606	0.0024	0.0067
Gm15294	ENSMUSG00000081607	predicted gene 15294	-5.467	0.0259	0.0550
Gm15559	ENSMUSG00000086401	predicted gene 15559	-2.668	0.0399	0.0797
Gm15743	ENSMUSG00000086645	predicted gene 15743	-3.384	0.0001	0.0002
Gm15760	ENSMUSG00000080797	predicted gene 15760	-2.798	0.0405	0.0808
Gm15772	ENSMUSG00000062353	predicted gene 15772	-3.167	0.0425	0.0842
Gm15931	ENSMUSG00000081723	predicted gene 15931	-3.123	0.0004	0.0014
Gm15998	ENSMUSG00000086389	predicted gene 15998	-11.058	0.0312	0.0646
Gm1600	ENSMUSG00000116270	predicted gene 1600	-2.089	0.0153	0.0349
Gm16118	ENSMUSG00000089797	predicted gene 16118	-14.160	0.0235	0.0504
Gm16141	ENSMUSG00000087507	predicted gene 16141	-2.716	0.0367	0.0741
Gm16230	ENSMUSG00000087163	predicted gene 16230	-12.725	0.0179	0.0399
Gm16251	ENSMUSG00000090075	predicted gene 16251	-3.082	0.0409	0.0815
Gm16283	ENSMUSG00000087020	predicted gene 16283	-4.707	0.0495	0.0957
Gm16364	ENSMUSG00000086915	predicted gene 16364	-4.040	0.0022	0.0064
Gm16374	ENSMUSG00000115205	predicted pseudogene 16374	-4.745	0.0004	0.0013
Gm16439	ENSMUSG00000072594	predicted pseudogene 16439	-2.447	0.0419	0.0832
Gm16494	ENSMUSG00000091775	predicted gene 16494	-6.928	0.0376	0.0758
Gm16537	ENSMUSG00000089671	predicted gene 16537	-1.705	0.0163	0.0368
Gm17276	ENSMUSG00000097305	predicted gene, 17276	-3.107	0.0003	0.0010
Gm17455	ENSMUSG00000090439	predicted gene, 17455	-9.587	0.0457	0.0895
Gm17690	ENSMUSG00000097204	predicted gene, 17690	-2.167	0.0007	0.0021
Gm17709	ENSMUSG00000091952	predicted gene, 17709	-4.849	0.0400	0.0799
Gm17753	ENSMUSG00000115867	predicted gene, 17753	-1.720	0.0379	0.0762
Gm18001	ENSMUSG00000110690	predicted gene, 18001	-6.575	0.0443	0.0872
Gm1826	ENSMUSG00000082028	predicted gene 1826	-21.367	0.0039	0.0105
Gm1833	ENSMUSG00000100362	predicted gene 1833	-27.234	0.0005	0.0015

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm18584	ENSMUSG00000107853	predicted gene, 18584	-18.476	0.0027	0.0075
Gm19277	ENSMUSG00000115924	predicted gene, 19277	-3.606	0.0007	0.0021
Gm19522	ENSMUSG00000116903	predicted gene, 19522	-2.113	0.0001	0.0004
Gm19680	ENSMUSG00000070960	predicted gene, 19680	-5.963	0.0310	0.0643
Gm19710	ENSMUSG00000105552	predicted gene, 19710	-9.585	0.0291	0.0608
Gm2174	ENSMUSG00000058932	predicted gene 2174	-6.166	0.0008	0.0025
Gm2420	ENSMUSG00000082305	predicted gene 2420	-7.346	0.0412	0.0819
Gm2423	ENSMUSG00000061724	predicted gene 2423	-5.905	0.0004	0.0013
Gm25612	ENSMUSG00000077202	predicted gene, 25612	-4.797	0.0338	0.0692
Gm26782	ENSMUSG00000097431	predicted gene, 26782	-2.026	0.0000	0.0000
Gm26877	ENSMUSG00000097373	predicted gene, 26877	-26.866	0.0022	0.0063
Gm26947	ENSMUSG00000098055	predicted gene, 26947	-1.987	0.0231	0.0498
Gm27252	ENSMUSG00000098708	predicted gene 27252	-2.720	0.0174	0.0389
Gm2805	ENSMUSG00000116536	predicted gene 2805	-3.926	0.0342	0.0698
Gm28119	ENSMUSG00000100158	predicted gene 28119	-8.135	0.0440	0.0867
Gm29188	ENSMUSG00000099622	predicted gene 29188	-2.118	0.0030	0.0082
Gm2a	ENSMUSG00000000594	GM2 ganglioside activator protein	-1.639	0.0000	0.0000
Gm3052	ENSMUSG00000101462	predicted gene 3052	-7.320	0.0298	0.0621
Gm30556	ENSMUSG00000115180	predicted gene, 30556	-1.776	0.0012	0.0037
Gm31036	ENSMUSG00000110475	predicted gene, 31036	-11.833	0.0134	0.0311
Gm3235	ENSMUSG00000090778	predicted gene 3235	-1.846	0.0507	0.0977
Gm33474	ENSMUSG00000106554	predicted gene, 33474	-11.747	0.0121	0.0283
Gm33609	ENSMUSG00000104736	predicted gene, 33609	-2.981	0.0000	0.0001
Gm35021	ENSMUSG00000109714	predicted gene, 35021	-1.733	0.0058	0.0148
Gm36371	ENSMUSG00000109108	predicted gene, 36371	-1.826	0.0017	0.0050
Gm36535	ENSMUSG00000105376	predicted gene, 36535	-2.184	0.0285	0.0597
Gm3695	ENSMUSG00000067224	predicted gene 3695	-3.615	0.0004	0.0013
Gm37784	ENSMUSG00000102525	predicted gene, 37784	-18.411	0.0053	0.0138
Gm37981	ENSMUSG00000103137	predicted gene, 37981	-10.969	0.0135	0.0312
Gm38250	ENSMUSG00000104168	predicted gene, 38250	-2.111	0.0468	0.0915
Gm38534	ENSMUSG00000108634	predicted gene, 38534	-2.664	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm38832	ENSMUSG00000108371	predicted gene, 38832	-3.574	0.0417	0.0828
Gm39317	ENSMUSG00000111056	predicted gene, 39317	-4.543	0.0039	0.0103
Gm40457	ENSMUSG00000108626	predicted gene, 40457	-2.811	0.0000	0.0000
Gm42208	ENSMUSG00000106140	predicted gene, 42208	-31.318	0.0003	0.0009
Gm42917	ENSMUSG00000104985	predicted gene 42917	-13.877	0.0084	0.0206
Gm43080	ENSMUSG00000105556	predicted gene 43080	-1.532	0.0309	0.0640
Gm43660	ENSMUSG00000107352	predicted gene 43660	-3.489	0.0391	0.0783
Gm43691	ENSMUSG00000104776	predicted gene 43691	-5.780	0.0182	0.0404
Gm43860	ENSMUSG00000106928	predicted gene 43860	-3.365	0.0111	0.0264
Gm45151	ENSMUSG00000108736	predicted gene 45151	-4.996	0.0398	0.0796
Gm45203	ENSMUSG00000108494	predicted gene 45203	-2.349	0.0166	0.0374
Gm45441	ENSMUSG00000110020	predicted gene 45441	-5.292	0.0254	0.0540
Gm45777	ENSMUSG00000110677	predicted gene 45777	-2.772	0.0200	0.0441
Gm4681	ENSMUSG00000115146	predicted gene 4681	-5.205	0.0281	0.0590
Gm47283	ENSMUSG00000096768	predicted gene, 47283	-1.955	0.0190	0.0419
Gm47322	ENSMUSG00000113789	predicted gene, 47322	-2.798	0.0086	0.0209
Gm47438	ENSMUSG00000111947	predicted gene, 47438	-18.479	0.0038	0.0102
Gm47708	ENSMUSG00000112188	predicted gene, 47708	-8.487	0.0062	0.0157
Gm48194	ENSMUSG00000114835	predicted gene, 48194	-4.741	0.0125	0.0293
Gm48336	ENSMUSG00000112952	predicted gene, 48336	-1.909	0.0290	0.0606
Gm49249	ENSMUSG00000115480	predicted gene, 49249	-15.557	0.0113	0.0268
Gm49327	ENSMUSG00000113536	predicted gene, 49327	-2.139	0.0374	0.0754
Gm4953	ENSMUSG00000061992	predicted pseudogene 4953	-7.623	0.0039	0.0105
Gm49593	ENSMUSG00000116081	predicted gene, 49593	-6.367	0.0106	0.0252
Gm49601	ENSMUSG00000116594	predicted gene, 49601	-6.538	0.0479	0.0933
Gm50203	ENSMUSG00000118243	predicted gene, 50203	-17.208	0.0058	0.0147
Gm50357	ENSMUSG00000117951	predicted gene, 50357	-1.750	0.0026	0.0071
Gm5040	ENSMUSG00000111880	predicted gene 5040	-18.682	0.0061	0.0154
Gm50419	ENSMUSG00000118024	predicted gene, 50419	-2.867	0.0051	0.0133
Gm5069	ENSMUSG00000055676	predicted pseudogene 5069	-1.708	0.0001	0.0005
Gm5431	ENSMUSG00000058163	predicted gene 5431	-2.106	0.0498	0.0963

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5454	ENSMUSG00000047643	predicted gene 5454	-20.462	0.0007	0.0022
Gm5463	ENSMUSG00000114892	predicted gene 5463	-2.174	0.0117	0.0275
Gm5801	ENSMUSG00000058581	predicted pseudogene 5801	-1.897	0.0056	0.0143
Gm5863	ENSMUSG00000082927	predicted gene 5863	-3.762	0.0002	0.0006
Gm5864	ENSMUSG00000107211	predicted gene 5864	-2.944	0.0050	0.0130
Gm5903	ENSMUSG00000082988	predicted gene 5903	-5.982	0.0457	0.0895
Gm5944	ENSMUSG00000081034	predicted gene 5944	-2.879	0.0489	0.0949
Gm6136	ENSMUSG00000084106	predicted pseudogene 6136	-1.807	0.0406	0.0809
Gm6169	ENSMUSG00000057762	predicted gene 6169	-21.506	0.0022	0.0063
Gm6180	ENSMUSG00000053038	predicted pseudogene 6180	-15.440	0.0041	0.0109
Gm6210	ENSMUSG00000107951	predicted gene 6210	-1.794	0.0257	0.0546
Gm6218	ENSMUSG00000112145	predicted gene 6218	-18.704	0.0020	0.0058
Gm6463	ENSMUSG00000098231	predicted gene 6463	-23.061	0.0032	0.0087
Gm6665	ENSMUSG00000091561	predicted gene 6665	-6.075	0.0048	0.0126
Gm6705	ENSMUSG00000116958	predicted gene 6705	-7.970	0.0478	0.0931
Gm6969	ENSMUSG00000066553	predicted pseudogene 6969	-1.786	0.0000	0.0000
Gm7084	ENSMUSG00000114894	predicted gene 7084	-4.535	0.0378	0.0761
Gm7357	ENSMUSG00000102269	predicted gene 7357	-5.557	0.0039	0.0105
Gm7488	ENSMUSG00000039617	predicted gene 7488	-17.783	0.0023	0.0064
Gm7507	ENSMUSG00000098142	predicted gene 7507	-2.631	0.0010	0.0029
Gm7543	ENSMUSG00000115738	predicted gene 7543	-6.270	0.0379	0.0763
Gm7598	ENSMUSG00000087390	predicted gene 7598	-2.168	0.0237	0.0508
Gm7607	ENSMUSG00000111085	predicted gene 7607	-15.693	0.0190	0.0421
Gm7633	ENSMUSG00000114606	predicted gene 7633	-3.468	0.0375	0.0756
Gm7658	ENSMUSG00000082935	predicted gene 7658	-1.581	0.0032	0.0087
Gm7879	ENSMUSG00000033036	predicted pseudogene 7879	-4.742	0.0003	0.0011
Gm8100	ENSMUSG00000098056	predicted gene 8100	-3.216	0.0373	0.0751
Gm8186	ENSMUSG00000049124	predicted gene 8186	-4.079	0.0000	0.0001
Gm8355	ENSMUSG00000093798	predicted pseudogene 8355	-2.064	0.0325	0.0670
Gm8615	ENSMUSG00000024437	predicted pseudogene 8615	-2.086	0.0000	0.0001
Gm8692	ENSMUSG00000082755	predicted gene 8692	-7.342	0.0476	0.0927

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm8825	ENSMUSG00000098105	predicted gene 8825	-3.565	0.0469	0.0915
Gm9108	ENSMUSG00000115819	predicted gene 9108	-3.418	0.0002	0.0008
Gm9164	ENSMUSG00000082322	predicted gene 9164	-3.389	0.0446	0.0877
Gm9294	ENSMUSG00000044609	predicted pseudogene 9294	-6.380	0.0241	0.0517
Gm9416	ENSMUSG00000117476	predicted gene 9416	-10.864	0.0441	0.0869
Gm9512	ENSMUSG00000113389	predicted gene 9512	-3.136	0.0100	0.0240
Gm9762	ENSMUSG00000037096	predicted pseudogene 9762	-2.990	0.0001	0.0002
Gm9796	ENSMUSG00000045075	predicted gene 9796	-4.515	0.0036	0.0097
Gm9816	ENSMUSG00000085783	predicted pseudogene 9816	-7.387	0.0025	0.0069
Gm9961	ENSMUSG00000055015	predicted gene 9961	-3.515	0.0188	0.0416
Gna14	ENSMUSG00000024697	guanine nucleotide binding protein, alpha 14	-2.354	0.0092	0.0222
Gna15	ENSMUSG00000034792	guanine nucleotide binding protein, alpha 15	-1.904	0.0487	0.0945
Gnb1l	ENSMUSG00000000884	guanine nucleotide binding protein (G protein), beta polypeptide 1-like	-1.632	0.0022	0.0063
Gnb2	ENSMUSG00000029713	guanine nucleotide binding protein (G protein), beta 2	-1.581	0.0000	0.0000
Gnb3	ENSMUSG00000023439	guanine nucleotide binding protein (G protein), beta 3	-2.931	0.0000	0.0000
Gnmt	ENSMUSG00000002769	glycine N-methyltransferase	-3.232	0.0001	0.0002
Gnpda2	ENSMUSG00000029209	glucosamine-6-phosphate deaminase 2	-1.571	0.0006	0.0020
Gnptg	ENSMUSG00000035521	N-acetylglucosamine-1-phosphotransferase, gamma subunit	-1.722	0.0000	0.0000
Got1	ENSMUSG00000025190	glutamic-oxaloacetic transaminase 1, soluble	-1.661	0.0012	0.0036
Gpc2	ENSMUSG00000029510	glypican 2 (cerebroglycan)	-11.106	0.0294	0.0614
Gpr137c	ENSMUSG00000049092	G protein-coupled receptor 137C	-1.868	0.0002	0.0009
Gpr160	ENSMUSG00000037661	G protein-coupled receptor 160	-2.307	0.0206	0.0451
Gprc5a	ENSMUSG00000046733	G protein-coupled receptor, family C, group 5, member A	-5.272	0.0038	0.0101
Greb1	ENSMUSG00000036523	gene regulated by estrogen in breast cancer protein	-3.455	0.0449	0.0881
Grhpr	ENSMUSG00000035637	glyoxylate reductase/hydroxypyruvate reductase	-1.601	0.0000	0.0000
Grip2	ENSMUSG00000030098	glutamate receptor interacting protein 2	-2.045	0.0019	0.0054
Grn	ENSMUSG00000034708	granulin	-1.584	0.0000	0.0002
Grwd1	ENSMUSG00000053801	glutamate-rich WD repeat containing 1	-1.510	0.0000	0.0000
Gsn	ENSMUSG00000026879	gelsolin	-1.789	0.0000	0.0000
Gss	ENSMUSG00000027610	glutathione synthetase	-1.520	0.0001	0.0003
Gstm7	ENSMUSG00000004035	glutathione S-transferase, mu 7	-2.130	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gstp2	ENSMUSG00000038155	glutathione S-transferase, pi 2	-2.174	0.0281	0.0589
Gstt3	ENSMUSG00000001665	glutathione S-transferase, theta 3	-1.571	0.0160	0.0362
Gtpbp8	ENSMUSG00000022668	GTP-binding protein 8 (putative)	-1.526	0.0007	0.0023
Gys1	ENSMUSG00000003865	glycogen synthase 1, muscle	-1.555	0.0015	0.0045
H13	ENSMUSG00000019188	histocompatibility 13	-1.530	0.0000	0.0000
H2ac19	ENSMUSG00000063954	H2A clustered histone 19	-5.848	0.0348	0.0710
H2aj	ENSMUSG00000060032	H2J.A histone	-1.636	0.0000	0.0000
H2bc8	ENSMUSG00000058385	H2B clustered histone 8	-19.127	0.0021	0.0059
H2bu1-ps	ENSMUSG00000080712	H2B.U histone 1, pseudogene	-12.378	0.0118	0.0279
H2-Eb1	ENSMUSG00000060586	histocompatibility 2, class II antigen E beta	-1.998	0.0300	0.0625
H2-Oa	ENSMUSG00000024334	histocompatibility 2, O region alpha locus	-4.959	0.0357	0.0724
Hacd4	ENSMUSG00000028497	3-hydroxyacyl-CoA dehydratase 4	-1.526	0.0105	0.0251
Has1	ENSMUSG00000003665	hyaluronan synthase 1	-9.892	0.0442	0.0870
Hdac5	ENSMUSG00000008855	histone deacetylase 5	-1.629	0.0000	0.0000
Hdhd3	ENSMUSG00000038422	haloacid dehalogenase-like hydrolase domain containing 3	-2.118	0.0097	0.0233
Heatr6	ENSMUSG00000000976	HEAT repeat containing 6	-1.555	0.0000	0.0000
Hebp1	ENSMUSG00000042770	heme binding protein 1	-1.701	0.0000	0.0000
Hemk1	ENSMUSG00000032579	HemK methyltransferase family member 1	-1.664	0.0000	0.0000
Herpud1	ENSMUSG00000031770	homocysteine-inducible, endoplasmic reticulum stress-inducible, ubiquitin-like domain member 1	-2.327	0.0428	0.0845
Hexb	ENSMUSG00000021665	hexosaminidase B	-1.559	0.0000	0.0000
Hgh1	ENSMUSG00000022554	HGH1 homolog	-2.363	0.0000	0.0000
Hic2	ENSMUSG00000050240	hypermethylated in cancer 2	-1.533	0.0437	0.0862
Hid1	ENSMUSG00000034586	HID1 domain containing	-1.769	0.0027	0.0076
Hipk4	ENSMUSG00000040424	homeodomain interacting protein kinase 4	-13.381	0.0121	0.0283
Hk1os	ENSMUSG00000085347	hexokinase 1, opposite strand	-5.118	0.0413	0.0822
Hmgn2	ENSMUSG00000003038	high mobility group nucleosomal binding domain 2	-1.686	0.0011	0.0033
Hmox1	ENSMUSG00000005413	heme oxygenase 1	-3.335	0.0016	0.0046
Hpcal4	ENSMUSG00000046093	hippocalcin-like 4	-8.139	0.0505	0.0974
Hpn	ENSMUSG00000001249	hepsin	-1.672	0.0016	0.0047
Hps6	ENSMUSG00000074811	HPS6, biogenesis of lysosomal organelles complex 2 subunit 3	-1.534	0.0000	0.0000
Hrh1	ENSMUSG00000053004	histamine receptor H1	-2.129	0.0134	0.0309

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hrob	ENSMUSG00000034773	homologous recombination factor with OB-fold	-2.645	0.0421	0.0836
Hs3st1	ENSMUSG00000051022	heparan sulfate (glucosamine) 3-O-sulfotransferase 1	-1.773	0.0100	0.0241
Hspb6	ENSMUSG00000036854	heat shock protein, alpha-crystallin-related, B6	-1.528	0.0000	0.0000
Hspb7	ENSMUSG00000006221	heat shock protein family, member 7 (cardiovascular)	-2.242	0.0000	0.0000
Htr2b	ENSMUSG00000026228	5-hydroxytryptamine (serotonin) receptor 2B	-39.725	0.0005	0.0017
Hvcn1	ENSMUSG00000064267	hydrogen voltage-gated channel 1	-1.745	0.0027	0.0074
Hyal3	ENSMUSG00000036091	hyaluronoglucosaminidase 3	-3.640	0.0285	0.0597
Idh2	ENSMUSG00000030541	isocitrate dehydrogenase 2 (NADP+), mitochondrial	-1.986	0.0000	0.0000
Ido1	ENSMUSG00000031551	indoleamine 2,3-dioxygenase 1	-2.161	0.0487	0.0946
Ifi203-ps	ENSMUSG00000090222	interferon activated gene 203, pseudogene	-1.592	0.0049	0.0128
Ifi27	ENSMUSG00000064215	interferon, alpha-inducible protein 27	-1.609	0.0000	0.0001
Ifit1bl1	ENSMUSG00000079339	interferon induced protein with tetratricpeptide repeats 1B like 1	-1.567	0.0001	0.0003
Ifitm10	ENSMUSG00000045777	interferon induced transmembrane protein 10	-2.111	0.0046	0.0120
Ifitm3	ENSMUSG00000025492	interferon induced transmembrane protein 3	-1.507	0.0001	0.0004
Ift140	ENSMUSG00000024169	intraflagellar transport 140	-1.528	0.0006	0.0018
Ift22	ENSMUSG00000007987	intraflagellar transport 22	-1.560	0.0000	0.0000
Igfals	ENSMUSG00000046070	insulin-like growth factor binding protein, acid labile subunit	-3.090	0.0092	0.0222
Igfbp6	ENSMUSG00000023046	insulin-like growth factor binding protein 6	-1.875	0.0000	0.0001
Ighm	ENSMUSG00000076617	immunoglobulin heavy constant mu	-1.920	0.0013	0.0039
Igkc	ENSMUSG00000076609	immunoglobulin kappa constant	-2.841	0.0008	0.0026
Iglc2	ENSMUSG00000076937	immunoglobulin lambda constant 2	-14.437	0.0416	0.0826
Il11ra1	ENSMUSG00000073889	interleukin 11 receptor, alpha chain 1	-1.783	0.0000	0.0000
Il16	ENSMUSG00000001741	interleukin 16	-1.509	0.0002	0.0008
Impdh1	ENSMUSG00000003500	inosine monophosphate dehydrogenase 1	-1.675	0.0000	0.0000
Inha	ENSMUSG00000032968	inhibin alpha	-1.869	0.0000	0.0001
Inmt	ENSMUSG00000003477	indolethylamine N-methyltransferase	-2.326	0.0006	0.0018
Inpp5b	ENSMUSG00000028894	inositol polyphosphate-5-phosphatase B	-1.585	0.0000	0.0000
Insc	ENSMUSG00000048782	INSC spindle orientation adaptor protein	-7.266	0.0020	0.0057
Ints1	ENSMUSG00000029547	integrator complex subunit 1	-1.711	0.0000	0.0000
Invs	ENSMUSG00000028344	inversin	-1.724	0.0017	0.0049
Ip6k3	ENSMUSG00000024210	inositol hexaphosphate kinase 3	-1.853	0.0068	0.0170

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ipo11	ENSMUSG00000042590	importin 11	-1.539	0.0000	0.0000
Iqce	ENSMUSG00000036555	IQ motif containing E	-1.502	0.0214	0.0466
Iqgap2	ENSMUSG00000021676	IQ motif containing GTPase activating protein 2	-1.984	0.0000	0.0000
Irf3	ENSMUSG00000003184	interferon regulatory factor 3	-1.508	0.0001	0.0002
Isoc2b	ENSMUSG00000052605	isochorismatase domain containing 2b	-2.153	0.0029	0.0080
Itga10	ENSMUSG00000090210	integrin, alpha 10	-2.323	0.0108	0.0258
Itga7	ENSMUSG00000025348	integrin alpha 7	-1.530	0.0000	0.0000
Itgb4	ENSMUSG00000020758	integrin beta 4	-1.601	0.0475	0.0925
Itgb7	ENSMUSG00000001281	integrin beta 7	-2.111	0.0286	0.0599
Itih6	ENSMUSG00000087149	inter-alpha-trypsin inhibitor heavy chain family member 6	-5.514	0.0179	0.0398
Itpa-ps1	ENSMUSG00000081476	inosine triphosphatase (nucleoside triphosphate pyrophosphatase) pseudogene 1	-3.469	0.0043	0.0114
Itpr3	ENSMUSG00000042644	inositol 1,4,5-triphosphate receptor 3	-1.826	0.0000	0.0000
Jam2	ENSMUSG00000053062	junction adhesion molecule 2	-1.877	0.0000	0.0000
Kansl2-ps	ENSMUSG00000097530	KAT8 regulatory NSL complex subunit 2, pseudogene	-2.703	0.0031	0.0084
Kat2b-ps	ENSMUSG00000053208	K(lysine) acetyltransferase 2B, pseudogene	-4.216	0.0458	0.0896
Kcne1	ENSMUSG00000039639	potassium voltage-gated channel, Isk-related subfamily, member 1	-2.127	0.0306	0.0636
Kcne1l	ENSMUSG00000090122	potassium voltage-gated channel, Isk-related family, member 1-like, pseudogene	-4.653	0.0388	0.0778
Kcnj11	ENSMUSG00000096146	potassium inwardly rectifying channel, subfamily J, member 11	-1.655	0.0000	0.0000
Kcnj8	ENSMUSG00000030247	potassium inwardly-rectifying channel, subfamily J, member 8	-1.548	0.0000	0.0000
Kcnk1	ENSMUSG00000033998	potassium channel, subfamily K, member 1	-2.935	0.0066	0.0166
Kcnmb2	ENSMUSG00000037610	potassium large conductance calcium-activated channel, subfamily M, beta member 2	-5.993	0.0197	0.0435
Kcnq1	ENSMUSG00000009545	potassium voltage-gated channel, subfamily Q, member 1	-1.580	0.0000	0.0000
Kcnv2	ENSMUSG00000047298	potassium channel, subfamily V, member 2	-1.603	0.0134	0.0310
Kif21b	ENSMUSG00000041642	kinesin family member 21B	-1.567	0.0148	0.0338
Kif26b	ENSMUSG00000026494	kinesin family member 26B	-1.891	0.0001	0.0003
Kif28	ENSMUSG00000087236	kinesin family member 28	-2.179	0.0021	0.0059
Kifc2	ENSMUSG00000004187	kinesin family member C2	-1.596	0.0059	0.0151
Klf8	ENSMUSG00000041649	Kruppel-like factor 8	-4.872	0.0019	0.0054
Klrb1c	ENSMUSG00000030325	killer cell lectin-like receptor subfamily B member 1C	-6.688	0.0211	0.0461
Krt19	ENSMUSG00000020911	keratin 19	-2.996	0.0170	0.0381
Krt80	ENSMUSG00000037185	keratin 80	-1.809	0.0189	0.0418

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kyat3	ENSMUSG00000040213	kynurenine aminotransferase 3	-2.104	0.0000	0.0000
L1cam	ENSMUSG00000031391	L1 cell adhesion molecule	-1.568	0.0132	0.0305
Lad1	ENSMUSG00000041782	ladinin	-1.921	0.0116	0.0273
Lair1	ENSMUSG00000055541	leukocyte-associated Ig-like receptor 1	-1.919	0.0347	0.0707
Lamtor4	ENSMUSG00000050552	late endosomal/lysosomal adaptor, MAPK and MTOR activator 4	-1.706	0.0000	0.0000
Lbp	ENSMUSG00000016024	lipopolysaccharide binding protein	-2.237	0.0056	0.0143
Lcn2	ENSMUSG00000026822	lipocalin 2	-2.903	0.0297	0.0620
Ldhd	ENSMUSG00000031958	lactate dehydrogenase D	-1.806	0.0000	0.0000
Lgals3	ENSMUSG00000050335	lectin, galactose binding, soluble 3	-3.630	0.0002	0.0006
Lgals9	ENSMUSG00000001123	lectin, galactose binding, soluble 9	-1.830	0.0000	0.0000
Lhcgr	ENSMUSG00000024107	luteinizing hormone/choriogonadotropin receptor	-8.884	0.0458	0.0897
Lilra6	ENSMUSG00000030427	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 6	-2.656	0.0137	0.0316
Lims2	ENSMUSG00000024395	LIM and senescent cell antigen like domains 2	-1.675	0.0000	0.0000
Lin7b	ENSMUSG00000003872	lin-7 homolog B, crumbs cell polarity complex component	-2.149	0.0350	0.0713
Lnx1	ENSMUSG00000029228	ligand of numb-protein X 1	-1.830	0.0066	0.0165
Loxl3	ENSMUSG00000000693	lysyl oxidase-like 3	-1.581	0.0046	0.0120
Lpin3	ENSMUSG00000027412	lipin 3	-1.647	0.0077	0.0190
Lrg1	ENSMUSG00000037095	leucine-rich alpha-2-glycoprotein 1	-2.337	0.0052	0.0135
Lrp2	ENSMUSG00000027070	low density lipoprotein receptor-related protein 2	-6.754	0.0412	0.0819
Lrrc14b	ENSMUSG00000021579	leucine rich repeat containing 14B	-1.616	0.0000	0.0001
Lrrc8c	ENSMUSG00000054720	leucine rich repeat containing 8 family, member C	-1.509	0.0004	0.0014
Lrrk1	ENSMUSG00000015133	leucine-rich repeat kinase 1	-1.661	0.0000	0.0000
Lrrn2	ENSMUSG00000026443	leucine rich repeat protein 2, neuronal	-1.765	0.0284	0.0595
Lrrn4	ENSMUSG00000043110	leucine rich repeat neuronal 4	-22.490	0.0073	0.0181
Lrsam1	ENSMUSG00000026792	leucine rich repeat and sterile alpha motif containing 1	-1.593	0.0000	0.0000
Lrwd1	ENSMUSG00000029703	leucine-rich repeats and WD repeat domain containing 1	-2.092	0.0000	0.0000
Lss	ENSMUSG00000033105	lanosterol synthase	-1.573	0.0392	0.0785
Lypd6	ENSMUSG00000050447	LY6/PLAUR domain containing 6	-2.354	0.0000	0.0000
Lysmd4	ENSMUSG00000043831	LysM, putative peptidoglycan-binding, domain containing 4	-1.542	0.0000	0.0000
Lzts1	ENSMUSG00000036306	leucine zipper, putative tumor suppressor 1	-1.720	0.0041	0.0109
Mag	ENSMUSG00000036634	myelin-associated glycoprotein	-18.489	0.0026	0.0073

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Magee1	ENSMUSG00000031227	MAGE family member E1	-1.510	0.0115	0.0271
Maml3	ENSMUSG00000061143	mastermind like transcriptional coactivator 3	-1.593	0.0007	0.0021
Mamld1	ENSMUSG00000059401	mastermind-like domain containing 1	-1.515	0.0094	0.0227
Mamstr	ENSMUSG00000042918	MEF2 activating motif and SAP domain containing transcriptional regulator	-1.788	0.0000	0.0000
Man2b1	ENSMUSG00000005142	mannosidase 2, alpha B1	-1.827	0.0000	0.0000
Man2c1	ENSMUSG00000032295	mannosidase, alpha, class 2C, member 1	-1.579	0.0000	0.0000
Map3k21	ENSMUSG00000031853	mitogen-activated protein kinase kinase kinase 21	-1.904	0.0029	0.0080
Map6d1	ENSMUSG00000041205	MAP6 domain containing 1	-2.662	0.0256	0.0544
Marchf3	ENSMUSG00000032656	membrane associated ring-CH-type finger 3	-1.730	0.0002	0.0007
Mbp	ENSMUSG00000041607	myelin basic protein	-2.014	0.0000	0.0001
Mdfi	ENSMUSG00000032717	MyoD family inhibitor	-2.377	0.0155	0.0353
Med9	ENSMUSG00000061650	mediator complex subunit 9	-1.706	0.0000	0.0000
Mettl11b	ENSMUSG00000040113	methyltransferase like 11B	-3.708	0.0002	0.0008
Mettl26	ENSMUSG00000025731	methyltransferase like 26	-1.786	0.0000	0.0000
Mettl27	ENSMUSG00000040557	methyltransferase like 27	-1.823	0.0012	0.0037
Mettl5os	ENSMUSG00000085735	methyltransferase like 5, opposite strand	-6.808	0.0144	0.0329
Mfap4	ENSMUSG00000042436	microfibrillar-associated protein 4	-2.562	0.0132	0.0307
Mfng	ENSMUSG00000018169	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.503	0.0000	0.0001
Mfsd13a	ENSMUSG00000025227	major facilitator superfamily domain containing 13a	-1.765	0.0010	0.0030
Mfsd2b	ENSMUSG00000037336	major facilitator superfamily domain containing 2B	-2.142	0.0301	0.0627
Mfsd4b3-ps	ENSMUSG00000071335	major facilitator superfamily domain containing 4B3, pseudogene	-1.772	0.0014	0.0040
Mgmt	ENSMUSG00000054612	O-6-methylguanine-DNA methyltransferase	-1.657	0.0002	0.0008
Mid1	ENSMUSG00000035299	midline 1	-1.581	0.0399	0.0798
Mindy4	ENSMUSG00000038022	MINDY lysine 48 deubiquitinase 4	-1.592	0.0260	0.0551
Mir5125	ENSMUSG00000092981	microRNA 5125	-5.618	0.0007	0.0022
Misp3	ENSMUSG00000074217	MISP family member 3	-2.023	0.0004	0.0014
Mllt1	ENSMUSG00000024212	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 1	-1.604	0.0000	0.0000
Mmel1	ENSMUSG00000058183	membrane metallo-endopeptidase-like 1	-2.378	0.0020	0.0059
Mmp2	ENSMUSG00000031740	matrix metallopeptidase 2	-1.548	0.0031	0.0084
Mmp28	ENSMUSG00000020682	matrix metallopeptidase 28 (epilysin)	-1.989	0.0004	0.0014
Mmp9	ENSMUSG00000017737	matrix metallopeptidase 9	-2.725	0.0003	0.0010

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mmrn1	ENSMUSG00000054641	multimerin 1	-1.720	0.0403	0.0804
Mov10l1	ENSMUSG00000015365	Mov10 like RISC complex RNA helicase 1	-1.522	0.0006	0.0020
Mpg	ENSMUSG00000020287	N-methylpurine-DNA glycosylase	-1.663	0.0000	0.0001
Mpp2	ENSMUSG00000017314	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)	-1.612	0.0000	0.0002
Mrgprd	ENSMUSG00000051207	MAS-related GPR, member D	-9.947	0.0432	0.0853
Mrm2	ENSMUSG00000029557	mitochondrial rRNA methyltransferase 2	-1.882	0.0005	0.0017
Mrpl10	ENSMUSG00000001445	mitochondrial ribosomal protein L10	-1.543	0.0000	0.0000
Mrpl17	ENSMUSG00000030879	mitochondrial ribosomal protein L17	-1.666	0.0000	0.0000
Mrpl22	ENSMUSG00000020514	mitochondrial ribosomal protein L22	-1.644	0.0000	0.0000
Mrpl23-ps1	ENSMUSG00000075279	mitichondrial ribosomal protein L23, pseudogene 1	-2.423	0.0126	0.0294
Mrpl28	ENSMUSG00000024181	mitochondrial ribosomal protein L28	-1.631	0.0000	0.0000
Mrpl37	ENSMUSG00000028622	mitochondrial ribosomal protein L37	-1.706	0.0000	0.0000
Mrpl38	ENSMUSG00000020775	mitochondrial ribosomal protein L38	-1.949	0.0000	0.0000
Mrpl41	ENSMUSG00000036850	mitochondrial ribosomal protein L41	-1.632	0.0000	0.0000
Mrpl58	ENSMUSG00000018858	mitochondrial ribosomal protein L58	-1.673	0.0000	0.0000
Mrps26	ENSMUSG00000037740	mitochondrial ribosomal protein S26	-1.568	0.0000	0.0000
Mrps34	ENSMUSG00000038880	mitochondrial ribosomal protein S34	-1.503	0.0000	0.0000
Mrtfa	ENSMUSG00000042292	myocardin related transcription factor A	-1.808	0.0000	0.0000
Ms4a14	ENSMUSG00000099398	membrane-spanning 4-domains, subfamily A, member 14	-2.880	0.0501	0.0967
Msantd1	ENSMUSG00000051246	Myb/SANT-like DNA-binding domain containing 1	-5.129	0.0027	0.0075
Msln	ENSMUSG00000063011	mesothelin	-16.377	0.0012	0.0037
Mst1r	ENSMUSG00000032584	macrophage stimulating 1 receptor (c-met-related tyrosine kinase)	-2.110	0.0002	0.0005
Mt1	ENSMUSG00000031765	metallothionein 1	-2.236	0.0463	0.0905
Mt2	ENSMUSG00000031762	metallothionein 2	-4.938	0.0294	0.0613
Muc1	ENSMUSG00000042784	mucin 1, transmembrane	-2.744	0.0350	0.0712
Muc16	ENSMUSG00000109564	mucin 16	-28.942	0.0005	0.0017
Mvd	ENSMUSG00000006517	mevalonate (diphospho) decarboxylase	-1.852	0.0000	0.0000
Myadml2os	ENSMUSG00000084822	myeloid-associated differentiation marker-like 2, opposite strand	-2.800	0.0289	0.0605
Myc	ENSMUSG00000022346	myelocytomatosis oncogene	-1.909	0.0113	0.0268
Myl3	ENSMUSG00000059741	myosin, light polypeptide 3	-1.534	0.0000	0.0000
Myoc	ENSMUSG00000026697	myocilin	-1.949	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Myrf	ENSMUSG00000036098	myelin regulatory factor	-1.864	0.0001	0.0005
Myrip	ENSMUSG00000041794	myosin VIIA and Rab interacting protein	-1.762	0.0006	0.0018
Mzb1	ENSMUSG00000024353	marginal zone B and B1 cell-specific protein 1	-5.195	0.0001	0.0005
Mzf1	ENSMUSG00000030380	myeloid zinc finger 1	-2.870	0.0153	0.0347
Mzt2	ENSMUSG00000022671	mitotic spindle organizing protein 2	-1.521	0.0004	0.0012
N4bp3	ENSMUSG00000001053	NEDD4 binding protein 3	-1.825	0.0000	0.0000
Nadsyn1	ENSMUSG00000031090	NAD synthetase 1	-1.947	0.0000	0.0000
Nagpa	ENSMUSG00000023143	N-acetylglucosamine-1-phosphodiester alpha-N-acetylglucosaminidase	-1.672	0.0000	0.0000
Naprt	ENSMUSG00000022574	nicotinate phosphoribosyltransferase	-1.639	0.0000	0.0000
Ncaph2	ENSMUSG00000008690	non-SMC condensin II complex, subunit H2	-1.765	0.0000	0.0000
Ncor2	ENSMUSG00000029478	nuclear receptor co-repressor 2	-1.720	0.0000	0.0000
Ncr1	ENSMUSG00000062524	natural cytotoxicity triggering receptor 1	-3.916	0.0320	0.0661
Ndor1	ENSMUSG00000006471	NADPH dependent diflavin oxidoreductase 1	-1.635	0.0014	0.0041
Ndrg3	ENSMUSG00000027634	N-myc downstream regulated gene 3	-1.514	0.0046	0.0120
Ndufc2	ENSMUSG00000030647	NADH:ubiquinone oxidoreductase subunit C2	-1.604	0.0000	0.0000
Necap2	ENSMUSG00000028923	NECAP endocytosis associated 2	-1.512	0.0001	0.0002
Neil2	ENSMUSG00000035121	nei like 2 (E. coli)	-1.711	0.0449	0.0882
Nek6	ENSMUSG00000026749	NIMA (never in mitosis gene a)-related expressed kinase 6	-2.160	0.0000	0.0000
Neurl2	ENSMUSG00000039873	neuralized E3 ubiquitin protein ligase 2	-1.769	0.0000	0.0000
Nfkbid	ENSMUSG00000036931	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, delta	-5.302	0.0111	0.0263
Nfkbie	ENSMUSG00000023947	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, epsilon	-1.884	0.0179	0.0398
Ngfr	ENSMUSG00000000120	nerve growth factor receptor (TNFR superfamily, member 16)	-2.573	0.0391	0.0783
Nipal3	ENSMUSG00000028803	NIPA-like domain containing 3	-1.592	0.0000	0.0000
Nkain4	ENSMUSG00000027574	Na+/K+ transporting ATPase interacting 4	-3.689	0.0204	0.0448
Nol12	ENSMUSG00000033099	nucleolar protein 12	-1.683	0.0000	0.0000
Nos1	ENSMUSG00000029361	nitric oxide synthase 1, neuronal	-11.561	0.0011	0.0033
Nos2	ENSMUSG00000020826	nitric oxide synthase 2, inducible	-1.517	0.0129	0.0300
Nox4	ENSMUSG00000030562	NADPH oxidase 4	-1.786	0.0401	0.0802
Npffr1	ENSMUSG00000020090	neuropeptide FF receptor 1	-17.225	0.0064	0.0162
Nppa	ENSMUSG00000041616	natriuretic peptide type A	-4.261	0.0024	0.0069
Npr1	ENSMUSG00000027931	natriuretic peptide receptor 1	-1.645	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Npy4r	ENSMUSG00000048337	neuropeptide Y receptor Y4	-3.154	0.0002	0.0009
Nr1h3	ENSMUSG00000002108	nuclear receptor subfamily 1, group H, member 3	-1.615	0.0001	0.0003
Nrap	ENSMUSG00000049134	nebulin-related anchoring protein	-1.557	0.0000	0.0000
Nrde2	ENSMUSG00000021179	nrde-2 necessary for RNA interference, domain containing	-1.867	0.0000	0.0000
Nubp2	ENSMUSG00000039183	nucleotide binding protein 2	-1.735	0.0000	0.0000
Nudt16	ENSMUSG00000032565	nudix (nucleoside diphosphate linked moiety X)-type motif 16	-1.591	0.0000	0.0001
Nudt16l1	ENSMUSG00000022516	nudix (nucleoside diphosphate linked moiety X)-type motif 16-like 1	-1.512	0.0000	0.0000
Nudt8	ENSMUSG00000110949	nudix (nucleoside diphosphate linked moiety X)-type motif 8	-2.634	0.0019	0.0056
Nup214	ENSMUSG00000001855	nucleoporin 214	-1.648	0.0000	0.0000
Nup85	ENSMUSG00000020739	nucleoporin 85	-1.621	0.0000	0.0000
Nupr1	ENSMUSG00000030717	nuclear protein transcription regulator 1	-1.701	0.0247	0.0528
Nxpe4	ENSMUSG00000044229	neurexophilin and PC-esterase domain family, member 4	-2.329	0.0059	0.0150
Ocln	ENSMUSG00000021638	occludin	-3.318	0.0329	0.0675
Ogdh	ENSMUSG00000020456	oxoglutarate (alpha-ketoglutarate) dehydrogenase (lipoamide)	-1.505	0.0000	0.0000
Oip5	ENSMUSG00000072980	Opa interacting protein 5	-3.361	0.0241	0.0516
Oplah	ENSMUSG00000022562	5-oxoprolinase (ATP-hydrolysing)	-1.845	0.0000	0.0000
Opn3	ENSMUSG00000026525	opsin 3	-1.721	0.0251	0.0534
Opn4	ENSMUSG00000021799	opsin 4 (melanopsin)	-2.313	0.0001	0.0003
Osbp2	ENSMUSG00000020435	oxysterol binding protein 2	-1.636	0.0000	0.0000
Oser1	ENSMUSG00000035399	oxidative stress responsive serine rich 1	-1.554	0.0035	0.0094
Otub1	ENSMUSG00000024767	OTU domain, ubiquitin aldehyde binding 1	-1.617	0.0000	0.0000
Oxa1l	ENSMUSG00000000959	oxidase assembly 1-like	-1.567	0.0000	0.0000
P2rx6	ENSMUSG00000022758	purinergic receptor P2X, ligand-gated ion channel, 6	-1.728	0.0034	0.0092
P2rx7	ENSMUSG00000029468	purinergic receptor P2X, ligand-gated ion channel, 7	-1.559	0.0013	0.0038
P2ry12	ENSMUSG00000036353	purinergic receptor P2Y, G-protein coupled 12	-3.125	0.0001	0.0003
Padi2	ENSMUSG00000028927	peptidyl arginine deiminase, type II	-3.186	0.0000	0.0000
Padi4	ENSMUSG00000025330	peptidyl arginine deiminase, type IV	-23.121	0.0086	0.0209
Pak5	ENSMUSG00000039913	p21 (RAC1) activated kinase 5	-9.604	0.0277	0.0583
Papln	ENSMUSG00000021223	papilin, proteoglycan-like sulfated glycoprotein	-1.896	0.0054	0.0139
Paqr7	ENSMUSG00000037348	progestin and adipoQ receptor family member VII	-1.840	0.0004	0.0012
Pbld1	ENSMUSG00000112129	phenazine biosynthesis-like protein domain containing 1	-2.293	0.0289	0.0605

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pcdhga4	ENSMUSG00000103677	protocadherin gamma subfamily A, 4	-2.450	0.0047	0.0124
Pcdhgc3	ENSMUSG00000102918	protocadherin gamma subfamily C, 3	-1.546	0.0002	0.0006
Pcif1	ENSMUSG00000039849	phosphorylated CTD interacting factor 1	-2.105	0.0000	0.0000
Pcolce2	ENSMUSG00000015354	procollagen C-endopeptidase enhancer 2	-1.629	0.0000	0.0000
Pcsk6	ENSMUSG00000030513	proprotein convertase subtilisin/kexin type 6	-1.527	0.0002	0.0006
Pcx	ENSMUSG00000024892	pyruvate carboxylase	-2.917	0.0000	0.0000
Pcyt2	ENSMUSG00000025137	phosphate cytidylyltransferase 2, ethanolamine	-1.575	0.0000	0.0000
Pdzd3	ENSMUSG00000032105	PDZ domain containing 3	-2.005	0.0008	0.0025
Peds1	ENSMUSG00000090213	plasmanylethanolamine desaturase 1	-1.708	0.0000	0.0000
Pelo	ENSMUSG00000042275	pelota mRNA surveillance and ribosome rescue factor	-1.958	0.0000	0.0000
Pepd	ENSMUSG00000063931	peptidase D	-1.516	0.0000	0.0000
Perm1	ENSMUSG00000078486	PPARGC1 and ESRR induced regulator, muscle 1	-1.554	0.0000	0.0001
Pex26	ENSMUSG00000067825	peroxisomal biogenesis factor 26	-1.557	0.0004	0.0013
Pgap2	ENSMUSG00000030990	post-GPI attachment to proteins 2	-1.748	0.0000	0.0000
Phykpl	ENSMUSG00000020359	5-phosphohydroxy-L-lysine phospholyase	-1.871	0.0000	0.0000
Pi16	ENSMUSG00000024011	peptidase inhibitor 16	-1.761	0.0015	0.0045
Pigl	ENSMUSG00000014245	phosphatidylinositol glycan anchor biosynthesis, class L	-1.584	0.0015	0.0045
Pigz	ENSMUSG00000045625	phosphatidylinositol glycan anchor biosynthesis, class Z	-4.232	0.0000	0.0000
Pik3ap1	ENSMUSG00000025017	phosphoinositide-3-kinase adaptor protein 1	-1.751	0.0107	0.0255
Pim2	ENSMUSG00000031155	proviral integration site 2	-1.650	0.0142	0.0326
Pisd-ps1	ENSMUSG00000082286	phosphatidylserine decarboxylase, pseudogene 1	-2.344	0.0292	0.0610
Pisd-ps2	ENSMUSG00000023795	phosphatidylserine decarboxylase, pseudogene 2	-2.790	0.0365	0.0739
Pitpnm2	ENSMUSG00000029406	phosphatidylinositol transfer protein, membrane-associated 2	-1.735	0.0000	0.0000
Pla2g15	ENSMUSG00000031903	phospholipase A2, group XV	-1.602	0.0000	0.0000
Plcd3	ENSMUSG00000020937	phospholipase C, delta 3	-1.816	0.0000	0.0002
Plch2	ENSMUSG00000029055	phospholipase C, eta 2	-4.078	0.0049	0.0129
Plekha7	ENSMUSG00000045659	pleckstrin homology domain containing, family A member 7	-1.511	0.0247	0.0528
Plekhf1	ENSMUSG00000074170	pleckstrin homology domain containing, family F (with FYVE domain) member 1	-1.844	0.0000	0.0000
Plekhn1	ENSMUSG00000078485	pleckstrin homology domain containing, family N member 1	-1.792	0.0310	0.0642
Plxdc1	ENSMUSG00000017417	plexin domain containing 1	-1.767	0.0000	0.0000
Plxna3	ENSMUSG00000031398	plexin A3	-2.496	0.0016	0.0048

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Plxnb1	ENSMUSG00000053646	plexin B1	-1.675	0.0000	0.0000
Pml	ENSMUSG00000036986	promyelocytic leukemia	-2.128	0.0000	0.0000
Pmp22	ENSMUSG00000018217	peripheral myelin protein 22	-1.551	0.0001	0.0004
Pnkp	ENSMUSG00000002963	polynucleotide kinase 3'- phosphatase	-1.615	0.0000	0.0000
Pno1	ENSMUSG00000020116	partner of NOB1 homolog	-1.506	0.0000	0.0000
Pole2	ENSMUSG00000020974	polymerase (DNA directed), epsilon 2 (p59 subunit)	-1.771	0.0318	0.0656
Poll	ENSMUSG00000025218	polymerase (DNA directed), lambda	-1.984	0.0000	0.0000
Polrmt	ENSMUSG00000020329	polymerase (RNA) mitochondrial (DNA directed)	-1.766	0.0000	0.0000
Ppan	ENSMUSG00000004100	peter pan homolog	-1.755	0.0000	0.0000
Ppara	ENSMUSG00000022383	peroxisome proliferator activated receptor alpha	-1.545	0.0000	0.0000
Ppard	ENSMUSG00000002250	peroxisome proliferator activator receptor delta	-1.700	0.0000	0.0000
Ppdpf	ENSMUSG00000016344	pancreatic progenitor cell differentiation and proliferation factor	-1.559	0.0000	0.0000
Ppm1j	ENSMUSG00000002228	protein phosphatase 1J	-1.729	0.0000	0.0000
Ppp1r3g	ENSMUSG00000050423	protein phosphatase 1, regulatory subunit 3G	-5.245	0.0230	0.0495
Ppp2r1a	ENSMUSG00000007564	protein phosphatase 2, regulatory subunit A, alpha	-1.523	0.0000	0.0000
Ppp5c	ENSMUSG00000003099	protein phosphatase 5, catalytic subunit	-1.686	0.0000	0.0000
Pradc1	ENSMUSG00000030008	protease-associated domain containing 1	-1.740	0.0000	0.0000
Prelid1	ENSMUSG00000021486	PRELI domain containing 1	-1.753	0.0000	0.0000
Prelp	ENSMUSG00000041577	proline arginine-rich end leucine-rich repeat	-1.907	0.0007	0.0022
Prim2	ENSMUSG00000026134	DNA primase, p58 subunit	-1.551	0.0038	0.0101
Prima1	ENSMUSG00000041669	proline rich membrane anchor 1	-11.002	0.0086	0.0210
Prkar1b	ENSMUSG00000025855	protein kinase, cAMP dependent regulatory, type I beta	-1.672	0.0003	0.0009
Prlr	ENSMUSG00000005268	prolactin receptor	-1.601	0.0055	0.0141
Prmt2	ENSMUSG00000020230	protein arginine N-methyltransferase 2	-1.588	0.0024	0.0067
Psmb10	ENSMUSG00000031897	proteasome (prosome, macropain) subunit, beta type 10	-1.816	0.0000	0.0000
Psmd13	ENSMUSG00000025487	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13	-1.530	0.0000	0.0000
Psmg4	ENSMUSG00000071451	proteasome (prosome, macropain) assembly chaperone 4	-1.676	0.0000	0.0001
Ptch2	ENSMUSG00000028681	patched 2	-3.857	0.0000	0.0000
Ptgds	ENSMUSG00000015090	prostaglandin D2 synthase (brain)	-4.062	0.0000	0.0000
Ptger4	ENSMUSG00000039942	prostaglandin E receptor 4 (subtype EP4)	-1.757	0.0002	0.0008
Ptgis	ENSMUSG00000017969	prostaglandin I2 (prostacyclin) synthase	-1.579	0.0121	0.0284

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ptpn22	ENSMUSG00000027843	protein tyrosine phosphatase, non-receptor type 22 (lymphoid)	-2.009	0.0303	0.0630
Ptpn23	ENSMUSG00000036057	protein tyrosine phosphatase, non-receptor type 23	-1.597	0.0000	0.0000
Ptprf	ENSMUSG00000033295	protein tyrosine phosphatase, receptor type, F	-1.510	0.0090	0.0218
Ptprn2	ENSMUSG00000056553	protein tyrosine phosphatase, receptor type, N polypeptide 2	-1.787	0.0142	0.0325
Ptrh1	ENSMUSG00000053746	peptidyl-tRNA hydrolase 1 homolog	-2.773	0.0000	0.0000
Pttg1	ENSMUSG00000020415	pituitary tumor-transforming gene 1	-1.581	0.0017	0.0050
Pusl1	ENSMUSG00000051557	pseudouridylate synthase-like 1	-1.754	0.0001	0.0002
Pycard	ENSMUSG00000030793	PYD and CARD domain containing	-2.225	0.0000	0.0001
Pycr1	ENSMUSG00000025140	pyrroline-5-carboxylate reductase 1	-2.275	0.0005	0.0015
Pycr2	ENSMUSG00000026520	pyrroline-5-carboxylate reductase family, member 2	-1.665	0.0001	0.0005
Rab29	ENSMUSG00000026433	RAB29, member RAS oncogene family	-1.901	0.0000	0.0000
Rab33a	ENSMUSG00000031104	RAB33A, member RAS oncogene family	-11.750	0.0113	0.0268
Rab34	ENSMUSG00000002059	RAB34, member RAS oncogene family	-1.877	0.0000	0.0000
Rab37	ENSMUSG00000020732	RAB37, member RAS oncogene family	-1.809	0.0106	0.0253
Rab3d	ENSMUSG00000019066	RAB3D, member RAS oncogene family	-1.641	0.0000	0.0000
Rabep2	ENSMUSG00000030727	rabaptin, RAB GTPase binding effector protein 2	-1.654	0.0001	0.0003
Rac2	ENSMUSG00000033220	Rac family small GTPase 2	-2.892	0.0000	0.0001
Rad1	ENSMUSG00000022248	RAD1 checkpoint DNA exonuclease	-1.831	0.0002	0.0007
Ramp1	ENSMUSG00000034353	receptor (calcitonin) activity modifying protein 1	-1.508	0.0105	0.0251
Ranbp17	ENSMUSG00000040594	RAN binding protein 17	-3.374	0.0004	0.0014
Rap1gap	ENSMUSG00000041351	Rap1 GTPase-activating protein	-1.792	0.0001	0.0004
Rapsn	ENSMUSG00000002104	receptor-associated protein of the synapse	-1.714	0.0001	0.0003
Rarg	ENSMUSG00000001288	retinoic acid receptor, gamma	-1.806	0.0000	0.0000
Rasa4	ENSMUSG00000004952	RAS p21 protein activator 4	-1.676	0.0002	0.0007
Rasgef1c	ENSMUSG00000020374	RasGEF domain family, member 1C	-2.281	0.0292	0.0610
Rasl11a	ENSMUSG00000029641	RAS-like, family 11, member A	-1.557	0.0139	0.0320
Rassf4	ENSMUSG00000042129	Ras association (RalGDS/AF-6) domain family member 4	-1.611	0.0141	0.0324
Rassf7	ENSMUSG00000038618	Ras association (RalGDS/AF-6) domain family (N-terminal) member 7	-1.854	0.0140	0.0322
Raver2	ENSMUSG00000035275	ribonucleoprotein, PTB-binding 2	-1.688	0.0046	0.0121
Rbm22	ENSMUSG00000024604	RNA binding motif protein 22	-1.516	0.0000	0.0000
Rdh12	ENSMUSG00000021123	retinol dehydrogenase 12	-2.835	0.0291	0.0609

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rdh5	ENSMUSG00000025350	retinol dehydrogenase 5	-1.891	0.0041	0.0107
Reln	ENSMUSG00000042453	reelin	-2.376	0.0000	0.0000
Relt	ENSMUSG00000008318	RELT tumor necrosis factor receptor	-1.530	0.0135	0.0311
Reps2	ENSMUSG00000040855	RALBP1 associated Eps domain containing protein 2	-1.681	0.0059	0.0149
Retnla	ENSMUSG00000061100	resistin like alpha	-2.577	0.0001	0.0004
Rfng	ENSMUSG00000025158	RFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase	-1.598	0.0000	0.0000
Rfx1	ENSMUSG00000031706	regulatory factor X, 1 (influences HLA class II expression)	-1.581	0.0042	0.0111
Rgs12	ENSMUSG00000029101	regulator of G-protein signaling 12	-1.766	0.0000	0.0000
Rgs14	ENSMUSG00000052087	regulator of G-protein signaling 14	-3.122	0.0074	0.0185
Rhof	ENSMUSG00000029449	ras homolog family member F (in filopodia)	-2.556	0.0002	0.0007
Rhog	ENSMUSG00000073982	ras homolog family member G	-1.787	0.0000	0.0000
Riiad1	ENSMUSG00000028139	regulatory subunit of type II PKA R-subunit (RIIa) domain containing 1	-3.061	0.0345	0.0704
Rint1	ENSMUSG00000028999	RAD50 interactor 1	-1.519	0.0000	0.0000
Ripor2	ENSMUSG00000036006	RHO family interacting cell polarization regulator 2	-1.659	0.0086	0.0209
Ripor3	ENSMUSG00000074577	RIPOR family member 3	-2.165	0.0427	0.0845
Rnase1	ENSMUSG00000035896	ribonuclease, RNase A family, 1 (pancreatic)	-5.670	0.0001	0.0003
Rnd2	ENSMUSG00000001313	Rho family GTPase 2	-1.554	0.0010	0.0032
Rnf113a1	ENSMUSG00000036537	ring finger protein 113A1	-2.968	0.0007	0.0021
Rnf31	ENSMUSG00000047098	ring finger protein 31	-1.681	0.0000	0.0000
Rnf41	ENSMUSG00000025373	ring finger protein 41	-1.745	0.0000	0.0000
Rnh1	ENSMUSG00000038650	ribonuclease/angiogenin inhibitor 1	-1.705	0.0000	0.0000
Rnps1-ps	ENSMUSG00000096403	RNA binding protein with serine rich domain 1, pseudogene	-1.515	0.0001	0.0002
Rogdi	ENSMUSG00000022540	rogdi homolog	-2.285	0.0000	0.0000
Rpl23a-ps3	ENSMUSG00000078126	ribosomal protein L23A, pseudogene 3	-2.117	0.0330	0.0678
Rpl28-ps1	ENSMUSG00000058603	ribosomal protein L28, pseudogene 1	-5.340	0.0114	0.0269
Rpl32l	ENSMUSG00000111356	ribosomal protein L32-like	-18.469	0.0226	0.0489
Rpl6	ENSMUSG00000029614	ribosomal protein L6	-1.504	0.0000	0.0000
Rpl6l	ENSMUSG00000091086	ribosomal protein L6-like	-3.783	0.0047	0.0122
Rplp2	ENSMUSG00000025508	ribosomal protein, large P2	-1.584	0.0000	0.0000
Rps15a-ps5	ENSMUSG00000067058	ribosomal protein S15A, pseudogene 5	-6.937	0.0333	0.0684
Rps15a-ps7	ENSMUSG00000081087	ribosomal protein S15A, pseudogene 7	-3.153	0.0010	0.0030

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rps15-ps2	ENSMUSG00000071419	ribosomal protein S15, pseudogene 2	-6.376	0.0005	0.0015
Rps18-ps6	ENSMUSG00000069117	ribosomal protein S18, pseudogene 6	-1.605	0.0000	0.0000
Rps26	ENSMUSG00000025362	ribosomal protein S26	-1.562	0.0000	0.0000
Rpsa-ps10	ENSMUSG00000047676	ribosomal protein SA, pseudogene 10	-4.015	0.0002	0.0007
Rpsa-ps7	ENSMUSG00000117438	ribosomal protein SA, pseudogene 7	-3.702	0.0451	0.0885
Rpsa-ps9	ENSMUSG00000082895	ribosomal protein SA, pseudogene 9	-3.631	0.0302	0.0628
Rrnad1	ENSMUSG00000004896	ribosomal RNA adenine dimethylase domain containing 1	-1.543	0.0088	0.0214
Rsl1d1	ENSMUSG00000005846	ribosomal L1 domain containing 1	-1.561	0.0000	0.0000
Rspo1	ENSMUSG00000028871	R-spondin 1	-2.557	0.0451	0.0884
Rtn2	ENSMUSG00000030401	reticulon 2 (Z-band associated protein)	-1.612	0.0000	0.0000
Rubcn	ENSMUSG00000035629	RUN domain and cysteine-rich domain containing, Beclin 1-interacting protein	-1.549	0.0000	0.0000
Rxfp1	ENSMUSG00000034009	relaxin/insulin-like family peptide receptor 1	-4.718	0.0002	0.0005
S100a8	ENSMUSG00000056054	S100 calcium binding protein A8 (calgranulin A)	-2.910	0.0183	0.0406
S100a9	ENSMUSG00000056071	S100 calcium binding protein A9 (calgranulin B)	-2.593	0.0401	0.0801
S1pr4	ENSMUSG00000044199	sphingosine-1-phosphate receptor 4	-3.337	0.0000	0.0001
Samd4b	ENSMUSG00000109336	sterile alpha motif domain containing 4B	-1.638	0.0000	0.0000
Sbf1	ENSMUSG00000036529	SET binding factor 1	-1.590	0.0000	0.0000
Sbk1	ENSMUSG00000042978	SH3-binding kinase 1	-1.790	0.0000	0.0000
Sbno2	ENSMUSG00000035673	strawberry notch 2	-1.859	0.0000	0.0000
Scarb1	ENSMUSG00000037936	scavenger receptor class B, member 1	-1.656	0.0000	0.0000
Scn3b	ENSMUSG00000049281	sodium channel, voltage-gated, type III, beta	-1.622	0.0029	0.0080
Scnn1a	ENSMUSG00000030340	sodium channel, nonvoltage-gated 1 alpha	-3.539	0.0000	0.0001
Scrib	ENSMUSG00000022568	scribbled planar cell polarity	-1.566	0.0000	0.0001
Sdc1	ENSMUSG00000020592	syndecan 1	-1.504	0.0061	0.0156
Sec14l2	ENSMUSG00000003585	SEC14-like lipid binding 2	-2.502	0.0219	0.0476
Sec61b	ENSMUSG00000053317	Sec61 beta subunit	-1.734	0.0000	0.0000
Selenbp2	ENSMUSG00000068877	selenium binding protein 2	-1.951	0.0007	0.0023
Selenon	ENSMUSG00000050989	selenoprotein N	-1.583	0.0002	0.0007
Selenos	ENSMUSG00000075701	selenoprotein S	-1.937	0.0000	0.0000
Selplg	ENSMUSG00000048163	selectin, platelet (p-selectin) ligand	-3.134	0.0000	0.0001
Sema3e	ENSMUSG00000063531	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3E	-3.183	0.0198	0.0436

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sema5a	ENSMUSG00000022231	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5A	-1.676	0.0486	0.0944
Sema5b	ENSMUSG00000052133	sema domain, seven thrombospondin repeats (type 1 and type 1-like), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 5B	-4.087	0.0025	0.0071
Sergef	ENSMUSG00000030839	secretion regulating guanine nucleotide exchange factor	-1.678	0.0000	0.0002
Serinc2	ENSMUSG00000023232	serine incorporator 2	-2.283	0.0428	0.0845
Setd4	ENSMUSG00000022948	SET domain containing 4	-2.301	0.0005	0.0016
Setmar	ENSMUSG00000034639	SET domain without mariner transposase fusion	-1.549	0.0023	0.0066
Sgip1	ENSMUSG00000028524	SH3-domain GRB2-like (endophilin) interacting protein 1	-1.747	0.0019	0.0055
Sgsh	ENSMUSG00000005043	N-sulfoglucosamine sulfohydrolase (sulfamidase)	-1.743	0.0000	0.0001
Sh3bp1	ENSMUSG00000022436	SH3-domain binding protein 1	-2.901	0.0002	0.0008
Shd	ENSMUSG00000039154	src homology 2 domain-containing transforming protein D	-2.470	0.0017	0.0049
Shisa6	ENSMUSG00000053930	shisa family member 6	-10.299	0.0157	0.0357
Shmt1	ENSMUSG00000020534	serine hydroxymethyltransferase 1 (soluble)	-1.841	0.0000	0.0000
Shmt2	ENSMUSG00000025403	serine hydroxymethyltransferase 2 (mitochondrial)	-1.726	0.0000	0.0000
Shroom1	ENSMUSG00000018387	shroom family member 1	-1.796	0.0440	0.0867
Sidt1	ENSMUSG00000022696	SID1 transmembrane family, member 1	-1.961	0.0387	0.0777
Sirt2	ENSMUSG00000015149	sirtuin 2	-1.855	0.0000	0.0000
Sirt4	ENSMUSG00000029524	sirtuin 4	-1.667	0.0000	0.0000
Siva1	ENSMUSG00000064326	SIVA1, apoptosis-inducing factor	-1.800	0.0000	0.0000
Six5	ENSMUSG00000040841	sine oculis-related homeobox 5	-1.527	0.0009	0.0027
Slamf8	ENSMUSG00000053318	SLAM family member 8	-2.803	0.0490	0.0949
Slc12a8	ENSMUSG00000035506	solute carrier family 12 (potassium/chloride transporters), member 8	-1.901	0.0399	0.0798
Slc12a9	ENSMUSG00000037344	solute carrier family 12 (potassium/chloride transporters), member 9	-1.571	0.0193	0.0426
Slc16a8	ENSMUSG00000032988	solute carrier family 16 (monocarboxylic acid transporters), member 8	-3.493	0.0068	0.0171
Slc19a3	ENSMUSG00000038496	solute carrier family 19, member 3	-1.950	0.0144	0.0329
Slc1a4	ENSMUSG00000020142	solute carrier family 1 (glutamate/neutral amino acid transporter), member 4	-1.875	0.0001	0.0005
Slc1a5	ENSMUSG00000001918	solute carrier family 1 (neutral amino acid transporter), member 5	-1.537	0.0003	0.0009
Slc1a7	ENSMUSG00000008932	solute carrier family 1 (glutamate transporter), member 7	-11.056	0.0064	0.0163
Slc25a31	ENSMUSG00000069041	solute carrier family 25 (mitochondrial carrier; adenine nucleotide translocator), member 31	-3.052	0.0205	0.0449
Slc25a35	ENSMUSG00000018740	solute carrier family 25, member 35	-1.944	0.0005	0.0017

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc25a45	ENSMUSG00000024818	solute carrier family 25, member 45	-1.871	0.0000	0.0000
Slc25a5	ENSMUSG00000016319	solute carrier family 25 (mitochondrial carrier, adenine nucleotide translocator), member 5	-1.551	0.0000	0.0000
Slc26a3	ENSMUSG00000001225	solute carrier family 26, member 3	-22.653	0.0014	0.0042
Slc27a1	ENSMUSG00000031808	solute carrier family 27 (fatty acid transporter), member 1	-1.588	0.0000	0.0000
Slc2a1	ENSMUSG00000028645	solute carrier family 2 (facilitated glucose transporter), member 1	-2.452	0.0120	0.0281
Slc2a9	ENSMUSG00000005107	solute carrier family 2 (facilitated glucose transporter), member 9	-1.967	0.0003	0.0009
Slc35c1	ENSMUSG00000049922	solute carrier family 35, member C1	-1.861	0.0000	0.0000
Slc37a2	ENSMUSG00000032122	solute carrier family 37 (glycerol-3-phosphate transporter), member 2	-1.792	0.0000	0.0001
Slc39a13	ENSMUSG00000002105	solute carrier family 39 (metal ion transporter), member 13	-1.525	0.0000	0.0000
Slc43a1	ENSMUSG00000027075	solute carrier family 43, member 1	-1.588	0.0445	0.0875
Slc43a3	ENSMUSG00000027074	solute carrier family 43, member 3	-1.526	0.0428	0.0846
Slc51a	ENSMUSG00000035699	solute carrier family 51, alpha subunit	-2.498	0.0049	0.0127
Slc5a11	ENSMUSG00000030769	solute carrier family 5 (sodium/glucose cotransporter), member 11	-7.067	0.0456	0.0893
Slc5a6	ENSMUSG00000006641	solute carrier family 5 (sodium-dependent vitamin transporter), member 6	-2.011	0.0000	0.0000
Slc9a1	ENSMUSG00000028854	solute carrier family 9 (sodium/hydrogen exchanger), member 1	-1.912	0.0000	0.0000
Slc9a2	ENSMUSG00000026062	solute carrier family 9 (sodium/hydrogen exchanger), member 2	-1.701	0.0018	0.0053
Slc9a4	ENSMUSG00000026065	solute carrier family 9 (sodium/hydrogen exchanger), member 4	-9.349	0.0009	0.0028
Slco2b1	ENSMUSG00000030737	solute carrier organic anion transporter family, member 2b1	-1.683	0.0000	0.0000
Slco4a1	ENSMUSG00000038963	solute carrier organic anion transporter family, member 4a1	-7.382	0.0503	0.0970
Slfn2	ENSMUSG00000072620	schlafen 2	-1.812	0.0000	0.0001
Slfn8	ENSMUSG00000035208	schlafen 8	-1.947	0.0009	0.0027
Slit1	ENSMUSG00000025020	slit guidance ligand 1	-6.744	0.0050	0.0129
Slit3	ENSMUSG00000056427	slit guidance ligand 3	-1.676	0.0109	0.0259
Smg9	ENSMUSG00000002210	SMG9 nonsense mediated mRNA decay factor	-1.528	0.0000	0.0000
Smim4	ENSMUSG00000058351	small integral membrane protein 4	-1.505	0.0040	0.0105
Smpd2	ENSMUSG00000019822	sphingomyelin phosphodiesterase 2, neutral	-1.501	0.0000	0.0000
Smpd3	ENSMUSG00000031906	sphingomyelin phosphodiesterase 3, neutral	-3.052	0.0000	0.0000
Snap29	ENSMUSG00000022765	synaptosomal-associated protein 29	-1.534	0.0000	0.0000
Snapc4	ENSMUSG00000036281	small nuclear RNA activating complex, polypeptide 4	-1.560	0.0166	0.0374
Snx32	ENSMUSG00000056185	sorting nexin 32	-1.954	0.0007	0.0022
Socs3	ENSMUSG00000053113	suppressor of cytokine signaling 3	-1.622	0.0297	0.0619

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sp2	ENSMUSG00000018678	Sp2 transcription factor	-1.600	0.0000	0.0000
Spata17	ENSMUSG00000026611	spermatogenesis associated 17	-2.800	0.0101	0.0242
Spats2l	ENSMUSG00000038305	spermatogenesis associated, serine-rich 2-like	-1.542	0.0001	0.0003
Spc24	ENSMUSG00000074476	SPC24, NDC80 kinetochore complex component, homolog (S. cerevisiae)	-1.578	0.0057	0.0147
Sphk2	ENSMUSG00000057342	sphingosine kinase 2	-2.120	0.0000	0.0000
Spint2	ENSMUSG00000074227	serine protease inhibitor, Kunitz type 2	-1.689	0.0000	0.0000
Spns2	ENSMUSG00000040447	spinster homolog 2	-1.828	0.0000	0.0001
Spon2	ENSMUSG00000037379	spondin 2, extracellular matrix protein	-2.496	0.0322	0.0663
Spsb2	ENSMUSG00000038451	splA/ryanodine receptor domain and SOCS box containing 2	-1.722	0.0201	0.0442
Srebf2	ENSMUSG00000022463	sterol regulatory element binding factor 2	-1.768	0.0000	0.0000
Srpk3	ENSMUSG00000002007	serine/arginine-rich protein specific kinase 3	-1.536	0.0003	0.0011
Srpx2	ENSMUSG00000031253	sushi-repeat-containing protein, X-linked 2	-1.655	0.0002	0.0009
Ssc4d	ENSMUSG00000029699	scavenger receptor cysteine rich family, 4 domains	-2.168	0.0053	0.0137
St3gal1	ENSMUSG00000013846	ST3 beta-galactoside alpha-2,3-sialyltransferase 1	-1.518	0.0004	0.0014
Stac2	ENSMUSG00000017400	SH3 and cysteine rich domain 2	-1.933	0.0081	0.0199
Steap3	ENSMUSG00000026389	STEAP family member 3	-1.625	0.0002	0.0005
Stk36	ENSMUSG00000033276	serine/threonine kinase 36	-2.153	0.0355	0.0721
Stmnd1	ENSMUSG00000063529	stathmin domain containing 1	-4.023	0.0420	0.0834
Ston1	ENSMUSG00000033855	stonin 1	-1.552	0.0256	0.0545
Sult6b2	ENSMUSG00000048473	sulfotransferase family 6B, member 2	-5.108	0.0243	0.0519
Surf1	ENSMUSG00000015790	surfeit gene 1	-1.511	0.0000	0.0000
Susd2	ENSMUSG00000006342	sushi domain containing 2	-2.090	0.0003	0.0011
Sv2b	ENSMUSG00000053025	synaptic vesicle glycoprotein 2 b	-2.597	0.0011	0.0033
Sv2c	ENSMUSG00000051111	synaptic vesicle glycoprotein 2c	-2.691	0.0276	0.0581
Syde1	ENSMUSG00000032714	synapse defective 1, Rho GTPase, homolog 1 (C. elegans)	-1.592	0.0000	0.0000
Sys1	ENSMUSG00000045503	SYS1 Golgi-localized integral membrane protein homolog (S. cerevisiae)	-1.549	0.0000	0.0000
Syt15	ENSMUSG00000041479	synaptotagmin XV	-1.591	0.0427	0.0844
Syt5	ENSMUSG00000004961	synaptotagmin V	-3.466	0.0092	0.0223
Taco1os	ENSMUSG00000085255	translational activator of mitochondrially encoded cytochrome c oxidase I, opposite strand	-7.302	0.0188	0.0417
Tada3	ENSMUSG00000048930	transcriptional adaptor 3	-1.651	0.0000	0.0000
Taf1c	ENSMUSG00000031832	TATA-box binding protein associated factor, RNA polymerase I, C	-1.591	0.0027	0.0074

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tagap	ENSMUSG00000033450	T cell activation Rho GTPase activating protein	-1.734	0.0076	0.0188
Tap1	ENSMUSG00000037321	transporter 1, ATP-binding cassette, sub-family B (MDR/TAP)	-1.896	0.0103	0.0247
Tas1r3	ENSMUSG00000029072	taste receptor, type 1, member 3	-3.243	0.0039	0.0103
Tat	ENSMUSG00000001670	tyrosine aminotransferase	-19.793	0.0314	0.0650
Tbc1d2b	ENSMUSG00000037410	TBC1 domain family, member 2B	-1.628	0.0000	0.0000
Tbc1d9b	ENSMUSG00000036644	TBC1 domain family, member 9B	-1.752	0.0000	0.0000
Tbrg4	ENSMUSG00000000384	transforming growth factor beta regulated gene 4	-1.733	0.0000	0.0000
Tcf21	ENSMUSG00000045680	transcription factor 21	-2.000	0.0000	0.0000
Tcof1	ENSMUSG00000024613	treacle ribosome biogenesis factor 1	-1.938	0.0000	0.0000
Tctn2	ENSMUSG00000118662	tectonic family member 2	-1.508	0.0011	0.0034
Tdg-ps2	ENSMUSG00000085666	thymine DNA glycosylase, pseudogene 2	-2.190	0.0000	0.0001
Telo2	ENSMUSG00000024170	telomere maintenance 2	-1.707	0.0000	0.0002
Tep1	ENSMUSG00000006281	telomerase associated protein 1	-1.519	0.0000	0.0000
Tespa1	ENSMUSG00000034833	thymocyte expressed, positive selection associated 1	-8.837	0.0276	0.0581
Tex11	ENSMUSG00000009670	testis expressed gene 11	-2.032	0.0256	0.0544
Tex261	ENSMUSG00000014748	testis expressed gene 261	-1.540	0.0000	0.0000
Tex38	ENSMUSG00000044556	testis expressed 38	-4.703	0.0069	0.0172
Tex49	ENSMUSG00000022993	testis expressed 49	-16.989	0.0068	0.0170
Tfb2m	ENSMUSG00000026492	transcription factor B2, mitochondrial	-1.683	0.0000	0.0000
Tfip11	ENSMUSG00000029345	tuftelin interacting protein 11	-1.697	0.0000	0.0000
Tgfbi	ENSMUSG00000035493	transforming growth factor, beta induced	-1.585	0.0011	0.0032
Tgtp2	ENSMUSG00000078921	T cell specific GTPase 2	-2.582	0.0175	0.0392
Tha1	ENSMUSG00000017713	threonine aldolase 1	-1.592	0.0003	0.0010
Thap3	ENSMUSG00000039759	THAP domain containing, apoptosis associated protein 3	-1.591	0.0006	0.0018
Thbs3	ENSMUSG00000028047	thrombospondin 3	-1.624	0.0066	0.0167
Them6	ENSMUSG00000056665	thioesterase superfamily member 6	-1.611	0.0003	0.0009
Thsd1	ENSMUSG00000031480	thrombospondin, type I, domain 1	-1.598	0.0000	0.0000
Tie1	ENSMUSG00000033191	tyrosine kinase with immunoglobulin-like and EGF-like domains 1	-1.643	0.0000	0.0000
Timm23	ENSMUSG00000013701	translocase of inner mitochondrial membrane 23	-1.540	0.0000	0.0000
Tlr2	ENSMUSG00000027995	toll-like receptor 2	-1.692	0.0034	0.0093
Tm4sf5	ENSMUSG00000018919	transmembrane 4 superfamily member 5	-12.942	0.0109	0.0260

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tm6sf2	ENSMUSG00000036151	transmembrane 6 superfamily member 2	-2.391	0.0388	0.0778
Tm7sf2	ENSMUSG00000024799	transmembrane 7 superfamily member 2	-1.929	0.0019	0.0055
Tmbim4	ENSMUSG00000020225	transmembrane BAX inhibitor motif containing 4	-1.537	0.0000	0.0000
Tmc4	ENSMUSG00000019734	transmembrane channel-like gene family 4	-2.980	0.0081	0.0199
Tmem102	ENSMUSG00000089876	transmembrane protein 102	-2.128	0.0145	0.0333
Tmem106a	ENSMUSG00000034947	transmembrane protein 106A	-1.693	0.0012	0.0037
Tmem107	ENSMUSG00000020895	transmembrane protein 107	-2.119	0.0000	0.0001
Tmem116	ENSMUSG00000029452	transmembrane protein 116	-2.042	0.0000	0.0001
Tmem119	ENSMUSG00000054675	transmembrane protein 119	-1.886	0.0499	0.0965
Tmem17	ENSMUSG00000049904	transmembrane protein 17	-1.549	0.0237	0.0508
Tmem176a	ENSMUSG00000023367	transmembrane protein 176A	-1.502	0.0107	0.0255
Tmem198	ENSMUSG00000051703	transmembrane protein 198	-2.304	0.0394	0.0788
Tmem221	ENSMUSG00000043664	transmembrane protein 221	-25.442	0.0058	0.0148
Tmem222	ENSMUSG00000028857	transmembrane protein 222	-1.737	0.0000	0.0000
Tmem255b	ENSMUSG00000038457	transmembrane protein 255B	-2.281	0.0013	0.0039
Tmem256	ENSMUSG00000070394	transmembrane protein 256	-1.841	0.0000	0.0000
Tmem266	ENSMUSG00000032313	transmembrane protein 266	-1.547	0.0098	0.0237
Tmod4	ENSMUSG00000005628	tropomodulin 4	-1.717	0.0001	0.0004
Tmprss4	ENSMUSG00000032091	transmembrane protease, serine 4	-2.002	0.0155	0.0351
Tmprss5	ENSMUSG00000032268	transmembrane protease, serine 5 (spinesin)	-8.577	0.0057	0.0146
Tmub2	ENSMUSG00000034757	transmembrane and ubiquitin-like domain containing 2	-1.610	0.0000	0.0000
Tnfrsf10b	ENSMUSG00000022074	tumor necrosis factor receptor superfamily, member 10b	-1.548	0.0077	0.0190
Tnfrsf11b	ENSMUSG00000063727	tumor necrosis factor receptor superfamily, member 11b (osteoprotegerin)	-5.673	0.0211	0.0461
Tnfrsf23	ENSMUSG00000037613	tumor necrosis factor receptor superfamily, member 23	-1.790	0.0017	0.0050
Tnfrsf8	ENSMUSG00000028602	tumor necrosis factor receptor superfamily, member 8	-10.259	0.0222	0.0482
Tnfsf13b	ENSMUSG00000031497	tumor necrosis factor (ligand) superfamily, member 13b	-1.960	0.0106	0.0253
Tnfsfm13	ENSMUSG00000018752	tumor necrosis factor (ligand) superfamily, membrane-bound member 13	-3.644	0.0380	0.0764
Tnip3	ENSMUSG00000044162	TNFAIP3 interacting protein 3	-1.745	0.0474	0.0923
Togaram2	ENSMUSG00000045761	TOG array regulator of axonemal microtubules 2	-2.659	0.0000	0.0000
Tor4a	ENSMUSG00000059555	torsin family 4, member A	-1.615	0.0001	0.0003
Tpcn1	ENSMUSG00000032741	two pore channel 1	-1.595	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Traf3ip2	ENSMUSG00000019842	TRAF3 interacting protein 2	-1.557	0.0004	0.0014
Traf5	ENSMUSG00000026637	TNF receptor-associated factor 5	-1.587	0.0009	0.0027
Trf	ENSMUSG00000032554	transferrin	-1.946	0.0000	0.0000
Tril	ENSMUSG00000043496	TLR4 interactor with leucine-rich repeats	-1.587	0.0001	0.0005
Trmt1	ENSMUSG00000001909	tRNA methyltransferase 1	-1.930	0.0000	0.0000
Trmt112	ENSMUSG00000038812	tRNA methyltransferase 11-2	-1.717	0.0000	0.0000
Tro	ENSMUSG00000025272	trophinin	-2.110	0.0468	0.0914
Troap	ENSMUSG00000032783	trophinin associated protein	-2.805	0.0243	0.0520
Trpm4	ENSMUSG00000038260	transient receptor potential cation channel, subfamily M, member 4	-1.746	0.0000	0.0000
Tspan10	ENSMUSG00000039691	tetraspanin 10	-6.638	0.0045	0.0118
Tspyl3	ENSMUSG00000074671	TSPY-like 3	-1.951	0.0006	0.0018
Tst	ENSMUSG00000044986	thiosulfate sulfurtransferase, mitochondrial	-2.002	0.0000	0.0000
Ttc13	ENSMUSG00000037300	tetratricopeptide repeat domain 13	-1.521	0.0000	0.0001
Ttc28	ENSMUSG00000033209	tetratricopeptide repeat domain 28	-1.721	0.0000	0.0000
Ttc39a	ENSMUSG00000028555	tetratricopeptide repeat domain 39A	-2.065	0.0233	0.0501
Ttc7	ENSMUSG00000036918	tetratricopeptide repeat domain 7	-1.946	0.0000	0.0000
Ttll12	ENSMUSG00000016757	tubulin tyrosine ligase-like family, member 12	-1.524	0.0001	0.0002
Ttpa	ENSMUSG00000073988	tocopherol (alpha) transfer protein	-2.728	0.0210	0.0460
Ttr	ENSMUSG00000061808	transthyretin	-4.887	0.0475	0.0926
Tuba3b	ENSMUSG00000067338	tubulin, alpha 3B	-41.503	0.0001	0.0003
Tubg2	ENSMUSG00000045007	tubulin, gamma 2	-1.610	0.0262	0.0554
Tubgcp2	ENSMUSG00000025474	tubulin, gamma complex associated protein 2	-1.776	0.0000	0.0000
Tvp23a	ENSMUSG00000050908	trans-golgi network vesicle protein 23A	-3.355	0.0010	0.0030
Tyro3	ENSMUSG00000027298	TYRO3 protein tyrosine kinase 3	-1.783	0.0005	0.0016
Uba7	ENSMUSG00000032596	ubiquitin-like modifier activating enzyme 7	-1.682	0.0109	0.0260
Ubac2	ENSMUSG00000041765	ubiquitin associated domain containing 2	-1.507	0.0000	0.0000
Ubald1	ENSMUSG00000039568	UBA-like domain containing 1	-1.581	0.0002	0.0008
Ugt1a6a	ENSMUSG00000054545	UDP glucuronosyltransferase 1 family, polypeptide A6A	-15.919	0.0112	0.0265
Upb1	ENSMUSG00000033427	ureidopropionase, beta	-7.694	0.0000	0.0000
Upk1b	ENSMUSG00000049436	uroplakin 1B	-7.469	0.0023	0.0065
Upk2	ENSMUSG00000041523	uroplakin 2	-4.309	0.0340	0.0695

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Upk3b	ENSMUSG00000042985	uroplakin 3B	-34.446	0.0001	0.0003
Urah	ENSMUSG00000025481	urate (5-hydroxyiso-) hydrolase	-3.306	0.0232	0.0499
Use1	ENSMUSG00000002395	unconventional SNARE in the ER 1 homolog (S. cerevisiae)	-1.721	0.0000	0.0000
Usf1	ENSMUSG00000026641	upstream transcription factor 1	-1.607	0.0000	0.0000
Usp18	ENSMUSG00000030107	ubiquitin specific peptidase 18	-1.682	0.0190	0.0419
Vasn	ENSMUSG00000039646	vasorin	-1.675	0.0004	0.0014
Vdr	ENSMUSG00000022479	vitamin D (1,25-dihydroxyvitamin D3) receptor	-1.989	0.0350	0.0713
Vegfd	ENSMUSG00000031380	vascular endothelial growth factor D	-1.936	0.0011	0.0034
Vps11	ENSMUSG00000032127	VPS11, CORVET/HOPS core subunit	-1.545	0.0008	0.0025
Vps29	ENSMUSG00000029462	VPS29 retromer complex component	-1.554	0.0000	0.0000
Vps37b	ENSMUSG00000066278	vacuolar protein sorting 37B	-1.545	0.0000	0.0002
Vps9d1	ENSMUSG00000001062	VPS9 domain containing 1	-1.701	0.0000	0.0000
Vwa7	ENSMUSG00000007030	von Willebrand factor A domain containing 7	-1.578	0.0000	0.0000
Was	ENSMUSG00000031165	Wiskott-Aldrich syndrome	-2.037	0.0006	0.0019
Washc3	ENSMUSG00000020056	WASH complex subunit 3	-1.639	0.0000	0.0000
Wdfy4	ENSMUSG00000051506	WD repeat and FYVE domain containing 4	-1.846	0.0015	0.0044
Wdr19	ENSMUSG00000037890	WD repeat domain 19	-1.807	0.0008	0.0026
Wdr54	ENSMUSG00000030032	WD repeat domain 54	-2.246	0.0084	0.0205
Wdr70	ENSMUSG00000039828	WD repeat domain 70	-1.508	0.0004	0.0012
Wdr73	ENSMUSG00000025722	WD repeat domain 73	-1.859	0.0000	0.0000
Wdr86	ENSMUSG00000055235	WD repeat domain 86	-5.260	0.0004	0.0012
Wfikkn1	ENSMUSG00000071192	WAP, FS, Ig, KU, and NTR-containing protein 1	-10.380	0.0208	0.0456
Wif1	ENSMUSG00000020218	Wnt inhibitory factor 1	-1.733	0.0012	0.0036
Wrap53	ENSMUSG00000041346	WD repeat containing, antisense to Trp53	-1.579	0.0000	0.0000
Wwp2	ENSMUSG00000031930	WW domain containing E3 ubiquitin protein ligase 2	-1.637	0.0000	0.0000
Xaf1	ENSMUSG00000040483	XIAP associated factor 1	-1.716	0.0039	0.0105
Xirp1	ENSMUSG00000079243	xin actin-binding repeat containing 1	-1.919	0.0000	0.0000
Xlr4a	ENSMUSG00000079845	X-linked lymphocyte-regulated 4A	-33.769	0.0343	0.0700
Xpnpep2	ENSMUSG00000037005	X-prolyl aminopeptidase (aminopeptidase P) 2, membrane-bound	-10.703	0.0004	0.0013
Xrcc1	ENSMUSG00000051768	X-ray repair complementing defective repair in Chinese hamster cells 1	-1.606	0.0000	0.0000
Xrcc3	ENSMUSG00000021287	X-ray repair complementing defective repair in Chinese hamster cells 3	-1.870	0.0445	0.0874

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Yjefn3	ENSMUSG00000048967	YjeF N-terminal domain containing 3	-1.731	0.0011	0.0035
Yju2	ENSMUSG00000003208	YJU2 splicing factor	-1.506	0.0001	0.0003
Zbed5-ps	ENSMUSG00000110424	zinc finger, BED type containing 5, pseudogene	-1.861	0.0161	0.0363
Zbtb48	ENSMUSG00000028952	zinc finger and BTB domain containing 48	-1.728	0.0001	0.0002
Zc2hc1c	ENSMUSG00000045064	zinc finger, C2HC-type containing 1C	-1.549	0.0391	0.0783
Zc3hc1	ENSMUSG00000039130	zinc finger, C3HC type 1	-1.516	0.0000	0.0000
Zdhhc24	ENSMUSG00000006463	zinc finger, DHHC domain containing 24	-1.523	0.0001	0.0004
Zdhhc8	ENSMUSG00000060166	zinc finger, DHHC domain containing 8	-1.622	0.0000	0.0000
Zfp185	ENSMUSG00000031351	zinc finger protein 185	-2.341	0.0101	0.0243
Zfp263	ENSMUSG00000022529	zinc finger protein 263	-1.557	0.0000	0.0000
Zfp296	ENSMUSG00000011267	zinc finger protein 296	-3.070	0.0015	0.0044
Zfp358	ENSMUSG00000047264	zinc finger protein 358	-1.686	0.0000	0.0000
Zfp410	ENSMUSG00000042472	zinc finger protein 410	-1.514	0.0203	0.0446
Zfp418	ENSMUSG00000034538	zinc finger protein 418	-1.521	0.0448	0.0880
Zfp458	ENSMUSG00000055480	zinc finger protein 458	-1.652	0.0479	0.0931
Zfp469	ENSMUSG00000043903	zinc finger protein 469	-2.069	0.0000	0.0000
Zfp524	ENSMUSG00000051184	zinc finger protein 524	-2.809	0.0000	0.0000
Zfp707	ENSMUSG00000034429	zinc finger protein 707	-1.752	0.0001	0.0004
Zfp788	ENSMUSG00000074165	zinc finger protein 788	-1.601	0.0000	0.0001
Zfp862-ps	ENSMUSG00000107476	zinc finger protein 862, pseudogene	-1.517	0.0000	0.0000
Zfp87	ENSMUSG00000097333	zinc finger protein 87	-1.844	0.0000	0.0000
Zfp956	ENSMUSG00000045466	zinc finger protein 956	-1.795	0.0010	0.0031
Zfp964	ENSMUSG00000091764	zinc finger protein 964	-1.626	0.0062	0.0156
Zfp977	ENSMUSG00000092335	zinc finger protein 977	-8.399	0.0001	0.0003
Zfp983	ENSMUSG00000035868	zinc finger protein 983	-1.995	0.0047	0.0123
Zkscan5	ENSMUSG00000055991	zinc finger with KRAB and SCAN domains 5	-1.601	0.0002	0.0008
Zmat5	ENSMUSG00000009076	zinc finger, matrin type 5	-1.589	0.0000	0.0000
Zmiz1os1	ENSMUSG00000087535	Zmiz1 opposite strand 1	-2.980	0.0110	0.0261
Zmiz2	ENSMUSG00000041164	zinc finger, MIZ-type containing 2	-1.544	0.0000	0.0000
Zmym3	ENSMUSG00000031310	zinc finger, MYM-type 3	-1.509	0.0000	0.0000
Znhit1	ENSMUSG00000059518	zinc finger, HIT domain containing 1	-1.605	0.0000	0.0000

• **Table S3: Differentially expressed transcripts specific to mG4H-ON (Venn Diagram: Group I)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Znhit3	ENSMUSG00000020526	zinc finger, HIT type 3	-1.989	0.0000	0.0000
Zp2	ENSMUSG00000030911	zona pellucida glycoprotein 2	-2.784	0.0042	0.0110
Zswim3	ENSMUSG00000045822	zinc finger SWIM-type containing 3	-1.530	0.0227	0.0491

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
1500011B03Rik	ENSMUSG00000072694	RIKEN cDNA 1500011B03 gene	1.576	0.0060	0.0168
1700048O20Rik	ENSMUSG00000043773	RIKEN cDNA 1700048O20 gene	2.572	0.0168	0.0411
1700063J08Rik	ENSMUSG00000117080	RIKEN cDNA 1700063J08 gene	3.062	0.0400	0.0861
1700081N11Rik	ENSMUSG00000113209	RIKEN cDNA 1700081N11 gene	2.585	0.0005	0.0017
1810009A15Rik	ENSMUSG00000071653	RIKEN cDNA 1810009A15 gene	5.807	0.0426	0.0906
1810019N24Rik	ENSMUSG00000097115	RIKEN cDNA 1810019N24 gene	2.310	0.0477	0.0995
1810034E14Rik	ENSMUSG00000097101	RIKEN cDNA 1810034E14 gene	1.501	0.0179	0.0435
1810073O08Rik	ENSMUSG00000117442	RIKEN cDNA 1810073O08 gene	2.295	0.0135	0.0341
2310001H17Rik	ENSMUSG00000097354	RIKEN cDNA 2310001H17 gene	1.655	0.0179	0.0434
2310014F06Rik	ENSMUSG00000085945	RIKEN cDNA 2310014F06 gene	2.237	0.0056	0.0157
2810021J22Rik	ENSMUSG00000020491	RIKEN cDNA 2810021J22 gene	1.586	0.0041	0.0120
2810405F17Rik	ENSMUSG00000101493	RIKEN cDNA 2810405F17 gene	2.166	0.0473	0.0988
4933431K14Rik	ENSMUSG00000103715	RIKEN cDNA 4933431K14 gene	1.580	0.0037	0.0111
5033417F24Rik	ENSMUSG00000097251	RIKEN cDNA 5033417F24 gene	1.713	0.0140	0.0351
6430710C18Rik	ENSMUSG00000085427	RIKEN cDNA 6430710C18 gene	1.682	0.0466	0.0977
8030453O22Rik	ENSMUSG00000085058	RIKEN cDNA 8030453O22 gene	2.449	0.0450	0.0947
A530072M11Rik	ENSMUSG00000085112	RIKEN cDNA gene A530072M11	2.199	0.0233	0.0544
AA414768	ENSMUSG00000083307	expressed sequence AA414768	1.924	0.0136	0.0344
Abcc3	ENSMUSG00000020865	ATP-binding cassette, sub-family C (CFTR/MRP), member 3	1.516	0.0397	0.0855
Ackr4	ENSMUSG00000079355	atypical chemokine receptor 4	1.829	0.0116	0.0297
Adamts8	ENSMUSG00000031994	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 8	2.357	0.0279	0.0636
Adgrl1	ENSMUSG00000013033	adhesion G protein-coupled receptor L1	1.508	0.0001	0.0004
Agbl5	ENSMUSG00000029165	ATP/GTP binding protein-like 5	1.634	0.0000	0.0002
Agpat4	ENSMUSG00000023827	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	1.553	0.0001	0.0003
Aif1l	ENSMUSG00000001864	allograft inflammatory factor 1-like	1.958	0.0000	0.0002
Akr1c13	ENSMUSG00000021213	aldo-keto reductase family 1, member C13	2.043	0.0082	0.0220
Alk	ENSMUSG00000055471	anaplastic lymphoma kinase	9.753	0.0128	0.0325
Alox8	ENSMUSG00000020891	arachidonate 8-lipoxygenase	7.373	0.0266	0.0609
Als2	ENSMUSG00000026024	alsin Rho guanine nucleotide exchange factor	1.561	0.0000	0.0000
Amy1	ENSMUSG00000074264	amylase 1, salivary	1.550	0.0170	0.0416
Ankle1	ENSMUSG00000046295	ankyrin repeat and LEM domain containing 1	3.333	0.0195	0.0467

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ankrd1	ENSMUSG00000024803	ankyrin repeat domain 1 (cardiac muscle)	1.755	0.0066	0.0182
Ankrd13a	ENSMUSG00000041870	ankyrin repeat domain 13a	1.650	0.0000	0.0000
Anks1b	ENSMUSG00000058589	ankyrin repeat and sterile alpha motif domain containing 1B	2.046	0.0245	0.0568
Anp32b-ps1	ENSMUSG00000081792	Bacidic (leucine-rich) nuclear phosphoprotein 32 family, member B, pseudogene 1	10.362	0.0014	0.0047
Anxa8	ENSMUSG00000021950	annexin A8	2.855	0.0442	0.0932
Aplf	ENSMUSG00000030051	aprataxin and PNKP like factor	1.742	0.0000	0.0000
Aplp1	ENSMUSG00000006651	amyloid beta (A4) precursor-like protein 1	1.795	0.0000	0.0001
Apoe	ENSMUSG00000002985	apolipoprotein E	1.707	0.0001	0.0004
Apol8	ENSMUSG00000056656	apolipoprotein L 8	3.937	0.0378	0.0821
Aptx	ENSMUSG00000028411	aprataxin	1.551	0.0000	0.0000
Arhgap22	ENSMUSG00000063506	Rho GTPase activating protein 22	1.793	0.0104	0.0271
Ascc2	ENSMUSG00000020412	activating signal cointegrator 1 complex subunit 2	1.550	0.0000	0.0000
Asprv1	ENSMUSG00000033508	aspartic peptidase, retroviral-like 1	32.090	0.0021	0.0067
Atp6v0d2	ENSMUSG00000028238	ATPase, H+ transporting, lysosomal V0 subunit D2	4.124	0.0035	0.0105
Atp6v1g2	ENSMUSG00000024403	ATPase, H+ transporting, lysosomal V1 subunit G2	1.592	0.0023	0.0073
Atp8b5	ENSMUSG00000028457	ATPase, class I, type 8B, member 5	3.463	0.0109	0.0284
Atxn7l3	ENSMUSG00000059995	ataxin 7-like 3	1.585	0.0001	0.0003
AV099323	ENSMUSG00000087377	expressed sequence AV099323	3.006	0.0265	0.0607
AV356131	ENSMUSG00000108461	expressed sequence AV356131	2.320	0.0304	0.0682
Azin2	ENSMUSG00000028789	antizyme inhibitor 2	1.617	0.0018	0.0057
B130046B21Rik	ENSMUSG00000097414	RIKEN cDNA B130046B21 gene	4.685	0.0027	0.0084
B230217O12Rik	ENSMUSG00000097785	RIKEN cDNA B230217O12 gene	2.971	0.0079	0.0213
B230317F23Rik	ENSMUSG00000045746	RIKEN cDNA B230317F23 gene	7.002	0.0073	0.0200
B3gat3	ENSMUSG00000071649	beta-1,3-glucuronyltransferase 3 (glucuronosyltransferase I)	1.533	0.0000	0.0000
B930095G15Rik	ENSMUSG00000085133	RIKEN cDNA B930095G15 gene	1.584	0.0005	0.0018
BC051226	ENSMUSG00000092564	cDNA sequence BC051226	2.120	0.0037	0.0110
Bend4	ENSMUSG00000092060	BEN domain containing 4	1.555	0.0003	0.0010
Bmp6	ENSMUSG00000039004	bone morphogenetic protein 6	1.658	0.0102	0.0267
Bod1-ps	ENSMUSG00000116936	biorientation of chromosomes in cell division 1, pseudogene	1.734	0.0001	0.0005
Brd8	ENSMUSG00000003778	bromodomain containing 8	1.513	0.0000	0.0000
C130046K22Rik	ENSMUSG00000085154	RIKEN cDNA C130046K22 gene	1.791	0.0305	0.0683

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
C1qb	ENSMUSG00000036905	complement component 1, q subcomponent, beta polypeptide	1.620	0.0028	0.0087
C1ql3	ENSMUSG00000049630	C1q-like 3	3.409	0.0081	0.0218
C230034O21Rik	ENSMUSG00000086181	RIKEN cDNA C230034O21 gene	3.180	0.0159	0.0394
C230062I16Rik	ENSMUSG00000063623	RIKEN cDNA C230062I16 gene	1.658	0.0053	0.0152
Camk4	ENSMUSG00000038128	calcium/calmodulin-dependent protein kinase IV	4.605	0.0393	0.0849
Ccdc102a	ENSMUSG00000063605	coiled-coil domain containing 102A	1.680	0.0000	0.0000
Ccdc149	ENSMUSG00000045790	coiled-coil domain containing 149	1.594	0.0016	0.0053
Ccdc160	ENSMUSG00000073207	coiled-coil domain containing 160	2.078	0.0352	0.0773
Ccdc28a	ENSMUSG00000059554	coiled-coil domain containing 28A	1.575	0.0002	0.0007
Ccdc62	ENSMUSG00000061882	coiled-coil domain containing 62	1.637	0.0330	0.0731
Ccdc80	ENSMUSG00000022665	coiled-coil domain containing 80	1.666	0.0012	0.0039
Ccdc88b	ENSMUSG00000047810	coiled-coil domain containing 88B	2.025	0.0055	0.0155
Ccdc96	ENSMUSG00000050677	coiled-coil domain containing 96	2.030	0.0005	0.0017
Ccl6	ENSMUSG00000018927	chemokine (C-C motif) ligand 6	1.715	0.0133	0.0336
Ccnjl	ENSMUSG00000044707	cyclin J-like	1.532	0.0168	0.0412
Cd248	ENSMUSG00000056481	CD248 antigen, endosialin	1.725	0.0154	0.0384
Cd2bp2	ENSMUSG00000042502	CD2 cytoplasmic tail binding protein 2	1.582	0.0000	0.0000
Cd300e	ENSMUSG00000048498	CD300E molecule	3.525	0.0185	0.0447
Cd79b	ENSMUSG00000040592	CD79B antigen	2.062	0.0285	0.0646
Cdc34	ENSMUSG00000020307	cell division cycle 34	1.646	0.0000	0.0000
Cdh24	ENSMUSG00000059674	cadherin-like 24	2.998	0.0171	0.0417
Cdv3-ps	ENSMUSG00000090389	Cdv3 retrotransposed pseudogene	3.863	0.0066	0.0182
Celf4	ENSMUSG00000024268	CUGBP, Elav-like family member 4	3.031	0.0115	0.0295
Cep131	ENSMUSG00000039781	centrosomal protein 131	1.577	0.0032	0.0097
Cep164	ENSMUSG00000043987	centrosomal protein 164	1.637	0.0000	0.0000
Cerkl	ENSMUSG00000075256	ceramide kinase-like	1.943	0.0161	0.0398
Cetn4	ENSMUSG00000045031	centrin 4	2.011	0.0372	0.0810
Cfap45	ENSMUSG00000026546	cilia and flagella associated protein 45	2.018	0.0374	0.0813
Cfap53	ENSMUSG00000035394	cilia and flagella associated protein 53	6.971	0.0334	0.0738
Chd3	ENSMUSG00000018474	chromodomain helicase DNA binding protein 3	1.599	0.0000	0.0000
Chmp2a	ENSMUSG00000033916	charged multivesicular body protein 2A	1.658	0.0000	0.0000

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Chsy3	ENSMUSG00000058152	chondroitin sulfate synthase 3	2.655	0.0058	0.0164
Chtf18	ENSMUSG00000019214	CTF18, chromosome transmission fidelity factor 18	1.771	0.0057	0.0162
Clec4d	ENSMUSG00000030144	C-type lectin domain family 4, member d	3.668	0.0428	0.0909
Clmp	ENSMUSG00000032024	CXADR-like membrane protein	1.622	0.0003	0.0011
Clstn1	ENSMUSG00000039953	calsyntenin 1	1.518	0.0000	0.0000
Col11a1	ENSMUSG00000027966	collagen, type XI, alpha 1	5.413	0.0164	0.0403
Coq10a	ENSMUSG00000039914	coenzyme Q10A	1.695	0.0000	0.0000
Cpsf4	ENSMUSG00000029625	cleavage and polyadenylation specific factor 4	1.604	0.0012	0.0039
Csnk1e	ENSMUSG00000022433	casein kinase 1, epsilon	1.613	0.0003	0.0013
Csnk1g2	ENSMUSG00000003345	casein kinase 1, gamma 2	1.736	0.0000	0.0000
Ctdsp1	ENSMUSG00000026176	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 1	1.676	0.0000	0.0000
Ctdsp2	ENSMUSG00000078429	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) small phosphatase 2	1.602	0.0004	0.0016
Cthrc1	ENSMUSG00000054196	collagen triple helix repeat containing 1	3.735	0.0041	0.0121
Ctnnbip1	ENSMUSG00000028988	catenin beta interacting protein 1	1.543	0.0001	0.0005
Ctss	ENSMUSG00000038642	cathepsin S	1.665	0.0037	0.0111
Cwc25	ENSMUSG00000018541	CWC25 spliceosome-associated protein	1.532	0.0000	0.0000
Cyhr1	ENSMUSG00000053929	cysteine and histidine rich 1	1.774	0.0000	0.0000
D830035M03Rik	ENSMUSG00000111828	RIKEN cDNA D830035M03 gene	1.909	0.0065	0.0179
Ddc	ENSMUSG00000020182	dopa decarboxylase	2.703	0.0000	0.0000
Ddx43	ENSMUSG00000070291	DEAD box helicase 43	2.104	0.0252	0.0583
Dhx16	ENSMUSG00000024422	DEAH (Asp-Glu-Ala-His) box polypeptide 16	1.642	0.0000	0.0000
Dhx38	ENSMUSG00000037993	DEAH (Asp-Glu-Ala-His) box polypeptide 38	1.581	0.0000	0.0000
Dmwd	ENSMUSG00000030410	dystrophia myotonica-containing WD repeat motif	1.504	0.0001	0.0003
Dnajc17	ENSMUSG00000034278	DnaJ heat shock protein family (Hsp40) member C17	1.566	0.0013	0.0043
Dnmt3b	ENSMUSG00000027478	DNA methyltransferase 3B	1.688	0.0131	0.0331
Doc2g	ENSMUSG00000024871	double C2, gamma	1.570	0.0000	0.0000
Dtnbp1	ENSMUSG00000057531	dystrobrevin binding protein 1	1.549	0.0000	0.0001
Dusp18	ENSMUSG00000047205	dual specificity phosphatase 18	1.596	0.0037	0.0110
Ebf1	ENSMUSG00000057098	early B cell factor 1	1.627	0.0000	0.0000
Efcab9	ENSMUSG00000044056	EF-hand calcium binding domain 9	3.805	0.0442	0.0933
Efhd2	ENSMUSG00000040659	EF hand domain containing 2	1.623	0.0112	0.0289

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Efna2	ENSMUSG00000003070	ephrin A2	1.897	0.0024	0.0074
Egln1	ENSMUSG00000031987	egl-9 family hypoxia-inducible factor 1	1.523	0.0000	0.0000
Eif2b5	ENSMUSG00000003235	eukaryotic translation initiation factor 2B, subunit 5 epsilon	1.633	0.0000	0.0000
Eif4b	ENSMUSG00000058655	eukaryotic translation initiation factor 4B	1.608	0.0000	0.0000
Eif4e	ENSMUSG00000028156	eukaryotic translation initiation factor 4E	1.610	0.0001	0.0004
Eipr1	ENSMUSG00000036613	EARP complex and GARP complex interacting protein 1	1.501	0.0000	0.0000
Eldr	ENSMUSG00000087060	Egfr long non-coding downstream RNA	2.840	0.0035	0.0105
Epb41l4b	ENSMUSG00000028434	erythrocyte membrane protein band 4.1 like 4b	1.677	0.0025	0.0079
Ephb3	ENSMUSG00000005958	Eph receptor B3	1.719	0.0018	0.0059
Erf	ENSMUSG00000040857	Ets2 repressor factor	1.766	0.0000	0.0001
Exd1	ENSMUSG00000048647	exonuclease 3'-5' domain containing 1	1.586	0.0116	0.0299
Faap20	ENSMUSG00000073684	Fanconi anemia core complex associated protein 20	1.582	0.0054	0.0154
Fads3	ENSMUSG00000024664	fatty acid desaturase 3	1.556	0.0008	0.0028
Faim2	ENSMUSG00000023011	Fas apoptotic inhibitory molecule 2	7.468	0.0472	0.0986
Fam131b	ENSMUSG00000029861	family with sequence similarity 131, member B	2.288	0.0021	0.0066
Fam131c	ENSMUSG00000006218	family with sequence similarity 131, member C	1.602	0.0012	0.0040
Fam167b	ENSMUSG00000050493	family with sequence similarity 167, member B	2.360	0.0209	0.0496
Fam174c	ENSMUSG00000035595	family with sequence similarity 174, member C	1.530	0.0286	0.0648
Fam184a	ENSMUSG00000019856	family with sequence similarity 184, member A	1.593	0.0480	0.0999
Fam32a	ENSMUSG00000003039	family with sequence similarity 32, member A	1.587	0.0000	0.0000
Fbxw8	ENSMUSG00000032867	F-box and WD-40 domain protein 8	1.534	0.0009	0.0032
Fer	ENSMUSG00000000127	fer (fms/fps related) protein kinase	1.524	0.0000	0.0000
Fgf7	ENSMUSG00000027208	fibroblast growth factor 7	1.767	0.0104	0.0272
Fkbp4	ENSMUSG00000030357	FK506 binding protein 4	1.506	0.0003	0.0010
Fndc5	ENSMUSG00000001334	fibronectin type III domain containing 5	1.602	0.0000	0.0000
G430095P16Rik	ENSMUSG00000074203	RIKEN cDNA G430095P16 gene	3.287	0.0319	0.0710
Galnt3	ENSMUSG00000026994	polypeptide N-acetylgalactosaminyltransferase 3	3.592	0.0400	0.0861
Gart	ENSMUSG00000022962	phosphoribosylglycinamide formyltransferase	1.501	0.0000	0.0000
Gas7	ENSMUSG00000033066	growth arrest specific 7	1.686	0.0009	0.0030
Gatad2a	ENSMUSG00000036180	GATA zinc finger domain containing 2A	1.541	0.0000	0.0000
Gbp2	ENSMUSG00000028270	guanylate binding protein 2	1.509	0.0061	0.0170

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gbp8	ENSMUSG00000034438	guanylate-binding protein 8	3.031	0.0295	0.0666
Gcnt2	ENSMUSG00000021360	glucosaminyl (N-acetyl) transferase 2, I-branching enzyme	1.702	0.0092	0.0245
Gimap1os	ENSMUSG00000044867	GTPase, IMAP family member 1, opposite strand	7.161	0.0005	0.0018
Glp2r	ENSMUSG00000049928	glucagon-like peptide 2 receptor	1.997	0.0367	0.0800
Gm10043	ENSMUSG00000109793	predicted pseudogene 10043	3.191	0.0437	0.0924
Gm10080	ENSMUSG00000060467	predicted gene 10080	4.530	0.0278	0.0633
Gm10138	ENSMUSG00000100954	predicted gene 10138	1.724	0.0007	0.0025
Gm10254	ENSMUSG00000069011	predicted gene 10254	2.874	0.0105	0.0274
Gm10356	ENSMUSG00000072387	predicted gene 10356	4.507	0.0421	0.0898
Gm10657	ENSMUSG00000103486	predicted gene 10657	5.875	0.0053	0.0151
Gm10941	ENSMUSG00000078444	predicted gene 10941	7.014	0.0193	0.0463
Gm11223	ENSMUSG00000046341	predicted gene 11223	3.805	0.0008	0.0029
Gm11407	ENSMUSG00000082179	predicted gene 11407	2.197	0.0166	0.0407
Gm11423	ENSMUSG00000085175	predicted gene 11423	1.658	0.0467	0.0977
Gm11488	ENSMUSG00000081871	predicted gene 11488	4.541	0.0416	0.0888
Gm11638	ENSMUSG00000086487	predicted gene 11638	6.096	0.0213	0.0504
Gm11732	ENSMUSG00000085336	predicted gene 11732	1.974	0.0003	0.0013
Gm11756	ENSMUSG00000093962	predicted gene 11756	2.590	0.0198	0.0473
Gm11821	ENSMUSG00000081884	predicted gene 11821	5.701	0.0019	0.0061
Gm12100	ENSMUSG00000087474	predicted gene 12100	5.938	0.0014	0.0047
Gm12183	ENSMUSG00000082454	predicted gene 12183	1.673	0.0134	0.0339
Gm12346	ENSMUSG00000083899	predicted gene 12346	1.994	0.0155	0.0385
Gm12430	ENSMUSG00000081152	predicted gene 12430	7.243	0.0445	0.0938
Gm12669	ENSMUSG00000100863	predicted gene 12669	1.527	0.0092	0.0244
Gm12688	ENSMUSG00000086096	predicted gene 12688	7.059	0.0044	0.0128
Gm13528	ENSMUSG00000085087	predicted gene 13528	1.781	0.0297	0.0668
Gm13620	ENSMUSG00000086603	predicted gene 13620	3.958	0.0050	0.0145
Gm13657	ENSMUSG00000086813	predicted gene 13657	2.264	0.0032	0.0097
Gm13886	ENSMUSG00000083856	predicted gene 13886	3.659	0.0115	0.0297
Gm14703	ENSMUSG00000087644	predicted gene 14703	1.695	0.0158	0.0391
Gm15445	ENSMUSG00000085311	predicted gene 15445	9.674	0.0046	0.0134

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm15793	ENSMUSG00000082769	predicted gene 15793	6.117	0.0402	0.0864
Gm15934	ENSMUSG00000090088	predicted gene 15934	2.174	0.0211	0.0499
Gm16754	ENSMUSG00000097439	predicted gene, 16754	10.359	0.0465	0.0973
Gm16845	ENSMUSG00000096981	predicted gene, 16845	2.524	0.0422	0.0899
Gm17334	ENSMUSG00000091191	predicted gene, 17334	2.754	0.0407	0.0872
Gm17396	ENSMUSG00000079669	predicted gene, 17396	2.253	0.0068	0.0187
Gm17484	ENSMUSG00000091514	predicted gene, 17484	2.198	0.0396	0.0854
Gm19557	ENSMUSG00000097990	predicted gene, 19557	3.195	0.0000	0.0002
Gm20036	ENSMUSG00000093579	predicted gene, 20036	1.840	0.0290	0.0655
Gm20045	ENSMUSG00000103983	predicted gene, 20045	2.024	0.0239	0.0556
Gm20125	ENSMUSG00000101969	predicted gene, 20125	5.286	0.0339	0.0747
Gm20457	ENSMUSG00000092187	predicted gene 20457	2.019	0.0000	0.0000
Gm2223	ENSMUSG00000079297	predicted pseudogene 2223	1.882	0.0310	0.0692
Gm2415	ENSMUSG00000086119	predicted gene 2415	1.530	0.0161	0.0398
Gm26586	ENSMUSG00000097472	predicted gene, 26586	7.847	0.0395	0.0851
Gm26704	ENSMUSG00000097875	predicted gene, 26704	2.352	0.0392	0.0847
Gm2710	ENSMUSG00000060128	predicted gene 2710	42.607	0.0005	0.0019
Gm27184	ENSMUSG00000098447	predicted gene 27184	4.897	0.0161	0.0398
Gm29675	ENSMUSG00000113515	predicted gene, 29675	2.321	0.0295	0.0666
Gm29686	ENSMUSG00000116725	predicted gene, 29686	2.613	0.0114	0.0294
Gm30025	ENSMUSG00000112278	predicted gene, 30025	2.073	0.0020	0.0063
Gm30873	ENSMUSG00000109341	predicted gene, 30873	2.332	0.0297	0.0669
Gm36033	ENSMUSG00000111058	predicted gene, 36033	7.233	0.0019	0.0062
Gm36827	ENSMUSG00000112327	predicted gene, 36827	1.753	0.0002	0.0007
Gm37694	ENSMUSG00000102562	predicted gene, 37694	2.291	0.0051	0.0146
Gm37711	ENSMUSG00000102796	predicted gene, 37711	3.583	0.0234	0.0546
Gm37786	ENSMUSG00000102632	predicted gene, 37786	3.403	0.0192	0.0461
Gm37969	ENSMUSG00000102577	predicted gene, 37969	10.783	0.0133	0.0338
Gm41144	ENSMUSG00000115846	predicted gene, 41144	7.163	0.0021	0.0067
Gm4202	ENSMUSG00000091421	predicted gene 4202	1.789	0.0048	0.0140
Gm43011	ENSMUSG00000106475	predicted gene 43011	1.847	0.0459	0.0964

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm43062	ENSMUSG00000104671	predicted gene 43062	7.159	0.0033	0.0101
Gm43324	ENSMUSG00000105487	predicted gene 43324	8.302	0.0004	0.0015
Gm43481	ENSMUSG00000107000	predicted gene 43481	2.476	0.0021	0.0066
Gm43500	ENSMUSG00000107296	predicted gene 43500	7.794	0.0212	0.0502
Gm43568	ENSMUSG00000106365	predicted gene 43568	4.894	0.0304	0.0682
Gm43573	ENSMUSG00000104786	predicted gene 43573	4.529	0.0000	0.0001
Gm43712	ENSMUSG00000104649	predicted gene 43712	3.598	0.0180	0.0435
Gm44421	ENSMUSG00000107451	predicted gene, 44421	2.392	0.0000	0.0001
Gm44837	ENSMUSG00000108723	predicted gene 44837	18.931	0.0178	0.0433
Gm44950	ENSMUSG00000108350	predicted gene 44950	1.626	0.0001	0.0005
Gm45074	ENSMUSG00000109568	predicted gene 45074	13.572	0.0098	0.0259
Gm45897	ENSMUSG00000110676	predicted gene 45897	2.838	0.0177	0.0431
Gm47210	ENSMUSG00000113647	predicted gene, 47210	5.019	0.0004	0.0014
Gm47863	ENSMUSG00000113165	predicted gene, 47863	1.739	0.0031	0.0096
Gm48295	ENSMUSG00000114309	predicted gene, 48295	1.907	0.0419	0.0894
Gm48607	ENSMUSG00000113735	predicted gene, 48607	2.098	0.0322	0.0717
Gm4925	ENSMUSG00000069540	predicted gene 4925	2.647	0.0117	0.0300
Gm49284	ENSMUSG00000114995	predicted gene, 49284	1.617	0.0049	0.0142
Gm49727	ENSMUSG00000116836	predicted gene, 49727	3.289	0.0175	0.0427
Gm49768	ENSMUSG00000115220	predicted gene, 49768	2.311	0.0000	0.0001
Gm5577	ENSMUSG00000084950	predicted gene 5577	5.060	0.0281	0.0639
Gm5620	ENSMUSG00000056904	predicted gene 5620	3.213	0.0022	0.0068
Gm5819	ENSMUSG00000092097	predicted gene 5819	9.822	0.0041	0.0122
Gm5904	ENSMUSG00000109894	predicted gene 5904	4.288	0.0231	0.0540
Gm6444	ENSMUSG00000080836	predicted gene 6444	1.837	0.0374	0.0813
Gm6457	ENSMUSG00000053740	predicted pseudogene 6457	3.387	0.0446	0.0939
Gm6685	ENSMUSG00000032889	predicted pseudogene 6685	1.644	0.0368	0.0802
Gm6974	ENSMUSG00000117673	predicted gene 6974	23.221	0.0011	0.0038
Gm7198	ENSMUSG00000112395	predicted gene 7198	36.495	0.0421	0.0897
Gm8518	ENSMUSG00000115312	predicted gene 8518	2.342	0.0058	0.0163
Gm8546	ENSMUSG00000094463	predicted gene 8546	2.642	0.0191	0.0459

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm8717	ENSMUSG00000117935	predicted gene 8717	4.438	0.0030	0.0091
Gm9118	ENSMUSG00000112825	predicted gene 9118	3.811	0.0345	0.0759
Gm9202	ENSMUSG00000114066	predicted gene 9202	3.222	0.0100	0.0264
Gm9316	ENSMUSG00000117262	predicted gene 9316	4.383	0.0001	0.0005
Gm9442	ENSMUSG00000104241	predicted gene 9442	3.049	0.0228	0.0535
Gm9755	ENSMUSG00000030735	predicted pseudogene 9755	1.934	0.0079	0.0213
Gm9828	ENSMUSG00000048603	predicted gene 9828	2.064	0.0284	0.0644
Gm9847	ENSMUSG00000050974	predicted pseudogene 9847	2.031	0.0009	0.0032
Gm9959	ENSMUSG00000054957	predicted gene 9959	24.038	0.0219	0.0515
Gnai2	ENSMUSG00000032562	guanine nucleotide binding protein (G protein), alpha inhibiting 2	1.557	0.0000	0.0000
Golga2	ENSMUSG00000002546	golgi autoantigen, golgin subfamily a, 2	1.578	0.0000	0.0000
Gon7	ENSMUSG00000091931	GON7 subunit of KEOPS complex	1.570	0.0053	0.0151
Gpc1	ENSMUSG00000034220	glypican 1	1.560	0.0000	0.0000
Gpr141	ENSMUSG00000053101	G protein-coupled receptor 141	3.877	0.0215	0.0508
Gpr63	ENSMUSG00000040372	G protein-coupled receptor 63	2.404	0.0118	0.0303
Gpsm3	ENSMUSG00000034786	G-protein signalling modulator 3 (AGS3-like, C. elegans)	1.540	0.0027	0.0085
Grap2	ENSMUSG00000042351	GRB2-related adaptor protein 2	2.109	0.0239	0.0556
Gripap1	ENSMUSG00000031153	GRIP1 associated protein 1	1.534	0.0000	0.0000
Gzmm	ENSMUSG00000054206	granzyme M (lymphocyte met-ase 1)	1.581	0.0016	0.0054
H2-DMb1	ENSMUSG00000079547	histocompatibility 2, class II, locus Mb1	2.163	0.0389	0.0841
H2-M5	ENSMUSG00000024459	histocompatibility 2, M region locus 5	5.840	0.0130	0.0329
H2-Q1	ENSMUSG00000079507	histocompatibility 2, Q region locus 1	3.246	0.0000	0.0001
H2-Q6	ENSMUSG00000073409	histocompatibility 2, Q region locus 6	2.881	0.0124	0.0316
H2-T10	ENSMUSG00000079491	histocompatibility 2, T region locus 10	1.503	0.0056	0.0159
H2-T-ps	ENSMUSG00000073405	histocompatibility 2, T region locus, pseudogene	1.529	0.0175	0.0425
Hars	ENSMUSG00000001380	histidyl-tRNA synthetase	1.579	0.0000	0.0000
Hax1	ENSMUSG00000027944	HCLS1 associated X-1	1.597	0.0000	0.0000
Hes7	ENSMUSG00000023781	hes family bHLH transcription factor 7	10.463	0.0370	0.0805
Hoxa3	ENSMUSG00000079560	homeobox A3	1.978	0.0043	0.0127
Hoxa4	ENSMUSG00000000942	homeobox A4	8.845	0.0000	0.0000
Hoxb4	ENSMUSG00000038692	homeobox B4	1.956	0.0030	0.0093

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hsbp1l1	ENSMUSG00000078963	heat shock factor binding protein 1-like 1	1.637	0.0187	0.0451
Hscb	ENSMUSG00000043510	HscB iron-sulfur cluster co-chaperone	1.509	0.0000	0.0000
Ift172	ENSMUSG00000038564	intraflagellar transport 172	1.565	0.0000	0.0000
Ighj1	ENSMUSG00000076621	immunoglobulin heavy joining 1	5.444	0.0055	0.0155
Il1rl1	ENSMUSG00000026069	interleukin 1 receptor-like 1	2.344	0.0198	0.0473
Ildr2	ENSMUSG00000040612	immunoglobulin-like domain containing receptor 2	2.224	0.0297	0.0668
Ilk	ENSMUSG00000030890	integrin linked kinase	1.506	0.0000	0.0000
Ing1	ENSMUSG00000045969	inhibitor of growth family, member 1	1.559	0.0002	0.0009
Iqcg	ENSMUSG00000035578	IQ motif containing G	2.711	0.0012	0.0039
Irf2bp1	ENSMUSG00000044030	interferon regulatory factor 2 binding protein 1	1.674	0.0000	0.0001
Irf7	ENSMUSG00000025498	interferon regulatory factor 7	1.689	0.0316	0.0704
Itgb3	ENSMUSG00000020689	integrin beta 3	2.014	0.0056	0.0158
Itpka	ENSMUSG00000027296	inositol 1,4,5-trisphosphate 3-kinase A	2.377	0.0004	0.0017
Kazald1	ENSMUSG00000025213	Kazal-type serine peptidase inhibitor domain 1	2.053	0.0001	0.0003
Kazn	ENSMUSG00000040606	kazrin, periplakin interacting protein	1.783	0.0000	0.0000
Kbtbd11	ENSMUSG00000055675	kelch repeat and BTB (POZ) domain containing 11	1.624	0.0007	0.0026
Kcna1	ENSMUSG00000047976	potassium voltage-gated channel, shaker-related subfamily, member 1	1.550	0.0188	0.0452
Kcnab1	ENSMUSG00000027827	potassium voltage-gated channel, shaker-related subfamily, beta member 1	1.583	0.0027	0.0083
Kcnc3	ENSMUSG00000062785	potassium voltage gated channel, Shaw-related subfamily, member 3	1.694	0.0000	0.0002
Kcnip2	ENSMUSG00000025221	Kv channel-interacting protein 2	1.785	0.0000	0.0000
Kcnk3	ENSMUSG00000049265	potassium channel, subfamily K, member 3	1.590	0.0000	0.0000
Kcnmb4	ENSMUSG00000054934	potassium large conductance calcium-activated channel, subfamily M, beta member 4	4.689	0.0114	0.0293
Kctd15	ENSMUSG00000030499	potassium channel tetramerisation domain containing 15	1.680	0.0216	0.0510
Kif5a	ENSMUSG00000074657	kinesin family member 5A	1.527	0.0164	0.0403
Kin	ENSMUSG00000037262	Kin17 DNA and RNA binding protein	1.607	0.0000	0.0002
Klc1	ENSMUSG00000021288	kinesin light chain 1	1.566	0.0000	0.0000
Klhl17	ENSMUSG00002076083	kelch-like 17	1.710	0.0000	0.0000
Kmt2b	ENSMUSG00000006307	lysine (K)-specific methyltransferase 2B	1.540	0.0001	0.0003
Lamtor2	ENSMUSG00000028062	late endosomal/lysosomal adaptor, MAPK and MTOR activator 2	1.567	0.0000	0.0000
Larp1	ENSMUSG00000037331	La ribonucleoprotein domain family, member 1	1.594	0.0000	0.0000
Lat	ENSMUSG00000030742	linker for activation of T cells	2.845	0.0131	0.0333

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lig4	ENSMUSG00000049717	ligase IV, DNA, ATP-dependent	1.573	0.0000	0.0000
Limd2	ENSMUSG00000040699	LIM domain containing 2	2.184	0.0000	0.0002
Lmcd1	ENSMUSG00000057604	LIM and cysteine-rich domains 1	1.748	0.0000	0.0000
Lrrc38	ENSMUSG00000028584	leucine rich repeat containing 38	5.500	0.0217	0.0511
Lsm11	ENSMUSG00000044847	U7 snRNP-specific Sm-like protein LSM11	1.510	0.0003	0.0013
Lsmem1	ENSMUSG00000071342	leucine-rich single-pass membrane protein 1	1.827	0.0378	0.0821
Lsp1	ENSMUSG00000018819	lymphocyte specific 1	1.617	0.0000	0.0000
Lzts3	ENSMUSG00000037703	leucine zipper, putative tumor suppressor family member 3	1.585	0.0010	0.0034
Macroh2a1	ENSMUSG00000015937	macroH2A.1 histone	1.523	0.0000	0.0000
Mapkapk2	ENSMUSG00000016528	MAP kinase-activated protein kinase 2	1.511	0.0000	0.0001
Mb	ENSMUSG00000018893	myoglobin	1.684	0.0000	0.0000
Mcf2l	ENSMUSG00000031442	mcf.2 transforming sequence-like	1.644	0.0337	0.0744
Mcm9	ENSMUSG00000058298	minichromosome maintenance 9 homologous recombination repair factor	1.593	0.0003	0.0011
Mdga2	ENSMUSG00000034912	MAM domain containing glycosylphosphatidylinositol anchor 2	1.833	0.0345	0.0759
Med4	ENSMUSG00000022109	mediator complex subunit 4	1.661	0.0000	0.0000
Mia3	ENSMUSG00000056050	MIA SH3 domain ER export factor 3	1.599	0.0000	0.0000
Mib2	ENSMUSG00000029060	mindbomb E3 ubiquitin protein ligase 2	1.645	0.0000	0.0000
Mir1943	ENSMUSG00000088901	microRNA 1943	8.044	0.0323	0.0719
Mir208a	ENSMUSG00000065432	microRNA 208a	3.829	0.0318	0.0708
Mir7052	ENSMUSG00000098661	microRNA 7052	5.611	0.0334	0.0738
Mmab	ENSMUSG00000029575	methylmalonic aciduria (cobalamin deficiency) cblB type homolog (human)	1.686	0.0000	0.0000
Mmp3	ENSMUSG00000043613	matrix metallopeptidase 3	2.734	0.0127	0.0323
Mpdz	ENSMUSG00000028402	multiple PDZ domain crumbs cell polarity complex component	1.527	0.0000	0.0000
Mpzl3	ENSMUSG00000070305	myelin protein zero-like 3	1.528	0.0002	0.0006
Mras	ENSMUSG00000032470	muscle and microspikes RAS	1.614	0.0000	0.0000
Mrln	ENSMUSG00000019933	myoregulin	1.717	0.0480	0.0999
Msl3	ENSMUSG00000031358	MSL complex subunit 3	1.929	0.0012	0.0039
Msx2	ENSMUSG00000021469	msh homeobox 2	3.723	0.0325	0.0721
Mt3	ENSMUSG00000031760	metallothionein 3	1.883	0.0103	0.0269
Mthfd1l	ENSMUSG00000040675	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 1-like	1.755	0.0341	0.0751

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mthfd2	ENSMUSG00000005667	methylenetetrahydrofolate dehydrogenase (NAD+ dependent), methenyltetrahydrofolate cyclohydrolase	1.756	0.0052	0.0149
Mtss2	ENSMUSG00000033763	MTSS I-BAR domain containing 2	1.795	0.0000	0.0000
Mvp	ENSMUSG00000030681	major vault protein	1.752	0.0000	0.0000
Myh7	ENSMUSG00000053093	myosin, heavy polypeptide 7, cardiac muscle, beta	1.559	0.0035	0.0107
Mylk4	ENSMUSG00000044951	myosin light chain kinase family, member 4	1.610	0.0054	0.0154
Myo1e	ENSMUSG00000032220	myosin IE	1.580	0.0000	0.0000
Nabp1	ENSMUSG00000026107	nucleic acid binding protein 1	1.569	0.0004	0.0016
Nacc1	ENSMUSG00000001910	nucleus accumbens associated 1, BEN and BTB (POZ) domain containing	1.604	0.0000	0.0000
Nat14	ENSMUSG00000035285	N-acetyltransferase 14	1.877	0.0003	0.0011
Ncf2	ENSMUSG00000026480	neutrophil cytosolic factor 2	1.609	0.0037	0.0112
Ndufaf2	ENSMUSG00000068184	NADH:ubiquinone oxidoreductase complex assembly factor 2	1.571	0.0000	0.0000
Ndufb10	ENSMUSG00000040048	NADH:ubiquinone oxidoreductase subunit B10	1.841	0.0000	0.0000
Neat1	ENSMUSG00000092274	nuclear paraspeckle assembly transcript 1 (non-protein coding)	2.035	0.0454	0.0955
Nefl	ENSMUSG00000022055	neurofilament, light polypeptide	10.169	0.0448	0.0943
Nkain1	ENSMUSG00000078532	Na+/K+ transporting ATPase interacting 1	1.869	0.0020	0.0063
Nlgn3	ENSMUSG00000031302	neuroligin 3	2.516	0.0248	0.0573
Nop2	ENSMUSG00000038279	NOP2 nucleolar protein	1.582	0.0000	0.0000
Noxred1	ENSMUSG00000072919	NADP+ dependent oxidoreductase domain containing 1	3.282	0.0156	0.0387
Npc2	ENSMUSG00000021242	NPC intracellular cholesterol transporter 2	1.614	0.0000	0.0000
Npnt	ENSMUSG00000040998	nephronectin	2.024	0.0176	0.0428
Nrn1	ENSMUSG00000039114	neuritin 1	2.002	0.0112	0.0291
Nucb1	ENSMUSG00000030824	nucleobindin 1	1.861	0.0000	0.0000
Nudt13	ENSMUSG00000021809	nudix (nucleoside diphosphate linked moiety X)-type motif 13	1.563	0.0000	0.0000
Numbl	ENSMUSG00000063160	numb-like	1.583	0.0057	0.0162
Nyap1	ENSMUSG00000045348	neuronal tyrosine-phosphorylated phosphoinositide 3-kinase adaptor 1	2.135	0.0000	0.0000
Oas3	ENSMUSG00000032661	2'-5' oligoadenylate synthetase 3	4.099	0.0249	0.0577
Odaph	ENSMUSG00000096035	odontogenesis associated phosphoprotein	2.052	0.0344	0.0757
Optn	ENSMUSG00000026672	optineurin	1.508	0.0002	0.0006
Os9	ENSMUSG00000040462	amplified in osteosarcoma	1.628	0.0000	0.0000
Parp2	ENSMUSG00000036023	poly (ADP-ribose) polymerase family, member 2	1.514	0.0001	0.0003

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pcdh20	ENSMUSG00000050505	protocadherin 20	3.010	0.0195	0.0467
Pcdhb2	ENSMUSG00000051599	protocadherin beta 2	2.757	0.0226	0.0529
Pcnt	ENSMUSG00000001151	pericentrin (kendrin)	1.526	0.0008	0.0028
Pdlim2	ENSMUSG00000022090	PDZ and LIM domain 2	1.755	0.0001	0.0004
Pdrg1	ENSMUSG00000027472	p53 and DNA damage regulated 1	1.508	0.0000	0.0000
Pdxp	ENSMUSG00000116165	pyridoxal (pyridoxine, vitamin B6) phosphatase	2.808	0.0327	0.0725
Peli3	ENSMUSG00000024901	pellino 3	1.708	0.0000	0.0000
Pex16	ENSMUSG00000027222	peroxisomal biogenesis factor 16	1.504	0.0003	0.0010
Pheta2	ENSMUSG00000049687	PH domain containing endocytic trafficking adaptor 2	1.786	0.0031	0.0096
Phf21a	ENSMUSG00000058318	PHD finger protein 21A	1.536	0.0000	0.0000
Phf21b	ENSMUSG00000016624	PHD finger protein 21B	1.616	0.0172	0.0420
Piezo2	ENSMUSG00000041482	piezo-type mechanosensitive ion channel component 2	2.249	0.0253	0.0583
Plet1os	ENSMUSG00000101304	placenta expressed transcript 1, opposite strand	1.759	0.0000	0.0001
Pmepa1	ENSMUSG00000038400	prostate transmembrane protein, androgen induced 1	1.563	0.0000	0.0000
Pmvk	ENSMUSG00000027952	phosphomevalonate kinase	1.778	0.0000	0.0000
Polr2a	ENSMUSG00000005198	polymerase (RNA) II (DNA directed) polypeptide A	1.602	0.0000	0.0001
Pou2f2	ENSMUSG00000008496	POU domain, class 2, transcription factor 2	2.107	0.0173	0.0421
Ppfia3	ENSMUSG00000003863	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3	3.470	0.0146	0.0366
Ppih	ENSMUSG00000060288	peptidyl prolyl isomerase H	1.500	0.0000	0.0002
Ppl	ENSMUSG00000039457	periplakin	1.714	0.0013	0.0044
Ppm1m	ENSMUSG00000020253	protein phosphatase 1M	1.542	0.0000	0.0000
Ppp1r18	ENSMUSG00000034595	protein phosphatase 1, regulatory subunit 18	1.693	0.0000	0.0000
Ppp1r37	ENSMUSG00000051403	protein phosphatase 1, regulatory subunit 37	1.753	0.0000	0.0000
Ppp6r1	ENSMUSG00000052296	protein phosphatase 6, regulatory subunit 1	1.713	0.0000	0.0000
Prdm6	ENSMUSG00000069378	PR domain containing 6	6.608	0.0048	0.0140
Prdx5	ENSMUSG00000024953	peroxiredoxin 5	1.774	0.0000	0.0000
Prmt6	ENSMUSG00000049300	protein arginine N-methyltransferase 6	1.505	0.0000	0.0002
Prpf40b	ENSMUSG00000023007	pre-mRNA processing factor 40B	1.677	0.0000	0.0000
Prpf6	ENSMUSG00000002455	pre-mRNA splicing factor 6	1.639	0.0000	0.0000
Prr13	ENSMUSG00000023048	proline rich 13	1.568	0.0000	0.0000

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

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Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Prr15	ENSMUSG00000045725	proline rich 15	2.097	0.0125	0.0318
Prr3	ENSMUSG00000038500	proline-rich polypeptide 3	1.742	0.0004	0.0016
Prx	ENSMUSG00000053198	periaxin	1.608	0.0439	0.0928
Psmc3	ENSMUSG00000002102	proteasome (prosome, macropain) 26S subunit, ATPase 3	1.613	0.0000	0.0000
Pstpip1	ENSMUSG00000032322	proline-serine-threonine phosphatase-interacting protein 1	1.924	0.0041	0.0121
Ptges3-ps	ENSMUSG00000040078	prostaglandin E synthase 3, pseudogene	1.787	0.0209	0.0495
Ptma-ps2	ENSMUSG00000084274	prothymosin alpha, pseudogene 2	11.122	0.0000	0.0000
Ptpdc1	ENSMUSG00000038042	protein tyrosine phosphatase domain containing 1	1.509	0.0000	0.0002
Ptprc	ENSMUSG00000026395	protein tyrosine phosphatase, receptor type, C	1.744	0.0109	0.0284
Pym1	ENSMUSG00000064030	PYM homolog 1, exon junction complex associated factor	1.719	0.0000	0.0001
Rab11fip1	ENSMUSG00000031488	RAB11 family interacting protein 1 (class I)	2.266	0.0121	0.0309
Rab6b	ENSMUSG00000032549	RAB6B, member RAS oncogene family	2.287	0.0190	0.0456
Rab9b	ENSMUSG00000043463	RAB9B, member RAS oncogene family	2.408	0.0121	0.0311
Rabl6	ENSMUSG00000015087	RAB, member RAS oncogene family-like 6	1.512	0.0000	0.0000
Rangrf	ENSMUSG00000032892	RAN guanine nucleotide release factor	1.902	0.0000	0.0000
Rasgef1a	ENSMUSG00000030134	RasGEF domain family, member 1A	1.882	0.0055	0.0157
Rassf10	ENSMUSG00000098132	Ras association (RalGDS/AF-6) domain family (N-terminal) member 10	1.893	0.0000	0.0000
Rassf8	ENSMUSG00000030259	Ras association (RalGDS/AF-6) domain family (N-terminal) member 8	1.517	0.0000	0.0000
Rbm5	ENSMUSG00000032580	RNA binding motif protein 5	1.616	0.0000	0.0001
Rbp1	ENSMUSG00000046402	retinol binding protein 1, cellular	1.878	0.0000	0.0001
Rcc2	ENSMUSG00000040945	regulator of chromosome condensation 2	1.694	0.0000	0.0000
Rcn3	ENSMUSG00000019539	reticulocalbin 3, EF-hand calcium binding domain	1.622	0.0027	0.0084
Rcor2	ENSMUSG00000024968	REST corepressor 2	1.829	0.0000	0.0001
Rexo4	ENSMUSG00000052406	REX4, 3'-5' exonuclease	1.657	0.0000	0.0000
Rilpl2	ENSMUSG00000029401	Rab interacting lysosomal protein-like 2	1.694	0.0000	0.0000
Rnf40	ENSMUSG00000030816	ring finger protein 40	1.521	0.0000	0.0000
Robo1	ENSMUSG00000022883	roundabout guidance receptor 1	1.730	0.0042	0.0124
Robo2	ENSMUSG00000052516	roundabout guidance receptor 2	2.125	0.0021	0.0067
Rpain	ENSMUSG00000018449	RPA interacting protein	1.509	0.0001	0.0004
Rps15a-ps6	ENSMUSG00000083022	ribosomal protein S15A, pseudogene 6	2.737	0.0396	0.0853
Rps6-ps4	ENSMUSG00000081406	ribosomal protein S6, pseudogene 4	2.797	0.0035	0.0106

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rrp7a	ENSMUSG00000018040	ribosomal RNA processing 7 homolog A	1.586	0.0000	0.0000
Rtf2	ENSMUSG00000027502	replication termination factor 2	1.541	0.0000	0.0000
Runx2	ENSMUSG00000039153	runt related transcription factor 2	1.800	0.0005	0.0019
Runx3	ENSMUSG00000070691	runt related transcription factor 3	2.080	0.0071	0.0194
Sbsn	ENSMUSG00000046056	suprabasin	2.307	0.0213	0.0504
Scml4	ENSMUSG00000044770	Scm polycomb group protein like 4	1.936	0.0304	0.0682
Scn1b	ENSMUSG00000019194	sodium channel, voltage-gated, type I, beta	1.834	0.0000	0.0001
Sdsl	ENSMUSG00000029596	serine dehydratase-like	1.689	0.0000	0.0000
Sec22c	ENSMUSG00000061536	SEC22 homolog C, vesicle trafficking protein	1.848	0.0000	0.0000
Septin3	ENSMUSG00000022456	septin 3	1.992	0.0036	0.0109
Serpinb1c	ENSMUSG00000079049	serine (or cysteine) peptidase inhibitor, clade B, member 1c	6.650	0.0059	0.0166
Setd1b	ENSMUSG00000038384	SET domain containing 1B	1.536	0.0001	0.0004
Sf3a3	ENSMUSG00000028902	splicing factor 3a, subunit 3	1.619	0.0000	0.0000
Shank1	ENSMUSG00000038738	SH3 and multiple ankyrin repeat domains 1	1.763	0.0119	0.0307
Shc2	ENSMUSG00000020312	SHC (Src homology 2 domain containing) transforming protein 2	1.585	0.0014	0.0047
Shisa2	ENSMUSG00000044461	shisa family member 2	1.751	0.0228	0.0535
Shisa4	ENSMUSG00000041889	shisa family member 4	1.822	0.0026	0.0082
Shtn1	ENSMUSG00000041362	shootin 1	1.949	0.0000	0.0000
Siglece	ENSMUSG00000030474	sialic acid binding Ig-like lectin E	1.938	0.0163	0.0401
Sla	ENSMUSG00000022372	src-like adaptor	1.885	0.0014	0.0046
Slc24a1	ENSMUSG00000034452	solute carrier family 24 (sodium/potassium/calcium exchanger), member 1	1.663	0.0260	0.0598
Slc28a2b	ENSMUSG00000079071	solute carrier family 28 member 2b	1.569	0.0002	0.0007
Slc38a1	ENSMUSG00000023169	solute carrier family 38, member 1	1.551	0.0212	0.0500
Slfn1	ENSMUSG00000078763	schlafen 1	2.886	0.0296	0.0668
Smarca4	ENSMUSG00000032187	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 4	1.541	0.0000	0.0000
Smtnl1	ENSMUSG00000027077	smoothelin-like 1	10.468	0.0002	0.0008
Sncg	ENSMUSG00000023064	synuclein, gamma	1.521	0.0000	0.0001
Snord73b	ENSMUSG00000064390	small nucleolar RNA, C/D box U73B	3.852	0.0455	0.0956
Sost	ENSMUSG00000001494	sclerostin	3.303	0.0019	0.0060
Spa17	ENSMUSG00000001948	sperm autoantigenic protein 17	1.835	0.0001	0.0003

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Spag6	ENSMUSG00000037708	sperm associated antigen 6	6.670	0.0224	0.0526
Spin2c	ENSMUSG00000046550	spindlin family, member 2C	4.264	0.0048	0.0140
Spindoc	ENSMUSG00000024970	spindlin interactor and repressor of chromatin binding	1.573	0.0001	0.0005
Spred3	ENSMUSG00000037239	sprouty-related EVH1 domain containing 3	2.140	0.0256	0.0590
Srgap3	ENSMUSG00000030257	SLIT-ROBO Rho GTPase activating protein 3	1.998	0.0017	0.0057
Srrm4	ENSMUSG00000063919	serine/arginine repetitive matrix 4	1.639	0.0000	0.0001
Ssc5d	ENSMUSG00000035279	scavenger receptor cysteine rich family, 5 domains	1.654	0.0051	0.0147
Stk10	ENSMUSG00000020272	serine/threonine kinase 10	1.602	0.0001	0.0004
Stk39	ENSMUSG00000027030	serine/threonine kinase 39	1.768	0.0000	0.0000
Stmn1	ENSMUSG00000028832	stathmin 1	2.212	0.0000	0.0000
Stx1a	ENSMUSG00000007207	syntaxin 1A (brain)	1.692	0.0297	0.0669
Stx1b	ENSMUSG00000030806	syntaxin 1B	2.557	0.0003	0.0012
Sun2	ENSMUSG00000042524	Sad1 and UNC84 domain containing 2	1.506	0.0076	0.0208
Supt5	ENSMUSG00000003435	suppressor of Ty 5, DSIF elongation factor subunit	1.591	0.0000	0.0000
Supt6	ENSMUSG00000002052	SPT6, histone chaperone and transcription elongation factor	1.574	0.0000	0.0000
Suv39h2	ENSMUSG00000026646	suppressor of variegation 3-9 2	1.897	0.0072	0.0198
Tceal3	ENSMUSG00000044550	transcription elongation factor A (SII)-like 3	7.220	0.0003	0.0013
Tfap2a	ENSMUSG00000021359	transcription factor AP-2, alpha	4.015	0.0040	0.0119
Tfap2e	ENSMUSG00000042477	transcription factor AP-2, epsilon	8.652	0.0069	0.0190
Thbs4	ENSMUSG00000021702	thrombospondin 4	2.282	0.0454	0.0955
Tigd5	ENSMUSG00000103906	tigger transposable element derived 5	1.552	0.0045	0.0132
Timd4	ENSMUSG00000055546	T cell immunoglobulin and mucin domain containing 4	1.811	0.0423	0.0901
Tmem179	ENSMUSG00000054013	transmembrane protein 179	2.073	0.0222	0.0521
Tmem240	ENSMUSG00000084845	transmembrane protein 240	2.216	0.0202	0.0480
Tnks1bp1	ENSMUSG00000033955	tankyrase 1 binding protein 1	1.647	0.0000	0.0000
Tnni3	ENSMUSG00000035458	troponin I, cardiac 3	1.639	0.0000	0.0000
Tox3	ENSMUSG00000043668	TOX high mobility group box family member 3	1.767	0.0000	0.0001
Trim21	ENSMUSG00000030966	tripartite motif-containing 21	1.912	0.0000	0.0000
Trim45	ENSMUSG00000033233	tripartite motif-containing 45	1.725	0.0001	0.0002
Trim54	ENSMUSG00000062077	tripartite motif-containing 54	1.772	0.0000	0.0001
Trip10	ENSMUSG00000019487	thyroid hormone receptor interactor 10	1.563	0.0007	0.0025

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Trmt6	ENSMUSG00000037376	tRNA methyltransferase 6	1.565	0.0000	0.0000
Tspan33	ENSMUSG00000001763	tetraspanin 33	1.502	0.0159	0.0393
Tsr2	ENSMUSG00000025264	TSR2 20S rRNA accumulation	1.693	0.0000	0.0000
Ttc39aos1	ENSMUSG00000085873	Ttc39a opposite strand RNA 1	2.272	0.0155	0.0385
Ttc5	ENSMUSG00000006288	tetratricopeptide repeat domain 5	1.557	0.0000	0.0000
Ttyh1	ENSMUSG00000030428	tweety family member 1	2.358	0.0332	0.0734
Txnrd1	ENSMUSG00000020250	thioredoxin reductase 1	1.547	0.0033	0.0100
U2af1	ENSMUSG00000061613	U2 small nuclear ribonucleoprotein auxiliary factor (U2AF) 1	1.695	0.0000	0.0000
Uaca	ENSMUSG00000034485	uveal autoantigen with coiled-coil domains and ankyrin repeats	1.590	0.0000	0.0000
Usb1	ENSMUSG00000031792	U6 snRNA biogenesis 1	1.515	0.0000	0.0000
Ush1c	ENSMUSG00000030838	USH1 protein network component harmonin	1.824	0.0053	0.0152
Vil1	ENSMUSG00000026175	villin 1	1.845	0.0331	0.0731
Vps37d	ENSMUSG00000043614	vacuolar protein sorting 37D	1.776	0.0151	0.0376
Vps72	ENSMUSG00000008958	vacuolar protein sorting 72	1.559	0.0000	0.0000
Vstm2b	ENSMUSG00000039257	V-set and transmembrane domain containing 2B	4.233	0.0055	0.0156
Zbtb7c	ENSMUSG00000044646	zinc finger and BTB domain containing 7C	1.810	0.0028	0.0086
Zc3h6	ENSMUSG00000042851	zinc finger CCCH type containing 6	1.715	0.0001	0.0005
Zfhx3	ENSMUSG00000038872	zinc finger homeobox 3	1.558	0.0000	0.0000
Zfp316	ENSMUSG00000046658	zinc finger protein 316	1.643	0.0000	0.0000
Zfp385a	ENSMUSG00000000552	zinc finger protein 385A	1.595	0.0001	0.0006
Zfp385c	ENSMUSG00000014198	zinc finger protein 385C	2.279	0.0243	0.0563
Zfp697	ENSMUSG00000050064	zinc finger protein 697	1.577	0.0129	0.0328
Zhx2	ENSMUSG00000071757	zinc fingers and homeoboxes 2	1.563	0.0000	0.0000

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
1110032A03Rik	ENSMUSG00000037971	RIKEN cDNA 1110032A03 gene	-1.675	0.0000	0.0000
1500004A13Rik	ENSMUSG00000098912	RIKEN cDNA 1500004A13 gene	-2.918	0.0403	0.0865
1500026H17Rik	ENSMUSG00000097383	RIKEN cDNA 1500026H17 gene	-2.804	0.0062	0.0173
1700022N22Rik	ENSMUSG00000097523	RIKEN cDNA 1700022N22 gene	-17.537	0.0063	0.0176
1700066B19Rik	ENSMUSG00000073598	RIKEN cDNA 1700066B19 gene	-8.651	0.0409	0.0875
1810010H24Rik	ENSMUSG00000078607	RIKEN cDNA 1810010H24 gene	-1.851	0.0155	0.0384
1810019D21Rik	ENSMUSG00000086390	RIKEN cDNA 1810019D21 gene	-3.813	0.0312	0.0696
2010001K21Rik	ENSMUSG00000051606	RIKEN cDNA 2010001K21 gene	-1.526	0.0042	0.0123
2210408I21Rik	ENSMUSG00000071252	RIKEN cDNA 2210408I21 gene	-1.731	0.0000	0.0000
2310020H05Rik	ENSMUSG00000100410	RIKEN cDNA 2310020H05 gene	-1.679	0.0178	0.0432
2500002B13Rik	ENSMUSG00000096917	RIKEN cDNA 2500002B13 gene	-1.554	0.0003	0.0010
2510016D11Rik	ENSMUSG00000106825	RIKEN cDNA 2510016D11 gene	-3.698	0.0040	0.0118
2610306O10Rik	ENSMUSG00000108614	RIKEN cDNA 2610306O10 gene	-3.345	0.0408	0.0875
3110009E18Rik	ENSMUSG00000026388	RIKEN cDNA 3110009E18 gene	-3.243	0.0000	0.0001
3222401L13Rik	ENSMUSG00000073590	RIKEN cDNA 3222401L13 gene	-1.511	0.0095	0.0252
3300002I08Rik	ENSMUSG00000063364	RIKEN cDNA 3300002I08 gene	-15.706	0.0004	0.0016
4631405J19Rik	ENSMUSG00000075027	RIKEN cDNA 4631405J19 gene	-1.630	0.0002	0.0006
4833419F23Rik	ENSMUSG00000117401	RIKEN cDNA 4833419F23 gene	-2.085	0.0395	0.0853
4833445I07Rik	ENSMUSG00000103103	RIKEN cDNA 4833445I07 gene	-4.375	0.0151	0.0377
4921507P07Rik	ENSMUSG00000029828	RIKEN cDNA 4921507P07 gene	-3.466	0.0020	0.0065
4921536K21Rik	ENSMUSG00000020434	RIKEN cDNA 4921536K21 gene	-2.426	0.0008	0.0028
4930431P22Rik	ENSMUSG00000115709	RIKEN cDNA 4930431P22 gene	-8.272	0.0377	0.0819
4930506C21Rik	ENSMUSG00000087478	RIKEN cDNA 4930506C21 gene	-14.961	0.0074	0.0203
4930522L14Rik	ENSMUSG00000072762	RIKEN cDNA 4930522L14 gene	-2.047	0.0106	0.0276
4930525G20Rik	ENSMUSG00000097276	RIKEN cDNA 4930525G20 gene	-12.451	0.0160	0.0396
4930581F22Rik	ENSMUSG00000070315	RIKEN cDNA 4930581F22 gene	-1.567	0.0288	0.0651
4933440J02Rik	ENSMUSG00000097082	RIKEN cDNA 4933440J02 gene	-17.586	0.0066	0.0183
5530601H04Rik	ENSMUSG00000087174	RIKEN cDNA 5530601H04 gene	-1.741	0.0015	0.0049
5830432E09Rik	ENSMUSG00000097471	RIKEN cDNA 5830432E09 gene	-1.968	0.0472	0.0986
6430584L05Rik	ENSMUSG00000108228	RIKEN cDNA 6430584L05 gene	-3.499	0.0083	0.0224
6720489N17Rik	ENSMUSG00000072066	RIKEN cDNA 6720489N17 gene	-3.423	0.0000	0.0002

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
8430437L04Rik	ENSMUSG00000085252	RIKEN cDNA 8430437L04 gene	-11.618	0.0266	0.0610
9330020H09Rik	ENSMUSG00000091050	RIKEN cDNA 9330020H09 gene	-4.574	0.0000	0.0001
9430015G10Rik	ENSMUSG00000059939	RIKEN cDNA 9430015G10 gene	-1.754	0.0019	0.0062
9530026P05Rik	ENSMUSG00000097462	RIKEN cDNA 9530026P05 gene	-1.760	0.0348	0.0765
9630013D21Rik	ENSMUSG00000059027	RIKEN cDNA 9630013D21 gene	-2.534	0.0003	0.0010
9930111J21Rik2	ENSMUSG00000069892	RIKEN cDNA 9930111J21 gene 2	-1.695	0.0004	0.0016
A230009B12Rik	ENSMUSG00000089633	RIKEN cDNA A230009B12 gene	-15.725	0.0020	0.0065
A630076J17Rik	ENSMUSG00000094613	RIKEN cDNA A630076J17 gene	-16.275	0.0106	0.0276
A730011C13Rik	ENSMUSG00000084846	RIKEN cDNA A730011C13 gene	-4.771	0.0012	0.0040
A930007I19Rik	ENSMUSG00000097855	RIKEN cDNA A930007I19 gene	-2.414	0.0476	0.0993
A930012L18Rik	ENSMUSG00000097610	RIKEN cDNA A930012L18 gene	-12.521	0.0110	0.0285
A930024E05Rik	ENSMUSG00000056735	RIKEN cDNA A930024E05 gene	-2.940	0.0475	0.0991
Abhd18	ENSMUSG00000037818	abhydrolase domain containing 18	-1.549	0.0000	0.0001
Acod1	ENSMUSG00000022126	aconitate decarboxylase 1	-13.828	0.0182	0.0441
Acot2	ENSMUSG00000021226	acyl-CoA thioesterase 2	-1.794	0.0001	0.0003
Acox2	ENSMUSG00000021751	acyl-Coenzyme A oxidase 2, branched chain	-18.657	0.0079	0.0213
Acsbg1	ENSMUSG00000032281	acyl-CoA synthetase bubblegum family member 1	-3.763	0.0081	0.0218
Acss3	ENSMUSG00000035948	acyl-CoA synthetase short-chain family member 3	-1.592	0.0128	0.0325
Acta2	ENSMUSG00000035783	actin alpha 2, smooth muscle, aorta	-1.622	0.0006	0.0023
Adal	ENSMUSG00000027259	adenosine deaminase-like	-1.863	0.0000	0.0000
Adrm1	ENSMUSG00000039041	adhesion regulating molecule 1	-1.500	0.0008	0.0027
AI838599	ENSMUSG00000085180	expressed sequence AI838599	-8.703	0.0023	0.0074
Airn	ENSMUSG00000078247	antisense Igf2r RNA	-1.757	0.0002	0.0007
Ak3	ENSMUSG00000024782	adenylate kinase 3	-1.942	0.0000	0.0000
Alg9	ENSMUSG00000032059	asparagine-linked glycosylation 9 (alpha 1,2 mannosyltransferase)	-1.541	0.0001	0.0005
Alkal2	ENSMUSG00000054204	ALK and LTK ligand 2	-3.293	0.0099	0.0261
Ang	ENSMUSG00000072115	angiogenin, ribonuclease, RNase A family, 5	-2.504	0.0175	0.0425
Angptl2	ENSMUSG00000004105	angiopoietin-like 2	-1.565	0.0011	0.0038
Angptl4	ENSMUSG00000002289	angiopoietin-like 4	-2.312	0.0323	0.0718
Ankrd10	ENSMUSG00000031508	ankyrin repeat domain 10	-1.566	0.0000	0.0000
Ankrd54	ENSMUSG00000033055	ankyrin repeat domain 54	-1.745	0.0009	0.0032

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Aoah	ENSMUSG00000021322	acyloxyacyl hydrolase	-2.538	0.0163	0.0401
Aopep	ENSMUSG00000021458	aminopeptidase O	-1.601	0.0000	0.0000
Arhgap28	ENSMUSG00000024043	Rho GTPase activating protein 28	-1.713	0.0006	0.0023
Arl11	ENSMUSG00000043157	ADP-ribosylation factor-like 11	-2.170	0.0343	0.0755
Arl5c	ENSMUSG00000038352	ADP-ribosylation factor-like 5C	-1.669	0.0176	0.0428
Arntl2	ENSMUSG00000040187	aryl hydrocarbon receptor nuclear translocator-like 2	-6.734	0.0245	0.0567
Arsk	ENSMUSG00000021592	arylsulfatase K	-2.263	0.0000	0.0000
Asb12	ENSMUSG00000031204	ankyrin repeat and SOCS box-containing 12	-1.517	0.0002	0.0009
Asb5	ENSMUSG00000031519	ankyrin repeat and SOCs box-containing 5	-1.641	0.0097	0.0257
Asxl3	ENSMUSG00000045215	ASXL transcriptional regulator 3	-1.652	0.0170	0.0415
Atf1-ps	ENSMUSG00000080968	activating transcription factor 1, pseudogene	-6.682	0.0055	0.0155
Atp10d	ENSMUSG00000046808	ATPase, class V, type 10D	-1.583	0.0020	0.0065
Atpsckmt	ENSMUSG00000039065	ATP synthase C subunit lysine N-methyltransferase	-1.548	0.0001	0.0004
AU041133	ENSMUSG00000078435	expressed sequence AU041133	-1.680	0.0478	0.0996
Aurka	ENSMUSG00000027496	aurora kinase A	-2.535	0.0006	0.0023
Avl9	ENSMUSG00000029787	AVL9 cell migration associated	-1.559	0.0000	0.0000
Bax	ENSMUSG00000003873	BCL2-associated X protein	-1.586	0.0008	0.0028
Bbip1	ENSMUSG00000084957	BBSome interacting protein 1	-1.595	0.0000	0.0000
BC028528	ENSMUSG00000038543	cDNA sequence BC028528	-1.582	0.0005	0.0020
Bche	ENSMUSG00000027792	butyrylcholinesterase	-1.732	0.0000	0.0000
Bdh2	ENSMUSG00000028167	3-hydroxybutyrate dehydrogenase, type 2	-3.075	0.0438	0.0926
Bmp10	ENSMUSG00000030046	bone morphogenetic protein 10	-83.565	0.0011	0.0039
Bmp2	ENSMUSG00000027358	bone morphogenetic protein 2	-1.615	0.0122	0.0312
Brca1	ENSMUSG00000017146	breast cancer 1, early onset	-2.358	0.0324	0.0719
Brinp2	ENSMUSG00000004031	bone morphogenic protein/retinoic acid inducible neural-specific 2	-19.441	0.0017	0.0055
Btf3l4b	ENSMUSG00000114133	basic transcription factor 3 like 4B	-2.134	0.0001	0.0005
Cab39l	ENSMUSG00000021981	calcium binding protein 39-like	-1.578	0.0118	0.0302
Calhm5	ENSMUSG00000049872	calcium homeostasis modulator family member 5	-1.665	0.0168	0.0411
Camk1g	ENSMUSG00000016179	calcium/calmodulin-dependent protein kinase I gamma	-6.808	0.0467	0.0977
Car3	ENSMUSG00000027559	carbonic anhydrase 3	-2.688	0.0446	0.0939
Cass4	ENSMUSG00000074570	Cas scaffolding protein family member 4	-2.613	0.0443	0.0934

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cat	ENSMUSG00000027187	catalase	-1.536	0.0024	0.0075
Catsperg1	ENSMUSG00000049676	cation channel sperm associated auxiliary subunit gamma 1	-3.821	0.0218	0.0513
Cav1	ENSMUSG00000007655	caveolin 1, caveolae protein	-1.662	0.0000	0.0000
Cbln1	ENSMUSG00000031654	cerebellin 1 precursor protein	-2.975	0.0385	0.0833
Ccdc103	ENSMUSG00000020930	coiled-coil domain containing 103	-4.949	0.0282	0.0641
Ccdc116	ENSMUSG00000022768	coiled-coil domain containing 116	-11.607	0.0152	0.0379
Ccdc130	ENSMUSG00000004994	coiled-coil domain containing 130	-1.614	0.0001	0.0005
Ccdc134	ENSMUSG00000068114	coiled-coil domain containing 134	-1.533	0.0004	0.0015
Ccdc162	ENSMUSG00000075225	coiled-coil domain containing 162	-8.413	0.0203	0.0483
Ccdc40	ENSMUSG00000039963	coiled-coil domain containing 40	-28.732	0.0007	0.0024
Ccdc73	ENSMUSG00000045106	coiled-coil domain containing 73	-5.224	0.0000	0.0000
Ccr1	ENSMUSG00000025804	chemokine (C-C motif) receptor 1	-2.260	0.0196	0.0469
Cd207	ENSMUSG00000034783	CD207 antigen	-22.672	0.0118	0.0304
Cd48	ENSMUSG00000015355	CD48 antigen	-2.276	0.0085	0.0229
Cdca5	ENSMUSG00000024791	cell division cycle associated 5	-4.009	0.0262	0.0601
Cdk1	ENSMUSG00000019942	cyclin-dependent kinase 1	-2.146	0.0188	0.0453
Cdkl1	ENSMUSG00000020990	cyclin-dependent kinase-like 1 (CDC2-related kinase)	-1.591	0.0037	0.0111
Ceacam2	ENSMUSG00000054385	carcinoembryonic antigen-related cell adhesion molecule 2	-4.196	0.0241	0.0560
Cela1	ENSMUSG00000023031	chymotrypsin-like elastase family, member 1	-2.493	0.0090	0.0240
Cenpn	ENSMUSG00000031756	centromere protein N	-5.248	0.0000	0.0001
Cep72	ENSMUSG00000021572	centrosomal protein 72	-2.000	0.0393	0.0848
Cep83os	ENSMUSG00000097164	centrosomal protein 83, opposite strand	-1.664	0.0020	0.0063
Cept1	ENSMUSG00000040774	choline/ethanolaminephosphotransferase 1	-1.920	0.0000	0.0000
Cerox1	ENSMUSG00000091475	cytoplasmic endogenous regulator of oxidative phosphorylation 1	-2.050	0.0330	0.0731
Ces1f	ENSMUSG00000031725	carboxylesterase 1F	-17.783	0.0037	0.0111
Chchd10	ENSMUSG00000049422	coiled-coil-helix-coiled-coil-helix domain containing 10	-2.644	0.0107	0.0279
Chic1	ENSMUSG00000031327	cysteine-rich hydrophobic domain 1	-1.684	0.0422	0.0899
Chka	ENSMUSG00000024843	choline kinase alpha	-1.720	0.0472	0.0987
Chrdl2	ENSMUSG00000030732	chordin-like 2	-16.640	0.0037	0.0110
Cidea	ENSMUSG00000024526	cell death-inducing DNA fragmentation factor, alpha subunit-like effector A	-1.735	0.0000	0.0000
Cidec	ENSMUSG00000030278	cell death-inducing DFFA-like effector c	-7.910	0.0003	0.0010

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ciita	ENSMUSG00000022504	class II transactivator	-2.500	0.0211	0.0499
Cklf	ENSMUSG00000054400	chemokine-like factor	-1.661	0.0195	0.0468
Cks1b	ENSMUSG00000028044	CDC28 protein kinase 1b	-1.726	0.0050	0.0145
Clca2	ENSMUSG00000036960	chloride channel accessory 2	-19.023	0.0015	0.0050
Cldn12	ENSMUSG00000046798	claudin 12	-1.697	0.0000	0.0000
Cldn34c1	ENSMUSG00000079450	claudin 34C1	-2.625	0.0171	0.0419
Clec18a	ENSMUSG00000033633	C-type lectin domain family 18, member A	-2.370	0.0193	0.0463
Clec4e	ENSMUSG00000030142	C-type lectin domain family 4, member e	-10.228	0.0478	0.0996
Cln5	ENSMUSG00000022125	ceroid-lipofuscinosis, neuronal 5	-1.648	0.0000	0.0000
Clstn3	ENSMUSG00000008153	calsyntenin 3	-2.912	0.0460	0.0964
Cmtm7	ENSMUSG00000032436	CKLF-like MARVEL transmembrane domain containing 7	-2.440	0.0199	0.0475
Cmtr2	ENSMUSG00000046441	cap methyltransferase 2	-1.515	0.0012	0.0040
Cox6c2	ENSMUSG00000066491	cytochrome c oxidase subunit 6C2	-2.899	0.0017	0.0056
Cox7b2	ENSMUSG00000049387	cytochrome c oxidase subunit 7B2	-4.617	0.0023	0.0072
Cpm	ENSMUSG00000020183	carboxypeptidase M	-1.632	0.0046	0.0134
Creb3l4	ENSMUSG00000027938	cAMP responsive element binding protein 3-like 4	-4.657	0.0036	0.0107
Cse1l	ENSMUSG00000002718	chromosome segregation 1-like (S. cerevisiae)	-1.593	0.0000	0.0000
Cstf2	ENSMUSG00000031256	cleavage stimulation factor, 3' pre-RNA subunit 2	-1.510	0.0006	0.0021
Ctsh	ENSMUSG00000032359	cathepsin H	-1.541	0.0046	0.0134
Ctso	ENSMUSG00000028015	cathepsin O	-1.683	0.0000	0.0000
Cttnbp2	ENSMUSG00000000416	cortactin binding protein 2	-1.538	0.0463	0.0971
Cul2	ENSMUSG00000024231	cullin 2	-1.518	0.0000	0.0000
Cxcr6	ENSMUSG00000048521	chemokine (C-X-C motif) receptor 6	-18.578	0.0021	0.0067
Cyp1a1	ENSMUSG00000032315	cytochrome P450, family 1, subfamily a, polypeptide 1	-14.849	0.0052	0.0149
Cyp2ab1	ENSMUSG00000022818	cytochrome P450, family 2, subfamily ab, polypeptide 1	-7.010	0.0153	0.0381
Cyp4f18	ENSMUSG00000003484	cytochrome P450, family 4, subfamily f, polypeptide 18	-9.303	0.0186	0.0449
D430040D24Rik	ENSMUSG00000087589	RIKEN cDNA D430040D24 gene	-1.608	0.0021	0.0067
D630036H23Rik	ENSMUSG00000091007	RIKEN cDNA D630036H23 gene	-11.217	0.0023	0.0073
D930030I03Rik	ENSMUSG00000097576	RIKEN cDNA D930030I03 gene	-11.469	0.0248	0.0574
Dbil5	ENSMUSG00000038057	diazepam binding inhibitor-like 5	-3.312	0.0289	0.0654
Dcp1b	ENSMUSG00000041477	decapping mRNA 1B	-1.737	0.0008	0.0028

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dctn4	ENSMUSG00000024603	dynactin 4	-1.575	0.0000	0.0000
Defb42	ENSMUSG00000054763	defensin beta 42	-4.738	0.0059	0.0165
Dennd10	ENSMUSG00000024993	DENN domain containing 10	-1.525	0.0000	0.0000
Derl1	ENSMUSG00000022365	Der1-like domain family, member 1	-1.536	0.0000	0.0000
Dgkeos	ENSMUSG00000063109	diacylglycerol kinase, epsilon, opposite strand	-2.046	0.0425	0.0904
Dhrs13	ENSMUSG00000020834	dehydrogenase/reductase (SDR family) member 13	-1.831	0.0000	0.0000
Dhx32	ENSMUSG00000030986	DEAH (Asp-Glu-Ala-His) box polypeptide 32	-1.633	0.0000	0.0000
Dio3os	ENSMUSG00000113581	deiodinase, iodothyronine type III, opposite strand	-14.495	0.0105	0.0274
Dipk2b	ENSMUSG00000037358	divergent protein kinase domain 2B	-1.748	0.0000	0.0001
Disp3	ENSMUSG00000041544	dispatched RND transporter family member 3	-11.277	0.0311	0.0694
Dlk2	ENSMUSG00000047428	delta like non-canonical Notch ligand 2	-3.208	0.0408	0.0875
Dnajc5b	ENSMUSG00000027606	DnaJ heat shock protein family (Hsp40) member C5 beta	-6.557	0.0280	0.0637
Dnph1	ENSMUSG00000040658	2'-deoxynucleoside 5'-phosphate N-hydrolase 1	-1.710	0.0327	0.0725
Dop1a	ENSMUSG00000034973	DOP1 leucine zipper like protein A	-1.848	0.0000	0.0000
Dusp14	ENSMUSG00000018648	dual specificity phosphatase 14	-2.325	0.0420	0.0897
E130215H24Rik	ENSMUSG00000087406	RIKEN cDNA E130215H24 gene	-4.740	0.0171	0.0417
Eaf2	ENSMUSG00000022838	ELL associated factor 2	-2.231	0.0025	0.0079
Efr3a	ENSMUSG00000015002	EFR3 homolog A	-1.511	0.0000	0.0000
Eif3s6-ps4	ENSMUSG00000106885	eukaryotic translation initiation factor 3, subunit 6, pseudogene 4	-8.511	0.0338	0.0745
Eif4g2	ENSMUSG00000005610	eukaryotic translation initiation factor 4, gamma 2	-1.509	0.0000	0.0000
Elmo3	ENSMUSG00000014791	engulfment and cell motility 3	-1.886	0.0014	0.0047
Elobl	ENSMUSG00000057534	elongin B-like	-3.618	0.0155	0.0384
Elovl4	ENSMUSG00000032262	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 4	-8.692	0.0376	0.0817
Eme2	ENSMUSG00000073436	essential meiotic structure-specific endonuclease subunit 2	-1.788	0.0001	0.0005
Emid1	ENSMUSG00000034164	EMI domain containing 1	-1.684	0.0160	0.0395
Enox1	ENSMUSG00000022012	ecto-NOX disulfide-thiol exchanger 1	-1.770	0.0296	0.0667
Enpp6	ENSMUSG00000038173	ectonucleotide pyrophosphatase/phosphodiesterase 6	-1.691	0.0000	0.0001
Epcam	ENSMUSG00000045394	epithelial cell adhesion molecule	-11.474	0.0271	0.0620
Erap1	ENSMUSG00000021583	endoplasmic reticulum aminopeptidase 1	-1.530	0.0000	0.0000
Ermard	ENSMUSG00000036552	ER membrane associated RNA degradation	-1.880	0.0000	0.0000
Ext2	ENSMUSG00000027198	exostosin glycosyltransferase 2	-1.791	0.0001	0.0003

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
F2rl3	ENSMUSG00000050147	coagulation factor II (thrombin) receptor-like 3	-4.555	0.0001	0.0004
F8	ENSMUSG00000031196	coagulation factor VIII	-1.791	0.0001	0.0004
Fam228b	ENSMUSG00000050545	family with sequence similarity 228, member B	-2.076	0.0002	0.0008
Fam72a	ENSMUSG00000055184	family with sequence similarity 72, member A	-1.836	0.0127	0.0322
Fanci	ENSMUSG00000039187	Fanconi anemia, complementation group I	-3.048	0.0405	0.0869
Fap	ENSMUSG00000000392	fibroblast activation protein	-1.671	0.0007	0.0024
Fastkd1	ENSMUSG00000027086	FAST kinase domains 1	-1.760	0.0000	0.0000
Fastkd2	ENSMUSG00000025962	FAST kinase domains 2	-1.623	0.0000	0.0000
Fbxo21	ENSMUSG00000032898	F-box protein 21	-1.576	0.0000	0.0000
Fbxo42	ENSMUSG00000028920	F-box protein 42	-1.551	0.0000	0.0002
Fbxo48	ENSMUSG00000044966	F-box protein 48	-20.121	0.0015	0.0051
Fgf10	ENSMUSG00000021732	fibroblast growth factor 10	-1.796	0.0096	0.0253
Fgf12	ENSMUSG00000022523	fibroblast growth factor 12	-3.586	0.0002	0.0009
Fggy	ENSMUSG00000028573	FGGY carbohydrate kinase domain containing	-1.832	0.0008	0.0030
Fhl1	ENSMUSG00000023092	four and a half LIM domains 1	-1.583	0.0002	0.0006
Fiz1	ENSMUSG00000061374	Flt3 interacting zinc finger protein 1	-1.557	0.0038	0.0113
Fmo4	ENSMUSG00000026692	flavin containing monooxygenase 4	-11.281	0.0259	0.0596
Frem2	ENSMUSG00000037016	Fras1 related extracellular matrix protein 2	-1.581	0.0098	0.0259
Fxyd7	ENSMUSG00000036578	FXYD domain-containing ion transport regulator 7	-5.653	0.0148	0.0370
Gdnf	ENSMUSG00000022144	glial cell line derived neurotrophic factor	-3.418	0.0362	0.0790
Gfer	ENSMUSG00000040888	growth factor, augmenter of liver regeneration	-1.697	0.0000	0.0000
Glb1l	ENSMUSG00000026200	galactosidase, beta 1-like	-1.501	0.0127	0.0324
Glis1	ENSMUSG00000034762	GLIS family zinc finger 1	-4.998	0.0266	0.0610
Gm10053	ENSMUSG00000058927	predicted gene 10053	-2.137	0.0024	0.0076
Gm10097	ENSMUSG00000096553	predicted gene 10097	-2.370	0.0331	0.0731
Gm10131	ENSMUSG00000063412	predicted pseudogene 10131	-2.763	0.0347	0.0763
Gm10146	ENSMUSG00000064317	predicted gene 10146	-17.559	0.0041	0.0122
Gm10382	ENSMUSG00000072612	predicted gene 10382	-9.130	0.0138	0.0347
Gm10557	ENSMUSG00000073647	predicted gene 10557	-1.716	0.0034	0.0101
Gm10570	ENSMUSG00000073752	predicted gene 10570	-1.556	0.0071	0.0195
Gm10605	ENSMUSG00000097974	predicted gene 10605	-3.207	0.0216	0.0510

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm10608	ENSMUSG00000111197	predicted gene 10608	-25.535	0.0020	0.0064
Gm10863	ENSMUSG00000075555	predicted gene 10863	-6.316	0.0256	0.0589
Gm11451	ENSMUSG00000083567	predicted gene 11451	-2.985	0.0009	0.0030
Gm11470	ENSMUSG00000082665	predicted gene 11470	-13.759	0.0095	0.0251
Gm11993	ENSMUSG00000101841	predicted gene 11993	-11.380	0.0121	0.0310
Gm12250	ENSMUSG00000082292	predicted gene 12250	-3.074	0.0007	0.0024
Gm12319	ENSMUSG00000087523	predicted gene 12319	-2.725	0.0000	0.0000
Gm12350	ENSMUSG00000095588	predicted gene 12350	-4.177	0.0017	0.0056
Gm12416	ENSMUSG00000083044	predicted gene 12416	-2.002	0.0058	0.0162
Gm12426	ENSMUSG00000087500	predicted gene 12426	-12.926	0.0059	0.0166
Gm12454	ENSMUSG00000087142	predicted gene 12454	-3.172	0.0324	0.0719
Gm12519	ENSMUSG00000085643	predicted gene 12519	-1.672	0.0269	0.0616
Gm12592	ENSMUSG00000053263	predicted gene 12592	-2.715	0.0072	0.0197
Gm12655	ENSMUSG00000087128	predicted gene 12655	-1.843	0.0000	0.0002
Gm12791	ENSMUSG00000081121	predicted gene 12791	-4.084	0.0274	0.0625
Gm12925	ENSMUSG00000087307	predicted gene 12925	-2.420	0.0208	0.0493
Gm12963	ENSMUSG00000085517	predicted gene 12963	-4.192	0.0178	0.0432
Gm13090	ENSMUSG00000078491	predicted gene 13090	-6.840	0.0022	0.0069
Gm13215	ENSMUSG00000081394	predicted gene 13215	-23.964	0.0007	0.0025
Gm13292	ENSMUSG00000082424	predicted gene 13292	-3.163	0.0184	0.0445
Gm13324	ENSMUSG00000085100	predicted gene 13324	-7.136	0.0305	0.0684
Gm13410	ENSMUSG00000083116	predicted gene 13410	-7.104	0.0007	0.0026
Gm13563	ENSMUSG00000085767	predicted gene 13563	-3.832	0.0005	0.0019
Gm13707	ENSMUSG00000085768	predicted gene 13707	-9.724	0.0275	0.0627
Gm13919	ENSMUSG00000085417	predicted gene 13919	-12.262	0.0273	0.0624
Gm14117	ENSMUSG00000042938	predicted gene 14117	-3.360	0.0003	0.0013
Gm14122	ENSMUSG00000083964	predicted gene 14122	-5.056	0.0039	0.0116
Gm14321	ENSMUSG00000084797	predicted gene 14321	-21.854	0.0021	0.0066
Gm14327	ENSMUSG00000074521	predicted gene 14327	-3.191	0.0001	0.0003
Gm14403	ENSMUSG00000094786	predicted gene 14403	-1.855	0.0000	0.0000
Gm14902	ENSMUSG00000086736	predicted gene 14902	-25.174	0.0003	0.0010

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm15499	ENSMUSG00000086722	predicted gene 15499	-14.999	0.0084	0.0226
Gm15626	ENSMUSG00000081822	predicted gene 15626	-4.139	0.0121	0.0309
Gm15651	ENSMUSG00000089663	predicted gene 15651	-2.194	0.0445	0.0938
Gm15703	ENSMUSG00000083890	predicted gene 15703	-6.871	0.0322	0.0717
Gm15753	ENSMUSG00000082088	predicted gene 15753	-16.178	0.0048	0.0140
Gm15832	ENSMUSG00000085894	predicted gene 15832	-5.145	0.0273	0.0624
Gm15932	ENSMUSG00000086341	predicted gene 15932	-3.467	0.0194	0.0465
Gm16253	ENSMUSG00000087610	predicted gene 16253	-1.610	0.0008	0.0029
Gm16418	ENSMUSG00000084093	predicted pseudogene 16418	-2.184	0.0267	0.0612
Gm16534	ENSMUSG00000090157	predicted gene 16534	-2.246	0.0002	0.0008
Gm17799	ENSMUSG00000097945	predicted gene, 17799	-5.725	0.0047	0.0137
Gm18194	ENSMUSG00000109724	predicted gene, 18194	-4.670	0.0425	0.0904
Gm18283	ENSMUSG00000115920	predicted gene, 18283	-6.244	0.0401	0.0862
Gm18943	ENSMUSG00000109472	predicted gene, 18943	-15.273	0.0066	0.0184
Gm19052	ENSMUSG00000117492	predicted gene, 19052	-8.906	0.0406	0.0871
Gm19412	ENSMUSG00000101438	predicted gene, 19412	-6.720	0.0466	0.0976
Gm19503	ENSMUSG00000100551	predicted gene, 19503	-3.802	0.0471	0.0984
Gm19689	ENSMUSG00000117399	predicted gene, 19689	-15.226	0.0063	0.0175
Gm19810	ENSMUSG00000111897	predicted gene, 19810	-18.145	0.0049	0.0143
Gm20559	ENSMUSG00000106734	predicted gene, 20559	-1.850	0.0261	0.0601
Gm20667	ENSMUSG00000093726	predicted gene 20667	-13.892	0.0062	0.0173
Gm20685	ENSMUSG00000093380	predicted gene 20685	-14.058	0.0332	0.0733
Gm21811	ENSMUSG00000096401	predicted gene, 21811	-2.157	0.0310	0.0692
Gm25135	ENSMUSG00000064582	predicted gene, 25135	-9.750	0.0436	0.0922
Gm25788	ENSMUSG00000064655	predicted gene, 25788	-16.104	0.0067	0.0186
Gm26397	ENSMUSG00000065637	predicted gene, 26397	-12.849	0.0135	0.0341
Gm26569	ENSMUSG00000097313	predicted gene, 26569	-35.211	0.0002	0.0008
Gm26621	ENSMUSG00000096967	predicted gene, 26621	-2.265	0.0296	0.0667
Gm27232	ENSMUSG00000098573	predicted gene 27232	-8.587	0.0112	0.0290
Gm28386	ENSMUSG00000101849	predicted gene 28386	-19.321	0.0027	0.0085
Gm28578	ENSMUSG00000100417	predicted gene 28578	-6.824	0.0018	0.0060

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm28610	ENSMUSG00000100685	predicted gene 28610	-15.608	0.0244	0.0567
Gm28723	ENSMUSG00000101028	predicted gene 28723	-2.068	0.0268	0.0615
Gm28874	ENSMUSG00000100813	predicted gene 28874	-8.925	0.0299	0.0673
Gm28932	ENSMUSG00000101445	predicted gene 28932	-11.758	0.0120	0.0307
Gm2897	ENSMUSG00000079410	predicted gene 2897	-16.551	0.0133	0.0336
Gm29427	ENSMUSG00000101904	predicted gene 29427	-9.725	0.0382	0.0829
Gm29460	ENSMUSG00000099686	predicted gene 29460	-9.888	0.0408	0.0875
Gm30292	ENSMUSG00000104109	predicted gene, 30292	-11.301	0.0172	0.0421
Gm30382	ENSMUSG00000106515	predicted gene, 30382	-3.809	0.0155	0.0384
Gm30984	ENSMUSG00000117361	predicted gene, 30984	-29.777	0.0005	0.0020
Gm31105	ENSMUSG00000109587	predicted gene, 31105	-1.605	0.0087	0.0234
Gm31812	ENSMUSG00000109599	predicted gene, 31812	-5.181	0.0010	0.0034
Gm32369	ENSMUSG00000112950	predicted gene, 32369	-17.569	0.0110	0.0286
Gm33940	ENSMUSG00000109733	predicted gene, 33940	-4.679	0.0426	0.0906
Gm34121	ENSMUSG00000108659	predicted gene, 34121	-11.410	0.0120	0.0308
Gm34276	ENSMUSG00000113977	predicted gene, 34276	-22.424	0.0026	0.0082
Gm3435	ENSMUSG00000116895	predicted gene 3435	-23.863	0.0010	0.0034
Gm35167	ENSMUSG00000115680	predicted gene, 35167	-14.951	0.0055	0.0156
Gm3604	ENSMUSG00000094942	predicted gene 3604	-2.442	0.0120	0.0307
Gm36173	ENSMUSG00000112835	predicted gene, 36173	-11.186	0.0177	0.0431
Gm36298	ENSMUSG00000114172	predicted gene, 36298	-2.315	0.0259	0.0596
Gm36738	ENSMUSG00000116097	predicted gene, 36738	-28.224	0.0003	0.0013
Gm37254	ENSMUSG00000104394	predicted gene, 37254	-2.281	0.0024	0.0076
Gm3815	ENSMUSG00000118088	predicted gene 3815	-3.740	0.0475	0.0991
Gm39168	ENSMUSG00000110179	predicted gene, 39168	-6.434	0.0105	0.0273
Gm42528	ENSMUSG00000107134	predicted gene 42528	-2.099	0.0011	0.0038
Gm42688	ENSMUSG00000079511	predicted gene 42688	-2.135	0.0262	0.0602
Gm42732	ENSMUSG00000107331	predicted gene 42732	-1.558	0.0010	0.0034
Gm4287	ENSMUSG00000092552	predicted gene 4287	-14.358	0.0418	0.0892
Gm43081	ENSMUSG00000106103	predicted gene 43081	-21.661	0.0041	0.0122
Gm43101	ENSMUSG00000106754	predicted gene 43101	-19.051	0.0051	0.0147

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm43185	ENSMUSG00000104621	predicted gene 43185	-2.041	0.0034	0.0103
Gm43197	ENSMUSG00000107215	predicted gene 43197	-2.461	0.0139	0.0351
Gm43327	ENSMUSG00000105695	predicted gene 43327	-6.477	0.0321	0.0715
Gm4335	ENSMUSG00000097989	predicted gene 4335	-2.298	0.0174	0.0425
Gm43598	ENSMUSG00000106927	predicted gene 43598	-15.129	0.0104	0.0272
Gm43682	ENSMUSG00000107019	predicted gene 43682	-2.231	0.0017	0.0055
Gm43693	ENSMUSG00000105929	predicted gene 43693	-23.067	0.0019	0.0062
Gm4419	ENSMUSG00000097055	predicted gene 4419	-24.069	0.0002	0.0010
Gm44220	ENSMUSG00000107655	predicted gene, 44220	-1.668	0.0198	0.0474
Gm44623	ENSMUSG00000108883	predicted gene 44623	-12.454	0.0104	0.0272
Gm44717	ENSMUSG00000109029	predicted gene 44717	-13.074	0.0089	0.0237
Gm44878	ENSMUSG00000108477	predicted gene 44878	-10.250	0.0282	0.0641
Gm44929	ENSMUSG00000109009	predicted gene 44929	-11.291	0.0206	0.0489
Gm45114	ENSMUSG00000109136	predicted gene 45114	-5.127	0.0083	0.0224
Gm45137	ENSMUSG00000109206	predicted gene 45137	-2.355	0.0438	0.0927
Gm45187	ENSMUSG00000109130	predicted gene 45187	-11.197	0.0161	0.0398
Gm45378	ENSMUSG00000110326	predicted gene 45378	-14.829	0.0259	0.0595
Gm45889	ENSMUSG00000109936	predicted gene 45889	-3.732	0.0184	0.0444
Gm4596	ENSMUSG00000082394	predicted gene 4596	-3.718	0.0347	0.0763
Gm46620	ENSMUSG00000118012	predicted gene, 46620	-1.573	0.0063	0.0175
Gm47232	ENSMUSG00000111656	predicted gene, 47232	-11.682	0.0303	0.0679
Gm47794	ENSMUSG00000114907	predicted gene, 47794	-9.641	0.0184	0.0445
Gm47826	ENSMUSG00000113650	predicted gene, 47826	-13.930	0.0226	0.0529
Gm47962	ENSMUSG00000111583	predicted gene, 47962	-20.502	0.0030	0.0093
Gm47976	ENSMUSG00000112300	predicted gene, 47976	-3.454	0.0361	0.0788
Gm4804	ENSMUSG00000098158	predicted gene 4804	-14.323	0.0035	0.0105
Gm48357	ENSMUSG00000114524	predicted gene, 48357	-14.271	0.0241	0.0561
Gm4840	ENSMUSG00000118282	predicted gene 4840	-2.750	0.0165	0.0405
Gm48483	ENSMUSG00000111318	predicted gene, 48483	-2.081	0.0168	0.0413
Gm48630	ENSMUSG00000113682	predicted gene, 48630	-3.784	0.0163	0.0401
Gm4875	ENSMUSG00000082791	predicted gene 4875	-2.092	0.0388	0.0839

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm48796	ENSMUSG00000111390	predicted gene, 48796	-4.126	0.0405	0.0869
Gm49494	ENSMUSG00000116518	predicted gene, 49494	-2.438	0.0475	0.0991
Gm49539	ENSMUSG00000116004	predicted gene, 49539	-6.799	0.0288	0.0651
Gm49980	ENSMUSG00000117465	predicted gene, 49980	-9.920	0.0199	0.0475
Gm50020	ENSMUSG00000117444	predicted gene, 50020	-11.963	0.0206	0.0490
Gm50402	ENSMUSG00000118159	predicted gene, 50402	-18.991	0.0024	0.0076
Gm50415	ENSMUSG00000118387	predicted gene, 50415	-5.616	0.0027	0.0083
Gm50455	ENSMUSG00000118071	predicted gene, 50455	-2.526	0.0469	0.0981
Gm5075	ENSMUSG00000105944	predicted gene 5075	-8.903	0.0379	0.0822
Gm5105	ENSMUSG00000049349	predicted gene 5105	-2.654	0.0003	0.0013
Gm5187	ENSMUSG00000082362	predicted gene 5187	-6.979	0.0183	0.0443
Gm5507	ENSMUSG00000069376	predicted gene 5507	-2.345	0.0121	0.0310
Gm55073	ENSMUSG00002075637	predicted gene, 55073	-43.849	0.0001	0.0006
Gm55371	ENSMUSG00002074854	predicted gene, 55371	-21.764	0.0026	0.0081
Gm5540	ENSMUSG00000048916	predicted pseudogene 5540	-2.137	0.0359	0.0784
Gm5621	ENSMUSG00000101597	predicted gene 5621	-29.193	0.0002	0.0008
Gm5687	ENSMUSG00000080866	predicted gene 5687	-4.609	0.0052	0.0148
Gm5737	ENSMUSG00000109392	predicted gene 5737	-4.120	0.0183	0.0443
Gm5791	ENSMUSG00000113753	predicted gene 5791	-7.747	0.0467	0.0977
Gm5865	ENSMUSG00000104923	predicted gene 5865	-15.202	0.0005	0.0020
Gm5920	ENSMUSG00000100839	predicted gene 5920	-11.628	0.0180	0.0435
Gm6054	ENSMUSG00000057157	predicted gene 6054	-9.916	0.0284	0.0643
Gm6206	ENSMUSG00000048949	predicted pseudogene 6206	-1.750	0.0000	0.0000
Gm6322	ENSMUSG00000082018	predicted gene 6322	-9.257	0.0086	0.0230
Gm6475	ENSMUSG00000116838	predicted gene 6475	-4.292	0.0219	0.0516
Gm6542	ENSMUSG00000085172	predicted gene 6542	-1.929	0.0313	0.0698
Gm6644	ENSMUSG00000100309	predicted gene 6644	-7.246	0.0004	0.0016
Gm6645	ENSMUSG00000083554	predicted gene 6645	-6.391	0.0001	0.0003
Gm6967	ENSMUSG00000097937	predicted gene 6967	-8.321	0.0355	0.0778
Gm6988	ENSMUSG00000113198	predicted gene 6988	-12.599	0.0010	0.0035
Gm7027	ENSMUSG00000067121	predicted gene 7027	-3.438	0.0246	0.0571

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm7293	ENSMUSG00000111162	predicted gene 7293	-2.628	0.0225	0.0527
Gm7368	ENSMUSG00000110867	predicted gene 7368	-18.893	0.0046	0.0133
Gm7741	ENSMUSG00000097713	predicted gene 7741	-16.227	0.0090	0.0240
Gm7808	ENSMUSG00000091460	predicted pseudogene 7808	-8.900	0.0112	0.0289
Gm7862	ENSMUSG00000046580	predicted gene 7862	-2.283	0.0345	0.0760
Gm8069	ENSMUSG00000105143	predicted pseudogene 8069	-20.097	0.0008	0.0029
Gm807	ENSMUSG00000097848	predicted gene 807	-10.076	0.0443	0.0934
Gm8129	ENSMUSG00000059159	predicted pseudogene 8129	-5.703	0.0384	0.0831
Gm8188	ENSMUSG00000112163	predicted gene 8188	-3.072	0.0000	0.0001
Gm8242	ENSMUSG00000102827	predicted gene 8242	-3.393	0.0241	0.0560
Gm8494	ENSMUSG00000094090	predicted gene 8494	-2.155	0.0050	0.0144
Gm8539	ENSMUSG00000106294	predicted gene 8539	-16.396	0.0042	0.0124
Gm8566	ENSMUSG00000047905	predicted pseudogene 8566	-3.363	0.0296	0.0667
Gm8722	ENSMUSG00000081164	predicted gene 8722	-8.462	0.0376	0.0817
Gm8864	ENSMUSG00000081892	predicted gene 8864	-3.194	0.0072	0.0197
Gm9204	ENSMUSG00000110562	predicted gene 9204	-3.083	0.0358	0.0783
Gm9260	ENSMUSG00000106239	predicted gene 9260	-3.558	0.0096	0.0254
Gm9843	ENSMUSG00000050299	predicted gene 9843	-2.861	0.0003	0.0011
Gm9951	ENSMUSG00000054618	predicted gene 9951	-12.588	0.0144	0.0361
Gm9967	ENSMUSG00000055323	predicted gene 9967	-7.229	0.0435	0.0922
Gnat3	ENSMUSG00000028777	guanine nucleotide binding protein, alpha transducing 3	-1.758	0.0253	0.0584
Golt1b	ENSMUSG00000030245	golgi transport 1B	-1.586	0.0001	0.0003
Gpc6	ENSMUSG00000058571	glypican 6	-1.583	0.0023	0.0073
Gpn2	ENSMUSG00000028848	GPN-loop GTPase 2	-2.051	0.0000	0.0000
Gpr135	ENSMUSG00000043398	G protein-coupled receptor 135	-2.384	0.0054	0.0154
Gpr18	ENSMUSG00000050350	G protein-coupled receptor 18	-13.826	0.0167	0.0410
Gpr22	ENSMUSG00000044067	G protein-coupled receptor 22	-1.681	0.0003	0.0010
Gpr35	ENSMUSG00000026271	G protein-coupled receptor 35	-5.054	0.0007	0.0025
Gpr4	ENSMUSG00000044317	G protein-coupled receptor 4	-1.984	0.0000	0.0000
Gpr52	ENSMUSG00000118401	G protein-coupled receptor 52	-15.099	0.0065	0.0180
Gpt2	ENSMUSG00000031700	glutamic pyruvate transaminase (alanine aminotransferase) 2	-1.502	0.0217	0.0511

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Grin2a	ENSMUSG00000059003	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	-4.517	0.0214	0.0506
Gsdma	ENSMUSG00000017204	gasdermin A	-5.754	0.0054	0.0154
Gsto2	ENSMUSG00000025069	glutathione S-transferase omega 2	-1.812	0.0135	0.0342
Gtse1	ENSMUSG00000022385	G two S phase expressed protein 1	-5.193	0.0003	0.0011
Guk1	ENSMUSG00000020444	guanylate kinase 1	-2.103	0.0000	0.0000
H2-Ea	ENSMUSG00000036322	histocompatibility 2, class II antigen E alpha	-4.159	0.0099	0.0261
H4c4	ENSMUSG00000061482	H4 clustered histone 4	-20.150	0.0025	0.0079
Hacd2	ENSMUSG00000035376	3-hydroxyacyl-CoA dehydratase 2	-1.742	0.0000	0.0001
Hacl1	ENSMUSG00000021884	2-hydroxyacyl-CoA lyase 1	-2.295	0.0234	0.0546
Has3	ENSMUSG00000031910	hyaluronan synthase 3	-2.143	0.0066	0.0182
Haus2	ENSMUSG00000027285	HAUS augmin-like complex, subunit 2	-1.535	0.0000	0.0001
Hbp1	ENSMUSG00000002996	high mobility group box transcription factor 1	-1.551	0.0014	0.0048
Hcst	ENSMUSG00000064109	hematopoietic cell signal transducer	-11.339	0.0169	0.0413
Hepacam2	ENSMUSG00000044156	HEPACAM family member 2	-4.905	0.0435	0.0922
Hes6	ENSMUSG00000067071	hairy and enhancer of split 6	-1.949	0.0093	0.0247
Hmgcs2	ENSMUSG00000027875	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 2	-1.608	0.0022	0.0070
Hsf2	ENSMUSG00000019878	heat shock factor 2	-1.526	0.0000	0.0000
Hspa1a	ENSMUSG00000091971	heat shock protein 1A	-3.094	0.0053	0.0152
Htr2a	ENSMUSG00000034997	5-hydroxytryptamine (serotonin) receptor 2A	-1.666	0.0200	0.0477
Htt	ENSMUSG00000029104	huntingtin	-1.504	0.0000	0.0000
Ifi203	ENSMUSG00000039997	interferon activated gene 203	-1.627	0.0017	0.0056
Ifi205	ENSMUSG00000054203	interferon activated gene 205	-1.657	0.0228	0.0535
Igsf6	ENSMUSG00000035004	immunoglobulin superfamily, member 6	-2.153	0.0015	0.0048
Il2rb	ENSMUSG00000068227	interleukin 2 receptor, beta chain	-2.445	0.0043	0.0126
Il2rg	ENSMUSG00000031304	interleukin 2 receptor, gamma chain	-1.608	0.0080	0.0216
Ints12	ENSMUSG00000028016	integrator complex subunit 12	-1.575	0.0007	0.0024
Kcnc2	ENSMUSG00000035681	potassium voltage gated channel, Shaw-related subfamily, member 2	-2.046	0.0326	0.0724
Kcnd1	ENSMUSG00000009731	potassium voltage-gated channel, Shal-related family, member 1	-2.980	0.0107	0.0279
Kcnip1	ENSMUSG00000053519	Kv channel-interacting protein 1	-15.109	0.0266	0.0610
Kics2	ENSMUSG00000053684	KICSTOR subunit 2	-1.513	0.0012	0.0041
Kif18a	ENSMUSG00000027115	kinesin family member 18A	-1.803	0.0431	0.0914

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kif9	ENSMUSG00000032489	kinesin family member 9	-3.029	0.0194	0.0464
Kifc5b	ENSMUSG00000024301	kinesin family member C5B	-2.235	0.0182	0.0441
Klra8	ENSMUSG00000089727	killer cell lectin-like receptor, subfamily A, member 8	-11.376	0.0205	0.0488
Krt18	ENSMUSG00000023043	keratin 18	-1.729	0.0326	0.0724
Lancl2	ENSMUSG00000062190	LanC (bacterial lantibiotic synthetase component C)-like 2	-1.553	0.0000	0.0000
Laptm4a	ENSMUSG00000020585	lysosomal-associated protein transmembrane 4A	-1.555	0.0000	0.0000
Ldlrad3	ENSMUSG00000048058	low density lipoprotein receptor class A domain containing 3	-1.554	0.0007	0.0025
Leat1	ENSMUSG00000109056	lncRNA Efnb2 associated transcript 1	-10.906	0.0165	0.0405
Lims1	ENSMUSG00000019920	LIM and senescent cell antigen-like domains 1	-1.566	0.0000	0.0000
Lingo4	ENSMUSG00000044505	leucine rich repeat and Ig domain containing 4	-3.289	0.0380	0.0824
Lipo2	ENSMUSG00000087303	lipase, member O2	-1.791	0.0004	0.0014
Lipt2	ENSMUSG00000030725	lipoyl(octanoyl) transferase 2 (putative)	-1.689	0.0018	0.0059
Lman2	ENSMUSG00000021484	lectin, mannose-binding 2	-1.508	0.0140	0.0353
Lpar6	ENSMUSG00000033446	lysophosphatidic acid receptor 6	-1.990	0.0000	0.0000
Lpcat3	ENSMUSG00000004270	lysophosphatidylcholine acyltransferase 3	-1.927	0.0000	0.0000
Lrrc56	ENSMUSG00000038637	leucine rich repeat containing 56	-2.006	0.0004	0.0015
Ltb4r1	ENSMUSG00000046908	leukotriene B4 receptor 1	-3.992	0.0419	0.0894
Lum	ENSMUSG00000036446	lumican	-1.502	0.0257	0.0592
Ly6g6d	ENSMUSG00000073413	lymphocyte antigen 6 complex, locus G6D	-15.222	0.0050	0.0145
Lypd8l	ENSMUSG00000037145	LY6/PLAUR domain containing 8 like	-2.798	0.0430	0.0913
Lypla1	ENSMUSG00000025903	lysophospholipase 1	-1.775	0.0001	0.0004
Lysmd2	ENSMUSG00000032184	LysM, putative peptidoglycan-binding, domain containing 2	-1.707	0.0013	0.0044
Lztfl1	ENSMUSG00000025245	leucine zipper transcription factor-like 1	-1.539	0.0000	0.0000
Mad2l1bp	ENSMUSG00000034509	MAD2L1 binding protein	-1.506	0.0000	0.0000
Maip1	ENSMUSG00000025971	matrix AAA peptidase interacting protein 1	-1.593	0.0000	0.0000
Mamdc4	ENSMUSG00000026941	MAM domain containing 4	-2.881	0.0056	0.0159
Manea	ENSMUSG00000040520	mannosidase, endo-alpha	-1.717	0.0000	0.0000
Map10	ENSMUSG00000050930	microtubule-associated protein 10	-1.657	0.0001	0.0003
Map3k11	ENSMUSG00000004054	mitogen-activated protein kinase kinase kinase 11	-1.720	0.0005	0.0019
Mast3	ENSMUSG00000031833	microtubule associated serine/threonine kinase 3	-1.502	0.0288	0.0652
Mbip	ENSMUSG00000021028	MAP3K12 binding inhibitory protein 1	-1.626	0.0000	0.0001

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mcts2	ENSMUSG00000042814	malignant T cell amplified sequence 2	-1.614	0.0000	0.0000
Mdm4-ps	ENSMUSG00000081739	transformed mouse 3T3 cell double minute 4, pseudogene	-28.081	0.0007	0.0024
Med21	ENSMUSG00000030291	mediator complex subunit 21	-1.631	0.0000	0.0001
Megf11	ENSMUSG00000036466	multiple EGF-like-domains 11	-8.940	0.0374	0.0813
Mettl8	ENSMUSG00000041975	methyltransferase like 8	-1.674	0.0019	0.0061
Mfsd14a	ENSMUSG00000089911	major facilitator superfamily domain containing 14A	-1.507	0.0000	0.0000
Mfsd14b	ENSMUSG00000038212	major facilitator superfamily domain containing 14B	-1.634	0.0000	0.0000
Mfsd4b1	ENSMUSG00000038522	major facilitator superfamily domain containing 4B1	-1.968	0.0002	0.0008
Mgat2	ENSMUSG00000043998	mannoside acetylglucosaminyltransferase 2	-1.606	0.0123	0.0314
Milr1	ENSMUSG00000040528	mast cell immunoglobulin like receptor 1	-4.309	0.0012	0.0041
Mir6240	ENSMUSG00000098343	microRNA 6240	-3.083	0.0448	0.0943
Mir703	ENSMUSG00000105814	microRNA 703	-4.400	0.0196	0.0469
Mis18bp1	ENSMUSG00000047534	MIS18 binding protein 1	-2.623	0.0188	0.0452
Mkrn3	ENSMUSG00000070527	makorin, ring finger protein, 3	-2.670	0.0314	0.0701
Mmp27	ENSMUSG00000070323	matrix metallopeptidase 27	-7.000	0.0195	0.0468
Mndal	ENSMUSG00000090272	myeloid nuclear differentiation antigen like	-2.215	0.0235	0.0547
Mob4	ENSMUSG00000025979	MOB family member 4, phocein	-1.627	0.0000	0.0000
Mok	ENSMUSG00000056458	MOK protein kinase	-3.797	0.0051	0.0146
Msmo1	ENSMUSG00000031604	methylsterol monoxygenase 1	-1.542	0.0003	0.0012
Msx1	ENSMUSG00000048450	msh homeobox 1	-2.152	0.0006	0.0021
Mtpap	ENSMUSG00000024234	mitochondrial poly(A) polymerase	-1.744	0.0000	0.0000
mt-Rnr2	ENSMUSG00000064339	mitochondrially encoded 16S rRNA	-1.921	0.0000	0.0002
mt-Ty	ENSMUSG00000064350	mitochondrially encoded tRNA tyrosine	-19.200	0.0020	0.0064
Mylpf	ENSMUSG00000030672	myosin light chain, phosphorylatable, fast skeletal muscle	-3.339	0.0018	0.0059
Nadk	ENSMUSG00000029063	NAD kinase	-1.676	0.0000	0.0000
Napsa	ENSMUSG00000002204	napsin A aspartic peptidase	-5.041	0.0057	0.0161
Nars2	ENSMUSG00000018995	asparaginyl-tRNA synthetase 2 (mitochondrial)(putative)	-1.627	0.0000	0.0000
Nat8f4	ENSMUSG00000068299	N-acetyltransferase 8 (GCN5-related) family member 4	-2.031	0.0018	0.0060
Nbdy	ENSMUSG00000086316	negative regulator of P-body association	-1.621	0.0000	0.0000
Ncapd3	ENSMUSG00000035024	non-SMC condensin II complex, subunit D3	-1.668	0.0000	0.0000
Ndufc1	ENSMUSG00000037152	NADH:ubiquinone oxidoreductase subunit C1	-1.595	0.0000	0.0000

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Neb	ENSMUSG00000026950	nebulin	-1.750	0.0152	0.0378
Necab1	ENSMUSG00000040536	N-terminal EF-hand calcium binding protein 1	-3.438	0.0005	0.0018
Nfatc1	ENSMUSG00000033016	nuclear factor of activated T cells, cytoplasmic, calcineurin dependent 1	-1.504	0.0005	0.0020
Nfe2l2	ENSMUSG00000015839	nuclear factor, erythroid derived 2, like 2	-1.510	0.0000	0.0000
Nlrp1b	ENSMUSG00000070390	NLR family, pyrin domain containing 1B	-3.910	0.0152	0.0379
Nmbr	ENSMUSG00000019865	neuromedin B receptor	-11.751	0.0096	0.0253
Nme2	ENSMUSG00000020857	NME/NM23 nucleoside diphosphate kinase 2	-3.330	0.0004	0.0014
Nme5	ENSMUSG00000035984	NME/NM23 family member 5	-1.577	0.0275	0.0628
Nnmt	ENSMUSG00000032271	nicotinamide N-methyltransferase	-1.598	0.0305	0.0684
Npm3	ENSMUSG00000056209	nucleoplasmin 3	-1.554	0.0010	0.0035
Npm3-ps1	ENSMUSG00000081669	nucleoplasmin 3, pseudogene 1	-1.942	0.0218	0.0514
Nqo1	ENSMUSG00000003849	NAD(P)H dehydrogenase, quinone 1	-1.500	0.0000	0.0000
Nsmf	ENSMUSG00000006476	NMDA receptor synaptonuclear signaling and neuronal migration factor	-1.666	0.0000	0.0000
Nt5c3b	ENSMUSG00000017176	5'-nucleotidase, cytosolic IIIB	-1.527	0.0000	0.0000
Nt5dc1	ENSMUSG00000039480	5'-nucleotidase domain containing 1	-1.565	0.0000	0.0001
Nt5e	ENSMUSG00000032420	5' nucleotidase, ecto	-1.524	0.0004	0.0015
Ntf3	ENSMUSG00000049107	neurotrophin 3	-1.625	0.0005	0.0020
Nudt11	ENSMUSG00000073295	nudix (nucleoside diphosphate linked moiety X)-type motif 11	-1.628	0.0104	0.0272
Nudt15	ENSMUSG00000033405	nudix (nucleoside diphosphate linked moiety X)-type motif 15	-1.955	0.0021	0.0068
Nudt7	ENSMUSG00000031767	nudix (nucleoside diphosphate linked moiety X)-type motif 7	-1.681	0.0000	0.0000
Nusap1	ENSMUSG00000027306	nucleolar and spindle associated protein 1	-2.148	0.0101	0.0264
Ocel1	ENSMUSG00000002396	occludin/ELL domain containing 1	-1.719	0.0182	0.0440
Odf3l1	ENSMUSG00000045620	outer dense fiber of sperm tails 3-like 1	-10.842	0.0148	0.0370
Onecut2	ENSMUSG00000045991	one cut domain, family member 2	-9.457	0.0442	0.0933
Optc	ENSMUSG00000010311	opticin	-11.618	0.0166	0.0406
P2ry10b	ENSMUSG00000054293	purinergic receptor P2Y, G-protein coupled 10B	-2.573	0.0012	0.0040
P4ha1	ENSMUSG00000019916	procollagen-proline, 2-oxoglutarate 4-dioxygenase (proline 4-hydroxylase), alpha 1 polypeptide	-1.506	0.0005	0.0019
P4htm	ENSMUSG00000006675	prolyl 4-hydroxylase, transmembrane (endoplasmic reticulum)	-1.871	0.0000	0.0000
Padi3	ENSMUSG00000025328	peptidyl arginine deiminase, type III	-17.633	0.0090	0.0239
Pakap	ENSMUSG00000038729	paralemmin A kinase anchor protein	-8.507	0.0302	0.0678

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pcdhb21	ENSMUSG00000044022	protocadherin beta 21	-2.036	0.0257	0.0592
Pcdhb6	ENSMUSG00000051678	protocadherin beta 6	-2.065	0.0398	0.0856
Pcdhga1	ENSMUSG00000103144	protocadherin gamma subfamily A, 1	-2.199	0.0055	0.0155
Pcdhga6	ENSMUSG00000103793	protocadherin gamma subfamily A, 6	-2.228	0.0220	0.0518
Pcdhga7	ENSMUSG00000103472	protocadherin gamma subfamily A, 7	-2.050	0.0000	0.0000
Pcdhga9	ENSMUSG00000102440	protocadherin gamma subfamily A, 9	-3.650	0.0050	0.0144
Pcdhgb2	ENSMUSG00000102748	protocadherin gamma subfamily B, 2	-1.626	0.0060	0.0168
Pcdhgb4	ENSMUSG00000103585	protocadherin gamma subfamily B, 4	-1.500	0.0278	0.0634
Pcdhgb7	ENSMUSG00000104063	protocadherin gamma subfamily B, 7	-1.626	0.0094	0.0249
Pcdhgc4	ENSMUSG00000023036	protocadherin gamma subfamily C, 4	-3.886	0.0063	0.0175
Pcgf1	ENSMUSG00000069678	polycomb group ring finger 1	-1.501	0.0016	0.0053
Pck1	ENSMUSG00000027513	phosphoenolpyruvate carboxykinase 1, cytosolic	-2.416	0.0335	0.0740
Pck2	ENSMUSG00000040618	phosphoenolpyruvate carboxykinase 2 (mitochondrial)	-1.520	0.0064	0.0177
Pdcd2	ENSMUSG00000014771	programmed cell death 2	-1.652	0.0012	0.0040
Pdcd6	ENSMUSG00000021576	programmed cell death 6	-1.509	0.0000	0.0000
Pex2	ENSMUSG00000040374	peroxisomal biogenesis factor 2	-1.737	0.0000	0.0000
Pex3	ENSMUSG00000019809	peroxisomal biogenesis factor 3	-1.670	0.0000	0.0000
Pgam5	ENSMUSG00000029500	phosphoglycerate mutase family member 5	-1.678	0.0000	0.0000
Pgpep1l	ENSMUSG00000030553	pyroglutamyl-peptidase I-like	-30.796	0.0003	0.0013
Pigb	ENSMUSG00000079469	phosphatidylinositol glycan anchor biosynthesis, class B	-2.156	0.0000	0.0000
Pih1d2	ENSMUSG00000000167	PIH1 domain containing 2	-3.174	0.0208	0.0493
Pik3cg	ENSMUSG00000020573	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma	-1.880	0.0160	0.0396
Pilrb1	ENSMUSG00000066684	paired immunoglobin-like type 2 receptor beta 1	-8.660	0.0212	0.0501
Piwil2	ENSMUSG00000033644	piwi-like RNA-mediated gene silencing 2	-1.818	0.0413	0.0882
Plag1	ENSMUSG00000003282	pleiomorphic adenoma gene 1	-1.540	0.0162	0.0399
Platr25	ENSMUSG00000074863	pluripotency associated transcript 25	-3.084	0.0000	0.0000
Plbd1	ENSMUSG00000030214	phospholipase B domain containing 1	-1.523	0.0001	0.0002
Plekhg1	ENSMUSG00000040624	pleckstrin homology domain containing, family G (with RhoGef domain) member 1	-1.548	0.0024	0.0074
Plin5	ENSMUSG00000011305	perilipin 5	-1.654	0.0013	0.0044
Pllp	ENSMUSG00000031775	plasma membrane proteolipid	-2.963	0.0176	0.0428
Plpp2	ENSMUSG00000052151	phospholipid phosphatase 2	-1.754	0.0101	0.0266

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pon1	ENSMUSG00000002588	paraoxonase 1	-27.553	0.0027	0.0085
Ppcdc	ENSMUSG00000063849	phosphopantothenoylcysteine decarboxylase	-1.612	0.0001	0.0005
Ppp1r27	ENSMUSG00000025129	protein phosphatase 1, regulatory subunit 27	-12.300	0.0090	0.0239
Prkab1	ENSMUSG00000029513	protein kinase, AMP-activated, beta 1 non-catalytic subunit	-1.564	0.0020	0.0065
Proser2	ENSMUSG00000045319	proline and serine rich 2	-1.959	0.0238	0.0555
Prr14	ENSMUSG00000030822	proline rich 14	-1.837	0.0002	0.0008
Prss45	ENSMUSG00000047257	protease, serine 45	-18.073	0.0089	0.0238
Pskh1	ENSMUSG00000048310	protein serine kinase H1	-1.528	0.0001	0.0003
Ptdss2	ENSMUSG00000025495	phosphatidylserine synthase 2	-1.534	0.0133	0.0337
Ptger3	ENSMUSG00000040016	prostaglandin E receptor 3 (subtype EP3)	-2.749	0.0464	0.0973
Ptpn4	ENSMUSG00000026384	protein tyrosine phosphatase, non-receptor type 4	-1.618	0.0000	0.0000
Ptpro	ENSMUSG00000030223	protein tyrosine phosphatase, receptor type, O	-1.657	0.0002	0.0008
Pwp1	ENSMUSG00000001785	PWP1 homolog, endonuclein	-1.550	0.0000	0.0000
Rab27b	ENSMUSG00000024511	RAB27B, member RAS oncogene family	-3.211	0.0046	0.0135
Rab3b	ENSMUSG00000003411	RAB3B, member RAS oncogene family	-1.963	0.0472	0.0986
Rab7-ps1	ENSMUSG00000111686	RAB7, member RAS oncogene family, pseudogene 1	-3.049	0.0184	0.0445
Rae1	ENSMUSG00000027509	ribonucleic acid export 1	-2.195	0.0001	0.0003
Ralgapa1	ENSMUSG00000021027	Ral GTPase activating protein, alpha subunit 1	-1.584	0.0000	0.0000
Rapgef3os2	ENSMUSG00000087397	Rap guanine nucleotide exchange factor (GEF) 3, opposite strand 2	-2.865	0.0453	0.0953
Rapgef5	ENSMUSG00000041992	Rap guanine nucleotide exchange factor (GEF) 5	-1.552	0.0000	0.0000
Rara	ENSMUSG00000037992	retinoic acid receptor, alpha	-1.846	0.0000	0.0000
Rasl2-9	ENSMUSG00000083649	RAS-like, family 2, locus 9	-1.652	0.0002	0.0007
Rbfa	ENSMUSG00000024570	ribosome binding factor A	-1.504	0.0019	0.0062
Rbfaos	ENSMUSG00000118061	ribosome binding factor A, opposite strand	-2.702	0.0397	0.0856
Rbks	ENSMUSG00000029136	ribokinase	-1.570	0.0293	0.0662
Rbm41	ENSMUSG00000031433	RNA binding motif protein 41	-1.556	0.0001	0.0004
Rcc1	ENSMUSG00000028896	regulator of chromosome condensation 1	-1.531	0.0001	0.0004
Retsat	ENSMUSG00000056666	retinol saturase (all trans retinol 13,14 reductase)	-1.753	0.0000	0.0000
Rfc3	ENSMUSG00000033970	replication factor C (activator 1) 3	-1.956	0.0003	0.0011
Rffl	ENSMUSG00000020696	ring finger and FYVE like domain containing protein	-1.662	0.0022	0.0071
Rfx2	ENSMUSG00000024206	regulatory factor X, 2 (influences HLA class II expression)	-1.879	0.0209	0.0496

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rgs18	ENSMUSG00000026357	regulator of G-protein signaling 18	-2.542	0.0076	0.0208
Rhebl1	ENSMUSG00000023755	Ras homolog enriched in brain like 1	-2.171	0.0016	0.0053
Ric8b	ENSMUSG00000035620	RIC8 guanine nucleotide exchange factor B	-1.551	0.0000	0.0000
Rims2	ENSMUSG00000037386	regulating synaptic membrane exocytosis 2	-4.284	0.0203	0.0483
Ripk4	ENSMUSG00000005251	receptor-interacting serine-threonine kinase 4	-3.562	0.0183	0.0442
Rn18s-rs5	ENSMUSG00000119584	18s RNA, related sequence 5	-2.184	0.0079	0.0214
Rn7sk	ENSMUSG00002076161	RNA, 7SK, nuclear	-2.056	0.0462	0.0969
Rnaseh2b	ENSMUSG00000021932	ribonuclease H2, subunit B	-1.530	0.0000	0.0000
Rnd1	ENSMUSG00000054855	Rho family GTPase 1	-1.650	0.0228	0.0534
Rnf138	ENSMUSG00000024317	ring finger protein 138	-1.756	0.0000	0.0000
Rnf180	ENSMUSG00000021720	ring finger protein 180	-2.303	0.0478	0.0996
Rnf208	ENSMUSG00000044628	ring finger protein 208	-2.753	0.0181	0.0438
Rnf32	ENSMUSG00000029130	ring finger protein 32	-15.184	0.0062	0.0173
Rnf39	ENSMUSG00000036492	ring finger protein 39	-7.675	0.0003	0.0012
Rph3al	ENSMUSG00000020847	rabphilin 3A-like (without C2 domains)	-1.874	0.0052	0.0149
Rpl18-ps1	ENSMUSG00000081382	ribosomal protein L18, pseudogene 1	-4.010	0.0173	0.0421
Rpl19-ps1	ENSMUSG00000064281	ribosomal protein L19, pseudogene 1	-5.638	0.0390	0.0844
Rpl30	ENSMUSG00000058600	ribosomal protein L30	-1.634	0.0000	0.0000
Rpl31	ENSMUSG00000073702	ribosomal protein L31	-1.710	0.0000	0.0000
Rps12-ps1	ENSMUSG00000082746	ribosomal protein S12, pseudogene 1	-3.825	0.0096	0.0253
Rps3a3	ENSMUSG00000059751	ribosomal protein S3A3	-3.197	0.0275	0.0628
Rrp1b	ENSMUSG00000058392	ribosomal RNA processing 1B	-1.752	0.0000	0.0000
Rsph9	ENSMUSG00000023966	radial spoke head 9 homolog (Chlamydomonas)	-2.983	0.0067	0.0186
Rtl10	ENSMUSG00000086965	retrotransposon Gag like 10	-3.033	0.0170	0.0415
Rtp4	ENSMUSG00000033355	receptor transporter protein 4	-1.568	0.0211	0.0499
Sac3d1	ENSMUSG00000024790	SAC3 domain containing 1	-1.836	0.0113	0.0292
Samd10	ENSMUSG00000038605	sterile alpha motif domain containing 10	-1.655	0.0037	0.0110
Samd13	ENSMUSG00000048652	sterile alpha motif domain containing 13	-2.766	0.0029	0.0090
Sdcbp	ENSMUSG00000028249	syndecan binding protein	-1.558	0.0000	0.0000
Sdhaf2	ENSMUSG00000024668	succinate dehydrogenase complex assembly factor 2	-1.581	0.0000	0.0000
Sdhaf3	ENSMUSG00000042505	succinate dehydrogenase complex assembly factor 3	-1.541	0.0043	0.0126

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sema3a	ENSMUSG00000028883	sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3A	-2.055	0.0009	0.0031
Sema4c	ENSMUSG00000026121	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4C	-1.589	0.0000	0.0000
Serpina3h	ENSMUSG00000041449	serine (or cysteine) peptidase inhibitor, clade A, member 3H	-5.269	0.0008	0.0027
Serpina3m	ENSMUSG00000079012	serine (or cysteine) peptidase inhibitor, clade A, member 3M	-13.830	0.0163	0.0402
Serpinb9	ENSMUSG00000045827	serine (or cysteine) peptidase inhibitor, clade B, member 9	-1.734	0.0000	0.0001
Sertad1	ENSMUSG00000008384	SERTA domain containing 1	-1.526	0.0010	0.0033
Sft2d3	ENSMUSG00000044982	SFT2 domain containing 3	-1.944	0.0002	0.0009
Sgsm1	ENSMUSG00000042216	small G protein signaling modulator 1	-3.628	0.0003	0.0012
Sh2b3	ENSMUSG00000042594	SH2B adaptor protein 3	-2.069	0.0003	0.0012
Shld3	ENSMUSG00000118537	shieldin complex subunit 3	-5.493	0.0003	0.0011
Siglech	ENSMUSG00000051504	sialic acid binding Ig-like lectin H	-21.264	0.0005	0.0018
Skp2	ENSMUSG00000054115	S-phase kinase-associated protein 2	-1.683	0.0464	0.0973
Slc13a3	ENSMUSG00000018459	solute carrier family 13 (sodium-dependent dicarboxylate transporter), member 3	-4.643	0.0070	0.0193
Slc15a4	ENSMUSG00000029416	solute carrier family 15, member 4	-1.603	0.0033	0.0099
Slc16a2	ENSMUSG00000033965	solute carrier family 16 (monocarboxylic acid transporters), member 2	-1.590	0.0011	0.0037
Slc17a5	ENSMUSG00000049624	solute carrier family 17 (anion/sugar transporter), member 5	-1.563	0.0091	0.0243
Slc22a18	ENSMUSG00000000154	solute carrier family 22 (organic cation transporter), member 18	-2.661	0.0178	0.0431
Slc23a4	ENSMUSG00000029847	solute carrier family 23 member 4	-21.495	0.0016	0.0052
Slc25a12	ENSMUSG00000027010	solute carrier family 25 (mitochondrial carrier, Aralar), member 12	-1.612	0.0000	0.0000
Slc25a43	ENSMUSG00000037636	solute carrier family 25, member 43	-17.816	0.0028	0.0085
Slc2a4	ENSMUSG00000018566	solute carrier family 2 (facilitated glucose transporter), member 4	-1.923	0.0000	0.0000
Slc35d2	ENSMUSG00000033114	solute carrier family 35, member D2	-2.768	0.0002	0.0008
Slc4a11	ENSMUSG00000074796	solute carrier family 4, sodium bicarbonate transporter-like, member 11	-14.042	0.0070	0.0194
Slc52a3	ENSMUSG00000027463	solute carrier protein family 52, member 3	-1.842	0.0046	0.0134
Sned1	ENSMUSG00000047793	sushi, nidogen and EGF-like domains 1	-1.592	0.0025	0.0079
Snx14	ENSMUSG00000032422	sorting nexin 14	-1.533	0.0000	0.0000
Sorcs2	ENSMUSG00000029093	sortilin-related VPS10 domain containing receptor 2	-1.949	0.0019	0.0062
Sowaha	ENSMUSG00000044352	sosondowah ankyrin repeat domain family member A	-3.005	0.0415	0.0886
Sowahc	ENSMUSG00000098188	sosondowah ankyrin repeat domain family member C	-1.910	0.0001	0.0004
Sp4	ENSMUSG00000025323	trans-acting transcription factor 4	-1.506	0.0094	0.0248

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Spag8	ENSMUSG00000066196	sperm associated antigen 8	-13.872	0.0229	0.0536
Spata6	ENSMUSG00000034401	spermatogenesis associated 6	-2.008	0.0000	0.0000
Spcs1	ENSMUSG00000021917	signal peptidase complex subunit 1 homolog (S. cerevisiae)	-1.585	0.0000	0.0000
Spic	ENSMUSG00000004359	Spi-C transcription factor (Spi-1/PU.1 related)	-9.150	0.0062	0.0174
Spsb4	ENSMUSG00000046997	splA/ryanodine receptor domain and SOCS box containing 4	-1.901	0.0005	0.0018
Sptssa	ENSMUSG00000044408	serine palmitoyltransferase, small subunit A	-1.650	0.0000	0.0002
Srgn	ENSMUSG00000020077	serglycin	-1.523	0.0000	0.0000
Srms	ENSMUSG00000027579	src-related kinase lacking C-terminal regulatory tyrosine and N-terminal myristylation sites	-2.914	0.0142	0.0357
St8sia2	ENSMUSG00000025789	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2	-17.933	0.0044	0.0128
St8sia4	ENSMUSG00000040710	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4	-1.709	0.0003	0.0010
Stat5a	ENSMUSG00000004043	signal transducer and activator of transcription 5A	-1.569	0.0002	0.0009
Stpg1	ENSMUSG00000028801	sperm tail PG rich repeat containing 1	-2.392	0.0298	0.0672
Susd3	ENSMUSG00000021384	sushi domain containing 3	-2.774	0.0367	0.0800
Swt1	ENSMUSG00000052748	SWT1 RNA endoribonuclease homolog (S. cerevisiae)	-1.653	0.0000	0.0000
Syt17	ENSMUSG00000058420	synaptotagmin XVII	-1.582	0.0342	0.0752
Taf4b	ENSMUSG00000054321	TATA-box binding protein associated factor 4b	-1.731	0.0007	0.0025
Tbc1d25	ENSMUSG00000039201	TBC1 domain family, member 25	-1.558	0.0081	0.0219
Tex15	ENSMUSG00000009628	testis expressed gene 15	-25.034	0.0016	0.0052
Tlr13	ENSMUSG00000033777	toll-like receptor 13	-1.686	0.0260	0.0599
Tlr3	ENSMUSG00000031639	toll-like receptor 3	-1.593	0.0001	0.0003
Tlr4	ENSMUSG00000039005	toll-like receptor 4	-1.849	0.0003	0.0012
Tm9sf2	ENSMUSG00000025544	transmembrane 9 superfamily member 2	-1.564	0.0000	0.0000
Tmc5	ENSMUSG00000030650	transmembrane channel-like gene family 5	-2.203	0.0022	0.0069
Tmed5	ENSMUSG00000063406	transmembrane p24 trafficking protein 5	-1.668	0.0000	0.0001
Tmem147os	ENSMUSG00000097320	transmembrane protein 147, opposite strand	-1.865	0.0242	0.0562
Tmem167	ENSMUSG00000012422	transmembrane protein 167	-1.614	0.0000	0.0000
Tmem198b	ENSMUSG00000047090	transmembrane protein 198b	-1.546	0.0087	0.0234
Tmem203	ENSMUSG00000078201	transmembrane protein 203	-5.748	0.0000	0.0000
Tmem229b	ENSMUSG00000046157	transmembrane protein 229B	-1.731	0.0002	0.0009
Tmem232	ENSMUSG00000045036	transmembrane protein 232	-5.752	0.0122	0.0311
Tmem255a	ENSMUSG00000036502	transmembrane protein 255A	-2.353	0.0002	0.0007

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem267	ENSMUSG00000074634	transmembrane protein 267	-1.698	0.0011	0.0039
Tmem30b	ENSMUSG00000034435	transmembrane protein 30B	-17.857	0.0027	0.0084
Tmem70	ENSMUSG00000025940	transmembrane protein 70	-1.801	0.0000	0.0000
Tnfrsf4	ENSMUSG00000029075	tumor necrosis factor receptor superfamily, member 4	-6.217	0.0477	0.0995
Tnfsf13	ENSMUSG00000089669	tumor necrosis factor (ligand) superfamily, member 13	-5.445	0.0037	0.0112
Tomm40	ENSMUSG00000002984	translocase of outer mitochondrial membrane 40	-1.592	0.0001	0.0002
Tomm6os	ENSMUSG00000084880	translocase of outer mitochondrial membrane 6, opposite strand	-4.246	0.0473	0.0988
Tpmt	ENSMUSG00000021376	thiopurine methyltransferase	-1.756	0.0000	0.0001
Trappc2	ENSMUSG00000079317	trafficking protein particle complex 2	-1.698	0.0000	0.0000
Trem2	ENSMUSG00000023992	triggering receptor expressed on myeloid cells 2	-1.917	0.0361	0.0788
Trim28	ENSMUSG00000005566	tripartite motif-containing 28	-1.586	0.0000	0.0000
Trim9	ENSMUSG00000021071	tripartite motif-containing 9	-32.741	0.0001	0.0006
Trpv1	ENSMUSG00000005952	transient receptor potential cation channel, subfamily V, member 1	-9.727	0.0244	0.0566
Tspan6	ENSMUSG00000067377	tetraspanin 6	-1.520	0.0020	0.0063
Tssk4	ENSMUSG00000007591	testis-specific serine kinase 4	-5.725	0.0432	0.0916
Ttc36	ENSMUSG00000039438	tetratricopeptide repeat domain 36	-16.480	0.0053	0.0152
Ttll3	ENSMUSG00000030276	tubulin tyrosine ligase-like family, member 3	-2.909	0.0094	0.0249
Ttyh2	ENSMUSG00000034714	tweety family member 2	-1.683	0.0062	0.0174
Txndc12	ENSMUSG00000028567	thioredoxin domain containing 12 (endoplasmic reticulum)	-1.530	0.0001	0.0005
Ubald2	ENSMUSG00000050628	UBA-like domain containing 2	-1.956	0.0007	0.0026
Ube2v1	ENSMUSG00000078923	ubiquitin-conjugating enzyme E2 variant 1	-7.135	0.0294	0.0664
Ubl4a	ENSMUSG00000015290	ubiquitin-like 4A	-1.574	0.0000	0.0000
Ubxn10	ENSMUSG00000043621	UBX domain protein 10	-1.656	0.0015	0.0051
Unkl	ENSMUSG00000015127	unkempt family like zinc finger	-1.881	0.0046	0.0135
Uqcrh-ps2	ENSMUSG00000081413	ubiquinol-cytochrome c reductase hinge protein, pseudogene 2	-31.572	0.0003	0.0010
Usp38	ENSMUSG00000038250	ubiquitin specific peptidase 38	-1.782	0.0000	0.0000
Uts2r	ENSMUSG00000039321	urotensin 2 receptor	-4.279	0.0102	0.0267
Vars	ENSMUSG00000007029	valyl-tRNA synthetase	-1.549	0.0028	0.0088
Vps35	ENSMUSG00000031696	VPS35 retromer complex component	-1.524	0.0000	0.0000
Wdfy2	ENSMUSG00000014547	WD repeat and FYVE domain containing 2	-1.632	0.0000	0.0000
Wfdc17	ENSMUSG00000069792	WAP four-disulfide core domain 17	-1.846	0.0032	0.0098

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Xbp1	ENSMUSG00000020484	X-box binding protein 1	-1.935	0.0000	0.0001
Zc2hc1a	ENSMUSG00000043542	zinc finger, C2HC-type containing 1A	-1.668	0.0000	0.0000
Zc3h12b	ENSMUSG00000035045	zinc finger CCCH-type containing 12B	-2.940	0.0007	0.0024
Zdhhc13	ENSMUSG00000030471	zinc finger, DHHC domain containing 13	-1.555	0.0000	0.0000
Zdhhc15	ENSMUSG00000033906	zinc finger, DHHC domain containing 15	-1.715	0.0350	0.0768
Zfp101	ENSMUSG00000055240	zinc finger protein 101	-1.559	0.0014	0.0048
Zfp119b	ENSMUSG00000062101	zinc finger protein 119b	-1.707	0.0087	0.0234
Zfp184	ENSMUSG00000006720	zinc finger protein 184 (Kruppel-like)	-5.473	0.0010	0.0035
Zfp202	ENSMUSG00000025602	zinc finger protein 202	-1.540	0.0006	0.0021
Zfp260	ENSMUSG00000049421	zinc finger protein 260	-1.681	0.0000	0.0000
Zfp354a	ENSMUSG00000020364	zinc finger protein 354A	-1.679	0.0076	0.0206
Zfp382	ENSMUSG00000074220	zinc finger protein 382	-4.814	0.0000	0.0002
Zfp40	ENSMUSG00000002617	zinc finger protein 40	-2.379	0.0000	0.0001
Zfp459	ENSMUSG00000055560	zinc finger protein 459	-3.532	0.0003	0.0010
Zfp472	ENSMUSG00000053600	zinc finger protein 472	-2.095	0.0000	0.0000
Zfp54	ENSMUSG00000023882	zinc finger protein 54	-2.086	0.0005	0.0019
Zfp558	ENSMUSG00000074500	zinc finger protein 558	-2.641	0.0025	0.0078
Zfp560	ENSMUSG00000045519	zinc finger protein 560	-1.644	0.0002	0.0007
Zfp574	ENSMUSG00000045252	zinc finger protein 574	-1.767	0.0035	0.0106
Zfp623	ENSMUSG00000050846	zinc finger protein 623	-1.501	0.0004	0.0016
Zfp652os	ENSMUSG00000086191	zinc finger protein 652, opposite strand	-13.376	0.0010	0.0036
Zfp655	ENSMUSG00000007812	zinc finger protein 655	-1.662	0.0000	0.0000
Zfp677	ENSMUSG00000062743	zinc finger protein 677	-2.398	0.0029	0.0089
Zfp7	ENSMUSG00000033669	zinc finger protein 7	-1.854	0.0249	0.0576
Zfp715	ENSMUSG00000012640	zinc finger protein 715	-1.784	0.0000	0.0000
Zfp72	ENSMUSG00000069184	zinc finger protein 72	-1.856	0.0012	0.0042
Zfp758	ENSMUSG00000044501	zinc finger protein 758	-1.809	0.0000	0.0000
Zfp759	ENSMUSG00000057396	zinc finger protein 759	-1.690	0.0020	0.0064
Zfp772	ENSMUSG00000066838	zinc finger protein 772	-1.613	0.0062	0.0174
Zfp811	ENSMUSG00000055202	zinc finger protein 811	-18.866	0.0021	0.0068
Zfp820	ENSMUSG00000069743	zinc finger protein 820	-2.440	0.0009	0.0032

• **Table S4: Differentially expressed transcripts specific to mG4H-OFF (Venn Diagram: Group II)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp853	ENSMUSG00000093910	zinc finger protein 853	-22.884	0.0009	0.0031
Zfp882	ENSMUSG00000089857	zinc finger protein 882	-2.052	0.0003	0.0011
Zfp930	ENSMUSG00000059897	zinc finger protein 930	-2.238	0.0000	0.0000
Zfp931	ENSMUSG00000078861	zinc finger protein 931	-1.614	0.0133	0.0336
Zfp932	ENSMUSG00000066613	zinc finger protein 932	-1.801	0.0013	0.0043
Zfp934	ENSMUSG00000074865	zinc finger protein 934	-1.695	0.0082	0.0220
Zfp942	ENSMUSG00000071267	zinc finger protein 942	-1.742	0.0000	0.0000
Zfp944	ENSMUSG00000033972	zinc finger protein 944	-1.845	0.0000	0.0000
Zfp947	ENSMUSG00000063383	zinc finger protein 947	-3.063	0.0005	0.0018
Zfp948	ENSMUSG00000067931	zinc finger protein 948	-1.535	0.0052	0.0149
Zfp951	ENSMUSG00000072774	zinc finger protein 951	-2.355	0.0201	0.0478
Zfp955a	ENSMUSG00000094441	zinc finger protein 955A	-1.659	0.0000	0.0000
Zfp959	ENSMUSG00000003198	zinc finger protein 959	-1.829	0.0000	0.0001
Zfp960	ENSMUSG00000096696	zinc finger protein 960	-13.131	0.0000	0.0002
Zfp978	ENSMUSG00000078497	zinc finger protein 978	-27.426	0.0009	0.0032
Zfp979	ENSMUSG00000066000	zinc finger protein 979	-1.800	0.0003	0.0012
Zfp995	ENSMUSG00000078546	zinc finger protein 995	-2.199	0.0221	0.0519
Zkscan6	ENSMUSG00000018347	zinc finger with KRAB and SCAN domains 6	-1.516	0.0115	0.0296
Zmat4	ENSMUSG00000037492	zinc finger, matrin type 4	-3.201	0.0003	0.0012
Zpr1	ENSMUSG00000032078	ZPR1 zinc finger	-1.592	0.0016	0.0054
Zscan30	ENSMUSG00000024274	zinc finger and SCAN domain containing 30	-2.988	0.0007	0.0026
Zyg11a	ENSMUSG00000034645	zyg-11 family member A, cell cycle regulator	-15.509	0.0143	0.0360

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610009L18Rik	ENSMUSG00000043644	RIKEN cDNA 0610009L18 gene	5.210	0.0000	0.0000	4.378	0.0000	0.0000
1110004F10Rik	ENSMUSG00000030663	RIKEN cDNA 1110004F10 gene	1.621	0.0000	0.0000	1.658	0.0000	0.0000
1110018N20Rik	ENSMUSG00000085151	RIKEN cDNA 1110018N20 gene	2.369	0.0000	0.0000	2.370	0.0000	0.0000
1110032F04Rik	ENSMUSG00000046999	RIKEN cDNA 1110032F04 gene	3.754	0.0004	0.0015	4.323	0.0003	0.0011
1110038F14Rik	ENSMUSG00000063236	RIKEN cDNA 1110038F14 gene	1.663	0.0000	0.0000	1.848	0.0000	0.0000
1110065P20Rik	ENSMUSG00000078570	RIKEN cDNA 1110065P20 gene	2.464	0.0001	0.0005	1.612	0.0447	0.0941
1190005I06Rik	ENSMUSG00000043687	RIKEN cDNA 1190005I06 gene	6.380	0.0000	0.0000	5.736	0.0000	0.0000
1300002E11Rik	ENSMUSG00000097290	RIKEN cDNA 1300002E11 gene	2.439	0.0000	0.0000	2.146	0.0000	0.0000
1600014C23Rik	ENSMUSG00000094690	RIKEN cDNA 1600014C23 gene	2.765	0.0069	0.0174	4.303	0.0001	0.0006
1700018L02Rik	ENSMUSG00000100075	RIKEN cDNA 1700018L02 gene	1.706	0.0489	0.0949	1.791	0.0397	0.0855
1700034H15Rik	ENSMUSG00000055833	RIKEN cDNA 1700034H15 gene	2.371	0.0002	0.0009	3.746	0.0000	0.0000
1700084E18Rik	ENSMUSG00000100747	RIKEN cDNA 1700084E18 gene	4.583	0.0000	0.0000	3.881	0.0000	0.0000
1700095B10Rik	ENSMUSG00000098230	RIKEN cDNA 1700095B10 gene	22.426	0.0000	0.0000	30.945	0.0001	0.0002
1700119I11Rik	ENSMUSG00000082488	RIKEN cDNA 1700119I11 gene	26.015	0.0001	0.0004	5.654	0.0357	0.0781
1810037I17Rik	ENSMUSG00000054091	RIKEN cDNA 1810037I17 gene	1.711	0.0000	0.0000	1.769	0.0000	0.0000
1810049J17Rik	ENSMUSG00000097221	RIKEN cDNA 1810049J17 gene	50.484	0.0000	0.0000	59.315	0.0000	0.0000
2010001A14Rik	ENSMUSG00000087165	RIKEN cDNA 2010001A14 gene	4.281	0.0000	0.0000	5.474	0.0000	0.0000
2300009A05Rik	ENSMUSG00000032403	RIKEN cDNA 2300009A05 gene	2.517	0.0000	0.0000	2.070	0.0000	0.0001
2310009B15Rik	ENSMUSG00000079283	RIKEN cDNA 2310009B15 gene	1.508	0.0007	0.0023	1.778	0.0000	0.0000
2310010J17Rik	ENSMUSG00000097162	RIKEN cDNA 2310010J17 gene	2.945	0.0000	0.0000	2.980	0.0000	0.0000
2310061I04Rik	ENSMUSG00000050705	RIKEN cDNA 2310061I04 gene	3.196	0.0000	0.0001	2.311	0.0026	0.0081
2410004B18Rik	ENSMUSG00000036873	RIKEN cDNA 2410004B18 gene	2.307	0.0000	0.0000	1.557	0.0065	0.0180
2410022M11Rik	ENSMUSG00000100017	RIKEN cDNA 2410022M11 gene	3.434	0.0000	0.0000	2.692	0.0001	0.0005
2510039O18Rik	ENSMUSG00000044496	RIKEN cDNA 2510039O18 gene	1.785	0.0002	0.0008	1.736	0.0005	0.0018
2610037D02Rik	ENSMUSG00000097536	RIKEN cDNA 2610037D02 gene	1.736	0.0465	0.0908	2.051	0.0120	0.0307
2610306M01Rik	ENSMUSG00000100164	RIKEN cDNA 2610306M01 gene	2.273	0.0000	0.0000	2.124	0.0000	0.0000
2810002D19Rik	ENSMUSG00000045464	RIKEN cDNA 2810002D19 gene	2.606	0.0000	0.0000	2.284	0.0001	0.0003
2900005J15Rik	ENSMUSG00000043833	RIKEN cDNA 2900005J15 gene	2.860	0.0044	0.0116	4.676	0.0001	0.0002
2900089D17Rik	ENSMUSG00000087484	RIKEN cDNA 2900089D17 gene	2.209	0.0004	0.0013	2.583	0.0000	0.0001
3110021N24Rik	ENSMUSG00000094958	RIKEN cDNA 3110021N24 gene	9.782	0.0000	0.0000	10.525	0.0000	0.0000
3110040N11Rik	ENSMUSG00000025102	RIKEN cDNA 3110040N11 gene	1.579	0.0000	0.0000	1.944	0.0000	0.0000
3110082I17Rik	ENSMUSG00000053553	RIKEN cDNA 3110082I17 gene	1.796	0.0000	0.0000	2.094	0.0000	0.0000
4833403J16Rik	ENSMUSG00000107481	RIKEN cDNA 4833403J16 gene	1.656	0.0126	0.0293	2.119	0.0002	0.0010
4833438C02Rik	ENSMUSG00000118087	RIKEN cDNA 4833438C02 gene	1.765	0.0074	0.0183	2.014	0.0009	0.0031
4921504A21Rik	ENSMUSG00000097626	RIKEN cDNA 4921504A21 gene	2.006	0.0000	0.0000	2.147	0.0000	0.0000
4921524J17Rik	ENSMUSG00000036934	RIKEN cDNA 4921524J17 gene	1.759	0.0000	0.0000	1.705	0.0000	0.0000
4921531C22Rik	ENSMUSG00000085704	RIKEN cDNA 4921531C22 gene	2.556	0.0000	0.0000	1.804	0.0051	0.0146
4930412F12Rik	ENSMUSG00000110289	RIKEN cDNA 4930412F12 gene	5.261	0.0000	0.0001	2.785	0.0100	0.0262
4930500M09Rik	ENSMUSG00000044306	RIKEN cDNA 4930500M09 gene	18.436	0.0070	0.0174	19.383	0.0062	0.0172
4930507D05Rik	ENSMUSG00000097129	RIKEN cDNA 4930507D05 gene	3.447	0.0001	0.0005	4.256	0.0001	0.0003
4930526A20Rik	ENSMUSG00000085521	RIKEN cDNA 4930526A20 gene	22.888	0.0000	0.0000	12.011	0.0000	0.0000
4930577N17Rik	ENSMUSG00000087440	RIKEN cDNA 4930577N17 gene	7.547	0.0000	0.0000	8.191	0.0000	0.0000
4930597O21Rik	ENSMUSG00000053442	RIKEN cDNA 4930597O21 gene	28.932	0.0169	0.0380	18.762	0.0389	0.0842

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
4931403E22Rik	ENSMUSG00000093772	RIKEN cDNA 4931403E22 gene	29.442	0.0000	0.0000	12.952	0.0000	0.0000
4931440P22Rik	ENSMUSG00000074580	RIKEN cDNA 4931440P22 gene	9.222	0.0000	0.0000	7.419	0.0000	0.0000
4933412E12Rik	ENSMUSG00000112627	RIKEN cDNA 4933412E12 gene	1.612	0.0187	0.0414	2.101	0.0004	0.0013
4933415A04Rik	ENSMUSG00000045877	RIKEN cDNA 4933415A04 gene	4.537	0.0002	0.0008	6.148	0.0000	0.0001
4933421O10Rik	ENSMUSG00000085037	RIKEN cDNA 4933421O10 gene	2.476	0.0000	0.0000	2.097	0.0000	0.0001
4933427D14Rik	ENSMUSG00000107877	RIKEN cDNA 4933427D14 gene	3.101	0.0028	0.0077	3.771	0.0006	0.0023
5330439K02Rik	ENSMUSG00000097827	RIKEN cDNA 5330439K02 gene	5.154	0.0000	0.0000	5.432	0.0000	0.0000
5730409E04Rik	ENSMUSG00000073755	RIKEN cDNA 5730409E04Rik gene	1.559	0.0000	0.0000	1.953	0.0000	0.0000
5730480H06Rik	ENSMUSG00000029089	RIKEN cDNA 5730480H06 gene	2.456	0.0000	0.0000	1.753	0.0000	0.0001
5830454E08Rik	ENSMUSG00000052658	RIKEN cDNA 5830454E08 gene	2.044	0.0070	0.0175	2.782	0.0001	0.0006
6330562C20Rik	ENSMUSG00000093424	RIKEN cDNA 6330562C20 gene	2.880	0.0004	0.0014	2.356	0.0051	0.0146
6430573P05Rik	ENSMUSG00000102545	RIKEN cDNA 6430573P05 gene	3.704	0.0000	0.0000	3.034	0.0000	0.0000
6530402F18Rik	ENSMUSG00000079499	RIKEN cDNA 6530402F18 gene	3.284	0.0000	0.0000	3.561	0.0000	0.0000
9030407P20Rik	ENSMUSG00000097343	RIKEN cDNA 9030407P20 gene	1.697	0.0088	0.0214	1.706	0.0092	0.0244
9130017K11Rik	ENSMUSG00000055134	RIKEN cDNA 9130017K11 gene	2.217	0.0284	0.0595	2.759	0.0049	0.0141
9130230N09Rik	ENSMUSG00000092626	RIKEN cDNA 9130230N09 gene	4.363	0.0033	0.0090	3.302	0.0153	0.0380
9130401M01Rik	ENSMUSG00000101892	RIKEN cDNA 9130401M01 gene	2.115	0.0000	0.0000	1.815	0.0000	0.0000
9330160F10Rik	ENSMUSG00000072809	RIKEN cDNA 9330160F10 gene	2.987	0.0000	0.0001	2.007	0.0097	0.0256
9330162012Rik	ENSMUSG00000086448	cDNA RIKEN 9330162012 gene	3.854	0.0000	0.0000	2.328	0.0002	0.0008
9330162G02Rik	ENSMUSG00000109536	RIKEN cDNA 9330162G02 gene	1.986	0.0005	0.0017	1.897	0.0015	0.0051
9430062P05Rik	ENSMUSG00000104263	RIKEN cDNA 9430062P05 gene	3.148	0.0003	0.0010	2.341	0.0088	0.0235
A330041J22Rik	ENSMUSG00000087466	RIKEN cDNA A330041J22 gene	6.539	0.0000	0.0000	5.935	0.0000	0.0000
A430027H14Rik	ENSMUSG00000104507	RIKEN cDNA A430027H14 gene	4.436	0.0174	0.0389	6.618	0.0007	0.0026
A530058N18Rik	ENSMUSG00000092201	RIKEN cDNA A530058N18 gene	4.198	0.0000	0.0000	2.092	0.0216	0.0509
A630019I02Rik	ENSMUSG00000114968	RIKEN cDNA A630019I02 gene	13.032	0.0000	0.0000	5.917	0.0000	0.0001
A830035O19Rik	ENSMUSG00000111329	RIKEN cDNA A830035O19 gene	2.006	0.0029	0.0080	2.498	0.0001	0.0004
A930015D03Rik	ENSMUSG00000092368	RIKEN cDNA A930015D03 gene	1.924	0.0000	0.0001	2.409	0.0000	0.0000
A930016O22Rik	ENSMUSG00000040705	RIKEN cDNA A930016O22 gene	6.746	0.0000	0.0000	5.082	0.0000	0.0000
A930018P22Rik	ENSMUSG00000032671	RIKEN cDNA A930018P22 gene	9.505	0.0000	0.0000	6.698	0.0002	0.0009
A930035D04Rik	ENSMUSG00000052241	RIKEN cDNA A930035D04 gene	6.313	0.0000	0.0000	5.402	0.0000	0.0000
Aatf	ENSMUSG00000018697	apoptosis antagonizing transcription factor	2.126	0.0000	0.0000	1.933	0.0000	0.0000
Abcf1	ENSMUSG00000038762	ATP-binding cassette, sub-family F (GCN20), member 1	1.840	0.0000	0.0000	2.050	0.0000	0.0000
Abhd11os	ENSMUSG00000085042	abhydrolase domain containing 11, opposite strand	4.459	0.0039	0.0104	3.701	0.0111	0.0287
Abhd17a	ENSMUSG00000003346	abhydrolase domain containing 17A	2.262	0.0000	0.0000	1.512	0.0263	0.0604
Abhd17b	ENSMUSG00000047368	abhydrolase domain containing 17B	1.858	0.0000	0.0000	1.615	0.0000	0.0002
Abl2	ENSMUSG00000026596	v-abl Abelson murine leukemia viral oncogene 2 (arg, Abelson-related gene)	1.685	0.0000	0.0000	1.595	0.0000	0.0001
Abracl	ENSMUSG00000078453	ABRA C-terminal like	2.431	0.0000	0.0000	1.779	0.0000	0.0000
Acbd3	ENSMUSG00000026499	acyl-Coenzyme A binding domain containing 3	3.473	0.0000	0.0000	3.341	0.0000	0.0000
Acbd6	ENSMUSG00000033701	acyl-Coenzyme A binding domain containing 6	3.941	0.0000	0.0000	1.886	0.0384	0.0831
Acin1	ENSMUSG00000022185	apoptotic chromatin condensation inducer 1	1.902	0.0000	0.0000	2.055	0.0000	0.0000
Acot4	ENSMUSG00000052392	acyl-CoA thioesterase 4	2.991	0.0000	0.0000	1.530	0.0331	0.0731
Acsm5	ENSMUSG00000030972	acyl-CoA synthetase medium-chain family member 5	1.508	0.0224	0.0486	2.140	0.0000	0.0001
Actr3-ps	ENSMUSG00000082319	actin related protein 3, pseudogene	2.589	0.0000	0.0000	2.212	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Acvr1b	ENSMUSG00000000532	activin A receptor, type 1B	1.739	0.0000	0.0000	1.810	0.0000	0.0000
Acvr2b	ENSMUSG00000061393	activin receptor IIB	1.699	0.0001	0.0002	1.861	0.0000	0.0000
Adam23	ENSMUSG00000025964	a disintegrin and metallopeptidase domain 23	2.078	0.0000	0.0000	1.735	0.0000	0.0000
Adamts19	ENSMUSG00000053441	a disintegrin-like and metallopeptidase (reprolysin type) with thrombospondin type 1 motif, 19	2.118	0.0015	0.0045	2.066	0.0025	0.0079
Adat2	ENSMUSG00000019808	adenosine deaminase, tRNA-specific 2	2.550	0.0000	0.0000	2.590	0.0000	0.0000
Adgrb2	ENSMUSG00000028782	adhesion G protein-coupled receptor B2	1.856	0.0140	0.0322	2.242	0.0014	0.0045
Adipor1	ENSMUSG00000026457	adiponectin receptor 1	1.613	0.0000	0.0000	1.660	0.0000	0.0000
Adnp	ENSMUSG00000051149	activity-dependent neuroprotective protein	25.375	0.0000	0.0000	23.217	0.0000	0.0000
Adra1d	ENSMUSG00000027335	adrenergic receptor, alpha 1d	2.452	0.0000	0.0002	2.544	0.0000	0.0001
Adra2c	ENSMUSG00000045318	adrenergic receptor, alpha 2c	4.255	0.0003	0.0010	4.541	0.0002	0.0007
Adrb1	ENSMUSG00000035283	adrenergic receptor, beta 1	3.139	0.0000	0.0000	2.727	0.0000	0.0000
Adssl1	ENSMUSG00000011148	adenylosuccinate synthetase like 1	1.626	0.0000	0.0002	1.781	0.0000	0.0000
Aebp2	ENSMUSG00000030232	AE binding protein 2	2.644	0.0000	0.0000	2.580	0.0000	0.0000
Aga	ENSMUSG00000031521	aspartylglucosaminidase	1.848	0.0000	0.0000	1.946	0.0000	0.0000
Agap3	ENSMUSG00000023353	ArfGAP with GTPase domain, ankyrin repeat and PH domain 3	2.265	0.0000	0.0000	2.481	0.0000	0.0000
Agpat5	ENSMUSG00000031467	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)	1.704	0.0000	0.0000	1.554	0.0000	0.0000
Agtpbp1	ENSMUSG00000021557	ATP/GTP binding protein 1	1.726	0.0000	0.0001	1.807	0.0000	0.0000
Ahcyl1	ENSMUSG00000027893	S-adenosylhomocysteine hydrolase-like 1	2.125	0.0000	0.0000	1.851	0.0000	0.0000
Ahcyl2	ENSMUSG00000029772	S-adenosylhomocysteine hydrolase-like 2	1.562	0.0000	0.0000	1.752	0.0000	0.0000
Ahsa2	ENSMUSG00000020288	AHA1, activator of heat shock protein ATPase 2	1.656	0.0000	0.0000	1.663	0.0000	0.0000
AI662270	ENSMUSG00000087107	expressed sequence AI662270	4.132	0.0000	0.0002	2.284	0.0206	0.0490
Aif1	ENSMUSG00000024397	allograft inflammatory factor 1	2.331	0.0029	0.0080	2.395	0.0024	0.0075
Aifm1	ENSMUSG00000036932	apoptosis-inducing factor, mitochondrion-associated 1	2.012	0.0000	0.0000	2.051	0.0000	0.0000
Ak6	ENSMUSG00000078941	adenylate kinase 6	2.347	0.0000	0.0000	1.997	0.0000	0.0000
Akap7	ENSMUSG00000039166	A kinase (PRKA) anchor protein 7	1.961	0.0000	0.0000	1.943	0.0000	0.0000
Akap8	ENSMUSG00000024045	A kinase (PRKA) anchor protein 8	2.100	0.0000	0.0000	2.122	0.0000	0.0000
Akap9	ENSMUSG00000040407	A kinase (PRKA) anchor protein (yotiao) 9	1.512	0.0003	0.0009	1.551	0.0001	0.0005
Akirin2	ENSMUSG00000028291	akirin 2	2.638	0.0000	0.0000	2.208	0.0000	0.0000
Aktip	ENSMUSG00000031667	AKT interacting protein	1.648	0.0000	0.0000	1.500	0.0000	0.0000
Aldoa	ENSMUSG00000114515	aldolase A, fructose-bisphosphate	3.882	0.0015	0.0044	3.355	0.0078	0.0211
Aldoart1	ENSMUSG00000059343	aldolase 1 A, retrogene 1	8.690	0.0000	0.0000	8.125	0.0000	0.0000
Alyref	ENSMUSG00000025134	Aly/REF export factor	6.207	0.0000	0.0000	6.399	0.0000	0.0000
Alyref2	ENSMUSG00000060244	Aly/REF export factor 2	1.812	0.0009	0.0027	1.828	0.0007	0.0027
Anapc13	ENSMUSG00000035048	anaphase promoting complex subunit 13	4.213	0.0000	0.0000	4.278	0.0000	0.0000
Anapc15	ENSMUSG00000030649	anaphase promoting complex C subunit 15	2.097	0.0000	0.0000	1.939	0.0000	0.0000
Ank1	ENSMUSG00000031543	ankyrin 1, erythroid	1.945	0.0000	0.0000	1.867	0.0000	0.0000
Ankhd1	ENSMUSG00000024483	ankyrin repeat and KH domain containing 1	1.757	0.0000	0.0000	1.537	0.0000	0.0001
Ankrd11	ENSMUSG00000035569	ankyrin repeat domain 11	1.506	0.0000	0.0000	1.611	0.0000	0.0000
Ankrd35	ENSMUSG00000038354	ankyrin repeat domain 35	1.987	0.0167	0.0376	2.480	0.0017	0.0056
Ankrd40	ENSMUSG00000020864	ankyrin repeat domain 40	2.182	0.0000	0.0000	2.204	0.0000	0.0000
Ankrd63	ENSMUSG00000078137	ankyrin repeat domain 63	1.803	0.0172	0.0385	2.012	0.0058	0.0164
Ano8	ENSMUSG00000034863	anoctamin 8	3.905	0.0000	0.0000	3.821	0.0000	0.0000
Anp32a	ENSMUSG00000032249	acidic (leucine-rich) nuclear phosphoprotein 32 family, member A	2.317	0.0000	0.0000	2.455	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Anp32b	ENSMUSG00000028333	acidic (leucine-rich) nuclear phosphoprotein 32 family, member B	7.305	0.0000	0.0000	7.115	0.0000	0.0000
Anp32e	ENSMUSG00000015749	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E	2.708	0.0000	0.0000	2.359	0.0000	0.0000
Anxa5	ENSMUSG00000027712	annexin A5	1.842	0.0000	0.0000	1.943	0.0000	0.0000
Ap1ar	ENSMUSG00000074238	adaptor-related protein complex 1 associated regulatory protein	1.738	0.0000	0.0000	1.516	0.0001	0.0003
Ap3b1	ENSMUSG00000021686	adaptor-related protein complex 3, beta 1 subunit	1.793	0.0000	0.0000	2.057	0.0000	0.0000
Ap3s1	ENSMUSG00000024480	adaptor-related protein complex 3, sigma 1 subunit	3.382	0.0000	0.0000	3.656	0.0000	0.0000
Apip	ENSMUSG00000010911	APAF1 interacting protein	1.543	0.0000	0.0000	1.538	0.0000	0.0000
Aplp2	ENSMUSG00000031996	amyloid beta (A4) precursor-like protein 2	1.509	0.0000	0.0000	1.589	0.0000	0.0000
Apobr	ENSMUSG00000042759	apolipoprotein B receptor	1.997	0.0044	0.0117	2.660	0.0001	0.0003
Apol10b	ENSMUSG00000050014	apolipoprotein L 10B	2.216	0.0013	0.0039	2.174	0.0016	0.0052
Apold1	ENSMUSG00000090698	apolipoprotein L domain containing 1	1.873	0.0002	0.0007	1.543	0.0099	0.0262
Apoo-ps	ENSMUSG00000049233	apolipoprotein O, pseudogene	1.891	0.0001	0.0002	1.787	0.0003	0.0011
App	ENSMUSG00000022892	amyloid beta (A4) precursor protein	1.566	0.0000	0.0000	1.699	0.0000	0.0000
Arf3	ENSMUSG00000051853	ADP-ribosylation factor 3	2.283	0.0000	0.0000	2.301	0.0000	0.0000
Arf5	ENSMUSG00000020440	ADP-ribosylation factor 5	2.546	0.0000	0.0000	2.569	0.0000	0.0000
Arf6	ENSMUSG00000044147	ADP-ribosylation factor 6	3.998	0.0000	0.0000	3.558	0.0000	0.0000
Arglu1	ENSMUSG00000040459	arginine and glutamate rich 1	3.016	0.0000	0.0000	2.781	0.0000	0.0000
Arhgap11a	ENSMUSG00000041219	Rho GTPase activating protein 11A	2.475	0.0000	0.0000	2.287	0.0000	0.0000
Arhgap19	ENSMUSG00000025154	Rho GTPase activating protein 19	1.897	0.0000	0.0000	1.620	0.0001	0.0006
Arhgap23	ENSMUSG00000049807	Rho GTPase activating protein 23	2.589	0.0000	0.0000	2.810	0.0000	0.0000
Arhgap30	ENSMUSG00000048865	Rho GTPase activating protein 30	2.002	0.0001	0.0003	2.269	0.0000	0.0000
Arhgap44	ENSMUSG00000033389	Rho GTPase activating protein 44	1.664	0.0000	0.0001	1.630	0.0000	0.0002
Arhgef9	ENSMUSG00000025656	CDC42 guanine nucleotide exchange factor (GEF) 9	1.714	0.0000	0.0000	1.614	0.0000	0.0000
Arid4a	ENSMUSG00000048118	AT rich interactive domain 4A (RBP1-like)	2.183	0.0000	0.0000	1.928	0.0000	0.0000
Arid4b	ENSMUSG00000039219	AT rich interactive domain 4B (RBP1-like)	1.894	0.0000	0.0000	1.731	0.0000	0.0000
Arih1	ENSMUSG00000025234	ariadne RBR E3 ubiquitin protein ligase 1	1.791	0.0000	0.0000	1.515	0.0000	0.0000
Arl1	ENSMUSG00000060904	ADP-ribosylation factor-like 1	1.981	0.0000	0.0000	2.048	0.0000	0.0000
Arl10	ENSMUSG00000025870	ADP-ribosylation factor-like 10	2.700	0.0000	0.0000	2.564	0.0000	0.0001
Arl2bp	ENSMUSG00000031776	ADP-ribosylation factor-like 2 binding protein	1.504	0.0000	0.0000	1.611	0.0000	0.0000
Arl4a	ENSMUSG00000047446	ADP-ribosylation factor-like 4A	2.153	0.0001	0.0002	2.173	0.0000	0.0002
Arl4c	ENSMUSG00000049866	ADP-ribosylation factor-like 4C	1.924	0.0000	0.0000	2.010	0.0000	0.0000
Arl4d	ENSMUSG00000034936	ADP-ribosylation factor-like 4D	1.660	0.0003	0.0011	1.822	0.0000	0.0001
Arl6ip4	ENSMUSG00000029404	ADP-ribosylation factor-like 6 interacting protein 4	1.790	0.0000	0.0000	1.895	0.0000	0.0000
Arl6ip5	ENSMUSG00000035199	ADP-ribosylation factor-like 6 interacting protein 5	1.747	0.0000	0.0000	1.553	0.0000	0.0000
Arl6ip6	ENSMUSG00000026960	ADP-ribosylation factor-like 6 interacting protein 6	1.845	0.0000	0.0000	1.627	0.0000	0.0000
Arl8a	ENSMUSG00000026426	ADP-ribosylation factor-like 8A	2.604	0.0000	0.0000	2.852	0.0000	0.0000
Armcx6	ENSMUSG00000050394	armadillo repeat containing, X-linked 6	2.657	0.0000	0.0000	2.005	0.0012	0.0041
Arnt	ENSMUSG00000015522	aryl hydrocarbon receptor nuclear translocator	1.654	0.0000	0.0000	1.572	0.0000	0.0000
Arpc2	ENSMUSG00000006304	actin related protein 2/3 complex, subunit 2	1.593	0.0000	0.0000	1.524	0.0000	0.0000
Arpc5l	ENSMUSG00000026755	actin related protein 2/3 complex, subunit 5-like	1.522	0.0000	0.0000	1.532	0.0000	0.0000
Arpp19	ENSMUSG00000007656	cAMP-regulated phosphoprotein 19	1.919	0.0000	0.0000	2.036	0.0000	0.0000
Asf1a	ENSMUSG00000019857	anti-silencing function 1A histone chaperone	2.616	0.0000	0.0000	2.678	0.0000	0.0000
Ash2l	ENSMUSG00000031575	ASH2 like histone lysine methyltransferase complex subunit	2.302	0.0000	0.0000	2.362	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Asph	ENSMUSG00000028207	aspartate-beta-hydroxylase	2.046	0.0000	0.0000	1.732	0.0000	0.0000
Asrgl1	ENSMUSG00000024654	asparaginase like 1	1.951	0.0000	0.0000	1.820	0.0000	0.0000
Atad1	ENSMUSG00000013662	ATPase family, AAA domain containing 1	1.940	0.0000	0.0000	1.819	0.0000	0.0000
Atad2	ENSMUSG00000022360	ATPase family, AAA domain containing 2	2.313	0.0000	0.0000	1.510	0.0114	0.0294
Atad2b	ENSMUSG00000052812	ATPase family, AAA domain containing 2B	1.984	0.0000	0.0000	1.506	0.0000	0.0000
Atad3a	ENSMUSG00000029036	ATPase family, AAA domain containing 3A	2.149	0.0000	0.0000	1.929	0.0000	0.0000
Atf1	ENSMUSG00000023027	activating transcription factor 1	2.810	0.0000	0.0000	1.892	0.0000	0.0000
Atf2	ENSMUSG00000027104	activating transcription factor 2	1.565	0.0000	0.0000	1.525	0.0000	0.0000
Atf5	ENSMUSG00000038539	activating transcription factor 5	3.062	0.0000	0.0000	2.308	0.0002	0.0009
Atg10	ENSMUSG00000021619	autophagy related 10	1.725	0.0000	0.0000	1.561	0.0000	0.0000
Atg3	ENSMUSG00000022663	autophagy related 3	4.076	0.0000	0.0000	3.644	0.0000	0.0000
Atn1	ENSMUSG00000004263	atrophin 1	6.372	0.0000	0.0000	5.929	0.0000	0.0000
Atp1b3	ENSMUSG00000032412	ATPase, Na+/K+ transporting, beta 3 polypeptide	1.853	0.0000	0.0000	1.789	0.0000	0.0000
Atp2a2	ENSMUSG00000029467	ATPase, Ca++ transporting, cardiac muscle, slow twitch 2	1.878	0.0000	0.0000	2.011	0.0000	0.0000
Atp6v1g1	ENSMUSG00000039105	ATPase, H+ transporting, lysosomal V1 subunit G1	1.987	0.0000	0.0000	1.773	0.0000	0.0000
Atxn7	ENSMUSG00000021738	ataxin 7	1.779	0.0000	0.0000	1.531	0.0000	0.0000
Aven	ENSMUSG00000003604	apoptosis, caspase activation inhibitor	4.911	0.0000	0.0000	5.515	0.0000	0.0000
AW046200	ENSMUSG00000110419	expressed sequence AW046200	3.660	0.0001	0.0003	4.242	0.0000	0.0001
Axin1	ENSMUSG00000024182	axin 1	1.567	0.0007	0.0021	1.662	0.0001	0.0005
Axin2	ENSMUSG00000000142	axin 2	1.835	0.0002	0.0007	2.143	0.0000	0.0000
B230216N24Rik	ENSMUSG00000089706	RIKEN cDNA B230216N24 gene	2.020	0.0469	0.0915	2.491	0.0103	0.0269
B230322F03Rik	ENSMUSG00000097509	RIKEN cDNA B230322F03 gene	2.451	0.0034	0.0091	2.189	0.0069	0.0189
B230377A18Rik	ENSMUSG00000104195	RIKEN cDNA B230377A18 gene	8.191	0.0000	0.0000	7.030	0.0000	0.0000
B330016D10Rik	ENSMUSG00000048406	RIKEN cDNA B330016D10 gene	2.360	0.0000	0.0000	2.347	0.0000	0.0000
B3gnt2	ENSMUSG00000051650	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2	14.044	0.0000	0.0000	10.456	0.0000	0.0000
B430319G15Rik	ENSMUSG00000103622	RIKEN cDNA B430319G15 gene	1.925	0.0162	0.0366	1.938	0.0159	0.0393
B4galt2	ENSMUSG00000028541	UDP-Gal:betaGlcNAc beta 1,4- galactosyltransferase, polypeptide 2	3.571	0.0000	0.0000	3.918	0.0000	0.0000
B630019K06Rik	ENSMUSG00000052364	RIKEN cDNA B630019K06 gene	2.132	0.0003	0.0012	1.845	0.0046	0.0134
Bag1	ENSMUSG00000028416	BCL2-associated athanogene 1	2.497	0.0000	0.0000	2.375	0.0000	0.0000
Basp1	ENSMUSG00000045763	brain abundant, membrane attached signal protein 1	8.773	0.0000	0.0000	7.375	0.0000	0.0000
Baz1b	ENSMUSG00000002748	bromodomain adjacent to zinc finger domain, 1B	2.344	0.0000	0.0000	2.147	0.0000	0.0000
Bbc3	ENSMUSG00000002083	BCL2 binding component 3	5.699	0.0000	0.0000	6.174	0.0000	0.0000
Bbof1	ENSMUSG00000057265	basal body orientation factor 1	1.582	0.0012	0.0035	1.864	0.0000	0.0001
BC002189	ENSMUSG00000104465	cDNA sequence BC002189	2.664	0.0103	0.0247	2.347	0.0235	0.0549
BC005624	ENSMUSG00000026851	cDNA sequence BC005624	2.291	0.0000	0.0000	2.465	0.0000	0.0000
Bcas2	ENSMUSG00000005687	BCAS2 pre-mRNA processing factor	1.714	0.0000	0.0000	1.572	0.0000	0.0000
Bccip	ENSMUSG00000030983	BRCA2 and CDKN1A interacting protein	2.553	0.0000	0.0000	2.747	0.0000	0.0000
Bcl2a1b	ENSMUSG00000089929	B cell leukemia/lymphoma 2 related protein A1b	18.966	0.0078	0.0192	10.910	0.0198	0.0473
Bcl2l2	ENSMUSG00000089682	BCL2-like 2	2.090	0.0000	0.0000	2.116	0.0000	0.0000
Bcl3	ENSMUSG00000053175	B cell leukemia/lymphoma 3	3.629	0.0000	0.0000	4.117	0.0000	0.0000
Bcl7c	ENSMUSG00000030814	B cell CLL/lymphoma 7C	5.806	0.0000	0.0000	5.583	0.0000	0.0000
Bdp1	ENSMUSG00000049658	B double prime 1, subunit of RNA polymerase III transcription initiation factor IIIB	1.952	0.0000	0.0000	1.609	0.0000	0.0000
Bean1	ENSMUSG00000031872	brain expressed, associated with Nedd4, 1	1.637	0.0216	0.0471	1.834	0.0050	0.0145

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Becn1	ENSMUSG00000035086	beclin 1, autophagy related	1.958	0.0000	0.0000	1.955	0.0000	0.0000
Bend5	ENSMUSG00000028545	BEN domain containing 5	1.787	0.0000	0.0000	1.786	0.0000	0.0000
Bex1	ENSMUSG00000050071	brain expressed X-linked 1	1.754	0.0075	0.0185	3.048	0.0000	0.0000
Bex4	ENSMUSG00000047844	brain expressed X-linked 4	4.390	0.0080	0.0196	7.887	0.0009	0.0033
Bhlhe22	ENSMUSG00000025128	basic helix-loop-helix family, member e22	2.597	0.0038	0.0100	2.367	0.0176	0.0429
Bhlhe41	ENSMUSG00000030256	basic helix-loop-helix family, member e41	2.720	0.0000	0.0000	1.785	0.0035	0.0105
Bicd2	ENSMUSG00000037933	BICD cargo adaptor 2	1.666	0.0000	0.0000	1.688	0.0000	0.0000
Bloc1s4	ENSMUSG00000060708	biogenesis of lysosomal organelles complex-1, subunit 4, cappuccino	3.365	0.0000	0.0000	2.658	0.0000	0.0000
Bms1	ENSMUSG00000030138	BMS1, ribosome biogenesis factor	2.490	0.0000	0.0000	2.654	0.0000	0.0000
Bmx	ENSMUSG00000031377	BMX non-receptor tyrosine kinase	1.815	0.0002	0.0007	2.023	0.0000	0.0001
Bnip2	ENSMUSG00000011958	BCL2/adenovirus E1B interacting protein 2	1.884	0.0000	0.0000	1.679	0.0000	0.0000
Bod1	ENSMUSG00000044502	biorientation of chromosomes in cell division 1	1.559	0.0000	0.0000	1.572	0.0000	0.0000
Bod1l	ENSMUSG00000061755	biorientation of chromosomes in cell division 1-like	1.898	0.0000	0.0000	1.797	0.0000	0.0000
Borcs6	ENSMUSG00000045176	BLOC-1 related complex subunit 6	2.977	0.0000	0.0001	2.273	0.0011	0.0037
Brd7	ENSMUSG00000031660	bromodomain containing 7	1.613	0.0000	0.0000	1.856	0.0000	0.0000
Brd9	ENSMUSG00000057649	bromodomain containing 9	1.529	0.0000	0.0000	1.714	0.0000	0.0000
Brf1	ENSMUSG00000011158	BRF1, RNA polymerase III transcription initiation factor 90 kDa subunit	1.722	0.0000	0.0000	1.752	0.0000	0.0000
Bri3	ENSMUSG00000047843	brain protein I3	7.344	0.0000	0.0000	9.261	0.0000	0.0000
Brsk1	ENSMUSG00000035390	BR serine/threonine kinase 1	2.030	0.0001	0.0002	2.181	0.0000	0.0000
Btbd1	ENSMUSG00000025103	BTB (POZ) domain containing 1	2.444	0.0000	0.0000	2.063	0.0000	0.0000
Btf3	ENSMUSG00000021660	basic transcription factor 3	1.941	0.0000	0.0000	1.688	0.0000	0.0000
Btf3l4	ENSMUSG00000028568	basic transcription factor 3-like 4	2.240	0.0000	0.0000	2.172	0.0000	0.0000
Btg1	ENSMUSG00000036478	BTG anti-proliferation factor 1	4.328	0.0000	0.0000	4.591	0.0000	0.0000
Btg3	ENSMUSG00000022863	BTG anti-proliferation factor 3	2.838	0.0000	0.0000	2.861	0.0000	0.0000
Bud13	ENSMUSG00000032077	BUD13 homolog	1.611	0.0000	0.0000	1.784	0.0000	0.0000
C030037D09Rik	ENSMUSG00000087574	RIKEN cDNA C030037D09 gene	1.504	0.0002	0.0007	1.691	0.0000	0.0000
C130074G19Rik	ENSMUSG00000039349	RIKEN cDNA C130074G19 gene	2.344	0.0000	0.0000	2.178	0.0000	0.0000
C1galt1c1	ENSMUSG00000048970	C1GALT1-specific chaperone 1	1.818	0.0000	0.0000	1.546	0.0000	0.0002
C1qc	ENSMUSG00000036896	complement component 1, q subcomponent, C chain	4.478	0.0003	0.0009	3.933	0.0008	0.0030
C1qtnf9	ENSMUSG00000071347	C1q and tumor necrosis factor related protein 9	1.686	0.0001	0.0005	1.713	0.0001	0.0004
C1rb	ENSMUSG00000098470	complement component 1, r subcomponent B	3.681	0.0000	0.0000	3.491	0.0000	0.0000
C230013L11Rik	ENSMUSG00000117171	RIKEN cDNA C230013L11 gene	5.086	0.0000	0.0000	3.591	0.0000	0.0000
C230096K16Rik	ENSMUSG00000106205	RIKEN cDNA C230096K16 gene	3.997	0.0000	0.0000	3.904	0.0000	0.0000
C330011M18Rik	ENSMUSG00000056753	RIKEN cDNA C330011M18 gene	2.001	0.0000	0.0000	1.887	0.0000	0.0000
C430014B12Rik	ENSMUSG00000097564	RIKEN cDNA C430014B12 gene	3.941	0.0000	0.0002	2.410	0.0120	0.0307
C430049B03Rik	ENSMUSG00000087365	RIKEN cDNA C430049B03 gene	2.739	0.0015	0.0044	2.343	0.0085	0.0229
C5ar1	ENSMUSG00000049130	complement component 5a receptor 1	2.330	0.0000	0.0001	2.972	0.0000	0.0000
C630043F03Rik	ENSMUSG00000084910	RIKEN cDNA C630043F03 gene	3.117	0.0000	0.0000	2.072	0.0025	0.0077
Caap1	ENSMUSG00000028578	caspase activity and apoptosis inhibitor 1	2.132	0.0000	0.0000	1.795	0.0000	0.0000
Cab39	ENSMUSG00000036707	calcium binding protein 39	2.034	0.0000	0.0000	1.870	0.0000	0.0000
Cables1	ENSMUSG00000040957	CDK5 and Abl enzyme substrate 1	1.894	0.0000	0.0000	1.972	0.0000	0.0000
Cables2	ENSMUSG00000038990	CDK5 and Abl enzyme substrate 2	1.663	0.0000	0.0000	1.688	0.0000	0.0000
Cacfd1	ENSMUSG00000015488	calcium channel flower domain containing 1	2.143	0.0000	0.0000	1.952	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cacna2d2	ENSMUSG00000010066	calcium channel, voltage-dependent, alpha 2/delta subunit 2	1.702	0.0119	0.0280	1.849	0.0029	0.0088
Cacng7	ENSMUSG00000069806	calcium channel, voltage-dependent, gamma subunit 7	2.223	0.0000	0.0000	3.068	0.0000	0.0000
Cadm1	ENSMUSG00000032076	cell adhesion molecule 1	1.649	0.0002	0.0008	1.857	0.0000	0.0000
Cald1	ENSMUSG00000029761	caldesmon 1	1.927	0.0000	0.0000	1.944	0.0000	0.0000
Calm2	ENSMUSG00000036438	calmodulin 2	2.332	0.0000	0.0000	1.872	0.0000	0.0000
Calm3	ENSMUSG00000019370	calmodulin 3	2.343	0.0000	0.0000	2.237	0.0000	0.0000
Calr	ENSMUSG00000003814	calreticulin	1.702	0.0000	0.0000	1.893	0.0000	0.0000
Camk1	ENSMUSG00000030272	calcium/calmodulin-dependent protein kinase I	2.493	0.0000	0.0000	2.598	0.0000	0.0000
Camk2n1	ENSMUSG00000046447	calcium/calmodulin-dependent protein kinase II inhibitor 1	5.358	0.0000	0.0000	5.034	0.0000	0.0000
Camk2n2	ENSMUSG00000051146	calcium/calmodulin-dependent protein kinase II inhibitor 2	3.200	0.0000	0.0000	3.813	0.0000	0.0000
Canx	ENSMUSG00000020368	calnexin	1.795	0.0000	0.0000	1.715	0.0000	0.0000
Caprin1	ENSMUSG00000027184	cell cycle associated protein 1	1.945	0.0000	0.0000	1.796	0.0000	0.0000
Carnmt1	ENSMUSG00000024726	carnosine N-methyltransferase 1	3.294	0.0000	0.0000	2.890	0.0000	0.0000
Casc3	ENSMUSG00000078676	cancer susceptibility candidate 3	1.967	0.0000	0.0000	1.779	0.0000	0.0000
Casz1	ENSMUSG00000028977	castor zinc finger 1	1.851	0.0000	0.0000	1.681	0.0000	0.0000
Cavin1	ENSMUSG00000004044	caveolae associated 1	2.460	0.0000	0.0000	2.375	0.0000	0.0000
Cbfb	ENSMUSG00000031885	core binding factor beta	2.615	0.0000	0.0000	2.388	0.0000	0.0000
Cbx1	ENSMUSG00000018666	chromobox 1	2.642	0.0000	0.0000	2.429	0.0000	0.0000
Cbx3	ENSMUSG00000029836	chromobox 3	2.486	0.0000	0.0000	2.491	0.0000	0.0000
Ccar1	ENSMUSG00000020074	cell division cycle and apoptosis regulator 1	2.464	0.0000	0.0000	2.232	0.0000	0.0000
Ccdc112	ENSMUSG00000071855	coiled-coil domain containing 112	1.555	0.0360	0.0729	1.868	0.0038	0.0112
Ccdc117	ENSMUSG00000020482	coiled-coil domain containing 117	2.112	0.0000	0.0000	2.062	0.0000	0.0000
Ccdc12	ENSMUSG00000019659	coiled-coil domain containing 12	1.863	0.0000	0.0000	2.180	0.0000	0.0000
Ccdc122	ENSMUSG00000034795	coiled-coil domain containing 122	2.290	0.0000	0.0000	2.999	0.0000	0.0000
Ccdc124	ENSMUSG00000007721	coiled-coil domain containing 124	2.263	0.0000	0.0000	2.866	0.0000	0.0000
Ccdc142os	ENSMUSG00000087578	coiled-coil domain containing 142, opposite strand	1.720	0.0168	0.0378	1.680	0.0264	0.0607
Ccdc146	ENSMUSG00000064280	coiled-coil domain containing 146	1.849	0.0000	0.0000	1.942	0.0000	0.0000
Ccdc173	ENSMUSG00000070883	coiled-coil domain containing 173	3.320	0.0000	0.0000	3.273	0.0000	0.0000
Ccdc174	ENSMUSG00000034083	coiled-coil domain containing 174	1.826	0.0000	0.0000	2.147	0.0000	0.0000
Ccdc181	ENSMUSG00000026578	coiled-coil domain containing 181	1.894	0.0000	0.0000	2.324	0.0000	0.0000
Ccdc191	ENSMUSG00000022701	coiled-coil domain containing 191	1.952	0.0000	0.0001	2.428	0.0000	0.0000
Ccdc25	ENSMUSG00000022035	coiled-coil domain containing 25	2.111	0.0000	0.0000	2.051	0.0000	0.0000
Ccdc28b	ENSMUSG00000028795	coiled coil domain containing 28B	1.506	0.0010	0.0030	1.834	0.0000	0.0000
Ccdc34	ENSMUSG00000027160	coiled-coil domain containing 34	3.968	0.0000	0.0000	4.215	0.0000	0.0000
Ccdc47	ENSMUSG00000078622	coiled-coil domain containing 47	2.602	0.0000	0.0000	2.273	0.0000	0.0000
Ccdc66	ENSMUSG00000046753	coiled-coil domain containing 66	1.502	0.0001	0.0003	1.518	0.0001	0.0003
Ccdc71l	ENSMUSG00000090946	coiled-coil domain containing 71 like	3.095	0.0000	0.0000	2.375	0.0000	0.0000
Ccdc82	ENSMUSG00000079084	coiled-coil domain containing 82	1.911	0.0000	0.0000	1.729	0.0000	0.0000
Ccdc85c	ENSMUSG00000084883	coiled-coil domain containing 85C	1.741	0.0000	0.0000	1.998	0.0000	0.0000
Ccdc9	ENSMUSG00000041375	coiled-coil domain containing 9	1.987	0.0000	0.0000	2.423	0.0000	0.0000
Ccdc91	ENSMUSG00000030301	coiled-coil domain containing 91	1.943	0.0000	0.0000	2.300	0.0000	0.0000
Cchcr1	ENSMUSG00000040312	coiled-coil alpha-helical rod protein 1	1.557	0.0069	0.0173	2.394	0.0000	0.0000
Ccm2l	ENSMUSG00000027474	cerebral cavernous malformation 2-like	1.549	0.0021	0.0060	1.706	0.0002	0.0007

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ccnd1	ENSMUSG00000070348	cyclin D1	2.050	0.0001	0.0004	1.907	0.0005	0.0018
Ccng2	ENSMUSG00000029385	cyclin G2	2.429	0.0000	0.0000	2.275	0.0000	0.0000
Ccni	ENSMUSG00000063015	cyclin I	2.340	0.0000	0.0000	2.044	0.0000	0.0000
Ccnj	ENSMUSG00000025010	cyclin J	2.412	0.0000	0.0000	2.144	0.0000	0.0000
Ccnt1	ENSMUSG00000011960	cyclin T1	1.530	0.0000	0.0000	1.602	0.0000	0.0000
Ccs	ENSMUSG00000034108	copper chaperone for superoxide dismutase	1.831	0.0000	0.0000	1.946	0.0000	0.0000
Ccsap	ENSMUSG00000031971	centriole, cilia and spindle associated protein	3.235	0.0000	0.0000	2.308	0.0002	0.0007
Ccz1	ENSMUSG00000029617	CCZ1 vacuolar protein trafficking and biogenesis associated	2.053	0.0000	0.0000	2.296	0.0000	0.0000
Cd163	ENSMUSG00000008845	CD163 antigen	1.780	0.0135	0.0313	1.910	0.0057	0.0160
Cd300a	ENSMUSG00000034652	CD300A molecule	1.755	0.0081	0.0199	1.982	0.0016	0.0052
Cd3e	ENSMUSG00000032093	CD3 antigen, epsilon polypeptide	3.972	0.0000	0.0000	3.726	0.0000	0.0001
Cd63	ENSMUSG00000025351	CD63 antigen	1.665	0.0000	0.0000	1.831	0.0000	0.0000
Cd72	ENSMUSG00000028459	CD72 antigen	2.879	0.0125	0.0291	3.465	0.0033	0.0101
Cd9	ENSMUSG00000030342	CD9 antigen	1.913	0.0000	0.0000	1.711	0.0000	0.0001
Cdc25a	ENSMUSG00000032477	cell division cycle 25A	1.693	0.0000	0.0000	1.605	0.0000	0.0000
Cdc26	ENSMUSG00000066149	cell division cycle 26	1.988	0.0000	0.0000	1.802	0.0000	0.0000
Cdc37	ENSMUSG00000019471	cell division cycle 37	2.061	0.0000	0.0000	2.291	0.0000	0.0000
Cdk11b	ENSMUSG00000029062	cyclin-dependent kinase 11B	2.385	0.0000	0.0000	2.619	0.0000	0.0000
Cdk13	ENSMUSG00000041297	cyclin-dependent kinase 13	1.851	0.0000	0.0000	1.537	0.0002	0.0007
Cdk18	ENSMUSG00000026437	cyclin-dependent kinase 18	1.563	0.0000	0.0000	1.675	0.0000	0.0000
Cdk2ap1	ENSMUSG00000029394	CDK2 (cyclin-dependent kinase 2)-associated protein 1	2.197	0.0000	0.0001	1.741	0.0021	0.0067
Cdk5rap3	ENSMUSG00000018669	CDK5 regulatory subunit associated protein 3	1.800	0.0000	0.0000	2.090	0.0000	0.0000
Cdk8	ENSMUSG00000029635	cyclin-dependent kinase 8	1.852	0.0000	0.0000	1.912	0.0000	0.0000
Cdkn1c	ENSMUSG00000037664	cyclin-dependent kinase inhibitor 1C (P57)	4.230	0.0000	0.0000	3.382	0.0000	0.0000
Cdkn2c	ENSMUSG00000028551	cyclin dependent kinase inhibitor 2C	2.091	0.0000	0.0000	1.792	0.0000	0.0000
Cdnf	ENSMUSG00000039496	cerebral dopamine neurotrophic factor	1.848	0.0000	0.0000	1.886	0.0000	0.0000
Cdr2	ENSMUSG00000030878	cerebellar degeneration-related 2	2.279	0.0000	0.0000	2.386	0.0000	0.0000
Cdr2l	ENSMUSG00000050910	cerebellar degeneration-related protein 2-like	2.006	0.0000	0.0000	2.398	0.0000	0.0000
Cds1	ENSMUSG00000029330	CDP-diacylglycerol synthase 1	1.760	0.0008	0.0025	2.363	0.0000	0.0000
Cdv3	ENSMUSG00000032803	carnitine deficiency-associated gene expressed in ventricle 3	2.896	0.0000	0.0000	3.299	0.0000	0.0000
Cdyl	ENSMUSG00000059288	chromodomain protein, Y chromosome-like	1.797	0.0000	0.0000	1.810	0.0000	0.0000
Cebpa	ENSMUSG00000034957	CCAAT/enhancer binding protein (C/EBP), alpha	4.478	0.0000	0.0000	4.284	0.0000	0.0000
Cebpb	ENSMUSG00000056501	CCAAT/enhancer binding protein (C/EBP), beta	11.498	0.0000	0.0000	9.906	0.0000	0.0000
Cebpg	ENSMUSG00000056216	CCAAT/enhancer binding protein (C/EBP), gamma	1.759	0.0000	0.0000	1.526	0.0000	0.0000
Cenpb	ENSMUSG00000068267	centromere protein B	1.643	0.0000	0.0000	1.795	0.0000	0.0000
Cenps	ENSMUSG00000073705	centromere protein S	1.968	0.0046	0.0121	2.497	0.0001	0.0006
Cenpv	ENSMUSG00000018509	centromere protein V	2.600	0.0000	0.0000	2.859	0.0000	0.0000
Cep250	ENSMUSG00000038241	centrosomal protein 250	1.682	0.0000	0.0000	1.776	0.0000	0.0000
Cep63	ENSMUSG00000032534	centrosomal protein 63	2.280	0.0000	0.0000	2.477	0.0000	0.0000
Cep83	ENSMUSG00000020024	centrosomal protein 83	2.278	0.0000	0.0000	1.688	0.0000	0.0000
Cep89	ENSMUSG00000023072	centrosomal protein 89	1.737	0.0000	0.0000	2.038	0.0000	0.0000
Cep97	ENSMUSG00000022604	centrosomal protein 97	2.136	0.0000	0.0000	2.138	0.0000	0.0000
Cetn3	ENSMUSG00000021537	centrin 3	4.023	0.0000	0.0000	3.684	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cfap298	ENSMUSG00000022972	cilia and flagella associate protien 298	2.087	0.0000	0.0000	2.366	0.0000	0.0000
Cfap36	ENSMUSG00000020462	cilia and flagella associated protein 36	1.799	0.0000	0.0000	1.977	0.0000	0.0000
Cfdp1	ENSMUSG00000031954	craniofacial development protein 1	2.788	0.0000	0.0000	2.671	0.0000	0.0000
Cflar	ENSMUSG00000026031	CASP8 and FADD-like apoptosis regulator	1.746	0.0000	0.0000	1.585	0.0000	0.0000
Cgnl1	ENSMUSG00000032232	cingulin-like 1	1.503	0.0000	0.0000	1.677	0.0000	0.0000
Cgref1	ENSMUSG00000029161	cell growth regulator with EF hand domain 1	4.750	0.0000	0.0000	3.042	0.0002	0.0007
Chaf1a	ENSMUSG00000002835	chromatin assembly factor 1, subunit A (p150)	2.259	0.0000	0.0000	2.938	0.0000	0.0000
Chaserr	ENSMUSG00000101970	CHD2 adjacent suppressive regulatory RNA	3.468	0.0000	0.0000	2.780	0.0000	0.0000
Chchd4	ENSMUSG00000034203	coiled-coil-helix-coiled-coil-helix domain containing 4	1.683	0.0000	0.0000	1.617	0.0000	0.0000
Chd1	ENSMUSG00000023852	chromodomain helicase DNA binding protein 1	1.879	0.0000	0.0000	1.795	0.0000	0.0000
Chd2	ENSMUSG00000078671	chromodomain helicase DNA binding protein 2	1.790	0.0000	0.0000	1.705	0.0000	0.0000
Chd4	ENSMUSG00000063870	chromodomain helicase DNA binding protein 4	1.812	0.0000	0.0000	1.826	0.0000	0.0000
Chgb	ENSMUSG00000027350	chromogranin B	2.261	0.0132	0.0307	4.769	0.0000	0.0000
Chic2	ENSMUSG00000029229	cysteine-rich hydrophobic domain 2	5.125	0.0000	0.0000	4.662	0.0000	0.0000
Chmp3	ENSMUSG00000053119	charged multivesicular body protein 3	1.994	0.0000	0.0000	1.930	0.0000	0.0000
Chmp4b	ENSMUSG00000038467	charged multivesicular body protein 4B	2.337	0.0000	0.0000	2.340	0.0000	0.0000
Chmp4c	ENSMUSG00000027536	charged multivesicular body protein 4C	1.749	0.0000	0.0000	1.610	0.0000	0.0000
Chmp7	ENSMUSG00000034190	charged multivesicular body protein 7	2.262	0.0000	0.0000	2.404	0.0000	0.0000
Chst14	ENSMUSG00000074916	carbohydrate sulfotransferase 14	1.802	0.0000	0.0001	1.888	0.0000	0.0000
Chst2	ENSMUSG00000033350	carbohydrate sulfotransferase 2	3.099	0.0000	0.0000	2.726	0.0000	0.0000
Chsy1	ENSMUSG00000032640	chondroitin sulfate synthase 1	2.336	0.0000	0.0000	2.180	0.0000	0.0000
Chuk	ENSMUSG00000025199	conserved helix-loop-helix ubiquitous kinase	1.713	0.0000	0.0000	1.537	0.0000	0.0000
Cib2	ENSMUSG00000037493	calcium and integrin binding family member 2	3.185	0.0000	0.0000	2.560	0.0003	0.0013
Cideb	ENSMUSG00000022219	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	1.582	0.0279	0.0586	1.727	0.0082	0.0220
Cir1	ENSMUSG00000041777	corepressor interacting with RBPJ, 1	1.964	0.0004	0.0014	2.275	0.0000	0.0001
Cirbp	ENSMUSG00000045193	cold inducible RNA binding protein	1.774	0.0001	0.0004	1.960	0.0000	0.0000
Cited2	ENSMUSG00000039910	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 2	1.902	0.0023	0.0064	1.731	0.0092	0.0244
Cited4	ENSMUSG00000070803	Cbp/p300-interacting transactivator, with Glu/Asp-rich carboxy-terminal domain, 4	4.217	0.0001	0.0003	3.045	0.0022	0.0071
Ckap4	ENSMUSG00000046841	cytoskeleton-associated protein 4	2.019	0.0000	0.0000	2.065	0.0000	0.0000
Clasrp	ENSMUSG00000061028	CLK4-associating serine/arginine rich protein	1.539	0.0068	0.0171	1.775	0.0003	0.0013
Clint1	ENSMUSG00000006169	clathrin interactor 1	1.778	0.0000	0.0000	1.747	0.0000	0.0000
Clk1	ENSMUSG00000026034	CDC-like kinase 1	1.744	0.0032	0.0087	1.524	0.0259	0.0596
Clptm1	ENSMUSG00000002981	cleft lip and palate associated transmembrane protein 1	1.881	0.0000	0.0002	1.892	0.0000	0.0002
Cltb	ENSMUSG00000047547	clathrin, light polypeptide (Lcb)	2.478	0.0000	0.0000	2.522	0.0000	0.0000
Cluap1	ENSMUSG00000014232	clusterin associated protein 1	2.049	0.0000	0.0000	1.864	0.0000	0.0000
Cmas	ENSMUSG00000030282	cytidine monophospho-N-acetylneuraminic acid synthetase	2.833	0.0000	0.0000	2.992	0.0000	0.0000
Cmpk1	ENSMUSG00000028719	cytidine monophosphate (UMP-CMP) kinase 1	2.144	0.0000	0.0000	1.584	0.0000	0.0000
Cmtm6	ENSMUSG00000032434	CKLF-like MARVEL transmembrane domain containing 6	1.602	0.0000	0.0000	1.558	0.0000	0.0000
Cnot11	ENSMUSG00000003135	CCR4-NOT transcription complex, subunit 11	2.110	0.0000	0.0000	1.912	0.0000	0.0000
Cnpy4	ENSMUSG00000036968	canopy FGF signaling regulator 4	1.814	0.0000	0.0000	1.861	0.0000	0.0000
Cntf	ENSMUSG00000079415	ciliary neurotrophic factor	8.064	0.0035	0.0095	11.432	0.0006	0.0023
Col13a1	ENSMUSG00000058806	collagen, type XIII, alpha 1	2.403	0.0025	0.0070	2.516	0.0015	0.0051
Commd1	ENSMUSG00000051355	COMM domain containing 1	1.725	0.0000	0.0000	1.780	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Coprs	ENSMUSG00000031458	coordinator of PRMT5, differentiation stimulator	1.837	0.0000	0.0001	1.684	0.0004	0.0014
Copz2	ENSMUSG00000018672	coatomer protein complex, subunit zeta 2	3.014	0.0000	0.0000	3.727	0.0000	0.0000
Cox11	ENSMUSG00000020544	cytochrome c oxidase assembly protein 11, copper chaperone	3.073	0.0000	0.0000	2.378	0.0000	0.0000
Cox20	ENSMUSG00000026500	cytochrome c oxidase assembly protein 20	1.809	0.0000	0.0000	1.574	0.0000	0.0000
Cox7c	ENSMUSG00000017778	cytochrome c oxidase subunit 7C	2.732	0.0000	0.0000	2.500	0.0000	0.0000
Cpe	ENSMUSG00000037852	carboxypeptidase E	2.105	0.0000	0.0000	1.687	0.0000	0.0000
Cpeb2	ENSMUSG00000039782	cytoplasmic polyadenylation element binding protein 2	2.822	0.0000	0.0000	2.180	0.0000	0.0000
Cpne2	ENSMUSG00000034361	copine II	1.593	0.0125	0.0293	1.753	0.0027	0.0085
Cpox	ENSMUSG00000022742	coproporphyrinogen oxidase	2.986	0.0000	0.0000	2.341	0.0000	0.0000
Cracr2b	ENSMUSG00000048200	calcium release activated channel regulator 2B	1.563	0.0000	0.0000	1.902	0.0000	0.0000
Creb3	ENSMUSG00000028466	cAMP responsive element binding protein 3	2.724	0.0000	0.0000	2.772	0.0000	0.0000
Creb3l1	ENSMUSG00000027230	cAMP responsive element binding protein 3-like 1	1.848	0.0001	0.0003	1.746	0.0004	0.0013
Crebzf	ENSMUSG00000051451	CREB/ATF bZIP transcription factor	3.044	0.0000	0.0000	3.154	0.0000	0.0000
Creld2	ENSMUSG00000023272	cysteine-rich with EGF-like domains 2	1.850	0.0000	0.0000	1.570	0.0000	0.0001
Crim1	ENSMUSG00000024074	cysteine rich transmembrane BMP regulator 1 (chordin like)	1.593	0.0000	0.0000	1.551	0.0000	0.0000
Crlf1	ENSMUSG00000007888	cytokine receptor-like factor 1	4.081	0.0032	0.0086	4.690	0.0013	0.0045
Crls1	ENSMUSG00000027357	cardiolipin synthase 1	1.962	0.0000	0.0000	2.049	0.0000	0.0000
Crnkl1	ENSMUSG00000001767	crooked neck pre-mRNA splicing factor 1	1.818	0.0000	0.0000	1.571	0.0000	0.0000
Csde1	ENSMUSG00000068823	cold shock domain containing E1, RNA binding	1.978	0.0000	0.0000	1.894	0.0000	0.0000
Csk	ENSMUSG00000032312	c-src tyrosine kinase	1.939	0.0000	0.0000	2.224	0.0000	0.0000
Csnk1g3	ENSMUSG00000073563	casein kinase 1, gamma 3	2.210	0.0000	0.0000	1.994	0.0000	0.0000
Csnk2a1	ENSMUSG00000074698	casein kinase 2, alpha 1 polypeptide	2.408	0.0000	0.0000	2.181	0.0000	0.0000
Cspp1	ENSMUSG00000056763	centrosome and spindle pole associated protein 1	1.797	0.0000	0.0000	1.828	0.0000	0.0000
Csrp2	ENSMUSG00000020186	cysteine and glycine-rich protein 2	2.325	0.0000	0.0000	2.065	0.0000	0.0000
Ctcf	ENSMUSG00000005698	CCCTC-binding factor	1.666	0.0000	0.0000	1.530	0.0000	0.0000
Ctdnep1	ENSMUSG00000018559	CTD nuclear envelope phosphatase 1	1.670	0.0001	0.0004	1.611	0.0003	0.0012
Ctdp1	ENSMUSG00000033323	CTD (carboxy-terminal domain, RNA polymerase II, polypeptide A) phosphatase, subunit 1	1.916	0.0000	0.0000	1.863	0.0000	0.0000
Ctnnbl1	ENSMUSG00000027649	catenin, beta like 1	1.764	0.0000	0.0000	1.832	0.0000	0.0000
Ctnnd1	ENSMUSG00000034101	catenin (cadherin associated protein), delta 1	2.490	0.0000	0.0000	2.843	0.0000	0.0000
Cul4a	ENSMUSG00000031446	cullin 4A	2.249	0.0000	0.0000	1.934	0.0000	0.0000
Cutal	ENSMUSG00000026870	cutA divalent cation tolerance homolog-like	2.334	0.0000	0.0002	2.182	0.0001	0.0004
Cutc	ENSMUSG00000025193	cutC copper transporter	2.321	0.0000	0.0000	2.218	0.0000	0.0000
Cwc15	ENSMUSG00000004096	CWC15 spliceosome-associated protein	2.050	0.0000	0.0000	2.136	0.0000	0.0000
Cwc27	ENSMUSG00000021715	CWC27 spliceosome-associated protein	3.630	0.0000	0.0000	3.434	0.0000	0.0000
Cyb5d1	ENSMUSG00000044795	cytochrome b5 domain containing 1	2.085	0.0000	0.0000	1.816	0.0000	0.0000
Cyb5r4	ENSMUSG00000032872	cytochrome b5 reductase 4	2.446	0.0000	0.0000	2.181	0.0000	0.0000
Cyp51	ENSMUSG00000001467	cytochrome P450, family 51	1.662	0.0000	0.0000	1.770	0.0000	0.0000
Cyrib	ENSMUSG00000022378	CYFIP related Rac1 interactor B	2.152	0.0000	0.0000	1.964	0.0000	0.0000
Cys1	ENSMUSG00000062563	cystin 1	3.275	0.0000	0.0000	4.652	0.0000	0.0000
Cyth2	ENSMUSG00000003269	cytohesin 2	1.963	0.0001	0.0005	2.030	0.0001	0.0003
D330050I16Rik	ENSMUSG00000117959	RIKEN cDNA D330050I16 gene	7.677	0.0000	0.0000	6.731	0.0000	0.0000
D630033A02Rik	ENSMUSG00000112237	RIKEN cDNA D630033A02 gene	5.503	0.0000	0.0000	3.023	0.0010	0.0033
D830050J10Rik	ENSMUSG00000107994	RIKEN cDNA D830050J10 gene	4.504	0.0000	0.0000	2.919	0.0000	0.0001

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
D8Ertd738e	ENSMUSG00000019362	DNA segment, Chr 8, ERATO Doi 738, expressed	1.746	0.0000	0.0000	1.836	0.0000	0.0000
Dact1	ENSMUSG00000044548	dishevelled-binding antagonist of beta-catenin 1	1.773	0.0008	0.0026	1.792	0.0007	0.0025
Dact3	ENSMUSG00000078794	dishevelled-binding antagonist of beta-catenin 3	7.079	0.0000	0.0000	5.233	0.0000	0.0000
Dazap1	ENSMUSG00000069565	DAZ associated protein 1	2.470	0.0000	0.0000	2.442	0.0000	0.0000
Dbf4	ENSMUSG00000002297	DBF4 zinc finger	1.907	0.0012	0.0037	1.832	0.0029	0.0088
Dbn1	ENSMUSG00000034675	drebrin 1	1.566	0.0043	0.0113	2.172	0.0000	0.0000
Dbndd2	ENSMUSG00000017734	dysbindin (dystrobrevin binding protein 1) domain containing 2	2.239	0.0000	0.0000	1.817	0.0000	0.0000
Dbp	ENSMUSG00000059824	D site albumin promoter binding protein	3.059	0.0023	0.0064	2.196	0.0316	0.0705
Dcaf13	ENSMUSG00000022300	DDB1 and CUL4 associated factor 13	1.761	0.0000	0.0000	1.517	0.0000	0.0000
Dctn5	ENSMUSG00000030868	dynactin 5	1.803	0.0000	0.0000	1.597	0.0000	0.0000
Dcun1d5	ENSMUSG00000032002	DCN1, defective in cullin neddylation 1, domain containing 5 (S. cerevisiae)	4.345	0.0000	0.0000	4.412	0.0000	0.0000
Ddrgk1	ENSMUSG00000068290	DDRGK domain containing 1	1.853	0.0000	0.0000	2.249	0.0000	0.0000
Ddx10	ENSMUSG00000053289	DEAD box helicase 10	2.554	0.0000	0.0000	2.302	0.0000	0.0000
Ddx19b	ENSMUSG00000033658	DEAD box helicase 19b	1.744	0.0000	0.0000	1.666	0.0000	0.0000
Ddx23	ENSMUSG00000003360	DEAD box helicase 23	1.568	0.0000	0.0000	1.654	0.0000	0.0000
Ddx27	ENSMUSG00000017999	DEAD box helicase 27	2.138	0.0000	0.0000	2.273	0.0000	0.0000
Ddx3x	ENSMUSG00000000787	DEAD box helicase 3, X-linked	2.538	0.0000	0.0000	2.202	0.0000	0.0000
Ddx42	ENSMUSG00000020705	DEAD box helicase 42	1.687	0.0000	0.0000	1.629	0.0000	0.0000
Ddx46	ENSMUSG00000021500	DEAD box helicase 46	2.173	0.0000	0.0000	2.096	0.0000	0.0000
Ddx55	ENSMUSG00000029389	DEAD box helicase 55	1.876	0.0000	0.0000	2.065	0.0000	0.0000
Deaf1	ENSMUSG00000058886	DEAF1, transcription factor	1.666	0.0021	0.0060	1.753	0.0007	0.0026
Decr1	ENSMUSG00000028223	2,4-dienoyl CoA reductase 1, mitochondrial	2.116	0.0000	0.0000	1.620	0.0000	0.0000
Dek	ENSMUSG00000021377	DEK proto-oncogene (DNA binding)	2.481	0.0000	0.0000	1.892	0.0000	0.0000
Denr	ENSMUSG00000023106	density-regulated protein	2.483	0.0000	0.0000	2.302	0.0000	0.0000
Dexi	ENSMUSG00000038055	dexamethasone-induced transcript	3.297	0.0000	0.0000	3.765	0.0000	0.0000
Dhdh	ENSMUSG00000011382	dihydrodiol dehydrogenase (dimeric)	2.213	0.0000	0.0000	2.388	0.0000	0.0000
Dhrs4	ENSMUSG00000022210	dehydrogenase/reductase (SDR family) member 4	2.550	0.0000	0.0000	2.189	0.0000	0.0000
Dhrs7	ENSMUSG00000021094	dehydrogenase/reductase (SDR family) member 7	1.917	0.0000	0.0000	1.861	0.0000	0.0000
Diaph1	ENSMUSG00000024456	diaphanous related formin 1	1.661	0.0000	0.0000	1.626	0.0000	0.0000
Dmrt2	ENSMUSG00000048138	doublesex and mab-3 related transcription factor 2	9.422	0.0402	0.0803	18.899	0.0120	0.0308
Dmrta2	ENSMUSG00000047143	doublesex and mab-3 related transcription factor like family A2	6.913	0.0001	0.0004	5.962	0.0013	0.0044
Dnaja4	ENSMUSG00000032285	DnaJ heat shock protein family (Hsp40) member A4	2.584	0.0000	0.0000	2.728	0.0000	0.0000
Dnajb11	ENSMUSG00000004460	DnaJ heat shock protein family (Hsp40) member B11	3.931	0.0000	0.0000	3.122	0.0000	0.0000
Dnajb2	ENSMUSG00000026203	DnaJ heat shock protein family (Hsp40) member B2	2.028	0.0000	0.0000	2.141	0.0000	0.0000
Dnajb6	ENSMUSG00000029131	DnaJ heat shock protein family (Hsp40) member B6	2.145	0.0000	0.0000	2.375	0.0000	0.0000
Dnajb6-ps	ENSMUSG00000091905	DnaJ heat shock protein family (Hsp40) member B6, pseudogene	11.852	0.0000	0.0000	4.277	0.0025	0.0078
Dnajc11	ENSMUSG00000039768	DnaJ heat shock protein family (Hsp40) member C11	1.838	0.0000	0.0000	1.811	0.0000	0.0000
Dnajc14	ENSMUSG00000025354	DnaJ heat shock protein family (Hsp40) member C14	1.767	0.0000	0.0000	1.857	0.0000	0.0000
Dnajc2	ENSMUSG00000029014	DnaJ heat shock protein family (Hsp40) member C2	2.378	0.0000	0.0000	2.219	0.0000	0.0000
Dnajc21	ENSMUSG00000044224	DnaJ heat shock protein family (Hsp40) member C21	4.289	0.0000	0.0000	4.789	0.0000	0.0000
Dnajc25	ENSMUSG00000070972	DnaJ heat shock protein family (Hsp40) member C25	2.380	0.0000	0.0000	2.058	0.0000	0.0000
Dnajc8	ENSMUSG00000054405	DnaJ heat shock protein family (Hsp40) member C8	3.239	0.0000	0.0000	3.255	0.0000	0.0000
Dnlz	ENSMUSG00000075467	DNL-type zinc finger	2.955	0.0000	0.0000	2.616	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dnm1	ENSMUSG00000026825	dynamin 1	1.760	0.0004	0.0015	2.112	0.0000	0.0000
Dnttip1	ENSMUSG00000017299	deoxynucleotidyltransferase, terminal, interacting protein 1	2.732	0.0000	0.0000	2.680	0.0000	0.0000
Dok5	ENSMUSG00000027560	docking protein 5	2.177	0.0003	0.0009	1.864	0.0045	0.0132
Donson	ENSMUSG00000022960	downstream neighbor of SON	1.826	0.0006	0.0019	1.784	0.0010	0.0036
Dpcd	ENSMUSG00000041035	deleted in primary ciliary dyskinesia	2.474	0.0000	0.0000	3.297	0.0000	0.0000
Dpy30	ENSMUSG00000024067	dpy-30, histone methyltransferase complex regulatory subunit	1.585	0.0000	0.0000	1.634	0.0000	0.0000
Dpysl2	ENSMUSG00000022048	dihydropyrimidinase-like 2	1.547	0.0000	0.0000	1.576	0.0000	0.0000
Dpysl3	ENSMUSG00000024501	dihydropyrimidinase-like 3	1.585	0.0187	0.0414	1.635	0.0121	0.0310
Drap1	ENSMUSG00000024914	Dr1 associated protein 1 (negative cofactor 2 alpha)	3.913	0.0000	0.0000	4.289	0.0000	0.0000
Dusp26	ENSMUSG00000039661	dual specificity phosphatase 26 (putative)	2.837	0.0000	0.0000	2.391	0.0000	0.0002
Dusp27	ENSMUSG00000026564	dual specificity phosphatase 27 (putative)	2.489	0.0000	0.0000	2.534	0.0000	0.0000
Dusp7	ENSMUSG00000053716	dual specificity phosphatase 7	1.550	0.0000	0.0000	1.662	0.0000	0.0000
Dusp8	ENSMUSG00000037887	dual specificity phosphatase 8	1.951	0.0003	0.0012	1.511	0.0272	0.0621
Dync1li2	ENSMUSG00000035770	dynein, cytoplasmic 1 light intermediate chain 2	2.319	0.0000	0.0000	2.284	0.0000	0.0000
Dync2i1	ENSMUSG00000042050	dynein 2 intermediate chain 1	1.606	0.0008	0.0024	1.877	0.0000	0.0000
Dynll2	ENSMUSG00000020483	dynein light chain LC8-type 2	2.265	0.0000	0.0000	2.391	0.0000	0.0000
Dynlt2b	ENSMUSG00000014075	dynein light chain Tctex-type 2B	2.303	0.0000	0.0000	1.969	0.0000	0.0000
Dynlt3	ENSMUSG00000031176	dynein light chain Tctex-type 3	2.401	0.0000	0.0000	1.733	0.0000	0.0000
E130102H24Rik	ENSMUSG00000086782	RIKEN cDNA E130102H24 gene	1.947	0.0122	0.0285	1.878	0.0176	0.0427
E130201H02Rik	ENSMUSG00000044141	RIKEN cDNA E130201H02 gene	9.858	0.0009	0.0027	39.282	0.0002	0.0007
E130208F15Rik	ENSMUSG00000074210	RIKEN cDNA E130208F15 gene	5.658	0.0000	0.0000	2.672	0.0001	0.0004
E2f1	ENSMUSG00000027490	E2F transcription factor 1	1.904	0.0062	0.0158	2.678	0.0000	0.0002
E2f4	ENSMUSG00000014859	E2F transcription factor 4	1.655	0.0000	0.0000	1.828	0.0000	0.0000
E330034L11Rik	ENSMUSG00000106383	RIKEN cDNA E330034L11 gene	1.771	0.0044	0.0116	1.931	0.0007	0.0025
Ebag9	ENSMUSG00000022339	estrogen receptor-binding fragment-associated gene 9	3.561	0.0000	0.0000	3.322	0.0000	0.0000
Echdc1	ENSMUSG00000019883	enoyl Coenzyme A hydratase domain containing 1	1.958	0.0000	0.0000	1.731	0.0000	0.0000
Edem3	ENSMUSG00000043019	ER degradation enhancer, mannosidase alpha-like 3	2.060	0.0000	0.0000	1.748	0.0000	0.0000
Eea1	ENSMUSG00000036499	early endosome antigen 1	1.810	0.0000	0.0000	1.717	0.0000	0.0000
Eed	ENSMUSG00000030619	embryonic ectoderm development	1.788	0.0000	0.0000	1.567	0.0000	0.0000
Efcab2	ENSMUSG00000026495	EF-hand calcium binding domain 2	2.246	0.0000	0.0000	2.129	0.0000	0.0000
Efhd1	ENSMUSG00000026255	EF hand domain containing 1	1.898	0.0000	0.0002	1.836	0.0001	0.0006
Efnb2	ENSMUSG00000001300	ephrin B2	1.937	0.0000	0.0000	1.744	0.0000	0.0000
Egln2	ENSMUSG00000058709	egl-9 family hypoxia-inducible factor 2	1.932	0.0001	0.0002	1.705	0.0010	0.0036
Ehbp1	ENSMUSG00000042302	EH domain binding protein 1	2.036	0.0000	0.0000	1.858	0.0000	0.0000
Ehbp1l1	ENSMUSG00000024937	EH domain binding protein 1-like 1	1.527	0.0000	0.0000	1.623	0.0000	0.0000
Ei24	ENSMUSG00000062762	etoposide induced 2.4 mRNA	2.136	0.0000	0.0000	1.900	0.0000	0.0000
Eid1	ENSMUSG00000091337	EP300 interacting inhibitor of differentiation 1	3.089	0.0000	0.0000	2.946	0.0000	0.0000
Eid2	ENSMUSG00000046058	EP300 interacting inhibitor of differentiation 2	4.388	0.0000	0.0000	4.807	0.0000	0.0000
Eid2b	ENSMUSG00000070705	EP300 interacting inhibitor of differentiation 2B	2.576	0.0000	0.0000	1.621	0.0095	0.0251
Eif1a	ENSMUSG00000057561	eukaryotic translation initiation factor 1A	1.698	0.0000	0.0000	1.690	0.0000	0.0000
Eif1ad	ENSMUSG00000024841	eukaryotic translation initiation factor 1A domain containing	2.143	0.0000	0.0000	2.107	0.0000	0.0000
Eif3a	ENSMUSG00000024991	eukaryotic translation initiation factor 3, subunit A	3.646	0.0000	0.0000	3.676	0.0000	0.0000
Eif3b	ENSMUSG00000056076	eukaryotic translation initiation factor 3, subunit B	2.767	0.0000	0.0000	2.655	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Eif3f	ENSMUSG00000031029	eukaryotic translation initiation factor 3, subunit F	2.203	0.0001	0.0003	1.689	0.0089	0.0238
Eif3j1	ENSMUSG00000027236	eukaryotic translation initiation factor 3, subunit J1	4.837	0.0000	0.0000	4.060	0.0000	0.0000
Eif3j2	ENSMUSG00000043424	eukaryotic translation initiation factor 3, subunit J2	2.839	0.0000	0.0000	2.326	0.0000	0.0000
Eif4e2	ENSMUSG00000026254	eukaryotic translation initiation factor 4E member 2	2.015	0.0000	0.0000	1.852	0.0000	0.0000
Eif4g1	ENSMUSG00000045983	eukaryotic translation initiation factor 4, gamma 1	1.914	0.0000	0.0000	2.133	0.0000	0.0000
Eif5b	ENSMUSG00000026083	eukaryotic translation initiation factor 5B	2.772	0.0000	0.0000	2.657	0.0000	0.0000
Elac1	ENSMUSG00000036941	elaC ribonuclease Z 1	1.667	0.0000	0.0000	1.502	0.0000	0.0000
Ell2	ENSMUSG00000001542	elongation factor for RNA polymerase II 2	2.223	0.0000	0.0000	1.766	0.0006	0.0023
Eln	ENSMUSG00000029675	elastin	2.468	0.0000	0.0000	3.014	0.0000	0.0000
Eloc	ENSMUSG00000079658	elongin C	2.140	0.0000	0.0000	1.828	0.0000	0.0000
Emc10	ENSMUSG00000008140	ER membrane protein complex subunit 10	2.270	0.0000	0.0000	2.357	0.0000	0.0000
Enah	ENSMUSG00000022995	ENAH actin regulator	1.742	0.0000	0.0000	1.558	0.0000	0.0002
Endog	ENSMUSG00000015337	endonuclease G	2.557	0.0000	0.0001	2.080	0.0008	0.0028
Engase	ENSMUSG00000033857	endo-beta-N-acetylglucosaminidase	2.510	0.0000	0.0000	3.239	0.0000	0.0000
Enho	ENSMUSG00000028445	energy homeostasis associated	2.408	0.0000	0.0000	3.233	0.0000	0.0000
Entr1	ENSMUSG00000026927	endosome associated trafficking regulator 1	1.522	0.0000	0.0000	1.529	0.0000	0.0000
Eny2	ENSMUSG00000022338	ENY2 transcription and export complex 2 subunit	1.795	0.0000	0.0000	1.662	0.0000	0.0000
Epb41l2	ENSMUSG00000019978	erythrocyte membrane protein band 4.1 like 2	1.503	0.0000	0.0000	1.549	0.0000	0.0000
Epha7	ENSMUSG00000028289	Eph receptor A7	1.853	0.0000	0.0000	1.596	0.0008	0.0029
Epop	ENSMUSG00000043439	elongin BC and polycomb repressive complex 2 associated protein	2.764	0.0224	0.0486	4.076	0.0015	0.0051
Erh	ENSMUSG00000021131	ERH mRNA splicing and mitosis factor	4.003	0.0000	0.0000	3.269	0.0000	0.0000
Eri3	ENSMUSG00000033423	exoribonuclease 3	2.104	0.0000	0.0001	1.672	0.0033	0.0101
Erich3	ENSMUSG00000078161	glutamate rich 3	1.788	0.0317	0.0656	3.288	0.0000	0.0002
Erlec1	ENSMUSG00000020311	endoplasmic reticulum lectin 1	1.831	0.0000	0.0000	1.718	0.0000	0.0000
Esf1	ENSMUSG00000045624	ESF1 nucleolar pre-rRNA processing protein homolog	2.031	0.0000	0.0000	1.945	0.0000	0.0000
Esm1	ENSMUSG00000042379	endothelial cell-specific molecule 1	2.685	0.0000	0.0002	2.166	0.0013	0.0043
Espn	ENSMUSG00000028943	espin	2.006	0.0000	0.0001	2.066	0.0000	0.0000
Esrra	ENSMUSG00000024955	estrogen related receptor, alpha	1.893	0.0000	0.0000	2.154	0.0000	0.0000
Etfb	ENSMUSG00000004610	electron transferring flavoprotein, beta polypeptide	1.810	0.0000	0.0000	1.796	0.0000	0.0000
Eva1b	ENSMUSG00000050212	eva-1 homolog B (C. elegans)	2.660	0.0000	0.0001	1.936	0.0045	0.0132
Evl	ENSMUSG00000021262	Ena-vasodilator stimulated phosphoprotein	2.321	0.0000	0.0000	2.521	0.0000	0.0000
Ewsr1	ENSMUSG00000009079	Ewing sarcoma breakpoint region 1	2.459	0.0000	0.0000	2.408	0.0000	0.0000
Exo5	ENSMUSG00000028629	exonuclease 5	1.742	0.0000	0.0000	1.611	0.0001	0.0005
Exosc2	ENSMUSG00000039356	exosome component 2	2.122	0.0000	0.0000	2.115	0.0000	0.0000
Exosc3	ENSMUSG00000028322	exosome component 3	2.480	0.0000	0.0000	2.372	0.0000	0.0000
Exosc7	ENSMUSG00000025785	exosome component 7	2.058	0.0000	0.0000	2.449	0.0000	0.0000
Exosc9	ENSMUSG00000027714	exosome component 9	2.259	0.0000	0.0000	2.190	0.0000	0.0000
Fabp4	ENSMUSG00000062515	fatty acid binding protein 4, adipocyte	2.411	0.0000	0.0000	2.214	0.0000	0.0000
Fabp5	ENSMUSG00000027533	fatty acid binding protein 5, epidermal	2.223	0.0000	0.0000	2.113	0.0000	0.0000
Fabp7	ENSMUSG00000019874	fatty acid binding protein 7, brain	2.240	0.0010	0.0031	3.130	0.0000	0.0000
Fahd1	ENSMUSG00000045316	fumarylacetoacetate hydrolase domain containing 1	2.353	0.0000	0.0000	2.446	0.0000	0.0000
Faim	ENSMUSG00000032463	Fas apoptotic inhibitory molecule	2.939	0.0000	0.0000	2.076	0.0000	0.0000
Fam104a	ENSMUSG00000041629	family with sequence similarity 104, member A	2.482	0.0000	0.0000	1.762	0.0027	0.0085

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fam110d	ENSMUSG00000050105	family with sequence similarity 110, member D	1.864	0.0052	0.0134	1.811	0.0079	0.0215
Fam122a	ENSMUSG00000074922	family with sequence similarity 122, member A	4.496	0.0000	0.0000	4.400	0.0000	0.0000
Fam133b	ENSMUSG00000058503	family with sequence similarity 133, member B	2.065	0.0000	0.0000	2.016	0.0000	0.0000
Fam149b	ENSMUSG00000039599	family with sequence similarity 149, member B	2.111	0.0000	0.0000	2.303	0.0000	0.0000
Fam171a2	ENSMUSG00000034685	family with sequence similarity 171, member A2	4.995	0.0000	0.0000	3.548	0.0000	0.0000
Fam174a	ENSMUSG00000051185	family with sequence similarity 174, member A	2.361	0.0000	0.0000	1.501	0.0050	0.0144
Fam193a	ENSMUSG00000037210	family with sequence homology 193, member A	1.529	0.0000	0.0000	1.776	0.0000	0.0000
Fam204a	ENSMUSG00000057858	family with sequence similarity 204, member A	2.856	0.0000	0.0000	2.639	0.0000	0.0000
Fam219a	ENSMUSG00000028439	family with sequence similarity 219, member A	1.671	0.0000	0.0000	1.540	0.0000	0.0000
Fam219b	ENSMUSG00000032305	family with sequence similarity 219, member B	2.015	0.0001	0.0002	1.675	0.0030	0.0091
Fam241a	ENSMUSG00000050549	family with sequence similarity 241, member A	5.066	0.0000	0.0000	4.792	0.0000	0.0000
Fam3c	ENSMUSG00000029672	FAM3 metabolism regulating signaling molecule C	3.623	0.0000	0.0000	3.074	0.0000	0.0000
Fam50a	ENSMUSG00000001962	family with sequence similarity 50, member A	2.655	0.0000	0.0000	2.725	0.0000	0.0000
Fam53c	ENSMUSG00000034300	family with sequence similarity 53, member C	2.074	0.0000	0.0000	1.870	0.0000	0.0000
Fam76b	ENSMUSG00000037808	family with sequence similarity 76, member B	1.824	0.0000	0.0000	1.734	0.0000	0.0001
Fam89a	ENSMUSG00000043068	family with sequence similarity 89, member A	2.718	0.0000	0.0001	2.162	0.0008	0.0030
Fam8a1	ENSMUSG00000069237	family with sequence similarity 8, member A1	2.555	0.0000	0.0000	2.136	0.0000	0.0000
Faxc	ENSMUSG00000028246	failed axon connections homolog	2.120	0.0024	0.0067	1.946	0.0094	0.0249
Fbl	ENSMUSG00000046865	fibrillarin	2.559	0.0000	0.0000	2.501	0.0000	0.0000
Fbrs	ENSMUSG00000042423	fibrosin	1.899	0.0000	0.0002	1.557	0.0051	0.0147
Fbxl14	ENSMUSG00000030019	F-box and leucine-rich repeat protein 14	3.239	0.0000	0.0000	3.132	0.0000	0.0000
Fbxl19	ENSMUSG00000030811	F-box and leucine-rich repeat protein 19	2.173	0.0000	0.0002	2.191	0.0000	0.0002
Fbxl3	ENSMUSG00000022124	F-box and leucine-rich repeat protein 3	1.942	0.0000	0.0000	1.665	0.0002	0.0007
Fbxo28	ENSMUSG00000047539	F-box protein 28	1.576	0.0000	0.0000	1.553	0.0000	0.0000
Fbxo4	ENSMUSG00000022184	F-box protein 4	1.836	0.0000	0.0001	1.525	0.0042	0.0124
Fbxo45	ENSMUSG00000035764	F-box protein 45	2.090	0.0000	0.0000	2.019	0.0000	0.0000
Fbxw11	ENSMUSG00000020271	F-box and WD-40 domain protein 11	1.730	0.0000	0.0000	1.582	0.0000	0.0000
Fbxw4	ENSMUSG00000040913	F-box and WD-40 domain protein 4	1.714	0.0000	0.0000	1.964	0.0000	0.0000
Fgf16	ENSMUSG00000031230	fibroblast growth factor 16	2.684	0.0000	0.0000	2.822	0.0000	0.0000
Fgf20	ENSMUSG00000031603	fibroblast growth factor 20	8.023	0.0000	0.0000	10.071	0.0000	0.0000
Fgf9	ENSMUSG00000021974	fibroblast growth factor 9	1.915	0.0000	0.0000	1.639	0.0000	0.0002
Fgfbp3	ENSMUSG00000047632	fibroblast growth factor binding protein 3	3.120	0.0000	0.0000	2.329	0.0000	0.0000
Fhip2b	ENSMUSG00000022095	FHF complex subunit HOOK interacting protein 2B	2.420	0.0000	0.0000	2.603	0.0000	0.0000
Fignl2	ENSMUSG00000095440	fidgetin-like 2	2.131	0.0002	0.0006	2.152	0.0002	0.0008
Filip1	ENSMUSG00000034898	filamin A interacting protein 1	1.825	0.0000	0.0000	1.875	0.0000	0.0000
Fip1l1	ENSMUSG00000029227	FIP1 like 1 (S. cerevisiae)	1.797	0.0000	0.0000	1.676	0.0000	0.0000
Firre	ENSMUSG00000085396	functional intergenic repeating RNA element	1.799	0.0125	0.0291	1.745	0.0180	0.0435
Fkbp1a	ENSMUSG00000032966	FK506 binding protein 1a	2.007	0.0000	0.0000	1.865	0.0000	0.0000
Fkbp1b	ENSMUSG00000020635	FK506 binding protein 1b	2.444	0.0060	0.0154	4.826	0.0000	0.0000
Fkbp2	ENSMUSG00000056629	FK506 binding protein 2	4.010	0.0000	0.0000	4.473	0.0000	0.0000
Fkbp8	ENSMUSG00000019428	FK506 binding protein 8	1.530	0.0000	0.0000	1.949	0.0000	0.0000
Fkbp9	ENSMUSG00000029781	FK506 binding protein 9	1.843	0.0000	0.0000	1.815	0.0000	0.0000
Fkbpl	ENSMUSG00000033739	FK506 binding protein-like	2.276	0.0000	0.0000	2.598	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Flvcr1	ENSMUSG00000066595	feline leukemia virus subgroup C cellular receptor 1	1.663	0.0000	0.0000	1.631	0.0000	0.0000
Fmnl2	ENSMUSG00000036053	formin-like 2	1.677	0.0000	0.0000	1.653	0.0000	0.0000
Fn3krp	ENSMUSG00000039253	fructosamine 3 kinase related protein	1.556	0.0001	0.0002	1.721	0.0000	0.0000
Fnbp1l	ENSMUSG00000039735	formin binding protein 1-like	1.985	0.0000	0.0000	1.694	0.0000	0.0000
Fndc4	ENSMUSG00000038552	fibronectin type III domain containing 4	2.410	0.0000	0.0000	2.205	0.0000	0.0001
Fnta	ENSMUSG00000015994	farnesyltransferase, CAAX box, alpha	2.346	0.0000	0.0000	2.182	0.0000	0.0000
Foxc1	ENSMUSG00000050295	forkhead box C1	3.647	0.0000	0.0000	3.916	0.0000	0.0000
Foxd1	ENSMUSG00000078302	forkhead box D1	8.112	0.0135	0.0311	4.643	0.0465	0.0975
Foxd2	ENSMUSG00000055210	forkhead box D2	4.276	0.0000	0.0000	3.548	0.0000	0.0000
Foxd3	ENSMUSG00000067261	forkhead box D3	5.484	0.0000	0.0000	4.341	0.0000	0.0002
Foxf1	ENSMUSG00000042812	forkhead box F1	3.655	0.0002	0.0008	2.310	0.0122	0.0312
Foxk2	ENSMUSG00000039275	forkhead box K2	1.639	0.0000	0.0000	1.509	0.0000	0.0000
Foxo4	ENSMUSG00000042903	forkhead box O4	1.653	0.0000	0.0000	1.628	0.0000	0.0000
Foxo6	ENSMUSG00000052135	forkhead box O6	5.344	0.0000	0.0000	4.380	0.0000	0.0001
Foxp4	ENSMUSG00000023991	forkhead box P4	2.831	0.0000	0.0000	2.362	0.0000	0.0000
Foxq1	ENSMUSG00000038415	forkhead box Q1	3.873	0.0194	0.0429	5.715	0.0019	0.0062
Fra10ac1	ENSMUSG00000054237	FRA10AC1 homolog (human)	3.077	0.0000	0.0000	2.464	0.0000	0.0000
Frat1	ENSMUSG00000067199	frequently rearranged in advanced T cell lymphomas	2.698	0.0000	0.0000	2.631	0.0000	0.0000
Frat2	ENSMUSG00000047604	frequently rearranged in advanced T cell lymphomas 2	6.004	0.0000	0.0000	4.685	0.0000	0.0000
Frg1	ENSMUSG00000031590	FSHD region gene 1	1.812	0.0000	0.0000	1.684	0.0000	0.0000
Ftsj3	ENSMUSG00000020706	FtsJ RNA methyltransferase homolog 3 (E. coli)	2.051	0.0000	0.0000	2.141	0.0000	0.0000
Fubp1	ENSMUSG00000028034	far upstream element (FUSE) binding protein 1	2.407	0.0000	0.0000	2.185	0.0000	0.0000
Fubp3	ENSMUSG00000026843	far upstream element (FUSE) binding protein 3	2.522	0.0000	0.0000	2.411	0.0000	0.0000
Fv1	ENSMUSG00000070583	Friend virus susceptibility 1	2.909	0.0000	0.0000	2.901	0.0000	0.0000
Fxr2	ENSMUSG00000018765	FMR1 autosomal homolog 2	1.848	0.0000	0.0000	2.130	0.0000	0.0000
Fyb	ENSMUSG00000022148	FYN binding protein	1.557	0.0155	0.0351	2.252	0.0000	0.0001
Fyn	ENSMUSG00000019843	Fyn proto-oncogene	3.192	0.0000	0.0000	3.018	0.0000	0.0000
Fzd1	ENSMUSG00000044674	frizzled class receptor 1	2.615	0.0000	0.0000	2.176	0.0000	0.0001
Fzd2	ENSMUSG00000050288	frizzled class receptor 2	1.980	0.0001	0.0004	2.400	0.0000	0.0000
Fzd6	ENSMUSG00000022297	frizzled class receptor 6	2.000	0.0000	0.0000	1.871	0.0000	0.0000
Fzd7	ENSMUSG00000041075	frizzled class receptor 7	1.864	0.0000	0.0000	1.753	0.0000	0.0001
Fzd8	ENSMUSG00000036904	frizzled class receptor 8	1.692	0.0009	0.0029	1.641	0.0018	0.0058
Gadd45a	ENSMUSG00000036390	growth arrest and DNA-damage-inducible 45 alpha	2.166	0.0000	0.0000	2.312	0.0000	0.0000
Galnt1	ENSMUSG00000000420	polypeptide N-acetylgalactosaminyltransferase 1	1.980	0.0000	0.0000	1.813	0.0000	0.0000
Galnt2	ENSMUSG00000089704	polypeptide N-acetylgalactosaminyltransferase 2	108.290	0.0000	0.0000	36.401	0.0000	0.0000
Gar1	ENSMUSG00000028010	GAR1 ribonucleoprotein	2.015	0.0000	0.0000	1.867	0.0000	0.0000
Gas1	ENSMUSG00000052957	growth arrest specific 1	2.798	0.0000	0.0000	2.155	0.0001	0.0002
Gas2l1	ENSMUSG00000034201	growth arrest-specific 2 like 1	2.109	0.0002	0.0007	1.615	0.0175	0.0425
Gas5	ENSMUSG00000053332	growth arrest specific 5	3.296	0.0000	0.0000	2.694	0.0000	0.0000
Gas8	ENSMUSG00000040220	growth arrest specific 8	2.196	0.0000	0.0000	3.059	0.0000	0.0000
Gata6	ENSMUSG00000005836	GATA binding protein 6	1.886	0.0000	0.0000	1.664	0.0002	0.0007
Gatad1	ENSMUSG00000007415	GATA zinc finger domain containing 1	2.069	0.0000	0.0000	1.909	0.0000	0.0000
Gatad2b	ENSMUSG00000042390	GATA zinc finger domain containing 2B	1.594	0.0004	0.0013	1.532	0.0012	0.0041

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gbp3	ENSMUSG00000028268	guanylate binding protein 3	1.793	0.0061	0.0154	2.015	0.0010	0.0034
Gcfc2	ENSMUSG00000035125	GC-rich sequence DNA binding factor 2	1.879	0.0004	0.0013	1.539	0.0180	0.0437
Gch1	ENSMUSG00000037580	GTP cyclohydrolase 1	2.191	0.0000	0.0000	1.965	0.0000	0.0000
Gclc	ENSMUSG00000032350	glutamate-cysteine ligase, catalytic subunit	1.784	0.0003	0.0009	1.840	0.0001	0.0005
Gcsh	ENSMUSG00000034424	glycine cleavage system protein H (aminomethyl carrier)	1.779	0.0000	0.0000	1.865	0.0000	0.0000
Gdf11	ENSMUSG00000025352	growth differentiation factor 11	1.599	0.0056	0.0143	2.161	0.0000	0.0000
Gdf6	ENSMUSG00000051279	growth differentiation factor 6	2.246	0.0009	0.0027	2.388	0.0006	0.0022
Gemin2	ENSMUSG00000060121	gem nuclear organelle associated protein 2	1.716	0.0000	0.0000	1.628	0.0000	0.0000
Gemin6	ENSMUSG00000055760	gem nuclear organelle associated protein 6	1.536	0.0004	0.0015	1.600	0.0002	0.0007
Gfra2	ENSMUSG00000022103	glial cell line derived neurotrophic factor family receptor alpha 2	1.550	0.0158	0.0358	2.128	0.0000	0.0002
Ggct	ENSMUSG00000002797	gamma-glutamyl cyclotransferase	2.098	0.0000	0.0000	2.078	0.0000	0.0000
Gid4	ENSMUSG00000018415	GID complex subunit 4, VID24 homolog	1.696	0.0000	0.0000	1.582	0.0000	0.0000
Gigyf2	ENSMUSG00000048000	GRB10 interacting GYF protein 2	1.627	0.0000	0.0000	1.663	0.0000	0.0000
Gimap4	ENSMUSG00000054435	GTPase, IMAP family member 4	2.326	0.0000	0.0000	1.956	0.0000	0.0001
Gimap8	ENSMUSG00000064262	GTPase, IMAP family member 8	1.677	0.0000	0.0000	1.502	0.0000	0.0001
Ginm1	ENSMUSG00000040006	glycoprotein integral membrane 1	2.147	0.0000	0.0000	1.676	0.0000	0.0000
Gins2	ENSMUSG00000031821	GINS complex subunit 2 (Psf2 homolog)	1.593	0.0261	0.0553	1.574	0.0327	0.0724
Gja1	ENSMUSG00000050953	gap junction protein, alpha 1	1.728	0.0000	0.0000	1.606	0.0000	0.0000
Gjc1	ENSMUSG00000034520	gap junction protein, gamma 1	1.809	0.0000	0.0000	1.898	0.0000	0.0000
Gkap1	ENSMUSG00000021552	G kinase anchoring protein 1	2.326	0.0000	0.0000	2.408	0.0000	0.0000
Glcci1	ENSMUSG00000029638	glucocorticoid induced transcript 1	13.434	0.0000	0.0000	11.828	0.0000	0.0000
Glrx5	ENSMUSG00000021102	glutaredoxin 5	3.953	0.0000	0.0000	4.300	0.0000	0.0000
Gm10052	ENSMUSG00000058922	predicted pseudogene 10052	16.128	0.0000	0.0000	19.262	0.0000	0.0000
Gm10060	ENSMUSG00000110669	predicted gene 10060	2.871	0.0001	0.0004	2.977	0.0002	0.0010
Gm10086	ENSMUSG00000060730	predicted pseudogene 10086	10.022	0.0000	0.0000	5.276	0.0001	0.0003
Gm10095	ENSMUSG00000113555	predicted gene 10095	1.892	0.0001	0.0004	1.598	0.0040	0.0118
Gm10125	ENSMUSG00000063087	predicted gene 10125	2.030	0.0042	0.0111	1.795	0.0261	0.0601
Gm10209	ENSMUSG00000108080	predicted gene 10209	6.902	0.0000	0.0000	4.461	0.0001	0.0003
Gm10222	ENSMUSG00000067736	predicted gene 10222	2.232	0.0066	0.0167	2.570	0.0014	0.0046
Gm10232	ENSMUSG00000068141	predicted pseudogene 10232	5.991	0.0000	0.0000	3.111	0.0001	0.0004
Gm10244	ENSMUSG00000068601	predicted gene 10244	6.414	0.0000	0.0000	6.824	0.0000	0.0001
Gm10293	ENSMUSG00000070490	predicted pseudogene 10293	1.537	0.0179	0.0398	2.027	0.0001	0.0006
Gm10371	ENSMUSG00000072589	predicted gene 10371	16.411	0.0000	0.0000	10.062	0.0000	0.0001
Gm10524	ENSMUSG00000097141	predicted gene 10524	2.319	0.0000	0.0000	2.362	0.0000	0.0000
Gm10575	ENSMUSG00000073787	predicted gene 10575	1.789	0.0006	0.0018	1.682	0.0028	0.0087
Gm10638	ENSMUSG00000074178	predicted gene 10638	11.484	0.0000	0.0000	9.048	0.0000	0.0000
Gm10642	ENSMUSG00000074213	predicted gene 10642	6.780	0.0000	0.0000	3.641	0.0004	0.0015
Gm10705	ENSMUSG00000074506	predicted gene 10705	6.025	0.0000	0.0000	7.705	0.0000	0.0000
Gm10762	ENSMUSG00000074807	predicted gene 10762	2.782	0.0000	0.0000	3.142	0.0000	0.0000
Gm10925	ENSMUSG00000100862	predicted gene 10925	33.630	0.0000	0.0000	19.369	0.0000	0.0000
Gm11175	ENSMUSG00000080058	predicted gene 11175	15.629	0.0000	0.0000	14.925	0.0000	0.0000
Gm11478	ENSMUSG00000083992	predicted gene 11478	3.354	0.0000	0.0000	2.506	0.0000	0.0000
Gm11560	ENSMUSG00000086688	predicted gene 11560	3.088	0.0000	0.0000	4.010	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm11642	ENSMUSG00000086794	predicted gene 11642	3.004	0.0000	0.0000	2.889	0.0000	0.0000
Gm11696	ENSMUSG00000056687	predicted gene 11696	2.728	0.0000	0.0000	2.714	0.0000	0.0000
Gm11748	ENSMUSG00000087036	predicted gene 11748	169.340	0.0000	0.0000	77.664	0.0000	0.0000
Gm11940	ENSMUSG00000087692	predicted gene 11940	1.708	0.0059	0.0151	1.754	0.0030	0.0091
Gm11973	ENSMUSG00000086839	predicted gene 11973	5.426	0.0000	0.0002	4.377	0.0004	0.0016
Gm12129	ENSMUSG00000082587	predicted gene 12129	8.596	0.0026	0.0071	64.561	0.0000	0.0001
Gm12138	ENSMUSG00000082087	predicted gene 12138	9.402	0.0000	0.0000	6.830	0.0000	0.0000
Gm12184	ENSMUSG00000078154	predicted gene 12184	2.040	0.0000	0.0000	2.878	0.0000	0.0000
Gm12191	ENSMUSG00000083061	predicted gene 12191	5.492	0.0000	0.0000	2.999	0.0001	0.0005
Gm12312	ENSMUSG00000082145	predicted gene 12312	2.290	0.0000	0.0001	2.707	0.0000	0.0000
Gm12444	ENSMUSG00000082194	predicted gene 12444	6.299	0.0116	0.0274	5.064	0.0288	0.0651
Gm12473	ENSMUSG00000086043	predicted gene 12473	38.870	0.0044	0.0116	23.508	0.0155	0.0385
Gm12693	ENSMUSG00000083179	predicted gene 12693	8.071	0.0000	0.0000	13.481	0.0000	0.0000
Gm12844	ENSMUSG00000084260	predicted gene 12844	2.576	0.0196	0.0433	2.372	0.0314	0.0701
Gm12905	ENSMUSG00000085875	predicted gene 12905	3.434	0.0004	0.0013	3.509	0.0004	0.0013
Gm12966	ENSMUSG00000070729	predicted gene 12966	4.794	0.0000	0.0000	4.610	0.0000	0.0000
Gm12992	ENSMUSG00000085667	predicted gene 12992	2.367	0.0000	0.0000	3.191	0.0000	0.0000
Gm12999	ENSMUSG00000087352	predicted gene 12999	2.200	0.0024	0.0067	2.504	0.0002	0.0010
Gm13161	ENSMUSG00000082248	predicted gene 13161	25.616	0.0000	0.0000	29.590	0.0000	0.0000
Gm13162	ENSMUSG00000082779	predicted pseudogene 13162	10.596	0.0268	0.0566	70.205	0.0002	0.0007
Gm13243	ENSMUSG00000094417	predicted gene 13243	9.605	0.0002	0.0006	66.554	0.0000	0.0000
Gm13339	ENSMUSG00000082884	predicted gene 13339	2.884	0.0001	0.0004	3.357	0.0000	0.0001
Gm13341	ENSMUSG00000083863	predicted gene 13341	2.114	0.0000	0.0000	1.762	0.0001	0.0006
Gm13369	ENSMUSG00000083796	predicted gene 13369	17.939	0.0049	0.0127	7.424	0.0356	0.0779
Gm13430	ENSMUSG00000083101	predicted gene 13430	29.264	0.0196	0.0432	41.024	0.0100	0.0262
Gm13453	ENSMUSG00000083240	predicted gene 13453	3.128	0.0000	0.0000	4.070	0.0000	0.0000
Gm13577	ENSMUSG00000082127	predicted gene 13577	8.188	0.0000	0.0000	10.708	0.0000	0.0000
Gm13594	ENSMUSG00000086881	predicted gene 13594	14.909	0.0000	0.0000	17.730	0.0000	0.0000
Gm13601	ENSMUSG00000087467	predicted gene 13601	15.796	0.0002	0.0008	12.916	0.0131	0.0332
Gm13712	ENSMUSG00000082534	predicted gene 13712	7.147	0.0000	0.0000	3.938	0.0000	0.0000
Gm13736	ENSMUSG00000082908	predicted gene 13736	1.523	0.0000	0.0000	1.536	0.0000	0.0000
Gm13889	ENSMUSG00000087006	predicted gene 13889	3.173	0.0000	0.0000	2.268	0.0001	0.0003
Gm14057	ENSMUSG00000089662	predicted gene 14057	1.932	0.0113	0.0268	1.988	0.0068	0.0188
Gm14221	ENSMUSG00000078956	predicted gene 14221	3.165	0.0001	0.0003	4.319	0.0000	0.0000
Gm14398	ENSMUSG00000083993	predicted gene 14398	9.793	0.0000	0.0001	6.161	0.0001	0.0005
Gm14964	ENSMUSG00000052188	predicted gene 14964	2.257	0.0001	0.0002	2.532	0.0000	0.0000
Gm15163	ENSMUSG00000085711	predicted gene 15163	3.976	0.0000	0.0000	3.763	0.0000	0.0000
Gm15270	ENSMUSG00000087400	predicted gene 15270	1.652	0.0027	0.0074	1.820	0.0002	0.0009
Gm15285	ENSMUSG00000081277	predicted gene 15285	4.734	0.0000	0.0000	4.189	0.0000	0.0000
Gm15327	ENSMUSG00000085204	predicted gene 15327	3.512	0.0054	0.0140	3.063	0.0147	0.0367
Gm15387	ENSMUSG00000082585	predicted gene 15387	5.600	0.0372	0.0751	5.041	0.0271	0.0620
Gm15441	ENSMUSG00000074398	predicted gene 15441	6.200	0.0000	0.0000	4.381	0.0000	0.0000
Gm15500	ENSMUSG00000086583	predicted pseudogene 15500	1.581	0.0144	0.0329	1.855	0.0010	0.0034

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm15542	ENSMUSG00000083396	predicted gene 15542	3.790	0.0000	0.0001	5.530	0.0000	0.0000
Gm15609	ENSMUSG00000086602	predicted gene 15609	9.153	0.0000	0.0000	18.971	0.0000	0.0000
Gm15610	ENSMUSG00000078183	predicted gene 15610	1.767	0.0000	0.0002	2.176	0.0000	0.0000
Gm15706	ENSMUSG00000086013	predicted gene 15706	1.929	0.0106	0.0254	2.201	0.0029	0.0089
Gm15801	ENSMUSG00000096592	predicted gene 15801	16.999	0.0000	0.0000	27.027	0.0000	0.0000
Gm15853	ENSMUSG00000103400	predicted gene 15853	3.204	0.0000	0.0000	1.858	0.0099	0.0262
Gm15860	ENSMUSG00000087336	predicted gene 15860	4.691	0.0000	0.0000	3.038	0.0000	0.0001
Gm15906	ENSMUSG00000087416	predicted gene 15906	79.916	0.0000	0.0000	139.414	0.0000	0.0000
Gm15952	ENSMUSG00000085655	predicted gene 15952	12.740	0.0000	0.0000	6.338	0.0004	0.0015
Gm16089	ENSMUSG00000081228	predicted gene 16089	2.094	0.0020	0.0057	3.548	0.0000	0.0000
Gm16124	ENSMUSG00000086914	predicted gene 16124	3.339	0.0000	0.0000	3.589	0.0000	0.0000
Gm16136	ENSMUSG00000089804	predicted gene 16136	2.169	0.0013	0.0040	2.362	0.0006	0.0021
Gm16140	ENSMUSG00000084085	predicted gene 16140	2.693	0.0250	0.0533	3.023	0.0138	0.0347
Gm16409	ENSMUSG00000075581	predicted gene 16409	5.594	0.0019	0.0056	10.399	0.0004	0.0015
Gm16437	ENSMUSG00000024761	predicted pseudogene 16437	2.198	0.0065	0.0164	2.570	0.0009	0.0032
Gm16701	ENSMUSG00000097823	predicted gene, 16701	2.181	0.0059	0.0150	2.563	0.0013	0.0043
Gm16861	ENSMUSG00000097397	predicted gene, 16861	3.673	0.0039	0.0105	7.249	0.0004	0.0017
Gm16933	ENSMUSG00000086289	predicted gene, 16933	53.949	0.0007	0.0022	17.416	0.0055	0.0156
Gm17082	ENSMUSG00000090674	predicted gene 17082	30.775	0.0021	0.0059	8.816	0.0212	0.0501
Gm17092	ENSMUSG00000091623	predicted gene 17092	12.983	0.0000	0.0000	9.212	0.0000	0.0000
Gm17110	ENSMUSG00000090779	predicted gene 17110	25.660	0.0000	0.0000	21.889	0.0000	0.0000
Gm17251	ENSMUSG00000090952	predicted gene, 17251	2.675	0.0000	0.0000	2.320	0.0001	0.0004
Gm17349	ENSMUSG00000091604	predicted gene, 17349	14.749	0.0000	0.0002	4.630	0.0192	0.0462
Gm17382	ENSMUSG00000078838	predicted gene, 17382	4.519	0.0022	0.0062	2.487	0.0389	0.0841
Gm17428	ENSMUSG00000090889	predicted gene, 17428	5.052	0.0000	0.0000	5.256	0.0000	0.0000
Gm17606	ENSMUSG00000091306	predicted gene, 17606	27.424	0.0008	0.0024	7.852	0.0429	0.0912
Gm17661	ENSMUSG00000091037	predicted gene, 17661	25.268	0.0000	0.0000	20.880	0.0000	0.0000
Gm18860	ENSMUSG00000110569	predicted gene, 18860	1.838	0.0000	0.0001	1.870	0.0000	0.0000
Gm18911	ENSMUSG00000116438	predicted gene, 18911	4.956	0.0012	0.0037	21.572	0.0000	0.0000
Gm19221	ENSMUSG00000113491	predicted gene, 19221	13.120	0.0018	0.0053	5.864	0.0143	0.0360
Gm19426	ENSMUSG00000097187	predicted gene, 19426	1.883	0.0031	0.0085	1.686	0.0137	0.0345
Gm2000	ENSMUSG00000078193	predicted gene 2000	1.553	0.0005	0.0016	1.797	0.0000	0.0000
Gm20033	ENSMUSG00000097640	predicted gene, 20033	8.475	0.0000	0.0000	5.641	0.0000	0.0000
Gm20091	ENSMUSG00000094249	predicted gene, 20091	4.548	0.0054	0.0139	6.381	0.0010	0.0035
Gm20186	ENSMUSG00000106874	predicted gene, 20186	2.711	0.0003	0.0010	2.714	0.0003	0.0011
Gm20300	ENSMUSG00000111080	predicted gene, 20300	1.589	0.0000	0.0000	1.616	0.0000	0.0000
Gm20379	ENSMUSG00000100622	predicted gene, 20379	17.264	0.0014	0.0041	34.131	0.0003	0.0013
Gm20400	ENSMUSG00000092500	predicted gene 20400	6.000	0.0041	0.0110	5.807	0.0057	0.0161
Gm20421	ENSMUSG00000092483	predicted gene 20421	7.029	0.0001	0.0003	6.508	0.0003	0.0013
Gm20522	ENSMUSG00000092241	predicted gene 20522	2.191	0.0018	0.0053	2.183	0.0020	0.0064
Gm20544	ENSMUSG00000092569	predicted gene 20544	3.162	0.0000	0.0000	2.651	0.0000	0.0000
Gm2058	ENSMUSG00000074903	predicted gene 2058	3.531	0.0000	0.0000	3.027	0.0000	0.0000
Gm20721	ENSMUSG00000090625	predicted gene, 20721	20.669	0.0000	0.0000	22.563	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm21399	ENSMUSG00000094530	predicted gene, 21399	2.183	0.0000	0.0001	2.811	0.0000	0.0000
Gm21596	ENSMUSG00000096006	predicted gene, 21596	10.607	0.0000	0.0000	9.080	0.0000	0.0000
Gm21926	ENSMUSG00000116995	predicted gene, 21926	1.815	0.0000	0.0001	1.847	0.0000	0.0001
Gm22009	ENSMUSG00000089417	predicted gene, 22009	3.306	0.0000	0.0000	2.942	0.0000	0.0000
Gm22953	ENSMUSG00000080374	predicted gene, 22953	3.584	0.0111	0.0264	3.898	0.0129	0.0329
Gm2296	ENSMUSG00000118653	predicted gene 2296	4.175	0.0001	0.0004	13.855	0.0000	0.0000
Gm2308	ENSMUSG00000092257	predicted gene 2308	1.780	0.0052	0.0136	2.055	0.0006	0.0020
Gm23119	ENSMUSG00000089235	predicted gene, 23119	8.743	0.0003	0.0011	3.218	0.0179	0.0434
Gm24045	ENSMUSG00000065047	predicted gene, 24045	4.761	0.0188	0.0416	5.279	0.0171	0.0418
Gm26558	ENSMUSG00000097025	predicted gene, 26558	8.242	0.0008	0.0025	6.810	0.0027	0.0083
Gm26631	ENSMUSG00000097445	predicted gene, 26631	18.006	0.0000	0.0000	12.095	0.0006	0.0023
Gm26881	ENSMUSG00000096974	predicted gene, 26881	1.828	0.0000	0.0000	1.757	0.0000	0.0001
Gm26910	ENSMUSG00000097835	predicted gene, 26910	2.963	0.0000	0.0001	2.509	0.0002	0.0006
Gm28035	ENSMUSG00000099041	predicted gene, 28035	14.137	0.0074	0.0184	12.667	0.0045	0.0131
Gm2830	ENSMUSG00000086567	predicted gene 2830	3.053	0.0000	0.0000	2.695	0.0000	0.0000
Gm28424	ENSMUSG00000101037	predicted gene 28424	2.518	0.0442	0.0870	2.474	0.0446	0.0939
Gm28437	ENSMUSG00000101111	predicted gene 28437	5.104	0.0000	0.0000	6.568	0.0000	0.0000
Gm28439	ENSMUSG00000100131	predicted gene 28439	6.353	0.0000	0.0000	4.453	0.0000	0.0000
Gm28529	ENSMUSG00000101320	predicted gene 28529	5.973	0.0000	0.0000	3.711	0.0000	0.0000
Gm28661	ENSMUSG00000102070	predicted gene 28661	3.037	0.0000	0.0000	2.867	0.0000	0.0000
Gm29216	ENSMUSG00000101249	predicted gene 29216	21.481	0.0000	0.0000	16.994	0.0000	0.0000
Gm29246	ENSMUSG00000102062	predicted gene 29246	5.342	0.0000	0.0000	4.627	0.0000	0.0002
Gm29346	ENSMUSG00000101386	predicted gene 29346	3.317	0.0034	0.0091	3.179	0.0045	0.0131
Gm2962	ENSMUSG00000089838	predicted pseudogene 2962	6.306	0.0000	0.0000	4.732	0.0000	0.0000
Gm29629	ENSMUSG00000099874	predicted gene 29629	76.072	0.0000	0.0000	31.965	0.0000	0.0000
Gm31166	ENSMUSG00000109695	predicted gene, 31166	4.855	0.0000	0.0000	4.335	0.0000	0.0000
Gm32282	ENSMUSG00000117648	predicted gene, 32282	2.690	0.0001	0.0005	2.606	0.0003	0.0010
Gm32699	ENSMUSG00000113528	predicted gene, 32699	2.844	0.0002	0.0006	1.828	0.0299	0.0672
Gm34220	ENSMUSG00000114045	predicted gene, 34220	7.154	0.0000	0.0000	6.073	0.0000	0.0000
Gm35558	ENSMUSG00000113662	predicted gene, 35558	2.950	0.0000	0.0000	2.494	0.0001	0.0006
Gm3625	ENSMUSG00000118449	predicted gene 3625	1.762	0.0000	0.0001	2.017	0.0000	0.0000
Gm37116	ENSMUSG00000103574	predicted gene, 37116	4.033	0.0000	0.0000	4.471	0.0000	0.0000
Gm37123	ENSMUSG00000103039	predicted gene, 37123	2.699	0.0012	0.0037	2.518	0.0029	0.0090
Gm3716	ENSMUSG00000105402	predicted gene 3716	1.664	0.0368	0.0742	1.732	0.0244	0.0566
Gm37194	ENSMUSG00000102189	predicted gene, 37194	46.655	0.0000	0.0000	47.504	0.0000	0.0000
Gm37201	ENSMUSG00000103658	predicted gene, 37201	5.417	0.0000	0.0000	7.264	0.0000	0.0000
Gm37376	ENSMUSG00000102349	predicted gene, 37376	7.111	0.0227	0.0490	8.898	0.0264	0.0606
Gm37563	ENSMUSG00000104040	predicted gene, 37563	5.969	0.0508	0.0978	16.950	0.0114	0.0294
Gm3788	ENSMUSG00000094392	predicted gene 3788	39.980	0.0003	0.0010	13.231	0.0005	0.0020
Gm39302	ENSMUSG00000111172	predicted gene, 39302	3.415	0.0004	0.0014	3.733	0.0000	0.0002
Gm40466	ENSMUSG00000110649	predicted gene, 40466	1.552	0.0362	0.0733	1.877	0.0030	0.0093
Gm4076	ENSMUSG00000096449	predicted gene 4076	2.002	0.0000	0.0001	2.056	0.0000	0.0001
Gm41381	ENSMUSG00000118456	predicted gene, 41381	7.068	0.0000	0.0000	3.607	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm41505	ENSMUSG00000116641	predicted gene, 41505	2.212	0.0176	0.0392	3.937	0.0001	0.0003
Gm41760	ENSMUSG00000117992	predicted gene, 41760	2.241	0.0000	0.0000	2.381	0.0000	0.0000
Gm42462	ENSMUSG00000104728	predicted gene 42462	5.047	0.0021	0.0061	4.131	0.0084	0.0226
Gm42517	ENSMUSG00000105867	predicted gene 42517	4.908	0.0000	0.0000	3.713	0.0000	0.0000
Gm42547	ENSMUSG00000106990	predicted gene 42547	2.019	0.0000	0.0001	1.582	0.0056	0.0159
Gm42596	ENSMUSG00000105482	predicted gene 42596	30.511	0.0000	0.0001	26.542	0.0002	0.0009
Gm42922	ENSMUSG00000104605	predicted gene 42922	7.141	0.0000	0.0001	4.213	0.0007	0.0027
Gm42984	ENSMUSG00000104784	predicted gene 42984	9.296	0.0000	0.0000	6.999	0.0000	0.0000
Gm43034	ENSMUSG00000106662	predicted gene 43034	1.843	0.0013	0.0039	1.549	0.0234	0.0546
Gm43075	ENSMUSG00000105004	predicted gene 43075	10.020	0.0000	0.0000	2.978	0.0158	0.0392
Gm43196	ENSMUSG00000107017	predicted gene 43196	2.433	0.0299	0.0622	3.191	0.0052	0.0149
Gm43361	ENSMUSG00000106375	predicted gene 43361	17.021	0.0000	0.0000	4.129	0.0011	0.0039
Gm4366	ENSMUSG00000107383	predicted gene 4366	2.433	0.0000	0.0000	2.215	0.0000	0.0000
Gm44136	ENSMUSG00000107524	predicted gene, 44136	4.134	0.0398	0.0796	5.330	0.0192	0.0462
Gm44250	ENSMUSG00000107881	predicted gene, 44250	1.532	0.0000	0.0000	1.578	0.0000	0.0000
Gm44423	ENSMUSG00000108064	predicted gene, 44423	3.592	0.0036	0.0097	2.942	0.0173	0.0421
Gm44731	ENSMUSG00000108190	predicted gene 44731	4.211	0.0010	0.0030	6.447	0.0000	0.0002
Gm44732	ENSMUSG00000108934	predicted gene 44732	23.224	0.0000	0.0000	17.750	0.0000	0.0000
Gm44899	ENSMUSG00000109008	predicted gene 44899	4.612	0.0000	0.0000	4.202	0.0000	0.0000
Gm4524	ENSMUSG00000090257	predicted gene 4524	3.096	0.0001	0.0002	2.415	0.0023	0.0072
Gm45246	ENSMUSG00000109645	predicted gene 45246	4.575	0.0000	0.0000	2.904	0.0001	0.0003
Gm45250	ENSMUSG00000110317	predicted gene 45250	2.607	0.0026	0.0071	2.583	0.0027	0.0084
Gm45371	ENSMUSG00000109954	predicted gene 45371	13.887	0.0105	0.0252	21.774	0.0095	0.0252
Gm45380	ENSMUSG00000110360	predicted gene 45380	1.887	0.0010	0.0031	1.973	0.0006	0.0021
Gm45494	ENSMUSG00000110161	predicted gene 45494	3.468	0.0000	0.0000	2.803	0.0000	0.0000
Gm4617	ENSMUSG00000096544	predicted pseudogene 4617	6.130	0.0000	0.0000	4.446	0.0000	0.0000
Gm4673	ENSMUSG00000097750	predicted gene 4673	2.163	0.0010	0.0030	3.467	0.0000	0.0000
Gm47155	ENSMUSG00000114019	predicted gene, 47155	3.508	0.0000	0.0000	2.424	0.0000	0.0000
Gm47205	ENSMUSG00000111312	predicted gene, 47205	5.476	0.0018	0.0053	8.142	0.0013	0.0042
Gm4734	ENSMUSG00000106208	predicted gene 4734	4.841	0.0363	0.0735	9.000	0.0058	0.0164
Gm4754	ENSMUSG00000106895	predicted gene 4754	6.436	0.0027	0.0074	3.629	0.0313	0.0699
Gm47766	ENSMUSG00000112336	predicted gene, 47766	140.587	0.0000	0.0000	19.770	0.0000	0.0000
Gm4811	ENSMUSG00000113263	predicted gene 4811	1.822	0.0215	0.0469	2.297	0.0016	0.0051
Gm48226	ENSMUSG00000112302	predicted gene, 48226	2.120	0.0000	0.0000	2.073	0.0000	0.0000
Gm4835	ENSMUSG00000043223	predicted pseudogene 4835	7.835	0.0000	0.0000	4.914	0.0001	0.0002
Gm4853	ENSMUSG00000081473	predicted pseudogene 4853	1.901	0.0310	0.0641	2.609	0.0009	0.0032
Gm48604	ENSMUSG00000111291	predicted gene, 48604	2.759	0.0000	0.0000	1.543	0.0107	0.0279
Gm48623	ENSMUSG00000112941	predicted gene, 48623	3.022	0.0112	0.0264	2.548	0.0369	0.0804
Gm4864	ENSMUSG00000112003	predicted gene 4864	1.909	0.0069	0.0172	1.928	0.0076	0.0207
Gm48667	ENSMUSG00000113964	predicted gene, 48667	12.841	0.0001	0.0002	66.637	0.0000	0.0001
Gm48705	ENSMUSG00000114834	predicted gene, 48705	44.248	0.0005	0.0015	15.316	0.0130	0.0329
Gm48768	ENSMUSG00000112346	predicted gene, 48768	2.620	0.0000	0.0000	2.404	0.0000	0.0001
Gm48933	ENSMUSG00000115003	predicted gene, 48933	13.294	0.0000	0.0001	12.583	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm4895	ENSMUSG00000044268	predicted gene 4895	2.987	0.0004	0.0014	3.423	0.0002	0.0009
Gm49041	ENSMUSG00000115026	predicted gene, 49041	2.039	0.0029	0.0081	1.936	0.0074	0.0202
Gm49130	ENSMUSG00000115234	predicted gene, 49130	10.337	0.0000	0.0000	7.674	0.0000	0.0000
Gm49207	ENSMUSG00000115497	predicted gene, 49207	5.158	0.0168	0.0378	6.477	0.0130	0.0330
Gm49330	ENSMUSG00000113234	predicted gene, 49330	64.478	0.0001	0.0005	10.568	0.0077	0.0210
Gm49492	ENSMUSG00000116180	predicted gene, 49492	1.774	0.0000	0.0000	1.737	0.0000	0.0000
Gm49540	ENSMUSG00000116272	predicted gene, 49540	3.560	0.0000	0.0001	3.219	0.0001	0.0005
Gm49544	ENSMUSG00000116262	predicted gene, 49544	36.236	0.0000	0.0000	40.185	0.0000	0.0000
Gm49741	ENSMUSG00000116571	predicted gene, 49741	7.085	0.0000	0.0000	4.563	0.0000	0.0000
Gm49864	ENSMUSG00000117255	predicted gene, 49864	6.155	0.0000	0.0001	18.030	0.0000	0.0000
Gm49883	ENSMUSG00000117113	predicted gene, 49883	1.840	0.0168	0.0378	2.312	0.0009	0.0031
Gm49894	ENSMUSG00000117069	predicted gene, 49894	2.836	0.0391	0.0784	7.495	0.0010	0.0034
Gm50069	ENSMUSG00000117634	predicted gene, 50069	3.131	0.0001	0.0003	2.508	0.0011	0.0037
Gm50144	ENSMUSG00000118184	predicted gene, 50144	2.806	0.0000	0.0001	3.534	0.0000	0.0000
Gm50163	ENSMUSG00000118030	predicted gene, 50163	5.794	0.0184	0.0410	6.528	0.0306	0.0685
Gm50240	ENSMUSG00000117725	predicted gene, 50240	1.600	0.0009	0.0027	2.031	0.0000	0.0000
Gm50251	ENSMUSG00000117839	predicted gene, 50251	8.871	0.0001	0.0003	3.824	0.0168	0.0412
Gm50253	ENSMUSG00000117819	predicted gene, 50253	4.923	0.0000	0.0000	5.430	0.0000	0.0000
Gm50464	ENSMUSG00000118487	predicted gene, 50464	3.223	0.0486	0.0943	4.666	0.0148	0.0370
Gm5216	ENSMUSG00000116398	predicted gene 5216	30.621	0.0000	0.0000	30.594	0.0000	0.0000
Gm527	ENSMUSG00000047227	predicted gene 527	2.038	0.0000	0.0000	2.271	0.0000	0.0000
Gm53012	ENSMUSG00000118504	predicted gene, 53012	2.304	0.0001	0.0004	2.266	0.0002	0.0007
Gm53023	ENSMUSG00000118572	predicted gene, 53023	17.987	0.0000	0.0000	10.307	0.0000	0.0000
Gm5422	ENSMUSG00000039684	predicted pseudogene 5422	5.018	0.0000	0.0000	3.602	0.0000	0.0000
Gm5469	ENSMUSG00000116083	predicted gene 5469	14.974	0.0000	0.0001	4.669	0.0019	0.0062
Gm55094	ENSMUSG00002075524	predicted gene, 55094	4.466	0.0171	0.0383	6.773	0.0024	0.0075
Gm55118	ENSMUSG00002076173	predicted gene, 55118	22.681	0.0000	0.0000	42.138	0.0000	0.0000
Gm5512	ENSMUSG00000112693	predicted gene 5512	23.691	0.0000	0.0000	30.352	0.0000	0.0000
Gm5526	ENSMUSG00000084817	predicted pseudogene 5526	4.952	0.0040	0.0107	3.147	0.0413	0.0884
Gm55276	ENSMUSG00002075551	predicted gene, 55276	6.726	0.0000	0.0002	3.260	0.0048	0.0140
Gm5550	ENSMUSG00000106419	predicted gene 5550	6.852	0.0291	0.0608	44.942	0.0007	0.0025
Gm55594	ENSMUSG00000095562	predicted gene, 55594	7.931	0.0000	0.0000	3.293	0.0011	0.0038
Gm55632	ENSMUSG00002075486	predicted gene, 55632	53.764	0.0000	0.0000	50.703	0.0000	0.0000
Gm55936	ENSMUSG00002075188	predicted gene, 55936	12.613	0.0001	0.0003	15.760	0.0000	0.0001
Gm55944	ENSMUSG00002076463	predicted gene, 55944	29.197	0.0000	0.0000	20.293	0.0000	0.0000
Gm5602	ENSMUSG00000086108	predicted gene 5602	2.473	0.0001	0.0003	2.064	0.0027	0.0084
Gm5611	ENSMUSG00000090602	predicted gene 5611	3.653	0.0229	0.0494	4.975	0.0064	0.0178
Gm56171	ENSMUSG00002075501	predicted gene, 56171	21.274	0.0000	0.0000	22.337	0.0000	0.0000
Gm56228	ENSMUSG00002075075	predicted gene, 56228	3.899	0.0000	0.0000	3.960	0.0000	0.0000
Gm56257	ENSMUSG00002075231	predicted gene, 56257	20.838	0.0000	0.0000	16.681	0.0000	0.0000
Gm56478	ENSMUSG00002076074	predicted gene, 56478	3.933	0.0000	0.0000	4.154	0.0000	0.0000
Gm5778	ENSMUSG00000091825	predicted gene 5778	3.262	0.0004	0.0012	2.368	0.0115	0.0296
Gm5805	ENSMUSG00000061848	predicted gene 5805	13.100	0.0000	0.0000	12.301	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5828	ENSMUSG00000091020	predicted gene 5828	1.956	0.0121	0.0283	3.143	0.0000	0.0001
Gm5898	ENSMUSG00000081788	predicted gene 5898	6.047	0.0000	0.0000	6.314	0.0000	0.0000
Gm5909	ENSMUSG00000082491	predicted gene 5909	2.091	0.0009	0.0029	1.722	0.0214	0.0505
Gm5921	ENSMUSG00000074034	predicted gene 5921	2.401	0.0256	0.0543	3.672	0.0029	0.0090
Gm6139	ENSMUSG00000057244	predicted gene 6139	4.335	0.0020	0.0057	3.688	0.0103	0.0269
Gm6204	ENSMUSG00000105879	predicted gene 6204	11.616	0.0000	0.0000	11.773	0.0000	0.0000
Gm6254	ENSMUSG00000066538	predicted gene 6254	5.657	0.0043	0.0113	5.716	0.0049	0.0140
Gm6277	ENSMUSG00000097440	predicted gene 6277	2.485	0.0001	0.0004	1.768	0.0159	0.0394
Gm6363	ENSMUSG00000114993	predicted gene 6363	27.220	0.0007	0.0022	5.022	0.0123	0.0313
Gm6433	ENSMUSG00000083382	predicted gene 6433	5.788	0.0006	0.0019	3.552	0.0241	0.0560
Gm6445	ENSMUSG00000100141	predicted gene 6445	7.773	0.0000	0.0001	24.611	0.0000	0.0000
Gm6477	ENSMUSG00000111877	predicted gene 6477	4.849	0.0006	0.0018	4.045	0.0010	0.0034
Gm6556	ENSMUSG00000097806	predicted gene 6556	2.966	0.0172	0.0385	4.387	0.0009	0.0033
Gm6579	ENSMUSG00000109565	predicted gene 6579	8.649	0.0046	0.0121	9.820	0.0290	0.0656
Gm6682	ENSMUSG00000091269	predicted gene 6682	2.658	0.0016	0.0048	2.520	0.0022	0.0068
Gm6728	ENSMUSG00000091408	predicted gene 6728	3.012	0.0000	0.0000	2.325	0.0001	0.0006
Gm6877	ENSMUSG00000083557	predicted pseudogene 6877	3.357	0.0115	0.0272	19.908	0.0003	0.0011
Gm6916	ENSMUSG00000108608	predicted pseudogene 6916	3.222	0.0000	0.0000	3.004	0.0000	0.0000
Gm7292	ENSMUSG00000104222	predicted gene 7292	2.981	0.0000	0.0000	3.302	0.0000	0.0000
Gm7334	ENSMUSG00000044645	predicted gene 7334	2.644	0.0267	0.0563	4.270	0.0014	0.0048
Gm7335	ENSMUSG00000067189	predicted gene 7335	5.257	0.0335	0.0686	5.174	0.0370	0.0806
Gm7390	ENSMUSG00000110644	predicted gene 7390	8.611	0.0000	0.0000	11.337	0.0000	0.0000
Gm7466	ENSMUSG00000117359	predicted gene 7466	3.739	0.0030	0.0083	2.385	0.0249	0.0576
Gm7467	ENSMUSG00000098449	predicted gene 7467	7.725	0.0000	0.0000	7.779	0.0000	0.0000
Gm7591	ENSMUSG00000114349	predicted gene 7591	4.202	0.0000	0.0000	2.798	0.0001	0.0004
Gm7666	ENSMUSG00000067547	predicted pseudogene 7666	1.525	0.0023	0.0066	1.960	0.0000	0.0000
Gm7729	ENSMUSG00000046636	predicted gene 7729	6.372	0.0000	0.0000	7.060	0.0000	0.0000
Gm7803	ENSMUSG00000083754	predicted gene 7803	9.674	0.0183	0.0408	5.320	0.0432	0.0916
Gm7809	ENSMUSG00000099397	predicted gene 7809	4.518	0.0000	0.0000	4.487	0.0000	0.0000
Gm7887	ENSMUSG00000044211	predicted gene 7887	2.494	0.0000	0.0000	2.289	0.0000	0.0000
Gm7895	ENSMUSG00000100347	predicted gene 7895	2.588	0.0058	0.0147	3.329	0.0002	0.0009
Gm7984	ENSMUSG00000049891	predicted gene 7984	1.504	0.0292	0.0610	2.356	0.0000	0.0001
Gm8066	ENSMUSG00000106237	predicted gene 8066	8.323	0.0000	0.0000	8.575	0.0000	0.0000
Gm8098	ENSMUSG00000073073	predicted gene 8098	2.810	0.0028	0.0076	3.455	0.0002	0.0007
Gm8116	ENSMUSG00000059422	predicted gene 8116	5.384	0.0000	0.0000	4.582	0.0000	0.0000
Gm8130	ENSMUSG00000116637	predicted gene 8130	2.201	0.0214	0.0466	3.265	0.0009	0.0031
Gm8451	ENSMUSG00000099471	predicted gene 8451	10.399	0.0000	0.0000	9.720	0.0000	0.0000
Gm8643	ENSMUSG00000102809	predicted gene 8643	5.548	0.0341	0.0697	5.367	0.0080	0.0217
Gm8806	ENSMUSG00000083367	predicted gene 8806	5.591	0.0005	0.0016	3.706	0.0122	0.0311
Gm8826	ENSMUSG00000102268	predicted gene 8826	16.633	0.0012	0.0036	14.982	0.0020	0.0063
Gm8991	ENSMUSG00000059179	predicted pseudogene 8991	85.606	0.0000	0.0000	18.517	0.0010	0.0033
Gm9162	ENSMUSG00000098044	predicted gene 9162	12.419	0.0000	0.0000	16.368	0.0000	0.0000
Gm9276	ENSMUSG00000118377	predicted gene 9276	3.171	0.0506	0.0975	3.889	0.0251	0.0581

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm9358	ENSMUSG00000098199	predicted gene 9358	7.773	0.0000	0.0000	6.735	0.0000	0.0000
Gm9392	ENSMUSG00000087298	predicted pseudogene 9392	16.835	0.0000	0.0000	9.831	0.0000	0.0000
Gm9431	ENSMUSG00000083468	predicted gene 9431	13.672	0.0001	0.0003	17.179	0.0001	0.0004
Gm9761	ENSMUSG00000034437	predicted gene 9761	2.862	0.0000	0.0001	1.771	0.0220	0.0518
Gm9800	ENSMUSG00000045799	predicted gene 9800	35.976	0.0000	0.0000	13.698	0.0000	0.0000
Gm9812	ENSMUSG00000046747	predicted gene 9812	6.378	0.0000	0.0000	6.820	0.0000	0.0000
Gm9856	ENSMUSG00000110945	predicted gene 9856	1.753	0.0488	0.0947	2.993	0.0001	0.0006
Gm9870	ENSMUSG00000052154	predicted gene 9870	2.429	0.0000	0.0001	1.909	0.0025	0.0078
Gm9905	ENSMUSG00000053358	predicted gene 9905	4.043	0.0000	0.0000	3.135	0.0000	0.0000
Gm9939	ENSMUSG00000054247	predicted gene 9939	2.141	0.0004	0.0012	1.993	0.0020	0.0063
Gmfg	ENSMUSG00000060791	glia maturation factor, gamma	2.114	0.0000	0.0001	1.966	0.0001	0.0006
Gmpr2	ENSMUSG00000002326	guanosine monophosphate reductase 2	1.770	0.0000	0.0000	1.886	0.0000	0.0000
Gngt2	ENSMUSG00000038811	guanine nucleotide binding protein (G protein), gamma transducing activity polypeptide 2	1.907	0.0000	0.0000	2.170	0.0000	0.0000
Gnl1	ENSMUSG00000024429	guanine nucleotide binding protein-like 1	1.790	0.0000	0.0000	2.143	0.0000	0.0000
Gnl3	ENSMUSG00000042354	guanine nucleotide binding protein-like 3 (nucleolar)	1.580	0.0000	0.0000	1.532	0.0000	0.0002
Golga4	ENSMUSG00000038708	golgi autoantigen, golgin subfamily a, 4	2.268	0.0000	0.0000	2.591	0.0000	0.0000
Golim4	ENSMUSG00000034109	golgi integral membrane protein 4	2.143	0.0000	0.0000	1.982	0.0000	0.0000
Golph3	ENSMUSG00000022200	golgi phosphoprotein 3	2.438	0.0000	0.0000	2.138	0.0000	0.0000
Gopc	ENSMUSG00000019861	golgi associated PDZ and coiled-coil motif containing	1.677	0.0000	0.0000	1.530	0.0000	0.0000
Gpatch11	ENSMUSG00000050668	G patch domain containing 11	1.985	0.0000	0.0000	2.016	0.0000	0.0000
Gpatch3	ENSMUSG00000028850	G patch domain containing 3	2.865	0.0000	0.0000	3.001	0.0000	0.0000
Gpatch4	ENSMUSG00000028069	G patch domain containing 4	4.780	0.0000	0.0000	5.863	0.0000	0.0000
Gpc3	ENSMUSG00000055653	glypican 3	1.518	0.0473	0.0922	2.145	0.0003	0.0013
Gpc4	ENSMUSG00000031119	glypican 4	2.084	0.0000	0.0000	1.735	0.0000	0.0000
Gpr27	ENSMUSG00000072875	G protein-coupled receptor 27	3.686	0.0000	0.0000	3.282	0.0000	0.0000
Gps2	ENSMUSG00000023170	G protein pathway suppressor 2	2.621	0.0000	0.0000	2.873	0.0000	0.0000
Gpx4-ps2	ENSMUSG00000110841	glutathione peroxidase 4, pseudogene 2	1.597	0.0000	0.0000	1.892	0.0000	0.0000
Grik5	ENSMUSG00000003378	glutamate receptor, ionotropic, kainate 5 (gamma 2)	2.112	0.0000	0.0000	2.374	0.0000	0.0000
Grin2d	ENSMUSG00000002771	glutamate receptor, ionotropic, NMDA2D (epsilon 4)	2.904	0.0001	0.0004	2.943	0.0001	0.0003
Grk3	ENSMUSG00000042249	G protein-coupled receptor kinase 3	1.517	0.0001	0.0003	1.520	0.0001	0.0004
Grsf1	ENSMUSG00000044221	G-rich RNA sequence binding factor 1	1.787	0.0000	0.0000	1.569	0.0000	0.0000
Gsg1l	ENSMUSG00000046182	GSG1-like	2.672	0.0000	0.0000	1.701	0.0002	0.0008
Gsk3a	ENSMUSG00000057177	glycogen synthase kinase 3 alpha	1.534	0.0000	0.0000	1.697	0.0000	0.0000
Gsr	ENSMUSG00000031584	glutathione reductase	2.369	0.0000	0.0000	2.423	0.0000	0.0000
Gsta4	ENSMUSG00000032348	glutathione S-transferase, alpha 4	1.564	0.0000	0.0000	1.872	0.0000	0.0000
Gstp-ps	ENSMUSG00000103653	glutathione S-transferase, pi, pseudogene	2.772	0.0000	0.0000	2.866	0.0000	0.0000
Gtf2a1	ENSMUSG00000020962	general transcription factor II A, 1	2.672	0.0000	0.0000	2.114	0.0000	0.0000
Gtf2e1	ENSMUSG00000022828	general transcription factor II E, polypeptide 1 (alpha subunit)	1.533	0.0001	0.0002	1.614	0.0000	0.0000
Gtf2f1	ENSMUSG00000002658	general transcription factor IIF, polypeptide 1	2.523	0.0000	0.0000	2.895	0.0000	0.0000
Gtf2h3	ENSMUSG00000029387	general transcription factor IIH, polypeptide 3	1.671	0.0003	0.0011	1.798	0.0000	0.0002
Gtf3c6	ENSMUSG00000019837	general transcription factor IIIC, polypeptide 6, alpha	2.843	0.0000	0.0000	2.753	0.0000	0.0000
Gtpbp4	ENSMUSG00000021149	GTP binding protein 4	1.765	0.0000	0.0000	1.721	0.0000	0.0000
Guf1	ENSMUSG00000029208	GUF1 homolog, GTPase	1.620	0.0000	0.0000	1.593	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gxylt1	ENSMUSG00000036197	glucoside xylosyltransferase 1	2.036	0.0000	0.0000	1.787	0.0000	0.0000
H19	ENSMUSG00000000031	H19, imprinted maternally expressed transcript	2.117	0.0001	0.0005	1.808	0.0026	0.0081
H1f10	ENSMUSG00000044927	H1.10 linker histone	6.314	0.0000	0.0000	8.300	0.0000	0.0000
H1f2	ENSMUSG00000036181	H1.2 linker histone, cluster member	1.643	0.0000	0.0002	1.516	0.0006	0.0023
H2aw	ENSMUSG00000078851	H2A.W histone	4.017	0.0000	0.0000	3.975	0.0000	0.0000
H2-Bl	ENSMUSG00000073406	histocompatibility 2, blastocyst	1.792	0.0001	0.0003	3.731	0.0000	0.0000
Habp4	ENSMUSG00000021476	hyaluronic acid binding protein 4	1.756	0.0000	0.0000	1.674	0.0000	0.0000
Hand2	ENSMUSG00000038193	heart and neural crest derivatives expressed 2	4.248	0.0000	0.0000	4.303	0.0000	0.0000
Haus3	ENSMUSG00000079555	HAUS augmin-like complex, subunit 3	1.929	0.0000	0.0000	1.561	0.0002	0.0009
Hccs	ENSMUSG00000031352	holocytochrome c synthetase	2.194	0.0000	0.0002	2.365	0.0000	0.0000
Hcls1	ENSMUSG00000022831	hematopoietic cell specific Lyn substrate 1	2.319	0.0000	0.0000	2.748	0.0000	0.0000
Hcn2	ENSMUSG00000020331	hyperpolarization-activated, cyclic nucleotide-gated K+ 2	3.753	0.0000	0.0000	3.828	0.0000	0.0000
Hdac2	ENSMUSG00000019777	histone deacetylase 2	4.277	0.0000	0.0000	3.842	0.0000	0.0000
Hdac7	ENSMUSG00000022475	histone deacetylase 7	1.529	0.0000	0.0000	1.642	0.0000	0.0000
Hdgf	ENSMUSG00000004897	heparin binding growth factor	1.837	0.0000	0.0000	2.062	0.0000	0.0000
Hdgfl3	ENSMUSG00000025104	HDGF like 3	2.294	0.0000	0.0000	1.987	0.0000	0.0000
Hdnr	ENSMUSG00000097910	Hand2 downstream lncRNA	1.781	0.0001	0.0005	1.829	0.0001	0.0004
Herc2	ENSMUSG00000030451	HECT and RLD domain containing E3 ubiquitin protein ligase 2	1.591	0.0000	0.0000	1.526	0.0000	0.0001
Hes1	ENSMUSG00000022528	hes family bHLH transcription factor 1	2.920	0.0000	0.0000	1.797	0.0042	0.0124
Hey2	ENSMUSG00000019789	hairy/enhancer-of-split related with YRPW motif 2	1.829	0.0019	0.0054	1.780	0.0033	0.0099
Hic1	ENSMUSG00000043099	hypermethylated in cancer 1	3.295	0.0000	0.0000	3.430	0.0000	0.0000
Hirip3	ENSMUSG00000042606	HIRA interacting protein 3	3.419	0.0000	0.0000	3.375	0.0000	0.0000
Hjv	ENSMUSG00000038403	hemojuvelin BMP co-receptor	2.128	0.0000	0.0000	2.386	0.0000	0.0000
Hk1	ENSMUSG00000037012	hexokinase 1	1.713	0.0000	0.0000	1.921	0.0000	0.0000
Hmga1	ENSMUSG00000046711	high mobility group AT-hook 1	5.143	0.0000	0.0000	6.605	0.0000	0.0000
Hmga1b	ENSMUSG00000078249	high mobility group AT-hook 1B	4.119	0.0000	0.0000	3.879	0.0000	0.0000
Hmgb1	ENSMUSG00000066551	high mobility group box 1	1.681	0.0000	0.0000	1.779	0.0000	0.0000
Hmgb1-ps7	ENSMUSG00000092281	high-mobility group high mobility group box 1, pseudogene 7	17.209	0.0000	0.0000	16.069	0.0000	0.0000
Hmgb3	ENSMUSG00000015217	high mobility group box 3	2.906	0.0000	0.0000	2.511	0.0000	0.0000
Hmgcs1	ENSMUSG00000093930	3-hydroxy-3-methylglutaryl-Coenzyme A synthase 1	1.805	0.0000	0.0000	1.514	0.0000	0.0000
Hmgn1	ENSMUSG00000040681	high mobility group nucleosomal binding domain 1	1.747	0.0000	0.0000	1.625	0.0000	0.0000
Hmgn3	ENSMUSG00000066456	high mobility group nucleosomal binding domain 3	3.847	0.0000	0.0000	3.346	0.0000	0.0000
Hmgn5	ENSMUSG00000031245	high-mobility group nucleosome binding domain 5	6.826	0.0000	0.0000	8.351	0.0000	0.0000
Hnrnpa0	ENSMUSG00000007836	heterogeneous nuclear ribonucleoprotein A0	4.069	0.0000	0.0000	3.001	0.0000	0.0000
Hnrnpa1	ENSMUSG00000046434	heterogeneous nuclear ribonucleoprotein A1	2.442	0.0000	0.0000	2.221	0.0000	0.0000
Hnrnpa1l2-ps2	ENSMUSG00000021927	heterogeneous nuclear ribonucleoprotein A1-like 2, pseudogene 2	59.076	0.0000	0.0000	18.153	0.0000	0.0000
Hnrnpa2b1	ENSMUSG00000004980	heterogeneous nuclear ribonucleoprotein A2/B1	2.665	0.0000	0.0000	2.298	0.0000	0.0000
Hnrnpa3	ENSMUSG00000059005	heterogeneous nuclear ribonucleoprotein A3	4.842	0.0000	0.0000	4.092	0.0000	0.0000
Hnrnpab	ENSMUSG00000020358	heterogeneous nuclear ribonucleoprotein A/B	4.438	0.0000	0.0000	4.851	0.0000	0.0000
Hnrnpc	ENSMUSG00000060373	heterogeneous nuclear ribonucleoprotein C	1.652	0.0000	0.0000	1.708	0.0000	0.0000
Hnrnpd	ENSMUSG00000000568	heterogeneous nuclear ribonucleoprotein D	3.351	0.0000	0.0000	3.084	0.0000	0.0000
Hnrnpdl	ENSMUSG00000029328	heterogeneous nuclear ribonucleoprotein D-like	1.957	0.0000	0.0000	1.888	0.0000	0.0000
Hnrnph1	ENSMUSG00000007850	heterogeneous nuclear ribonucleoprotein H1	3.319	0.0000	0.0000	2.921	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hnrnph2	ENSMUSG00000045427	heterogeneous nuclear ribonucleoprotein H2	2.561	0.0000	0.0000	2.244	0.0000	0.0000
Hnrnph3	ENSMUSG00000020069	heterogeneous nuclear ribonucleoprotein H3	2.736	0.0000	0.0000	2.684	0.0000	0.0000
Hnrnpk	ENSMUSG00000021546	heterogeneous nuclear ribonucleoprotein K	1.804	0.0000	0.0000	1.666	0.0000	0.0000
Hnrnpl	ENSMUSG00000015165	heterogeneous nuclear ribonucleoprotein L	1.992	0.0000	0.0000	1.913	0.0000	0.0000
Hnrnpll	ENSMUSG00000024095	heterogeneous nuclear ribonucleoprotein L-like	2.477	0.0000	0.0000	1.985	0.0000	0.0000
Hnrnpm	ENSMUSG00000059208	heterogeneous nuclear ribonucleoprotein M	3.747	0.0000	0.0000	3.128	0.0000	0.0000
Hnrnpr	ENSMUSG00000066037	heterogeneous nuclear ribonucleoprotein R	2.730	0.0000	0.0000	2.463	0.0000	0.0000
Hnrnpu	ENSMUSG00000039630	heterogeneous nuclear ribonucleoprotein U	3.396	0.0000	0.0000	2.273	0.0000	0.0000
Hnrnpul1	ENSMUSG00000040725	heterogeneous nuclear ribonucleoprotein U-like 1	2.605	0.0000	0.0000	2.855	0.0000	0.0000
Hnrnpul2	ENSMUSG00000071659	heterogeneous nuclear ribonucleoprotein U-like 2	2.984	0.0000	0.0000	2.924	0.0000	0.0000
Homer2	ENSMUSG00000025813	homer scaffolding protein 2	1.566	0.0000	0.0000	1.660	0.0000	0.0000
Hoxb3os	ENSMUSG00000084844	homeobox B3 and homeobox B2, opposite strand	2.291	0.0012	0.0037	2.047	0.0066	0.0182
Hoxd8	ENSMUSG00000027102	homeobox D8	2.305	0.0032	0.0087	3.664	0.0000	0.0000
Hoxd9	ENSMUSG00000043342	homeobox D9	3.857	0.0021	0.0059	6.922	0.0000	0.0001
Hpf1	ENSMUSG00000038005	histone PARylation factor 1	1.954	0.0000	0.0000	1.679	0.0000	0.0000
Hras	ENSMUSG00000025499	Harvey rat sarcoma virus oncogene	2.864	0.0000	0.0000	3.071	0.0000	0.0000
Hrc	ENSMUSG00000038239	histidine rich calcium binding protein	2.092	0.0000	0.0000	2.449	0.0000	0.0000
Hs3st3a1	ENSMUSG00000047759	heparan sulfate (glucosamine) 3-O-sulfotransferase 3A1	2.140	0.0016	0.0046	3.148	0.0000	0.0000
Hs3st3b1	ENSMUSG00000070407	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1	2.003	0.0000	0.0002	1.514	0.0158	0.0391
Hsd17b4	ENSMUSG00000024507	hydroxysteroid (17-beta) dehydrogenase 4	2.160	0.0000	0.0000	2.073	0.0000	0.0000
Hsd3b7	ENSMUSG00000042289	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 7	2.646	0.0127	0.0295	3.226	0.0022	0.0069
Hsdl2	ENSMUSG00000028383	hydroxysteroid dehydrogenase like 2	3.108	0.0000	0.0000	2.132	0.0000	0.0000
Hsp90aa1	ENSMUSG00000021270	heat shock protein 90, alpha (cytosolic), class A member 1	1.504	0.0003	0.0010	1.514	0.0002	0.0009
Hsp90ab1	ENSMUSG00000023944	heat shock protein 90 alpha (cytosolic), class B member 1	2.053	0.0000	0.0000	2.304	0.0000	0.0000
Hsp90b1	ENSMUSG00000020048	heat shock protein 90, beta (Grp94), member 1	2.058	0.0000	0.0000	1.863	0.0000	0.0000
Hspa4	ENSMUSG00000020361	heat shock protein 4	2.591	0.0000	0.0000	2.291	0.0000	0.0000
Hspa9	ENSMUSG00000024359	heat shock protein 9	1.761	0.0000	0.0000	1.796	0.0000	0.0000
Hspd1	ENSMUSG00000025980	heat shock protein 1 (chaperonin)	2.284	0.0000	0.0000	2.113	0.0000	0.0000
Hspd1-ps3	ENSMUSG00000058809	heat shock protein 1 (chaperonin), pseudogene 3	1.609	0.0346	0.0707	1.615	0.0381	0.0826
Hspe1	ENSMUSG00000073676	heat shock protein 1 (chaperonin 10)	1.847	0.0000	0.0000	1.930	0.0000	0.0000
Hspe1-rs1	ENSMUSG00000117621	heat shock protein 1 (chaperonin 10), related sequence 1	3.697	0.0000	0.0000	2.857	0.0000	0.0000
Hsph1	ENSMUSG00000029657	heat shock 105kDa/110kDa protein 1	1.616	0.0001	0.0005	1.820	0.0000	0.0000
Htatsf1	ENSMUSG00000067873	HIV TAT specific factor 1	3.078	0.0000	0.0000	2.924	0.0000	0.0000
Hyi	ENSMUSG00000006395	hydroxypyruvate isomerase (putative)	1.555	0.0145	0.0332	1.517	0.0263	0.0604
Hypk	ENSMUSG00000027245	huntingtin interacting protein K	3.092	0.0000	0.0000	2.682	0.0000	0.0000
Ier5	ENSMUSG00000056708	immediate early response 5	4.031	0.0000	0.0000	3.068	0.0000	0.0000
Ier5l	ENSMUSG00000089762	immediate early response 5-like	3.251	0.0000	0.0000	2.349	0.0006	0.0022
Iffo2	ENSMUSG00000041025	intermediate filament family orphan 2	1.653	0.0000	0.0000	1.673	0.0000	0.0000
Ifi204	ENSMUSG00000073489	interferon activated gene 204	2.113	0.0000	0.0001	1.753	0.0015	0.0048
Ifit3	ENSMUSG00000074896	interferon-induced protein with tetratricopeptide repeats 3	1.995	0.0004	0.0012	1.909	0.0009	0.0030
Ifrd1	ENSMUSG00000001627	interferon-related developmental regulator 1	2.967	0.0000	0.0000	2.229	0.0003	0.0011
Ift57	ENSMUSG00000032965	intraflagellar transport 57	2.346	0.0000	0.0000	1.981	0.0000	0.0001
Igf2	ENSMUSG00000048583	insulin-like growth factor 2	3.078	0.0000	0.0000	1.745	0.0180	0.0435

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Igfbp7	ENSMUSG00000036256	insulin-like growth factor binding protein 7	1.905	0.0001	0.0003	1.931	0.0001	0.0002
Igsf11	ENSMUSG00000022790	immunoglobulin superfamily, member 11	1.644	0.0080	0.0197	1.557	0.0198	0.0473
Ik	ENSMUSG00000024474	IK cytokine	2.324	0.0000	0.0000	2.281	0.0000	0.0000
Il17d	ENSMUSG00000050222	interleukin 17D	2.826	0.0000	0.0001	2.903	0.0000	0.0001
Ilkap	ENSMUSG00000026309	integrin-linked kinase-associated serine/threonine phosphatase 2C	1.605	0.0000	0.0000	1.549	0.0000	0.0000
Ilrun	ENSMUSG00000056692	inflammation and lipid regulator with UBA-like and NBR1-like domains	1.903	0.0000	0.0000	1.904	0.0000	0.0000
Inafm2	ENSMUSG00000074918	InaF motif containing 2	3.452	0.0000	0.0000	3.385	0.0000	0.0000
Incenp	ENSMUSG00000024660	inner centromere protein	2.177	0.0000	0.0000	2.337	0.0000	0.0000
Ing5	ENSMUSG00000026283	inhibitor of growth family, member 5	1.557	0.0000	0.0001	1.622	0.0000	0.0000
Inhba	ENSMUSG00000041324	inhibin beta-A	2.352	0.0000	0.0002	2.074	0.0005	0.0019
Inhbb	ENSMUSG00000037035	inhibin beta-B	2.663	0.0000	0.0000	2.419	0.0000	0.0000
Ino80b	ENSMUSG00000030034	INO80 complex subunit B	3.322	0.0000	0.0000	3.906	0.0000	0.0000
Ino80dos	ENSMUSG00000084799	INO80 complex subunit D, opposite strand	2.048	0.0001	0.0004	2.681	0.0000	0.0000
Inpp5a	ENSMUSG00000025477	inositol polyphosphate-5-phosphatase A	1.770	0.0000	0.0000	1.841	0.0000	0.0000
Ipo8	ENSMUSG00000040029	importin 8	1.803	0.0000	0.0000	1.608	0.0000	0.0000
Ipp	ENSMUSG00000028696	IAP promoted placental gene	1.592	0.0000	0.0000	1.527	0.0000	0.0000
Iqsec2	ENSMUSG00000041115	IQ motif and Sec7 domain 2	2.290	0.0000	0.0000	1.854	0.0000	0.0000
Irak4	ENSMUSG00000059883	interleukin-1 receptor-associated kinase 4	1.727	0.0000	0.0000	1.818	0.0000	0.0000
Irf2bp2	ENSMUSG00000051495	interferon regulatory factor 2 binding protein 2	2.520	0.0000	0.0000	2.302	0.0000	0.0000
Irx1	ENSMUSG00000060969	Iroquois homeobox 1	3.042	0.0000	0.0000	2.147	0.0014	0.0048
Irx3	ENSMUSG00000031734	Iroquois related homeobox 3	4.333	0.0000	0.0000	4.665	0.0000	0.0000
Irx3os	ENSMUSG00000046413	iroquois homeobox 3, opposite strand	3.078	0.0005	0.0017	3.200	0.0004	0.0017
Irx5	ENSMUSG00000031737	Iroquois homeobox 5	2.626	0.0000	0.0000	2.087	0.0000	0.0001
Iscu	ENSMUSG00000025825	iron-sulfur cluster assembly enzyme	3.680	0.0000	0.0000	2.947	0.0000	0.0000
Ism1	ENSMUSG00000074766	isthmin 1, angiogenesis inhibitor	2.163	0.0156	0.0353	2.257	0.0116	0.0299
Itgam	ENSMUSG00000030786	integrin alpha M	2.784	0.0000	0.0000	3.037	0.0000	0.0000
Itgb1	ENSMUSG00000025809	integrin beta 1 (fibronectin receptor beta)	2.303	0.0000	0.0000	1.904	0.0000	0.0000
Itgbl1	ENSMUSG00000032925	integrin, beta-like 1	2.618	0.0000	0.0000	3.627	0.0000	0.0000
Itpripl2	ENSMUSG00000095115	inositol 1,4,5-triphosphate receptor interacting protein-like 2	2.246	0.0000	0.0000	2.000	0.0000	0.0000
Itsn1	ENSMUSG00000022957	intersectin 1 (SH3 domain protein 1A)	1.735	0.0000	0.0000	1.960	0.0000	0.0000
Iws1	ENSMUSG00000024384	IWS1, SUPT6 interacting protein	2.074	0.0000	0.0000	1.829	0.0000	0.0000
Jdp2	ENSMUSG00000034271	Jun dimerization protein 2	1.867	0.0004	0.0012	1.792	0.0010	0.0033
Jph2	ENSMUSG00000017817	junctophilin 2	3.007	0.0000	0.0000	2.242	0.0000	0.0001
Jund	ENSMUSG00000071076	jun D proto-oncogene	9.236	0.0000	0.0000	9.349	0.0000	0.0000
Junos	ENSMUSG00000087366	jun proto-oncogene, opposite strand	1.803	0.0185	0.0412	4.197	0.0000	0.0000
K230015D01Rik	ENSMUSG00000110630	RIKEN cDNA K230015D01 gene	2.713	0.0001	0.0002	1.916	0.0131	0.0331
Kansl2	ENSMUSG00000022992	KAT8 regulatory NSL complex subunit 2	2.110	0.0000	0.0000	1.920	0.0000	0.0001
Kantr	ENSMUSG00000087403	Kdm5c adjacent non-coding transcript	1.712	0.0002	0.0008	1.781	0.0001	0.0005
Kcmf1	ENSMUSG00000055239	potassium channel modulatory factor 1	1.986	0.0000	0.0000	1.982	0.0000	0.0000
Kcnab3	ENSMUSG00000018470	potassium voltage-gated channel, shaker-related subfamily, beta member 3	2.359	0.0013	0.0038	2.544	0.0021	0.0067
Kcnd3os	ENSMUSG00000074346	potassium voltage-gated channel, Shal-related family, member 3, opposite strand	2.472	0.0005	0.0015	2.239	0.0027	0.0083
Kcng2	ENSMUSG00000059852	potassium voltage-gated channel, subfamily G, member 2	1.889	0.0000	0.0000	2.029	0.0000	0.0000
Kcnj12	ENSMUSG00000042529	potassium inwardly-rectifying channel, subfamily J, member 12	1.951	0.0000	0.0001	1.970	0.0000	0.0001

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kcnk2	ENSMUSG00000037624	potassium channel, subfamily K, member 2	1.535	0.0005	0.0017	2.117	0.0000	0.0000
Kctd1	ENSMUSG00000036225	potassium channel tetramerisation domain containing 1	1.870	0.0000	0.0000	1.573	0.0003	0.0010
Kctd18	ENSMUSG00000054770	potassium channel tetramerisation domain containing 18	1.880	0.0000	0.0000	1.562	0.0000	0.0001
Kctd2	ENSMUSG00000016940	potassium channel tetramerisation domain containing 2	2.576	0.0000	0.0000	3.250	0.0000	0.0000
Kctd3	ENSMUSG00000026608	potassium channel tetramerisation domain containing 3	1.971	0.0000	0.0000	1.901	0.0000	0.0000
Kctd6	ENSMUSG00000021752	potassium channel tetramerisation domain containing 6	2.243	0.0000	0.0000	1.738	0.0000	0.0002
Kctd9	ENSMUSG00000034327	potassium channel tetramerisation domain containing 9	1.795	0.0000	0.0000	1.757	0.0000	0.0000
Kdm1a	ENSMUSG00000036940	lysine (K)-specific demethylase 1A	2.328	0.0000	0.0000	2.441	0.0000	0.0000
Kdm6b	ENSMUSG00000018476	KDM1 lysine (K)-specific demethylase 6B	1.983	0.0001	0.0003	1.617	0.0052	0.0149
Kdr	ENSMUSG00000062960	kinase insert domain protein receptor	1.658	0.0000	0.0001	1.559	0.0002	0.0008
Khdrbs1	ENSMUSG00000028790	KH domain containing, RNA binding, signal transduction associated 1	1.821	0.0000	0.0000	1.679	0.0001	0.0006
Khdrbs3	ENSMUSG00000022332	KH domain containing, RNA binding, signal transduction associated 3	1.787	0.0000	0.0000	1.709	0.0000	0.0000
Khsrp	ENSMUSG00000007670	KH-type splicing regulatory protein	3.241	0.0000	0.0000	3.464	0.0000	0.0000
Kif1c	ENSMUSG00000020821	kinesin family member 1C	1.693	0.0000	0.0000	1.965	0.0000	0.0000
Kif21a	ENSMUSG00000022629	kinesin family member 21A	1.583	0.0000	0.0000	1.537	0.0000	0.0000
Kif2a	ENSMUSG00000021693	kinesin family member 2A	1.765	0.0000	0.0000	1.570	0.0000	0.0000
Kif3a	ENSMUSG00000018395	kinesin family member 3A	2.002	0.0000	0.0000	2.244	0.0000	0.0000
Kifbp	ENSMUSG00000036955	kinesin family binding protein	1.633	0.0000	0.0000	1.538	0.0000	0.0000
Klf16	ENSMUSG00000035397	Kruppel-like factor 16	1.853	0.0000	0.0000	1.801	0.0000	0.0001
Klf2	ENSMUSG00000055148	Kruppel-like factor 2 (lung)	2.888	0.0000	0.0000	2.331	0.0000	0.0000
Klf3	ENSMUSG00000029178	Kruppel-like factor 3 (basic)	1.843	0.0000	0.0000	1.598	0.0000	0.0000
Klf4	ENSMUSG00000003032	Kruppel-like factor 4 (gut)	1.994	0.0000	0.0000	1.815	0.0000	0.0000
Klhdc2	ENSMUSG00000020978	kelch domain containing 2	2.165	0.0000	0.0000	2.010	0.0000	0.0000
Klhdc4	ENSMUSG00000040263	kelch domain containing 4	2.171	0.0000	0.0000	2.616	0.0000	0.0000
Klhdc8b	ENSMUSG00000032609	kelch domain containing 8B	1.751	0.0001	0.0003	1.951	0.0000	0.0000
Klhl2	ENSMUSG00000031605	kelch-like 2, Mayven	1.705	0.0014	0.0042	1.606	0.0047	0.0137
Klhl8	ENSMUSG00000029312	kelch-like 8	1.536	0.0000	0.0000	1.596	0.0000	0.0000
Kpna2	ENSMUSG00000018362	karyopherin (importin) alpha 2	2.139	0.0000	0.0000	1.567	0.0001	0.0002
Kpnb1	ENSMUSG00000001440	karyopherin (importin) beta 1	1.522	0.0000	0.0000	1.504	0.0000	0.0000
Kras	ENSMUSG00000030265	Kirsten rat sarcoma viral oncogene homolog	2.105	0.0000	0.0000	1.761	0.0000	0.0000
Krcc1	ENSMUSG00000053012	lysine-rich coiled-coil 1	1.915	0.0000	0.0000	1.775	0.0000	0.0000
Lacc1	ENSMUSG00000044350	laccase domain containing 1	1.667	0.0002	0.0008	1.727	0.0001	0.0004
Lactb	ENSMUSG00000032370	lactamase, beta	2.281	0.0000	0.0000	2.178	0.0000	0.0000
Lamtor3	ENSMUSG00000091512	late endosomal/lysosomal adaptor, MAPK and MTOR activator 3	1.640	0.0000	0.0000	1.598	0.0000	0.0000
Larp1b	ENSMUSG00000025762	La ribonucleoprotein domain family, member 1B	2.440	0.0000	0.0000	2.498	0.0000	0.0000
Larp6	ENSMUSG00000034839	La ribonucleoprotein domain family, member 6	2.064	0.0006	0.0019	1.553	0.0391	0.0845
Las1l	ENSMUSG00000057421	LAS1-like (S. cerevisiae)	1.566	0.0000	0.0000	1.577	0.0000	0.0000
Lat2	ENSMUSG00000040751	linker for activation of T cells family, member 2	1.891	0.0026	0.0074	2.037	0.0009	0.0032
Lbhd1	ENSMUSG00000096740	LBH domain containing 1	1.991	0.0001	0.0005	1.684	0.0046	0.0134
Ldhb	ENSMUSG00000030246	lactate dehydrogenase B	1.690	0.0000	0.0000	1.860	0.0000	0.0000
Lemd2	ENSMUSG00000044857	LEM domain containing 2	3.168	0.0000	0.0000	3.005	0.0000	0.0000
Lemd3	ENSMUSG00000048661	LEM domain containing 3	2.389	0.0000	0.0000	2.233	0.0000	0.0000
Leng1	ENSMUSG00000078813	leukocyte receptor cluster (LRC) member 1	2.706	0.0000	0.0000	3.011	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Leng8	ENSMUSG00000035545	leukocyte receptor cluster (LRC) member 8	1.743	0.0037	0.0098	2.014	0.0003	0.0010
Leo1	ENSMUSG00000042487	Leo1, Paf1/RNA polymerase II complex component	1.976	0.0000	0.0000	1.956	0.0000	0.0000
Lhfpl4	ENSMUSG00000042873	lipoma HMGIC fusion partner-like protein 4	4.201	0.0000	0.0000	3.300	0.0000	0.0000
Lin7a	ENSMUSG00000019906	lin-7 homolog A, crumbs cell polarity complex component	2.012	0.0053	0.0137	2.542	0.0002	0.0010
Lipo4	ENSMUSG00000079344	lipase, member O4	2.870	0.0000	0.0000	1.570	0.0152	0.0378
Lix1l	ENSMUSG00000049288	Lix1-like	1.661	0.0000	0.0000	1.508	0.0000	0.0000
Llph-ps1	ENSMUSG00000081459	LLP homolog, pseudogene 1	6.582	0.0168	0.0377	85.398	0.0000	0.0000
Llph-ps2	ENSMUSG00000083364	LLP homolog, pseudogene 2	19.242	0.0000	0.0000	11.986	0.0000	0.0000
Lmln	ENSMUSG00000022802	leishmanolysin-like (metallopeptidase M8 family)	1.553	0.0012	0.0036	1.735	0.0001	0.0003
Lmnb1	ENSMUSG00000024590	lamin B1	2.010	0.0000	0.0002	1.765	0.0009	0.0032
Lmo2	ENSMUSG00000032698	LIM domain only 2	2.379	0.0000	0.0000	2.727	0.0000	0.0000
Lmod1	ENSMUSG00000048096	leiomodin 1 (smooth muscle)	2.508	0.0000	0.0000	3.452	0.0000	0.0000
Lmod2	ENSMUSG00000029683	leiomodin 2 (cardiac)	2.623	0.0000	0.0000	2.498	0.0000	0.0000
Lmod3	ENSMUSG00000044086	leiomodin 3 (fetal)	1.716	0.0218	0.0475	2.096	0.0017	0.0055
Lncob1	ENSMUSG00000092381	lncRNA osteoblastogenesis associated 1	4.900	0.0007	0.0022	5.823	0.0004	0.0017
Lonp1	ENSMUSG00000041168	lon peptidase 1, mitochondrial	2.056	0.0000	0.0000	2.152	0.0000	0.0000
Lonrf1	ENSMUSG00000039633	LON peptidase N-terminal domain and ring finger 1	2.705	0.0000	0.0000	2.506	0.0000	0.0000
Lpar1	ENSMUSG00000038668	lysophosphatidic acid receptor 1	2.286	0.0000	0.0000	2.308	0.0000	0.0000
Lpcat1	ENSMUSG00000021608	lysophosphatidylcholine acyltransferase 1	2.011	0.0000	0.0000	1.636	0.0000	0.0000
Lpcat4	ENSMUSG00000027134	lysophosphatidylcholine acyltransferase 4	2.440	0.0000	0.0000	3.405	0.0000	0.0000
Lrch1	ENSMUSG00000068015	leucine-rich repeats and calponin homology (CH) domain containing 1	1.638	0.0002	0.0007	1.651	0.0002	0.0007
Lrfn1	ENSMUSG00000030600	leucine rich repeat and fibronectin type III domain containing 1	4.063	0.0000	0.0000	4.002	0.0000	0.0000
Lrfn4	ENSMUSG00000045045	leucine rich repeat and fibronectin type III domain containing 4	2.691	0.0000	0.0000	2.158	0.0002	0.0007
Lrrc47	ENSMUSG00000029028	leucine rich repeat containing 47	4.454	0.0000	0.0000	4.025	0.0000	0.0000
Lrrc75a	ENSMUSG00000046417	leucine rich repeat containing 75A	1.634	0.0008	0.0025	1.550	0.0032	0.0098
Lrrc8a	ENSMUSG00000007476	leucine rich repeat containing 8A VRAC subunit A	1.722	0.0029	0.0080	1.751	0.0022	0.0069
Lsg1	ENSMUSG00000022538	large 60S subunit nuclear export GTPase 1	1.663	0.0000	0.0000	1.672	0.0000	0.0000
Lsm14a	ENSMUSG00000066568	LSM14A mRNA processing body assembly factor	1.754	0.0000	0.0000	1.584	0.0000	0.0000
Lsm6	ENSMUSG00000031683	LSM6 homolog, U6 small nuclear RNA and mRNA degradation associated	2.996	0.0000	0.0000	2.803	0.0000	0.0000
Lsm8	ENSMUSG00000044155	LSM8 homolog, U6 small nuclear RNA associated	2.652	0.0000	0.0000	2.176	0.0000	0.0000
Ltbp1	ENSMUSG00000001870	latent transforming growth factor beta binding protein 1	1.722	0.0000	0.0000	1.522	0.0000	0.0000
Ltv1	ENSMUSG00000019814	LTV1 ribosome biogenesis factor	2.123	0.0000	0.0000	1.925	0.0000	0.0000
Luc7l2	ENSMUSG00000029823	LUC7-like 2 (S. cerevisiae)	2.126	0.0000	0.0000	1.885	0.0000	0.0000
Luc7l3	ENSMUSG00000020863	LUC7-like 3 (S. cerevisiae)	2.284	0.0000	0.0000	2.258	0.0000	0.0000
Ly75	ENSMUSG00000026980	lymphocyte antigen 75	1.599	0.0019	0.0055	1.506	0.0060	0.0169
Lyar	ENSMUSG00000067367	Ly1 antibody reactive clone	1.758	0.0000	0.0000	1.946	0.0000	0.0000
Maco1	ENSMUSG00000028826	macoilin 1	2.131	0.0000	0.0000	2.101	0.0000	0.0000
Macrod1	ENSMUSG00000036278	mono-ADP ribosylhydrolase 1	2.273	0.0000	0.0000	2.225	0.0000	0.0000
Macrod2	ENSMUSG00000068205	mono-ADP ribosylhydrolase 2	2.301	0.0000	0.0000	2.142	0.0000	0.0000
Mad1l1	ENSMUSG00000029554	MAD1 mitotic arrest deficient 1-like 1	1.719	0.0000	0.0000	2.107	0.0000	0.0000
Madd	ENSMUSG00000040687	MAP-kinase activating death domain	1.518	0.0000	0.0000	1.540	0.0000	0.0000
Maf	ENSMUSG00000055435	avian musculoaponeurotic fibrosarcoma oncogene homolog	2.664	0.0000	0.0000	2.444	0.0000	0.0000
Mafa	ENSMUSG00000047591	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein A (avian)	7.029	0.0000	0.0000	6.488	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mafk	ENSMUSG00000018143	v-maf musculoaponeurotic fibrosarcoma oncogene family, protein K (avian)	1.575	0.0499	0.0964	1.684	0.0245	0.0568
Magohb	ENSMUSG00000030188	mago homolog B, exon junction complex core component	1.820	0.0001	0.0003	1.697	0.0005	0.0018
Mak16	ENSMUSG00000031578	MAK16 homolog	2.214	0.0000	0.0000	1.984	0.0000	0.0000
Malat1	ENSMUSG00000092341	metastasis associated lung adenocarcinoma transcript 1 (non-coding RNA)	3.422	0.0009	0.0027	2.989	0.0031	0.0094
Malsu1	ENSMUSG00000029815	mitochondrial assembly of ribosomal large subunit 1	2.034	0.0000	0.0000	2.078	0.0000	0.0000
Manf	ENSMUSG00000032575	mesencephalic astrocyte-derived neurotrophic factor	1.778	0.0000	0.0000	2.013	0.0000	0.0000
Map1lc3a	ENSMUSG00000027602	microtubule-associated protein 1 light chain 3 alpha	2.632	0.0000	0.0000	2.320	0.0000	0.0001
Map2k2	ENSMUSG00000035027	mitogen-activated protein kinase kinase 2	2.206	0.0001	0.0003	1.816	0.0030	0.0091
Map2k7	ENSMUSG00000002948	mitogen-activated protein kinase kinase 7	1.868	0.0000	0.0000	1.963	0.0000	0.0000
Map3k10	ENSMUSG00000040390	mitogen-activated protein kinase kinase kinase 10	3.154	0.0000	0.0000	3.112	0.0000	0.0000
Map3k5	ENSMUSG00000071369	mitogen-activated protein kinase kinase kinase 5	1.813	0.0000	0.0000	1.779	0.0000	0.0000
Map4	ENSMUSG00000032479	microtubule-associated protein 4	1.577	0.0000	0.0000	1.561	0.0000	0.0000
Map4k4	ENSMUSG00000026074	mitogen-activated protein kinase kinase kinase kinase 4	2.345	0.0000	0.0000	2.265	0.0000	0.0000
Map7	ENSMUSG00000019996	microtubule-associated protein 7	2.143	0.0000	0.0000	2.061	0.0000	0.0000
Map7d1	ENSMUSG00000028849	MAP7 domain containing 1	2.382	0.0000	0.0000	2.416	0.0000	0.0000
Map7d2	ENSMUSG00000041020	MAP7 domain containing 2	2.540	0.0000	0.0002	2.861	0.0000	0.0000
Mapk1ip1l	ENSMUSG00000021840	mitogen-activated protein kinase 1 interacting protein 1-like	1.830	0.0000	0.0000	1.775	0.0000	0.0000
Mapkapk5	ENSMUSG00000029454	MAP kinase-activated protein kinase 5	20.690	0.0000	0.0000	13.052	0.0000	0.0000
Marchf1	ENSMUSG00000036469	membrane associated ring-CH-type finger 1	1.555	0.0375	0.0755	1.929	0.0022	0.0069
Marchf11	ENSMUSG00000022269	membrane associated ring-CH-type finger 11	4.881	0.0000	0.0000	4.900	0.0000	0.0000
Marchf2	ENSMUSG00000079557	membrane associated ring-CH-type finger 2	1.517	0.0000	0.0000	1.780	0.0000	0.0000
Marchf5	ENSMUSG00000023307	membrane associated ring-CH-type finger 5	2.968	0.0000	0.0000	2.498	0.0000	0.0000
Marchf8	ENSMUSG00000025702	membrane associated ring-CH-type finger 8	1.732	0.0000	0.0000	1.579	0.0000	0.0000
Marchf9	ENSMUSG00000040502	membrane associated ring-CH-type finger 9	4.783	0.0000	0.0000	5.288	0.0000	0.0000
Marcks	ENSMUSG00000069662	myristoylated alanine rich protein kinase C substrate	3.884	0.0000	0.0000	3.896	0.0000	0.0000
Marcksl1	ENSMUSG00000047945	MARCKS-like 1	2.243	0.0001	0.0003	1.730	0.0080	0.0216
Mark2	ENSMUSG00000024969	MAP/microtubule affinity regulating kinase 2	1.615	0.0000	0.0000	1.539	0.0000	0.0000
Mark3	ENSMUSG00000007411	MAP/microtubule affinity regulating kinase 3	1.789	0.0000	0.0000	1.655	0.0000	0.0000
Mark4	ENSMUSG00000030397	MAP/microtubule affinity regulating kinase 4	2.647	0.0000	0.0000	1.956	0.0013	0.0043
Max	ENSMUSG00000059436	Max protein	1.756	0.0000	0.0000	1.655	0.0000	0.0002
Maz	ENSMUSG00000030678	MYC-associated zinc finger protein (purine-binding transcription factor)	2.529	0.0000	0.0000	2.476	0.0000	0.0000
Mbd2	ENSMUSG00000024513	methyl-CpG binding domain protein 2	3.308	0.0000	0.0000	3.427	0.0000	0.0000
Mbd3	ENSMUSG00000035478	methyl-CpG binding domain protein 3	1.669	0.0000	0.0001	1.571	0.0001	0.0006
Mcat	ENSMUSG00000048755	malonyl CoA:ACP acyltransferase (mitochondrial)	1.524	0.0000	0.0000	1.659	0.0000	0.0000
Mcl1	ENSMUSG00000038612	myeloid cell leukemia sequence 1	2.344	0.0000	0.0000	2.192	0.0000	0.0000
Mdfic	ENSMUSG00000041390	MyoD family inhibitor domain containing	2.271	0.0000	0.0000	1.914	0.0000	0.0000
Mdn1	ENSMUSG00000058006	midasin AAA ATPase 1	1.700	0.0000	0.0000	1.557	0.0000	0.0000
Mecomos	ENSMUSG00000085702	MDS1 and EVI1 complex locus, opposite strand	10.093	0.0000	0.0001	7.913	0.0000	0.0002
Med16	ENSMUSG00000013833	mediator complex subunit 16	1.578	0.0000	0.0000	1.759	0.0000	0.0000
Med30	ENSMUSG00000038622	mediator complex subunit 30	3.167	0.0000	0.0000	2.557	0.0000	0.0000
Medag	ENSMUSG00000029659	mesenteric estrogen dependent adipogenesis	3.143	0.0000	0.0000	2.955	0.0000	0.0000
Meig1	ENSMUSG00000026650	meiosis expressed gene 1	1.569	0.0025	0.0070	1.985	0.0000	0.0000
Meis1	ENSMUSG00000020160	Meis homeobox 1	1.518	0.0002	0.0006	1.713	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Meox1	ENSMUSG00000001493	mesenchyme homeobox 1	2.021	0.0214	0.0466	2.534	0.0024	0.0074
Mepce	ENSMUSG00000029726	methylphosphate capping enzyme	1.551	0.0000	0.0000	1.641	0.0000	0.0000
Mesd	ENSMUSG00000038503	mesoderm development LRP chaperone	1.706	0.0000	0.0000	1.635	0.0000	0.0000
Metap2	ENSMUSG00000036112	methionine aminopeptidase 2	1.848	0.0000	0.0000	1.867	0.0000	0.0000
Metrnl	ENSMUSG00000039208	meteorin, glial cell differentiation regulator-like	1.954	0.0000	0.0000	2.060	0.0000	0.0000
Mettl14	ENSMUSG00000028114	methyltransferase like 14	2.299	0.0000	0.0000	1.896	0.0000	0.0000
Mettl5	ENSMUSG00000051730	methyltransferase like 5	3.602	0.0000	0.0000	2.982	0.0000	0.0000
Mettl6	ENSMUSG00000021891	methyltransferase like 6	1.583	0.0000	0.0000	1.635	0.0000	0.0000
Mex3a	ENSMUSG00000074480	mex3 RNA binding family member A	2.265	0.0002	0.0009	1.711	0.0220	0.0517
Mex3d	ENSMUSG00000048696	mex3 RNA binding family member D	2.435	0.0000	0.0000	1.952	0.0000	0.0001
Mfn1	ENSMUSG00000027668	mitofusin 1	2.044	0.0000	0.0000	1.896	0.0000	0.0000
Mfsd1	ENSMUSG00000027775	major facilitator superfamily domain containing 1	1.895	0.0000	0.0000	1.897	0.0000	0.0000
Mfsd12	ENSMUSG00000034854	major facilitator superfamily domain containing 12	1.505	0.0001	0.0005	1.843	0.0000	0.0000
Mfsd6	ENSMUSG00000041439	major facilitator superfamily domain containing 6	1.578	0.0000	0.0000	1.649	0.0000	0.0000
Mgat4b	ENSMUSG00000036620	mannoside acetylglucosaminyltransferase 4, isoenzyme B	2.500	0.0000	0.0000	2.219	0.0000	0.0001
Mhrt	ENSMUSG00000097652	myosin heavy chain associated RNA transcript	2.276	0.0000	0.0000	3.082	0.0000	0.0000
Mib1	ENSMUSG00000024294	MIB E3 ubiquitin protein ligase 1	2.082	0.0000	0.0000	1.721	0.0000	0.0000
Micos13	ENSMUSG00000049760	mitochondrial contact site and cristae organizing system subunit 13	1.579	0.0000	0.0000	1.815	0.0000	0.0000
Micu2	ENSMUSG00000021973	mitochondrial calcium uptake 2	1.782	0.0000	0.0000	1.667	0.0000	0.0000
Midn	ENSMUSG00000035621	midnolin	1.806	0.0013	0.0038	1.880	0.0006	0.0021
Mios	ENSMUSG00000042447	meiosis regulator for oocyte development	2.686	0.0000	0.0000	2.295	0.0000	0.0000
Mipep	ENSMUSG00000021993	mitochondrial intermediate peptidase	1.574	0.0000	0.0000	1.632	0.0000	0.0000
Mipol1	ENSMUSG00000047022	mirror-image polydactyly 1	1.725	0.0000	0.0002	1.552	0.0012	0.0042
Mir762	ENSMUSG00000076454	microRNA 762	9.594	0.0001	0.0002	25.813	0.0000	0.0000
Mir8091	ENSMUSG00000098286	microRNA 8091	4.280	0.0001	0.0004	4.921	0.0001	0.0002
Mkrn1	ENSMUSG00000029922	makorin, ring finger protein, 1	2.666	0.0000	0.0000	2.954	0.0000	0.0000
Mlec	ENSMUSG00000048578	malectin	1.577	0.0000	0.0000	1.594	0.0000	0.0000
Mllt6	ENSMUSG00000038437	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6	1.539	0.0000	0.0000	1.540	0.0000	0.0000
Mlycd	ENSMUSG00000074064	malonyl-CoA decarboxylase	1.914	0.0000	0.0000	1.655	0.0003	0.0010
Mmadhc	ENSMUSG00000026766	methylmalonic aciduria (cobalamin deficiency) cblD type, with homocystinuria	1.786	0.0000	0.0000	1.502	0.0000	0.0000
Mmp14	ENSMUSG00000000957	matrix metallopeptidase 14 (membrane-inserted)	1.534	0.0068	0.0170	1.851	0.0001	0.0004
Mnat1	ENSMUSG00000021103	menage a trois 1	1.963	0.0000	0.0000	1.805	0.0000	0.0000
Mnd1	ENSMUSG00000033752	meiotic nuclear divisions 1	2.179	0.0021	0.0060	2.101	0.0049	0.0141
Mocs3	ENSMUSG00000074576	molybdenum cofactor synthesis 3	2.193	0.0002	0.0008	1.681	0.0153	0.0380
Mon1b	ENSMUSG00000078908	MON1 homolog B, secretory traffciking associated	1.600	0.0000	0.0000	1.625	0.0000	0.0000
Morf4l1	ENSMUSG00000062270	mortality factor 4 like 1	1.664	0.0000	0.0000	1.692	0.0000	0.0000
Morrbid	ENSMUSG00000074813	myeloid RNA regulator of BCL2L11 induced cell death	1.659	0.0003	0.0011	1.870	0.0000	0.0001
Mospd3	ENSMUSG00000037221	motile sperm domain containing 3	5.440	0.0000	0.0000	6.173	0.0000	0.0000
Mpeg1	ENSMUSG00000046805	macrophage expressed gene 1	1.639	0.0043	0.0113	1.823	0.0005	0.0019
Mphosph10	ENSMUSG00000030521	M-phase phosphoprotein 10 (U3 small nucleolar ribonucleoprotein)	1.703	0.0000	0.0000	1.561	0.0000	0.0001
Mphosph6	ENSMUSG00000031843	M phase phosphoprotein 6	2.679	0.0000	0.0000	2.414	0.0000	0.0000
Mphosph8	ENSMUSG00000079184	M-phase phosphoprotein 8	1.881	0.0000	0.0000	1.720	0.0000	0.0000
Mplkip	ENSMUSG00000012429	M-phase specific PLK1 intereacting protein	2.655	0.0000	0.0000	2.884	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mpnd	ENSMUSG00000003199	MPN domain containing	1.814	0.0000	0.0000	2.548	0.0000	0.0000
Mreg	ENSMUSG00000039395	melanoregulin	2.552	0.0000	0.0000	2.409	0.0000	0.0000
Mrfap1	ENSMUSG00000055302	Morf4 family associated protein 1	1.996	0.0000	0.0000	1.864	0.0000	0.0000
Mrgbp	ENSMUSG00000027569	MRG/MORF4L binding protein	2.261	0.0000	0.0000	2.314	0.0000	0.0000
Mrpl16	ENSMUSG00000024683	mitochondrial ribosomal protein L16	1.722	0.0000	0.0000	1.726	0.0000	0.0000
Mrpl18	ENSMUSG00000057388	mitochondrial ribosomal protein L18	1.505	0.0000	0.0000	1.545	0.0000	0.0000
Mrpl43	ENSMUSG00000025208	mitochondrial ribosomal protein L43	1.856	0.0000	0.0000	2.135	0.0000	0.0000
Mrpl50	ENSMUSG00000044018	mitochondrial ribosomal protein L50	1.658	0.0000	0.0000	1.554	0.0000	0.0000
Mrpl9	ENSMUSG00000028140	mitochondrial ribosomal protein L9	2.006	0.0000	0.0000	2.115	0.0000	0.0000
Mrps25	ENSMUSG00000014551	mitochondrial ribosomal protein S25	1.633	0.0000	0.0000	1.643	0.0000	0.0000
Mrps5	ENSMUSG00000027374	mitochondrial ribosomal protein S5	2.187	0.0000	0.0000	2.447	0.0000	0.0000
Msantd3	ENSMUSG00000039693	Myb/SANT-like DNA-binding domain containing 3	2.308	0.0000	0.0000	2.495	0.0000	0.0000
Msi1	ENSMUSG00000054256	musashi RNA-binding protein 1	1.666	0.0127	0.0295	3.345	0.0000	0.0000
Msl1	ENSMUSG00000052915	male specific lethal 1	2.742	0.0000	0.0000	2.245	0.0000	0.0000
mt-Atp6	ENSMUSG00000064357	mitochondrially encoded ATP synthase 6	162.310	0.0000	0.0000	119.215	0.0000	0.0000
mt-Atp8	ENSMUSG00000064356	mitochondrially encoded ATP synthase 8	587.642	0.0000	0.0000	682.269	0.0000	0.0000
Mtch1	ENSMUSG00000024012	mitochondrial carrier 1	2.193	0.0000	0.0000	2.324	0.0000	0.0000
Mtcl1	ENSMUSG00000052105	microtubule crosslinking factor 1	2.280	0.0000	0.0000	2.565	0.0000	0.0000
mt-Co2	ENSMUSG00000064354	mitochondrially encoded cytochrome c oxidase II	67.767	0.0000	0.0000	48.709	0.0000	0.0000
mt-Co3	ENSMUSG00000064358	mitochondrially encoded cytochrome c oxidase III	39.237	0.0000	0.0000	13.444	0.0000	0.0001
Mthfd2l	ENSMUSG00000029376	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2-like	2.980	0.0000	0.0000	2.214	0.0000	0.0000
Mtif2	ENSMUSG00000020459	mitochondrial translational initiation factor 2	1.908	0.0000	0.0000	1.781	0.0000	0.0000
mt-Nd4l	ENSMUSG00000065947	mitochondrially encoded NADH dehydrogenase 4L	1312.905	0.0000	0.0000	101.439	0.0000	0.0000
mt-Nd6	ENSMUSG00000064368	mitochondrially encoded NADH dehydrogenase 6	9.718	0.0000	0.0000	6.376	0.0000	0.0000
Mtres1	ENSMUSG00000019797	mitochondrial transcription rescue factor 1	2.366	0.0000	0.0000	2.590	0.0000	0.0000
Mtrf1l	ENSMUSG00000019774	mitochondrial translational release factor 1-like	2.351	0.0000	0.0000	2.112	0.0000	0.0000
Mtx3	ENSMUSG00000021704	metaxin 3	1.949	0.0002	0.0008	1.609	0.0087	0.0233
Mxra7	ENSMUSG00000020814	matrix-remodelling associated 7	4.263	0.0000	0.0000	4.029	0.0000	0.0000
Myadm	ENSMUSG00000068566	myeloid-associated differentiation marker	2.248	0.0000	0.0000	2.091	0.0000	0.0000
Mycl	ENSMUSG00000028654	v-myc avian myelocytomatosis viral oncogene lung carcinoma derived	2.704	0.0016	0.0048	3.212	0.0004	0.0015
Myef2	ENSMUSG00000027201	myelin basic protein expression factor 2, repressor	2.550	0.0000	0.0000	2.241	0.0000	0.0000
Myef2l	ENSMUSG00000049230	myelin expression factor 2 like	8.853	0.0000	0.0000	7.681	0.0000	0.0000
Myh10	ENSMUSG00000020900	myosin, heavy polypeptide 10, non-muscle	1.729	0.0000	0.0000	1.962	0.0000	0.0000
Myh11	ENSMUSG00000018830	myosin, heavy polypeptide 11, smooth muscle	1.754	0.0000	0.0001	1.962	0.0000	0.0000
Myh14	ENSMUSG00000030739	myosin, heavy polypeptide 14	1.915	0.0000	0.0000	1.899	0.0000	0.0000
Myh6	ENSMUSG00000040752	myosin, heavy polypeptide 6, cardiac muscle, alpha	1.772	0.0000	0.0000	1.928	0.0000	0.0000
Myh7b	ENSMUSG00000074652	myosin, heavy chain 7B, cardiac muscle, beta	1.599	0.0095	0.0230	1.866	0.0006	0.0021
Myh9	ENSMUSG00000022443	myosin, heavy polypeptide 9, non-muscle	2.075	0.0000	0.0000	2.165	0.0000	0.0000
Myl12b	ENSMUSG00000034868	myosin, light chain 12B, regulatory	2.745	0.0000	0.0000	1.856	0.0002	0.0009
Mylk	ENSMUSG00000022836	myosin, light polypeptide kinase	1.773	0.0000	0.0000	1.594	0.0000	0.0001
Myo18b	ENSMUSG00000072720	myosin XVIIIb	1.567	0.0000	0.0000	1.786	0.0000	0.0000
Mypop	ENSMUSG00000048481	Myb-related transcription factor, partner of profilin	1.798	0.0095	0.0229	2.004	0.0022	0.0070
Myzap	ENSMUSG00000041361	myocardial zonula adherens protein	1.554	0.0001	0.0003	1.700	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
N4bp2os	ENSMUSG00000106978	NEDD4 binding protein 2, opposite strand	8.537	0.0000	0.0000	8.252	0.0000	0.0000
Naa30	ENSMUSG00000036282	N(alpha)-acetyltransferase 30, NatC catalytic subunit	3.124	0.0000	0.0000	2.467	0.0000	0.0000
Naa50	ENSMUSG00000022698	N(alpha)-acetyltransferase 50, NatE catalytic subunit	2.713	0.0000	0.0000	1.850	0.0000	0.0000
Nab2	ENSMUSG00000025402	Ngfi-A binding protein 2	1.637	0.0003	0.0012	1.676	0.0002	0.0008
Naf1	ENSMUSG00000014907	nuclear assembly factor 1 ribonucleoprotein	3.636	0.0000	0.0000	2.301	0.0001	0.0002
Naif1	ENSMUSG00000039164	nuclear apoptosis inducing factor 1	1.964	0.0000	0.0000	1.805	0.0000	0.0000
Nanos3	ENSMUSG00000056155	nanos C2HC-type zinc finger 3	2.737	0.0072	0.0180	3.138	0.0011	0.0037
Nasp	ENSMUSG00000028693	nuclear autoantigenic sperm protein (histone-binding)	3.303	0.0000	0.0000	3.104	0.0000	0.0000
Nat10	ENSMUSG00000027185	N-acetyltransferase 10	1.571	0.0000	0.0000	1.609	0.0000	0.0000
Nat8l	ENSMUSG00000048142	N-acetyltransferase 8-like	1.931	0.0023	0.0065	2.526	0.0000	0.0001
Nbl1	ENSMUSG00000041120	NBL1, DAN family BMP antagonist	1.557	0.0271	0.0572	1.954	0.0009	0.0030
Ncbp1	ENSMUSG00000028330	nuclear cap binding protein subunit 1	1.811	0.0000	0.0000	1.570	0.0000	0.0000
Ncbp3	ENSMUSG00000020783	nuclear cap binding subunit 3	1.735	0.0000	0.0000	1.604	0.0000	0.0000
Nck2	ENSMUSG00000066877	non-catalytic region of tyrosine kinase adaptor protein 2	1.881	0.0000	0.0000	1.945	0.0000	0.0000
Ncl	ENSMUSG00000026234	nucleolin	2.915	0.0000	0.0000	2.591	0.0000	0.0000
Ncoa5	ENSMUSG00000039804	nuclear receptor coactivator 5	1.843	0.0000	0.0000	1.998	0.0000	0.0000
Ndfip2	ENSMUSG00000053253	Nedd4 family interacting protein 2	2.799	0.0000	0.0000	2.515	0.0000	0.0000
Ndufa12	ENSMUSG00000020022	NADH:ubiquinone oxidoreductase subunit A12	1.519	0.0000	0.0000	1.699	0.0000	0.0000
Ndufa5	ENSMUSG00000023089	NADH:ubiquinone oxidoreductase subunit A5	3.161	0.0000	0.0000	2.953	0.0000	0.0000
Ndufa9	ENSMUSG00000000399	NADH:ubiquinone oxidoreductase subunit A9	1.908	0.0000	0.0000	1.902	0.0000	0.0000
Ndufaf6	ENSMUSG00000050323	NADH:ubiquinone oxidoreductase complex assembly factor 6	3.047	0.0000	0.0000	2.398	0.0000	0.0000
Ndufb3	ENSMUSG00000026032	NADH:ubiquinone oxidoreductase subunit B3	1.867	0.0000	0.0000	1.754	0.0000	0.0000
Ndufb9	ENSMUSG00000022354	NADH:ubiquinone oxidoreductase subunit B9	1.686	0.0000	0.0000	1.809	0.0000	0.0000
Ndufs6b	ENSMUSG00000083820	NADH:ubiquinone oxidoreductase subunit S6B	4.034	0.0000	0.0001	7.135	0.0000	0.0000
Nedd8	ENSMUSG00000010376	neural precursor cell expressed, developmentally down-regulated gene 8	1.769	0.0000	0.0000	2.086	0.0000	0.0000
Nek2	ENSMUSG00000026622	NIMA (never in mitosis gene a)-related expressed kinase 2	1.859	0.0154	0.0349	1.843	0.0211	0.0500
Nek7	ENSMUSG00000026393	NIMA (never in mitosis gene a)-related expressed kinase 7	2.034	0.0000	0.0000	1.862	0.0000	0.0000
Nemf	ENSMUSG00000020982	nuclear export mediator factor	2.050	0.0000	0.0000	1.914	0.0000	0.0000
Nes	ENSMUSG00000004891	nestin	2.168	0.0000	0.0001	1.829	0.0008	0.0030
Net1	ENSMUSG00000021215	neuroepithelial cell transforming gene 1	1.956	0.0000	0.0000	2.046	0.0000	0.0000
Nexn	ENSMUSG00000039103	nexilin	3.192	0.0000	0.0000	3.138	0.0000	0.0000
Nfe2l1	ENSMUSG00000038615	nuclear factor, erythroid derived 2,-like 1	1.728	0.0000	0.0000	1.710	0.0000	0.0000
Nfix	ENSMUSG00000001911	nuclear factor I/X	2.099	0.0000	0.0000	2.155	0.0000	0.0000
Nfxl1	ENSMUSG00000072889	nuclear transcription factor, X-box binding-like 1	2.180	0.0000	0.0000	1.989	0.0000	0.0000
Nfyb	ENSMUSG00000020248	nuclear transcription factor-Y beta	3.118	0.0000	0.0000	2.803	0.0000	0.0000
Nkapd1	ENSMUSG00000059820	NKAP domain containing 1	1.910	0.0000	0.0000	1.549	0.0000	0.0000
Nkiras1	ENSMUSG00000021772	NFKB inhibitor interacting Ras-like protein 1	2.214	0.0000	0.0000	1.969	0.0000	0.0000
Nlgn2	ENSMUSG00000051790	neuroligin 2	1.522	0.0006	0.0018	1.980	0.0000	0.0000
Noc2l	ENSMUSG00000095567	NOC2 like nucleolar associated transcriptional repressor	1.924	0.0000	0.0000	2.101	0.0000	0.0000
Noc3l	ENSMUSG00000024999	NOC3 like DNA replication regulator	1.681	0.0000	0.0000	1.757	0.0000	0.0000
Nog	ENSMUSG00000048616	noggin	5.558	0.0019	0.0054	5.154	0.0044	0.0128
Nol7	ENSMUSG00000063200	nucleolar protein 7	3.346	0.0000	0.0000	2.061	0.0001	0.0002
Nol8	ENSMUSG00000021392	nucleolar protein 8	1.559	0.0000	0.0000	1.510	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nono	ENSMUSG00000031311	non-POU-domain-containing, octamer binding protein	2.364	0.0000	0.0000	2.238	0.0000	0.0000
Nop14	ENSMUSG00000036693	NOP14 nucleolar protein	1.773	0.0000	0.0000	1.756	0.0000	0.0000
Nop58	ENSMUSG00000026020	NOP58 ribonucleoprotein	2.006	0.0000	0.0000	1.846	0.0000	0.0000
Nop9	ENSMUSG00000019297	NOP9 nucleolar protein	1.912	0.0000	0.0000	1.777	0.0000	0.0000
Norad	ENSMUSG00000102869	non-coding RNA activated by DNA damage	2.515	0.0000	0.0000	2.406	0.0000	0.0000
Notumos	ENSMUSG00000053613	notum palmitoleoyl-protein carboxylesterase, opposite strand	4.916	0.0019	0.0055	7.005	0.0013	0.0043
Nova2	ENSMUSG00000030411	NOVA alternative splicing regulator 2	2.290	0.0000	0.0000	2.115	0.0000	0.0000
Nphp1	ENSMUSG00000027378	nephronophthisis 1 (juvenile) homolog (human)	1.796	0.0000	0.0000	2.174	0.0000	0.0000
Npm1	ENSMUSG00000057113	nucleophosmin 1	3.260	0.0000	0.0000	2.907	0.0000	0.0000
Nr2f1	ENSMUSG00000069171	nuclear receptor subfamily 2, group F, member 1	3.391	0.0000	0.0000	3.045	0.0000	0.0000
Nr2f2	ENSMUSG00000030551	nuclear receptor subfamily 2, group F, member 2	2.604	0.0000	0.0000	2.537	0.0000	0.0000
Nr2f6	ENSMUSG00000002393	nuclear receptor subfamily 2, group F, member 6	3.935	0.0000	0.0000	2.632	0.0000	0.0002
Nr4a2	ENSMUSG00000026826	nuclear receptor subfamily 4, group A, member 2	2.251	0.0020	0.0058	2.670	0.0002	0.0008
Nrarp	ENSMUSG00000078202	Notch-regulated ankyrin repeat protein	2.231	0.0000	0.0000	1.913	0.0000	0.0002
Nrd1	ENSMUSG00000053510	nardilysin, N-arginine dibasic convertase, NRD convertase 1	2.125	0.0000	0.0000	2.142	0.0000	0.0000
Nrgn	ENSMUSG00000053310	neurogranin	9.877	0.0000	0.0000	8.592	0.0000	0.0000
Nrtn	ENSMUSG00000039481	neurturin	10.540	0.0000	0.0000	8.582	0.0000	0.0000
Nsa2	ENSMUSG00000060739	NSA2 ribosome biogenesis homolog	3.467	0.0000	0.0000	3.005	0.0000	0.0000
Nsa2-ps1	ENSMUSG00000118353	NSA2 ribosome biogenesis homolog, pseudogene 1	3.611	0.0067	0.0168	3.005	0.0107	0.0280
Nsmce3	ENSMUSG00000070520	NSE3 homolog, SMC5-SMC6 complex component	2.401	0.0000	0.0000	2.081	0.0000	0.0000
Nsmce4a	ENSMUSG00000040331	NSE4 homolog A, SMC5-SMC6 complex component	2.197	0.0000	0.0000	2.392	0.0000	0.0000
Nsrp1	ENSMUSG00000037958	nuclear speckle regulatory protein 1	3.970	0.0000	0.0000	4.004	0.0000	0.0000
Ntn4	ENSMUSG00000020019	netrin 4	1.962	0.0000	0.0000	2.001	0.0000	0.0000
Ntng2	ENSMUSG00000035513	netrin G2	1.696	0.0032	0.0087	1.511	0.0219	0.0516
Nucb2	ENSMUSG00000030659	nucleobindin 2	2.018	0.0000	0.0000	2.016	0.0000	0.0000
Nucks1	ENSMUSG00000026434	nuclear casein kinase and cyclin-dependent kinase substrate 1	2.168	0.0000	0.0000	1.914	0.0000	0.0000
Nudc	ENSMUSG00000028851	nudC nuclear distribution protein	3.147	0.0000	0.0000	3.182	0.0000	0.0000
Nudc-ps1	ENSMUSG00000110331	nuclear distribution gene C homolog (Aspergillus), pseudogene 1	1.705	0.0000	0.0001	2.102	0.0000	0.0000
Nudt3	ENSMUSG00000024213	nudix (nucleotide diphosphate linked moiety X)-type motif 3	2.887	0.0000	0.0000	2.466	0.0000	0.0000
Nudt4	ENSMUSG00000020029	nudix (nucleoside diphosphate linked moiety X)-type motif 4	3.308	0.0000	0.0000	2.498	0.0000	0.0000
Nudt6	ENSMUSG00000050174	nudix (nucleoside diphosphate linked moiety X)-type motif 6	3.386	0.0000	0.0000	3.557	0.0000	0.0000
Nudt9	ENSMUSG00000029310	nudix (nucleoside diphosphate linked moiety X)-type motif 9	2.127	0.0000	0.0000	2.160	0.0000	0.0000
Nup107	ENSMUSG00000052798	nucleoporin 107	1.546	0.0000	0.0000	1.624	0.0000	0.0000
Nutf2-ps1	ENSMUSG00000071497	nuclear transport factor 2, pseudogene 1	6.719	0.0000	0.0000	20.547	0.0000	0.0000
Nxn	ENSMUSG00000020844	nucleoredoxin	1.586	0.0014	0.0041	1.741	0.0001	0.0005
Oaf	ENSMUSG00000032014	out at first homolog	1.605	0.0179	0.0399	1.614	0.0169	0.0414
Obi1	ENSMUSG00000022120	ORC ubiquitin ligase 1	1.743	0.0000	0.0000	1.618	0.0002	0.0006
Ociad2	ENSMUSG00000029153	OCIA domain containing 2	1.835	0.0000	0.0000	1.760	0.0000	0.0000
Odc1	ENSMUSG00000011179	ornithine decarboxylase, structural 1	1.765	0.0000	0.0001	1.907	0.0000	0.0000
Ogfrl1	ENSMUSG00000026158	opioid growth factor receptor-like 1	2.680	0.0000	0.0000	2.500	0.0000	0.0000
Olfm1	ENSMUSG00000026833	olfactomedin 1	2.350	0.0000	0.0000	2.481	0.0000	0.0000
Orai1	ENSMUSG00000049686	ORAI calcium release-activated calcium modulator 1	3.008	0.0000	0.0000	3.550	0.0000	0.0000
Osbpl10	ENSMUSG00000040875	oxysterol binding protein-like 10	1.663	0.0007	0.0022	2.045	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Otud1	ENSMUSG00000043415	OTU domain containing 1	3.134	0.0000	0.0000	2.305	0.0000	0.0000
Otud3	ENSMUSG00000041161	OTU domain containing 3	2.111	0.0000	0.0000	1.843	0.0000	0.0001
Otud6b	ENSMUSG00000040550	OTU domain containing 6B	2.047	0.0000	0.0000	1.834	0.0000	0.0000
Otud7b	ENSMUSG00000038495	OTU domain containing 7B	1.976	0.0000	0.0000	1.889	0.0000	0.0000
Otulin	ENSMUSG00000046034	OTU deubiquitinase with linear linkage specificity	2.565	0.0000	0.0000	3.128	0.0000	0.0000
Otulinl	ENSMUSG00000056069	OTU deubiquitinase with linear linkage specificity like	2.025	0.0001	0.0002	2.404	0.0000	0.0000
Oxsr1	ENSMUSG00000036737	oxidative-stress responsive 1	1.811	0.0000	0.0000	1.746	0.0000	0.0000
P3h3	ENSMUSG00000023191	prolyl 3-hydroxylase 3	1.673	0.0067	0.0168	1.756	0.0031	0.0094
Pabpc4	ENSMUSG00000011257	poly(A) binding protein, cytoplasmic 4	1.615	0.0000	0.0000	1.560	0.0000	0.0000
Pabpn1	ENSMUSG00000022194	poly(A) binding protein, nuclear 1	12.246	0.0000	0.0000	20.333	0.0000	0.0000
Pacsin3	ENSMUSG00000027257	protein kinase C and casein kinase substrate in neurons 3	1.713	0.0000	0.0000	1.921	0.0000	0.0000
Paf1	ENSMUSG00000003437	Paf1, RNA polymerase II complex component	2.592	0.0000	0.0000	2.835	0.0000	0.0000
Paip1	ENSMUSG00000025451	polyadenylate binding protein-interacting protein 1	2.708	0.0000	0.0000	2.722	0.0000	0.0000
Palm3	ENSMUSG00000047986	paralemmin 3	3.332	0.0007	0.0023	5.170	0.0000	0.0000
Pals2	ENSMUSG00000038388	protein associated with LIN7 2, MAGUK family member	1.848	0.0000	0.0000	1.856	0.0000	0.0000
Pan3	ENSMUSG00000029647	PAN3 poly(A) specific ribonuclease subunit	1.739	0.0000	0.0000	1.605	0.0000	0.0001
Pank1	ENSMUSG00000033610	pantothenate kinase 1	1.709	0.0000	0.0000	1.597	0.0000	0.0000
Pank2	ENSMUSG00000037514	pantothenate kinase 2	2.451	0.0000	0.0000	2.234	0.0000	0.0000
Paqr3	ENSMUSG00000055725	progestin and adipoQ receptor family member III	1.875	0.0001	0.0003	3.594	0.0000	0.0000
Paqr4	ENSMUSG00000023909	progestin and adipoQ receptor family member IV	2.292	0.0000	0.0000	2.702	0.0000	0.0000
Paqr9	ENSMUSG00000064225	progestin and adipoQ receptor family member IX	1.887	0.0000	0.0000	1.670	0.0002	0.0007
Pard3	ENSMUSG00000025812	par-3 family cell polarity regulator	1.939	0.0000	0.0000	1.866	0.0000	0.0000
Pard6b	ENSMUSG00000044641	par-6 family cell polarity regulator beta	2.305	0.0000	0.0000	2.079	0.0000	0.0000
Parn	ENSMUSG00000022685	poly(A)-specific ribonuclease (deadenylation nuclease)	1.689	0.0000	0.0000	1.620	0.0000	0.0000
Pawr	ENSMUSG00000035873	PRKC, apoptosis, WT1, regulator	4.498	0.0000	0.0000	4.358	0.0000	0.0000
Paxbp1	ENSMUSG00000022974	PAX3 and PAX7 binding protein 1	1.739	0.0000	0.0000	1.891	0.0000	0.0000
Pbdc1	ENSMUSG00000031226	polysaccharide biosynthesis domain containing 1	2.534	0.0000	0.0000	2.683	0.0000	0.0000
Pbx2	ENSMUSG00000034673	pre B cell leukemia homeobox 2	1.875	0.0000	0.0000	1.969	0.0000	0.0000
Pcbd2	ENSMUSG00000021496	pterin 4 alpha carbinolamine dehydratase/dimerization cofactor of hepatocyte nuclear factor 1 alpha (TCF1) 2	6.811	0.0000	0.0000	6.620	0.0000	0.0000
Pcdhb16	ENSMUSG00000047910	protocadherin beta 16	1.772	0.0017	0.0051	2.130	0.0000	0.0002
Pcdhb20	ENSMUSG00000046191	protocadherin beta 20	2.060	0.0000	0.0000	1.674	0.0001	0.0006
Pcf11	ENSMUSG00000041328	PCF11 cleavage and polyadenylation factor subunit	1.735	0.0000	0.0000	1.816	0.0000	0.0000
Pcgf3	ENSMUSG00000033623	polycomb group ring finger 3	2.076	0.0000	0.0000	1.747	0.0000	0.0000
Pcgf6	ENSMUSG00000025050	polycomb group ring finger 6	1.857	0.0000	0.0000	2.005	0.0000	0.0000
Pcm1	ENSMUSG00000031592	pericentriolar material 1	1.685	0.0000	0.0000	1.609	0.0000	0.0000
Pdap1	ENSMUSG00000029623	PDGFA associated protein 1	2.608	0.0000	0.0000	2.847	0.0000	0.0000
Pdcd4	ENSMUSG00000024975	programmed cell death 4	2.551	0.0000	0.0000	2.676	0.0000	0.0000
Pdcd5	ENSMUSG00000030417	programmed cell death 5	2.973	0.0000	0.0000	2.590	0.0000	0.0000
Pdcd7	ENSMUSG00000041837	programmed cell death 7	5.032	0.0000	0.0000	4.013	0.0000	0.0000
Pdcl	ENSMUSG00000009030	phosducin-like	1.708	0.0000	0.0000	1.527	0.0000	0.0000
Pdcl3	ENSMUSG00000026078	phosducin-like 3	2.777	0.0000	0.0000	2.557	0.0000	0.0000
Pde3b	ENSMUSG00000030671	phosphodiesterase 3B, cGMP-inhibited	2.169	0.0004	0.0012	1.865	0.0040	0.0119
Pde6d	ENSMUSG00000026239	phosphodiesterase 6D, cGMP-specific, rod, delta	2.011	0.0000	0.0000	1.686	0.0000	0.0002

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pdgfb	ENSMUSG00000000489	platelet derived growth factor, B polypeptide	1.828	0.0000	0.0000	1.906	0.0000	0.0000
Pdha1	ENSMUSG00000031299	pyruvate dehydrogenase E1 alpha 1	1.531	0.0000	0.0000	1.512	0.0000	0.0000
Pdhb	ENSMUSG00000021748	pyruvate dehydrogenase (lipoamide) beta	2.214	0.0000	0.0000	1.569	0.0000	0.0000
Pdia6	ENSMUSG00000020571	protein disulfide isomerase associated 6	1.747	0.0000	0.0000	1.766	0.0000	0.0000
Pdzd11	ENSMUSG00000015668	PDZ domain containing 11	1.530	0.0000	0.0000	1.626	0.0000	0.0000
Pdzrn4	ENSMUSG00000036218	PDZ domain containing RING finger 4	2.283	0.0087	0.0213	2.311	0.0075	0.0206
Peg12	ENSMUSG00000070526	paternally expressed 12	1.787	0.0176	0.0392	1.971	0.0057	0.0161
Peg3	ENSMUSG00000002265	paternally expressed 3	1.842	0.0002	0.0008	1.533	0.0103	0.0269
Pet100	ENSMUSG00000087687	PET100 homolog	2.148	0.0000	0.0000	2.278	0.0000	0.0000
Pfdn2	ENSMUSG00000006412	prefoldin 2	2.919	0.0000	0.0000	3.294	0.0000	0.0000
Pfdn6	ENSMUSG00000024309	prefoldin subunit 6	1.854	0.0000	0.0000	2.082	0.0000	0.0000
Pfn4	ENSMUSG00000020639	profilin family, member 4	1.535	0.0224	0.0485	1.577	0.0165	0.0406
Pgrmc2	ENSMUSG00000049940	progesterone receptor membrane component 2	2.410	0.0000	0.0000	2.345	0.0000	0.0000
Phactr3	ENSMUSG00000027525	phosphatase and actin regulator 3	3.466	0.0000	0.0000	2.297	0.0015	0.0048
Phc2	ENSMUSG00000028796	polyhomeotic 2	1.568	0.0002	0.0008	1.988	0.0000	0.0000
Phf1	ENSMUSG00000024193	PHD finger protein 1	1.902	0.0000	0.0000	1.921	0.0000	0.0000
Phf10	ENSMUSG00000023883	PHD finger protein 10	1.783	0.0000	0.0000	1.902	0.0000	0.0000
Phf13	ENSMUSG00000047777	PHD finger protein 13	2.270	0.0000	0.0000	2.527	0.0000	0.0000
Phlda3	ENSMUSG00000041801	pleckstrin homology like domain, family A, member 3	1.699	0.0149	0.0339	1.732	0.0121	0.0310
Phldb3	ENSMUSG00000074277	pleckstrin homology like domain, family B, member 3	2.701	0.0097	0.0234	2.676	0.0076	0.0206
Phospho1	ENSMUSG00000050860	phosphatase, orphan 1	12.572	0.0000	0.0000	8.823	0.0000	0.0000
Phox2a	ENSMUSG00000007946	paired-like homeobox 2a	3.301	0.0004	0.0012	2.469	0.0071	0.0194
Phtf1	ENSMUSG00000058388	putative homeodomain transcription factor 1	2.503	0.0000	0.0000	2.133	0.0000	0.0000
Pi4k2b	ENSMUSG00000029186	phosphatidylinositol 4-kinase type 2 beta	1.951	0.0011	0.0034	1.598	0.0232	0.0541
Pick1	ENSMUSG00000068206	protein interacting with C kinase 1	1.598	0.0004	0.0013	1.679	0.0001	0.0004
Pilra	ENSMUSG00000046245	paired immunoglobin-like type 2 receptor alpha	2.440	0.0016	0.0048	2.493	0.0016	0.0053
Pin4	ENSMUSG00000079480	peptidyl-prolyl cis/trans isomerase, NIMA-interacting, 4 (parvulin)	4.648	0.0000	0.0000	4.904	0.0000	0.0000
Pip4k2b	ENSMUSG00000018547	phosphatidylinositol-5-phosphate 4-kinase, type II, beta	1.634	0.0000	0.0000	1.733	0.0000	0.0000
Pip4p1	ENSMUSG00000035953	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 1	1.951	0.0000	0.0001	1.653	0.0018	0.0060
Pitpna	ENSMUSG00000017781	phosphatidylinositol transfer protein, alpha	2.662	0.0000	0.0000	2.794	0.0000	0.0000
Pitpnb	ENSMUSG00000050017	phosphatidylinositol transfer protein, beta	1.847	0.0000	0.0000	1.831	0.0000	0.0000
Pitx3	ENSMUSG00000025229	paired-like homeodomain transcription factor 3	5.374	0.0000	0.0001	4.276	0.0002	0.0009
Pkd2	ENSMUSG00000034462	polycystin 2, transient receptor potential cation channel	1.971	0.0000	0.0000	2.106	0.0000	0.0000
Pkdcc	ENSMUSG00000024247	protein kinase domain containing, cytoplasmic	1.791	0.0001	0.0002	2.081	0.0000	0.0000
Pkm	ENSMUSG00000032294	pyruvate kinase, muscle	2.658	0.0000	0.0000	2.524	0.0000	0.0000
Pkp2	ENSMUSG00000041957	plakophilin 2	1.634	0.0003	0.0010	1.512	0.0023	0.0072
Pla2g12a	ENSMUSG00000027999	phospholipase A2, group XIIA	2.686	0.0000	0.0000	3.535	0.0000	0.0000
Plcl1	ENSMUSG00000038349	phospholipase C-like 1	1.544	0.0004	0.0014	1.724	0.0000	0.0001
Plekha1	ENSMUSG00000040268	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 1	2.258	0.0000	0.0000	1.683	0.0000	0.0000
Plekha3	ENSMUSG00000002733	pleckstrin homology domain-containing, family A (phosphoinositide binding specific) member 3	2.026	0.0000	0.0000	1.863	0.0000	0.0000
Plekha8	ENSMUSG00000005225	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 8	1.568	0.0000	0.0000	1.564	0.0000	0.0000
Plekhd1	ENSMUSG00000066438	pleckstrin homology domain containing, family D (with coiled-coil domains) member 1	4.113	0.0149	0.0340	3.320	0.0364	0.0795
Plekhh3	ENSMUSG00000035172	pleckstrin homology domain containing, family H (with MyTH4 domain) member 3	2.052	0.0001	0.0005	1.788	0.0020	0.0065

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Plekhj1	ENSMUSG00000035278	pleckstrin homology domain containing, family J member 1	2.498	0.0000	0.0000	2.564	0.0000	0.0000
Plod2	ENSMUSG00000032374	procollagen lysine, 2-oxoglutarate 5-dioxygenase 2	1.813	0.0000	0.0000	1.530	0.0000	0.0002
Plpp6	ENSMUSG00000040105	phospholipid phosphatase 6	1.754	0.0000	0.0000	1.752	0.0000	0.0000
Plppr2	ENSMUSG00000040563	phospholipid phosphatase related 2	1.924	0.0003	0.0010	2.226	0.0000	0.0001
Pm20d2	ENSMUSG00000054659	peptidase M20 domain containing 2	2.281	0.0000	0.0001	1.565	0.0212	0.0500
Pnisr	ENSMUSG00000028248	PNN interacting serine/arginine-rich	2.413	0.0000	0.0000	2.067	0.0000	0.0000
Pnma8b	ENSMUSG00000070802	PNMA family member 8B	1.509	0.0007	0.0021	1.915	0.0000	0.0000
Pnn	ENSMUSG00000020994	pinin	4.660	0.0000	0.0000	3.805	0.0000	0.0000
Pnrc1	ENSMUSG00000040128	proline-rich nuclear receptor coactivator 1	2.517	0.0000	0.0000	2.101	0.0003	0.0012
Polr1c	ENSMUSG00000067148	polymerase (RNA) I polypeptide C	1.750	0.0000	0.0000	1.692	0.0000	0.0000
Polr1has	ENSMUSG00000036214	RNA polymerase I subunit H, antisense	1.728	0.0000	0.0000	1.692	0.0000	0.0000
Polr2m	ENSMUSG00000032199	polymerase (RNA) II (DNA directed) polypeptide M	1.830	0.0000	0.0000	1.543	0.0000	0.0000
Polr3d	ENSMUSG00000000776	polymerase (RNA) III (DNA directed) polypeptide D	1.517	0.0000	0.0001	1.560	0.0000	0.0000
Polr3g	ENSMUSG00000035834	polymerase (RNA) III (DNA directed) polypeptide G	2.318	0.0000	0.0000	1.879	0.0000	0.0000
Polr3gl	ENSMUSG00000028104	polymerase (RNA) III (DNA directed) polypeptide G like	1.992	0.0000	0.0000	2.332	0.0000	0.0000
Pou3f1	ENSMUSG00000090125	POU domain, class 3, transcription factor 1	5.364	0.0000	0.0001	5.884	0.0000	0.0000
Ppat	ENSMUSG00000029246	phosphoribosyl pyrophosphate amidotransferase	1.690	0.0000	0.0000	1.545	0.0000	0.0000
Ppfibp1	ENSMUSG00000016487	PTPRF interacting protein, binding protein 1 (liprin beta 1)	2.169	0.0000	0.0000	2.075	0.0000	0.0000
Ppid	ENSMUSG00000027804	peptidylprolyl isomerase D (cyclophilin D)	2.133	0.0000	0.0000	2.027	0.0000	0.0000
Ppig	ENSMUSG00000042133	peptidyl-prolyl isomerase G (cyclophilin G)	3.375	0.0000	0.0000	3.267	0.0000	0.0000
Ppil3	ENSMUSG00000026035	peptidylprolyl isomerase (cyclophilin)-like 3	2.115	0.0000	0.0000	2.183	0.0000	0.0000
Ppil4	ENSMUSG00000015757	peptidylprolyl isomerase (cyclophilin)-like 4	2.108	0.0000	0.0000	1.880	0.0000	0.0000
Ppm1a	ENSMUSG00000021096	protein phosphatase 1A, magnesium dependent, alpha isoform	2.450	0.0000	0.0000	2.553	0.0000	0.0000
Ppm1b	ENSMUSG00000061130	protein phosphatase 1B, magnesium dependent, beta isoform	3.075	0.0000	0.0000	3.146	0.0000	0.0000
Ppm1g	ENSMUSG00000029147	protein phosphatase 1G (formerly 2C), magnesium-dependent, gamma isoform	2.121	0.0000	0.0000	2.106	0.0000	0.0000
Ppp1cb	ENSMUSG00000014956	protein phosphatase 1 catalytic subunit beta	2.016	0.0000	0.0000	1.705	0.0000	0.0000
Ppp1cc	ENSMUSG00000004455	protein phosphatase 1 catalytic subunit gamma	1.676	0.0000	0.0000	1.741	0.0000	0.0000
Ppp1r11	ENSMUSG00000036398	protein phosphatase 1, regulatory inhibitor subunit 11	2.191	0.0000	0.0000	2.592	0.0000	0.0000
Ppp1r12a	ENSMUSG00000019907	protein phosphatase 1, regulatory subunit 12A	1.976	0.0000	0.0000	1.697	0.0000	0.0000
Ppp1r14a	ENSMUSG00000037166	protein phosphatase 1, regulatory inhibitor subunit 14A	3.535	0.0000	0.0000	1.894	0.0124	0.0315
Ppp1r14b	ENSMUSG00000056612	protein phosphatase 1, regulatory inhibitor subunit 14B	3.916	0.0000	0.0000	4.526	0.0000	0.0000
Ppp1r18os	ENSMUSG00000087443	protein phosphatase 1, regulatory subunit 18, opposite strand	3.009	0.0372	0.0750	3.232	0.0432	0.0916
Ppp1r1a	ENSMUSG00000022490	protein phosphatase 1, regulatory inhibitor subunit 1A	2.276	0.0002	0.0007	1.718	0.0156	0.0386
Ppp1r2-ps4	ENSMUSG00000059237	protein phosphatase 1, regulatory (inhibitor) subunit 2, pseudogene 4	3.337	0.0018	0.0052	2.521	0.0164	0.0403
Ppp1r35	ENSMUSG00000029725	protein phosphatase 1, regulatory subunit 35	4.189	0.0000	0.0000	3.962	0.0000	0.0000
Ppp1r3f	ENSMUSG00000039556	protein phosphatase 1, regulatory subunit 3F	4.485	0.0000	0.0000	4.459	0.0000	0.0000
Ppp1r9b	ENSMUSG00000038976	protein phosphatase 1, regulatory subunit 9B	3.857	0.0000	0.0000	3.945	0.0000	0.0000
Ppp2ca	ENSMUSG00000020349	protein phosphatase 2 (formerly 2A), catalytic subunit, alpha isoform	1.820	0.0000	0.0000	1.716	0.0000	0.0000
Ppp2r5a	ENSMUSG00000026626	protein phosphatase 2, regulatory subunit B', alpha	2.227	0.0000	0.0000	1.995	0.0000	0.0000
Ppp3cc	ENSMUSG00000022092	protein phosphatase 3, catalytic subunit, gamma isoform	2.039	0.0000	0.0000	2.009	0.0000	0.0000
Ppp4c	ENSMUSG00000030697	protein phosphatase 4, catalytic subunit	2.443	0.0000	0.0000	2.414	0.0000	0.0000
Ppp4r1l-ps	ENSMUSG00000055897	protein phosphatase 4, regulatory subunit 1-like, pseudogene	1.968	0.0000	0.0000	1.716	0.0002	0.0007
Ppp4r3a	ENSMUSG00000041846	protein phosphatase 4 regulatory subunit 3A	1.979	0.0000	0.0000	1.592	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ppwd1	ENSMUSG00000021713	peptidylprolyl isomerase domain and WD repeat containing 1	1.702	0.0000	0.0000	1.640	0.0000	0.0000
Prcd	ENSMUSG00000075410	photoreceptor disc component	1.874	0.0092	0.0223	2.423	0.0001	0.0006
Prdm10	ENSMUSG00000042496	PR domain containing 10	1.524	0.0000	0.0000	1.579	0.0000	0.0000
Prdm8	ENSMUSG00000035456	PR domain containing 8	4.430	0.0004	0.0012	6.438	0.0000	0.0000
Prkar1a	ENSMUSG00000020612	protein kinase, cAMP dependent regulatory, type I, alpha	1.650	0.0000	0.0000	1.529	0.0000	0.0000
Prkci	ENSMUSG00000037643	protein kinase C, iota	2.052	0.0000	0.0000	1.764	0.0000	0.0000
Prkg1	ENSMUSG00000052920	protein kinase, cGMP-dependent, type I	1.787	0.0000	0.0000	1.574	0.0000	0.0000
Prkrip1	ENSMUSG00000039737	Prkr interacting protein 1 (IL11 inducible)	1.550	0.0000	0.0000	1.618	0.0000	0.0000
Prmt9	ENSMUSG00000037134	protein arginine methyltransferase 9	2.296	0.0000	0.0000	2.208	0.0000	0.0000
Procr	ENSMUSG00000027611	protein C receptor, endothelial	1.903	0.0007	0.0023	2.750	0.0000	0.0000
Prpf18	ENSMUSG00000039449	pre-mRNA processing factor 18	1.578	0.0000	0.0000	1.523	0.0000	0.0000
Prpf3	ENSMUSG00000015748	pre-mRNA processing factor 3	2.193	0.0000	0.0000	2.072	0.0000	0.0000
Prpf31	ENSMUSG00000008373	pre-mRNA processing factor 31	2.594	0.0000	0.0000	2.615	0.0000	0.0000
Prpf38b	ENSMUSG00000027881	PRP38 pre-mRNA processing factor 38 (yeast) domain containing B	3.004	0.0000	0.0000	2.927	0.0000	0.0000
Prph	ENSMUSG00000023484	peripherin	3.652	0.0207	0.0454	5.139	0.0067	0.0186
Prr18	ENSMUSG00000055945	proline rich 18	2.895	0.0149	0.0340	2.850	0.0265	0.0607
Prr33	ENSMUSG00000043795	proline rich 33	1.885	0.0000	0.0001	1.724	0.0003	0.0011
Prr5	ENSMUSG00000036106	proline rich 5 (renal)	2.207	0.0000	0.0000	2.577	0.0000	0.0000
Prr7	ENSMUSG00000034686	proline rich 7 (synaptic)	6.984	0.0000	0.0000	2.566	0.0223	0.0523
Prrx2	ENSMUSG00000039476	paired related homeobox 2	4.541	0.0003	0.0009	8.978	0.0000	0.0000
Psip1	ENSMUSG00000028484	PC4 and SFRS1 interacting protein 1	2.345	0.0000	0.0000	2.502	0.0000	0.0000
Psma5	ENSMUSG00000068749	proteasome subunit alpha 5	1.728	0.0000	0.0000	1.572	0.0000	0.0000
Psmb7	ENSMUSG00000026750	proteasome (prosome, macropain) subunit, beta type 7	1.916	0.0000	0.0000	1.972	0.0000	0.0000
Psmd10	ENSMUSG00000031429	proteasome (prosome, macropain) 26S subunit, non-ATPase, 10	1.837	0.0000	0.0000	1.660	0.0000	0.0000
Psmd14	ENSMUSG00000026914	proteasome (prosome, macropain) 26S subunit, non-ATPase, 14	2.357	0.0000	0.0000	2.217	0.0000	0.0000
Psmd7	ENSMUSG00000039067	proteasome (prosome, macropain) 26S subunit, non-ATPase, 7	1.550	0.0002	0.0008	1.592	0.0001	0.0004
Psme2b	ENSMUSG00000078153	protease (prosome, macropain) activator subunit 2B	1.697	0.0007	0.0023	1.511	0.0100	0.0262
Pten	ENSMUSG00000013663	phosphatase and tensin homolog	1.763	0.0000	0.0000	1.580	0.0001	0.0006
Ptges2	ENSMUSG00000026820	prostaglandin E synthase 2	1.737	0.0000	0.0000	1.684	0.0000	0.0000
Ptges3	ENSMUSG00000071072	prostaglandin E synthase 3	3.143	0.0000	0.0000	2.224	0.0000	0.0000
Ptgr2	ENSMUSG00000072946	prostaglandin reductase 2	1.780	0.0000	0.0000	1.612	0.0000	0.0000
Ptma	ENSMUSG00000026238	prothymosin alpha	7.683	0.0000	0.0000	6.791	0.0000	0.0000
Ptms	ENSMUSG00000030122	parathymosin	5.617	0.0000	0.0000	4.979	0.0000	0.0000
Ptp4a3	ENSMUSG00000059895	protein tyrosine phosphatase 4a3	1.700	0.0000	0.0001	1.598	0.0001	0.0005
Ptpn11	ENSMUSG00000043733	protein tyrosine phosphatase, non-receptor type 11	1.618	0.0002	0.0007	1.573	0.0004	0.0016
Ptpra	ENSMUSG00000027303	protein tyrosine phosphatase, receptor type, A	1.658	0.0000	0.0000	1.795	0.0000	0.0000
Ptx3	ENSMUSG00000027832	pentraxin related gene	3.254	0.0026	0.0072	3.786	0.0006	0.0023
Pum3	ENSMUSG00000041360	pumilio RNA-binding family member 3	1.642	0.0000	0.0000	1.650	0.0000	0.0000
Pura	ENSMUSG00000043991	purine rich element binding protein A	1.770	0.0000	0.0000	1.552	0.0000	0.0000
Purb	ENSMUSG00000094483	purine rich element binding protein B	1.666	0.0000	0.0000	1.621	0.0000	0.0000
Pwwp2a	ENSMUSG00000044950	PWWP domain containing 2A	2.368	0.0000	0.0000	2.041	0.0000	0.0000
Pxdc1	ENSMUSG00000021411	PX domain containing 1	2.640	0.0000	0.0000	2.978	0.0000	0.0000
Pygo1	ENSMUSG00000034910	pygopus 1	2.044	0.0000	0.0000	1.670	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pygo2	ENSMUSG00000047824	pygopus 2	1.669	0.0000	0.0000	1.628	0.0000	0.0001
Qki	ENSMUSG00000062078	quaking, KH domain containing RNA binding	2.097	0.0000	0.0000	1.832	0.0000	0.0000
R3hcc1	ENSMUSG00000034194	R3H domain and coiled-coil containing 1	2.935	0.0000	0.0000	3.088	0.0000	0.0000
R3hdm4	ENSMUSG00000035781	R3H domain containing 4	1.856	0.0000	0.0000	2.096	0.0000	0.0000
Rab10os	ENSMUSG00000079179	RAB10, member RAS oncogene family, opposite strand	1.729	0.0000	0.0002	1.644	0.0003	0.0010
Rab12	ENSMUSG00000023460	RAB12, member RAS oncogene family	1.617	0.0000	0.0000	1.646	0.0000	0.0000
Rab18	ENSMUSG00000073639	RAB18, member RAS oncogene family	2.611	0.0000	0.0000	2.232	0.0000	0.0000
Rab21	ENSMUSG00000020132	RAB21, member RAS oncogene family	2.084	0.0000	0.0000	1.844	0.0000	0.0000
Rab22a	ENSMUSG00000027519	RAB22A, member RAS oncogene family	2.160	0.0000	0.0000	2.120	0.0000	0.0000
Rab24	ENSMUSG00000034789	RAB24, member RAS oncogene family	2.441	0.0000	0.0000	1.800	0.0034	0.0103
Rab27a	ENSMUSG00000032202	RAB27A, member RAS oncogene family	1.560	0.0101	0.0242	1.605	0.0063	0.0176
Rab28	ENSMUSG00000029128	RAB28, member RAS oncogene family	2.918	0.0000	0.0000	2.654	0.0000	0.0000
Rab2a	ENSMUSG00000047187	RAB2A, member RAS oncogene family	2.079	0.0000	0.0000	1.950	0.0000	0.0000
Rab43	ENSMUSG00000030055	RAB43, member RAS oncogene family	9.546	0.0000	0.0000	5.662	0.0000	0.0000
Rab5a	ENSMUSG00000017831	RAB5A, member RAS oncogene family	1.830	0.0000	0.0000	1.563	0.0001	0.0004
Rab5if	ENSMUSG00000027637	RAB5 interacting factor	3.150	0.0000	0.0000	3.088	0.0000	0.0000
Rab8a	ENSMUSG00000003037	RAB8A, member RAS oncogene family	2.866	0.0000	0.0000	2.994	0.0000	0.0000
Rabl3	ENSMUSG00000022827	RAB, member RAS oncogene family-like 3	1.528	0.0000	0.0000	1.570	0.0000	0.0000
Rac1	ENSMUSG00000001847	Rac family small GTPase 1	1.894	0.0000	0.0000	1.546	0.0000	0.0000
Rad23b	ENSMUSG00000028426	RAD23 homolog B, nucleotide excision repair protein	2.081	0.0000	0.0000	1.763	0.0000	0.0000
Rad51c	ENSMUSG00000007646	RAD51 paralog C	1.771	0.0014	0.0042	1.547	0.0172	0.0420
Rala	ENSMUSG00000008859	v-ral simian leukemia viral oncogene A (ras related)	2.229	0.0000	0.0000	1.794	0.0000	0.0000
Ramac	ENSMUSG00000038646	RNA guanine-7 methyltransferase activating subunit	2.317	0.0000	0.0000	1.939	0.0000	0.0000
Ranbp1	ENSMUSG00000005732	RAN binding protein 1	2.568	0.0000	0.0000	2.235	0.0000	0.0000
Ranbp9	ENSMUSG00000038546	RAN binding protein 9	1.768	0.0034	0.0093	1.708	0.0060	0.0168
Rap1a	ENSMUSG00000068798	RAS-related protein 1a	2.551	0.0000	0.0000	2.228	0.0000	0.0000
Rap1b	ENSMUSG00000052681	RAS related protein 1b	2.175	0.0000	0.0000	1.851	0.0000	0.0000
Rap2b	ENSMUSG00000036894	RAP2B, member of RAS oncogene family	2.030	0.0000	0.0000	2.328	0.0000	0.0000
Rars	ENSMUSG00000018848	arginyl-tRNA synthetase	1.505	0.0000	0.0000	1.518	0.0000	0.0000
Rasl10b	ENSMUSG00000020684	RAS-like, family 10, member B	1.749	0.0000	0.0000	2.111	0.0000	0.0000
Rassf3	ENSMUSG00000025795	Ras association (RalGDS/AF-6) domain family member 3	2.157	0.0000	0.0000	2.081	0.0000	0.0000
Rbm15b	ENSMUSG00000074102	RNA binding motif protein 15B	1.576	0.0000	0.0000	1.619	0.0000	0.0000
Rbm17	ENSMUSG00000037197	RNA binding motif protein 17	4.626	0.0000	0.0000	4.039	0.0000	0.0000
Rbm24	ENSMUSG00000038132	RNA binding motif protein 24	2.410	0.0000	0.0000	2.437	0.0000	0.0000
Rbm25	ENSMUSG00000010608	RNA binding motif protein 25	3.062	0.0000	0.0000	3.017	0.0000	0.0000
Rbm3	ENSMUSG00000031167	RNA binding motif (RNP1, RRM) protein 3	2.211	0.0000	0.0000	1.979	0.0000	0.0000
Rbm33	ENSMUSG00000048271	RNA binding motif protein 33	1.786	0.0007	0.0021	1.708	0.0017	0.0054
Rbm45	ENSMUSG00000042369	RNA binding motif protein 45	2.051	0.0000	0.0000	1.917	0.0000	0.0000
Rbm6	ENSMUSG00000032582	RNA binding motif protein 6	1.819	0.0000	0.0000	1.679	0.0000	0.0000
Rbm8a	ENSMUSG00000038374	RNA binding motif protein 8a	2.233	0.0000	0.0000	2.288	0.0000	0.0000
Rbpj-ps3	ENSMUSG00000079575	recombination signal binding protein for immunoglobulin kappa J region, pseudogene 3	1.804	0.0000	0.0000	1.980	0.0000	0.0000
Rbpms	ENSMUSG00000031586	RNA binding protein gene with multiple splicing	3.990	0.0000	0.0000	3.197	0.0000	0.0000
Rcan2	ENSMUSG00000039601	regulator of calcineurin 2	1.769	0.0000	0.0000	1.699	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rcn1	ENSMUSG00000005973	reticulocalbin 1	1.877	0.0000	0.0000	1.851	0.0000	0.0000
Rdh10	ENSMUSG00000025921	retinol dehydrogenase 10 (all-trans)	1.743	0.0000	0.0000	1.560	0.0000	0.0000
Rell1	ENSMUSG00000047881	RELT-like 1	1.846	0.0000	0.0000	1.722	0.0000	0.0000
Renbp	ENSMUSG00000031387	renin binding protein	1.938	0.0000	0.0000	2.424	0.0000	0.0000
Rest	ENSMUSG00000029249	RE1-silencing transcription factor	2.088	0.0000	0.0000	1.772	0.0000	0.0000
Rflnb	ENSMUSG00000020846	refilin B	2.419	0.0000	0.0000	1.961	0.0000	0.0000
Rfxap	ENSMUSG00000036615	regulatory factor X-associated protein	4.609	0.0000	0.0000	5.052	0.0000	0.0000
Rhbdl1	ENSMUSG00000025735	rhomboid like 1	4.482	0.0275	0.0578	14.849	0.0013	0.0044
Rhbdl3	ENSMUSG00000017692	rhomboid like 3	4.708	0.0000	0.0000	3.447	0.0000	0.0000
Rheb	ENSMUSG00000028945	Ras homolog enriched in brain	2.254	0.0000	0.0000	2.066	0.0000	0.0000
Rhoa	ENSMUSG00000007815	ras homolog family member A	2.111	0.0000	0.0000	1.885	0.0000	0.0000
Rhot2	ENSMUSG00000025733	ras homolog family member T2	1.710	0.0000	0.0000	1.894	0.0000	0.0000
Rhox5	ENSMUSG00000095180	reproductive homeobox 5	1.623	0.0191	0.0423	2.088	0.0004	0.0017
Ribc1	ENSMUSG00000025257	RIB43A domain with coiled-coils 1	2.023	0.0128	0.0298	2.623	0.0009	0.0032
Rida	ENSMUSG00000022323	reactive intermediate imine deaminase A homolog	1.960	0.0000	0.0000	1.789	0.0000	0.0000
Rilpl1	ENSMUSG00000029392	Rab interacting lysosomal protein-like 1	1.581	0.0000	0.0001	1.870	0.0000	0.0000
Rims4	ENSMUSG00000035226	regulating synaptic membrane exocytosis 4	1.967	0.0013	0.0038	1.707	0.0110	0.0285
Ring1	ENSMUSG00000024325	ring finger protein 1	2.136	0.0000	0.0001	1.745	0.0017	0.0056
Ripk1	ENSMUSG00000021408	receptor (TNFRSF)-interacting serine-threonine kinase 1	1.723	0.0000	0.0000	1.507	0.0000	0.0001
Rnf10	ENSMUSG00000041740	ring finger protein 10	2.875	0.0000	0.0000	1.748	0.0013	0.0045
Rnf103	ENSMUSG00000052656	ring finger protein 103	2.434	0.0000	0.0000	2.344	0.0000	0.0000
Rnf11	ENSMUSG00000028557	ring finger protein 11	2.116	0.0000	0.0000	1.702	0.0000	0.0000
Rnf113a2	ENSMUSG00000098134	ring finger protein 113A2	2.151	0.0000	0.0000	2.405	0.0000	0.0000
Rnf125	ENSMUSG00000033107	ring finger protein 125	1.943	0.0001	0.0002	1.729	0.0011	0.0036
Rnf146	ENSMUSG00000038876	ring finger protein 146	2.053	0.0000	0.0000	1.640	0.0000	0.0000
Rnf149	ENSMUSG00000048234	ring finger protein 149	2.457	0.0000	0.0000	2.379	0.0000	0.0000
Rnf166	ENSMUSG00000014470	ring finger protein 166	1.610	0.0000	0.0001	1.693	0.0000	0.0000
Rnf19b	ENSMUSG00000028793	ring finger protein 19B	2.190	0.0000	0.0000	2.483	0.0000	0.0000
Rnf20	ENSMUSG00000028309	ring finger protein 20	1.945	0.0000	0.0000	1.820	0.0000	0.0000
Rnf214	ENSMUSG00000042790	ring finger protein 214	1.652	0.0000	0.0000	1.694	0.0000	0.0000
Rnf217	ENSMUSG00000063760	ring finger protein 217	1.798	0.0000	0.0000	1.624	0.0000	0.0000
Rnf220	ENSMUSG00000028677	ring finger protein 220	2.106	0.0000	0.0000	2.612	0.0000	0.0000
Rnps1	ENSMUSG00000034681	RNA binding protein with serine rich domain 1	2.942	0.0000	0.0000	2.949	0.0000	0.0000
Rock1	ENSMUSG00000024290	Rho-associated coiled-coil containing protein kinase 1	2.451	0.0000	0.0000	1.857	0.0000	0.0000
Rock2	ENSMUSG00000020580	Rho-associated coiled-coil containing protein kinase 2	1.806	0.0000	0.0000	1.561	0.0000	0.0000
Rp9	ENSMUSG00000032239	retinitis pigmentosa 9 (human)	2.809	0.0000	0.0000	2.272	0.0000	0.0000
Rpia	ENSMUSG00000053604	ribose 5-phosphate isomerase A	2.390	0.0000	0.0000	1.707	0.0023	0.0074
Rpl11	ENSMUSG00000059291	ribosomal protein L11	2.844	0.0000	0.0000	2.809	0.0000	0.0000
Rpl14-ps1	ENSMUSG00000046721	ribosomal protein L14, pseudogene 1	1.735	0.0000	0.0000	1.588	0.0000	0.0001
Rpl15-ps6	ENSMUSG00000057262	ribosomal protein L15, pseudogene 6	9.077	0.0000	0.0002	6.326	0.0002	0.0010
Rpl30-ps11	ENSMUSG00000081461	ribosomal protein L30, pseudogene 11	2.858	0.0415	0.0824	3.829	0.0152	0.0379
Rpl5	ENSMUSG00000058558	ribosomal protein L5	2.597	0.0000	0.0000	2.219	0.0000	0.0000
Rpl5-ps2	ENSMUSG00000082064	ribisomal protein L5, pseudogene 2	5.263	0.0000	0.0000	3.616	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpl9	ENSMUSG00000047215	ribosomal protein L9	2.184	0.0000	0.0000	1.857	0.0000	0.0000
Rpl9-ps7	ENSMUSG00000047965	ribosomal protein L9, pseudogene 7	6.635	0.0000	0.0000	4.230	0.0000	0.0000
Rps12-ps4	ENSMUSG00000109509	ribosomal protein S12, pseudogene 4	7.743	0.0050	0.0130	5.876	0.0161	0.0398
Rps14	ENSMUSG00000024608	ribosomal protein S14	1.841	0.0000	0.0000	2.095	0.0000	0.0000
Rps18	ENSMUSG00000008668	ribosomal protein S18	2.072	0.0000	0.0000	2.280	0.0000	0.0000
Rps2	ENSMUSG00000044533	ribosomal protein S2	2.789	0.0000	0.0002	1.992	0.0063	0.0175
Rps23-ps1	ENSMUSG00000100755	ribosomal protein S23, pseudogene 1	1.713	0.0127	0.0296	1.957	0.0018	0.0060
Rps2-ps10	ENSMUSG00000091957	ribosomal protein S2, pseudogene 10	8.445	0.0000	0.0000	4.730	0.0000	0.0000
Rps2-ps13	ENSMUSG00000081684	ribosomal protein S2, pseudogene 13	3.766	0.0005	0.0017	3.848	0.0020	0.0063
Rps2-ps8	ENSMUSG00000118161	ribosomal protein S2, pseudogene 8	2.797	0.0454	0.0889	2.903	0.0447	0.0941
Rps3	ENSMUSG00000030744	ribosomal protein S3	1.821	0.0000	0.0000	1.846	0.0000	0.0000
Rps6	ENSMUSG00000028495	ribosomal protein S6	1.667	0.0000	0.0000	1.556	0.0000	0.0000
Rps6kb1	ENSMUSG00000020516	ribosomal protein S6 kinase, polypeptide 1	1.685	0.0000	0.0000	1.657	0.0000	0.0000
Rps6-ps3	ENSMUSG00000082465	ribosomal protein S6, pseudogene 3	23.307	0.0013	0.0039	4.280	0.0233	0.0543
Rras	ENSMUSG00000038387	related RAS viral (r-ras) oncogene	1.907	0.0000	0.0000	2.260	0.0000	0.0000
Rras2	ENSMUSG00000055723	related RAS viral (r-ras) oncogene 2	2.198	0.0000	0.0000	1.960	0.0000	0.0000
Rrbp1	ENSMUSG00000027422	ribosome binding protein 1	1.594	0.0000	0.0000	1.824	0.0000	0.0000
Rrp1	ENSMUSG00000061032	ribosomal RNA processing 1	2.124	0.0000	0.0000	2.393	0.0000	0.0000
Rrp15	ENSMUSG00000001305	ribosomal RNA processing 15 homolog	2.410	0.0000	0.0000	2.433	0.0000	0.0000
Rrp9	ENSMUSG00000041506	ribosomal RNA processing 9, U3 small nucleolar RNA binding protein	1.892	0.0000	0.0000	2.210	0.0000	0.0000
Rsad2	ENSMUSG00000020641	radical S-adenosyl methionine domain containing 2	1.520	0.0000	0.0001	1.508	0.0000	0.0002
Rsf1	ENSMUSG00000035623	remodeling and spacing factor 1	1.823	0.0000	0.0000	1.521	0.0001	0.0005
Rsl24d1	ENSMUSG00000032215	ribosomal L24 domain containing 1	2.718	0.0000	0.0000	2.577	0.0000	0.0000
Rsph3a	ENSMUSG00000073471	radial spoke 3A homolog (Chlamydomonas)	2.553	0.0000	0.0000	1.637	0.0000	0.0000
Rsph3b	ENSMUSG00000023806	radial spoke 3B homolog (Chlamydomonas)	2.758	0.0000	0.0000	1.724	0.0014	0.0046
Rsrc2	ENSMUSG00000029422	arginine/serine-rich coiled-coil 2	2.053	0.0000	0.0000	1.809	0.0000	0.0000
Rsu1	ENSMUSG00000026727	Ras suppressor protein 1	1.553	0.0000	0.0000	1.504	0.0000	0.0000
Rtcb	ENSMUSG00000001783	RNA 2',3'-cyclic phosphate and 5'-OH ligase	1.838	0.0000	0.0000	1.937	0.0000	0.0000
Rtn4	ENSMUSG00000020458	reticulon 4	2.375	0.0000	0.0000	2.148	0.0000	0.0000
Rtn4ip1	ENSMUSG00000019864	reticulon 4 interacting protein 1	1.962	0.0000	0.0000	1.997	0.0000	0.0000
Rtn4r	ENSMUSG00000043811	reticulon 4 receptor	2.594	0.0468	0.0914	3.138	0.0171	0.0417
Rtn4rl2	ENSMUSG00000050896	reticulon 4 receptor-like 2	2.423	0.0219	0.0476	2.342	0.0405	0.0869
Rufy1	ENSMUSG00000020375	RUN and FYVE domain containing 1	2.909	0.0000	0.0000	2.811	0.0000	0.0000
Rufy3	ENSMUSG00000029291	RUN and FYVE domain containing 3	1.855	0.0000	0.0000	1.563	0.0001	0.0005
Ruvbl1	ENSMUSG00000030079	RuvB-like protein 1	1.738	0.0000	0.0000	1.933	0.0000	0.0000
Rwdd3	ENSMUSG00000028133	RWD domain containing 3	1.588	0.0059	0.0151	1.532	0.0115	0.0296
Rwdd4a	ENSMUSG00000031568	RWD domain containing 4A	1.600	0.0000	0.0000	1.553	0.0000	0.0000
S1pr5	ENSMUSG00000045087	sphingosine-1-phosphate receptor 5	1.842	0.0018	0.0051	2.044	0.0002	0.0009
Safb	ENSMUSG00000071054	scaffold attachment factor B	2.179	0.0000	0.0000	2.313	0.0000	0.0000
Safb2	ENSMUSG00000042625	scaffold attachment factor B2	1.608	0.0001	0.0003	1.777	0.0000	0.0000
Sall4	ENSMUSG00000027547	spalt like transcription factor 4	2.151	0.0003	0.0011	1.728	0.0100	0.0264
Samd1	ENSMUSG00000079003	sterile alpha motif domain containing 1	3.077	0.0000	0.0000	3.265	0.0000	0.0000
Samd4	ENSMUSG00000021838	sterile alpha motif domain containing 4	1.724	0.0000	0.0000	1.531	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sap18	ENSMUSG00000021963	Sin3-associated polypeptide 18	1.782	0.0000	0.0000	1.694	0.0000	0.0000
Sap18b	ENSMUSG00000061104	Sin3-associated polypeptide 18B	2.785	0.0001	0.0002	3.846	0.0000	0.0000
Sap30	ENSMUSG00000031609	sin3 associated polypeptide	5.097	0.0000	0.0000	3.869	0.0000	0.0000
Sap30l	ENSMUSG00000020519	SAP30-like	9.281	0.0000	0.0000	10.074	0.0000	0.0000
Sarnp	ENSMUSG00000078427	SAP domain containing ribonucleoprotein	2.000	0.0000	0.0000	2.005	0.0000	0.0000
Sars	ENSMUSG00000068739	seryl-aminoacyl-tRNA synthetase	1.607	0.0000	0.0000	1.962	0.0000	0.0000
Sart1	ENSMUSG00000039148	squamous cell carcinoma antigen recognized by T cells 1	2.800	0.0000	0.0000	3.149	0.0000	0.0000
Sart3	ENSMUSG00000018974	squamous cell carcinoma antigen recognized by T cells 3	2.307	0.0000	0.0000	2.079	0.0000	0.0000
Satb1	ENSMUSG00000023927	special AT-rich sequence binding protein 1	2.183	0.0000	0.0000	1.753	0.0000	0.0000
Sbds	ENSMUSG00000025337	SBDS ribosome maturation factor	1.981	0.0000	0.0000	2.018	0.0000	0.0000
Sbk2	ENSMUSG00000030433	SH3-binding domain kinase family, member 2	2.431	0.0000	0.0000	2.289	0.0000	0.0000
Scaf4	ENSMUSG00000022983	SR-related CTD-associated factor 4	2.253	0.0000	0.0000	1.972	0.0000	0.0000
Scamp1	ENSMUSG00000021687	secretory carrier membrane protein 1	1.668	0.0000	0.0000	1.548	0.0000	0.0000
Scand1	ENSMUSG00000046229	SCAN domain-containing 1	12.419	0.0000	0.0000	6.347	0.0000	0.0001
Scarf2	ENSMUSG00000012017	scavenger receptor class F, member 2	2.800	0.0000	0.0000	2.699	0.0000	0.0000
Schip1	ENSMUSG00000027777	schwannomin interacting protein 1	2.751	0.0000	0.0000	1.938	0.0000	0.0000
Scn2b	ENSMUSG00000070304	sodium channel, voltage-gated, type II, beta	2.237	0.0033	0.0090	2.345	0.0019	0.0060
Scx	ENSMUSG00000034161	scleraxis	3.765	0.0000	0.0000	5.703	0.0000	0.0000
Sdc4	ENSMUSG00000017009	syndecan 4	2.489	0.0000	0.0000	2.263	0.0000	0.0000
Sdccag8	ENSMUSG00000026504	serologically defined colon cancer antigen 8	1.712	0.0000	0.0000	1.678	0.0000	0.0000
Sdf2l1	ENSMUSG00000022769	stromal cell-derived factor 2-like 1	1.658	0.0105	0.0251	1.810	0.0031	0.0095
Sdha	ENSMUSG00000021577	succinate dehydrogenase complex, subunit A, flavoprotein (Fp)	1.592	0.0000	0.0000	1.573	0.0000	0.0000
Sdhaf1	ENSMUSG00000074211	succinate dehydrogenase complex assembly factor 1	2.592	0.0000	0.0000	2.172	0.0000	0.0000
Sec11a	ENSMUSG00000025724	SEC11 homolog A, signal peptidase complex subunit	1.951	0.0000	0.0000	1.689	0.0000	0.0000
Sec11c	ENSMUSG00000024516	SEC11 homolog C, signal peptidase complex subunit	1.645	0.0000	0.0000	1.550	0.0000	0.0000
Sec62	ENSMUSG00000027706	SEC62 homolog (S. cerevisiae)	2.440	0.0000	0.0000	2.250	0.0000	0.0000
Sec63	ENSMUSG00000019802	SEC63-like (S. cerevisiae)	1.680	0.0000	0.0000	1.842	0.0000	0.0000
Secisbp2l	ENSMUSG00000035093	SECIS binding protein 2-like	2.076	0.0000	0.0000	1.857	0.0000	0.0000
Sem1	ENSMUSG00000042541	SEM1, 26S proteasome complex subunit	2.070	0.0000	0.0000	2.098	0.0000	0.0000
Sema6b	ENSMUSG00000001227	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6B	3.892	0.0000	0.0000	3.853	0.0000	0.0000
Sema6c	ENSMUSG00000038777	sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6C	2.642	0.0000	0.0000	1.983	0.0018	0.0058
Septin10	ENSMUSG00000019917	septin 10	2.413	0.0000	0.0000	2.131	0.0000	0.0000
Septin7	ENSMUSG00000001833	septin 7	2.494	0.0000	0.0000	2.205	0.0000	0.0000
Serbp1	ENSMUSG00000036371	serpine1 mRNA binding protein 1	3.088	0.0000	0.0000	2.602	0.0000	0.0000
Sertad4	ENSMUSG00000016262	SERTA domain containing 4	1.540	0.0173	0.0388	1.680	0.0042	0.0124
Set	ENSMUSG00000054766	SET nuclear oncogene	3.405	0.0000	0.0000	3.109	0.0000	0.0000
Setd3	ENSMUSG00000056770	SET domain containing 3	1.785	0.0000	0.0000	1.791	0.0000	0.0000
Setd6	ENSMUSG00000031671	SET domain containing 6	2.936	0.0000	0.0000	2.861	0.0000	0.0000
Sf3a1	ENSMUSG00000002129	splicing factor 3a, subunit 1	1.965	0.0000	0.0000	1.979	0.0000	0.0000
Sf3b2	ENSMUSG00000024853	splicing factor 3b, subunit 2	1.724	0.0000	0.0000	2.037	0.0000	0.0000
Sfpq	ENSMUSG00000028820	splicing factor proline/glutamine rich (polypyrimidine tract binding protein associated)	4.390	0.0000	0.0000	2.999	0.0000	0.0000
Sfr1	ENSMUSG00000025066	SWI5 dependent recombination repair 1	2.605	0.0000	0.0000	2.482	0.0000	0.0000
Sfrp5	ENSMUSG00000018822	secreted frizzled-related sequence protein 5	2.961	0.0001	0.0004	1.970	0.0157	0.0389

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sfswap	ENSMUSG00000029439	splicing factor SWAP	2.222	0.0000	0.0000	2.067	0.0000	0.0000
Sgpp1	ENSMUSG00000021054	sphingosine-1-phosphate phosphatase 1	1.800	0.0000	0.0000	1.602	0.0001	0.0005
Sh3bgr	ENSMUSG00000040666	SH3-binding domain glutamic acid-rich protein	1.913	0.0000	0.0000	2.006	0.0000	0.0000
Sh3gl3	ENSMUSG00000030638	SH3-domain GRB2-like 3	3.969	0.0000	0.0000	3.065	0.0000	0.0001
Sh3pxd2a	ENSMUSG00000053617	SH3 and PX domains 2A	1.534	0.0000	0.0000	1.577	0.0000	0.0000
Shc3	ENSMUSG00000021448	src homology 2 domain-containing transforming protein C3	2.249	0.0022	0.0063	1.978	0.0113	0.0292
Shf	ENSMUSG00000033256	Src homology 2 domain containing F	2.168	0.0000	0.0000	2.922	0.0000	0.0000
Shoc2	ENSMUSG00000024976	Shoc2, leucine rich repeat scaffold protein	1.734	0.0000	0.0000	1.652	0.0000	0.0000
Siah1a	ENSMUSG00000036840	siah E3 ubiquitin protein ligase 1A	2.229	0.0000	0.0000	1.916	0.0000	0.0000
Siah2	ENSMUSG00000036432	siah E3 ubiquitin protein ligase 2	3.072	0.0000	0.0000	2.636	0.0000	0.0000
Sinhcaf	ENSMUSG00000039985	SIN3-HDAC complex associated factor	2.382	0.0000	0.0001	2.010	0.0008	0.0027
Six1	ENSMUSG00000051367	sine oculis-related homeobox 1	1.826	0.0255	0.0542	1.792	0.0344	0.0756
Skap2	ENSMUSG00000059182	src family associated phosphoprotein 2	1.570	0.0000	0.0000	1.853	0.0000	0.0000
Slbp	ENSMUSG00000004642	stem-loop binding protein	1.752	0.0000	0.0000	1.507	0.0001	0.0002
Slc12a2	ENSMUSG00000024597	solute carrier family 12, member 2	1.755	0.0000	0.0000	1.556	0.0000	0.0000
Slc16a11	ENSMUSG00000040938	solute carrier family 16 (monocarboxylic acid transporters), member 11	4.951	0.0002	0.0008	3.357	0.0041	0.0122
Slc17a7	ENSMUSG00000070570	solute carrier family 17 (sodium-dependent inorganic phosphate cotransporter), member 7	1.766	0.0000	0.0001	1.930	0.0000	0.0000
Slc22a3	ENSMUSG00000023828	solute carrier family 22 (organic cation transporter), member 3	1.648	0.0194	0.0429	1.559	0.0379	0.0822
Slc24a3	ENSMUSG00000063873	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3	1.596	0.0001	0.0003	1.756	0.0000	0.0000
Slc25a15	ENSMUSG00000031482	solute carrier family 25 (mitochondrial carrier ornithine transporter), member 15	1.608	0.0000	0.0000	1.527	0.0000	0.0000
Slc25a38	ENSMUSG00000032519	solute carrier family 25, member 38	1.558	0.0038	0.0100	1.995	0.0000	0.0000
Slc35a2	ENSMUSG00000031156	solute carrier family 35 (UDP-galactose transporter), member A2	1.624	0.0000	0.0000	1.663	0.0000	0.0000
Slc35a3	ENSMUSG00000027957	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member 3	2.103	0.0000	0.0000	1.795	0.0000	0.0000
Slc35d1	ENSMUSG00000028521	solute carrier family 35 (UDP-glucuronic acid/UDP-N-acetylgalactosamine dual transporter), member D1	1.638	0.0000	0.0000	1.589	0.0000	0.0000
Slc49a4	ENSMUSG00000022848	solute carrier family 49 member 4	1.955	0.0000	0.0000	1.879	0.0000	0.0001
Slc4a1ap	ENSMUSG00000029141	solute carrier family 4 (anion exchanger), member 1, adaptor protein	1.738	0.0000	0.0000	2.040	0.0000	0.0000
Slc6a8	ENSMUSG00000019558	solute carrier family 6 (neurotransmitter transporter, creatine), member 8	2.025	0.0000	0.0000	2.196	0.0000	0.0000
Slc8a2	ENSMUSG00000030376	solute carrier family 8 (sodium/calcium exchanger), member 2	1.636	0.0118	0.0278	1.558	0.0272	0.0621
Slco5a1	ENSMUSG00000025938	solute carrier organic anion transporter family, member 5A1	1.728	0.0000	0.0000	1.652	0.0000	0.0000
Slk	ENSMUSG00000025060	STE20-like kinase	1.780	0.0000	0.0000	1.668	0.0000	0.0000
Slmap	ENSMUSG00000021870	sarcolemma associated protein	2.387	0.0000	0.0000	1.698	0.0000	0.0000
Sltm	ENSMUSG00000032212	SAFB-like, transcription modulator	1.783	0.0001	0.0003	1.884	0.0000	0.0001
Smad1	ENSMUSG00000031681	SMAD family member 1	1.768	0.0000	0.0000	1.706	0.0000	0.0000
Smad4	ENSMUSG00000024515	SMAD family member 4	1.942	0.0000	0.0000	1.982	0.0000	0.0000
Smad6	ENSMUSG00000036867	SMAD family member 6	2.440	0.0000	0.0000	2.847	0.0000	0.0000
Smad7	ENSMUSG00000025880	SMAD family member 7	4.345	0.0000	0.0000	3.717	0.0000	0.0000
Smagp	ENSMUSG00000053559	small cell adhesion glycoprotein	2.736	0.0000	0.0000	2.814	0.0000	0.0000
Smap1	ENSMUSG00000026155	small ArfGAP 1	1.797	0.0000	0.0000	1.629	0.0001	0.0003
Smap2	ENSMUSG00000032870	small ArfGAP 2	1.789	0.0000	0.0000	1.842	0.0000	0.0000
Smarca2	ENSMUSG00000024921	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 2	2.234	0.0000	0.0000	2.623	0.0000	0.0000
Smarca5	ENSMUSG00000031715	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 5	2.508	0.0000	0.0000	1.784	0.0000	0.0000
Smarcc2	ENSMUSG00000025369	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily c, member 2	1.916	0.0000	0.0000	2.176	0.0000	0.0000
Smarcd3	ENSMUSG00000028949	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily d, member 3	3.538	0.0000	0.0000	4.032	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Smarce1	ENSMUSG00000037935	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily e, member 1	1.796	0.0000	0.0000	1.686	0.0000	0.0000
Smc1a	ENSMUSG00000041133	structural maintenance of chromosomes 1A	1.958	0.0000	0.0000	1.991	0.0000	0.0000
Smc3	ENSMUSG00000024974	structural maintenance of chromosomes 3	2.267	0.0000	0.0000	2.061	0.0000	0.0000
Smc6	ENSMUSG00000020608	structural maintenance of chromosomes 6	2.177	0.0000	0.0000	1.759	0.0000	0.0000
Smco4	ENSMUSG00000058173	single-pass membrane protein with coiled-coil domains 4	2.362	0.0000	0.0000	2.436	0.0000	0.0000
Smim10l1	ENSMUSG00000072704	small integral membrane protein 10 like 1	2.150	0.0000	0.0000	1.759	0.0000	0.0000
Smim13	ENSMUSG00000091264	small integral membrane protein 13	1.686	0.0000	0.0000	1.510	0.0000	0.0001
Smim36	ENSMUSG00000110344	small integral membrane protein 36	1.545	0.0000	0.0000	1.513	0.0000	0.0000
Smndc1	ENSMUSG00000025024	survival motor neuron domain containing 1	2.037	0.0000	0.0000	1.914	0.0000	0.0000
Smox	ENSMUSG00000027333	spermine oxidase	1.575	0.0001	0.0005	1.512	0.0006	0.0021
Snapc5	ENSMUSG00000032398	small nuclear RNA activating complex, polypeptide 5	1.768	0.0000	0.0000	1.761	0.0000	0.0000
Snca	ENSMUSG00000025889	synuclein, alpha	3.489	0.0001	0.0003	3.615	0.0001	0.0002
Snhg3	ENSMUSG00000085241	small nucleolar RNA host gene 3	2.719	0.0000	0.0000	2.160	0.0000	0.0000
Snhg4	ENSMUSG00000117869	small nucleolar RNA host gene 4	2.115	0.0001	0.0004	1.727	0.0049	0.0143
Snhg5	ENSMUSG00000097195	small nucleolar RNA host gene 5	2.210	0.0027	0.0075	1.814	0.0254	0.0585
Snhg8	ENSMUSG00000104960	small nucleolar RNA host gene 8	2.077	0.0000	0.0000	1.502	0.0029	0.0089
Snora73b	ENSMUSG00000065353	small nucleolar RNA, H/ACA box 73b	5.434	0.0000	0.0000	4.676	0.0000	0.0000
Snord55	ENSMUSG00000092680	small nucleolar RNA, C/D box 55	53.000	0.0001	0.0004	7.366	0.0084	0.0227
Snrnp27	ENSMUSG00000001158	small nuclear ribonucleoprotein 27 (U4/U6.U5)	2.062	0.0000	0.0000	2.037	0.0000	0.0000
Snrnp35	ENSMUSG00000029402	small nuclear ribonucleoprotein 35 (U11/U12)	1.897	0.0000	0.0000	1.830	0.0000	0.0000
Snrnp48	ENSMUSG00000021431	small nuclear ribonucleoprotein 48 (U11/U12)	3.246	0.0000	0.0000	3.172	0.0000	0.0000
Snrnp70	ENSMUSG00000063511	small nuclear ribonucleoprotein 70 (U1)	1.511	0.0019	0.0055	1.863	0.0000	0.0000
Snrpd1	ENSMUSG00000002477	small nuclear ribonucleoprotein D1	2.073	0.0000	0.0000	1.546	0.0004	0.0014
Snw1	ENSMUSG00000021039	SNW domain containing 1	1.820	0.0000	0.0000	1.887	0.0000	0.0000
Snx12	ENSMUSG00000046032	sorting nexin 12	1.756	0.0000	0.0000	1.661	0.0000	0.0000
Snx2	ENSMUSG00000034484	sorting nexin 2	1.564	0.0000	0.0000	1.664	0.0000	0.0000
Snx7	ENSMUSG00000028007	sorting nexin 7	2.484	0.0000	0.0000	2.083	0.0000	0.0000
Snx9	ENSMUSG00000002365	sorting nexin 9	1.651	0.0000	0.0000	1.566	0.0000	0.0001
Sobp	ENSMUSG00000038248	sine oculis binding protein	2.163	0.0000	0.0000	2.258	0.0000	0.0000
Socs6	ENSMUSG00000056153	suppressor of cytokine signaling 6	2.059	0.0000	0.0000	1.651	0.0000	0.0000
Socs7	ENSMUSG00000038485	suppressor of cytokine signaling 7	2.546	0.0000	0.0000	2.125	0.0000	0.0000
Sox10	ENSMUSG00000033006	SRY (sex determining region Y)-box 10	2.367	0.0021	0.0060	2.410	0.0018	0.0060
Sox12	ENSMUSG00000051817	SRY (sex determining region Y)-box 12	4.549	0.0000	0.0000	5.623	0.0000	0.0000
Sox4	ENSMUSG00000076431	SRY (sex determining region Y)-box 4	2.768	0.0000	0.0000	2.531	0.0000	0.0000
Sp110	ENSMUSG00000070034	Sp110 nuclear body protein	1.803	0.0006	0.0019	2.078	0.0000	0.0001
Spaca6	ENSMUSG00000080316	sperm acrosome associated 6	2.005	0.0140	0.0323	1.939	0.0199	0.0475
Spata48	ENSMUSG00000020191	spermatogenesis associated 48	7.575	0.0000	0.0000	3.963	0.0000	0.0000
Spata5	ENSMUSG00000027722	spermatogenesis associated 5	1.996	0.0000	0.0000	1.844	0.0000	0.0000
Spats2	ENSMUSG00000051934	spermatogenesis associated, serine-rich 2	1.675	0.0000	0.0000	1.521	0.0000	0.0001
Spcs2	ENSMUSG00000035227	signal peptidase complex subunit 2 homolog (S. cerevisiae)	2.145	0.0000	0.0000	2.098	0.0000	0.0000
Spg7	ENSMUSG00000000738	SPG7, paraplegin matrix AAA peptidase subunit	2.077	0.0000	0.0000	2.168	0.0000	0.0000
Spn	ENSMUSG00000051457	sialophorin	1.976	0.0053	0.0137	3.242	0.0000	0.0000
Spop	ENSMUSG00000057522	speckle-type BTB/POZ protein	2.387	0.0000	0.0000	2.301	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Spopl	ENSMUSG00000026771	speckle-type BTB/POZ protein-like	2.125	0.0000	0.0000	1.880	0.0000	0.0000
Sppl3	ENSMUSG00000029550	signal peptide peptidase 3	1.929	0.0000	0.0000	1.855	0.0000	0.0000
Spred2	ENSMUSG00000045671	sprouty-related EVH1 domain containing 2	2.022	0.0000	0.0000	1.931	0.0000	0.0000
Spring1	ENSMUSG00000032840	SREBF pathway regulator in golgi 1	1.630	0.0000	0.0000	1.570	0.0000	0.0000
Spry1	ENSMUSG00000037211	sprouty RTK signaling antagonist 1	1.561	0.0010	0.0031	1.625	0.0003	0.0013
Spta1	ENSMUSG00000026532	spectrin alpha, erythrocytic 1	1.602	0.0008	0.0025	1.913	0.0000	0.0000
Srek1	ENSMUSG00000032621	splicing regulatory glutamine/lysine-rich protein 1	1.905	0.0000	0.0000	2.018	0.0000	0.0000
Srf	ENSMUSG00000015605	serum response factor	3.890	0.0000	0.0000	3.943	0.0000	0.0000
Srfbp1	ENSMUSG00000024528	serum response factor binding protein 1	1.827	0.0000	0.0000	1.817	0.0000	0.0000
Srp14	ENSMUSG00000009549	signal recognition particle 14	1.957	0.0000	0.0000	1.867	0.0000	0.0000
Srp54a	ENSMUSG00000073079	signal recognition particle 54A	1.905	0.0000	0.0000	2.052	0.0000	0.0000
Srp54c	ENSMUSG00000079108	signal recognition particle 54C	3.154	0.0000	0.0000	2.602	0.0000	0.0000
Srrd	ENSMUSG00000029346	SRR1 domain containing	2.832	0.0000	0.0000	3.416	0.0000	0.0000
Srrt	ENSMUSG00000037364	serrate RNA effector molecule homolog (Arabidopsis)	2.566	0.0000	0.0000	2.726	0.0000	0.0000
Srsf1	ENSMUSG00000018379	serine and arginine-rich splicing factor 1	3.252	0.0000	0.0000	2.687	0.0000	0.0000
Srsf11	ENSMUSG00000055436	serine and arginine-rich splicing factor 11	2.017	0.0000	0.0000	2.013	0.0000	0.0000
Srsf2	ENSMUSG00000034120	serine and arginine-rich splicing factor 2	2.306	0.0000	0.0000	1.981	0.0000	0.0000
Srsf5	ENSMUSG00000021134	serine and arginine-rich splicing factor 5	2.060	0.0000	0.0000	2.186	0.0000	0.0000
Srsf9	ENSMUSG00000029538	serine and arginine-rich splicing factor 9	2.381	0.0000	0.0000	2.504	0.0000	0.0000
Ss18l1	ENSMUSG00000039086	SS18, nBAF chromatin remodeling complex subunit like 1	2.288	0.0000	0.0000	1.739	0.0000	0.0000
Ssb	ENSMUSG00000068882	Sjogren syndrome antigen B	2.208	0.0000	0.0000	1.986	0.0000	0.0000
Ssbp1	ENSMUSG00000029911	single-stranded DNA binding protein 1	2.864	0.0000	0.0000	2.494	0.0000	0.0000
Ssbp3	ENSMUSG00000061887	single-stranded DNA binding protein 3	2.160	0.0000	0.0000	2.369	0.0000	0.0000
Ssbp4	ENSMUSG00000070003	single stranded DNA binding protein 4	3.125	0.0000	0.0000	3.119	0.0000	0.0000
Ssrp1	ENSMUSG00000027067	structure specific recognition protein 1	1.549	0.0000	0.0000	1.681	0.0000	0.0000
Ssx2ip	ENSMUSG00000036825	synovial sarcoma, X 2 interacting protein	1.659	0.0000	0.0000	1.644	0.0000	0.0000
St13	ENSMUSG00000022403	suppression of tumorigenicity 13	1.590	0.0000	0.0000	1.767	0.0000	0.0000
St3gal5	ENSMUSG00000056091	ST3 beta-galactoside alpha-2,3-sialyltransferase 5	1.762	0.0000	0.0000	2.284	0.0000	0.0000
Stard5	ENSMUSG00000046027	StAR-related lipid transfer (START) domain containing 5	1.561	0.0009	0.0029	1.749	0.0000	0.0002
Stbd1	ENSMUSG00000047963	starch binding domain 1	3.476	0.0000	0.0000	2.584	0.0007	0.0025
Stc2	ENSMUSG00000020303	stanniocalcin 2	2.081	0.0000	0.0000	1.934	0.0000	0.0000
Stim2	ENSMUSG00000039156	stromal interaction molecule 2	2.159	0.0000	0.0000	2.069	0.0000	0.0000
Stk11	ENSMUSG00000003068	serine/threonine kinase 11	1.651	0.0000	0.0000	1.775	0.0000	0.0000
Stk24	ENSMUSG00000063410	serine/threonine kinase 24	1.824	0.0000	0.0000	1.806	0.0000	0.0000
Stk32c	ENSMUSG00000015981	serine/threonine kinase 32C	1.725	0.0044	0.0116	1.538	0.0286	0.0649
Stk40	ENSMUSG00000042608	serine/threonine kinase 40	1.730	0.0000	0.0000	1.833	0.0000	0.0000
Strbp	ENSMUSG00000026915	spermatid perinuclear RNA binding protein	1.976	0.0000	0.0000	1.840	0.0000	0.0000
Strn3	ENSMUSG00000020954	striatin, calmodulin binding protein 3	3.154	0.0000	0.0000	3.119	0.0000	0.0000
Stt3b	ENSMUSG00000032437	STT3, subunit of the oligosaccharyltransferase complex, homolog B (S. cerevisiae)	2.574	0.0000	0.0000	2.339	0.0000	0.0000
Stx11	ENSMUSG00000039232	syntaxin 11	1.737	0.0033	0.0089	1.534	0.0242	0.0561
Stx4a	ENSMUSG00000030805	syntaxin 4A (placental)	1.535	0.0000	0.0000	1.702	0.0000	0.0000
Suds3	ENSMUSG00000066900	suppressor of defective silencing 3 homolog (S. cerevisiae)	2.501	0.0000	0.0000	2.788	0.0000	0.0000
Sumf1	ENSMUSG00000030101	sulfatase modifying factor 1	2.010	0.0000	0.0000	1.567	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Sumo1	ENSMUSG00000026021	small ubiquitin-like modifier 1	1.927	0.0000	0.0000	2.312	0.0000	0.0000
Suox	ENSMUSG00000049858	sulfite oxidase	1.804	0.0000	0.0000	2.007	0.0000	0.0000
Supt16	ENSMUSG00000035726	SPT16, facilitates chromatin remodeling subunit	1.899	0.0000	0.0000	1.766	0.0000	0.0000
Suz12	ENSMUSG00000017548	SUZ12 polycomb repressive complex 2 subunit	1.868	0.0000	0.0000	1.512	0.0000	0.0000
Svbp	ENSMUSG00000028643	small vasohibin binding protein	2.583	0.0000	0.0000	1.722	0.0087	0.0232
Swap70	ENSMUSG00000031015	SWA-70 protein	1.757	0.0000	0.0000	1.845	0.0000	0.0000
Syf2	ENSMUSG00000028821	SYF2 homolog, RNA splicing factor (S. cerevisiae)	2.319	0.0000	0.0000	2.613	0.0000	0.0000
Sync	ENSMUSG00000001333	syncoilin	1.748	0.0000	0.0000	1.714	0.0000	0.0000
Synj2bp	ENSMUSG00000090935	synaptojanin 2 binding protein	1.799	0.0000	0.0000	1.550	0.0000	0.0000
Synm	ENSMUSG00000030554	synemin, intermediate filament protein	1.615	0.0000	0.0001	1.719	0.0000	0.0000
Synpo2	ENSMUSG00000050315	synaptopodin 2	1.621	0.0000	0.0000	1.569	0.0000	0.0000
Syp	ENSMUSG00000031144	synaptophysin	2.686	0.0000	0.0000	3.404	0.0000	0.0000
Szrd1	ENSMUSG00000040842	SUZ RNA binding domain containing 1	1.599	0.0000	0.0000	1.502	0.0000	0.0000
Taf10	ENSMUSG00000043866	TATA-box binding protein associated factor 10	5.602	0.0000	0.0000	5.721	0.0000	0.0000
Taf12	ENSMUSG00000028899	TATA-box binding protein associated factor 12	1.719	0.0000	0.0000	1.758	0.0000	0.0000
Taf13	ENSMUSG00000048100	TATA-box binding protein associated factor 13	2.103	0.0000	0.0000	1.958	0.0000	0.0000
Taf15	ENSMUSG00000020680	TATA-box binding protein associated factor 15	4.208	0.0000	0.0000	4.053	0.0000	0.0000
Taf1a	ENSMUSG00000072258	TATA-box binding protein associated factor, RNA polymerase I, A	1.755	0.0000	0.0000	1.786	0.0000	0.0000
Taf3	ENSMUSG00000025782	TATA-box binding protein associated factor 3	2.252	0.0000	0.0000	2.238	0.0000	0.0000
Taf4	ENSMUSG00000039117	TATA-box binding protein associated factor 4	1.590	0.0000	0.0000	1.817	0.0000	0.0000
Taf5	ENSMUSG00000025049	TATA-box binding protein associated factor 5	3.071	0.0000	0.0000	3.104	0.0000	0.0000
Tagln	ENSMUSG00000032085	transgelin	1.610	0.0077	0.0191	1.917	0.0003	0.0011
Tamalin	ENSMUSG00000000531	trafficking regulator and scaffold protein tamalin	2.994	0.0000	0.0000	2.719	0.0000	0.0000
Taok3	ENSMUSG00000061288	TAO kinase 3	1.514	0.0006	0.0019	1.578	0.0002	0.0007
Tardbp	ENSMUSG00000041459	TAR DNA binding protein	1.961	0.0000	0.0000	1.653	0.0000	0.0000
Tbc1d12	ENSMUSG00000048720	TBC1D12: TBC1 domain family, member 12	1.983	0.0000	0.0000	1.766	0.0000	0.0000
Tbc1d20	ENSMUSG00000027465	TBC1 domain family, member 20	2.053	0.0000	0.0000	2.211	0.0000	0.0000
Tbcc	ENSMUSG00000036430	tubulin-specific chaperone C	2.878	0.0000	0.0000	2.634	0.0000	0.0000
Tbcel	ENSMUSG00000037287	tubulin folding cofactor E-like	1.951	0.0000	0.0000	2.277	0.0000	0.0000
Tbkbp1	ENSMUSG00000038517	TBK1 binding protein 1	2.221	0.0000	0.0001	1.717	0.0031	0.0094
Tbx1	ENSMUSG00000009097	T-box 1	3.566	0.0000	0.0000	2.402	0.0016	0.0054
Tbx15	ENSMUSG00000027868	T-box 15	1.969	0.0226	0.0488	2.236	0.0073	0.0198
Tbx2	ENSMUSG00000000093	T-box 2	3.685	0.0000	0.0000	2.996	0.0000	0.0000
Tbx3	ENSMUSG00000018604	T-box 3	1.612	0.0002	0.0007	1.991	0.0000	0.0000
Tcea1-ps1	ENSMUSG00000067869	transcription elongation factor A (SII) 1, pseudogene 1	2.277	0.0016	0.0047	2.092	0.0055	0.0157
Tceal1	ENSMUSG00000049536	transcription elongation factor A (SII)-like 1	1.736	0.0001	0.0002	1.765	0.0000	0.0002
Tceal9	ENSMUSG00000042712	transcription elongation factor A like 9	1.756	0.0000	0.0000	1.623	0.0000	0.0000
Tcerg1	ENSMUSG00000024498	transcription elongation regulator 1 (CA150)	2.207	0.0000	0.0000	1.972	0.0000	0.0000
Tcf15	ENSMUSG00000068079	transcription factor 15	3.610	0.0000	0.0000	3.840	0.0000	0.0000
Tcf3	ENSMUSG00000020167	transcription factor 3	1.787	0.0000	0.0001	1.580	0.0007	0.0025
Tcf7l1	ENSMUSG00000055799	transcription factor 7 like 1 (T cell specific, HMG box)	1.572	0.0000	0.0002	1.656	0.0000	0.0000
Tchp	ENSMUSG00000002486	trichoplein, keratin filament binding	2.225	0.0000	0.0000	2.764	0.0000	0.0000
Tcp11l1	ENSMUSG00000027175	t-complex 11 like 1	2.281	0.0000	0.0000	2.578	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tcte2	ENSMUSG00000038347	t-complex-associated testis expressed 2	1.905	0.0281	0.0591	2.275	0.0055	0.0155
Tdp2	ENSMUSG00000035958	tyrosyl-DNA phosphodiesterase 2	2.029	0.0000	0.0000	1.675	0.0000	0.0000
Tead2	ENSMUSG00000030796	TEA domain family member 2	1.846	0.0005	0.0015	1.773	0.0012	0.0041
Tead3	ENSMUSG00000002249	TEA domain family member 3	2.271	0.0000	0.0000	1.970	0.0000	0.0001
Tent4a	ENSMUSG00000034575	terminal nucleotidyltransferase 4A	1.974	0.0000	0.0000	2.008	0.0000	0.0000
Tent4b	ENSMUSG00000036779	terminal nucleotidyltransferase 4B	3.414	0.0000	0.0000	2.797	0.0000	0.0000
Terf1	ENSMUSG00000025925	telomeric repeat binding factor 1	2.903	0.0000	0.0000	2.508	0.0000	0.0000
Tesc	ENSMUSG00000029359	tescalcin	2.997	0.0000	0.0000	3.161	0.0000	0.0000
Tesk1	ENSMUSG00000028458	testis specific protein kinase 1	2.055	0.0000	0.0000	2.148	0.0000	0.0000
Tex9	ENSMUSG00000090626	testis expressed gene 9	1.902	0.0048	0.0125	2.018	0.0021	0.0067
Tfam	ENSMUSG00000003923	transcription factor A, mitochondrial	1.804	0.0000	0.0000	1.689	0.0000	0.0000
Tfdp1	ENSMUSG00000038482	transcription factor Dp 1	2.104	0.0000	0.0000	2.215	0.0000	0.0000
Tfpt	ENSMUSG00000006335	TCF3 (E2A) fusion partner	2.945	0.0000	0.0000	2.557	0.0000	0.0000
Tgfb1	ENSMUSG00000002603	transforming growth factor, beta 1	2.356	0.0000	0.0000	2.165	0.0000	0.0000
Tgfb3	ENSMUSG00000021253	transforming growth factor, beta 3	1.739	0.0000	0.0001	1.751	0.0000	0.0001
Thap12	ENSMUSG00000030753	THAP domain containing 12	1.627	0.0000	0.0000	1.526	0.0000	0.0000
Thg1l	ENSMUSG00000011254	tRNA-histidine guanylyltransferase 1-like (S. cerevisiae)	2.325	0.0000	0.0000	1.999	0.0000	0.0000
Thoc2	ENSMUSG00000037475	THO complex 2	1.662	0.0000	0.0000	1.519	0.0000	0.0000
Thoc2l	ENSMUSG00000097392	THO complex subunit 2-like	2.143	0.0000	0.0000	1.959	0.0000	0.0000
Thra	ENSMUSG00000058756	thyroid hormone receptor alpha	1.806	0.0000	0.0000	2.186	0.0000	0.0000
Thumpd1	ENSMUSG00000030942	THUMP domain containing 1	2.615	0.0000	0.0000	3.095	0.0000	0.0000
Timeless	ENSMUSG00000039994	timeless circadian clock 1	2.244	0.0000	0.0000	2.513	0.0000	0.0000
Timm10	ENSMUSG00000027076	translocase of inner mitochondrial membrane 10	1.625	0.0000	0.0000	2.008	0.0000	0.0000
Timm29	ENSMUSG00000048429	translocase of inner mitochondrial membrane 29	2.030	0.0000	0.0000	2.018	0.0000	0.0000
Timm44	ENSMUSG00000002949	translocase of inner mitochondrial membrane 44	1.696	0.0000	0.0000	1.945	0.0000	0.0000
Timm8b	ENSMUSG00000039016	translocase of inner mitochondrial membrane 8B	1.681	0.0000	0.0000	1.657	0.0000	0.0000
Timmdc1	ENSMUSG00000002846	translocase of inner mitochondrial membrane domain containing 1	1.657	0.0000	0.0000	1.745	0.0000	0.0000
Timp2	ENSMUSG00000017466	tissue inhibitor of metalloproteinase 2	1.672	0.0000	0.0002	1.780	0.0000	0.0000
Tle1	ENSMUSG00000008305	transducin-like enhancer of split 1	2.292	0.0000	0.0000	2.306	0.0000	0.0000
Tle5	ENSMUSG00000054452	TLE family member 5, transcriptional modulator	3.122	0.0000	0.0000	3.920	0.0000	0.0000
Tlk2	ENSMUSG00000020694	tousled-like kinase 2 (Arabidopsis)	1.866	0.0000	0.0000	1.727	0.0000	0.0000
Tm6sf1	ENSMUSG00000038623	transmembrane 6 superfamily member 1	2.042	0.0000	0.0000	2.477	0.0000	0.0000
Tm9sf3	ENSMUSG00000025016	transmembrane 9 superfamily member 3	2.175	0.0000	0.0000	1.939	0.0000	0.0000
Tma7	ENSMUSG00000091537	translational machinery associated 7	1.501	0.0000	0.0000	1.516	0.0000	0.0000
Tma7-ps	ENSMUSG00000059058	translational machinery associated 7 homolog (S. cerevisiae), pseudogene	2.935	0.0000	0.0000	2.908	0.0000	0.0000
Tmbim6	ENSMUSG00000023010	transmembrane BAX inhibitor motif containing 6	1.542	0.0000	0.0000	1.590	0.0000	0.0000
Tmc7	ENSMUSG00000042246	transmembrane channel-like gene family 7	1.777	0.0000	0.0000	1.545	0.0000	0.0002
Tmco6	ENSMUSG00000006850	transmembrane and coiled-coil domains 6	2.001	0.0000	0.0000	1.706	0.0007	0.0025
Tmed9	ENSMUSG00000058569	transmembrane p24 trafficking protein 9	1.630	0.0000	0.0000	1.663	0.0000	0.0000
Tmem101	ENSMUSG00000020921	transmembrane protein 101	3.265	0.0000	0.0000	3.932	0.0000	0.0000
Tmem127	ENSMUSG00000034850	transmembrane protein 127	1.752	0.0000	0.0000	1.843	0.0000	0.0000
Tmem150a	ENSMUSG00000055912	transmembrane protein 150A	2.177	0.0000	0.0000	2.382	0.0000	0.0000
Tmem158	ENSMUSG00000054871	transmembrane protein 158	5.720	0.0000	0.0000	4.780	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem160	ENSMUSG00000019158	transmembrane protein 160	5.004	0.0000	0.0000	4.627	0.0000	0.0000
Tmem164	ENSMUSG00000047045	transmembrane protein 164	1.806	0.0001	0.0005	1.691	0.0007	0.0026
Tmem165	ENSMUSG00000029234	transmembrane protein 165	3.166	0.0000	0.0000	2.693	0.0000	0.0000
Tmem181b-ps	ENSMUSG00000096780	transmembrane protein 181B, pseudogene	8.958	0.0002	0.0007	12.338	0.0000	0.0002
Tmem192	ENSMUSG00000025521	transmembrane protein 192	1.913	0.0000	0.0000	2.153	0.0000	0.0000
Tmem196	ENSMUSG00000048004	transmembrane protein 196	2.298	0.0000	0.0000	2.028	0.0001	0.0006
Tmem200b	ENSMUSG00000070720	transmembrane protein 200B	3.610	0.0000	0.0000	1.868	0.0247	0.0571
Tmem243	ENSMUSG00000079659	transmembrane protein 243, mitochondrial	1.861	0.0000	0.0000	2.004	0.0000	0.0000
Tmem248	ENSMUSG00000053094	transmembrane protein 248	1.622	0.0000	0.0000	1.655	0.0000	0.0000
Tmem251	ENSMUSG00000046675	transmembrane protein 251	2.307	0.0000	0.0000	1.922	0.0000	0.0000
Tmem259	ENSMUSG00000013858	transmembrane protein 259	2.365	0.0000	0.0000	1.771	0.0003	0.0011
Tmem38b	ENSMUSG00000028420	transmembrane protein 38B	1.770	0.0005	0.0018	1.729	0.0009	0.0033
Tmem51os1	ENSMUSG00000073728	Tmem51 opposite strand 1	2.798	0.0002	0.0008	2.238	0.0041	0.0123
Tmem64	ENSMUSG00000043252	transmembrane protein 64	1.825	0.0000	0.0000	1.536	0.0000	0.0000
Tmem65	ENSMUSG00000062373	transmembrane protein 65	2.228	0.0000	0.0000	2.070	0.0000	0.0000
Tmf1	ENSMUSG00000030059	TATA element modulatory factor 1	1.596	0.0000	0.0001	1.538	0.0001	0.0005
Tmpo	ENSMUSG00000019961	thymopoietin	1.855	0.0000	0.0000	1.563	0.0000	0.0000
Tmx1	ENSMUSG00000021072	thioredoxin-related transmembrane protein 1	2.124	0.0000	0.0000	1.642	0.0000	0.0000
Tnfrsf11a	ENSMUSG00000026321	tumor necrosis factor receptor superfamily, member 11a, NFKB activator	2.126	0.0005	0.0015	1.990	0.0015	0.0049
Tnip2	ENSMUSG00000059866	TNFAIP3 interacting protein 2	2.079	0.0000	0.0000	2.350	0.0000	0.0000
Tnnc1	ENSMUSG00000091898	troponin C, cardiac/slow skeletal	2.063	0.0000	0.0000	2.369	0.0000	0.0000
Tnnt1	ENSMUSG00000064179	troponin T1, skeletal, slow	1.631	0.0000	0.0000	1.529	0.0001	0.0004
Tnnt2	ENSMUSG00000026414	troponin T2, cardiac	3.295	0.0000	0.0000	4.134	0.0000	0.0000
Tnnt3	ENSMUSG00000061723	troponin T3, skeletal, fast	2.659	0.0153	0.0347	2.748	0.0068	0.0188
Tnrc18	ENSMUSG00000039477	trinucleotide repeat containing 18	1.771	0.0000	0.0000	1.719	0.0000	0.0000
Tnrc6c	ENSMUSG00000025571	trinucleotide repeat containing 6C	2.091	0.0000	0.0000	2.335	0.0000	0.0000
Tom1l1	ENSMUSG00000020541	target of myb1-like 1 (chicken)	1.602	0.0000	0.0000	1.545	0.0000	0.0000
Tomm70a	ENSMUSG00000022752	translocase of outer mitochondrial membrane 70A	2.173	0.0000	0.0000	1.574	0.0000	0.0000
Top1	ENSMUSG00000070544	topoisomerase (DNA) I	2.284	0.0000	0.0000	2.055	0.0000	0.0000
Tox2	ENSMUSG00000074607	TOX high mobility group box family member 2	2.414	0.0000	0.0001	2.643	0.0000	0.0000
Tpbg	ENSMUSG00000035274	trophoblast glycoprotein	1.834	0.0281	0.0590	2.570	0.0007	0.0026
Tpm1	ENSMUSG00000032366	tropomyosin 1, alpha	1.597	0.0000	0.0000	1.696	0.0000	0.0000
Tpm2	ENSMUSG00000028464	tropomyosin 2, beta	1.621	0.0004	0.0015	1.864	0.0000	0.0000
Tpm3	ENSMUSG00000027940	tropomyosin 3, gamma	2.598	0.0000	0.0000	2.411	0.0000	0.0000
Tpm3-rs7	ENSMUSG00000058126	tropomyosin 3, related sequence 7	3.147	0.0000	0.0001	4.861	0.0000	0.0000
Tpm4	ENSMUSG00000031799	tropomyosin 4	1.638	0.0000	0.0002	1.504	0.0007	0.0026
Tpr	ENSMUSG00000006005	translocated promoter region, nuclear basket protein	1.765	0.0000	0.0000	1.706	0.0000	0.0000
Tpt1	ENSMUSG00000060126	tumor protein, translationally-controlled 1	1.874	0.0000	0.0000	1.844	0.0000	0.0000
Traf3ip1	ENSMUSG00000034292	TRAF3 interacting protein 1	2.754	0.0000	0.0000	2.765	0.0000	0.0000
Trak1	ENSMUSG00000032536	trafficking protein, kinesin binding 1	1.719	0.0000	0.0000	1.551	0.0000	0.0000
Trappc3	ENSMUSG00000028847	trafficking protein particle complex 3	1.915	0.0000	0.0000	2.019	0.0000	0.0000
Trappc6b	ENSMUSG00000020993	trafficking protein particle complex 6B	3.242	0.0000	0.0000	2.980	0.0000	0.0000
Trim27	ENSMUSG00000021326	tripartite motif-containing 27	2.473	0.0000	0.0000	1.972	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Trim44	ENSMUSG00000027189	tripartite motif-containing 44	1.900	0.0000	0.0000	1.620	0.0000	0.0000
Trim68	ENSMUSG00000073968	tripartite motif-containing 68	1.579	0.0000	0.0000	1.504	0.0000	0.0000
Trim72	ENSMUSG00000042828	tripartite motif-containing 72	2.000	0.0000	0.0000	2.685	0.0000	0.0000
Trim8	ENSMUSG00000025034	tripartite motif-containing 8	3.322	0.0000	0.0000	3.317	0.0000	0.0000
Triobp	ENSMUSG00000033088	TRIO and F-actin binding protein	1.503	0.0000	0.0000	1.635	0.0000	0.0000
Trip13	ENSMUSG00000021569	thyroid hormone receptor interactor 13	2.418	0.0024	0.0068	2.296	0.0062	0.0173
Trir	ENSMUSG00000041203	telomerase RNA component interacting RNase	13.228	0.0000	0.0000	13.891	0.0000	0.0000
Trmt10a	ENSMUSG00000004127	tRNA methyltransferase 10A	2.105	0.0000	0.0000	1.898	0.0000	0.0000
Trnp1	ENSMUSG00000056596	TMF1-regulated nuclear protein 1	2.927	0.0111	0.0263	3.235	0.0020	0.0065
Trp53bp2	ENSMUSG00000026510	transformation related protein 53 binding protein 2	1.735	0.0000	0.0000	1.938	0.0000	0.0000
Trp53rkb	ENSMUSG00000042854	transformation related protein 53 regulating kinase B	2.232	0.0000	0.0000	2.052	0.0000	0.0000
Trub1	ENSMUSG00000025086	TruB pseudouridine (psi) synthase family member 1	2.264	0.0000	0.0000	2.185	0.0000	0.0000
Tsc22d2	ENSMUSG00000027806	TSC22 domain family, member 2	2.715	0.0000	0.0000	1.956	0.0000	0.0000
Tsen34	ENSMUSG00000035585	tRNA splicing endonuclease subunit 34	3.060	0.0000	0.0000	2.900	0.0000	0.0000
Tslp	ENSMUSG00000024379	thymic stromal lymphopoietin	2.324	0.0001	0.0002	2.914	0.0000	0.0000
Tsnax	ENSMUSG00000056820	translin-associated factor X	1.846	0.0000	0.0000	1.752	0.0000	0.0000
Tspan17	ENSMUSG00000025875	tetraspanin 17	2.588	0.0000	0.0000	3.125	0.0000	0.0000
Tspan5	ENSMUSG00000028152	tetraspanin 5	1.654	0.0002	0.0007	2.313	0.0000	0.0000
Tspyl2	ENSMUSG00000041096	TSPY-like 2	2.089	0.0000	0.0000	2.337	0.0000	0.0000
Tstd3	ENSMUSG00000028251	thiosulfate sulfurtransferase (rhodanese)-like domain containing 3	1.699	0.0000	0.0000	1.556	0.0001	0.0002
Ttc1	ENSMUSG00000041278	tetratricopeptide repeat domain 1	1.673	0.0000	0.0000	1.679	0.0000	0.0000
Ttc39c	ENSMUSG00000024424	tetratricopeptide repeat domain 39C	1.526	0.0010	0.0029	1.563	0.0006	0.0023
Ttc9	ENSMUSG00000042734	tetratricopeptide repeat domain 9	2.262	0.0006	0.0020	2.329	0.0005	0.0017
Ttll11	ENSMUSG00000026885	tubulin tyrosine ligase-like family, member 11	3.552	0.0000	0.0000	2.860	0.0000	0.0000
Tuba1a	ENSMUSG00000072235	tubulin, alpha 1A	1.705	0.0039	0.0103	1.644	0.0072	0.0196
Tuba1b	ENSMUSG00000023004	tubulin, alpha 1B	1.977	0.0005	0.0015	1.682	0.0076	0.0208
Tubb2a	ENSMUSG00000058672	tubulin, beta 2A class IIA	1.868	0.0000	0.0000	1.681	0.0000	0.0001
Tubb4b-ps1	ENSMUSG00000095159	tubulin, beta 4B class IVB, pseudogene 1	16.059	0.0000	0.0000	19.289	0.0000	0.0000
Tusc1	ENSMUSG00000054000	tumor suppressor candidate 1	4.275	0.0000	0.0000	4.873	0.0000	0.0000
Tut7	ENSMUSG00000035248	terminal uridylyl transferase 7	1.765	0.0000	0.0000	1.659	0.0000	0.0000
Tvp23b	ENSMUSG00000014177	trans-golgi network vesicle protein 23B	2.147	0.0000	0.0000	1.730	0.0000	0.0000
Twist1	ENSMUSG00000035799	twist basic helix-loop-helix transcription factor 1	2.509	0.0001	0.0002	3.708	0.0000	0.0000
Twist2	ENSMUSG00000007805	twist basic helix-loop-helix transcription factor 2	5.081	0.0000	0.0000	4.247	0.0000	0.0001
U2surp	ENSMUSG00000032407	U2 snRNP-associated SURP domain containing	1.728	0.0000	0.0000	1.621	0.0000	0.0000
Uba3	ENSMUSG00000030061	ubiquitin-like modifier activating enzyme 3	2.295	0.0000	0.0000	1.812	0.0000	0.0000
Uba5	ENSMUSG00000032557	ubiquitin-like modifier activating enzyme 5	1.796	0.0000	0.0000	1.635	0.0000	0.0000
Uba52	ENSMUSG00000090137	ubiquitin A-52 residue ribosomal protein fusion product 1	19.384	0.0000	0.0000	14.280	0.0000	0.0000
Ube2d3	ENSMUSG00000078578	ubiquitin-conjugating enzyme E2D 3	1.998	0.0000	0.0000	1.879	0.0000	0.0000
Ube2e2	ENSMUSG00000058317	ubiquitin-conjugating enzyme E2E 2	1.697	0.0000	0.0000	1.676	0.0000	0.0000
Ube2g2	ENSMUSG00000009293	ubiquitin-conjugating enzyme E2G 2	1.841	0.0000	0.0000	1.984	0.0000	0.0000
Ube2h	ENSMUSG00000039159	ubiquitin-conjugating enzyme E2H	3.095	0.0000	0.0000	3.120	0.0000	0.0000
Ube2j2	ENSMUSG00000023286	ubiquitin-conjugating enzyme E2J 2	2.595	0.0000	0.0000	2.208	0.0000	0.0000
Ube2k	ENSMUSG00000029203	ubiquitin-conjugating enzyme E2K	1.985	0.0000	0.0000	1.804	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ube2m	ENSMUSG00000005575	ubiquitin-conjugating enzyme E2M	2.338	0.0000	0.0000	3.185	0.0000	0.0000
Ube2q1	ENSMUSG00000042572	ubiquitin-conjugating enzyme E2Q family member 1	2.995	0.0000	0.0000	3.404	0.0000	0.0000
Ube2q2	ENSMUSG00000032307	ubiquitin-conjugating enzyme E2Q family member 2	1.953	0.0000	0.0000	1.790	0.0000	0.0000
Ube2r2	ENSMUSG00000036241	ubiquitin-conjugating enzyme E2R 2	3.692	0.0000	0.0000	4.190	0.0000	0.0000
Ube2s	ENSMUSG00000060860	ubiquitin-conjugating enzyme E2S	6.037	0.0000	0.0000	7.399	0.0000	0.0000
Ube2v2	ENSMUSG00000022674	ubiquitin-conjugating enzyme E2 variant 2	1.788	0.0001	0.0004	1.690	0.0006	0.0020
Ubfd1	ENSMUSG00000030870	ubiquitin family domain containing 1	2.127	0.0000	0.0000	1.703	0.0002	0.0007
Ubtd2	ENSMUSG00000044949	ubiquitin domain containing 2	2.622	0.0000	0.0000	2.264	0.0000	0.0000
Ubtf	ENSMUSG00000020923	upstream binding transcription factor, RNA polymerase I	2.648	0.0000	0.0000	2.665	0.0000	0.0000
Ubxn1	ENSMUSG00000071655	UBX domain protein 1	2.035	0.0000	0.0000	2.522	0.0000	0.0000
Uck2	ENSMUSG00000026558	uridine-cytidine kinase 2	1.613	0.0023	0.0064	1.534	0.0065	0.0180
Ugcg	ENSMUSG00000028381	UDP-glucose ceramide glucosyltransferase	1.819	0.0000	0.0000	1.689	0.0000	0.0000
Ugt1a7c	ENSMUSG00000090124	UDP glucuronosyltransferase 1 family, polypeptide A7C	3.472	0.0000	0.0002	2.685	0.0008	0.0029
Uhrf2	ENSMUSG00000024817	ubiquitin-like, containing PHD and RING finger domains 2	1.756	0.0001	0.0003	1.594	0.0011	0.0036
Uimc1	ENSMUSG00000025878	ubiquitin interaction motif containing 1	2.337	0.0000	0.0000	2.465	0.0000	0.0000
Unc119	ENSMUSG00000002058	unc-119 lipid binding chaperone	2.868	0.0000	0.0000	3.776	0.0000	0.0000
Upf1	ENSMUSG00000058301	UPF1 regulator of nonsense transcripts homolog (yeast)	2.065	0.0000	0.0000	2.141	0.0000	0.0000
Upf2	ENSMUSG00000043241	UPF2 regulator of nonsense transcripts homolog (yeast)	2.204	0.0000	0.0000	2.158	0.0000	0.0000
Upf3a	ENSMUSG00000038398	UPF3 regulator of nonsense transcripts homolog A (yeast)	3.316	0.0000	0.0000	3.360	0.0000	0.0000
Upf3b	ENSMUSG00000036572	UPF3 regulator of nonsense transcripts homolog B (yeast)	2.200	0.0000	0.0000	2.254	0.0000	0.0000
Upp2	ENSMUSG00000026839	uridine phosphorylase 2	5.696	0.0000	0.0000	6.343	0.0000	0.0000
Uqcrb	ENSMUSG00000021520	ubiquinol-cytochrome c reductase binding protein	2.496	0.0000	0.0000	2.075	0.0000	0.0000
Urm1	ENSMUSG00000069020	ubiquitin related modifier 1	1.643	0.0000	0.0000	1.766	0.0000	0.0000
Usf2	ENSMUSG00000058239	upstream transcription factor 2	2.971	0.0000	0.0000	1.946	0.0000	0.0001
Usp1	ENSMUSG00000028560	ubiquitin specific peptidase 1	2.146	0.0000	0.0000	1.611	0.0000	0.0001
Usp12	ENSMUSG00000029640	ubiquitin specific peptidase 12	1.652	0.0000	0.0000	1.603	0.0000	0.0000
Usp2	ENSMUSG00000032010	ubiquitin specific peptidase 2	1.655	0.0031	0.0085	1.743	0.0011	0.0038
Usp27x	ENSMUSG00000046269	ubiquitin specific peptidase 27, X chromosome	3.055	0.0000	0.0000	2.548	0.0000	0.0000
Usp31	ENSMUSG00000063317	ubiquitin specific peptidase 31	1.854	0.0000	0.0000	1.558	0.0000	0.0000
Utp14b	ENSMUSG00000079470	UTP14B small subunit processome component	2.567	0.0001	0.0002	2.804	0.0000	0.0001
Utp18	ENSMUSG00000054079	UTP18 small subunit processome component	4.081	0.0000	0.0000	3.322	0.0000	0.0000
Utp3	ENSMUSG00000070697	UTP3 small subunit processome component	2.827	0.0000	0.0000	2.930	0.0000	0.0000
Vamp1	ENSMUSG00000030337	vesicle-associated membrane protein 1	1.588	0.0000	0.0001	1.692	0.0000	0.0000
Vamp2	ENSMUSG00000020894	vesicle-associated membrane protein 2	1.962	0.0000	0.0000	2.047	0.0000	0.0000
Vamp8	ENSMUSG00000050732	vesicle-associated membrane protein 8	2.770	0.0000	0.0000	3.076	0.0000	0.0000
Vangl2	ENSMUSG00000026556	VANGL planar cell polarity 2	1.677	0.0000	0.0000	1.570	0.0001	0.0003
Vapb	ENSMUSG00000054455	vesicle-associated membrane protein, associated protein B and C	2.181	0.0000	0.0000	2.360	0.0000	0.0000
Vcp	ENSMUSG00000028452	valosin containing protein	1.989	0.0000	0.0000	1.957	0.0000	0.0000
Vdac1	ENSMUSG00000020402	voltage-dependent anion channel 1	1.831	0.0000	0.0000	1.731	0.0000	0.0000
Vdac3-ps1	ENSMUSG00000075053	voltage-dependent anion channel 3, pseudogene 1	3.988	0.0000	0.0000	3.213	0.0000	0.0000
Vegfa	ENSMUSG00000023951	vascular endothelial growth factor A	2.180	0.0000	0.0000	1.852	0.0004	0.0014
Vegfb	ENSMUSG00000024962	vascular endothelial growth factor B	1.717	0.0000	0.0002	2.044	0.0000	0.0000
Vopp1	ENSMUSG00000037788	vesicular, overexpressed in cancer, prosurvival protein 1	1.783	0.0000	0.0000	1.641	0.0000	0.0001

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Vwc2	ENSMUSG00000050830	von Willebrand factor C domain containing 2	4.001	0.0000	0.0000	3.323	0.0000	0.0000
Wapl	ENSMUSG00000041408	WAPL cohesin release factor	1.975	0.0000	0.0000	1.729	0.0000	0.0000
Wasf3	ENSMUSG00000029636	WASP family, member 3	1.543	0.0097	0.0234	1.857	0.0002	0.0009
Wbp11	ENSMUSG00000030216	WW domain binding protein 11	1.670	0.0000	0.0000	1.662	0.0000	0.0000
Wbp4	ENSMUSG00000022023	WW domain binding protein 4	1.748	0.0000	0.0000	1.662	0.0000	0.0000
Wdr26	ENSMUSG00000038733	WD repeat domain 26	1.835	0.0000	0.0000	1.628	0.0003	0.0012
Wdr43	ENSMUSG00000041057	WD repeat domain 43	1.904	0.0000	0.0000	1.738	0.0000	0.0000
Whamm	ENSMUSG00000045795	WAS protein homolog associated with actin, golgi membranes and microtubules	1.531	0.0329	0.0676	1.539	0.0311	0.0694
Whrn	ENSMUSG00000039137	whirlin	2.314	0.0000	0.0000	1.680	0.0044	0.0128
Wnt5a	ENSMUSG00000021994	wingless-type MMTV integration site family, member 5A	2.197	0.0000	0.0000	1.942	0.0000	0.0002
Wnt5b	ENSMUSG00000030170	wingless-type MMTV integration site family, member 5B	2.298	0.0000	0.0002	1.775	0.0046	0.0134
Wnt9a	ENSMUSG00000000126	wingless-type MMTV integration site family, member 9A	1.521	0.0004	0.0014	1.565	0.0002	0.0008
Wsb1	ENSMUSG00000017677	WD repeat and SOCS box-containing 1	1.774	0.0000	0.0000	1.616	0.0000	0.0001
Wtap	ENSMUSG00000060475	WT1 associating protein	3.047	0.0000	0.0000	2.974	0.0000	0.0000
Wtip	ENSMUSG00000036459	WT1 interacting protein	2.812	0.0000	0.0000	2.940	0.0000	0.0000
Xirp2	ENSMUSG00000027022	xin actin-binding repeat containing 2	1.585	0.0045	0.0117	1.642	0.0022	0.0069
Xkr6	ENSMUSG00000035067	X-linked Kx blood group related 6	1.620	0.0151	0.0343	2.047	0.0003	0.0011
Xkr8	ENSMUSG00000037752	X-linked Kx blood group related 8	1.756	0.0000	0.0001	1.877	0.0000	0.0000
Xndc1	ENSMUSG00000099481	Xrcc1 N-terminal domain containing 1	1.744	0.0189	0.0419	2.242	0.0007	0.0024
Xpa	ENSMUSG00000028329	xeroderma pigmentosum, complementation group A	3.005	0.0000	0.0000	2.632	0.0000	0.0000
Ybx1	ENSMUSG00000028639	Y box protein 1	4.441	0.0000	0.0000	4.452	0.0000	0.0000
Ybx2	ENSMUSG00000018554	Y box protein 2	2.499	0.0000	0.0000	2.319	0.0000	0.0002
Ybx3	ENSMUSG00000030189	Y box protein 3	3.668	0.0000	0.0000	4.168	0.0000	0.0000
Yeats4	ENSMUSG00000020171	YEATS domain containing 4	2.539	0.0000	0.0000	1.588	0.0002	0.0007
Ykt6	ENSMUSG00000002741	YKT6 v-SNARE homolog (S. cerevisiae)	1.945	0.0000	0.0000	1.732	0.0000	0.0000
Ylpm1	ENSMUSG00000021244	YLP motif containing 1	1.713	0.0000	0.0000	1.623	0.0000	0.0000
Ypel3	ENSMUSG00000042675	yippee like 3	4.519	0.0000	0.0000	4.769	0.0000	0.0000
Ythdc1	ENSMUSG00000035851	YTH domain containing 1	2.576	0.0000	0.0000	2.120	0.0000	0.0000
Ythdf1	ENSMUSG00000038848	YTH N6-methyladenosine RNA binding protein 1	1.830	0.0000	0.0000	1.906	0.0000	0.0000
Ywhae	ENSMUSG00000020849	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, epsilon polypeptide	2.865	0.0000	0.0000	2.641	0.0000	0.0000
Ywhah	ENSMUSG00000018965	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, eta polypeptide	3.246	0.0000	0.0000	2.703	0.0000	0.0000
Ywhaz	ENSMUSG00000022285	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, zeta polypeptide	2.442	0.0000	0.0000	2.077	0.0000	0.0000
Yy1	ENSMUSG00000021264	YY1 transcription factor	2.482	0.0000	0.0000	2.420	0.0000	0.0000
Zbtb11os1	ENSMUSG00000102101	zinc finger and BTB domain containing 11, opposite strand 1	4.356	0.0000	0.0000	3.046	0.0000	0.0000
Zbtb12	ENSMUSG00000049823	zinc finger and BTB domain containing 12	1.736	0.0000	0.0000	1.912	0.0000	0.0000
Zbtb18	ENSMUSG00000063659	zinc finger and BTB domain containing 18	1.670	0.0000	0.0000	1.543	0.0000	0.0000
Zbtb42	ENSMUSG00000037638	zinc finger and BTB domain containing 42	1.621	0.0001	0.0002	1.719	0.0000	0.0000
Zbtb44	ENSMUSG00000047412	zinc finger and BTB domain containing 44	2.028	0.0000	0.0000	1.578	0.0002	0.0010
Zbtb7a	ENSMUSG00000035011	zinc finger and BTB domain containing 7a	2.480	0.0000	0.0000	2.316	0.0000	0.0000
Zc3h12d	ENSMUSG00000039981	zinc finger CCCH type containing 12D	3.238	0.0003	0.0011	2.843	0.0014	0.0047
Zc3h13	ENSMUSG00000022000	zinc finger CCCH type containing 13	2.308	0.0000	0.0000	2.226	0.0000	0.0000
Zc3h15	ENSMUSG00000027091	zinc finger CCCH-type containing 15	2.534	0.0000	0.0000	2.287	0.0000	0.0000
Zc3h18	ENSMUSG00000017478	zinc finger CCCH-type containing 18	1.566	0.0000	0.0000	1.755	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zcchc10	ENSMUSG00000018239	zinc finger, CCHC domain containing 10	2.679	0.0000	0.0000	1.787	0.0003	0.0013
Zcchc17	ENSMUSG00000028772	zinc finger, CCHC domain containing 17	1.700	0.0000	0.0000	1.834	0.0000	0.0000
Zcchc2	ENSMUSG00000038866	zinc finger, CCHC domain containing 2	1.739	0.0000	0.0000	1.712	0.0000	0.0000
Zcchc3	ENSMUSG00000074682	zinc finger, CCHC domain containing 3	2.161	0.0000	0.0000	1.621	0.0059	0.0167
Zcrb1	ENSMUSG00000022635	zinc finger CCHC-type and RNA binding motif 1	2.252	0.0000	0.0000	2.657	0.0000	0.0000
Zdhhc14	ENSMUSG00000034265	zinc finger, DHHC domain containing 14	1.700	0.0001	0.0005	1.659	0.0003	0.0012
Zdhhc2	ENSMUSG00000039470	zinc finger, DHHC domain containing 2	1.656	0.0005	0.0016	1.847	0.0000	0.0001
Zeb2os	ENSMUSG00000052248	zinc finger E-box binding homeobox 2, opposite strand	4.609	0.0000	0.0000	3.784	0.0000	0.0000
Zfas1	ENSMUSG00000074578	zinc finger, NFX1-type containing 1, antisense RNA 1	2.953	0.0000	0.0002	3.351	0.0000	0.0000
Zfp207	ENSMUSG00000017421	zinc finger protein 207	2.027	0.0000	0.0000	2.097	0.0000	0.0000
Zfp251	ENSMUSG00000022526	zinc finger protein 251	1.613	0.0000	0.0000	1.604	0.0000	0.0000
Zfp330	ENSMUSG00000031711	zinc finger protein 330	2.721	0.0000	0.0000	2.498	0.0000	0.0000
Zfp335os	ENSMUSG00000085436	zinc finger protein 335, opposite strand	3.336	0.0000	0.0000	3.073	0.0000	0.0000
Zfp362	ENSMUSG00000028799	zinc finger protein 362	1.603	0.0000	0.0000	2.110	0.0000	0.0000
Zfp369	ENSMUSG00000021514	zinc finger protein 369	1.734	0.0000	0.0000	1.612	0.0000	0.0000
Zfp36l2	ENSMUSG00000045817	zinc finger protein 36, C3H type-like 2	2.881	0.0000	0.0000	2.073	0.0000	0.0002
Zfp451	ENSMUSG00000042197	zinc finger protein 451	1.774	0.0000	0.0000	1.513	0.0000	0.0000
Zfp462	ENSMUSG00000060206	zinc finger protein 462	1.652	0.0000	0.0000	1.518	0.0001	0.0004
Zfp513	ENSMUSG00000043059	zinc finger protein 513	2.424	0.0000	0.0000	2.651	0.0000	0.0000
Zfp593	ENSMUSG00000028840	zinc finger protein 593	2.825	0.0003	0.0011	2.724	0.0005	0.0019
Zfp622	ENSMUSG00000052253	zinc finger protein 622	4.051	0.0000	0.0000	3.705	0.0000	0.0000
Zfp628	ENSMUSG00000074406	zinc finger protein 628	1.678	0.0033	0.0089	1.649	0.0045	0.0132
Zfp667	ENSMUSG00000054893	zinc finger protein 667	1.855	0.0000	0.0000	1.674	0.0000	0.0000
Zfp703	ENSMUSG00000085795	zinc finger protein 703	2.014	0.0005	0.0017	1.560	0.0279	0.0636
Zfp710	ENSMUSG00000048897	zinc finger protein 710	1.579	0.0000	0.0000	1.621	0.0000	0.0000
Zfp740	ENSMUSG00000046897	zinc finger protein 740	1.607	0.0000	0.0000	1.676	0.0000	0.0000
Zfp787	ENSMUSG00000046792	zinc finger protein 787	1.787	0.0000	0.0000	1.574	0.0001	0.0005
Zfp821	ENSMUSG00000031728	zinc finger protein 821	2.266	0.0000	0.0000	2.526	0.0000	0.0000
Zfp827	ENSMUSG00000071064	zinc finger protein 827	2.050	0.0000	0.0000	1.936	0.0000	0.0000
Zfp830	ENSMUSG00000046010	zinc finger protein 830	2.568	0.0000	0.0000	2.601	0.0000	0.0000
Zfp839	ENSMUSG00000021271	zinc finger protein 839	2.315	0.0000	0.0000	2.828	0.0000	0.0000
Zfp84	ENSMUSG00000046185	zinc finger protein 84	1.916	0.0000	0.0000	1.685	0.0000	0.0000
Zfp938	ENSMUSG00000062931	zinc finger protein 938	3.868	0.0000	0.0000	3.496	0.0000	0.0000
Zfp982	ENSMUSG00000078496	zinc finger protein 982	1.756	0.0001	0.0004	1.651	0.0006	0.0022
Zfpm1	ENSMUSG00000049577	zinc finger protein, multitype 1	3.704	0.0000	0.0000	3.046	0.0000	0.0000
Zfr2	ENSMUSG00000034949	zinc finger RNA binding protein 2	1.543	0.0039	0.0104	1.580	0.0031	0.0094
Zfta	ENSMUSG00000053080	zinc finger translocation associated	2.333	0.0000	0.0000	2.276	0.0000	0.0000
Zmat2	ENSMUSG00000001383	zinc finger, matrin type 2	3.074	0.0000	0.0000	3.127	0.0000	0.0000
Zmynd19	ENSMUSG00000026974	zinc finger, MYND domain containing 19	1.906	0.0000	0.0000	2.200	0.0000	0.0000
Znhit6	ENSMUSG00000074182	zinc finger, HIT type 6	2.387	0.0000	0.0000	2.346	0.0000	0.0000
Znrf1	ENSMUSG00000033545	zinc and ring finger 1	2.403	0.0000	0.0000	2.085	0.0000	0.0000
Znrf2	ENSMUSG00000058446	zinc and ring finger 2	2.448	0.0000	0.0000	2.297	0.0000	0.0000
Zpbp	ENSMUSG00000020193	zona pellucida binding protein	2.641	0.0003	0.0009	2.376	0.0012	0.0041

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

UPREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zranb1	ENSMUSG00000030967	zinc finger, RAN-binding domain containing 1	1.583	0.0034	0.0092	1.515	0.0081	0.0218
Zranb2	ENSMUSG00000028180	zinc finger, RAN-binding domain containing 2	2.054	0.0000	0.0000	1.772	0.0000	0.0000
Zrsr1	ENSMUSG00000044068	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 1	1.899	0.0000	0.0000	1.974	0.0000	0.0000
Zrsr2	ENSMUSG00000031370	zinc finger (CCCH type), RNA binding motif and serine/arginine rich 2	3.234	0.0000	0.0000	3.084	0.0000	0.0000
Zscan29	ENSMUSG00000050619	zinc finger SCAN domains 29	1.818	0.0000	0.0000	1.724	0.0000	0.0000
Zswim4	ENSMUSG00000035671	zinc finger SWIM-type containing 4	1.592	0.0034	0.0092	1.860	0.0001	0.0004
Zswim9	ENSMUSG00000070814	zinc finger SWIM-type containing 9	1.962	0.0000	0.0000	2.309	0.0000	0.0000
Zxdc	ENSMUSG00000034430	ZXD family zinc finger C	1.743	0.0021	0.0061	1.522	0.0206	0.0489
	ENSMUSG00000095742		25.900	0.0000	0.0000	14.771	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

INVERSELY REGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm36235	ENSMUSG00000113930	predicted gene, 36235	6.272	0.0356	0.0723	-10.165	0.0309	0.0690
Gm48069	ENSMUSG00000111547	predicted gene, 48069	1.731	0.0259	0.0550	-1.741	0.0353	0.0774
Gm49326	ENSMUSG00000113294	predicted gene, 49326	4.696	0.0069	0.0173	-4.519	0.0350	0.0768
Rps6ka6	ENSMUSG00000025665	ribosomal protein S6 kinase polypeptide 6	4.872	0.0004	0.0013	-4.664	0.0273	0.0624
Tmem252	ENSMUSG00000048572	transmembrane protein 252	4.392	0.0349	0.0712	-21.208	0.0042	0.0123

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
0610012G03Rik	ENSMUSG00000107002	RIKEN cDNA 0610012G03 gene	-2.366	0.0000	0.0000	-2.224	0.0000	0.0000
1010001B22Rik	ENSMUSG00000097863	RIKEN cDNA 1010001B22 gene	-4.589	0.0002	0.0006	-5.163	0.0000	0.0002
1110002O04Rik	ENSMUSG00000102531	RIKEN cDNA 1110002O04 gene	-5.920	0.0039	0.0103	-4.813	0.0178	0.0432
1110019D14Rik	ENSMUSG00000097616	RIKEN cDNA 1110019D14 gene	-2.850	0.0046	0.0120	-8.030	0.0000	0.0001
1110038B12Rik	ENSMUSG00000092203	RIKEN cDNA 1110038B12 gene	-2.944	0.0001	0.0003	-2.307	0.0019	0.0062
1190007I07Rik	ENSMUSG00000063320	RIKEN cDNA 1190007I07 gene	-2.644	0.0000	0.0000	-2.834	0.0000	0.0000
1600020E01Rik	ENSMUSG00000097048	RIKEN cDNA 1600020E01 gene	-1.650	0.0162	0.0365	-1.606	0.0251	0.0580
1700001O22Rik	ENSMUSG00000044320	RIKEN cDNA 1700001O22 gene	-2.240	0.0030	0.0081	-2.248	0.0051	0.0148
1700008O03Rik	ENSMUSG00000008028	RIKEN cDNA 1700008O03 gene	-16.044	0.0159	0.0360	-16.430	0.0146	0.0365
1700017B05Rik	ENSMUSG00000032300	RIKEN cDNA 1700017B05 gene	-2.071	0.0000	0.0001	-1.609	0.0052	0.0148
1700037H04Rik	ENSMUSG00000027327	RIKEN cDNA 1700037H04 gene	-1.710	0.0002	0.0008	-1.633	0.0009	0.0031
1700088E04Rik	ENSMUSG00000033029	RIKEN cDNA 1700088E04 gene	-2.017	0.0023	0.0064	-3.275	0.0000	0.0000
1700101I11Rik	ENSMUSG00000097675	RIKEN cDNA 1700101I11 gene	-1.603	0.0150	0.0341	-2.136	0.0002	0.0006
1700120C14Rik	ENSMUSG00000100599	RIKEN cDNA 1700120C14 gene	-2.581	0.0000	0.0000	-2.204	0.0000	0.0000
1810021B22Rik	ENSMUSG00000087331	RIKEN cDNA 1810021B22 gene	-2.405	0.0000	0.0000	-1.700	0.0014	0.0045
1810024B03Rik	ENSMUSG00000044145	RIKEN cDNA 1810024B03 gene	-3.933	0.0002	0.0006	-2.154	0.0221	0.0519
1810044D09Rik	ENSMUSG00000100680	RIKEN cDNA 1810044D09 gene	-3.576	0.0000	0.0000	-1.659	0.0225	0.0528
1810055G02Rik	ENSMUSG00000035372	RIKEN cDNA 1810055G02 gene	-1.813	0.0000	0.0001	-1.597	0.0014	0.0047
1810058I24Rik	ENSMUSG00000073155	RIKEN cDNA 1810058I24 gene	-2.756	0.0000	0.0000	-2.328	0.0000	0.0000
2310001K24Rik	ENSMUSG00000053353	RIKEN cDNA 2310001K24 gene	-2.838	0.0103	0.0247	-4.452	0.0019	0.0062
2310002D06Rik	ENSMUSG00000112701	RIKEN cDNA 2310002D06 gene	-7.044	0.0000	0.0002	-19.718	0.0001	0.0004
2310011J03Rik	ENSMUSG00000020133	RIKEN cDNA 2310011J03 gene	-1.854	0.0000	0.0000	-1.649	0.0000	0.0000
2310016G11Rik	ENSMUSG00000070574	RIKEN cDNA 2310016G11 gene	-2.362	0.0005	0.0017	-2.688	0.0001	0.0005
2310022A10Rik	ENSMUSG00000049643	RIKEN cDNA 2310022A10 gene	-1.954	0.0000	0.0000	-1.589	0.0000	0.0000
2310039H08Rik	ENSMUSG00000062619	RIKEN cDNA 2310039H08 gene	-3.036	0.0000	0.0000	-2.888	0.0000	0.0000
2410002F23Rik	ENSMUSG00000045411	RIKEN cDNA 2410002F23 gene	-1.786	0.0001	0.0004	-1.551	0.0036	0.0108
2510002D24Rik	ENSMUSG00000071632	RIKEN cDNA 2510002D24 gene	-1.845	0.0000	0.0000	-1.525	0.0000	0.0001
2700046G09Rik	ENSMUSG00000097787	RIKEN cDNA 2700046G09 gene	-1.838	0.0026	0.0073	-2.078	0.0004	0.0015
2810403D21Rik	ENSMUSG00000086629	RIKEN cDNA 2810403D21 gene	-3.087	0.0000	0.0000	-1.864	0.0052	0.0149
2900009J06Rik	ENSMUSG00000102014	RIKEN cDNA 2900009J06 gene	-2.244	0.0126	0.0293	-2.111	0.0311	0.0694
3110070M22Rik	ENSMUSG00000074635	RIKEN cDNA 3110070M22 gene	-4.350	0.0000	0.0000	-2.095	0.0119	0.0304
4833408A19Rik	ENSMUSG00000118132	RIKEN cDNA 4833408A19 gene	-1.934	0.0110	0.0262	-1.930	0.0125	0.0319
4930466K18Rik	ENSMUSG00000112332	RIKEN cDNA 4930466K18 gene	-2.044	0.0355	0.0721	-2.305	0.0204	0.0485
4930523C07Rik	ENSMUSG00000090394	RIKEN cDNA 4930523C07 gene	-1.605	0.0000	0.0001	-1.533	0.0002	0.0008
4930592C13Rik	ENSMUSG00000105834	RIKEN cDNA 4930592C13 gene	-21.376	0.0018	0.0051	-8.770	0.0329	0.0728
4933406P04Rik	ENSMUSG00000069713	RIKEN cDNA 4933406P04 gene	-4.158	0.0000	0.0001	-3.434	0.0003	0.0013
4933434E20Rik	ENSMUSG00000027942	RIKEN cDNA 4933434E20 gene	-2.262	0.0000	0.0000	-1.885	0.0000	0.0000
5033430I15Rik	ENSMUSG00000038152	RIKEN cDNA 5033430I15 gene	-3.415	0.0000	0.0000	-2.755	0.0000	0.0000
5430403G16Rik	ENSMUSG00000072763	RIKEN cDNA 5430403G16 gene	-1.749	0.0307	0.0637	-1.947	0.0118	0.0302
5830448L01Rik	ENSMUSG00000115007	RIKEN cDNA 5830448L01 gene	-2.100	0.0130	0.0303	-2.065	0.0223	0.0524
5930430L01Rik	ENSMUSG00000106951	RIKEN cDNA 5930430L01 gene	-1.768	0.0000	0.0000	-1.790	0.0000	0.0000
6030443J06Rik	ENSMUSG00000097207	RIKEN cDNA 6030443J06 gene	-1.933	0.0155	0.0352	-2.564	0.0012	0.0040
6330549D23Rik	ENSMUSG00000045327	RIKEN cDNA 6330549D23 gene	-3.016	0.0060	0.0154	-6.216	0.0011	0.0037

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
9130604C24Rik	ENSMUSG00000105851	RIKEN cDNA 9130604C24 gene	-2.990	0.0125	0.0291	-5.683	0.0010	0.0035
9430091E24Rik	ENSMUSG00000084808	RIKEN cDNA 9430091E24 gene	-2.639	0.0258	0.0548	-3.777	0.0094	0.0249
9930111J21Rik1	ENSMUSG00000069893	RIKEN cDNA 9930111J21 gene 1	-2.032	0.0001	0.0003	-2.323	0.0000	0.0001
A230065N10Rik	ENSMUSG00000092071	RIKEN cDNA A230065N10 gene	-2.334	0.0313	0.0647	-3.213	0.0066	0.0182
A430005L14Rik	ENSMUSG00000047613	RIKEN cDNA A430005L14 gene	-1.676	0.0000	0.0000	-1.587	0.0000	0.0000
A530016L24Rik	ENSMUSG00000043122	RIKEN cDNA A530016L24 gene	-3.042	0.0000	0.0000	-1.859	0.0000	0.0001
A730020M07Rik	ENSMUSG00000044522	RIKEN cDNA A730020M07 gene	-2.535	0.0000	0.0000	-2.241	0.0001	0.0004
A930004D18Rik	ENSMUSG00000054057	RIKEN cDNA A930004D18 gene	-1.842	0.0017	0.0050	-1.631	0.0125	0.0318
AA986860	ENSMUSG00000042510	expressed sequence AA986860	-1.644	0.0432	0.0853	-1.927	0.0142	0.0356
Abca2	ENSMUSG00000026944	ATP-binding cassette, sub-family A (ABC1), member 2	-2.013	0.0000	0.0000	-1.578	0.0000	0.0001
Abca3	ENSMUSG00000024130	ATP-binding cassette, sub-family A (ABC1), member 3	-2.208	0.0000	0.0000	-1.838	0.0000	0.0000
Abca7	ENSMUSG00000035722	ATP-binding cassette, sub-family A (ABC1), member 7	-1.786	0.0007	0.0021	-1.540	0.0111	0.0289
Abcb8	ENSMUSG00000028973	ATP-binding cassette, sub-family B (MDR/TAP), member 8	-2.056	0.0000	0.0000	-1.842	0.0000	0.0000
Abcb9	ENSMUSG00000029408	ATP-binding cassette, sub-family B (MDR/TAP), member 9	-2.439	0.0000	0.0000	-1.880	0.0000	0.0001
Abcc8	ENSMUSG00000040136	ATP-binding cassette, sub-family C (CFTR/MRP), member 8	-2.802	0.0000	0.0000	-2.145	0.0000	0.0000
Abcd1	ENSMUSG00000031378	ATP-binding cassette, sub-family D (ALD), member 1	-1.731	0.0000	0.0000	-1.715	0.0000	0.0000
Abhd14b	ENSMUSG00000042073	abhydrolase domain containing 14b	-3.185	0.0000	0.0000	-2.461	0.0000	0.0000
Abhd4	ENSMUSG00000040997	abhydrolase domain containing 4	-2.696	0.0000	0.0000	-2.581	0.0000	0.0000
Abhd8	ENSMUSG00000007950	abhydrolase domain containing 8	-2.337	0.0000	0.0000	-2.166	0.0000	0.0000
Abi3	ENSMUSG00000018381	ABI family member 3	-1.667	0.0000	0.0000	-1.821	0.0000	0.0000
Abitram	ENSMUSG00000038827	actin binding transcription modulator	-1.733	0.0000	0.0001	-1.626	0.0003	0.0012
Acad10	ENSMUSG00000029456	acyl-Coenzyme A dehydrogenase family, member 10	-2.676	0.0000	0.0000	-2.377	0.0000	0.0000
Acad11	ENSMUSG00000090150	acyl-Coenzyme A dehydrogenase family, member 11	-1.676	0.0000	0.0000	-1.518	0.0000	0.0000
Acad12	ENSMUSG00000042647	acyl-Coenzyme A dehydrogenase family, member 12	-2.028	0.0000	0.0000	-1.562	0.0000	0.0000
Acad9	ENSMUSG00000027710	acyl-Coenzyme A dehydrogenase family, member 9	-1.614	0.0000	0.0000	-1.747	0.0000	0.0000
Acads	ENSMUSG00000029545	acyl-Coenzyme A dehydrogenase, short chain	-2.959	0.0000	0.0000	-2.492	0.0000	0.0000
Acd	ENSMUSG00000038000	adrenocortical dysplasia	-1.892	0.0000	0.0000	-1.621	0.0000	0.0001
Ace	ENSMUSG00000020681	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	-2.300	0.0000	0.0000	-1.744	0.0007	0.0025
Ache	ENSMUSG00000023328	acetylcholinesterase	-1.943	0.0000	0.0002	-1.943	0.0001	0.0004
Ackr3	ENSMUSG00000044337	atypical chemokine receptor 3	-1.859	0.0000	0.0000	-1.917	0.0000	0.0000
Acot8	ENSMUSG00000017307	acyl-CoA thioesterase 8	-2.147	0.0000	0.0000	-1.936	0.0000	0.0000
Acp1	ENSMUSG00000044573	acid phosphatase 1, soluble	-2.183	0.0000	0.0000	-1.950	0.0000	0.0000
Acp2	ENSMUSG00000002103	acid phosphatase 2, lysosomal	-2.042	0.0000	0.0000	-1.926	0.0000	0.0000
Acp5	ENSMUSG00000001348	acid phosphatase 5, tartrate resistant	-2.555	0.0072	0.0180	-2.238	0.0215	0.0508
Actc1	ENSMUSG00000068614	actin, alpha, cardiac muscle 1	-1.805	0.0000	0.0000	-1.982	0.0000	0.0000
Actg1	ENSMUSG00000062825	actin, gamma, cytoplasmic 1	-2.495	0.0000	0.0000	-2.036	0.0000	0.0000
Acy3	ENSMUSG00000024866	aspartoacylase (aminoacylase) 3	-4.088	0.0000	0.0000	-3.054	0.0000	0.0000
Ada	ENSMUSG00000017697	adenosine deaminase	-3.484	0.0004	0.0012	-2.304	0.0152	0.0379
Adam15	ENSMUSG00000028041	a disintegrin and metallopeptidase domain 15 (metargidin)	-1.810	0.0000	0.0000	-1.580	0.0000	0.0000
Adamtsl4	ENSMUSG00000015850	ADAMTS-like 4	-1.751	0.0001	0.0002	-1.683	0.0002	0.0007
Adamtsl5	ENSMUSG00000043822	ADAMTS-like 5	-1.842	0.0000	0.0000	-1.845	0.0000	0.0000
Adar	ENSMUSG00000027951	adenosine deaminase, RNA-specific	-1.736	0.0000	0.0000	-1.542	0.0000	0.0002
Adck1	ENSMUSG00000021044	aarF domain containing kinase 1	-2.013	0.0000	0.0000	-1.807	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Adck5	ENSMUSG00000022550	aarF domain containing kinase 5	-1.551	0.0275	0.0578	-1.707	0.0083	0.0224
Adcy4	ENSMUSG00000022220	adenylate cyclase 4	-1.960	0.0000	0.0000	-1.571	0.0006	0.0021
Adgre5	ENSMUSG00000002885	adhesion G protein-coupled receptor E5	-1.792	0.0000	0.0000	-1.581	0.0000	0.0000
Adgrg1	ENSMUSG00000031785	adhesion G protein-coupled receptor G1	-2.189	0.0004	0.0013	-1.729	0.0134	0.0338
Adgrg3	ENSMUSG00000060470	adhesion G protein-coupled receptor G3	-7.248	0.0000	0.0000	-2.303	0.0026	0.0082
Adsl	ENSMUSG00000022407	adenylosuccinate lyase	-2.259	0.0000	0.0000	-2.038	0.0000	0.0000
Afmid	ENSMUSG00000017718	arylformamidase	-2.886	0.0000	0.0002	-2.085	0.0034	0.0102
Agmo	ENSMUSG00000050103	alkylglycerol monooxygenase	-2.059	0.0013	0.0040	-2.221	0.0005	0.0017
Agt	ENSMUSG00000031980	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)	-2.258	0.0165	0.0372	-2.346	0.0140	0.0351
Ahcy	ENSMUSG00000027597	S-adenosylhomocysteine hydrolase	-3.356	0.0000	0.0000	-2.407	0.0000	0.0000
AI467606	ENSMUSG00000045165	expressed sequence AI467606	-2.458	0.0001	0.0003	-1.869	0.0062	0.0174
AI661453	ENSMUSG00000034382	expressed sequence AI661453	-2.348	0.0021	0.0060	-2.231	0.0108	0.0282
AK157302	ENSMUSG00000078139	cDNA sequence AK157302	-2.867	0.0000	0.0000	-2.553	0.0000	0.0000
Ak3l2-ps	ENSMUSG00000081957	adenylate kinase 3-like 2, pseudogene	-4.356	0.0001	0.0003	-15.806	0.0000	0.0001
Akna	ENSMUSG00000039158	AT-hook transcription factor	-1.896	0.0000	0.0000	-1.750	0.0000	0.0001
Akr1b10	ENSMUSG00000061758	aldo-keto reductase family 1, member B10 (aldose reductase)	-1.857	0.0000	0.0000	-1.676	0.0000	0.0000
Akr7a5	ENSMUSG00000028743	aldo-keto reductase family 7, member A5 (aflatoxin aldehyde reductase)	-3.746	0.0000	0.0000	-2.538	0.0000	0.0000
Alad	ENSMUSG00000028393	aminolevulinate, delta-, dehydratase	-3.262	0.0000	0.0000	-2.682	0.0000	0.0000
Aldh18a1	ENSMUSG00000025007	aldehyde dehydrogenase 18 family, member A1	-1.543	0.0103	0.0246	-1.577	0.0073	0.0201
Alg1	ENSMUSG00000039427	asparagine-linked glycosylation 1 (beta-1,4-mannosyltransferase)	-1.970	0.0000	0.0000	-1.732	0.0000	0.0000
Alg12	ENSMUSG00000035845	asparagine-linked glycosylation 12 (alpha-1,6-mannosyltransferase)	-2.463	0.0000	0.0000	-2.119	0.0000	0.0000
Alg8	ENSMUSG00000035704	asparagine-linked glycosylation 8 (alpha-1,3-glucosyltransferase)	-2.121	0.0000	0.0000	-1.867	0.0003	0.0013
Alkbh6	ENSMUSG00000042831	alkB homolog 6	-2.001	0.0000	0.0000	-2.023	0.0000	0.0000
Alkbh7	ENSMUSG00000002661	alkB homolog 7	-3.977	0.0000	0.0000	-2.823	0.0000	0.0000
Alox5ap	ENSMUSG00000060063	arachidonate 5-lipoxygenase activating protein	-2.304	0.0000	0.0001	-2.252	0.0000	0.0002
Amdhd2	ENSMUSG00000036820	amidohydrolase domain containing 2	-1.542	0.0039	0.0103	-1.565	0.0029	0.0089
Amigo3	ENSMUSG00000032593	adhesion molecule with Ig like domain 3	-3.723	0.0002	0.0007	-2.911	0.0026	0.0080
Anapc16	ENSMUSG00000020107	anaphase promoting complex subunit 16	-1.723	0.0001	0.0003	-1.741	0.0001	0.0003
Angel1	ENSMUSG00000021257	angel homolog 1	-1.682	0.0000	0.0000	-1.542	0.0001	0.0002
Angptl6	ENSMUSG00000038742	angiopoietin-like 6	-1.916	0.0000	0.0001	-1.779	0.0002	0.0007
Ankrd23	ENSMUSG00000067653	ankyrin repeat domain 23	-2.587	0.0000	0.0000	-2.707	0.0000	0.0000
Ankrd39	ENSMUSG00000079610	ankyrin repeat domain 39	-1.680	0.0003	0.0010	-1.613	0.0011	0.0037
Ankrd46	ENSMUSG00000048307	ankyrin repeat domain 46	-1.515	0.0000	0.0000	-1.511	0.0000	0.0000
Ap1b1	ENSMUSG00000009090	adaptor protein complex AP-1, beta 1 subunit	-1.717	0.0000	0.0000	-1.546	0.0000	0.0000
Ap2a1	ENSMUSG00000060279	adaptor-related protein complex 2, alpha 1 subunit	-1.866	0.0000	0.0000	-1.811	0.0000	0.0000
Ap2m1-ps	ENSMUSG00000081272	adaptor-related protein complex 2, mu 1 subunit, pseudogene	-3.051	0.0000	0.0000	-1.837	0.0000	0.0000
Ap5b1	ENSMUSG00000049562	adaptor-related protein complex 5, beta 1 subunit	-2.322	0.0000	0.0000	-2.407	0.0000	0.0000
Ap5m1	ENSMUSG00000036291	adaptor-related protein complex 5, mu 1 subunit	-1.569	0.0000	0.0000	-1.996	0.0000	0.0000
Ap5z1	ENSMUSG00000039623	adaptor-related protein complex 5, zeta 1 subunit	-1.768	0.0000	0.0000	-1.633	0.0000	0.0001
Apba3	ENSMUSG00000004931	amyloid beta (A4) precursor protein-binding, family A, member 3	-2.583	0.0000	0.0000	-1.846	0.0000	0.0000
Apc2	ENSMUSG00000020135	APC regulator of WNT signaling pathway 2	-2.337	0.0000	0.0001	-1.999	0.0005	0.0020
Apeh	ENSMUSG00000032590	acylpeptide hydrolase	-2.202	0.0000	0.0000	-1.919	0.0000	0.0000
Aph1b	ENSMUSG00000032375	aph1 homolog B, gamma secretase subunit	-2.306	0.0000	0.0000	-2.120	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Aph1c	ENSMUSG00000053040	aph1 homolog C, gamma secretase subunit	-2.520	0.0001	0.0002	-1.651	0.0286	0.0649
Apobec1	ENSMUSG00000040613	apolipoprotein B mRNA editing enzyme, catalytic polypeptide 1	-1.711	0.0001	0.0005	-1.513	0.0034	0.0101
Aprt	ENSMUSG00000006589	adenine phosphoribosyl transferase	-2.369	0.0000	0.0000	-1.661	0.0000	0.0000
Aqp1	ENSMUSG00000004655	aquaporin 1	-1.805	0.0101	0.0243	-1.740	0.0159	0.0394
Arfip1	ENSMUSG00000074513	ADP-ribosylation factor interacting protein 1	-2.027	0.0000	0.0000	-2.137	0.0000	0.0000
Arhgap1	ENSMUSG00000027247	Rho GTPase activating protein 1	-2.071	0.0000	0.0000	-1.984	0.0000	0.0000
Arhgap27	ENSMUSG00000034255	Rho GTPase activating protein 27	-1.960	0.0027	0.0074	-1.929	0.0035	0.0106
Arhgdia	ENSMUSG00000025132	Rho GDP dissociation inhibitor (GDI) alpha	-2.110	0.0000	0.0000	-1.649	0.0000	0.0000
Arl15	ENSMUSG00000042348	ADP-ribosylation factor-like 15	-1.800	0.0000	0.0000	-1.757	0.0000	0.0000
Arl2	ENSMUSG00000024944	ADP-ribosylation factor-like 2	-1.847	0.0000	0.0000	-1.549	0.0000	0.0000
Arl6	ENSMUSG00000022722	ADP-ribosylation factor-like 6	-1.799	0.0000	0.0000	-1.598	0.0001	0.0006
Armc6	ENSMUSG00000002343	armadillo repeat containing 6	-2.063	0.0000	0.0000	-1.845	0.0000	0.0000
Arpc3	ENSMUSG00000029465	actin related protein 2/3 complex, subunit 3	-2.173	0.0000	0.0000	-2.022	0.0000	0.0000
Arrdc1	ENSMUSG00000026972	arrestin domain containing 1	-2.118	0.0001	0.0003	-1.560	0.0168	0.0411
Arsa	ENSMUSG00000022620	arylsulfatase A	-1.705	0.0000	0.0000	-1.593	0.0000	0.0000
Arsg	ENSMUSG00000020604	arylsulfatase G	-2.173	0.0000	0.0000	-2.050	0.0001	0.0004
Art1	ENSMUSG00000030996	ADP-ribosyltransferase 1	-1.938	0.0000	0.0000	-1.568	0.0000	0.0002
Art4	ENSMUSG00000030217	ADP-ribosyltransferase 4	-1.897	0.0011	0.0034	-2.363	0.0000	0.0002
Asb11	ENSMUSG00000031382	ankyrin repeat and SOCS box-containing 11	-1.763	0.0000	0.0001	-1.524	0.0012	0.0040
Asb14	ENSMUSG00000021898	ankyrin repeat and SOCS box-containing 14	-2.295	0.0000	0.0000	-2.066	0.0000	0.0000
Asb18	ENSMUSG00000067081	ankyrin repeat and SOCS box-containing 18	-1.702	0.0000	0.0000	-1.787	0.0000	0.0000
Asb2	ENSMUSG00000021200	ankyrin repeat and SOCS box-containing 2	-1.900	0.0000	0.0000	-1.518	0.0000	0.0002
Asb6	ENSMUSG00000039483	ankyrin repeat and SOCS box-containing 6	-2.590	0.0000	0.0000	-1.816	0.0000	0.0000
Ascc1	ENSMUSG00000044475	activating signal cointegrator 1 complex subunit 1	-2.205	0.0000	0.0000	-1.872	0.0000	0.0001
Asf1b	ENSMUSG00000005470	anti-silencing function 1B histone chaperone	-1.648	0.0186	0.0413	-2.339	0.0002	0.0008
Asl	ENSMUSG00000025533	argininosuccinate lyase	-2.254	0.0000	0.0000	-2.011	0.0000	0.0002
Asns	ENSMUSG00000029752	asparagine synthetase	-1.721	0.0148	0.0338	-1.559	0.0456	0.0958
Asnsd1	ENSMUSG00000026095	asparagine synthetase domain containing 1	-1.517	0.0006	0.0019	-2.263	0.0000	0.0000
Aspa	ENSMUSG00000020774	aspartoacylase	-1.969	0.0024	0.0066	-2.264	0.0003	0.0013
Aspg	ENSMUSG00000037686	asparaginase	-6.945	0.0017	0.0051	-3.418	0.0366	0.0798
Atat1	ENSMUSG00000024426	alpha tubulin acetyltransferase 1	-1.828	0.0002	0.0006	-1.505	0.0110	0.0286
Atg2a	ENSMUSG00000024773	autophagy related 2A	-2.751	0.0000	0.0000	-2.117	0.0000	0.0000
Atg9a	ENSMUSG00000033124	autophagy related 9A	-2.449	0.0000	0.0000	-2.308	0.0000	0.0000
Atox1	ENSMUSG00000018585	antioxidant 1 copper chaperone	-3.492	0.0000	0.0000	-3.545	0.0000	0.0000
Atp5d	ENSMUSG00000003072	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	-3.893	0.0000	0.0000	-3.150	0.0000	0.0000
Atp5g2	ENSMUSG00000062683	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit C2 (subunit 9)	-4.492	0.0000	0.0000	-3.936	0.0000	0.0000
Atp5l	ENSMUSG00000038717	ATP synthase, H+ transporting, mitochondrial F0 complex, subunit G	-6.749	0.0000	0.0000	-5.764	0.0000	0.0000
Atp5mpl	ENSMUSG00000021290	ATP synthase membrane subunit 6.8PL	-1.536	0.0000	0.0000	-1.539	0.0000	0.0000
Atp5o	ENSMUSG00000022956	ATP synthase, H+ transporting, mitochondrial F1 complex, O subunit	-2.394	0.0000	0.0000	-2.515	0.0000	0.0000
Atp6v0c	ENSMUSG00000024121	ATPase, H+ transporting, lysosomal V0 subunit C	-5.543	0.0000	0.0000	-4.689	0.0000	0.0000
Atp6v0c-ps2	ENSMUSG00000080242	ATPase, H+ transporting, lysosomal V0 subunit C, pseudogene 2	-8.443	0.0000	0.0000	-7.059	0.0000	0.0000
Atp6v0d1	ENSMUSG00000013160	ATPase, H+ transporting, lysosomal V0 subunit D1	-2.975	0.0000	0.0000	-2.713	0.0000	0.0000
Atp6v0e	ENSMUSG00000015575	ATPase, H+ transporting, lysosomal V0 subunit E	-1.712	0.0000	0.0000	-1.644	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Atp6v0e2	ENSMUSG00000039347	ATPase, H+ transporting, lysosomal V0 subunit E2	-2.109	0.0000	0.0000	-1.910	0.0000	0.0000
Atp6v1b2	ENSMUSG00000006273	ATPase, H+ transporting, lysosomal V1 subunit B2	-1.573	0.0000	0.0000	-1.712	0.0000	0.0000
Atp6v1f	ENSMUSG00000004285	ATPase, H+ transporting, lysosomal V1 subunit F	-1.637	0.0000	0.0000	-1.575	0.0000	0.0000
Atraid	ENSMUSG00000013622	all-trans retinoic acid induced differentiation factor	-1.731	0.0000	0.0000	-1.592	0.0000	0.0000
Atrip	ENSMUSG00000025646	ATR interacting protein	-2.086	0.0000	0.0000	-1.954	0.0000	0.0000
Atxn7l2	ENSMUSG00000048997	ataxin 7-like 2	-2.172	0.0002	0.0006	-2.053	0.0006	0.0020
AU021092	ENSMUSG00000051669	expressed sequence AU021092	-3.793	0.0000	0.0000	-2.422	0.0000	0.0000
Aurkaip1	ENSMUSG00000065990	aurora kinase A interacting protein 1	-2.395	0.0000	0.0000	-1.841	0.0000	0.0000
Avpi1	ENSMUSG00000018821	arginine vasopressin-induced 1	-1.925	0.0000	0.0000	-1.662	0.0000	0.0000
AW112010	ENSMUSG00000075010	expressed sequence AW112010	-2.761	0.0000	0.0000	-2.958	0.0000	0.0000
B2m	ENSMUSG00000060802	beta-2 microglobulin	-2.407	0.0000	0.0000	-2.016	0.0000	0.0000
B3galt4	ENSMUSG00000067370	UDP-Gal:betaGlcNAc beta 1,3-galactosyltransferase, polypeptide 4	-3.086	0.0000	0.0000	-3.008	0.0000	0.0000
B3galt6	ENSMUSG00000050796	UDP-Gal:betaGal beta 1,3-galactosyltransferase, polypeptide 6	-1.907	0.0101	0.0242	-3.238	0.0000	0.0000
B3gntl1	ENSMUSG00000046605	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase-like 1	-2.035	0.0003	0.0012	-1.876	0.0016	0.0053
B9d2	ENSMUSG00000063439	B9 protein domain 2	-3.457	0.0000	0.0000	-2.860	0.0000	0.0000
Bace2	ENSMUSG00000040605	beta-site APP-cleaving enzyme 2	-1.835	0.0001	0.0004	-1.639	0.0017	0.0055
Baiap3	ENSMUSG00000047507	BAI1-associated protein 3	-3.522	0.0005	0.0017	-2.510	0.0159	0.0394
Bak1	ENSMUSG00000057789	BCL2-antagonist/killer 1	-2.229	0.0000	0.0000	-2.354	0.0000	0.0000
Bambi-ps1	ENSMUSG00000081219	BMP and activin membrane-bound inhibitor, pseudogene (Xenopus laevis)	-2.197	0.0022	0.0061	-3.127	0.0000	0.0002
Banf2os	ENSMUSG00000086384	barrier to autointegration factor 2, opposite strand	-2.747	0.0002	0.0008	-2.908	0.0002	0.0007
BB218582	ENSMUSG00000085218	expressed sequence BB218582	-1.697	0.0051	0.0132	-1.909	0.0006	0.0023
Bbs4	ENSMUSG00000025235	Bardet-Biedl syndrome 4 (human)	-2.576	0.0000	0.0000	-2.262	0.0000	0.0000
BC002059	ENSMUSG00000060149	cDNA sequence BC002059	-1.760	0.0000	0.0000	-1.967	0.0000	0.0000
BC004004	ENSMUSG00000052712	cDNA sequence BC004004	-2.423	0.0000	0.0000	-1.921	0.0000	0.0000
BC024063	ENSMUSG00000112160	cDNA sequence BC024063	-1.727	0.0378	0.0761	-1.859	0.0177	0.0431
BC029722	ENSMUSG00000074649	cDNA sequence BC029722	-1.653	0.0000	0.0000	-1.649	0.0000	0.0000
Bcam	ENSMUSG00000002980	basal cell adhesion molecule	-1.802	0.0000	0.0000	-1.774	0.0000	0.0000
Bckdha	ENSMUSG00000060376	branched chain ketoacid dehydrogenase E1, alpha polypeptide	-2.778	0.0000	0.0000	-1.849	0.0000	0.0000
Bckdhb	ENSMUSG00000032263	branched chain ketoacid dehydrogenase E1, beta polypeptide	-1.911	0.0000	0.0000	-1.634	0.0007	0.0023
Bckdk	ENSMUSG00000030802	branched chain ketoacid dehydrogenase kinase	-2.215	0.0000	0.0000	-1.844	0.0000	0.0000
Best3	ENSMUSG00000020169	bestrophin 3	-2.362	0.0000	0.0000	-1.999	0.0002	0.0008
Bfsp2	ENSMUSG00000032556	beaded filament structural protein 2, phakinin	-13.214	0.0000	0.0000	-2.389	0.0198	0.0473
Bicra	ENSMUSG00000070808	BRD4 interacting chromatin remodeling complex associated protein	-1.562	0.0001	0.0005	-1.602	0.0001	0.0003
Bicral	ENSMUSG00000036568	BRD4 interacting chromatin remodeling complex associated protein like	-1.634	0.0000	0.0000	-1.616	0.0000	0.0000
Bid	ENSMUSG00000004446	BH3 interacting domain death agonist	-2.660	0.0003	0.0010	-2.026	0.0091	0.0243
Bik	ENSMUSG00000016758	BCL2-interacting killer	-2.093	0.0000	0.0000	-1.513	0.0120	0.0307
Blnk	ENSMUSG00000061132	B cell linker	-2.080	0.0000	0.0001	-2.110	0.0000	0.0002
Bloc1s1	ENSMUSG00000090247	biogenesis of lysosomal organelles complex-1, subunit 1	-2.215	0.0001	0.0003	-2.370	0.0000	0.0001
Bloc1s6	ENSMUSG00000005804	biogenesis of lysosomal organelles complex-1, subunit 6, pallidin	-1.788	0.0000	0.0000	-1.726	0.0000	0.0000
Blvrb	ENSMUSG00000040466	biliverdin reductase B (flavin reductase (NADPH))	-2.796	0.0000	0.0000	-2.236	0.0000	0.0000
Bmp7	ENSMUSG00000008999	bone morphogenetic protein 7	-1.580	0.0151	0.0343	-2.308	0.0000	0.0001
Bmyc	ENSMUSG00000049086	brain expressed myelocytomatosis oncogene	-2.444	0.0000	0.0000	-1.560	0.0000	0.0000
Bnip1	ENSMUSG00000024191	BCL2/adenovirus E1B interacting protein 1	-2.046	0.0000	0.0000	-1.948	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Boc	ENSMUSG00000022687	biregional cell adhesion molecule-related/down-regulated by oncogenes (Cdon) binding protein	-1.993	0.0000	0.0000	-1.887	0.0000	0.0000
Bok	ENSMUSG00000026278	BCL2-related ovarian killer	-2.668	0.0000	0.0000	-2.647	0.0000	0.0001
Bola1	ENSMUSG00000015943	bolA-like 1 (E. coli)	-3.627	0.0000	0.0000	-2.389	0.0000	0.0000
Bop1	ENSMUSG00000022557	block of proliferation 1	-2.287	0.0000	0.0000	-1.506	0.0000	0.0000
Borcs8	ENSMUSG00000002345	BLOC-1 related complex subunit 8	-1.670	0.0000	0.0000	-1.518	0.0004	0.0015
Brd3os	ENSMUSG00000109946	bromodomain containing 3, opposite strand	-3.193	0.0000	0.0000	-1.837	0.0048	0.0138
Brf2	ENSMUSG00000031487	BRF2, RNA polymerase III transcription initiation factor 50kDa subunit	-1.870	0.0000	0.0000	-1.669	0.0000	0.0000
Brk1	ENSMUSG00000033940	BRICK1, SCAR/WAVE actin-nucleating complex subunit	-1.618	0.0000	0.0000	-1.614	0.0000	0.0000
Brme1	ENSMUSG00000008129	break repair meiotic recombinase recruitment factor 1	-4.440	0.0080	0.0197	-5.323	0.0022	0.0070
Bscl2	ENSMUSG00000071657	Berardinelli-Seip congenital lipodystrophy 2 (seipin)	-2.090	0.0000	0.0000	-1.685	0.0000	0.0002
Bst2	ENSMUSG00000046718	bone marrow stromal cell antigen 2	-2.116	0.0000	0.0000	-1.856	0.0000	0.0002
Btbd3	ENSMUSG00000062098	BTB (POZ) domain containing 3	-1.522	0.0000	0.0000	-1.767	0.0000	0.0000
Btbd6	ENSMUSG00000002803	BTB (POZ) domain containing 6	-2.941	0.0000	0.0000	-2.754	0.0000	0.0000
Btd	ENSMUSG00000021900	biotinidase	-2.430	0.0000	0.0000	-1.931	0.0000	0.0000
C030013G03Rik	ENSMUSG00000117314	RIKEN cDNA C030013G03 gene	-4.509	0.0025	0.0071	-4.969	0.0071	0.0194
C1qtnf12	ENSMUSG00000023571	C1q and tumor necrosis factor related 12	-3.214	0.0000	0.0000	-2.585	0.0000	0.0000
C1qtnf6	ENSMUSG00000022440	C1q and tumor necrosis factor related protein 6	-2.079	0.0000	0.0000	-1.711	0.0007	0.0024
C2cd3	ENSMUSG00000047248	C2 calcium-dependent domain containing 3	-1.606	0.0000	0.0000	-1.891	0.0000	0.0000
C87436	ENSMUSG00000046679	expressed sequence C87436	-2.000	0.0000	0.0000	-2.205	0.0000	0.0000
Cabin1	ENSMUSG00000020196	calcineurin binding protein 1	-1.969	0.0000	0.0000	-1.706	0.0000	0.0000
Cacna1s	ENSMUSG00000026407	calcium channel, voltage-dependent, L type, alpha 1S subunit	-2.739	0.0000	0.0000	-1.836	0.0002	0.0007
Calhm2	ENSMUSG00000033033	calcium homeostasis modulator family member 2	-2.099	0.0000	0.0000	-1.794	0.0000	0.0001
Cand2	ENSMUSG00000030319	cullin-associated and neddylation-dissociated 2 (putative)	-2.133	0.0000	0.0000	-1.863	0.0000	0.0000
Capn3	ENSMUSG00000079110	calpain 3	-1.752	0.0277	0.0582	-1.883	0.0151	0.0376
Capns1	ENSMUSG00000001794	calpain, small subunit 1	-2.217	0.0000	0.0000	-1.937	0.0000	0.0000
Car15	ENSMUSG00000090236	carbonic anhydrase 15	-6.382	0.0131	0.0304	-24.890	0.0007	0.0025
Car7	ENSMUSG00000031883	carbonic anhydrase 7	-2.864	0.0000	0.0000	-2.482	0.0000	0.0000
Carm1	ENSMUSG00000032185	coactivator-associated arginine methyltransferase 1	-1.983	0.0000	0.0000	-1.582	0.0000	0.0000
Carmil3	ENSMUSG00000022211	capping protein regulator and myosin 1 linker 3	-2.520	0.0000	0.0000	-1.519	0.0218	0.0514
Caskin2	ENSMUSG00000034471	CASK-interacting protein 2	-2.738	0.0000	0.0000	-2.487	0.0000	0.0000
Cav2	ENSMUSG00000000058	caveolin 2	-1.837	0.0000	0.0000	-2.125	0.0000	0.0000
Ccdc107	ENSMUSG00000028461	coiled-coil domain containing 107	-2.951	0.0000	0.0000	-2.311	0.0000	0.0000
Ccdc159	ENSMUSG00000006241	coiled-coil domain containing 159	-2.731	0.0000	0.0000	-1.888	0.0001	0.0003
Ccdc166	ENSMUSG00000098176	coiled-coil domain containing 166	-2.290	0.0001	0.0004	-3.689	0.0000	0.0000
Ccdc17	ENSMUSG00000034035	coiled-coil domain containing 17	-2.366	0.0021	0.0059	-2.478	0.0016	0.0052
Ccdc22	ENSMUSG00000031143	coiled-coil domain containing 22	-7.467	0.0002	0.0008	-3.898	0.0043	0.0126
Ccdc69	ENSMUSG00000049588	coiled-coil domain containing 69	-1.788	0.0177	0.0395	-1.905	0.0089	0.0237
Ccdc86	ENSMUSG00000024732	coiled-coil domain containing 86	-2.512	0.0000	0.0000	-2.258	0.0000	0.0000
Ccdc90b	ENSMUSG00000030613	coiled-coil domain containing 90B	-1.527	0.0000	0.0001	-1.700	0.0000	0.0000
Ccnq	ENSMUSG00000049489	cyclin Q	-1.629	0.0000	0.0000	-1.719	0.0000	0.0000
Ccrl2	ENSMUSG00000043953	chemokine (C-C motif) receptor-like 2	-2.039	0.0000	0.0001	-1.885	0.0002	0.0008
Cd109	ENSMUSG00000046186	CD109 antigen	-1.657	0.0138	0.0318	-2.388	0.0000	0.0002
Cd14	ENSMUSG00000051439	CD14 antigen	-2.645	0.0000	0.0000	-1.871	0.0002	0.0008

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cd151	ENSMUSG00000025510	CD151 antigen	-2.097	0.0000	0.0000	-2.107	0.0000	0.0000
Cd209b	ENSMUSG00000065987	CD209b antigen	-3.148	0.0338	0.0692	-34.175	0.0001	0.0006
Cd300ld	ENSMUSG00000034641	CD300 molecule like family member d	-1.779	0.0068	0.0170	-1.763	0.0086	0.0231
Cd302	ENSMUSG00000060703	CD302 antigen	-1.753	0.0000	0.0000	-1.983	0.0000	0.0000
Cd320	ENSMUSG00000002308	CD320 antigen	-3.285	0.0000	0.0000	-2.011	0.0000	0.0000
Cd40	ENSMUSG00000017652	CD40 antigen	-2.069	0.0002	0.0008	-2.644	0.0000	0.0000
Cd59b	ENSMUSG00000068686	CD59b antigen	-2.709	0.0000	0.0000	-2.052	0.0001	0.0002
Cd7	ENSMUSG00000025163	CD7 antigen	-20.063	0.0030	0.0081	-14.279	0.0076	0.0207
Cd74	ENSMUSG00000024610	CD74 antigen (invariant polypeptide of major histocompatibility complex, class II antigen-associated)	-2.456	0.0001	0.0002	-1.657	0.0244	0.0566
Cd83	ENSMUSG00000015396	CD83 antigen	-1.869	0.0037	0.0099	-1.950	0.0022	0.0070
Cda	ENSMUSG00000028755	cytidine deaminase	-4.657	0.0001	0.0003	-2.462	0.0165	0.0405
Cdc42ep2	ENSMUSG00000045664	CDC42 effector protein (Rho GTPase binding) 2	-1.686	0.0000	0.0001	-1.820	0.0000	0.0000
Cdcp3	ENSMUSG00000006204	CUB domain containing protein 3	-3.964	0.0000	0.0000	-1.557	0.0272	0.0621
Cdh13	ENSMUSG00000031841	cadherin 13	-1.546	0.0000	0.0000	-1.507	0.0000	0.0000
Cdh15	ENSMUSG00000031962	cadherin 15	-17.090	0.0045	0.0119	-8.765	0.0351	0.0771
Cdh16	ENSMUSG00000031881	cadherin 16	-5.483	0.0000	0.0000	-2.183	0.0000	0.0000
Cdh23	ENSMUSG00000012819	cadherin 23 (otocadherin)	-2.338	0.0000	0.0000	-2.176	0.0000	0.0000
Cdip1	ENSMUSG00000004071	cell death inducing Trp53 target 1	-1.761	0.0000	0.0000	-1.556	0.0000	0.0000
Cdipt	ENSMUSG00000030682	CDP-diacylglycerol--inositol 3-phosphatidyltransferase (phosphatidylinositol synthase)	-1.846	0.0000	0.0000	-1.680	0.0000	0.0000
Cdk2ap2	ENSMUSG00000024856	CDK2-associated protein 2	-3.128	0.0000	0.0000	-2.256	0.0000	0.0000
Cdk4	ENSMUSG00000006728	cyclin-dependent kinase 4	-2.044	0.0000	0.0000	-1.996	0.0000	0.0000
Cdpf1	ENSMUSG00000064284	cysteine rich, DPF motif domain containing 1	-2.139	0.0000	0.0000	-2.177	0.0000	0.0000
Cdt1	ENSMUSG00000006585	chromatin licensing and DNA replication factor 1	-1.825	0.0087	0.0211	-1.702	0.0245	0.0569
Celsr1	ENSMUSG00000016028	cadherin, EGF LAG seven-pass G-type receptor 1	-2.023	0.0001	0.0004	-1.656	0.0053	0.0152
Cenpa	ENSMUSG00000029177	centromere protein A	-1.560	0.0007	0.0021	-1.663	0.0001	0.0004
Cenpt	ENSMUSG00000036672	centromere protein T	-2.246	0.0030	0.0082	-1.832	0.0275	0.0627
Cenpw	ENSMUSG00000075266	centromere protein W	-2.407	0.0244	0.0522	-2.559	0.0185	0.0448
Cenpx	ENSMUSG00000025144	centromere protein X	-2.338	0.0000	0.0000	-2.206	0.0000	0.0000
Cep295	ENSMUSG00000046111	centrosomal protein 295	-1.540	0.0003	0.0010	-1.575	0.0002	0.0007
Ces2e	ENSMUSG00000031886	carboxylesterase 2E	-2.547	0.0018	0.0053	-1.904	0.0324	0.0720
Cfap126	ENSMUSG00000026649	cilia and flagella associated protein 126	-1.609	0.0407	0.0811	-1.774	0.0197	0.0471
Cfap20	ENSMUSG00000031796	cilia and flagella associated protein 20	-1.732	0.0000	0.0000	-1.663	0.0000	0.0001
Cfap418	ENSMUSG00000059482	cilia and flagella associated protein 418	-1.542	0.0048	0.0125	-1.679	0.0008	0.0029
Cfap54	ENSMUSG00000020014	cilia and flagella associated protein 54	-1.901	0.0014	0.0041	-2.605	0.0000	0.0000
Chchd1	ENSMUSG00000063787	coiled-coil-helix-coiled-coil-helix domain containing 1	-3.418	0.0000	0.0000	-3.161	0.0000	0.0000
Chchd2	ENSMUSG00000070493	coiled-coil-helix-coiled-coil-helix domain containing 2	-1.611	0.0000	0.0000	-1.737	0.0000	0.0000
Chchd2-ps	ENSMUSG00000094320	coiled-coil-helix-coiled-coil-helix domain containing 2, pseudogene	-12.941	0.0000	0.0000	-6.611	0.0010	0.0034
Chchd5	ENSMUSG00000037938	coiled-coil-helix-coiled-coil-helix domain containing 5	-1.655	0.0000	0.0000	-1.813	0.0000	0.0000
Chpf2	ENSMUSG00000038181	chondroitin polymerizing factor 2	-1.782	0.0008	0.0026	-1.646	0.0041	0.0121
Chrd	ENSMUSG00000006958	chordin	-1.943	0.0024	0.0068	-1.788	0.0091	0.0242
Chst12	ENSMUSG00000036599	carbohydrate sulfotransferase 12	-2.328	0.0000	0.0000	-1.846	0.0000	0.0000
Chst7	ENSMUSG00000037347	carbohydrate (N-acetylglucosamino) sulfotransferase 7	-1.956	0.0002	0.0006	-2.507	0.0000	0.0000
Churc1	ENSMUSG00000090258	churchill domain containing 1	-2.977	0.0000	0.0000	-2.741	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ciao3	ENSMUSG00000002280	cytosolic iron-sulfur assembly component 3	-2.185	0.0000	0.0000	-1.992	0.0000	0.0000
Cib1	ENSMUSG00000030538	calcium and integrin binding 1 (calmyrin)	-1.778	0.0000	0.0000	-1.895	0.0000	0.0000
Cipc	ENSMUSG00000034157	CLOCK interacting protein, circadian	-1.837	0.0001	0.0003	-1.802	0.0001	0.0006
Cisd3	ENSMUSG00000078695	CDGSH iron sulfur domain 3	-2.206	0.0000	0.0000	-1.578	0.0000	0.0000
Cish	ENSMUSG00000032578	cytokine inducible SH2-containing protein	-3.152	0.0000	0.0000	-1.914	0.0012	0.0039
Ckb	ENSMUSG00000001270	creatine kinase, brain	-5.942	0.0000	0.0000	-3.712	0.0000	0.0000
Ckm	ENSMUSG00000030399	creatine kinase, muscle	-2.310	0.0000	0.0000	-1.597	0.0000	0.0000
Clcn7	ENSMUSG00000036636	chloride channel, voltage-sensitive 7	-1.666	0.0000	0.0000	-1.693	0.0000	0.0000
Cldn5	ENSMUSG00000041378	claudin 5	-1.803	0.0000	0.0002	-1.814	0.0000	0.0002
Clec2d	ENSMUSG00000030157	C-type lectin domain family 2, member d	-2.971	0.0000	0.0000	-3.666	0.0000	0.0000
Clec3b	ENSMUSG00000025784	C-type lectin domain family 3, member b	-3.558	0.0000	0.0000	-2.707	0.0000	0.0000
Clec4a3	ENSMUSG00000043832	C-type lectin domain family 4, member a3	-1.733	0.0360	0.0730	-2.244	0.0036	0.0108
Clic1	ENSMUSG00000007041	chloride intracellular channel 1	-2.347	0.0000	0.0000	-2.163	0.0000	0.0000
Cmtm3	ENSMUSG00000031875	CKLF-like MARVEL transmembrane domain containing 3	-2.660	0.0000	0.0000	-2.296	0.0000	0.0000
Cmtm5	ENSMUSG00000040759	CKLF-like MARVEL transmembrane domain containing 5	-4.397	0.0167	0.0375	-4.478	0.0229	0.0535
Cmtr1	ENSMUSG00000024019	cap methyltransferase 1	-1.781	0.0000	0.0000	-1.839	0.0000	0.0000
Cnep1r1	ENSMUSG00000036810	CTD nuclear envelope phosphatase 1 regulatory subunit 1	-1.657	0.0000	0.0000	-1.931	0.0000	0.0000
Cnih1	ENSMUSG00000015759	cornichon family AMPA receptor auxiliary protein 1	-1.532	0.0000	0.0000	-1.724	0.0000	0.0000
Cnksr1	ENSMUSG00000028841	connector enhancer of kinase suppressor of Ras 1	-4.882	0.0000	0.0000	-2.256	0.0142	0.0356
Cnn3	ENSMUSG00000053931	calponin 3, acidic	-1.995	0.0000	0.0000	-1.826	0.0000	0.0000
Cntnap1	ENSMUSG00000017167	contactin associated protein-like 1	-1.847	0.0045	0.0119	-1.688	0.0165	0.0406
Coa3	ENSMUSG00000017188	cytochrome C oxidase assembly factor 3	-2.298	0.0000	0.0000	-2.063	0.0000	0.0000
Coa6	ENSMUSG00000051671	cytochrome c oxidase assembly factor 6	-1.914	0.0000	0.0000	-2.029	0.0000	0.0000
Cog8	ENSMUSG00000031916	component of oligomeric golgi complex 8	-1.788	0.0000	0.0001	-2.271	0.0000	0.0000
Col4a5	ENSMUSG00000031274	collagen, type IV, alpha 5	-1.988	0.0000	0.0000	-1.670	0.0000	0.0000
Colec12	ENSMUSG00000036103	collectin sub-family member 12	-1.708	0.0000	0.0000	-1.517	0.0000	0.0001
Commd2	ENSMUSG00000036513	COMM domain containing 2	-1.503	0.0000	0.0000	-1.664	0.0000	0.0000
Commd4	ENSMUSG00000032299	COMM domain containing 4	-3.257	0.0000	0.0000	-3.290	0.0000	0.0000
Commd9	ENSMUSG00000027163	COMM domain containing 9	-2.596	0.0000	0.0000	-2.170	0.0000	0.0000
Comt	ENSMUSG00000000326	catechol-O-methyltransferase	-2.278	0.0000	0.0000	-2.037	0.0000	0.0000
Comtd1	ENSMUSG00000021773	catechol-O-methyltransferase domain containing 1	-4.108	0.0000	0.0000	-2.569	0.0000	0.0000
Cope	ENSMUSG00000055681	coatomer protein complex, subunit epsilon	-3.064	0.0000	0.0000	-2.403	0.0000	0.0000
Cops3	ENSMUSG00000019373	COP9 signalosome subunit 3	-1.934	0.0000	0.0000	-1.862	0.0000	0.0000
Cops6	ENSMUSG00000019494	COP9 signalosome subunit 6	-1.952	0.0000	0.0000	-1.644	0.0000	0.0000
Cops7a	ENSMUSG00000030127	COP9 signalosome subunit 7A	-2.456	0.0000	0.0000	-2.014	0.0000	0.0000
Coq4	ENSMUSG00000026798	coenzyme Q4	-2.395	0.0000	0.0000	-2.223	0.0000	0.0000
Coq6	ENSMUSG00000021235	coenzyme Q6 monooxygenase	-1.786	0.0000	0.0000	-1.647	0.0000	0.0000
Coq8a	ENSMUSG00000026489	coenzyme Q8A	-1.777	0.0000	0.0000	-1.598	0.0001	0.0002
Coq9	ENSMUSG00000031782	coenzyme Q9	-1.934	0.0000	0.0000	-1.661	0.0000	0.0000
Coro1b	ENSMUSG00000024835	coronin, actin binding protein 1B	-2.408	0.0000	0.0000	-2.283	0.0000	0.0000
Cox14	ENSMUSG00000023020	cytochrome c oxidase assembly protein 14	-1.836	0.0000	0.0000	-1.633	0.0000	0.0000
Cox16	ENSMUSG00000091803	cytochrome c oxidase assembly protein 16	-7.547	0.0000	0.0000	-4.890	0.0000	0.0000
Cox18	ENSMUSG00000035505	cytochrome c oxidase assembly protein 18	-2.022	0.0000	0.0000	-1.809	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cox4i2	ENSMUSG00000009876	cytochrome c oxidase subunit 4I2	-2.655	0.0000	0.0000	-1.962	0.0000	0.0000
Cox6a1	ENSMUSG00000041697	cytochrome c oxidase subunit 6A1	-1.845	0.0000	0.0000	-1.727	0.0000	0.0000
Cox6a2	ENSMUSG00000030785	cytochrome c oxidase subunit 6A2	-5.350	0.0000	0.0000	-3.933	0.0000	0.0000
Cox6b1	ENSMUSG00000036751	cytochrome c oxidase, subunit 6B1	-2.577	0.0000	0.0000	-2.343	0.0000	0.0000
Cox7a1	ENSMUSG00000074218	cytochrome c oxidase subunit 7A1	-2.924	0.0000	0.0000	-2.638	0.0000	0.0000
Cox7a2	ENSMUSG00000032330	cytochrome c oxidase subunit 7A2	-3.664	0.0000	0.0000	-3.474	0.0000	0.0000
Cox7a2l	ENSMUSG00000024248	cytochrome c oxidase subunit 7A2 like	-2.082	0.0000	0.0000	-1.980	0.0000	0.0000
Cox7b	ENSMUSG00000031231	cytochrome c oxidase subunit 7B	-1.839	0.0000	0.0000	-1.980	0.0000	0.0000
Cox8a	ENSMUSG00000035885	cytochrome c oxidase subunit 8A	-3.913	0.0000	0.0000	-3.414	0.0000	0.0000
Cpt1b	ENSMUSG00000078937	carnitine palmitoyltransferase 1b, muscle	-5.923	0.0000	0.0000	-3.678	0.0000	0.0000
Cpt1c	ENSMUSG00000007783	carnitine palmitoyltransferase 1c	-1.776	0.0031	0.0086	-2.203	0.0001	0.0005
Cpt2	ENSMUSG00000028607	carnitine palmitoyltransferase 2	-1.794	0.0000	0.0000	-1.870	0.0000	0.0000
Cpxm1	ENSMUSG00000027408	carboxypeptidase X 1 (M14 family)	-4.446	0.0000	0.0000	-3.736	0.0000	0.0000
Crat	ENSMUSG00000026853	carnitine acetyltransferase	-2.260	0.0000	0.0000	-2.068	0.0000	0.0000
Crb2	ENSMUSG00000035403	crumbs family member 2	-24.646	0.0038	0.0102	-10.609	0.0354	0.0775
Crip2	ENSMUSG00000006356	cysteine rich protein 2	-1.892	0.0000	0.0000	-1.633	0.0000	0.0000
Crlf2	ENSMUSG00000033467	cytokine receptor-like factor 2	-3.627	0.0000	0.0000	-3.208	0.0000	0.0000
Crtc1	ENSMUSG00000003575	CREB regulated transcription coactivator 1	-2.170	0.0000	0.0000	-1.644	0.0000	0.0000
Cryab	ENSMUSG00000032060	crystallin, alpha B	-2.163	0.0000	0.0000	-1.553	0.0000	0.0000
Crybb1	ENSMUSG00000029343	crystallin, beta B1	-2.839	0.0000	0.0000	-2.416	0.0000	0.0001
Cs	ENSMUSG00000005683	citrate synthase	-1.785	0.0000	0.0000	-1.749	0.0000	0.0000
Csdc2	ENSMUSG00000042109	cold shock domain containing C2, RNA binding	-1.782	0.0014	0.0042	-1.516	0.0217	0.0511
Csf1r	ENSMUSG00000024621	colony stimulating factor 1 receptor	-1.947	0.0000	0.0000	-1.566	0.0011	0.0038
Csf2rb2	ENSMUSG00000071714	colony stimulating factor 2 receptor, beta 2, low-affinity (granulocyte-macrophage)	-2.599	0.0016	0.0046	-2.845	0.0015	0.0050
Csnk2a1-ps3	ENSMUSG00000101523	casein kinase 2, alpha 1 polypeptide, pseudogene 3	-1.629	0.0150	0.0342	-1.644	0.0145	0.0364
Csnk2b	ENSMUSG00000024387	casein kinase 2, beta polypeptide	-3.217	0.0000	0.0000	-2.686	0.0000	0.0000
Cspg4	ENSMUSG00000032911	chondroitin sulfate proteoglycan 4	-1.703	0.0000	0.0000	-1.712	0.0000	0.0000
Cst6	ENSMUSG00000024846	cystatin E/M	-5.301	0.0000	0.0000	-3.941	0.0000	0.0000
Cstf1	ENSMUSG00000027498	cleavage stimulation factor, 3' pre-RNA, subunit 1	-1.873	0.0000	0.0000	-1.762	0.0000	0.0000
Cstpp1	ENSMUSG00000040591	centriolar satellite-associated tubulin polyglutamylase complex regulator 1	-1.594	0.0002	0.0008	-1.722	0.0000	0.0001
Ctbp2	ENSMUSG00000030970	C-terminal binding protein 2	-1.893	0.0000	0.0000	-1.701	0.0000	0.0000
Ctc1	ENSMUSG00000020898	CTS telomere maintenance complex component 1	-1.929	0.0000	0.0000	-1.787	0.0000	0.0000
Ctsa	ENSMUSG00000017760	cathepsin A	-1.750	0.0000	0.0000	-1.512	0.0000	0.0000
Ctsb	ENSMUSG00000021939	cathepsin B	-1.826	0.0000	0.0000	-1.707	0.0000	0.0000
Ctsd	ENSMUSG00000007891	cathepsin D	-4.110	0.0000	0.0000	-3.353	0.0000	0.0000
Ctu2	ENSMUSG00000049482	cytosolic thiouridylase subunit 2	-2.378	0.0000	0.0000	-1.745	0.0000	0.0000
Cuta	ENSMUSG00000024194	cutA divalent cation tolerance homolog	-1.842	0.0000	0.0000	-1.578	0.0000	0.0000
Cuzd1	ENSMUSG00000040205	CUB and zona pellucida-like domains 1	-3.356	0.0000	0.0000	-2.666	0.0001	0.0005
Cx3cl1	ENSMUSG00000031778	chemokine (C-X3-C motif) ligand 1	-2.326	0.0000	0.0000	-1.680	0.0020	0.0064
Cyb561d2	ENSMUSG00000037190	cytochrome b-561 domain containing 2	-3.442	0.0000	0.0000	-2.235	0.0000	0.0000
Cyb5a	ENSMUSG00000024646	cytochrome b5 type A (microsomal)	-3.196	0.0000	0.0000	-2.608	0.0000	0.0000
Cyb5r1	ENSMUSG00000026456	cytochrome b5 reductase 1	-1.575	0.0000	0.0000	-1.611	0.0000	0.0000
Cyp27a1	ENSMUSG00000026170	cytochrome P450, family 27, subfamily a, polypeptide 1	-2.355	0.0000	0.0000	-2.108	0.0001	0.0003

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Cyp2d22	ENSMUSG00000061740	cytochrome P450, family 2, subfamily d, polypeptide 22	-2.076	0.0000	0.0000	-1.705	0.0000	0.0001
Cyp4f14	ENSMUSG00000024292	cytochrome P450, family 4, subfamily f, polypeptide 14	-13.816	0.0067	0.0169	-8.461	0.0295	0.0666
Cyp4f16	ENSMUSG00000048440	cytochrome P450, family 4, subfamily f, polypeptide 16	-2.234	0.0000	0.0000	-2.024	0.0000	0.0000
Cystm1	ENSMUSG00000046727	cysteine-rich transmembrane module containing 1	-2.332	0.0000	0.0000	-2.324	0.0000	0.0000
Cytl1	ENSMUSG00000062329	cytokine-like 1	-3.417	0.0000	0.0000	-2.342	0.0001	0.0005
D330023K18Rik	ENSMUSG00000087269	RIKEN cDNA D330023K18 gene	-2.743	0.0000	0.0000	-3.721	0.0000	0.0000
D630003M21Rik	ENSMUSG00000037813	RIKEN cDNA D630003M21 gene	-2.812	0.0000	0.0000	-1.943	0.0000	0.0000
D630024D03Rik	ENSMUSG00000085772	RIKEN cDNA D630024D03 gene	-10.594	0.0003	0.0009	-28.991	0.0001	0.0005
D830005E20Rik	ENSMUSG00000112707	RIKEN cDNA D830005E20 gene	-1.708	0.0000	0.0000	-1.511	0.0005	0.0017
Dad1	ENSMUSG00000022174	defender against cell death 1	-3.887	0.0000	0.0000	-3.838	0.0000	0.0000
Dap	ENSMUSG00000039168	death-associated protein	-2.863	0.0000	0.0000	-2.263	0.0000	0.0000
Dapp1	ENSMUSG00000028159	dual adaptor for phosphotyrosine and 3-phosphoinositides 1	-1.863	0.0001	0.0005	-1.622	0.0029	0.0088
Dcaf15	ENSMUSG00000037103	DDB1 and CUL4 associated factor 15	-1.852	0.0000	0.0000	-1.701	0.0000	0.0000
Dcaf4	ENSMUSG00000021222	DDB1 and CUL4 associated factor 4	-1.675	0.0002	0.0008	-1.731	0.0001	0.0005
Dcakd	ENSMUSG00000020935	dephospho-CoA kinase domain containing	-2.780	0.0000	0.0000	-2.513	0.0000	0.0000
Dclre1c	ENSMUSG00000026648	DNA cross-link repair 1C	-1.547	0.0091	0.0221	-1.588	0.0074	0.0203
Dcn	ENSMUSG00000019929	decorin	-2.477	0.0000	0.0000	-2.346	0.0000	0.0000
Dctpp1	ENSMUSG00000042462	dCTP pyrophosphatase 1	-2.283	0.0000	0.0000	-1.808	0.0000	0.0000
Dcxr	ENSMUSG00000039450	dicarbonyl L-xylulose reductase	-8.749	0.0000	0.0000	-3.418	0.0000	0.0000
Dda1	ENSMUSG00000074247	DET1 and DDB1 associated 1	-1.900	0.0000	0.0000	-2.270	0.0000	0.0000
Ddost	ENSMUSG00000028757	dolichyl-di-phosphooligosaccharide-protein glycotransferase	-1.678	0.0000	0.0000	-1.567	0.0000	0.0000
Ddx28	ENSMUSG00000045538	DEAD box helicase 28	-2.565	0.0000	0.0000	-2.146	0.0000	0.0000
Ddx39b	ENSMUSG00000019432	DEAD box helicase 39b	-1.672	0.0000	0.0000	-1.681	0.0000	0.0000
Ddx56	ENSMUSG00000004393	DEAD box helicase 56	-2.166	0.0000	0.0000	-1.975	0.0000	0.0000
Degs1	ENSMUSG00000038633	delta(4)-desaturase, sphingolipid 1	-1.579	0.0000	0.0000	-1.564	0.0000	0.0000
Dele1	ENSMUSG00000024442	DAP3 binding cell death enhancer 1	-3.126	0.0000	0.0000	-2.701	0.0000	0.0000
Dennd6b	ENSMUSG00000015377	DENN/MADD domain containing 6B	-1.968	0.0000	0.0000	-1.980	0.0000	0.0000
Dgkz	ENSMUSG00000040479	diacylglycerol kinase zeta	-2.247	0.0000	0.0000	-1.787	0.0000	0.0000
Dguok	ENSMUSG00000014554	deoxyguanosine kinase	-2.073	0.0000	0.0000	-2.003	0.0000	0.0000
Dhcr7	ENSMUSG00000058454	7-dehydrocholesterol reductase	-1.611	0.0009	0.0028	-1.655	0.0005	0.0018
Dhodh	ENSMUSG00000031730	dihydroorotate dehydrogenase	-1.645	0.0000	0.0000	-1.700	0.0000	0.0000
Dhrs11	ENSMUSG00000034449	dehydrogenase/reductase (SDR family) member 11	-2.178	0.0000	0.0000	-1.732	0.0000	0.0000
Dhrs7b	ENSMUSG00000042569	dehydrogenase/reductase (SDR family) member 7B	-1.984	0.0000	0.0000	-1.986	0.0000	0.0000
Dhx30	ENSMUSG00000032480	DEAH (Asp-Glu-Ala-His) box polypeptide 30	-1.699	0.0000	0.0000	-1.625	0.0000	0.0000
Dhx34	ENSMUSG00000006019	DEAH (Asp-Glu-Ala-His) box polypeptide 34	-2.124	0.0000	0.0000	-1.664	0.0000	0.0000
Dhx35	ENSMUSG00000027655	DEAH (Asp-Glu-Ala-His) box polypeptide 35	-1.586	0.0000	0.0000	-1.794	0.0000	0.0000
Dhx37	ENSMUSG00000029480	DEAH (Asp-Glu-Ala-His) box polypeptide 37	-1.912	0.0000	0.0000	-1.849	0.0000	0.0000
Diablo	ENSMUSG00000029433	diablo, IAP-binding mitochondrial protein	-1.664	0.0007	0.0021	-1.734	0.0002	0.0010
Dll4	ENSMUSG00000027314	delta like canonical Notch ligand 4	-2.353	0.0000	0.0000	-1.976	0.0000	0.0000
Dmap1	ENSMUSG00000009640	DNA methyltransferase 1-associated protein 1	-1.791	0.0000	0.0000	-1.562	0.0000	0.0000
Dnaaf2	ENSMUSG00000020973	dynein, axonemal assembly factor 2	-2.097	0.0098	0.0235	-2.148	0.0087	0.0233
Dnajc15	ENSMUSG00000022013	DnaJ heat shock protein family (Hsp40) member C15	-2.368	0.0000	0.0000	-2.575	0.0000	0.0000
Dnase1l2	ENSMUSG00000024136	deoxyribonuclease 1-like 2	-2.782	0.0198	0.0436	-8.389	0.0005	0.0019

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Dnase2a	ENSMUSG00000003812	deoxyribonuclease II alpha	-1.684	0.0000	0.0000	-1.511	0.0000	0.0000
Dnd1	ENSMUSG00000044595	DND microRNA-mediated repression inhibitor 1	-4.697	0.0000	0.0000	-2.726	0.0005	0.0020
Dnpep	ENSMUSG00000026209	aspartyl aminopeptidase	-2.544	0.0000	0.0000	-2.277	0.0000	0.0000
Dohh	ENSMUSG00000078440	deoxyhypusine hydroxylase/monooxygenase	-1.637	0.0000	0.0000	-1.530	0.0000	0.0001
Dok7	ENSMUSG00000044716	docking protein 7	-2.497	0.0000	0.0000	-2.565	0.0000	0.0000
Dolpp1	ENSMUSG00000026856	dolichyl pyrophosphate phosphatase 1	-1.594	0.0000	0.0001	-1.647	0.0000	0.0000
Dop1b	ENSMUSG00000022946	DOP1 leucine zipper like protein B	-1.986	0.0000	0.0000	-1.797	0.0000	0.0000
Dpagt1	ENSMUSG00000032123	dolichyl-phosphate (UDP-N-acetylglucosamine) acetylglucosaminephosphotransferase 1 (GlcNAc-1-P transferase)	-3.776	0.0000	0.0000	-2.951	0.0000	0.0000
Dpep1	ENSMUSG00000019278	dipeptidase 1	-1.786	0.0005	0.0017	-1.583	0.0060	0.0168
Dph1	ENSMUSG00000078789	diphthamide biosynthesis 1	-1.965	0.0000	0.0000	-1.944	0.0000	0.0000
Dpm2	ENSMUSG00000026810	dolichol-phosphate (beta-D) mannosyltransferase 2	-2.141	0.0000	0.0000	-2.982	0.0000	0.0000
Dpm3	ENSMUSG00000042737	dolichyl-phosphate mannosyltransferase polypeptide 3	-5.332	0.0000	0.0000	-4.702	0.0000	0.0000
Dpp7	ENSMUSG00000026958	dipeptidylpeptidase 7	-4.588	0.0000	0.0000	-2.635	0.0000	0.0000
Dpp9	ENSMUSG00000001229	dipeptidylpeptidase 9	-2.100	0.0000	0.0000	-1.874	0.0000	0.0000
Dpysl4	ENSMUSG00000025478	dihydropyrimidinase-like 4	-1.906	0.0000	0.0001	-1.613	0.0014	0.0047
Drg2	ENSMUSG00000020537	developmentally regulated GTP binding protein 2	-1.928	0.0000	0.0000	-1.637	0.0000	0.0000
Dstn	ENSMUSG00000015932	destrin	-1.713	0.0000	0.0000	-1.883	0.0000	0.0000
Dusp13	ENSMUSG00000021768	dual specificity phosphatase 13	-3.937	0.0506	0.0975	-5.422	0.0251	0.0580
Dusp23	ENSMUSG00000026544	dual specificity phosphatase 23	-1.894	0.0000	0.0000	-2.225	0.0000	0.0000
Dxo	ENSMUSG00000040482	decapping exoribonuclease	-2.308	0.0000	0.0000	-2.955	0.0000	0.0000
Dync2i2	ENSMUSG00000039715	dynein 2 intermediate chain 2	-2.260	0.0000	0.0000	-1.548	0.0122	0.0311
Dynll1	ENSMUSG00000009013	dynein light chain LC8-type 1	-1.710	0.0006	0.0019	-1.610	0.0023	0.0074
Dynlt1a	ENSMUSG00000092074	dynein light chain Tctex-type 1A	-6.776	0.0056	0.0145	-5.185	0.0041	0.0122
Dynlt1f	ENSMUSG00000095677	dynein light chain Tctex-type 1F	-4.651	0.0000	0.0001	-2.883	0.0013	0.0043
E130310I04Rik	ENSMUSG00000116665	RIKEN cDNA E130310I04 gene	-2.696	0.0002	0.0006	-2.000	0.0077	0.0209
E430024I08Rik	ENSMUSG00000112964	RIKEN cDNA E430024I08 gene	-1.626	0.0001	0.0002	-1.808	0.0000	0.0000
Ebi3	ENSMUSG00000003206	Epstein-Barr virus induced gene 3	-5.355	0.0030	0.0082	-10.980	0.0005	0.0020
Ebpl	ENSMUSG00000021928	emopamil binding protein-like	-1.992	0.0077	0.0189	-2.238	0.0021	0.0066
Ech1	ENSMUSG00000053898	enoyl coenzyme A hydratase 1, peroxisomal	-2.050	0.0000	0.0000	-2.103	0.0000	0.0000
Echs1	ENSMUSG00000025465	enoyl Coenzyme A hydratase, short chain, 1, mitochondrial	-2.237	0.0000	0.0000	-1.607	0.0000	0.0000
Edc3	ENSMUSG00000038957	enhancer of mRNA decapping 3	-1.937	0.0000	0.0000	-1.519	0.0001	0.0002
Edc4	ENSMUSG00000036270	enhancer of mRNA decapping 4	-1.995	0.0000	0.0000	-1.893	0.0000	0.0000
Eef1akmt1	ENSMUSG00000021951	EEF1A alpha lysine methyltransferase 1	-1.845	0.0000	0.0000	-1.722	0.0000	0.0000
Eef1akmt4	ENSMUSG00000115219	EEF1A lysine methyltransferase 4	-3.635	0.0001	0.0002	-3.699	0.0001	0.0006
Eef2kmt	ENSMUSG00000022544	eukaryotic elongation factor 2 lysine methyltransferase	-2.708	0.0000	0.0000	-2.297	0.0000	0.0000
Eefsec	ENSMUSG00000033216	eukaryotic elongation factor, selenocysteine-tRNA-specific	-2.784	0.0000	0.0000	-2.059	0.0000	0.0001
Efna1	ENSMUSG00000027954	ephrin A1	-2.040	0.0000	0.0000	-2.118	0.0000	0.0000
Efs	ENSMUSG00000022203	embryonal Fyn-associated substrate	-1.900	0.0000	0.0001	-1.559	0.0031	0.0096
Eif1	ENSMUSG00000035530	eukaryotic translation initiation factor 1	-2.698	0.0000	0.0000	-2.270	0.0000	0.0000
Eif2b3	ENSMUSG00000028683	eukaryotic translation initiation factor 2B, subunit 3	-1.676	0.0000	0.0000	-1.760	0.0000	0.0000
Eif2d	ENSMUSG00000026427	eukaryotic translation initiation factor 2D	-2.054	0.0000	0.0000	-1.817	0.0000	0.0000
Eif3h	ENSMUSG00000022312	eukaryotic translation initiation factor 3, subunit H	-2.016	0.0000	0.0000	-1.738	0.0000	0.0000
Eif3i	ENSMUSG00000028798	eukaryotic translation initiation factor 3, subunit I	-2.897	0.0000	0.0000	-2.894	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Eif3k	ENSMUSG00000053565	eukaryotic translation initiation factor 3, subunit K	-2.044	0.0000	0.0000	-1.955	0.0000	0.0000
Eif3l	ENSMUSG00000033047	eukaryotic translation initiation factor 3, subunit L	-1.998	0.0000	0.0000	-1.802	0.0000	0.0000
Eif3m	ENSMUSG00000027170	eukaryotic translation initiation factor 3, subunit M	-1.659	0.0000	0.0000	-1.790	0.0000	0.0000
Eif3s6-ps2	ENSMUSG00000091697	eukaryotic translation initiation factor 3, subunit 6, pseudogene 2	-1.982	0.0019	0.0054	-2.357	0.0001	0.0006
Eif5al3-ps	ENSMUSG00000043618	eukaryotic translation initiation factor 5A-like 3, pseudogene	-1.855	0.0000	0.0000	-1.527	0.0002	0.0008
Elmo1	ENSMUSG00000041112	engulfment and cell motility 1	-1.818	0.0012	0.0036	-1.822	0.0012	0.0041
Elmo2	ENSMUSG00000017670	engulfment and cell motility 2	-1.680	0.0000	0.0000	-1.585	0.0000	0.0000
Elmod3	ENSMUSG00000056698	ELMO/CED-12 domain containing 3	-2.106	0.0000	0.0000	-2.123	0.0000	0.0000
Elob	ENSMUSG00000055839	elongin B	-3.186	0.0000	0.0000	-2.571	0.0000	0.0000
Elof1	ENSMUSG00000013822	ELF1 homolog, elongation factor 1	-2.788	0.0000	0.0000	-2.183	0.0000	0.0000
Elovl1	ENSMUSG00000006390	elongation of very long chain fatty acids (FEN1/Elo2, SUR4/Elo3, yeast)-like 1	-1.873	0.0000	0.0000	-1.657	0.0000	0.0000
Elp4	ENSMUSG00000027167	elongator acetyltransferase complex subunit 4	-1.714	0.0000	0.0000	-1.667	0.0000	0.0000
Emc6	ENSMUSG00000047260	ER membrane protein complex subunit 6	-1.857	0.0000	0.0000	-1.847	0.0000	0.0000
Emcn	ENSMUSG00000054690	endomucin	-1.845	0.0000	0.0000	-1.705	0.0000	0.0000
Emd	ENSMUSG00000001964	emerin	-1.642	0.0000	0.0000	-1.641	0.0000	0.0000
Emp2	ENSMUSG00000022505	epithelial membrane protein 2	-1.860	0.0000	0.0000	-1.610	0.0000	0.0000
Emp3	ENSMUSG00000040212	epithelial membrane protein 3	-4.231	0.0000	0.0000	-4.186	0.0000	0.0000
Eng	ENSMUSG00000026814	endoglin	-2.612	0.0000	0.0000	-2.054	0.0000	0.0000
Eno1	ENSMUSG00000063524	enolase 1, alpha non-neuron	-1.898	0.0000	0.0000	-1.694	0.0000	0.0000
Eno1b	ENSMUSG00000059040	enolase 1B, retrotransposed	-5.345	0.0000	0.0000	-3.883	0.0000	0.0000
Eno3	ENSMUSG00000060600	enolase 3, beta muscle	-1.869	0.0000	0.0000	-1.586	0.0000	0.0000
Enpep	ENSMUSG00000028024	glutamyl aminopeptidase	-1.723	0.0000	0.0000	-1.706	0.0000	0.0000
Entpd2	ENSMUSG00000015085	ectonucleoside triphosphate diphosphohydrolase 2	-3.789	0.0000	0.0000	-3.529	0.0000	0.0000
Entpd6	ENSMUSG00000033068	ectonucleoside triphosphate diphosphohydrolase 6	-1.884	0.0000	0.0000	-1.633	0.0000	0.0000
Eola1	ENSMUSG00000045237	endothelium and lymphocyte associated ASCH domain 1	-1.849	0.0000	0.0000	-1.816	0.0000	0.0000
Epdr1	ENSMUSG00000002808	ependymin related protein 1 (zebrafish)	-1.534	0.0093	0.0226	-1.817	0.0003	0.0013
Epg5	ENSMUSG00000039840	ectopic P-granules autophagy protein 5 homolog (C. elegans)	-2.127	0.0000	0.0000	-1.855	0.0000	0.0000
Ephx1	ENSMUSG00000038776	epoxide hydrolase 1, microsomal	-2.074	0.0000	0.0000	-1.945	0.0000	0.0001
Ephx2	ENSMUSG00000022040	epoxide hydrolase 2, cytoplasmic	-1.702	0.0000	0.0000	-2.033	0.0000	0.0000
Ercc1	ENSMUSG00000003549	excision repair cross-complementing rodent repair deficiency, complementation group 1	-1.966	0.0000	0.0000	-1.912	0.0000	0.0000
Ercc2	ENSMUSG00000030400	excision repair cross-complementing rodent repair deficiency, complementation group 2	-2.428	0.0000	0.0000	-2.253	0.0000	0.0000
Esd	ENSMUSG00000021996	esterase D/formylglutathione hydrolase	-1.666	0.0000	0.0000	-1.657	0.0000	0.0000
Esrrb	ENSMUSG00000021255	estrogen related receptor, beta	-2.066	0.0000	0.0000	-1.601	0.0000	0.0000
Ethe1	ENSMUSG00000064254	ethylmalonic encephalopathy 1	-4.676	0.0000	0.0000	-4.026	0.0000	0.0000
Exoc3l4	ENSMUSG00000021280	exocyst complex component 3-like 4	-2.068	0.0008	0.0025	-2.300	0.0001	0.0006
Exoc7	ENSMUSG00000020792	exocyst complex component 7	-1.641	0.0000	0.0000	-1.500	0.0000	0.0000
Exosc5	ENSMUSG00000061286	exosome component 5	-2.395	0.0000	0.0000	-1.653	0.0000	0.0000
F8a	ENSMUSG00000078317	factor 8-associated gene A	-1.755	0.0000	0.0000	-1.693	0.0000	0.0000
Faap100	ENSMUSG00000025384	Fanconi anemia core complex associated protein 100	-3.254	0.0000	0.0000	-3.403	0.0000	0.0000
Faap24	ENSMUSG00000030493	Fanconi anemia core complex associated protein 24	-1.973	0.0012	0.0035	-1.579	0.0324	0.0720
Fah	ENSMUSG00000030630	fumarylacetoacetate hydrolase	-3.348	0.0000	0.0000	-2.158	0.0002	0.0009
Fam120b	ENSMUSG00000014763	family with sequence similarity 120, member B	-1.819	0.0000	0.0000	-1.585	0.0000	0.0000
Fam13c	ENSMUSG00000043259	family with sequence similarity 13, member C	-1.601	0.0000	0.0000	-1.513	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fam189b	ENSMUSG00000032657	family with sequence similarity 189, member B	-2.721	0.0000	0.0000	-1.841	0.0000	0.0000
Fam205c	ENSMUSG00000050141	family with sequence similarity 205, member C	-6.480	0.0000	0.0000	-3.731	0.0001	0.0003
Fam222b	ENSMUSG00000037750	family with sequence similarity 222, member B	-1.610	0.0000	0.0000	-1.759	0.0000	0.0000
Fam229b	ENSMUSG00000051736	family with sequence similarity 229, member B	-3.290	0.0000	0.0000	-2.309	0.0000	0.0000
Fam234a	ENSMUSG00000024187	family with sequence similarity 234, member A	-2.116	0.0000	0.0000	-2.048	0.0000	0.0000
Fam53b	ENSMUSG00000030956	family with sequence similarity 53, member B	-1.866	0.0000	0.0000	-1.774	0.0000	0.0000
Fan1	ENSMUSG00000033458	FANCD2/FANCI-associated nuclease 1	-1.760	0.0000	0.0000	-1.515	0.0005	0.0019
Fancb	ENSMUSG00000047757	Fanconi anemia, complementation group B	-1.751	0.0031	0.0084	-1.645	0.0086	0.0231
Fancg	ENSMUSG00000028453	Fanconi anemia, complementation group G	-1.640	0.0038	0.0101	-1.902	0.0004	0.0015
Fars2	ENSMUSG00000021420	phenylalanine-tRNA synthetase 2 (mitochondrial)	-2.060	0.0000	0.0000	-1.691	0.0000	0.0000
Farsb	ENSMUSG00000026245	phenylalanyl-tRNA synthetase, beta subunit	-2.280	0.0000	0.0000	-2.279	0.0000	0.0000
Fasn	ENSMUSG00000025153	fatty acid synthase	-1.631	0.0008	0.0025	-1.780	0.0001	0.0003
Fau	ENSMUSG00000038274	Finkel-Biskis-Reilly murine sarcoma virus (FBR-MuSV) ubiquitously expressed (fox derived)	-2.166	0.0000	0.0000	-1.943	0.0000	0.0000
Fbln2	ENSMUSG00000064080	fibulin 2	-1.877	0.0000	0.0001	-1.570	0.0022	0.0069
Fbln5	ENSMUSG00000021186	fibulin 5	-1.819	0.0000	0.0000	-1.593	0.0000	0.0000
Fbxl15	ENSMUSG00000025226	F-box and leucine-rich repeat protein 15	-5.361	0.0000	0.0000	-5.591	0.0000	0.0000
Fbxl22	ENSMUSG00000050503	F-box and leucine-rich repeat protein 22	-2.282	0.0000	0.0000	-2.111	0.0000	0.0001
Fbxl6	ENSMUSG00000022559	F-box and leucine-rich repeat protein 6	-2.877	0.0000	0.0000	-2.086	0.0000	0.0000
Fbxo6	ENSMUSG00000055401	F-box protein 6	-1.817	0.0000	0.0000	-1.683	0.0000	0.0000
Fbxo8	ENSMUSG00000038206	F-box protein 8	-1.632	0.0000	0.0000	-1.675	0.0000	0.0000
Fcer1g	ENSMUSG00000058715	Fc receptor, IgE, high affinity I, gamma polypeptide	-4.322	0.0000	0.0000	-2.872	0.0000	0.0000
Fcgr2b	ENSMUSG00000026656	Fc receptor, IgG, low affinity IIb	-2.146	0.0002	0.0006	-1.847	0.0028	0.0086
Fcgr3	ENSMUSG00000059498	Fc receptor, IgG, low affinity III	-2.656	0.0000	0.0000	-1.938	0.0004	0.0016
Fcna	ENSMUSG00000026938	ficolin A	-1.990	0.0003	0.0010	-1.599	0.0146	0.0365
Fcsk	ENSMUSG00000033703	fucose kinase	-1.714	0.0000	0.0001	-1.662	0.0001	0.0004
Fem1a	ENSMUSG00000043683	fem 1 homolog a	-2.116	0.0000	0.0000	-1.764	0.0000	0.0000
Fgfr3	ENSMUSG00000054252	fibroblast growth factor receptor 3	-1.875	0.0002	0.0006	-1.974	0.0001	0.0003
Fh1	ENSMUSG00000026526	fumarate hydratase 1	-1.657	0.0000	0.0000	-1.740	0.0000	0.0000
Fhip1a	ENSMUSG00000051000	FHF complex subunit HOOK interacting protein 1A	-1.816	0.0000	0.0000	-1.868	0.0000	0.0000
Fhl2	ENSMUSG00000008136	four and a half LIM domains 2	-2.297	0.0000	0.0000	-2.473	0.0000	0.0000
Ficd	ENSMUSG00000053334	FIC domain containing	-2.362	0.0000	0.0000	-1.868	0.0000	0.0000
Fitm1	ENSMUSG00000022215	fat storage-inducing transmembrane protein 1	-4.208	0.0000	0.0000	-3.736	0.0000	0.0000
Fkbp10	ENSMUSG00000001555	FK506 binding protein 10	-1.618	0.0000	0.0002	-1.914	0.0000	0.0000
Fkbp11	ENSMUSG00000003355	FK506 binding protein 11	-2.203	0.0000	0.0002	-2.041	0.0003	0.0012
Flad1	ENSMUSG00000042642	flavin adenine dinucleotide synthetase 1	-1.933	0.0000	0.0000	-1.525	0.0000	0.0000
Flnc	ENSMUSG00000068699	filamin C, gamma	-1.716	0.0000	0.0000	-1.589	0.0000	0.0001
Flrt3	ENSMUSG00000051379	fibronectin leucine rich transmembrane protein 3	-3.029	0.0173	0.0386	-2.327	0.0460	0.0966
Fndc1	ENSMUSG00000071984	fibronectin type III domain containing 1	-1.872	0.0081	0.0198	-1.639	0.0369	0.0803
Fndc10	ENSMUSG00000074738	fibronectin type III domain containing 10	-2.102	0.0001	0.0002	-1.906	0.0004	0.0015
Fntb	ENSMUSG00000033373	farnesyltransferase, CAAX box, beta	-1.780	0.0000	0.0000	-1.530	0.0000	0.0001
Focad	ENSMUSG00000038368	focadhesin	-2.057	0.0000	0.0000	-2.047	0.0000	0.0000
Folr2	ENSMUSG00000032725	folate receptor 2 (fetal)	-2.871	0.0000	0.0000	-2.362	0.0000	0.0000
Foxs1	ENSMUSG00000074676	forkhead box S1	-4.574	0.0000	0.0000	-3.234	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Fpgs	ENSMUSG00000009566	folylpolyglutamyl synthetase	-1.843	0.0001	0.0002	-1.796	0.0002	0.0007
Frg2f1	ENSMUSG00000087385	FSHD region gene 2 family member 1	-1.680	0.0003	0.0009	-2.004	0.0000	0.0000
Frmd5	ENSMUSG00000027238	FERM domain containing 5	-1.801	0.0000	0.0001	-1.509	0.0030	0.0092
Frmd8	ENSMUSG00000024816	FERM domain containing 8	-2.619	0.0000	0.0000	-2.072	0.0000	0.0000
Frmd8os	ENSMUSG00000043488	FERM domain containing 8, opposite strand	-2.841	0.0000	0.0000	-5.305	0.0000	0.0000
Fscn2	ENSMUSG00000025380	fascin actin-bundling protein 2	-15.709	0.0101	0.0242	-17.474	0.0070	0.0193
Fstl4	ENSMUSG00000036264	follistatin-like 4	-3.061	0.0000	0.0000	-1.838	0.0099	0.0261
Ftl1	ENSMUSG00000050708	ferritin light polypeptide 1	-3.238	0.0000	0.0000	-2.529	0.0000	0.0000
Fuom	ENSMUSG00000025466	fucose mutarotase	-2.056	0.0000	0.0000	-1.635	0.0000	0.0000
Fxn	ENSMUSG00000059363	frataxin	-4.071	0.0000	0.0000	-4.173	0.0000	0.0000
Fxyd1	ENSMUSG00000036570	FXYD domain-containing ion transport regulator 1	-2.503	0.0000	0.0000	-2.057	0.0000	0.0000
Fxyd2	ENSMUSG00000059412	FXYD domain-containing ion transport regulator 2	-3.281	0.0000	0.0000	-2.304	0.0002	0.0010
Fxyd5	ENSMUSG00000009687	FXYD domain-containing ion transport regulator 5	-2.177	0.0000	0.0000	-1.591	0.0006	0.0023
G0s2	ENSMUSG00000009633	G0/G1 switch gene 2	-3.409	0.0000	0.0000	-3.445	0.0000	0.0000
G6pc3	ENSMUSG00000034793	glucose 6 phosphatase, catalytic, 3	-2.628	0.0000	0.0000	-2.080	0.0000	0.0000
G6pdx	ENSMUSG00000031400	glucose-6-phosphate dehydrogenase X-linked	-1.690	0.0000	0.0000	-1.536	0.0000	0.0000
Gaa	ENSMUSG00000025579	glucosidase, alpha, acid	-2.859	0.0000	0.0000	-2.127	0.0000	0.0000
Gadd45g	ENSMUSG00000021453	growth arrest and DNA-damage-inducible 45 gamma	-1.877	0.0030	0.0083	-1.614	0.0236	0.0550
Galns	ENSMUSG00000015027	galactosamine (N-acetyl)-6-sulfate sulfatase	-1.796	0.0000	0.0000	-1.769	0.0000	0.0001
Galt	ENSMUSG00000036073	galactose-1-phosphate uridyl transferase	-2.655	0.0000	0.0000	-2.017	0.0000	0.0000
Gamt	ENSMUSG00000020150	guanidinoacetate methyltransferase	-2.467	0.0000	0.0000	-1.640	0.0143	0.0358
Ganab	ENSMUSG00000071650	alpha glucosidase 2 alpha neutral subunit	-1.773	0.0000	0.0000	-1.814	0.0000	0.0000
Garre1	ENSMUSG00000066571	granule associated Rac and RHOG effector 1	-1.504	0.0002	0.0007	-1.717	0.0000	0.0000
Gask1b	ENSMUSG00000027955	golgi associated kinase 1B	-1.541	0.0441	0.0869	-1.769	0.0080	0.0216
Gatd3a	ENSMUSG00000053329	glutamine amidotransferase like class 1 domain containing 3A	-1.926	0.0000	0.0000	-1.526	0.0000	0.0000
Gba	ENSMUSG00000028048	glucosidase, beta, acid	-1.675	0.0000	0.0000	-1.525	0.0003	0.0010
Gchfr	ENSMUSG00000046814	GTP cyclohydrolase I feedback regulator	-2.698	0.0000	0.0000	-1.522	0.0007	0.0025
Gcn1	ENSMUSG00000041638	GCN1 activator of EIF2AK4	-2.111	0.0000	0.0000	-1.672	0.0000	0.0000
Gde1	ENSMUSG00000033917	glycerophosphodiester phosphodiesterase 1	-1.618	0.0000	0.0000	-2.042	0.0000	0.0000
Gdf15	ENSMUSG00000038508	growth differentiation factor 15	-5.831	0.0000	0.0000	-4.639	0.0000	0.0000
Gdpd3	ENSMUSG00000030703	glycerophosphodiester phosphodiesterase domain containing 3	-1.653	0.0000	0.0000	-1.657	0.0000	0.0000
Gdpgp1	ENSMUSG00000050973	GDP-D-glucose phosphorylase 1	-1.520	0.0024	0.0068	-1.651	0.0004	0.0013
Gemin5	ENSMUSG00000037275	gem nuclear organelle associated protein 5	-1.960	0.0000	0.0000	-1.955	0.0000	0.0000
Get3	ENSMUSG00000052456	guided entry of tail-anchored proteins factor 3, ATPase	-2.110	0.0000	0.0000	-1.891	0.0000	0.0000
Gfra3	ENSMUSG00000024366	glial cell line derived neurotrophic factor family receptor alpha 3	-4.464	0.0000	0.0001	-2.439	0.0089	0.0237
Ggnbp1	ENSMUSG00000048731	gametogenetin binding protein 1	-2.030	0.0000	0.0000	-1.892	0.0000	0.0000
Ggt5	ENSMUSG00000006344	gamma-glutamyltransferase 5	-2.623	0.0000	0.0000	-2.165	0.0000	0.0000
Ggt7	ENSMUSG00000027603	gamma-glutamyltransferase 7	-1.568	0.0469	0.0915	-1.925	0.0085	0.0228
Gipc1	ENSMUSG00000019433	GIPC PDZ domain containing family, member 1	-1.970	0.0000	0.0000	-1.716	0.0000	0.0000
Git2	ENSMUSG00000041890	GIT ArfGAP 2	-1.670	0.0000	0.0000	-1.625	0.0000	0.0000
Gkn3	ENSMUSG00000030048	gastrokine 3	-8.422	0.0070	0.0175	-4.372	0.0345	0.0759
Glb1	ENSMUSG00000045594	galactosidase, beta 1	-2.298	0.0000	0.0000	-1.776	0.0000	0.0000
Glmp	ENSMUSG00000001418	glycosylated lysosomal membrane protein	-2.928	0.0000	0.0000	-2.285	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Glo1-ps	ENSMUSG00000075391	glyoxalase 1, pseudogene	-4.006	0.0000	0.0000	-3.849	0.0000	0.0000
Glt8d2	ENSMUSG00000020251	glycosyltransferase 8 domain containing 2	-2.285	0.0030	0.0082	-1.983	0.0153	0.0381
Gm10039	ENSMUSG00000091478	predicted pseudogene 10039	-3.235	0.0000	0.0000	-2.147	0.0000	0.0000
Gm10059	ENSMUSG00000059064	predicted pseudogene 10059	-19.206	0.0020	0.0058	-27.111	0.0006	0.0022
Gm10076	ENSMUSG00000060143	predicted gene 10076	-14.747	0.0000	0.0000	-26.767	0.0000	0.0000
Gm10123	ENSMUSG00000062933	predicted pseudogene 10123	-3.078	0.0129	0.0300	-6.576	0.0022	0.0071
Gm10226	ENSMUSG00000067929	predicted gene 10226	-33.760	0.0000	0.0002	-8.240	0.0000	0.0000
Gm10263	ENSMUSG00000066407	predicted gene 10263	-3.708	0.0000	0.0000	-2.833	0.0000	0.0000
Gm10275	ENSMUSG00000069682	predicted pseudogene 10275	-3.936	0.0000	0.0000	-3.617	0.0000	0.0000
Gm10288	ENSMUSG00000070343	predicted gene 10288	-6.493	0.0000	0.0000	-4.753	0.0000	0.0000
Gm10291	ENSMUSG00000070443	predicted pseudogene 10291	-2.239	0.0011	0.0032	-2.393	0.0016	0.0053
Gm10359	ENSMUSG00000094708	predicted gene 10359	-5.146	0.0099	0.0239	-10.510	0.0034	0.0104
Gm10435	ENSMUSG00000072902	predicted gene 10435	-1.768	0.0025	0.0069	-1.540	0.0220	0.0517
Gm10443	ENSMUSG00000072940	predicted pseudogene 10443	-2.088	0.0347	0.0707	-2.142	0.0270	0.0617
Gm10509	ENSMUSG00000073448	predicted gene 10509	-5.544	0.0000	0.0000	-4.921	0.0000	0.0001
Gm10736	ENSMUSG00000096842	predicted gene 10736	-96.240	0.0000	0.0000	-81.090	0.0000	0.0000
Gm10790	ENSMUSG00000113856	predicted gene 10790	-6.126	0.0362	0.0733	-29.305	0.0003	0.0012
Gm10819	ENSMUSG00000075268	predicted gene 10819	-5.790	0.0001	0.0004	-3.469	0.0015	0.0050
Gm11512	ENSMUSG00000081043	predicted gene 11512	-1.830	0.0159	0.0360	-2.068	0.0079	0.0214
Gm11517	ENSMUSG00000081249	predicted gene 11517	-4.277	0.0055	0.0142	-5.168	0.0033	0.0099
Gm11658	ENSMUSG00000081524	predicted gene 11658	-5.332	0.0035	0.0095	-6.681	0.0054	0.0153
Gm11702	ENSMUSG00000084277	predicted gene 11702	-5.776	0.0000	0.0000	-33.761	0.0000	0.0002
Gm11730	ENSMUSG00000087057	predicted gene 11730	-2.597	0.0121	0.0283	-2.513	0.0173	0.0422
Gm11734	ENSMUSG00000085419	predicted gene 11734	-2.143	0.0002	0.0008	-1.723	0.0101	0.0265
Gm11808	ENSMUSG00000068240	predicted gene 11808	-38.553	0.0000	0.0000	-4.199	0.0000	0.0000
Gm11816	ENSMUSG00000086233	predicted gene 11816	-2.052	0.0062	0.0156	-2.694	0.0004	0.0016
Gm11868	ENSMUSG00000050550	predicted gene 11868	-2.023	0.0000	0.0000	-1.892	0.0000	0.0000
Gm11942	ENSMUSG00000094344	predicted gene 11942	-1.625	0.0000	0.0000	-2.153	0.0000	0.0000
Gm11953	ENSMUSG00000082816	predicted gene 11953	-1.691	0.0471	0.0919	-3.104	0.0001	0.0006
Gm11960	ENSMUSG00000081974	predicted gene 11960	-1.719	0.0482	0.0937	-6.693	0.0000	0.0000
Gm12167	ENSMUSG00000085853	predicted gene 12167	-3.747	0.0000	0.0000	-4.067	0.0000	0.0000
Gm12182	ENSMUSG00000083460	predicted gene 12182	-3.024	0.0039	0.0103	-4.879	0.0003	0.0012
Gm12224	ENSMUSG00000085888	predicted gene 12224	-3.075	0.0002	0.0006	-1.939	0.0188	0.0453
Gm12337	ENSMUSG00000084224	predicted gene 12337	-3.614	0.0172	0.0386	-3.184	0.0287	0.0650
Gm12439	ENSMUSG00000080850	predicted gene 12439	-1.509	0.0026	0.0073	-1.913	0.0000	0.0000
Gm12537	ENSMUSG00000095042	predicted gene 12537	-3.853	0.0001	0.0004	-3.240	0.0017	0.0056
Gm12727	ENSMUSG00000082768	predicted gene 12727	-10.098	0.0407	0.0811	-16.001	0.0119	0.0304
Gm12751	ENSMUSG00000062554	predicted gene 12751	-5.179	0.0000	0.0000	-4.063	0.0000	0.0000
Gm12864	ENSMUSG00000082143	predicted gene 12864	-21.417	0.0020	0.0057	-17.689	0.0038	0.0114
Gm13092	ENSMUSG00000085787	predicted gene 13092	-9.131	0.0000	0.0000	-6.026	0.0000	0.0000
Gm13192	ENSMUSG00000069188	predicted gene 13192	-12.094	0.0029	0.0080	-24.231	0.0007	0.0026
Gm14022	ENSMUSG00000087151	predicted gene 14022	-2.613	0.0026	0.0073	-2.994	0.0007	0.0024
Gm14026	ENSMUSG00000082274	predicted gene 14026	-2.945	0.0001	0.0003	-1.785	0.0405	0.0868

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm14048	ENSMUSG00000080989	predicted gene 14048	-2.469	0.0262	0.0554	-2.832	0.0350	0.0768
Gm14097	ENSMUSG00000084839	predicted gene 14097	-1.713	0.0047	0.0122	-1.865	0.0025	0.0079
Gm14130	ENSMUSG00000081494	predicted gene 14130	-7.067	0.0000	0.0000	-6.508	0.0000	0.0000
Gm14165	ENSMUSG00000081434	predicted gene 14165	-16.119	0.0000	0.0000	-10.972	0.0000	0.0000
Gm14269	ENSMUSG00000084067	predicted gene 14269	-2.921	0.0383	0.0769	-3.116	0.0271	0.0620
Gm14292	ENSMUSG00000061897	predicted gene 14292	-1.809	0.0109	0.0259	-3.467	0.0000	0.0000
Gm14303	ENSMUSG00000081344	predicted gene 14303	-4.016	0.0000	0.0000	-1.976	0.0022	0.0069
Gm14539	ENSMUSG00000084830	predicted gene 14539	-2.494	0.0000	0.0000	-2.111	0.0000	0.0000
Gm15191	ENSMUSG00000082778	predicted gene 15191	-3.646	0.0000	0.0001	-2.225	0.0054	0.0154
Gm15361	ENSMUSG00000083283	predicted pseudogene 15361	-1.659	0.0063	0.0160	-2.316	0.0000	0.0001
Gm15420	ENSMUSG00000087387	predicted gene 15420	-7.958	0.0003	0.0012	-3.026	0.0034	0.0102
Gm15446	ENSMUSG00000090015	predicted gene 15446	-1.508	0.0292	0.0609	-2.251	0.0000	0.0001
Gm15545	ENSMUSG00000087138	predicted gene 15545	-2.077	0.0016	0.0047	-1.575	0.0399	0.0858
Gm15564	ENSMUSG00000086324	predicted gene 15564	-97.879	0.0000	0.0000	-4376.174	0.0000	0.0000
Gm15608	ENSMUSG00000112110	predicted gene 15608	-4.815	0.0331	0.0680	-14.553	0.0066	0.0182
Gm15879	ENSMUSG00000084790	predicted gene 15879	-4.162	0.0004	0.0013	-2.376	0.0258	0.0595
Gm15950	ENSMUSG00000089818	predicted gene 15950	-19.935	0.0043	0.0113	-20.142	0.0040	0.0119
Gm15972	ENSMUSG00000086287	predicted gene 15972	-4.557	0.0000	0.0000	-4.091	0.0000	0.0000
Gm16177	ENSMUSG00000082484	predicted gene 16177	-7.529	0.0000	0.0000	-4.626	0.0001	0.0003
Gm16378	ENSMUSG00000095762	predicted gene 16378	-3.385	0.0000	0.0000	-3.205	0.0000	0.0000
Gm16380	ENSMUSG00000059830	predicted pseudogene 16380	-1.778	0.0232	0.0499	-2.004	0.0073	0.0200
Gm16574	ENSMUSG00000089769	predicted gene 16574	-2.714	0.0027	0.0075	-2.053	0.0301	0.0676
Gm1673	ENSMUSG00000070858	predicted gene 1673	-4.925	0.0000	0.0001	-4.207	0.0002	0.0009
Gm16793	ENSMUSG00000097357	predicted gene, 16793	-2.710	0.0000	0.0000	-2.236	0.0001	0.0005
Gm17017	ENSMUSG00000090246	predicted gene 17017	-5.679	0.0029	0.0079	-23.713	0.0004	0.0016
Gm17068	ENSMUSG00000078528	predicted gene 17068	-7.283	0.0000	0.0001	-2.358	0.0305	0.0684
Gm17354	ENSMUSG00000091985	predicted gene, 17354	-1.671	0.0400	0.0799	-1.732	0.0273	0.0624
Gm17511	ENSMUSG00000090460	predicted gene, 17511	-14.181	0.0000	0.0000	-12.223	0.0000	0.0000
Gm18095	ENSMUSG00000115856	predicted gene, 18095	-2.827	0.0143	0.0327	-3.171	0.0057	0.0160
Gm18234	ENSMUSG00000116926	predicted gene, 18234	-5.304	0.0000	0.0000	-3.404	0.0000	0.0000
Gm18537	ENSMUSG00000108484	predicted gene, 18537	-3.712	0.0490	0.0950	-25.390	0.0005	0.0018
Gm18734	ENSMUSG00000092438	predicted gene, 18734	-7.075	0.0028	0.0076	-48.652	0.0000	0.0001
Gm18736	ENSMUSG00000117300	predicted gene, 18736	-2.176	0.0000	0.0000	-2.272	0.0000	0.0000
Gm1943	ENSMUSG00000110528	predicted gene 1943	-7.985	0.0044	0.0115	-32.630	0.0002	0.0007
Gm19605	ENSMUSG00000113585	predicted gene, 19605	-1.919	0.0057	0.0146	-1.957	0.0050	0.0145
Gm20490	ENSMUSG00000092596	predicted gene 20490	-3.201	0.0009	0.0028	-3.707	0.0008	0.0029
Gm20604	ENSMUSG00000041716	predicted gene 20604	-1.605	0.0035	0.0094	-2.677	0.0000	0.0000
Gm20619	ENSMUSG00000093482	predicted gene 20619	-3.024	0.0000	0.0000	-2.170	0.0002	0.0008
Gm20707	ENSMUSG00000093594	predicted gene 20707	-2.440	0.0159	0.0360	-2.793	0.0111	0.0287
Gm20939	ENSMUSG00000095193	predicted gene, 20939	-2.486	0.0248	0.0530	-3.090	0.0122	0.0312
Gm2199	ENSMUSG00000083829	predicted gene 2199	-4.962	0.0319	0.0658	-9.105	0.0207	0.0491
Gm23297	ENSMUSG00000065118	predicted gene, 23297	-14.130	0.0095	0.0231	-17.737	0.0043	0.0126
Gm2383	ENSMUSG00000097628	predicted gene 2383	-5.045	0.0043	0.0113	-2.965	0.0264	0.0606

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm2445	ENSMUSG00000098113	predicted gene 2445	-2.322	0.0013	0.0039	-3.585	0.0000	0.0002
Gm24474	ENSMUSG00000114005	predicted gene, 24474	-1.758	0.0081	0.0199	-1.723	0.0092	0.0245
Gm2573	ENSMUSG00000115017	predicted gene 2573	-25.068	0.0000	0.0000	-5.730	0.0000	0.0002
Gm2614	ENSMUSG00000113113	predicted gene 2614	-3.584	0.0025	0.0069	-6.469	0.0014	0.0046
Gm26493	ENSMUSG00000065089	predicted gene, 26493	-11.422	0.0218	0.0474	-18.785	0.0046	0.0134
Gm26620	ENSMUSG00000096968	predicted gene, 26620	-7.102	0.0002	0.0007	-2.780	0.0186	0.0448
Gm26795	ENSMUSG00000097776	predicted gene, 26795	-1.745	0.0073	0.0181	-1.633	0.0184	0.0444
Gm27030	ENSMUSG00000098221	predicted gene, 27030	-4.195	0.0187	0.0415	-26.729	0.0004	0.0013
Gm27045	ENSMUSG00000098211	predicted gene, 27045	-4.848	0.0017	0.0050	-3.376	0.0131	0.0332
Gm28231	ENSMUSG00000100782	predicted gene 28231	-2.155	0.0211	0.0462	-2.923	0.0046	0.0135
Gm28438	ENSMUSG00000101939	predicted gene 28438	-2.468	0.0000	0.0000	-3.014	0.0000	0.0000
Gm28455	ENSMUSG00000100490	predicted gene 28455	-18.402	0.0039	0.0104	-14.148	0.0091	0.0241
Gm29668	ENSMUSG00000099835	predicted gene 29668	-4.184	0.0000	0.0000	-3.099	0.0000	0.0000
Gm30373	ENSMUSG00000111758	predicted gene, 30373	-2.059	0.0022	0.0063	-2.019	0.0030	0.0092
Gm30970	ENSMUSG00000115637	predicted gene, 30970	-10.559	0.0000	0.0000	-7.294	0.0000	0.0000
Gm31663	ENSMUSG00000108994	predicted gene, 31663	-2.004	0.0000	0.0001	-1.912	0.0001	0.0003
Gm32031	ENSMUSG00000109118	predicted gene, 32031	-3.224	0.0000	0.0001	-3.538	0.0002	0.0008
Gm3226	ENSMUSG00000114547	predicted gene 3226	-3.533	0.0004	0.0012	-3.337	0.0017	0.0057
Gm32352	ENSMUSG00000110453	predicted gene, 32352	-2.131	0.0015	0.0044	-2.521	0.0002	0.0009
Gm32591	ENSMUSG00000108015	predicted gene, 32591	-4.992	0.0000	0.0001	-2.480	0.0081	0.0219
Gm33024	ENSMUSG00000107682	predicted gene, 33024	-2.389	0.0434	0.0857	-2.421	0.0438	0.0926
Gm33104	ENSMUSG00000110902	predicted gene, 33104	-14.245	0.0088	0.0214	-7.075	0.0300	0.0674
Gm3325	ENSMUSG00000113836	predicted gene 3325	-2.644	0.0063	0.0159	-9.182	0.0000	0.0000
Gm33424	ENSMUSG00000113101	predicted gene, 33424	-2.609	0.0000	0.0000	-1.522	0.0162	0.0400
Gm33543	ENSMUSG00000110353	predicted gene, 33543	-1.638	0.0237	0.0509	-1.559	0.0421	0.0898
Gm3375	ENSMUSG00000107470	predicted gene 3375	-3.164	0.0000	0.0000	-2.694	0.0000	0.0000
Gm3436	ENSMUSG00000096160	predicted pseudogene 3436	-6.682	0.0344	0.0702	-12.753	0.0116	0.0298
Gm34655	ENSMUSG00000110863	predicted gene, 34655	-2.161	0.0344	0.0703	-3.029	0.0032	0.0096
Gm34934	ENSMUSG00000115100	predicted gene, 34934	-2.299	0.0000	0.0000	-2.162	0.0000	0.0000
Gm35290	ENSMUSG00000117263	predicted gene, 35290	-3.892	0.0000	0.0000	-1.869	0.0225	0.0527
Gm3534	ENSMUSG00000098192	predicted pseudogene 3534	-3.175	0.0020	0.0058	-2.397	0.0175	0.0426
Gm35438	ENSMUSG00000118209	predicted gene, 35438	-6.079	0.0034	0.0093	-16.653	0.0029	0.0089
Gm3555	ENSMUSG00000089791	predicted pseudogene 3555	-1.527	0.0381	0.0766	-1.621	0.0436	0.0924
Gm35638	ENSMUSG00000113188	predicted gene, 35638	-2.927	0.0078	0.0192	-3.857	0.0046	0.0133
Gm3646	ENSMUSG00000091937	predicted gene 3646	-1.895	0.0020	0.0059	-1.505	0.0469	0.0980
Gm36569	ENSMUSG00000102191	predicted gene, 36569	-19.862	0.0021	0.0060	-23.952	0.0012	0.0040
Gm36684	ENSMUSG00000117278	predicted gene, 36684	-2.009	0.0004	0.0014	-1.800	0.0031	0.0095
Gm3671	ENSMUSG00000098232	predicted gene 3671	-2.401	0.0036	0.0097	-2.131	0.0183	0.0443
Gm3699	ENSMUSG00000094955	predicted gene 3699	-5.733	0.0000	0.0002	-8.354	0.0000	0.0001
Gm37486	ENSMUSG00000104126	predicted gene, 37486	-24.320	0.0009	0.0029	-7.898	0.0343	0.0755
Gm3756	ENSMUSG00000091639	predicted gene 3756	-3.647	0.0132	0.0305	-3.299	0.0281	0.0639
Gm37986	ENSMUSG00000104212	predicted gene, 37986	-9.003	0.0109	0.0259	-15.004	0.0048	0.0140
Gm3809	ENSMUSG00000097935	predicted gene 3809	-3.830	0.0079	0.0195	-3.752	0.0328	0.0727

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm38228	ENSMUSG00000103945	predicted gene, 38228	-4.650	0.0443	0.0872	-5.999	0.0373	0.0810
Gm39469	ENSMUSG00000110834	predicted gene, 39469	-1.866	0.0005	0.0015	-1.548	0.0114	0.0295
Gm4045	ENSMUSG00000108231	predicted gene 4045	-5.050	0.0000	0.0000	-4.914	0.0000	0.0000
Gm41341	ENSMUSG00000069996	predicted gene, 41341	-3.264	0.0000	0.0002	-2.160	0.0052	0.0149
Gm4149	ENSMUSG00000074800	predicted pseudogene 4149	-35.405	0.0001	0.0004	-28.134	0.0003	0.0013
Gm4217	ENSMUSG00000097954	predicted gene 4217	-1.722	0.0148	0.0338	-1.605	0.0378	0.0821
Gm42879	ENSMUSG00000106590	predicted gene 42879	-5.923	0.0149	0.0340	-20.286	0.0014	0.0048
Gm43247	ENSMUSG00000105406	predicted gene 43247	-4.422	0.0007	0.0023	-6.238	0.0007	0.0025
Gm4353	ENSMUSG00000091900	predicted gene 4353	-2.256	0.0043	0.0112	-2.598	0.0020	0.0064
Gm43667	ENSMUSG00000105135	predicted gene 43667	-2.300	0.0001	0.0005	-1.796	0.0097	0.0256
Gm43814	ENSMUSG00000104654	predicted gene 43814	-6.923	0.0012	0.0036	-3.817	0.0102	0.0267
Gm43823	ENSMUSG00000106224	predicted gene 43823	-3.827	0.0001	0.0005	-2.402	0.0067	0.0184
Gm44386	ENSMUSG00000107689	predicted gene, 44386	-2.983	0.0000	0.0000	-2.633	0.0000	0.0000
Gm4518	ENSMUSG00000098123	predicted gene 4518	-3.366	0.0004	0.0015	-4.332	0.0002	0.0010
Gm45353	ENSMUSG00000109957	predicted gene 45353	-3.581	0.0082	0.0202	-5.133	0.0097	0.0255
Gm45552	ENSMUSG00000110279	predicted gene 45552	-2.266	0.0011	0.0034	-2.031	0.0040	0.0118
Gm45871	ENSMUSG00000110277	predicted gene 45871	-1.731	0.0005	0.0016	-2.552	0.0000	0.0000
Gm4609	ENSMUSG00000078592	predicted gene 4609	-4.227	0.0020	0.0058	-4.022	0.0056	0.0159
Gm47021	ENSMUSG00000113036	predicted gene, 47021	-19.871	0.0016	0.0046	-14.232	0.0043	0.0128
Gm47108	ENSMUSG00000111000	predicted gene, 47108	-3.223	0.0045	0.0119	-2.544	0.0173	0.0422
Gm47547	ENSMUSG00000114196	predicted gene, 47547	-2.432	0.0001	0.0002	-3.929	0.0000	0.0000
Gm47604	ENSMUSG00000110946	predicted gene, 47604	-13.861	0.0000	0.0000	-5.828	0.0011	0.0039
Gm4800	ENSMUSG00000111759	predicted gene 4800	-4.789	0.0365	0.0738	-3.912	0.0325	0.0721
Gm4815	ENSMUSG00000114733	predicted gene 4815	-41.122	0.0000	0.0001	-8.272	0.0001	0.0004
Gm48496	ENSMUSG00000112969	predicted gene, 48496	-2.972	0.0006	0.0018	-4.547	0.0000	0.0002
Gm4890	ENSMUSG00000097174	predicted gene 4890	-5.168	0.0517	0.0994	-14.392	0.0038	0.0114
Gm48931	ENSMUSG00000115458	predicted gene, 48931	-2.938	0.0006	0.0019	-3.915	0.0000	0.0001
Gm49024	ENSMUSG00000115575	predicted gene, 49024	-2.172	0.0015	0.0045	-6.111	0.0000	0.0000
Gm49120	ENSMUSG00000115636	predicted gene, 49120	-14.673	0.0045	0.0119	-7.745	0.0162	0.0400
Gm49331	ENSMUSG00000114025	predicted gene, 49331	-3.668	0.0000	0.0001	-4.660	0.0000	0.0000
Gm49338	ENSMUSG00000111128	predicted gene, 49338	-2.264	0.0000	0.0000	-2.260	0.0000	0.0000
Gm4935	ENSMUSG00000113405	predicted gene 4935	-3.815	0.0041	0.0110	-2.550	0.0410	0.0877
Gm49390	ENSMUSG00000114898	predicted gene, 49390	-1.788	0.0090	0.0218	-2.217	0.0006	0.0021
Gm49395	ENSMUSG00000114470	predicted gene, 49395	-13.974	0.0081	0.0200	-15.456	0.0068	0.0187
Gm49477	ENSMUSG00000116066	predicted gene, 49477	-1.779	0.0004	0.0013	-1.891	0.0001	0.0004
Gm49486	ENSMUSG00000116121	predicted gene, 49486	-2.514	0.0409	0.0815	-2.669	0.0474	0.0988
Gm50114	ENSMUSG00000117692	predicted gene, 50114	-1.642	0.0019	0.0055	-1.507	0.0109	0.0283
Gm50145	ENSMUSG00000117731	predicted gene, 50145	-11.013	0.0000	0.0000	-3.960	0.0001	0.0004
Gm5131	ENSMUSG00000110715	predicted gene 5131	-3.390	0.0000	0.0000	-2.078	0.0000	0.0000
Gm5141	ENSMUSG00000091183	predicted gene 5141	-2.883	0.0037	0.0099	-2.558	0.0099	0.0260
Gm5165	ENSMUSG00000116802	predicted gene 5165	-2.618	0.0000	0.0000	-3.206	0.0000	0.0000
Gm5276	ENSMUSG00000105452	predicted gene 5276	-3.874	0.0001	0.0004	-5.723	0.0001	0.0004
Gm52948	ENSMUSG00000118521	predicted gene, 52948	-50.087	0.0000	0.0001	-7.905	0.0107	0.0278

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm5421	ENSMUSG00000097245	predicted gene 5421	-1.936	0.0051	0.0132	-2.098	0.0020	0.0065
Gm5425	ENSMUSG00000111875	predicted gene 5425	-7.285	0.0007	0.0023	-2.867	0.0169	0.0413
Gm5430	ENSMUSG00000098180	predicted gene 5430	-4.081	0.0001	0.0005	-4.020	0.0002	0.0008
Gm5436	ENSMUSG00000042962	predicted pseudogene 5436	-2.753	0.0000	0.0000	-2.950	0.0000	0.0000
Gm54867	ENSMUSG00002075795	predicted gene, 54867	-3.868	0.0159	0.0360	-12.539	0.0000	0.0000
Gm5503	ENSMUSG00000117730	predicted gene 5503	-5.309	0.0000	0.0000	-6.254	0.0000	0.0000
Gm5510	ENSMUSG00000083458	predicted pseudogene 5510	-21.432	0.0037	0.0099	-17.688	0.0066	0.0183
Gm5523	ENSMUSG00000097711	predicted pseudogene 5523	-1.737	0.0277	0.0583	-2.251	0.0042	0.0124
Gm5560	ENSMUSG00000067161	predicted pseudogene 5560	-6.821	0.0002	0.0006	-3.280	0.0038	0.0112
Gm5566	ENSMUSG00000080002	predicted pseudogene 5566	-16.771	0.0000	0.0000	-4.065	0.0001	0.0002
Gm5578	ENSMUSG00000029633	predicted pseudogene 5578	-3.767	0.0117	0.0276	-3.457	0.0232	0.0542
Gm5617	ENSMUSG00000042293	predicted gene 5617	-2.404	0.0000	0.0000	-2.926	0.0000	0.0000
Gm5693	ENSMUSG00000117793	predicted gene 5693	-2.826	0.0002	0.0008	-2.234	0.0055	0.0157
Gm5823	ENSMUSG00000117813	predicted gene 5823	-3.883	0.0000	0.0000	-4.382	0.0000	0.0000
Gm5824	ENSMUSG00000118241	predicted gene 5824	-3.404	0.0206	0.0452	-19.354	0.0012	0.0041
Gm5841	ENSMUSG00000103921	predicted gene 5841	-4.052	0.0107	0.0256	-12.395	0.0024	0.0075
Gm5855	ENSMUSG00000105558	predicted gene 5855	-6.984	0.0000	0.0000	-2.411	0.0016	0.0053
Gm5874	ENSMUSG00000071568	predicted gene 5874	-3.241	0.0001	0.0005	-13.560	0.0000	0.0000
Gm5884	ENSMUSG00000037827	predicted pseudogene 5884	-3.945	0.0000	0.0000	-3.883	0.0000	0.0000
Gm5900	ENSMUSG00000094685	predicted pseudogene 5900	-2.399	0.0000	0.0000	-1.876	0.0000	0.0001
Gm5913	ENSMUSG00000081111	predicted gene 5913	-3.896	0.0006	0.0019	-6.689	0.0001	0.0005
Gm6055	ENSMUSG00000062081	predicted gene 6055	-1.871	0.0088	0.0215	-2.478	0.0003	0.0010
Gm6278	ENSMUSG00000116972	predicted gene 6278	-43.639	0.0000	0.0000	-39.758	0.0000	0.0000
Gm6316	ENSMUSG00000078370	predicted pseudogene 6316	-4.937	0.0000	0.0000	-2.530	0.0001	0.0004
Gm6368	ENSMUSG00000080775	predicted gene 6368	-2.980	0.0002	0.0006	-4.883	0.0000	0.0000
Gm6402	ENSMUSG00000117962	predicted pseudogene 6402	-7.876	0.0131	0.0304	-6.663	0.0232	0.0542
Gm6419	ENSMUSG00000072407	predicted gene 6419	-3.262	0.0059	0.0149	-17.834	0.0002	0.0008
Gm6493	ENSMUSG00000090021	predicted gene 6493	-10.622	0.0065	0.0163	-10.489	0.0158	0.0391
Gm6505	ENSMUSG00000070522	predicted pseudogene 6505	-4.180	0.0000	0.0000	-3.201	0.0000	0.0000
Gm6517	ENSMUSG00000082420	predicted gene 6517	-6.052	0.0000	0.0000	-14.839	0.0000	0.0000
Gm6552	ENSMUSG00000117458	predicted gene 6552	-2.978	0.0115	0.0271	-3.471	0.0035	0.0105
Gm6712	ENSMUSG00000072761	predicted gene 6712	-2.611	0.0000	0.0001	-2.525	0.0001	0.0004
Gm6776	ENSMUSG00000047509	predicted pseudogene 6776	-14.448	0.0144	0.0329	-10.168	0.0354	0.0776
Gm6997	ENSMUSG00000115539	predicted gene 6997	-5.615	0.0451	0.0884	-9.065	0.0204	0.0485
Gm7114	ENSMUSG00000100481	predicted gene 7114	-5.360	0.0015	0.0043	-8.471	0.0085	0.0229
Gm7251	ENSMUSG00000069236	predicted pseudogene 7251	-4.999	0.0006	0.0019	-3.614	0.0030	0.0092
Gm7252	ENSMUSG00000114135	predicted gene 7252	-15.760	0.0058	0.0149	-21.791	0.0017	0.0056
Gm7278	ENSMUSG00000080950	predicted gene 7278	-11.654	0.0097	0.0234	-9.770	0.0166	0.0407
Gm7286	ENSMUSG00000098194	predicted gene 7286	-2.887	0.0149	0.0339	-6.534	0.0009	0.0031
Gm7353	ENSMUSG00000055452	predicted pseudogene 7353	-6.274	0.0001	0.0002	-3.277	0.0028	0.0087
Gm7367	ENSMUSG00000047370	predicted pseudogene 7367	-54.323	0.0000	0.0000	-11.020	0.0091	0.0243
Gm7481	ENSMUSG00000098219	predicted gene 7481	-6.572	0.0446	0.0877	-8.538	0.0354	0.0776
Gm7536	ENSMUSG00000057036	predicted gene 7536	-10.716	0.0000	0.0000	-15.555	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gm7665	ENSMUSG00000063628	predicted pseudogene 7665	-19.766	0.0015	0.0045	-5.623	0.0203	0.0483
Gm7832	ENSMUSG00000106917	predicted gene 7832	-3.872	0.0000	0.0000	-6.820	0.0000	0.0000
Gm8075	ENSMUSG00000113321	predicted gene 8075	-6.212	0.0000	0.0000	-5.625	0.0000	0.0000
Gm8121	ENSMUSG00000051116	predicted pseudogene 8121	-1.899	0.0000	0.0001	-1.915	0.0000	0.0002
Gm8189	ENSMUSG00000110298	predicted gene 8189	-1.849	0.0026	0.0074	-1.622	0.0143	0.0358
Gm8210	ENSMUSG00000094497	predicted pseudogene 8210	-3.284	0.0000	0.0000	-5.374	0.0000	0.0000
Gm8216	ENSMUSG00000084303	predicted gene 8216	-19.918	0.0030	0.0082	-13.755	0.0100	0.0262
Gm8330	ENSMUSG00000098048	predicted gene 8330	-4.033	0.0318	0.0656	-4.810	0.0136	0.0344
Gm8349	ENSMUSG00000098208	predicted gene 8349	-1.654	0.0388	0.0778	-2.135	0.0031	0.0094
Gm8606	ENSMUSG00000083362	predicted gene 8606	-27.349	0.0018	0.0053	-17.212	0.0080	0.0215
Gm8666	ENSMUSG00000048709	predicted gene 8666	-4.287	0.0081	0.0199	-10.792	0.0006	0.0022
Gm8730	ENSMUSG00000063696	predicted pseudogene 8730	-15.025	0.0000	0.0000	-10.364	0.0000	0.0000
Gm8741	ENSMUSG00000091655	predicted gene 8741	-13.280	0.0070	0.0174	-30.523	0.0003	0.0013
Gm8756	ENSMUSG00000098238	predicted gene 8756	-2.360	0.0001	0.0005	-1.769	0.0128	0.0325
Gm9008	ENSMUSG00000072476	predicted pseudogene 9008	-2.792	0.0000	0.0001	-3.230	0.0000	0.0000
Gm9247	ENSMUSG00000115505	predicted gene 9247	-3.117	0.0028	0.0078	-2.717	0.0138	0.0348
Gm9385	ENSMUSG00000080848	predicted pseudogene 9385	-4.311	0.0000	0.0000	-4.711	0.0000	0.0000
Gm9616	ENSMUSG00000114003	predicted gene 9616	-1.938	0.0338	0.0692	-1.962	0.0341	0.0752
Gm9625	ENSMUSG00000097906	predicted gene 9625	-5.659	0.0000	0.0000	-5.247	0.0000	0.0000
Gm9790	ENSMUSG00000044330	predicted gene 9790	-2.237	0.0028	0.0078	-5.876	0.0000	0.0000
Gm9892	ENSMUSG00000052825	predicted gene 9892	-2.551	0.0001	0.0003	-3.048	0.0000	0.0001
Gm9895	ENSMUSG00000118038	predicted gene 9895	-4.230	0.0003	0.0009	-3.596	0.0029	0.0089
Gm9903	ENSMUSG00000097271	predicted gene 9903	-2.209	0.0173	0.0388	-2.063	0.0323	0.0719
Gmppa	ENSMUSG00000033021	GDP-mannose pyrophosphorylase A	-3.159	0.0000	0.0000	-2.496	0.0000	0.0000
Gng5	ENSMUSG00000068523	guanine nucleotide binding protein (G protein), gamma 5	-4.058	0.0000	0.0000	-4.060	0.0000	0.0000
Gng7	ENSMUSG00000048240	guanine nucleotide binding protein (G protein), gamma 7	-2.995	0.0000	0.0000	-1.912	0.0005	0.0017
Gnpda1	ENSMUSG00000052102	glucosamine-6-phosphate deaminase 1	-2.057	0.0000	0.0000	-1.905	0.0000	0.0001
Gorasp1	ENSMUSG00000032513	golgi reassembly stacking protein 1	-2.420	0.0000	0.0000	-2.099	0.0000	0.0000
Got2	ENSMUSG00000031672	glutamatic-oxaloacetic transaminase 2, mitochondrial	-1.737	0.0000	0.0000	-1.646	0.0000	0.0000
Got2-ps1	ENSMUSG00000080935	glutamatic-oxaloacetic transaminase 2, mitochondrial, pseudogene 1	-1.683	0.0000	0.0000	-1.534	0.0000	0.0000
Gpaa1	ENSMUSG00000022561	GPI anchor attachment protein 1	-3.293	0.0000	0.0000	-2.863	0.0000	0.0000
Gpd1l	ENSMUSG00000050627	glycerol-3-phosphate dehydrogenase 1-like	-1.833	0.0000	0.0000	-1.656	0.0000	0.0000
Gper1	ENSMUSG00000053647	G protein-coupled estrogen receptor 1	-3.182	0.0000	0.0000	-2.201	0.0002	0.0009
Gpihbp1	ENSMUSG00000022579	GPI-anchored HDL-binding protein 1	-1.837	0.0016	0.0047	-1.603	0.0143	0.0360
Gpr132	ENSMUSG00000021298	G protein-coupled receptor 132	-8.902	0.0072	0.0180	-8.481	0.0080	0.0217
Gpr137	ENSMUSG00000024958	G protein-coupled receptor 137	-2.152	0.0000	0.0000	-1.731	0.0000	0.0000
Gpr137b-ps	ENSMUSG00000097715	G protein-coupled receptor 137B, pseudogene	-2.231	0.0000	0.0000	-1.707	0.0002	0.0007
Gpr146	ENSMUSG00000044197	G protein-coupled receptor 146	-2.197	0.0000	0.0000	-1.864	0.0000	0.0000
Gpr155	ENSMUSG00000041762	G protein-coupled receptor 155	-1.929	0.0000	0.0000	-1.610	0.0001	0.0003
Gpr182	ENSMUSG00000058396	G protein-coupled receptor 182	-1.761	0.0001	0.0004	-1.725	0.0002	0.0008
Gpr34	ENSMUSG00000040229	G protein-coupled receptor 34	-2.061	0.0073	0.0180	-2.571	0.0007	0.0024
Gpr37l1	ENSMUSG00000026424	G protein-coupled receptor 37-like 1	-1.864	0.0491	0.0951	-1.989	0.0394	0.0851
Gpr89	ENSMUSG00000028096	G protein-coupled receptor 89	-1.802	0.0000	0.0000	-1.744	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Gprc5c	ENSMUSG00000051043	G protein-coupled receptor, family C, group 5, member C	-2.326	0.0000	0.0000	-1.998	0.0000	0.0000
Gps1	ENSMUSG00000025156	G protein pathway suppressor 1	-2.813	0.0000	0.0000	-2.439	0.0000	0.0000
Gpsm1	ENSMUSG00000026930	G-protein signalling modulator 1 (AGS3-like, C. elegans)	-2.402	0.0000	0.0000	-1.909	0.0000	0.0000
Gpx3	ENSMUSG00000018339	glutathione peroxidase 3	-1.679	0.0002	0.0007	-1.516	0.0027	0.0085
Gpx7	ENSMUSG00000028597	glutathione peroxidase 7	-3.193	0.0000	0.0000	-2.175	0.0000	0.0000
Grina	ENSMUSG00000022564	glutamate receptor, ionotropic, N-methyl D-aspartate-associated protein 1 (glutamate binding)	-2.135	0.0000	0.0000	-1.667	0.0000	0.0000
Grpel1	ENSMUSG00000029198	GrpE-like 1, mitochondrial	-1.707	0.0000	0.0000	-1.638	0.0000	0.0000
Grpel2	ENSMUSG00000024580	GrpE-like 2, mitochondrial	-1.530	0.0000	0.0000	-1.632	0.0000	0.0000
Grtp1	ENSMUSG00000038515	GH regulated TBC protein 1	-2.198	0.0001	0.0005	-1.606	0.0231	0.0541
Gstk1	ENSMUSG00000029864	glutathione S-transferase kappa 1	-2.568	0.0000	0.0000	-1.804	0.0000	0.0000
Gstm1	ENSMUSG00000058135	glutathione S-transferase, mu 1	-2.253	0.0000	0.0000	-1.713	0.0000	0.0000
Gstm2	ENSMUSG00000040562	glutathione S-transferase, mu 2	-3.813	0.0000	0.0000	-2.066	0.0000	0.0000
Gstm2-ps1	ENSMUSG00000107369	glutathione S-transferase mu 2 (muscle), pseudogene 1	-4.982	0.0038	0.0103	-5.967	0.0042	0.0125
Gsto1	ENSMUSG00000025068	glutathione S-transferase omega 1	-1.802	0.0000	0.0000	-1.558	0.0000	0.0000
Gstt1	ENSMUSG00000001663	glutathione S-transferase, theta 1	-3.106	0.0000	0.0000	-1.872	0.0000	0.0000
Gstt2	ENSMUSG00000033318	glutathione S-transferase, theta 2	-1.749	0.0020	0.0056	-1.644	0.0053	0.0151
Gtdc1	ENSMUSG00000036890	glycosyltransferase-like domain containing 1	-1.671	0.0000	0.0001	-1.729	0.0000	0.0000
Gtf2h4	ENSMUSG00000001524	general transcription factor II H, polypeptide 4	-3.103	0.0000	0.0000	-2.278	0.0000	0.0000
Gtf3a	ENSMUSG00000016503	general transcription factor III A	-1.675	0.0000	0.0000	-1.828	0.0000	0.0000
Gvin1	ENSMUSG00000045868	GTPase, very large interferon inducible 1	-3.745	0.0012	0.0035	-2.625	0.0154	0.0383
Gypc	ENSMUSG00000090523	glycophorin C	-1.565	0.0000	0.0000	-1.708	0.0000	0.0000
H2-Ab1	ENSMUSG00000073421	histocompatibility 2, class II antigen A, beta 1	-2.440	0.0006	0.0018	-1.887	0.0141	0.0355
H2af-ps2	ENSMUSG00000091383	H2A histone family, pseudogene 2	-14.954	0.0000	0.0000	-6.281	0.0000	0.0000
H2ax	ENSMUSG00000049932	H2A.X variant histone	-1.757	0.0023	0.0066	-2.186	0.0000	0.0002
H2bc3	ENSMUSG00000075031	H2B clustered histone 3	-2.314	0.0443	0.0872	-4.378	0.0025	0.0079
H2bc4	ENSMUSG00000018102	H2B clustered histone 4	-4.102	0.0000	0.0000	-3.552	0.0000	0.0000
H2-T22	ENSMUSG00000056116	histocompatibility 2, T region locus 22	-3.172	0.0000	0.0000	-2.874	0.0000	0.0000
H3c15	ENSMUSG00000081058	H3 clustered histone 15	-4.723	0.0000	0.0000	-2.331	0.0061	0.0170
H3f3a-ps1	ENSMUSG00000082284	H3.3 histone A, pseudogene 1	-25.669	0.0002	0.0009	-8.869	0.0059	0.0166
H4c8	ENSMUSG00000060981	H4 clustered histone 8	-4.877	0.0000	0.0000	-3.624	0.0000	0.0000
H4c9	ENSMUSG00000060639	H4 clustered histone 9	-1.999	0.0000	0.0000	-1.504	0.0009	0.0031
Hadhb	ENSMUSG00000059447	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta	-1.884	0.0000	0.0000	-2.188	0.0000	0.0000
Hadhb-ps	ENSMUSG00000063684	hydroxyacyl-CoA dehydrogenase trifunctional multienzyme complex subunit beta, pseudogene	-1.735	0.0000	0.0000	-2.090	0.0000	0.0000
Hagh	ENSMUSG00000024158	hydroxyacyl glutathione hydrolase	-1.871	0.0000	0.0000	-1.784	0.0000	0.0000
Haus1	ENSMUSG00000041840	HAUS augmin-like complex, subunit 1	-1.543	0.0000	0.0000	-1.541	0.0000	0.0000
Hba-a1	ENSMUSG00000069919	hemoglobin alpha, adult chain 1	-4.927	0.0000	0.0000	-3.330	0.0000	0.0000
Hbb-bs	ENSMUSG00000052305	hemoglobin, beta adult s chain	-3.180	0.0000	0.0000	-2.593	0.0000	0.0000
Hbb-bt	ENSMUSG00000073940	hemoglobin, beta adult t chain	-11.186	0.0000	0.0000	-16.557	0.0000	0.0000
Hcfc1r1	ENSMUSG00000023904	host cell factor C1 regulator 1 (XPO1-dependent)	-4.587	0.0000	0.0000	-3.650	0.0000	0.0000
Hdac10	ENSMUSG00000062906	histone deacetylase 10	-1.748	0.0000	0.0001	-1.780	0.0000	0.0001
Hdc	ENSMUSG00000027360	histidine decarboxylase	-2.327	0.0002	0.0007	-2.421	0.0002	0.0006
Hddc2	ENSMUSG00000000295	HD domain containing 2	-1.666	0.0005	0.0015	-2.094	0.0000	0.0000
Hebp2	ENSMUSG00000019853	heme binding protein 2	-1.794	0.0048	0.0124	-1.671	0.0170	0.0415

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Hectd4	ENSMUSG00000042744	HECT domain E3 ubiquitin protein ligase 4	-1.701	0.0000	0.0000	-1.544	0.0000	0.0000
Hexdc	ENSMUSG00000039307	hexosaminidase (glycosyl hydrolase family 20, catalytic domain) containing	-1.906	0.0000	0.0000	-1.906	0.0000	0.0000
Hexim2	ENSMUSG00000043372	hexamethylene bis-acetamide inducible 2	-1.750	0.0226	0.0490	-2.416	0.0006	0.0021
Hfe	ENSMUSG00000006611	homeostatic iron regulator	-1.577	0.0000	0.0000	-1.854	0.0000	0.0000
Hhatl	ENSMUSG00000032523	hedgehog acyltransferase-like	-2.708	0.0000	0.0000	-2.262	0.0000	0.0000
Higd1b	ENSMUSG00000020928	HIG1 domain family, member 1B	-1.683	0.0000	0.0000	-2.059	0.0000	0.0000
Higd2a	ENSMUSG00000025868	HIG1 domain family, member 2A	-2.081	0.0000	0.0000	-1.860	0.0000	0.0000
Hint2	ENSMUSG00000028470	histidine triad nucleotide binding protein 2	-1.947	0.0000	0.0000	-1.898	0.0000	0.0000
Hmbs	ENSMUSG00000032126	hydroxymethylbilane synthase	-2.134	0.0000	0.0000	-1.919	0.0000	0.0000
Hmcn2	ENSMUSG00000055632	hemicentin 2	-2.073	0.0000	0.0000	-1.765	0.0002	0.0007
Hmgcl	ENSMUSG00000028672	3-hydroxy-3-methylglutaryl-Coenzyme A lyase	-2.487	0.0000	0.0000	-2.023	0.0000	0.0000
Hmgn2-ps	ENSMUSG00000070713	high mobility group nucleosomal binding domain 2, pseudogene	-18.359	0.0013	0.0040	-18.260	0.0013	0.0045
Hopx	ENSMUSG00000059325	HOP homeobox	-2.186	0.0000	0.0000	-2.110	0.0000	0.0000
Hpcal1	ENSMUSG00000071379	hippocalcin-like 1	-1.925	0.0009	0.0027	-1.835	0.0021	0.0068
Hpdl	ENSMUSG00000043155	4-hydroxyphenylpyruvate dioxygenase-like	-2.725	0.0000	0.0000	-2.313	0.0000	0.0001
Hpgd	ENSMUSG00000031613	hydroxyprostaglandin dehydrogenase 15 (NAD)	-1.565	0.0013	0.0040	-1.569	0.0017	0.0055
Hps1	ENSMUSG00000025188	HPS1, biogenesis of lysosomal organelles complex 3 subunit 1	-1.790	0.0052	0.0135	-2.426	0.0001	0.0003
Hps4	ENSMUSG00000042328	HPS4, biogenesis of lysosomal organelles complex 3 subunit 2	-1.860	0.0000	0.0000	-1.566	0.0000	0.0000
Hrct1	ENSMUSG00000071001	histidine rich carboxyl terminus 1	-2.233	0.0008	0.0024	-1.853	0.0095	0.0251
Hs1bp3	ENSMUSG00000020605	HCLS1 binding protein 3	-1.668	0.0000	0.0000	-1.527	0.0001	0.0003
Hsd11b1	ENSMUSG00000016194	hydroxysteroid 11-beta dehydrogenase 1	-1.616	0.0022	0.0063	-1.562	0.0047	0.0136
Hsd17b10	ENSMUSG00000025260	hydroxysteroid (17-beta) dehydrogenase 10	-1.922	0.0000	0.0000	-1.621	0.0000	0.0000
Hsf1	ENSMUSG00000022556	heat shock factor 1	-2.095	0.0000	0.0000	-1.660	0.0000	0.0000
Hsf4	ENSMUSG00000033249	heat shock transcription factor 4	-1.627	0.0035	0.0094	-2.117	0.0000	0.0001
Hspa1b	ENSMUSG00000090877	heat shock protein 1B	-2.278	0.0073	0.0181	-4.458	0.0000	0.0002
Hspa8	ENSMUSG00000015656	heat shock protein 8	-1.897	0.0000	0.0000	-1.740	0.0000	0.0000
Hspb1	ENSMUSG00000004951	heat shock protein 1	-4.296	0.0000	0.0000	-3.589	0.0000	0.0000
Hspb11	ENSMUSG00000063172	heat shock protein family B (small), member 11	-2.196	0.0000	0.0000	-2.474	0.0000	0.0000
Hspb3	ENSMUSG00000051456	heat shock protein 3	-2.100	0.0001	0.0003	-2.514	0.0000	0.0000
Hspbp1	ENSMUSG00000063802	HSPA (heat shock 70kDa) binding protein, cytoplasmic cochaperone 1	-2.378	0.0000	0.0000	-1.934	0.0000	0.0000
Hspg2	ENSMUSG00000028763	perlecan (heparan sulfate proteoglycan 2)	-2.186	0.0000	0.0000	-2.085	0.0000	0.0000
Htra3	ENSMUSG00000029096	HtrA serine peptidase 3	-3.616	0.0000	0.0000	-2.702	0.0000	0.0000
Hyal2	ENSMUSG00000010047	hyaluronoglucosaminidase 2	-3.177	0.0000	0.0000	-2.464	0.0000	0.0000
Iah1	ENSMUSG00000062054	isoamyl acetate-hydrolyzing esterase 1 homolog	-2.466	0.0000	0.0000	-2.269	0.0000	0.0000
Icam2	ENSMUSG00000001029	intercellular adhesion molecule 2	-3.580	0.0000	0.0000	-3.758	0.0000	0.0000
Id1	ENSMUSG00000042745	inhibitor of DNA binding 1, HLH protein	-4.398	0.0000	0.0000	-4.877	0.0000	0.0000
Id3	ENSMUSG00000007872	inhibitor of DNA binding 3	-2.034	0.0000	0.0000	-2.012	0.0000	0.0000
Ide	ENSMUSG00000056999	insulin degrading enzyme	-1.616	0.0000	0.0000	-1.643	0.0000	0.0000
Idh3g	ENSMUSG00000002010	isocitrate dehydrogenase 3 (NAD+), gamma	-1.872	0.0000	0.0000	-1.740	0.0000	0.0000
Idua	ENSMUSG00000033540	iduronidase, alpha-L	-1.661	0.0000	0.0000	-1.568	0.0000	0.0000
Ier3	ENSMUSG00000003541	immediate early response 3	-2.038	0.0000	0.0000	-2.618	0.0000	0.0000
Ifi27l2a	ENSMUSG00000079017	interferon, alpha-inducible protein 27 like 2A	-4.544	0.0000	0.0000	-2.395	0.0004	0.0016
Ifi47	ENSMUSG00000078920	interferon gamma inducible protein 47	-1.602	0.0262	0.0555	-1.772	0.0091	0.0241

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ifitm1	ENSMUSG00000025491	interferon induced transmembrane protein 1	-2.228	0.0023	0.0066	-1.981	0.0091	0.0243
Ifngr2	ENSMUSG00000022965	interferon gamma receptor 2	-1.794	0.0000	0.0001	-1.648	0.0004	0.0014
Ift27	ENSMUSG00000016637	intraflagellar transport 27	-2.057	0.0000	0.0000	-1.697	0.0000	0.0000
Il10ra	ENSMUSG00000032089	interleukin 10 receptor, alpha	-2.266	0.0001	0.0004	-1.611	0.0236	0.0550
Il15	ENSMUSG00000031712	interleukin 15	-1.923	0.0000	0.0000	-2.097	0.0000	0.0000
Il17rc	ENSMUSG00000030281	interleukin 17 receptor C	-3.945	0.0000	0.0000	-2.664	0.0000	0.0000
Il18bp	ENSMUSG00000070427	interleukin 18 binding protein	-2.244	0.0000	0.0000	-2.586	0.0000	0.0000
Il1rl2	ENSMUSG00000070942	interleukin 1 receptor-like 2	-2.349	0.0001	0.0004	-1.849	0.0054	0.0154
Il27ra	ENSMUSG00000005465	interleukin 27 receptor, alpha	-2.065	0.0003	0.0010	-1.581	0.0234	0.0546
Il34	ENSMUSG00000031750	interleukin 34	-3.111	0.0000	0.0000	-1.985	0.0000	0.0001
Il3ra	ENSMUSG00000068758	interleukin 3 receptor, alpha chain	-1.556	0.0161	0.0364	-1.957	0.0005	0.0017
Impdh2	ENSMUSG00000062867	inosine monophosphate dehydrogenase 2	-1.530	0.0000	0.0000	-1.599	0.0000	0.0000
Impdh2-ps	ENSMUSG00000071041	inosine monophosphate dehydrogenase 2, pseudogene	-6.549	0.0000	0.0000	-4.530	0.0001	0.0003
Inpp5j	ENSMUSG00000034570	inositol polyphosphate 5-phosphatase J	-2.134	0.0000	0.0000	-1.834	0.0004	0.0015
Inpp5k	ENSMUSG00000006127	inositol polyphosphate 5-phosphatase K	-1.878	0.0000	0.0000	-1.598	0.0000	0.0000
Insl6	ENSMUSG00000050957	insulin-like 6	-3.794	0.0013	0.0039	-3.143	0.0111	0.0288
Ints5	ENSMUSG00000071652	integrator complex subunit 5	-1.698	0.0000	0.0000	-1.816	0.0000	0.0000
Ints9	ENSMUSG00000021975	integrator complex subunit 9	-1.967	0.0000	0.0000	-1.738	0.0000	0.0000
Ipo13	ENSMUSG00000033365	importin 13	-1.859	0.0000	0.0000	-1.794	0.0000	0.0000
Ipo4	ENSMUSG00000002319	importin 4	-3.090	0.0000	0.0000	-2.740	0.0000	0.0000
Isca2	ENSMUSG00000021241	iron-sulfur cluster assembly 2	-1.559	0.0000	0.0000	-1.556	0.0000	0.0000
Islr	ENSMUSG00000037206	immunoglobulin superfamily containing leucine-rich repeat	-2.594	0.0000	0.0000	-1.970	0.0000	0.0001
Isyna1	ENSMUSG00000019139	myo-inositol 1-phosphate synthase A1	-3.812	0.0000	0.0000	-3.131	0.0000	0.0000
Itga11	ENSMUSG00000032243	integrin alpha 11	-1.709	0.0058	0.0149	-1.692	0.0074	0.0203
Itga3	ENSMUSG00000001507	integrin alpha 3	-1.798	0.0001	0.0003	-1.716	0.0003	0.0013
Itga5	ENSMUSG00000000555	integrin alpha 5 (fibronectin receptor alpha)	-1.913	0.0000	0.0000	-1.749	0.0000	0.0000
Itgb3bp	ENSMUSG00000028549	integrin beta 3 binding protein (beta3-endonexin)	-2.138	0.0000	0.0000	-1.818	0.0001	0.0003
Itm2a	ENSMUSG00000031239	integral membrane protein 2A	-2.422	0.0000	0.0000	-2.385	0.0000	0.0000
Itm2c	ENSMUSG00000026223	integral membrane protein 2C	-2.132	0.0000	0.0000	-1.533	0.0000	0.0000
Ivd	ENSMUSG00000027332	isovaleryl coenzyme A dehydrogenase	-2.921	0.0000	0.0000	-1.725	0.0000	0.0000
Izumo4	ENSMUSG00000055862	IZUMO family member 4	-2.180	0.0075	0.0185	-2.855	0.0007	0.0024
Jagn1	ENSMUSG00000051256	jagunal homolog 1	-2.316	0.0000	0.0000	-2.161	0.0000	0.0000
Jak3	ENSMUSG00000031805	Janus kinase 3	-1.744	0.0062	0.0157	-1.581	0.0246	0.0569
Josd2	ENSMUSG00000038695	Josephin domain containing 2	-1.901	0.0000	0.0000	-1.654	0.0000	0.0000
Jrk	ENSMUSG00000046380	jerky	-1.849	0.0000	0.0000	-1.701	0.0000	0.0002
Jtb	ENSMUSG00000027937	jumping translocation breakpoint	-1.562	0.0000	0.0000	-1.605	0.0000	0.0000
Kat8	ENSMUSG00000030801	K(lysine) acetyltransferase 8	-1.854	0.0000	0.0000	-1.690	0.0000	0.0000
Katnb1	ENSMUSG00000031787	katanin p80 (WD40-containing) subunit B 1	-2.312	0.0000	0.0000	-2.708	0.0000	0.0000
Kcp	ENSMUSG00000059022	kielin/chordin-like protein	-1.681	0.0011	0.0033	-1.640	0.0024	0.0074
Kctd21	ENSMUSG00000044952	potassium channel tetramerisation domain containing 21	-1.957	0.0000	0.0000	-1.786	0.0000	0.0001
Kdelr1	ENSMUSG00000002778	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 1	-2.238	0.0000	0.0000	-1.946	0.0000	0.0000
Kdelr2	ENSMUSG00000079111	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 2	-1.763	0.0000	0.0000	-1.838	0.0000	0.0000
Kdelr3	ENSMUSG00000010830	KDEL (Lys-Asp-Glu-Leu) endoplasmic reticulum protein retention receptor 3	-2.398	0.0000	0.0000	-2.232	0.0000	0.0001

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Kif26a	ENSMUSG00000021294	kinesin family member 26A	-2.168	0.0000	0.0000	-2.039	0.0000	0.0000
Klhl22	ENSMUSG00000022750	kelch-like 22	-1.778	0.0000	0.0000	-1.595	0.0001	0.0003
Klhl26	ENSMUSG00000055707	kelch-like 26	-1.851	0.0000	0.0000	-1.599	0.0000	0.0000
Klhl30	ENSMUSG00000026308	kelch-like 30	-2.060	0.0000	0.0000	-1.848	0.0001	0.0002
Klhl40	ENSMUSG00000074001	kelch-like 40	-2.211	0.0000	0.0000	-1.539	0.0070	0.0193
Klk10	ENSMUSG00000030693	kallikrein related-peptidase 10	-5.874	0.0005	0.0016	-5.158	0.0005	0.0018
Klk14	ENSMUSG00000044737	kallikrein related-peptidase 14	-2.110	0.0352	0.0717	-3.370	0.0028	0.0086
Klk8	ENSMUSG00000064023	kallikrein related-peptidase 8	-2.132	0.0000	0.0000	-1.777	0.0002	0.0009
Klra9	ENSMUSG00000033024	killer cell lectin-like receptor subfamily A, member 9	-1.987	0.0061	0.0156	-2.537	0.0003	0.0012
Kptn	ENSMUSG00000006021	kaptin	-2.270	0.0000	0.0000	-1.869	0.0000	0.0000
Krba1	ENSMUSG00000042810	KRAB-A domain containing 1	-1.920	0.0000	0.0000	-1.828	0.0000	0.0000
Krtcap2	ENSMUSG00000042747	keratinocyte associated protein 2	-5.451	0.0000	0.0000	-3.846	0.0000	0.0000
Kti12	ENSMUSG00000073775	KTI12 homolog, chromatin associated	-2.763	0.0000	0.0000	-2.432	0.0000	0.0000
Kyat1	ENSMUSG00000039648	kynurenine aminotransferase 1	-1.706	0.0000	0.0000	-1.660	0.0000	0.0000
Lage3	ENSMUSG00000015289	L antigen family, member 3	-2.274	0.0000	0.0000	-2.065	0.0000	0.0000
Lama5	ENSMUSG00000015647	laminin, alpha 5	-2.669	0.0000	0.0000	-2.133	0.0002	0.0008
Lamb2	ENSMUSG00000052911	laminin, beta 2	-1.936	0.0000	0.0000	-1.652	0.0000	0.0000
Lamc3	ENSMUSG00000026840	laminin gamma 3	-3.068	0.0014	0.0041	-2.221	0.0255	0.0588
Lancl1	ENSMUSG00000026000	LanC (bacterial lantibiotic synthetase component C)-like 1	-2.696	0.0000	0.0000	-2.576	0.0000	0.0000
Laptm5	ENSMUSG00000028581	lysosomal-associated protein transmembrane 5	-1.881	0.0000	0.0002	-1.523	0.0067	0.0185
Large1	ENSMUSG00000004383	LARGE xylosyl- and glucuronyltransferase 1	-1.591	0.0000	0.0000	-1.549	0.0000	0.0000
Lars2	ENSMUSG00000035202	leucyl-tRNA synthetase, mitochondrial	-8.337	0.0000	0.0000	-11.605	0.0000	0.0000
Lasp1	ENSMUSG00000038366	LIM and SH3 protein 1	-1.862	0.0000	0.0000	-1.713	0.0000	0.0000
Lcmt2	ENSMUSG00000074890	leucine carboxyl methyltransferase 2	-2.025	0.0000	0.0000	-1.743	0.0000	0.0000
Ldah	ENSMUSG00000037669	lipid droplet associated hydrolase	-1.707	0.0000	0.0000	-1.887	0.0000	0.0000
Ldb3	ENSMUSG00000021798	LIM domain binding 3	-1.661	0.0000	0.0000	-1.532	0.0000	0.0000
Ldhb-ps	ENSMUSG00000045104	lactate dehydrogenase B, pseudogene	-3.221	0.0000	0.0000	-2.555	0.0000	0.0000
Limd1	ENSMUSG00000025239	LIM domains containing 1	-1.631	0.0037	0.0099	-1.564	0.0080	0.0216
Lipe	ENSMUSG00000003123	lipase, hormone sensitive	-1.645	0.0007	0.0023	-1.549	0.0030	0.0092
Lipo3	ENSMUSG00000024766	lipase, member O3	-1.501	0.0458	0.0896	-2.216	0.0002	0.0007
Llgl1	ENSMUSG00000020536	LLGL1 scribble cell polarity complex component	-2.344	0.0000	0.0000	-2.128	0.0000	0.0000
Lman1l	ENSMUSG00000056271	lectin, mannose-binding 1 like	-4.126	0.0001	0.0003	-3.974	0.0002	0.0007
Lmbr1l	ENSMUSG00000022999	limb region 1 like	-1.647	0.0171	0.0384	-1.661	0.0158	0.0392
Lmf1	ENSMUSG00000002279	lipase maturation factor 1	-2.595	0.0000	0.0000	-2.419	0.0000	0.0000
Lmf2	ENSMUSG00000022614	lipase maturation factor 2	-1.947	0.0000	0.0000	-1.809	0.0000	0.0000
Lnx2	ENSMUSG00000016520	ligand of numb-protein X 2	-1.568	0.0079	0.0194	-1.964	0.0001	0.0003
Loxl1	ENSMUSG00000032334	lysyl oxidase-like 1	-2.260	0.0003	0.0012	-2.240	0.0004	0.0015
Lrfn3	ENSMUSG00000036957	leucine rich repeat and fibronectin type III domain containing 3	-2.313	0.0004	0.0014	-1.949	0.0077	0.0209
Lrp1	ENSMUSG00000040249	low density lipoprotein receptor-related protein 1	-1.904	0.0000	0.0000	-1.533	0.0008	0.0029
Lrrc10	ENSMUSG00000060187	leucine rich repeat containing 10	-2.726	0.0012	0.0037	-2.149	0.0137	0.0347
Lrrc24	ENSMUSG00000033707	leucine rich repeat containing 24	-1.778	0.0518	0.0997	-2.580	0.0024	0.0074
Lrrc25	ENSMUSG00000049988	leucine rich repeat containing 25	-2.110	0.0015	0.0044	-2.496	0.0001	0.0006
Lrrc28	ENSMUSG00000030556	leucine rich repeat containing 28	-1.993	0.0000	0.0000	-1.782	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Lrrc29	ENSMUSG00000041679	leucine rich repeat containing 29	-3.294	0.0023	0.0064	-8.340	0.0002	0.0009
Lrrc30	ENSMUSG00000073375	leucine rich repeat containing 30	-7.201	0.0000	0.0000	-3.040	0.0004	0.0013
Lrrc32	ENSMUSG00000090958	leucine rich repeat containing 32	-1.853	0.0001	0.0004	-1.636	0.0019	0.0062
Lrrc49	ENSMUSG00000047766	leucine rich repeat containing 49	-1.544	0.0007	0.0023	-1.748	0.0000	0.0001
Lrrc51	ENSMUSG00000064307	leucine rich repeat containing 51	-2.805	0.0000	0.0000	-1.580	0.0249	0.0576
Lrrc70	ENSMUSG00000118423	leucine rich repeat containing 70	-2.391	0.0021	0.0059	-2.336	0.0034	0.0102
Lsm10	ENSMUSG00000050188	U7 snRNP-specific Sm-like protein LSM10	-3.723	0.0000	0.0000	-2.953	0.0000	0.0000
Lsmem2	ENSMUSG00000103409	leucine-rich single-pass membrane protein 2	-1.783	0.0000	0.0002	-1.506	0.0040	0.0118
Lta4h	ENSMUSG00000015889	leukotriene A4 hydrolase	-1.740	0.0000	0.0000	-1.587	0.0000	0.0000
Ltc4s	ENSMUSG00000020377	leukotriene C4 synthase	-4.029	0.0000	0.0000	-2.970	0.0000	0.0002
Lxn	ENSMUSG00000047557	latexin	-1.576	0.0262	0.0555	-2.254	0.0001	0.0006
Ly6a	ENSMUSG00000075602	lymphocyte antigen 6 complex, locus A	-1.795	0.0000	0.0000	-1.796	0.0000	0.0000
Ly6c1	ENSMUSG00000079018	lymphocyte antigen 6 complex, locus C1	-1.901	0.0000	0.0000	-1.776	0.0000	0.0001
Ly6e	ENSMUSG00000022587	lymphocyte antigen 6 complex, locus E	-2.353	0.0000	0.0000	-1.824	0.0000	0.0000
Ly86	ENSMUSG00000021423	lymphocyte antigen 86	-3.834	0.0000	0.0000	-4.389	0.0000	0.0000
Ly96	ENSMUSG00000025779	lymphocyte antigen 96	-1.558	0.0250	0.0533	-2.282	0.0001	0.0003
Lyl1	ENSMUSG00000034041	lymphoblastomic leukemia 1	-2.405	0.0000	0.0000	-1.895	0.0010	0.0034
Lypd2	ENSMUSG00000022595	Ly6/Plaur domain containing 2	-3.961	0.0001	0.0005	-2.500	0.0068	0.0188
Lyrm1	ENSMUSG00000030922	LYR motif containing 1	-1.522	0.0040	0.0106	-1.554	0.0028	0.0086
Lyrm2	ENSMUSG00000045854	LYR motif containing 2	-1.639	0.0000	0.0000	-1.664	0.0000	0.0000
Lyz2	ENSMUSG00000069516	lysozyme 2	-2.036	0.0001	0.0002	-1.608	0.0069	0.0189
Macroh2a2	ENSMUSG00000020086	macroH2A.2 histone	-1.521	0.0140	0.0323	-1.792	0.0007	0.0025
Mad2l2	ENSMUSG00000029003	MAD2 mitotic arrest deficient-like 2	-1.742	0.0000	0.0000	-1.763	0.0000	0.0000
Maged1	ENSMUSG00000025151	MAGE family member D1	-2.286	0.0000	0.0000	-2.088	0.0000	0.0000
Maged2	ENSMUSG00000025268	MAGE family member D2	-2.016	0.0000	0.0000	-1.899	0.0000	0.0000
Maml2	ENSMUSG00000031925	mastermind like transcriptional coactivator 2	-1.563	0.0000	0.0001	-1.532	0.0000	0.0002
Man2b2	ENSMUSG00000029119	mannosidase 2, alpha B2	-2.600	0.0000	0.0000	-1.969	0.0000	0.0000
Manbal	ENSMUSG00000063019	mannosidase, beta A, lysosomal-like	-2.890	0.0000	0.0000	-2.686	0.0000	0.0000
Map1lc3b	ENSMUSG00000031812	microtubule-associated protein 1 light chain 3 beta	-2.027	0.0000	0.0000	-2.009	0.0000	0.0000
Map1s	ENSMUSG00000019261	microtubule-associated protein 1S	-2.684	0.0000	0.0000	-2.048	0.0000	0.0000
Map2k3os	ENSMUSG00000042549	mitogen-activated protein kinase kinase 3, opposite strand	-2.762	0.0000	0.0000	-2.065	0.0009	0.0030
Map3k14	ENSMUSG00000020941	mitogen-activated protein kinase kinase kinase 14	-1.766	0.0000	0.0001	-1.627	0.0002	0.0009
Mapk13	ENSMUSG00000004864	mitogen-activated protein kinase 13	-8.485	0.0002	0.0007	-10.569	0.0023	0.0072
Mapk1ip1	ENSMUSG00000041775	mitogen-activated protein kinase 1 interacting protein 1	-2.094	0.0000	0.0000	-1.947	0.0001	0.0002
Mapk3	ENSMUSG00000063065	mitogen-activated protein kinase 3	-2.475	0.0000	0.0000	-2.060	0.0000	0.0000
Mapkapk3	ENSMUSG00000032577	mitogen-activated protein kinase-activated protein kinase 3	-1.502	0.0000	0.0001	-1.532	0.0000	0.0000
Mavs	ENSMUSG00000037523	mitochondrial antiviral signaling protein	-2.424	0.0000	0.0000	-1.954	0.0000	0.0000
Mcfd2	ENSMUSG00000024150	multiple coagulation factor deficiency 2	-2.024	0.0000	0.0000	-2.362	0.0000	0.0000
Mcm8	ENSMUSG00000027353	minichromosome maintenance 8 homologous recombination repair factor	-1.638	0.0003	0.0010	-2.054	0.0000	0.0000
Mcrip2	ENSMUSG00000025732	MAPK regulated corepressor interacting protein 2	-1.607	0.0008	0.0026	-1.667	0.0003	0.0013
Mcrs1	ENSMUSG00000037570	microspherule protein 1	-2.702	0.0000	0.0000	-2.369	0.0000	0.0000
Mdh1	ENSMUSG00000020321	malate dehydrogenase 1, NAD (soluble)	-1.812	0.0000	0.0000	-1.696	0.0000	0.0000
Mdh2	ENSMUSG00000019179	malate dehydrogenase 2, NAD (mitochondrial)	-2.710	0.0000	0.0000	-2.469	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Mdp1	ENSMUSG00000002329	magnesium-dependent phosphatase 1	-1.519	0.0000	0.0000	-1.726	0.0000	0.0000
Med10	ENSMUSG00000021598	mediator complex subunit 10	-1.720	0.0000	0.0000	-1.655	0.0000	0.0000
Med11	ENSMUSG00000018923	mediator complex subunit 11	-1.537	0.0004	0.0012	-1.678	0.0000	0.0002
Med22	ENSMUSG00000015776	mediator complex subunit 22	-1.758	0.0000	0.0000	-1.601	0.0000	0.0000
Med24	ENSMUSG00000017210	mediator complex subunit 24	-2.225	0.0000	0.0000	-1.896	0.0000	0.0000
Med26	ENSMUSG00000045248	mediator complex subunit 26	-1.547	0.0004	0.0014	-1.677	0.0000	0.0002
Med27	ENSMUSG00000026799	mediator complex subunit 27	-1.831	0.0000	0.0000	-1.744	0.0000	0.0000
Med29	ENSMUSG00000003444	mediator complex subunit 29	-2.496	0.0000	0.0000	-2.586	0.0000	0.0000
Med7	ENSMUSG00000020397	mediator complex subunit 7	-1.518	0.0005	0.0017	-1.743	0.0000	0.0000
Mef2b	ENSMUSG00000079033	myocyte enhancer factor 2B	-2.762	0.0003	0.0009	-3.768	0.0001	0.0004
Megf6	ENSMUSG00000057751	multiple EGF-like-domains 6	-1.951	0.0024	0.0066	-1.954	0.0027	0.0084
Mest	ENSMUSG00000051855	mesoderm specific transcript	-2.207	0.0000	0.0001	-2.761	0.0000	0.0000
Metrn	ENSMUSG00000002274	meteorin, glial cell differentiation regulator	-1.829	0.0000	0.0000	-1.970	0.0000	0.0000
Mettl22	ENSMUSG00000039345	methyltransferase like 22	-3.220	0.0000	0.0000	-2.428	0.0000	0.0000
Mettl23	ENSMUSG00000090266	methyltransferase like 23	-1.587	0.0000	0.0000	-1.976	0.0000	0.0000
Mfap1b	ENSMUSG00000048222	microfibrillar-associated protein 1B	-2.345	0.0000	0.0000	-2.218	0.0000	0.0000
Mfap2	ENSMUSG00000060572	microfibrillar-associated protein 2	-3.275	0.0000	0.0001	-1.729	0.0448	0.0943
Mfge8	ENSMUSG00000030605	milk fat globule EGF and factor V/VIII domain containing	-1.925	0.0000	0.0000	-1.807	0.0000	0.0000
Mfsd10	ENSMUSG00000001082	major facilitator superfamily domain containing 10	-1.999	0.0000	0.0000	-1.540	0.0001	0.0003
Mfsd11	ENSMUSG00000020818	major facilitator superfamily domain containing 11	-1.753	0.0000	0.0000	-1.756	0.0000	0.0000
Mfsd3	ENSMUSG00000019080	major facilitator superfamily domain containing 3	-3.632	0.0000	0.0000	-1.742	0.0018	0.0059
Mfsd4a	ENSMUSG00000059149	major facilitator superfamily domain containing 4A	-3.160	0.0000	0.0000	-2.420	0.0000	0.0000
Mgp	ENSMUSG00000030218	matrix Gla protein	-2.914	0.0000	0.0000	-2.262	0.0000	0.0000
Mgrn1	ENSMUSG00000022517	mahogunin, ring finger 1	-1.703	0.0000	0.0000	-1.522	0.0000	0.0000
Mgst1	ENSMUSG00000008540	microsomal glutathione S-transferase 1	-1.719	0.0052	0.0135	-1.797	0.0026	0.0081
Mgst3	ENSMUSG00000026688	microsomal glutathione S-transferase 3	-3.100	0.0000	0.0000	-2.645	0.0000	0.0000
Micall2	ENSMUSG00000036718	MICAL-like 2	-2.074	0.0000	0.0001	-1.981	0.0001	0.0003
Mif	ENSMUSG00000033307	macrophage migration inhibitory factor (glycosylation-inhibiting factor)	-3.389	0.0000	0.0000	-2.315	0.0000	0.0000
Mif4gd	ENSMUSG00000020743	MIF4G domain containing	-1.845	0.0000	0.0000	-1.815	0.0000	0.0000
Miip	ENSMUSG00000029022	migration and invasion inhibitory protein	-2.926	0.0000	0.0000	-1.714	0.0009	0.0033
Mindy1	ENSMUSG00000038712	MINDY lysine 48 deubiquitinase 1	-2.339	0.0000	0.0000	-2.261	0.0000	0.0000
Mir133a-2	ENSMUSG00000065460	microRNA 133a-2	-30.296	0.0000	0.0000	-25.440	0.0000	0.0001
Mir7-1	ENSMUSG00000065434	microRNA 7-1	-37.166	0.0002	0.0006	-19.973	0.0020	0.0064
Mir7666	ENSMUSG00000098431	microRNA 7666	-5.071	0.0238	0.0511	-22.794	0.0007	0.0025
Mkks	ENSMUSG00000027274	McKusick-Kaufman syndrome	-1.892	0.0000	0.0000	-1.999	0.0000	0.0000
Mlst8	ENSMUSG00000024142	MTOR associated protein, LST8 homolog (S. cerevisiae)	-1.860	0.0000	0.0000	-1.617	0.0000	0.0001
Mlx	ENSMUSG00000017801	MAX-like protein X	-2.504	0.0000	0.0000	-2.135	0.0000	0.0000
Mmachc	ENSMUSG00000028690	methylmalonic aciduria cblC type, with homocystinuria	-1.640	0.0000	0.0000	-1.620	0.0000	0.0001
Mmp11	ENSMUSG00000000901	matrix metallopeptidase 11	-1.561	0.0009	0.0027	-1.665	0.0002	0.0007
Mmp23	ENSMUSG00000029061	matrix metallopeptidase 23	-2.329	0.0001	0.0003	-1.817	0.0057	0.0161
Mms19	ENSMUSG00000025159	MMS19 cytosolic iron-sulfur assembly component	-2.776	0.0000	0.0000	-2.153	0.0000	0.0000
Mocs1	ENSMUSG00000064120	molybdenum cofactor synthesis 1	-2.025	0.0006	0.0019	-1.623	0.0181	0.0438
Mon1a	ENSMUSG00000032583	MON1 homolog A, secretory traffciking associated	-2.966	0.0000	0.0000	-2.274	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Morf4l1-ps1	ENSMUSG00000116875	mortality factor 4 like 1, pseudogene 1	-2.650	0.0002	0.0007	-2.820	0.0001	0.0004
Mov10	ENSMUSG00000002227	Mov10 RISC complex RNA helicase	-2.037	0.0000	0.0000	-1.531	0.0014	0.0046
Mpc1	ENSMUSG00000023861	mitochondrial pyruvate carrier 1	-3.244	0.0000	0.0000	-2.783	0.0000	0.0000
Mpc1-ps	ENSMUSG00000091498	mitochondrial pyruvate carrier 1, pseudogene	-11.909	0.0000	0.0000	-10.359	0.0000	0.0000
Mpdu1	ENSMUSG00000018761	mannose-P-dolichol utilization defect 1	-1.688	0.0000	0.0000	-1.532	0.0000	0.0000
Mpst	ENSMUSG00000071711	mercaptopyruvate sulfurtransferase	-3.399	0.0000	0.0000	-1.759	0.0000	0.0000
Mpv17	ENSMUSG00000107283	MpV17 mitochondrial inner membrane protein	-1.656	0.0000	0.0000	-1.743	0.0000	0.0000
Mpv17l2	ENSMUSG00000035559	MPV17 mitochondrial membrane protein-like 2	-3.218	0.0000	0.0000	-2.445	0.0000	0.0000
Mrap	ENSMUSG00000039956	melanocortin 2 receptor accessory protein	-2.079	0.0000	0.0000	-1.834	0.0000	0.0000
Mrgpre	ENSMUSG00000048965	MAS-related GPR, member E	-2.848	0.0000	0.0000	-1.871	0.0005	0.0020
Mrgprf	ENSMUSG00000031070	MAS-related GPR, member F	-5.134	0.0000	0.0000	-2.875	0.0000	0.0000
Mrgprh	ENSMUSG00000059408	MAS-related GPR, member H	-1.569	0.0185	0.0411	-1.685	0.0074	0.0203
Mrip-ps	ENSMUSG00000098404	Mom radiation induced polyposis, pseudogene	-3.083	0.0000	0.0000	-2.504	0.0000	0.0000
Mroh1	ENSMUSG00000022558	maestro heat-like repeat family member 1	-2.350	0.0000	0.0000	-1.743	0.0000	0.0000
Mrpl11	ENSMUSG00000024902	mitochondrial ribosomal protein L11	-1.709	0.0000	0.0000	-1.536	0.0000	0.0000
Mrpl12	ENSMUSG00000039640	mitochondrial ribosomal protein L12	-2.437	0.0000	0.0000	-2.036	0.0000	0.0000
Mrpl14	ENSMUSG00000023939	mitochondrial ribosomal protein L14	-2.839	0.0000	0.0000	-2.776	0.0000	0.0000
Mrpl23	ENSMUSG00000037772	mitochondrial ribosomal protein L23	-2.121	0.0000	0.0000	-2.183	0.0000	0.0000
Mrpl27	ENSMUSG00000024414	mitochondrial ribosomal protein L27	-2.084	0.0000	0.0000	-1.709	0.0000	0.0000
Mrpl27-ps	ENSMUSG00000071867	mitochondrial ribosomal protein L27, pseudogene	-11.091	0.0167	0.0376	-13.928	0.0097	0.0255
Mrpl3	ENSMUSG00000032563	mitochondrial ribosomal protein L3	-1.655	0.0000	0.0000	-1.957	0.0000	0.0000
Mrpl30	ENSMUSG00000026087	mitochondrial ribosomal protein L30	-2.913	0.0000	0.0000	-2.590	0.0000	0.0000
Mrpl34	ENSMUSG00000034880	mitochondrial ribosomal protein L34	-2.595	0.0000	0.0000	-2.046	0.0000	0.0000
Mrpl36	ENSMUSG00000021607	mitochondrial ribosomal protein L36	-2.355	0.0000	0.0000	-2.158	0.0000	0.0000
Mrpl4	ENSMUSG00000003299	mitochondrial ribosomal protein L4	-3.175	0.0000	0.0000	-2.621	0.0000	0.0000
Mrpl52	ENSMUSG00000010406	mitochondrial ribosomal protein L52	-1.914	0.0000	0.0000	-1.544	0.0000	0.0000
Mrpl54	ENSMUSG00000034932	mitochondrial ribosomal protein L54	-3.850	0.0000	0.0000	-2.561	0.0000	0.0000
Mrpl57	ENSMUSG00000021967	mitochondrial ribosomal protein L57	-2.030	0.0000	0.0000	-2.401	0.0000	0.0000
Mrps11	ENSMUSG00000030611	mitochondrial ribosomal protein S11	-2.075	0.0000	0.0000	-1.697	0.0000	0.0000
Mrps12	ENSMUSG00000045948	mitochondrial ribosomal protein S12	-2.251	0.0000	0.0000	-1.933	0.0000	0.0000
Mrps14	ENSMUSG00000058267	mitochondrial ribosomal protein S14	-1.676	0.0000	0.0000	-1.923	0.0000	0.0000
Mrps16	ENSMUSG00000049960	mitochondrial ribosomal protein S16	-1.819	0.0000	0.0000	-1.913	0.0000	0.0000
Mrps17	ENSMUSG00000034211	mitochondrial ribosomal protein S17	-1.563	0.0000	0.0000	-1.554	0.0000	0.0000
Mrps18a	ENSMUSG00000023967	mitochondrial ribosomal protein S18A	-2.505	0.0000	0.0000	-1.862	0.0000	0.0000
Mrps18b	ENSMUSG00000024436	mitochondrial ribosomal protein S18B	-2.747	0.0000	0.0000	-2.420	0.0000	0.0000
Mrps24	ENSMUSG00000020477	mitochondrial ribosomal protein S24	-1.835	0.0040	0.0106	-3.032	0.0000	0.0000
Mrps27	ENSMUSG00000041632	mitochondrial ribosomal protein S27	-1.739	0.0000	0.0000	-1.776	0.0000	0.0000
Mrps28	ENSMUSG00000040269	mitochondrial ribosomal protein S28	-3.097	0.0000	0.0000	-2.575	0.0000	0.0000
Mrps30	ENSMUSG00000021731	mitochondrial ribosomal protein S30	-2.211	0.0000	0.0000	-2.201	0.0000	0.0000
Mrps36-ps1	ENSMUSG00000021631	mitichondrial ribosomal protein S36, pseudogene 1	-3.707	0.0003	0.0010	-1.933	0.0357	0.0781
Mrps7	ENSMUSG00000046756	mitchondrial ribosomal protein S7	-1.976	0.0000	0.0000	-1.546	0.0000	0.0000
Mrrf	ENSMUSG00000026887	mitochondrial ribosome recycling factor	-2.045	0.0000	0.0000	-2.002	0.0000	0.0000
Mrtfb	ENSMUSG00000009569	myocardin related transcription factor B	-1.557	0.0002	0.0008	-1.683	0.0000	0.0001

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ms4a6d	ENSMUSG00000024679	membrane-spanning 4-domains, subfamily A, member 6D	-2.928	0.0001	0.0005	-4.102	0.0000	0.0000
Msh5	ENSMUSG00000007035	mutS homolog 5	-3.249	0.0091	0.0220	-2.883	0.0356	0.0778
Msra	ENSMUSG00000054733	methionine sulfoxide reductase A	-1.741	0.0000	0.0000	-1.641	0.0000	0.0000
Msrb1	ENSMUSG00000075705	methionine sulfoxide reductase B1	-2.351	0.0000	0.0000	-2.190	0.0000	0.0000
Msto1	ENSMUSG00000068922	misato 1, mitochondrial distribution and morphology regulator	-2.092	0.0000	0.0000	-1.542	0.0004	0.0014
Mterf3	ENSMUSG00000021519	mitochondrial transcription termination factor 3	-1.988	0.0000	0.0000	-2.088	0.0000	0.0000
Mtg1	ENSMUSG00000039018	mitochondrial ribosome-associated GTPase 1	-1.892	0.0000	0.0000	-1.713	0.0000	0.0000
Mthfr	ENSMUSG00000029009	methylenetetrahydrofolate reductase	-2.078	0.0000	0.0000	-2.182	0.0000	0.0000
Mtln	ENSMUSG00000051319	mitoregulin	-2.497	0.0000	0.0000	-3.164	0.0000	0.0000
Mtmr10	ENSMUSG00000030522	myotubularin related protein 10	-1.600	0.0049	0.0127	-1.839	0.0003	0.0011
Mtmr11	ENSMUSG00000045934	myotubularin related protein 11	-1.665	0.0037	0.0099	-1.575	0.0103	0.0271
mt-Rnr1	ENSMUSG00000064337	mitochondrially encoded 12S rRNA	-1.801	0.0013	0.0039	-2.577	0.0000	0.0000
mt-Ta	ENSMUSG00000064347	mitochondrially encoded tRNA alanine	-2.826	0.0232	0.0499	-8.326	0.0006	0.0022
mt-Ti	ENSMUSG00000064342	mitochondrially encoded tRNA isoleucine	-2.429	0.0033	0.0090	-5.953	0.0000	0.0000
mt-Tl1	ENSMUSG00000064340	mitochondrially encoded tRNA leucine 1	-44.006	0.0000	0.0001	-50.127	0.0000	0.0001
mt-Tm	ENSMUSG00000064344	mitochondrially encoded tRNA methionine	-12.882	0.0000	0.0000	-19.101	0.0000	0.0000
mt-Tt	ENSMUSG00000064371	mitochondrially encoded tRNA threonine	-12.128	0.0000	0.0000	-17.224	0.0000	0.0000
mt-Tw	ENSMUSG00000064346	mitochondrially encoded tRNA tryptophan	-2.074	0.0008	0.0024	-3.158	0.0000	0.0000
Mtx1	ENSMUSG00000064068	metaxin 1	-1.657	0.0000	0.0000	-1.588	0.0000	0.0000
Muc3a	ENSMUSG00000094840	mucin 3A, cell surface associated	-3.630	0.0214	0.0466	-7.697	0.0015	0.0049
Mus81	ENSMUSG00000024906	MUS81 structure-specific endonuclease subunit	-2.482	0.0000	0.0000	-2.045	0.0000	0.0000
Mutyh	ENSMUSG00000028687	mutY DNA glycosylase	-2.301	0.0010	0.0030	-1.823	0.0239	0.0557
Myl12a	ENSMUSG00000024048	myosin, light chain 12A, regulatory, non-sarcomeric	-1.510	0.0000	0.0000	-1.714	0.0000	0.0000
Myl2	ENSMUSG00000013936	myosin, light polypeptide 2, regulatory, cardiac, slow	-2.088	0.0000	0.0000	-1.907	0.0000	0.0000
Myl6b	ENSMUSG00000039824	myosin, light polypeptide 6B	-2.034	0.0000	0.0002	-1.749	0.0007	0.0026
Myl9	ENSMUSG00000067818	myosin, light polypeptide 9, regulatory	-2.122	0.0000	0.0000	-2.072	0.0000	0.0000
Myo19	ENSMUSG00000020527	myosin XIX	-1.936	0.0016	0.0046	-1.817	0.0051	0.0148
Myo7a	ENSMUSG00000030761	myosin VIIA	-2.037	0.0000	0.0000	-1.500	0.0027	0.0083
Myo9b	ENSMUSG00000004677	myosin IXb	-1.875	0.0000	0.0000	-1.612	0.0000	0.0000
Myot	ENSMUSG00000024471	myotilin	-2.452	0.0000	0.0000	-2.026	0.0002	0.0008
Myoz2	ENSMUSG00000028116	myozenin 2	-1.897	0.0000	0.0000	-1.898	0.0000	0.0000
Naa38	ENSMUSG00000059278	N(alpha)-acetyltransferase 38, NatC auxiliary subunit	-2.569	0.0000	0.0000	-2.567	0.0000	0.0000
Naa60	ENSMUSG00000005982	N(alpha)-acetyltransferase 60, NatF catalytic subunit	-2.429	0.0000	0.0000	-2.073	0.0000	0.0000
Naa80	ENSMUSG00000079334	N(alpha)-acetyltransferase 80, NatH catalytic subunit	-3.031	0.0000	0.0000	-2.006	0.0000	0.0000
Naaa	ENSMUSG00000029413	N-acylethanolamine acid amidase	-1.648	0.0000	0.0001	-1.520	0.0004	0.0014
Naga	ENSMUSG00000022453	N-acetyl galactosaminidase, alpha	-2.394	0.0000	0.0000	-1.892	0.0000	0.0000
Naglu	ENSMUSG00000001751	alpha-N-acetylglucosaminidase (Sanfilippo disease IIIB)	-2.375	0.0000	0.0000	-1.676	0.0007	0.0024
Naip2	ENSMUSG00000078945	NLR family, apoptosis inhibitory protein 2	-1.608	0.0041	0.0109	-1.711	0.0027	0.0083
Napa	ENSMUSG00000006024	N-ethylmaleimide sensitive fusion protein attachment protein alpha	-2.563	0.0000	0.0000	-2.468	0.0000	0.0000
Nat8f1	ENSMUSG00000057103	N-acetyltransferase 8 (GCN5-related) family member 1	-2.413	0.0001	0.0004	-1.871	0.0054	0.0154
Natd1	ENSMUSG00000018931	N-acetyltransferase domain containing 1	-1.830	0.0000	0.0000	-1.771	0.0000	0.0001
Naxd	ENSMUSG00000031505	NAD(P)HX dehydratase	-1.750	0.0000	0.0000	-1.646	0.0000	0.0000
Nbeal2	ENSMUSG00000056724	neurobeachin-like 2	-1.930	0.0000	0.0000	-1.763	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ncdn	ENSMUSG00000028833	neurochondrin	-1.990	0.0000	0.0000	-1.606	0.0000	0.0000
Nckap5l	ENSMUSG00000023009	NCK-associated protein 5-like	-3.041	0.0000	0.0000	-1.760	0.0000	0.0000
Nckipsd	ENSMUSG00000032598	NCK interacting protein with SH3 domain	-2.380	0.0000	0.0000	-2.063	0.0000	0.0000
Ncln	ENSMUSG00000020238	nicalin	-3.754	0.0000	0.0000	-3.322	0.0000	0.0000
Ncoa4-ps	ENSMUSG00000021908	nuclear receptor coactivator 4, pseudogene	-4.490	0.0008	0.0024	-3.537	0.0018	0.0059
Ncstn	ENSMUSG00000003458	nicastrin	-1.532	0.0000	0.0000	-1.532	0.0000	0.0000
Ndufa11	ENSMUSG00000002379	NADH:ubiquinone oxidoreductase subunit A11	-3.010	0.0000	0.0000	-2.480	0.0000	0.0000
Ndufa12-ps	ENSMUSG00000080893	NADH:ubiquinone oxidoreductase subunit A12, pseudogene	-3.769	0.0000	0.0000	-3.625	0.0000	0.0000
Ndufa3	ENSMUSG00000035674	NADH:ubiquinone oxidoreductase subunit A3	-2.330	0.0000	0.0000	-2.215	0.0000	0.0000
Ndufa4l2	ENSMUSG00000040280	Ndufa4, mitochondrial complex associated like 2	-3.035	0.0000	0.0000	-2.519	0.0000	0.0000
Ndufa7	ENSMUSG00000041881	NADH:ubiquinone oxidoreductase subunit A7	-3.018	0.0000	0.0000	-2.416	0.0000	0.0000
Ndufab1-ps	ENSMUSG00000091989	NADH:ubiquinone oxidoreductase subunit AB1b	-2.872	0.0021	0.0060	-3.668	0.0004	0.0016
Ndufaf3	ENSMUSG00000070283	NADH:ubiquinone oxidoreductase complex assembly factor 3	-1.786	0.0000	0.0000	-1.654	0.0000	0.0000
Ndufaf8	ENSMUSG00000078572	NADH:ubiquinone oxidoreductase complex assembly factor 8	-2.100	0.0000	0.0000	-1.804	0.0000	0.0000
Ndufb1	ENSMUSG00000113902	NADH:ubiquinone oxidoreductase subunit B1	-2.426	0.0000	0.0000	-2.893	0.0000	0.0000
Ndufb11	ENSMUSG00000031059	NADH:ubiquinone oxidoreductase subunit B11	-2.609	0.0000	0.0000	-2.332	0.0000	0.0000
Ndufb2	ENSMUSG00000002416	NADH:ubiquinone oxidoreductase subunit B2	-3.772	0.0000	0.0000	-4.367	0.0000	0.0000
Ndufb5	ENSMUSG00000027673	NADH:ubiquinone oxidoreductase subunit B5	-2.289	0.0000	0.0000	-2.516	0.0000	0.0000
Ndufb6	ENSMUSG00000071014	NADH:ubiquinone oxidoreductase subunit B6	-1.794	0.0000	0.0000	-1.790	0.0000	0.0000
Ndufs5	ENSMUSG00000028648	NADH:ubiquinone oxidoreductase core subunit S5	-2.772	0.0000	0.0000	-5.076	0.0000	0.0000
Ndufs5-ps	ENSMUSG00000081824	NADH:ubiquinone oxidoreductase core subunit S5, pseudogene	-3.428	0.0000	0.0000	-2.849	0.0000	0.0000
Ndufs7	ENSMUSG00000020153	NADH:ubiquinone oxidoreductase core subunit S7	-3.422	0.0000	0.0000	-2.579	0.0000	0.0000
Ndufs8	ENSMUSG00000059734	NADH:ubiquinone oxidoreductase core subunit S8	-2.315	0.0000	0.0000	-1.870	0.0000	0.0000
Necab3	ENSMUSG00000027489	N-terminal EF-hand calcium binding protein 3	-13.082	0.0021	0.0061	-9.670	0.0075	0.0203
Nelfa	ENSMUSG00000029111	negative elongation factor complex member A, Whsc2	-1.609	0.0000	0.0000	-1.558	0.0000	0.0000
Nepn	ENSMUSG00000038624	nephrocan	-2.362	0.0004	0.0013	-1.666	0.0299	0.0673
Neurl1a	ENSMUSG00000006435	neuralized E3 ubiquitin protein ligase 1A	-2.202	0.0000	0.0000	-1.543	0.0053	0.0152
Nfkbib	ENSMUSG00000030595	nuclear factor of kappa light polypeptide gene enhancer in B cells inhibitor, beta	-4.088	0.0000	0.0000	-2.587	0.0000	0.0000
Nfs1	ENSMUSG00000027618	nitrogen fixation gene 1 (S. cerevisiae)	-2.663	0.0000	0.0000	-2.258	0.0000	0.0000
Nfyc	ENSMUSG00000032897	nuclear transcription factor-Y gamma	-1.912	0.0000	0.0000	-1.711	0.0000	0.0000
Nfyc-ps	ENSMUSG00000073233	nuclear transcription factor-Y gamma, pseudogene	-6.348	0.0009	0.0029	-25.843	0.0002	0.0009
Ngf	ENSMUSG00000027859	nerve growth factor	-1.927	0.0000	0.0002	-1.747	0.0006	0.0021
Nhej1	ENSMUSG00000026162	non-homologous end joining factor 1	-1.553	0.0001	0.0003	-1.668	0.0000	0.0000
Nicn1	ENSMUSG00000032606	nicolin 1	-1.562	0.0000	0.0000	-1.508	0.0000	0.0000
Nid2	ENSMUSG00000021806	nidogen 2	-1.727	0.0000	0.0000	-1.854	0.0000	0.0000
Ninj1	ENSMUSG00000037966	ninjurin 1	-2.763	0.0000	0.0000	-2.771	0.0000	0.0000
Nipsnap2	ENSMUSG00000029432	nipsnap homolog 2	-1.888	0.0000	0.0000	-1.789	0.0000	0.0000
Nipsnap3b	ENSMUSG00000015247	nipsnap homolog 3B	-1.641	0.0000	0.0000	-1.648	0.0000	0.0001
Nisch	ENSMUSG00000021910	nischarin	-1.799	0.0000	0.0000	-1.751	0.0000	0.0000
Nit1	ENSMUSG00000013997	nitrilase 1	-1.927	0.0000	0.0000	-1.509	0.0000	0.0000
Nit2	ENSMUSG00000022751	nitrilase family, member 2	-1.678	0.0000	0.0000	-1.664	0.0000	0.0000
Nkiras2	ENSMUSG00000017837	NFKB inhibitor interacting Ras-like protein 2	-1.835	0.0000	0.0000	-1.592	0.0000	0.0000
Nle1	ENSMUSG00000020692	notchless homolog 1	-1.907	0.0002	0.0008	-1.583	0.0090	0.0241

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Nlrc3	ENSMUSG00000049871	NLR family, CARD domain containing 3	-1.606	0.0119	0.0280	-1.682	0.0085	0.0229
Nmb	ENSMUSG00000025723	neuromedin B	-4.201	0.0001	0.0005	-2.245	0.0166	0.0407
Nmnat1	ENSMUSG00000028992	nicotinamide nucleotide adenylyltransferase 1	-1.704	0.0000	0.0000	-1.533	0.0000	0.0001
Nmral1	ENSMUSG00000063445	NmrA-like family domain containing 1	-2.564	0.0000	0.0000	-1.552	0.0187	0.0450
Noc4l	ENSMUSG00000033294	NOC4 like	-2.782	0.0000	0.0000	-2.203	0.0000	0.0000
Nod1	ENSMUSG00000038058	nucleotide-binding oligomerization domain containing 1	-2.146	0.0000	0.0000	-1.851	0.0000	0.0000
Nop10	ENSMUSG00000027133	NOP10 ribonucleoprotein	-2.225	0.0000	0.0000	-1.869	0.0000	0.0000
Nos3	ENSMUSG00000028978	nitric oxide synthase 3, endothelial cell	-1.916	0.0000	0.0000	-1.599	0.0000	0.0000
Nosip	ENSMUSG00000003421	nitric oxide synthase interacting protein	-2.025	0.0000	0.0000	-1.705	0.0000	0.0000
Notch1	ENSMUSG00000026923	notch 1	-1.639	0.0000	0.0000	-1.509	0.0002	0.0007
Npdc1	ENSMUSG00000015094	neural proliferation, differentiation and control 1	-2.396	0.0000	0.0000	-1.917	0.0000	0.0000
Npepl1	ENSMUSG00000039263	aminopeptidase-like 1	-1.758	0.0000	0.0000	-1.601	0.0000	0.0000
Nphp4	ENSMUSG00000039577	nephronophthisis 4 (juvenile) homolog (human)	-2.468	0.0098	0.0236	-2.302	0.0246	0.0571
Nprl2	ENSMUSG00000010057	NPR2 like, GATOR1 complex subunit	-3.957	0.0000	0.0000	-3.775	0.0000	0.0000
Nprl3	ENSMUSG00000020289	nitrogen permease regulator-like 3	-2.408	0.0000	0.0000	-1.827	0.0000	0.0000
Nr0b2	ENSMUSG00000037583	nuclear receptor subfamily 0, group B, member 2	-3.954	0.0000	0.0000	-3.449	0.0000	0.0000
Nr1d1	ENSMUSG00000020889	nuclear receptor subfamily 1, group D, member 1	-1.668	0.0002	0.0007	-1.638	0.0003	0.0012
Nr1h2	ENSMUSG00000060601	nuclear receptor subfamily 1, group H, member 2	-3.508	0.0000	0.0000	-2.560	0.0000	0.0000
Nr4a1	ENSMUSG00000023034	nuclear receptor subfamily 4, group A, member 1	-1.825	0.0072	0.0179	-1.742	0.0130	0.0330
Nradd	ENSMUSG00000032491	neurotrophin receptor associated death domain	-2.016	0.0368	0.0743	-1.985	0.0458	0.0962
Nrbf2	ENSMUSG00000075000	nuclear receptor binding factor 2	-2.849	0.0000	0.0000	-2.141	0.0001	0.0004
Nrm	ENSMUSG00000059791	nurim (nuclear envelope membrane protein)	-2.808	0.0000	0.0000	-4.443	0.0000	0.0000
Nrros	ENSMUSG00000052384	negative regulator of reactive oxygen species	-2.391	0.0000	0.0002	-2.118	0.0004	0.0015
Nsdhl	ENSMUSG00000031349	NAD(P) dependent steroid dehydrogenase-like	-1.777	0.0000	0.0000	-2.097	0.0000	0.0000
Nsun5	ENSMUSG00000000916	NOL1/NOP2/Sun domain family, member 5	-2.322	0.0000	0.0000	-2.189	0.0000	0.0000
Ntan1	ENSMUSG00000022681	N-terminal Asn amidase	-1.673	0.0000	0.0000	-1.730	0.0000	0.0000
Ntmt1	ENSMUSG00000026857	N-terminal Xaa-Pro-Lys N-methyltransferase 1	-1.873	0.0000	0.0000	-1.613	0.0000	0.0000
Ntsr2	ENSMUSG00000020591	neurotensin receptor 2	-2.187	0.0000	0.0000	-1.756	0.0006	0.0021
Nudt14	ENSMUSG00000002804	nudix (nucleoside diphosphate linked moiety X)-type motif 14	-2.616	0.0000	0.0000	-1.990	0.0000	0.0000
Nudt17	ENSMUSG00000028100	nudix (nucleoside diphosphate linked moiety X)-type motif 17	-2.766	0.0000	0.0000	-2.197	0.0000	0.0000
Nudt19	ENSMUSG00000034875	nudix (nucleoside diphosphate linked moiety X)-type motif 19	-1.994	0.0000	0.0000	-2.113	0.0000	0.0000
Nudt2	ENSMUSG00000028443	nudix (nucleoside diphosphate linked moiety X)-type motif 2	-3.935	0.0000	0.0000	-3.005	0.0000	0.0000
Nudt22	ENSMUSG00000037349	nudix (nucleoside diphosphate linked moiety X)-type motif 22	-2.484	0.0000	0.0000	-2.072	0.0000	0.0000
Nup133	ENSMUSG00000039509	nucleoporin 133	-1.666	0.0000	0.0000	-1.638	0.0000	0.0000
Nup188	ENSMUSG00000052533	nucleoporin 188	-1.944	0.0000	0.0000	-1.796	0.0000	0.0000
Nupr1l	ENSMUSG00000095789	nuclear protein transcriptional regulator 1 like	-6.496	0.0013	0.0039	-3.208	0.0278	0.0634
Nxpe3	ENSMUSG00000075033	neurexophilin and PC-esterase domain family, member 3	-1.735	0.0002	0.0008	-1.809	0.0001	0.0006
Oas2	ENSMUSG00000032690	2'-5' oligoadenylate synthetase 2	-1.897	0.0186	0.0412	-1.721	0.0477	0.0994
Oaz1	ENSMUSG00000035242	ornithine decarboxylase antizyme 1	-1.750	0.0000	0.0000	-1.575	0.0000	0.0000
Oaz2-ps	ENSMUSG00000083610	ornithine decarboxylase antizyme 2, pseudogene	-4.232	0.0000	0.0000	-3.306	0.0000	0.0000
Ogdhl	ENSMUSG00000021913	oxoglutarate dehydrogenase-like	-2.159	0.0000	0.0000	-1.613	0.0008	0.0029
Ogg1	ENSMUSG00000030271	8-oxoguanine DNA-glycosylase 1	-2.129	0.0000	0.0000	-2.243	0.0000	0.0000
Ogn	ENSMUSG00000021390	osteoglycin	-1.595	0.0014	0.0041	-1.786	0.0001	0.0003

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Olfml1	ENSMUSG00000051041	olfactomedin-like 1	-1.764	0.0072	0.0179	-1.554	0.0384	0.0832
Olfml2a	ENSMUSG00000046618	olfactomedin-like 2A	-1.790	0.0001	0.0003	-1.529	0.0042	0.0123
Olfr78	ENSMUSG00000043366	olfactory receptor 78	-2.660	0.0006	0.0021	-2.060	0.0116	0.0299
Orc5	ENSMUSG00000029012	origin recognition complex, subunit 5	-1.927	0.0000	0.0000	-2.025	0.0000	0.0000
Ormdl2	ENSMUSG00000025353	ORM1-like 2 (S. cerevisiae)	-2.004	0.0000	0.0000	-2.104	0.0000	0.0000
Osbpl5	ENSMUSG00000037606	oxysterol binding protein-like 5	-1.612	0.0001	0.0004	-1.650	0.0001	0.0003
Osgepl1	ENSMUSG00000026096	O-sialoglycoprotein endopeptidase-like 1	-2.146	0.0000	0.0000	-2.542	0.0000	0.0000
Osgin1	ENSMUSG00000074063	oxidative stress induced growth inhibitor 1	-3.014	0.0001	0.0003	-2.477	0.0011	0.0038
Osmr	ENSMUSG00000022146	oncostatin M receptor	-1.745	0.0003	0.0009	-1.996	0.0000	0.0000
Osr1	ENSMUSG00000048387	odd-skipped related transcription factor 1	-2.861	0.0000	0.0001	-2.079	0.0025	0.0077
Oxld1	ENSMUSG00000039670	oxidoreductase like domain containing 1	-2.124	0.0000	0.0000	-1.587	0.0000	0.0000
P2ry14	ENSMUSG00000036381	purinergic receptor P2Y, G-protein coupled, 14	-2.281	0.0000	0.0000	-2.089	0.0000	0.0000
P2ry6	ENSMUSG00000048779	pyrimidinergic receptor P2Y, G-protein coupled, 6	-2.467	0.0001	0.0003	-1.993	0.0025	0.0078
P3h1	ENSMUSG00000028641	prolyl 3-hydroxylase 1	-1.887	0.0000	0.0000	-2.019	0.0000	0.0000
Pacc1	ENSMUSG00000026627	proton activated chloride channel 1	-1.851	0.0000	0.0001	-1.853	0.0000	0.0001
Pafah2	ENSMUSG00000037366	platelet-activating factor acetylhydrolase 2	-1.654	0.0000	0.0002	-1.557	0.0003	0.0013
Pah	ENSMUSG00000020051	phenylalanine hydroxylase	-5.309	0.0000	0.0000	-2.529	0.0001	0.0005
Pam16	ENSMUSG00000014301	presequence translocase-asssociated motor 16	-3.436	0.0000	0.0000	-2.996	0.0000	0.0000
Pank4	ENSMUSG00000029056	pantothenate kinase 4	-1.717	0.0000	0.0000	-1.660	0.0000	0.0000
Pard6a	ENSMUSG00000005699	par-6 family cell polarity regulator alpha	-2.296	0.0000	0.0000	-2.140	0.0000	0.0000
Parp16	ENSMUSG00000032392	poly (ADP-ribose) polymerase family, member 16	-1.863	0.0000	0.0000	-1.887	0.0000	0.0000
Pars2	ENSMUSG00000043572	prolyl-tRNA synthetase (mitochondrial)(putative)	-1.556	0.0009	0.0028	-1.697	0.0001	0.0004
Parvb	ENSMUSG00000022438	parvin, beta	-1.525	0.0000	0.0000	-1.515	0.0000	0.0000
Patz1	ENSMUSG00000020453	POZ (BTB) and AT hook containing zinc finger 1	-1.836	0.0000	0.0001	-1.550	0.0022	0.0069
Paxx	ENSMUSG00000047617	non-homologous end joining factor	-2.706	0.0000	0.0000	-2.645	0.0000	0.0000
Pcdhga10	ENSMUSG00000102222	protocadherin gamma subfamily A, 10	-1.877	0.0000	0.0001	-2.469	0.0000	0.0000
Pcdhga2	ENSMUSG00000103332	protocadherin gamma subfamily A, 2	-1.967	0.0000	0.0000	-2.601	0.0000	0.0000
Pcdhga3	ENSMUSG00000104346	protocadherin gamma subfamily A, 3	-1.744	0.0056	0.0144	-1.823	0.0049	0.0140
Pcdhga5	ENSMUSG00000103567	protocadherin gamma subfamily A, 5	-1.895	0.0003	0.0011	-1.677	0.0039	0.0117
Pcolce	ENSMUSG00000029718	procollagen C-endopeptidase enhancer protein	-2.265	0.0000	0.0000	-1.739	0.0019	0.0062
Pcsk4	ENSMUSG00000020131	proprotein convertase subtilisin/kexin type 4	-1.906	0.0010	0.0032	-1.883	0.0032	0.0098
Pde1b	ENSMUSG00000022489	phosphodiesterase 1B, Ca2+-calmodulin dependent	-1.518	0.0096	0.0231	-1.569	0.0079	0.0215
Pdf	ENSMUSG00000078931	peptide deformylase (mitochondrial)	-4.223	0.0000	0.0000	-5.652	0.0000	0.0000
Pdgfrb	ENSMUSG00000024620	platelet derived growth factor receptor, beta polypeptide	-2.002	0.0000	0.0000	-1.741	0.0000	0.0000
Pdgfrl	ENSMUSG00000031595	platelet-derived growth factor receptor-like	-3.206	0.0000	0.0000	-2.398	0.0002	0.0010
Pdia5	ENSMUSG00000022844	protein disulfide isomerase associated 5	-2.056	0.0003	0.0010	-1.667	0.0103	0.0269
Pdk2	ENSMUSG00000038967	pyruvate dehydrogenase kinase, isoenzyme 2	-2.008	0.0000	0.0000	-1.693	0.0000	0.0000
Pdk3	ENSMUSG00000035232	pyruvate dehydrogenase kinase, isoenzyme 3	-1.660	0.0059	0.0150	-1.905	0.0012	0.0041
Pdlim1	ENSMUSG00000055044	PDZ and LIM domain 1 (elfin)	-1.734	0.0000	0.0000	-1.765	0.0000	0.0000
Pdlim4	ENSMUSG00000020388	PDZ and LIM domain 4	-2.595	0.0000	0.0000	-2.433	0.0000	0.0000
Pdlim7	ENSMUSG00000021493	PDZ and LIM domain 7	-1.535	0.0000	0.0000	-1.675	0.0000	0.0000
Pear1	ENSMUSG00000028073	platelet endothelial aggregation receptor 1	-2.402	0.0000	0.0000	-2.069	0.0000	0.0000
Pebp1	ENSMUSG00000032959	phosphatidylethanolamine binding protein 1	-1.972	0.0000	0.0000	-1.755	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Pef1	ENSMUSG00000028779	penta-EF hand domain containing 1	-2.377	0.0000	0.0000	-1.903	0.0000	0.0000
Pemt	ENSMUSG00000000301	phosphatidylethanolamine N-methyltransferase	-2.216	0.0022	0.0061	-5.229	0.0000	0.0000
Penk	ENSMUSG00000045573	preproenkephalin	-1.707	0.0012	0.0035	-1.632	0.0029	0.0090
Pex10	ENSMUSG00000029047	peroxisomal biogenesis factor 10	-2.807	0.0000	0.0000	-2.478	0.0000	0.0000
Pf4	ENSMUSG00000029373	platelet factor 4	-2.497	0.0009	0.0027	-2.111	0.0067	0.0186
Pfkfb1	ENSMUSG00000025271	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 1	-2.055	0.0010	0.0031	-1.862	0.0045	0.0131
Pfkfb4	ENSMUSG00000025648	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4	-3.166	0.0000	0.0000	-1.917	0.0000	0.0000
Pgam1	ENSMUSG00000011752	phosphoglycerate mutase 1	-2.911	0.0000	0.0000	-2.284	0.0000	0.0000
Pgam2	ENSMUSG00000020475	phosphoglycerate mutase 2	-2.164	0.0000	0.0000	-1.786	0.0000	0.0000
Pgap6	ENSMUSG00000024180	post-glycosylphosphatidylinositol attachment to proteins 6	-2.778	0.0000	0.0000	-2.494	0.0000	0.0000
Pgls	ENSMUSG00000031807	6-phosphogluconolactonase	-5.672	0.0000	0.0000	-4.524	0.0000	0.0000
Pgrmc1	ENSMUSG00000006373	progesterone receptor membrane component 1	-1.581	0.0000	0.0000	-1.534	0.0000	0.0000
Pheta1	ENSMUSG00000044134	PH domain containing endocytic trafficking adaptor 1	-1.848	0.0000	0.0000	-1.727	0.0000	0.0000
Phf7	ENSMUSG00000021902	PHD finger protein 7	-1.805	0.0002	0.0006	-1.657	0.0016	0.0052
Phkg2	ENSMUSG00000030815	phosphorylase kinase, gamma 2 (testis)	-1.877	0.0000	0.0000	-1.640	0.0002	0.0008
Pias3	ENSMUSG00000028101	protein inhibitor of activated STAT 3	-2.026	0.0000	0.0000	-2.037	0.0000	0.0000
Pias4	ENSMUSG00000004934	protein inhibitor of activated STAT 4	-1.668	0.0003	0.0011	-1.675	0.0003	0.0012
Pidd1	ENSMUSG00000025507	p53 induced death domain protein 1	-2.001	0.0067	0.0169	-2.070	0.0105	0.0273
Pierce2	ENSMUSG00000086158	piercer of microtubule wall 2	-2.215	0.0000	0.0000	-2.514	0.0000	0.0000
Pigf	ENSMUSG00000024145	phosphatidylinositol glycan anchor biosynthesis, class F	-2.007	0.0001	0.0002	-2.110	0.0001	0.0004
Pigo	ENSMUSG00000028454	phosphatidylinositol glycan anchor biosynthesis, class O	-2.338	0.0000	0.0000	-2.125	0.0000	0.0000
Pigp	ENSMUSG00000022940	phosphatidylinositol glycan anchor biosynthesis, class P	-1.774	0.0000	0.0000	-1.634	0.0000	0.0000
Pigq	ENSMUSG00000025728	phosphatidylinositol glycan anchor biosynthesis, class Q	-1.787	0.0000	0.0000	-1.615	0.0000	0.0000
Pigs	ENSMUSG00000041958	phosphatidylinositol glycan anchor biosynthesis, class S	-1.844	0.0000	0.0000	-1.796	0.0000	0.0000
Pigt	ENSMUSG00000017721	phosphatidylinositol glycan anchor biosynthesis, class T	-2.397	0.0000	0.0000	-1.940	0.0000	0.0000
Pigv	ENSMUSG00000043257	phosphatidylinositol glycan anchor biosynthesis, class V	-2.035	0.0000	0.0000	-1.770	0.0000	0.0000
Pih1d1	ENSMUSG00000003423	PIH1 domain containing 1	-2.050	0.0000	0.0000	-1.811	0.0000	0.0000
Pik3r6	ENSMUSG00000046207	phosphoinositide-3-kinase regulatory subunit 5	-1.721	0.0001	0.0003	-1.709	0.0001	0.0005
Pin1	ENSMUSG00000032171	peptidyl-prolyl cis/trans isomerase, NIMA-interacting 1	-2.095	0.0000	0.0000	-1.875	0.0000	0.0000
Pip4p2	ENSMUSG00000028221	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 2	-1.692	0.0000	0.0000	-1.798	0.0000	0.0000
Pip5k1b	ENSMUSG00000024867	phosphatidylinositol-4-phosphate 5-kinase, type 1 beta	-1.776	0.0000	0.0000	-2.008	0.0000	0.0000
Pira12	ENSMUSG00000074417	paired-Ig-like receptor A12	-2.560	0.0105	0.0252	-7.611	0.0000	0.0002
Pitpnm1	ENSMUSG00000024851	phosphatidylinositol transfer protein, membrane-associated 1	-2.458	0.0000	0.0000	-2.070	0.0000	0.0000
Pkd1	ENSMUSG00000032855	polycystin 1, transient receptor potential channel interacting	-1.810	0.0000	0.0000	-1.619	0.0000	0.0000
Pkmyt1	ENSMUSG00000023908	protein kinase, membrane associated tyrosine/threonine 1	-2.569	0.0095	0.0229	-2.056	0.0380	0.0825
Pla1a	ENSMUSG00000002847	phospholipase A1 member A	-1.590	0.0004	0.0012	-1.556	0.0008	0.0027
Pla2g4e	ENSMUSG00000050211	phospholipase A2, group IVE	-1.727	0.0195	0.0430	-1.815	0.0113	0.0291
Pla2g6	ENSMUSG00000042632	phospholipase A2, group VI	-1.881	0.0000	0.0000	-1.565	0.0000	0.0001
Plb1	ENSMUSG00000029134	phospholipase B1	-2.118	0.0018	0.0053	-1.934	0.0135	0.0341
Plcd1	ENSMUSG00000010660	phospholipase C, delta 1	-2.170	0.0000	0.0000	-1.662	0.0000	0.0000
Pld3	ENSMUSG00000003363	phospholipase D family, member 3	-3.514	0.0000	0.0000	-2.689	0.0000	0.0000
Pld4	ENSMUSG00000052160	phospholipase D family, member 4	-2.962	0.0000	0.0000	-1.855	0.0002	0.0007
Plekhg2	ENSMUSG00000037552	pleckstrin homology domain containing, family G (with RhoGef domain) member 2	-2.099	0.0000	0.0000	-1.823	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Plekhm1	ENSMUSG00000034247	pleckstrin homology domain containing, family M (with RUN domain) member 1	-2.007	0.0000	0.0000	-1.616	0.0009	0.0032
Plekho1	ENSMUSG00000015745	pleckstrin homology domain containing, family O member 1	-2.602	0.0000	0.0000	-2.294	0.0000	0.0000
Plet1	ENSMUSG00000032068	placenta expressed transcript 1	-2.946	0.0072	0.0179	-3.063	0.0061	0.0171
Plin4	ENSMUSG00000002831	perilipin 4	-1.977	0.0020	0.0058	-1.769	0.0098	0.0259
Plk5	ENSMUSG00000035486	polo like kinase 5	-4.296	0.0000	0.0000	-2.007	0.0008	0.0029
Pln	ENSMUSG00000038583	phospholamban	-1.679	0.0000	0.0000	-1.741	0.0000	0.0000
Plod1	ENSMUSG00000019055	procollagen-lysine, 2-oxoglutarate 5-dioxygenase 1	-1.572	0.0000	0.0000	-1.506	0.0000	0.0000
Plp2	ENSMUSG00000031146	proteolipid protein 2	-2.962	0.0000	0.0000	-2.360	0.0000	0.0000
Plpbp	ENSMUSG00000031485	pyridoxal phosphate binding protein	-2.415	0.0000	0.0000	-2.191	0.0000	0.0000
Plpp1	ENSMUSG00000021759	phospholipid phosphatase 1	-1.742	0.0000	0.0000	-1.846	0.0000	0.0000
Plpp5	ENSMUSG00000031570	phospholipid phosphatase 5	-1.586	0.0003	0.0010	-1.805	0.0000	0.0000
Plpp7	ENSMUSG00000051373	phospholipid phosphatase 7 (inactive)	-2.204	0.0000	0.0000	-1.632	0.0000	0.0000
Plscr2	ENSMUSG00000032372	phospholipid scramblase 2	-1.707	0.0000	0.0000	-1.544	0.0000	0.0002
Pltp	ENSMUSG00000017754	phospholipid transfer protein	-2.821	0.0000	0.0000	-2.426	0.0000	0.0000
Plxnb2	ENSMUSG00000036606	plexin B2	-2.173	0.0000	0.0000	-1.871	0.0000	0.0000
Plxnb3	ENSMUSG00000031385	plexin B3	-2.621	0.0000	0.0000	-1.707	0.0001	0.0004
Plxnd1	ENSMUSG00000030123	plexin D1	-1.888	0.0000	0.0000	-1.845	0.0000	0.0000
Pmf1	ENSMUSG00000028066	polyamine-modulated factor 1	-2.402	0.0000	0.0000	-1.984	0.0000	0.0000
Pnck	ENSMUSG00000002012	pregnancy upregulated non-ubiquitously expressed CaM kinase	-2.170	0.0000	0.0000	-1.620	0.0000	0.0001
Pnkd	ENSMUSG00000026179	paroxysmal nonkinesiogenic dyskinesia	-1.916	0.0000	0.0000	-1.671	0.0000	0.0000
Pnp	ENSMUSG00000115338	purine-nucleoside phosphorylase	-2.409	0.0000	0.0000	-1.809	0.0013	0.0045
Pnpla3	ENSMUSG00000041653	patatin-like phospholipase domain containing 3	-4.418	0.0003	0.0010	-5.260	0.0003	0.0011
Pnpo	ENSMUSG00000018659	pyridoxine 5'-phosphate oxidase	-2.937	0.0000	0.0000	-2.138	0.0000	0.0000
Poc1a	ENSMUSG00000023345	POC1 centriolar protein A	-2.093	0.0000	0.0001	-1.648	0.0055	0.0157
Pola2	ENSMUSG00000024833	polymerase (DNA directed), alpha 2	-2.925	0.0000	0.0000	-2.549	0.0000	0.0000
Pold1	ENSMUSG00000038644	polymerase (DNA directed), delta 1, catalytic subunit	-2.192	0.0000	0.0000	-1.524	0.0000	0.0002
Pold2	ENSMUSG00000020471	polymerase (DNA directed), delta 2, regulatory subunit	-2.396	0.0000	0.0000	-1.813	0.0000	0.0000
Pold4	ENSMUSG00000024854	polymerase (DNA-directed), delta 4	-4.686	0.0000	0.0000	-2.591	0.0000	0.0000
Pole	ENSMUSG00000007080	polymerase (DNA directed), epsilon	-1.690	0.0084	0.0205	-1.751	0.0065	0.0180
Polg2	ENSMUSG00000020718	polymerase (DNA directed), gamma 2, accessory subunit	-1.875	0.0000	0.0001	-1.616	0.0012	0.0041
Polm	ENSMUSG00000020474	polymerase (DNA directed), mu	-2.159	0.0000	0.0000	-3.136	0.0000	0.0000
Poln	ENSMUSG00000045102	DNA polymerase N	-3.178	0.0000	0.0000	-1.833	0.0157	0.0389
Polr1b	ENSMUSG00000027395	polymerase (RNA) I polypeptide B	-1.944	0.0000	0.0000	-2.074	0.0000	0.0000
Polr1d	ENSMUSG00000029642	polymerase (RNA) I polypeptide D	-2.094	0.0000	0.0000	-2.236	0.0000	0.0000
Polr2c	ENSMUSG00000031783	polymerase (RNA) II (DNA directed) polypeptide C	-2.849	0.0000	0.0000	-2.561	0.0000	0.0000
Polr2d	ENSMUSG00000024258	polymerase (RNA) II (DNA directed) polypeptide D	-2.061	0.0000	0.0000	-1.854	0.0000	0.0000
Polr2e	ENSMUSG00000004667	polymerase (RNA) II (DNA directed) polypeptide E	-2.515	0.0000	0.0000	-1.888	0.0000	0.0000
Polr2i	ENSMUSG00000019738	polymerase (RNA) II (DNA directed) polypeptide I	-2.195	0.0000	0.0000	-2.064	0.0000	0.0000
Polr2l	ENSMUSG00000038489	polymerase (RNA) II (DNA directed) polypeptide L	-2.354	0.0000	0.0000	-2.141	0.0000	0.0000
Pop4	ENSMUSG00000030423	processing of precursor 4, ribonuclease P/MRP family, (S. cerevisiae)	-2.712	0.0000	0.0000	-2.399	0.0000	0.0000
Pop7	ENSMUSG00000029715	processing of precursor 7, ribonuclease P family, (S. cerevisiae)	-2.823	0.0000	0.0000	-2.275	0.0000	0.0000
Ppia	ENSMUSG00000071866	peptidylprolyl isomerase A	-1.531	0.0000	0.0000	-1.651	0.0000	0.0000
Ppif	ENSMUSG00000021868	peptidylprolyl isomerase F (cyclophilin F)	-2.011	0.0000	0.0000	-1.674	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ppil2	ENSMUSG00000022771	peptidylprolyl isomerase (cyclophilin)-like 2	-2.000	0.0000	0.0000	-1.778	0.0000	0.0000
Ppp2r3d	ENSMUSG00000093803	protein phosphatase 2 (formerly 2A), regulatory subunit B", delta	-2.044	0.0000	0.0000	-1.961	0.0000	0.0000
Pqlc3	ENSMUSG00000045679	PQ loop repeat containing	-2.573	0.0014	0.0043	-2.553	0.0020	0.0063
Praf2	ENSMUSG00000031149	PRA1 domain family 2	-4.451	0.0000	0.0000	-4.008	0.0000	0.0000
Prdm5	ENSMUSG00000029913	PR domain containing 5	-1.566	0.0018	0.0052	-1.572	0.0018	0.0057
Prdx2	ENSMUSG00000005161	peroxiredoxin 2	-2.680	0.0000	0.0000	-2.506	0.0000	0.0000
Prdx2-ps1	ENSMUSG00000082431	peroxiredoxin 2, pseudogene 1	-11.154	0.0000	0.0000	-10.469	0.0000	0.0000
Prdx4	ENSMUSG00000025289	peroxiredoxin 4	-2.032	0.0000	0.0000	-1.818	0.0000	0.0000
Prickle3	ENSMUSG00000031145	prickle planar cell polarity protein 3	-1.921	0.0002	0.0008	-1.795	0.0009	0.0032
Prkag3	ENSMUSG00000006542	protein kinase, AMP-activated, gamma 3 non-catalytic subunit	-1.501	0.0411	0.0818	-1.690	0.0099	0.0261
Prkcz	ENSMUSG00000029053	protein kinase C, zeta	-3.208	0.0000	0.0000	-1.609	0.0005	0.0020
Prkd2	ENSMUSG00000041187	protein kinase D2	-1.932	0.0000	0.0000	-1.676	0.0003	0.0013
Prkra	ENSMUSG00000002731	protein kinase, interferon inducible double stranded RNA dependent activator	-2.040	0.0000	0.0000	-1.711	0.0000	0.0000
Prnp	ENSMUSG00000079037	prion protein	-1.939	0.0000	0.0000	-1.656	0.0000	0.0000
Proscos	ENSMUSG00000091154	proline synthetase co-transcribed, opposite strand	-2.138	0.0000	0.0001	-1.833	0.0003	0.0010
Proser3	ENSMUSG00000036864	proline and serine rich 3	-2.230	0.0001	0.0004	-2.562	0.0000	0.0000
Prpf8	ENSMUSG00000020850	pre-mRNA processing factor 8	-1.567	0.0000	0.0000	-1.538	0.0000	0.0000
Prpsap1	ENSMUSG00000015869	phosphoribosyl pyrophosphate synthetase-associated protein 1	-2.431	0.0000	0.0000	-1.892	0.0000	0.0000
Prpsap2	ENSMUSG00000020528	phosphoribosyl pyrophosphate synthetase-associated protein 2	-1.501	0.0132	0.0306	-1.830	0.0003	0.0012
Prrg2	ENSMUSG00000007837	proline-rich Gla (G-carboxyglutamic acid) polypeptide 2	-2.089	0.0000	0.0000	-1.665	0.0001	0.0003
Prss36	ENSMUSG00000070371	protease, serine 36	-2.455	0.0000	0.0000	-2.052	0.0000	0.0000
Psenen	ENSMUSG00000036835	presenilin enhancer gamma secretase subunit	-2.743	0.0000	0.0000	-2.924	0.0000	0.0000
Psenen-ps	ENSMUSG00000056412	presenilin enhancer gamma secretase subunit, pseudogene	-3.771	0.0228	0.0493	-19.097	0.0015	0.0049
Psmb3	ENSMUSG00000069744	proteasome (prosome, macropain) subunit, beta type 3	-1.790	0.0000	0.0000	-1.703	0.0000	0.0000
Psmd5	ENSMUSG00000026869	proteasome (prosome, macropain) 26S subunit, non-ATPase, 5	-1.565	0.0000	0.0000	-1.606	0.0000	0.0000
Psmd8	ENSMUSG00000030591	proteasome (prosome, macropain) 26S subunit, non-ATPase, 8	-1.623	0.0000	0.0000	-1.550	0.0000	0.0000
Psmf1	ENSMUSG00000032869	proteasome (prosome, macropain) inhibitor subunit 1	-2.152	0.0000	0.0000	-2.015	0.0000	0.0000
Psmg2	ENSMUSG00000024537	proteasome (prosome, macropain) assembly chaperone 2	-2.099	0.0000	0.0000	-2.341	0.0000	0.0000
Psmg3	ENSMUSG00000029551	proteasome (prosome, macropain) assembly chaperone 3	-2.645	0.0000	0.0000	-2.236	0.0000	0.0001
Ptbp1	ENSMUSG00000006498	polypyrimidine tract binding protein 1	-2.114	0.0000	0.0000	-2.023	0.0000	0.0000
Ptcd1	ENSMUSG00000029624	pentatricopeptide repeat domain 1	-1.864	0.0000	0.0002	-1.791	0.0001	0.0005
Ptpn18	ENSMUSG00000026126	protein tyrosine phosphatase, non-receptor type 18	-1.643	0.0362	0.0733	-3.200	0.0000	0.0000
Ptprn	ENSMUSG00000026204	protein tyrosine phosphatase, receptor type, N	-2.038	0.0006	0.0020	-1.628	0.0185	0.0446
Ptprv	ENSMUSG00000097993	protein tyrosine phosphatase, receptor type, V	-3.838	0.0029	0.0081	-7.149	0.0007	0.0024
Ptrhd1	ENSMUSG00000096199	peptidyl-tRNA hydrolase domain containing 1	-1.761	0.0000	0.0000	-1.760	0.0000	0.0000
Pvr	ENSMUSG00000040511	poliovirus receptor	-1.762	0.0000	0.0000	-1.858	0.0000	0.0000
Pxdn	ENSMUSG00000020674	peroxidasin	-1.808	0.0000	0.0000	-1.839	0.0000	0.0000
Pxmp4	ENSMUSG00000000876	peroxisomal membrane protein 4	-1.712	0.0000	0.0000	-1.720	0.0000	0.0000
Pycrl	ENSMUSG00000022571	pyrroline-5-carboxylate reductase-like	-2.254	0.0000	0.0000	-2.191	0.0000	0.0000
Pyroxd2	ENSMUSG00000060224	pyridine nucleotide-disulphide oxidoreductase domain 2	-2.789	0.0000	0.0000	-2.631	0.0000	0.0000
Pyurf	ENSMUSG00000043162	Pigy upstream reading frame	-1.587	0.0000	0.0000	-1.883	0.0000	0.0000
Pzp	ENSMUSG00000030359	PZP, alpha-2-macroglobulin like	-2.522	0.0083	0.0202	-2.234	0.0245	0.0569
Qpct	ENSMUSG00000024084	glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	-1.823	0.0001	0.0003	-1.662	0.0009	0.0032

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rab11b-ps2	ENSMUSG00000095690	RAB11B, member RAS oncogene family, pseudogene 2	-2.884	0.0000	0.0000	-2.483	0.0000	0.0000
Rab1b	ENSMUSG00000024870	RAB1B, member RAS oncogene family	-1.762	0.0000	0.0000	-1.500	0.0000	0.0000
Rab20	ENSMUSG00000031504	RAB20, member RAS oncogene family	-1.862	0.0000	0.0000	-1.672	0.0000	0.0000
Rab36	ENSMUSG00000020175	RAB36, member RAS oncogene family	-4.149	0.0000	0.0000	-1.991	0.0209	0.0496
Rab3a	ENSMUSG00000031840	RAB3A, member RAS oncogene family	-2.054	0.0000	0.0000	-1.943	0.0000	0.0000
Rab3il1	ENSMUSG00000024663	RAB3A interacting protein (rabin3)-like 1	-1.790	0.0041	0.0109	-1.505	0.0448	0.0943
Rab42	ENSMUSG00000089687	RAB42, member RAS oncogene family	-3.867	0.0001	0.0003	-2.304	0.0114	0.0295
Rabac1	ENSMUSG00000003380	Rab acceptor 1 (prenylated)	-2.384	0.0000	0.0000	-2.065	0.0000	0.0000
Rabggta	ENSMUSG00000040472	Rab geranylgeranyl transferase, a subunit	-2.370	0.0000	0.0000	-2.043	0.0000	0.0000
Rabif	ENSMUSG00000042229	RAB interacting factor	-1.666	0.0118	0.0277	-1.617	0.0178	0.0433
Rabl2	ENSMUSG00000022621	RAB, member RAS oncogene family-like 2	-3.894	0.0000	0.0000	-2.109	0.0006	0.0023
Rack1	ENSMUSG00000020372	receptor for activated C kinase 1	-3.712	0.0000	0.0000	-3.337	0.0000	0.0000
Rad9a	ENSMUSG00000024824	RAD9 checkpoint clamp component A	-1.840	0.0000	0.0000	-1.627	0.0000	0.0001
Radil	ENSMUSG00000029576	Ras association and DIL domains	-1.884	0.0003	0.0011	-1.589	0.0094	0.0248
Ralgds	ENSMUSG00000026821	ral guanine nucleotide dissociation stimulator	-1.588	0.0000	0.0000	-1.621	0.0000	0.0000
Ramp3	ENSMUSG00000041046	receptor (calcitonin) activity modifying protein 3	-1.939	0.0000	0.0000	-1.520	0.0029	0.0090
Rap1gapos	ENSMUSG00000087476	RAP1 GTPase activating protein, opposite strand	-3.243	0.0005	0.0017	-3.287	0.0009	0.0033
Rarres2	ENSMUSG00000009281	retinoic acid receptor responder (tazarotene induced) 2	-2.922	0.0000	0.0000	-2.108	0.0000	0.0000
Rasl12	ENSMUSG00000041696	RAS-like, family 12	-2.276	0.0000	0.0000	-2.628	0.0000	0.0000
Rbck1	ENSMUSG00000027466	RanBP-type and C3HC4-type zinc finger containing 1	-2.834	0.0000	0.0000	-2.430	0.0000	0.0000
Rbis	ENSMUSG00000078784	ribosomal biogenesis factor	-1.529	0.0003	0.0009	-1.550	0.0002	0.0008
Rbx1-ps	ENSMUSG00000049832	ring-box 1, pseudogene	-4.941	0.0000	0.0001	-3.449	0.0005	0.0018
Rce1	ENSMUSG00000024889	Ras converting CAAX endopeptidase 1	-2.638	0.0000	0.0000	-1.803	0.0000	0.0000
Rcl1	ENSMUSG00000024785	RNA terminal phosphate cyclase-like 1	-2.012	0.0000	0.0000	-1.667	0.0000	0.0000
Rdh13	ENSMUSG00000008435	retinol dehydrogenase 13 (all-trans and 9-cis)	-1.505	0.0000	0.0001	-1.558	0.0000	0.0000
Rdm1	ENSMUSG00000010362	RAD52 motif 1	-1.851	0.0000	0.0000	-1.636	0.0000	0.0000
Reep4	ENSMUSG00000033589	receptor accessory protein 4	-1.603	0.0166	0.0374	-1.856	0.0026	0.0082
Reep6	ENSMUSG00000035504	receptor accessory protein 6	-2.458	0.0000	0.0000	-1.780	0.0005	0.0017
Relb	ENSMUSG00000002983	avian reticuloendotheliosis viral (v-rel) oncogene related B	-1.620	0.0001	0.0003	-1.507	0.0009	0.0032
Rem1	ENSMUSG00000000359	rad and gem related GTP binding protein 1	-1.703	0.0008	0.0025	-1.582	0.0039	0.0116
Rer1	ENSMUSG00000029048	retention in endoplasmic reticulum sorting receptor 1	-1.782	0.0000	0.0000	-1.886	0.0000	0.0000
Rfc5	ENSMUSG00000029363	replication factor C (activator 1) 5	-3.031	0.0000	0.0000	-2.098	0.0000	0.0000
Rgcc	ENSMUSG00000022018	regulator of cell cycle	-3.516	0.0000	0.0000	-2.766	0.0000	0.0000
Rgl3	ENSMUSG00000040146	ral guanine nucleotide dissociation stimulator-like 3	-1.793	0.0000	0.0000	-1.592	0.0000	0.0001
Rgs11	ENSMUSG00000024186	regulator of G-protein signaling 11	-2.899	0.0292	0.0610	-2.831	0.0394	0.0851
Rgs19	ENSMUSG00000002458	regulator of G-protein signaling 19	-2.403	0.0000	0.0000	-1.726	0.0028	0.0086
Rgs3	ENSMUSG00000059810	regulator of G-protein signaling 3	-1.673	0.0000	0.0000	-1.503	0.0000	0.0002
Rhbdd1	ENSMUSG00000026142	rhomboid domain containing 1	-1.601	0.0000	0.0000	-1.543	0.0000	0.0000
Rhbdd2	ENSMUSG00000039917	rhomboid domain containing 2	-1.969	0.0000	0.0000	-2.166	0.0000	0.0000
Rhbdd3	ENSMUSG00000034175	rhomboid domain containing 3	-2.248	0.0000	0.0000	-2.490	0.0000	0.0000
Rhbdf2	ENSMUSG00000020806	rhomboid 5 homolog 2	-2.347	0.0000	0.0000	-2.017	0.0000	0.0000
Rhd	ENSMUSG00000028825	Rh blood group, D antigen	-2.536	0.0000	0.0000	-1.670	0.0001	0.0004
Rhod	ENSMUSG00000041845	ras homolog family member D	-2.966	0.0000	0.0000	-3.370	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Ric8a	ENSMUSG00000025485	RIC8 guanine nucleotide exchange factor A	-1.955	0.0000	0.0000	-1.724	0.0000	0.0000
Rilp	ENSMUSG00000038195	Rab interacting lysosomal protein	-1.978	0.0000	0.0000	-1.821	0.0000	0.0000
Rimkla	ENSMUSG00000048899	ribosomal modification protein rimK-like family member A	-2.027	0.0088	0.0215	-2.165	0.0075	0.0205
Rimoc1	ENSMUSG00000041935	RAB7A interacting MON1-CCZ1 complex subunit 1	-1.559	0.0000	0.0001	-1.780	0.0000	0.0000
Rin1	ENSMUSG00000024883	Ras and Rab interactor 1	-1.824	0.0077	0.0191	-1.897	0.0075	0.0203
Ripk3	ENSMUSG00000022221	receptor-interacting serine-threonine kinase 3	-1.700	0.0035	0.0094	-1.570	0.0141	0.0355
Rita1	ENSMUSG00000029600	RBPJ interacting and tubulin associated 1	-1.978	0.0000	0.0000	-1.545	0.0004	0.0016
Rmnd5b	ENSMUSG00000001054	required for meiotic nuclear division 5 homolog B	-2.987	0.0000	0.0000	-2.793	0.0000	0.0000
Rnase4	ENSMUSG00000021876	ribonuclease, RNase A family 4	-1.885	0.0000	0.0001	-1.671	0.0005	0.0018
Rnf122	ENSMUSG00000039328	ring finger protein 122	-2.014	0.0000	0.0000	-1.747	0.0000	0.0000
Rnf123	ENSMUSG00000041528	ring finger protein 123	-1.563	0.0000	0.0000	-1.504	0.0000	0.0000
Rnf13	ENSMUSG00000036503	ring finger protein 13	-1.604	0.0000	0.0000	-1.712	0.0000	0.0000
Rnf135	ENSMUSG00000020707	ring finger protein 135	-1.640	0.0032	0.0086	-1.593	0.0062	0.0173
Rnf181	ENSMUSG00000055850	ring finger protein 181	-2.162	0.0000	0.0000	-1.913	0.0000	0.0000
Rnf225	ENSMUSG00000033967	ring finger protein 225	-11.142	0.0031	0.0086	-4.349	0.0156	0.0387
Rnf25	ENSMUSG00000026171	ring finger protein 25	-2.785	0.0000	0.0000	-2.548	0.0000	0.0000
Rnls	ENSMUSG00000071573	renalase, FAD-dependent amine oxidase	-1.779	0.0000	0.0000	-1.689	0.0000	0.0000
Rnpep	ENSMUSG00000041926	arginyl aminopeptidase (aminopeptidase B)	-1.866	0.0000	0.0000	-1.599	0.0000	0.0000
Robo4	ENSMUSG00000032125	roundabout guidance receptor 4	-1.868	0.0000	0.0000	-1.524	0.0001	0.0003
Romo1	ENSMUSG00000067847	reactive oxygen species modulator 1	-1.980	0.0000	0.0000	-2.063	0.0000	0.0000
Rpl10	ENSMUSG00000008682	ribosomal protein L10	-2.887	0.0000	0.0000	-3.071	0.0000	0.0000
Rpl10a	ENSMUSG00000037805	ribosomal protein L10A	-2.221	0.0000	0.0000	-2.518	0.0000	0.0000
Rpl10a-ps1	ENSMUSG00000084416	ribosomal protein L10A, pseudogene 1	-2.292	0.0009	0.0028	-1.904	0.0103	0.0270
Rpl12	ENSMUSG00000038900	ribosomal protein L12	-2.581	0.0000	0.0000	-2.534	0.0000	0.0000
Rpl13	ENSMUSG00000000740	ribosomal protein L13	-4.710	0.0000	0.0000	-4.407	0.0000	0.0000
Rpl19-ps11	ENSMUSG00000081094	ribosomal protein L19, pseudogene 11	-2.083	0.0004	0.0015	-2.568	0.0000	0.0001
Rpl21-ps8	ENSMUSG00000061684	ribosomal protein L21, pseudogene 8	-3.312	0.0152	0.0345	-9.268	0.0010	0.0033
Rpl22l1	ENSMUSG00000039221	ribosomal protein L22 like 1	-1.982	0.0000	0.0000	-2.216	0.0000	0.0000
Rpl26	ENSMUSG00000060938	ribosomal protein L26	-4.452	0.0000	0.0000	-4.663	0.0000	0.0000
Rpl27	ENSMUSG00000063316	ribosomal protein L27	-2.849	0.0000	0.0000	-2.885	0.0000	0.0000
Rpl29	ENSMUSG00000048758	ribosomal protein L29	-2.580	0.0000	0.0000	-2.386	0.0000	0.0000
Rpl3	ENSMUSG00000060036	ribosomal protein L3	-1.966	0.0000	0.0000	-2.041	0.0000	0.0000
Rpl31-ps8	ENSMUSG00000067870	ribosomal protein L31, pseudogene 8	-2.265	0.0054	0.0139	-2.127	0.0148	0.0370
Rpl32	ENSMUSG00000057841	ribosomal protein L32	-3.119	0.0000	0.0000	-2.832	0.0000	0.0000
Rpl34	ENSMUSG00000062006	ribosomal protein L34	-3.085	0.0000	0.0000	-2.724	0.0000	0.0000
Rpl34-ps1	ENSMUSG00000068396	ribosomal protein L34, pseudogene 1	-4.941	0.0000	0.0000	-5.177	0.0000	0.0000
Rpl34-ps2	ENSMUSG00000061669	ribosomal protein L34, pseudogene 2	-21.281	0.0011	0.0033	-33.605	0.0001	0.0006
Rpl35a	ENSMUSG00000060636	ribosomal protein L35A	-3.280	0.0000	0.0000	-3.426	0.0000	0.0000
Rpl36	ENSMUSG00000057863	ribosomal protein L36	-4.879	0.0000	0.0000	-4.184	0.0000	0.0000
Rpl36a	ENSMUSG00000079435	ribosomal protein L36A	-2.350	0.0000	0.0000	-2.912	0.0000	0.0000
Rpl36-ps12	ENSMUSG00000091845	ribosomal protein L36, pseudogene 12	-5.851	0.0065	0.0163	-9.458	0.0056	0.0158
Rpl37	ENSMUSG00000041841	ribosomal protein L37	-3.486	0.0000	0.0000	-3.625	0.0000	0.0000
Rpl37a	ENSMUSG00000046330	ribosomal protein L37a	-2.715	0.0000	0.0000	-2.760	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpl38	ENSMUSG00000057322	ribosomal protein L38	-2.567	0.0000	0.0000	-2.032	0.0000	0.0000
Rpl38-ps2	ENSMUSG00000080921	ribosomal protein L38, pseudogene 2	-10.208	0.0000	0.0000	-8.825	0.0000	0.0000
Rpl39l	ENSMUSG00000039209	ribosomal protein L39-like	-9.128	0.0157	0.0357	-12.938	0.0131	0.0332
Rpl3-ps1	ENSMUSG00000084349	ribosomal protein L3, pseudogene 1	-2.343	0.0000	0.0000	-2.051	0.0000	0.0000
Rpl7	ENSMUSG00000043716	ribosomal protein L7	-1.557	0.0000	0.0000	-1.571	0.0000	0.0000
Rpl8	ENSMUSG00000003970	ribosomal protein L8	-2.366	0.0000	0.0000	-2.063	0.0000	0.0000
Rplp0	ENSMUSG00000067274	ribosomal protein, large, P0	-2.960	0.0000	0.0000	-2.793	0.0000	0.0000
Rplp1	ENSMUSG00000007892	ribosomal protein, large, P1	-4.855	0.0000	0.0000	-4.449	0.0000	0.0000
Rpp21	ENSMUSG00000024446	ribonuclease P 21 subunit	-4.658	0.0000	0.0000	-3.473	0.0000	0.0000
Rpp25l	ENSMUSG00000036114	ribonuclease P/MRP 25 subunit-like	-3.126	0.0000	0.0000	-2.687	0.0000	0.0000
Rpp40	ENSMUSG00000021418	ribonuclease P 40 subunit	-2.410	0.0000	0.0000	-2.681	0.0000	0.0000
Rprd1b	ENSMUSG00000027651	regulation of nuclear pre-mRNA domain containing 1B	-1.612	0.0000	0.0000	-1.540	0.0000	0.0000
Rps10-ps1	ENSMUSG00000060438	ribosomal protein S10, pseudogene 1	-11.687	0.0000	0.0000	-8.162	0.0000	0.0000
Rps10-ps2	ENSMUSG00000099764	ribosomal protein S10, pseudogene 2	-4.500	0.0018	0.0053	-9.105	0.0007	0.0026
Rps11	ENSMUSG00000003429	ribosomal protein S11	-2.023	0.0000	0.0000	-1.863	0.0000	0.0000
Rps12	ENSMUSG00000061983	ribosomal protein S12	-2.399	0.0000	0.0000	-2.631	0.0000	0.0000
Rps13	ENSMUSG00000090862	ribosomal protein S13	-3.186	0.0000	0.0000	-2.999	0.0000	0.0000
Rps13-ps2	ENSMUSG00000069972	ribosomal protein S13, pseudogene 2	-4.558	0.0000	0.0000	-5.383	0.0000	0.0000
Rps15	ENSMUSG00000063457	ribosomal protein S15	-2.483	0.0000	0.0000	-2.031	0.0000	0.0000
Rps15a	ENSMUSG00000008683	ribosomal protein S15A	-2.516	0.0000	0.0000	-2.936	0.0000	0.0000
Rps15a-ps3	ENSMUSG00000084314	ribosomal protein S15A, pseudogene 3	-6.523	0.0061	0.0155	-38.281	0.0000	0.0002
Rps15a-ps4	ENSMUSG00000083757	ribosomal protein S15A, pseudogene 4	-34.308	0.0001	0.0003	-3.767	0.0362	0.0790
Rps18-ps3	ENSMUSG00000057657	ribosomal protein S18, pseudogene 3	-5.150	0.0129	0.0300	-14.735	0.0038	0.0115
Rps18-ps5	ENSMUSG00000113061	ribosomal protein S18, pseudogene 5	-1.886	0.0000	0.0001	-1.813	0.0001	0.0004
Rps19	ENSMUSG00000040952	ribosomal protein S19	-3.380	0.0000	0.0000	-3.153	0.0000	0.0000
Rps19-ps3	ENSMUSG00000080059	ribosomal protein S19, pseudogene 3	-3.600	0.0003	0.0009	-2.838	0.0020	0.0063
Rps19-ps6	ENSMUSG00000096942	ribosomal protein S19, pseudogene 6	-26.442	0.0002	0.0006	-63.195	0.0000	0.0000
Rps21	ENSMUSG00000039001	ribosomal protein S21	-2.492	0.0000	0.0000	-2.721	0.0000	0.0000
Rps24	ENSMUSG00000025290	ribosomal protein S24	-1.552	0.0000	0.0000	-1.636	0.0000	0.0000
Rps24-ps3	ENSMUSG00000081049	ribosomal protein S24, pseudogene 3	-3.728	0.0000	0.0000	-3.351	0.0000	0.0000
Rps25	ENSMUSG00000009927	ribosomal protein S25	-3.112	0.0000	0.0000	-3.471	0.0000	0.0000
Rps27	ENSMUSG00000090733	ribosomal protein S27	-4.340	0.0000	0.0000	-4.585	0.0000	0.0000
Rps27l	ENSMUSG00000036781	ribosomal protein S27-like	-2.236	0.0000	0.0000	-2.101	0.0000	0.0000
Rps27rt	ENSMUSG00000050621	ribosomal protein S27, retrogene	-13.703	0.0000	0.0000	-2.577	0.0097	0.0256
Rps28	ENSMUSG00000067288	ribosomal protein S28	-2.230	0.0000	0.0000	-2.528	0.0000	0.0000
Rps29	ENSMUSG00000034892	ribosomal protein S29	-4.430	0.0000	0.0000	-4.888	0.0000	0.0000
Rps4l	ENSMUSG00000063171	ribosomal protein S4-like	-2.484	0.0000	0.0000	-2.136	0.0000	0.0000
Rps5	ENSMUSG00000012848	ribosomal protein S5	-2.343	0.0000	0.0000	-2.199	0.0000	0.0000
Rps6kb2	ENSMUSG00000024830	ribosomal protein S6 kinase, polypeptide 2	-2.444	0.0000	0.0000	-1.877	0.0000	0.0000
Rps6kl1	ENSMUSG00000019235	ribosomal protein S6 kinase-like 1	-2.410	0.0001	0.0004	-1.632	0.0296	0.0668
Rps7-ps3	ENSMUSG00000095597	ribosomal protein S7, pseudogene 3	-11.492	0.0000	0.0000	-9.195	0.0000	0.0000
Rpsa	ENSMUSG00000032518	ribosomal protein SA	-2.020	0.0000	0.0000	-2.015	0.0000	0.0000
Rpsa-ps11	ENSMUSG00000082978	ribosomal protein SA, pseudogene 11	-13.939	0.0008	0.0024	-3.749	0.0209	0.0495

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Rpusd1	ENSMUSG00000041199	RNA pseudouridylate synthase domain containing 1	-2.500	0.0000	0.0000	-2.207	0.0000	0.0000
Rpusd3	ENSMUSG00000051169	RNA pseudouridylate synthase domain containing 3	-2.410	0.0000	0.0000	-1.978	0.0000	0.0000
Rrp36	ENSMUSG00000023971	ribosomal RNA processing 36	-2.268	0.0000	0.0000	-1.862	0.0000	0.0000
Rsl1	ENSMUSG00000058900	regulator of sex limited protein 1	-1.954	0.0137	0.0315	-1.775	0.0368	0.0802
Rtel1	ENSMUSG00000038685	regulator of telomere elongation helicase 1	-2.036	0.0000	0.0000	-1.773	0.0003	0.0012
Rtl8a	ENSMUSG00000067925	retrotransposon Gag like 8A	-4.605	0.0000	0.0000	-2.880	0.0000	0.0000
Rtl8b	ENSMUSG00000067924	retrotransposon Gag like 8B	-6.103	0.0000	0.0000	-3.587	0.0000	0.0000
Rtl9	ENSMUSG00000085584	retrotransposon Gag like 9	-2.618	0.0400	0.0800	-3.344	0.0145	0.0364
Rtn1	ENSMUSG00000021087	reticulon 1	-1.655	0.0220	0.0478	-2.045	0.0013	0.0045
Rtraf	ENSMUSG00000021807	RNA transcription, translation and transport factor	-1.866	0.0000	0.0000	-1.759	0.0000	0.0000
Rtraf-ps	ENSMUSG00000074479	RNA transcription, translation and transport factor, pseudogene	-2.147	0.0000	0.0000	-2.255	0.0000	0.0000
S100a11	ENSMUSG00000027907	S100 calcium binding protein A11	-2.100	0.0001	0.0002	-1.981	0.0002	0.0009
S100a13	ENSMUSG00000042312	S100 calcium binding protein A13	-2.366	0.0000	0.0000	-2.420	0.0000	0.0000
S100a6	ENSMUSG00000001025	S100 calcium binding protein A6 (calcyclin)	-3.504	0.0000	0.0000	-2.816	0.0000	0.0000
Sars2	ENSMUSG00000070699	seryl-aminoacyl-tRNA synthetase 2	-2.210	0.0000	0.0000	-1.759	0.0000	0.0000
Sash3	ENSMUSG00000031101	SAM and SH3 domain containing 3	-2.526	0.0001	0.0003	-2.099	0.0016	0.0054
Scamp2	ENSMUSG00000040188	secretory carrier membrane protein 2	-1.906	0.0000	0.0000	-1.655	0.0000	0.0000
Scamp3	ENSMUSG00000028049	secretory carrier membrane protein 3	-2.027	0.0000	0.0000	-1.841	0.0000	0.0000
Scap	ENSMUSG00000032485	SREBF chaperone	-1.732	0.0000	0.0000	-1.708	0.0000	0.0000
Scarf1	ENSMUSG00000038188	scavenger receptor class F, member 1	-1.946	0.0000	0.0000	-1.577	0.0001	0.0005
Scgb1c1	ENSMUSG00000038801	secretoglobin, family 1C, member 1	-6.686	0.0000	0.0000	-2.037	0.0086	0.0230
Scgb3a1	ENSMUSG00000064057	secretoglobin, family 3A, member 1	-2.931	0.0312	0.0646	-36.517	0.0001	0.0002
Scmh1	ENSMUSG00000000085	sex comb on midleg homolog 1	-1.515	0.0000	0.0000	-1.549	0.0000	0.0000
Scn4a	ENSMUSG00000001027	sodium channel, voltage-gated, type IV, alpha	-1.743	0.0011	0.0032	-1.612	0.0050	0.0143
Sco2	ENSMUSG00000091780	SCO2 cytochrome c oxidase assembly protein	-7.675	0.0000	0.0000	-4.932	0.0000	0.0000
Scp2-ps2	ENSMUSG00000058492	sterol carrier protein 2, pseudogene 2	-1.562	0.0058	0.0149	-1.550	0.0081	0.0219
Scube2	ENSMUSG00000007279	signal peptide, CUB domain, EGF-like 2	-1.545	0.0050	0.0130	-1.640	0.0015	0.0050
Sdhaf4	ENSMUSG00000026154	succinate dehydrogenase complex assembly factor 4	-1.693	0.0001	0.0002	-1.712	0.0000	0.0002
Sdhb	ENSMUSG00000009863	succinate dehydrogenase complex, subunit B, iron sulfur (Ip)	-2.078	0.0000	0.0000	-1.742	0.0000	0.0000
Sec22a	ENSMUSG00000034473	SEC22 homolog A, vesicle trafficking protein	-1.710	0.0000	0.0000	-1.807	0.0000	0.0000
Sec61a1	ENSMUSG00000030082	Sec61 alpha 1 subunit (S. cerevisiae)	-1.634	0.0000	0.0000	-1.607	0.0000	0.0000
Sec61g	ENSMUSG00000078974	SEC61, gamma subunit	-2.849	0.0000	0.0000	-2.759	0.0000	0.0000
Selenbp1	ENSMUSG00000068874	selenium binding protein 1	-2.149	0.0000	0.0000	-1.623	0.0021	0.0067
Selenoh	ENSMUSG00000076437	selenoprotein H	-2.336	0.0000	0.0000	-1.991	0.0000	0.0000
Selenom	ENSMUSG00000075702	selenoprotein M	-2.491	0.0000	0.0000	-1.796	0.0000	0.0000
Selenop	ENSMUSG00000064373	selenoprotein P	-1.629	0.0000	0.0000	-1.756	0.0000	0.0000
Sema4a	ENSMUSG00000028064	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A	-3.298	0.0000	0.0000	-3.490	0.0000	0.0000
Sema4b	ENSMUSG00000030539	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4B	-1.746	0.0000	0.0000	-1.652	0.0000	0.0000
Sema4d	ENSMUSG00000021451	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4D	-1.703	0.0000	0.0000	-1.551	0.0000	0.0000
Sema7a	ENSMUSG00000038264	sema domain, immunoglobulin domain (Ig), and GPI membrane anchor, (semaphorin) 7A	-1.871	0.0000	0.0002	-1.852	0.0001	0.0003
Serhl	ENSMUSG00000058586	serine hydrolase-like	-1.849	0.0000	0.0000	-1.507	0.0000	0.0000
Serpina3c	ENSMUSG00000066361	serine (or cysteine) peptidase inhibitor, clade A, member 3C	-2.406	0.0000	0.0001	-2.422	0.0000	0.0001

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Serpina3i	ENSMUSG00000079014	serine (or cysteine) peptidase inhibitor, clade A, member 3I	-3.717	0.0125	0.0291	-12.502	0.0019	0.0061
Serpinb10	ENSMUSG00000092572	serine (or cysteine) peptidase inhibitor, clade B (ovalbumin), member 10	-25.807	0.0022	0.0062	-14.083	0.0141	0.0355
Serpinf1	ENSMUSG00000000753	serine (or cysteine) peptidase inhibitor, clade F, member 1	-2.352	0.0000	0.0001	-1.678	0.0081	0.0218
Serping1	ENSMUSG00000023224	serine (or cysteine) peptidase inhibitor, clade G, member 1	-3.038	0.0000	0.0000	-2.098	0.0000	0.0000
Sesn2	ENSMUSG00000028893	sestrin 2	-1.946	0.0001	0.0003	-1.759	0.0011	0.0038
Sez6l2	ENSMUSG00000030683	seizure related 6 homolog like 2	-2.523	0.0000	0.0001	-2.698	0.0000	0.0000
Sf3b4	ENSMUSG00000068856	splicing factor 3b, subunit 4	-2.446	0.0000	0.0000	-2.074	0.0000	0.0000
Sf3b5	ENSMUSG00000078348	splicing factor 3b, subunit 5	-3.703	0.0000	0.0000	-3.102	0.0000	0.0000
Sf3b6	ENSMUSG00000037361	splicing factor 3B, subunit 6	-1.948	0.0000	0.0000	-2.247	0.0000	0.0000
Sgca	ENSMUSG00000001508	sarcoglycan, alpha (dystrophin-associated glycoprotein)	-3.500	0.0000	0.0000	-2.607	0.0000	0.0000
Sgf29	ENSMUSG00000030714	SAGA complex associated factor 29	-1.844	0.0000	0.0000	-1.745	0.0000	0.0000
Sgsm3	ENSMUSG00000042303	small G protein signaling modulator 3	-3.179	0.0000	0.0000	-2.169	0.0000	0.0000
Sh2d3c	ENSMUSG00000059013	SH2 domain containing 3C	-2.666	0.0000	0.0000	-1.959	0.0003	0.0013
Sh3bgrl3	ENSMUSG00000028843	SH3 domain binding glutamic acid-rich protein-like 3	-4.065	0.0000	0.0000	-2.909	0.0000	0.0000
Sh3bp4	ENSMUSG00000036206	SH3-domain binding protein 4	-1.534	0.0014	0.0040	-1.527	0.0015	0.0049
Sh3gl1	ENSMUSG00000003200	SH3-domain GRB2-like 1	-2.039	0.0000	0.0000	-1.515	0.0000	0.0000
Sh3glb2	ENSMUSG00000026860	SH3-domain GRB2-like endophilin B2	-2.435	0.0000	0.0000	-2.026	0.0000	0.0000
Sh3tc1	ENSMUSG00000036553	SH3 domain and tetratricopeptide repeats 1	-1.520	0.0048	0.0124	-1.565	0.0028	0.0086
Sh3tc2	ENSMUSG00000045629	SH3 domain and tetratricopeptide repeats 2	-2.328	0.0000	0.0000	-3.161	0.0000	0.0000
Shkbp1	ENSMUSG00000089832	Sh3kbp1 binding protein 1	-2.219	0.0000	0.0000	-1.709	0.0000	0.0000
Shld1	ENSMUSG00000044991	shieldin complex subunit 1	-4.466	0.0000	0.0001	-3.621	0.0003	0.0012
Sigirr	ENSMUSG00000025494	single immunoglobulin and toll-interleukin 1 receptor (TIR) domain	-1.537	0.0005	0.0017	-1.730	0.0000	0.0001
Sik2	ENSMUSG00000037112	salt inducible kinase 2	-1.735	0.0000	0.0001	-1.997	0.0000	0.0000
Slamf9	ENSMUSG00000026548	SLAM family member 9	-2.549	0.0058	0.0147	-2.651	0.0043	0.0126
Slc10a3	ENSMUSG00000032806	solute carrier family 10 (sodium/bile acid cotransporter family), member 3	-2.297	0.0000	0.0000	-2.911	0.0000	0.0000
Slc11a1	ENSMUSG00000026177	solute carrier family 11 (proton-coupled divalent metal ion transporters), member 1	-3.250	0.0000	0.0000	-1.707	0.0071	0.0195
Slc12a4	ENSMUSG00000017765	solute carrier family 12, member 4	-1.737	0.0000	0.0000	-1.566	0.0000	0.0000
Slc16a12	ENSMUSG00000009378	solute carrier family 16 (monocarboxylic acid transporters), member 12	-2.022	0.0000	0.0000	-2.707	0.0000	0.0000
Slc16a3	ENSMUSG00000025161	solute carrier family 16 (monocarboxylic acid transporters), member 3	-1.767	0.0324	0.0668	-2.026	0.0113	0.0291
Slc17a9	ENSMUSG00000023393	solute carrier family 17, member 9	-3.005	0.0377	0.0759	-4.471	0.0311	0.0694
Slc19a1	ENSMUSG00000001436	solute carrier family 19 (folate transporter), member 1	-3.516	0.0000	0.0000	-2.909	0.0000	0.0000
Slc22a21	ENSMUSG00000063652	solute carrier family 22 (organic cation transporter), member 21	-3.209	0.0013	0.0038	-3.507	0.0004	0.0014
Slc22a5	ENSMUSG00000018900	solute carrier family 22 (organic cation transporter), member 5	-2.010	0.0000	0.0000	-1.856	0.0000	0.0000
Slc25a10	ENSMUSG00000025792	solute carrier family 25 (mitochondrial carrier, dicarboxylate transporter), member 10	-3.156	0.0000	0.0000	-2.321	0.0000	0.0000
Slc25a22	ENSMUSG00000019082	solute carrier family 25 (mitochondrial carrier, glutamate), member 22	-1.645	0.0000	0.0001	-1.673	0.0000	0.0001
Slc25a29	ENSMUSG00000021265	solute carrier family 25 (mitochondrial carrier, palmitoylcarnitine transporter), member 29	-3.483	0.0000	0.0000	-2.728	0.0000	0.0000
Slc25a3	ENSMUSG00000061904	solute carrier family 25 (mitochondrial carrier, phosphate carrier), member 3	-1.904	0.0000	0.0000	-2.008	0.0000	0.0000
Slc25a34	ENSMUSG00000040740	solute carrier family 25, member 34	-2.037	0.0000	0.0000	-1.710	0.0000	0.0000
Slc25a42	ENSMUSG00000002346	solute carrier family 25, member 42	-1.543	0.0000	0.0000	-1.584	0.0000	0.0000
Slc26a11	ENSMUSG00000039908	solute carrier family 26, member 11	-1.842	0.0050	0.0130	-2.054	0.0012	0.0041
Slc26a6	ENSMUSG00000023259	solute carrier family 26, member 6	-1.824	0.0000	0.0000	-1.688	0.0000	0.0000
Slc29a1	ENSMUSG00000023942	solute carrier family 29 (nucleoside transporters), member 1	-2.286	0.0000	0.0000	-1.973	0.0000	0.0000
Slc29a2	ENSMUSG00000024891	solute carrier family 29 (nucleoside transporters), member 2	-2.880	0.0000	0.0000	-3.995	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Slc2a10	ENSMUSG00000027661	solute carrier family 2 (facilitated glucose transporter), member 10	-1.986	0.0003	0.0011	-1.555	0.0192	0.0460
Slc2a12	ENSMUSG00000037490	solute carrier family 2 (facilitated glucose transporter), member 12	-1.990	0.0000	0.0000	-2.056	0.0000	0.0000
Slc2a8	ENSMUSG00000026791	solute carrier family 2, (facilitated glucose transporter), member 8	-3.535	0.0000	0.0000	-2.772	0.0000	0.0000
Slc30a6	ENSMUSG00000024069	solute carrier family 30 (zinc transporter), member 6	-1.629	0.0000	0.0000	-1.590	0.0000	0.0000
Slc31a2	ENSMUSG00000066152	solute carrier family 31, member 2	-1.850	0.0000	0.0000	-2.208	0.0000	0.0000
Slc35a4	ENSMUSG00000033272	solute carrier family 35, member A4	-2.119	0.0000	0.0000	-2.042	0.0000	0.0000
Slc35b1	ENSMUSG00000020873	solute carrier family 35, member B1	-1.744	0.0000	0.0000	-1.601	0.0000	0.0000
Slc35c2	ENSMUSG00000017664	solute carrier family 35, member C2	-1.854	0.0000	0.0000	-1.611	0.0000	0.0000
Slc35e4	ENSMUSG00000048807	solute carrier family 35, member E4	-1.555	0.0396	0.0792	-1.917	0.0028	0.0085
Slc35f6	ENSMUSG00000029175	solute carrier family 35, member F6	-1.624	0.0000	0.0000	-1.583	0.0000	0.0000
Slc36a2	ENSMUSG00000020264	solute carrier family 36 (proton/amino acid symporter), member 2	-2.546	0.0000	0.0000	-2.424	0.0000	0.0000
Slc37a1	ENSMUSG00000024036	solute carrier family 37 (glycerol-3-phosphate transporter), member 1	-1.901	0.0000	0.0000	-2.799	0.0000	0.0000
Slc38a11	ENSMUSG00000061171	solute carrier family 38, member 11	-1.956	0.0018	0.0051	-1.632	0.0207	0.0492
Slc38a3	ENSMUSG00000010064	solute carrier family 38, member 3	-2.535	0.0000	0.0000	-2.380	0.0000	0.0000
Slc38a7	ENSMUSG00000036534	solute carrier family 38, member 7	-1.837	0.0000	0.0000	-1.773	0.0000	0.0000
Slc39a14	ENSMUSG00000022094	solute carrier family 39 (zinc transporter), member 14	-1.581	0.0000	0.0000	-1.649	0.0000	0.0000
Slc39a3	ENSMUSG00000046822	solute carrier family 39 (zinc transporter), member 3	-1.598	0.0000	0.0000	-1.788	0.0000	0.0000
Slc3a2	ENSMUSG00000010095	solute carrier family 3 (activators of dibasic and neutral amino acid transport), member 2	-2.018	0.0000	0.0000	-1.642	0.0005	0.0017
Slc40a1	ENSMUSG00000025993	solute carrier family 40 (iron-regulated transporter), member 1	-1.823	0.0001	0.0003	-1.848	0.0001	0.0003
Slc41a3	ENSMUSG00000030089	solute carrier family 41, member 3	-1.641	0.0000	0.0000	-1.525	0.0000	0.0000
Slc46a1	ENSMUSG00000020829	solute carrier family 46, member 1	-3.815	0.0000	0.0001	-3.379	0.0002	0.0009
Slc46a3	ENSMUSG00000029650	solute carrier family 46, member 3	-2.260	0.0000	0.0000	-1.988	0.0000	0.0001
Slc48a1	ENSMUSG00000081534	solute carrier family 48 (heme transporter), member 1	-2.197	0.0000	0.0000	-1.840	0.0000	0.0000
Slc50a1	ENSMUSG00000027953	solute carrier family 50 (sugar transporter), member 1	-3.461	0.0000	0.0000	-3.083	0.0000	0.0000
Slc52a2	ENSMUSG00000022560	solute carrier protein 52, member 2	-1.954	0.0000	0.0000	-1.563	0.0018	0.0059
Slc66a1	ENSMUSG00000028744	solute carrier family 66 member 1	-2.838	0.0000	0.0000	-2.304	0.0000	0.0000
Slc6a9	ENSMUSG00000028542	solute carrier family 6 (neurotransmitter transporter, glycine), member 9	-1.898	0.0017	0.0050	-1.537	0.0410	0.0878
Slc7a4	ENSMUSG00000022756	solute carrier family 7 (cationic amino acid transporter, y+ system), member 4	-3.657	0.0000	0.0000	-2.278	0.0001	0.0004
Slc7a6	ENSMUSG00000031904	solute carrier family 7 (cationic amino acid transporter, y+ system), member 6	-1.920	0.0000	0.0000	-1.789	0.0000	0.0002
Slc9a8	ENSMUSG00000039463	solute carrier family 9 (sodium/hydrogen exchanger), member 8	-1.556	0.0000	0.0000	-1.595	0.0000	0.0000
Smarcal1	ENSMUSG00000039354	SWI/SNF related matrix associated, actin dependent regulator of chromatin, subfamily a-like 1	-2.058	0.0000	0.0000	-1.743	0.0000	0.0000
Smarcb1	ENSMUSG00000000902	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily b, member 1	-1.955	0.0000	0.0000	-1.775	0.0000	0.0000
Smco1	ENSMUSG00000046345	single-pass membrane protein with coiled-coil domains 1	-1.895	0.0000	0.0000	-1.675	0.0001	0.0004
Smim15	ENSMUSG00000071180	small integral membrane protein 15	-1.588	0.0000	0.0000	-1.835	0.0000	0.0000
Smim27	ENSMUSG00000028407	small integral membrane protein 27	-4.292	0.0000	0.0000	-4.024	0.0000	0.0000
Smim5	ENSMUSG00000048442	small integral membrane protein 5	-2.451	0.0000	0.0000	-2.185	0.0000	0.0002
Smim8	ENSMUSG00000028295	small integral membrane protein 8	-1.513	0.0000	0.0000	-1.625	0.0000	0.0000
Smpd1	ENSMUSG00000037049	sphingomyelin phosphodiesterase 1, acid lysosomal	-2.319	0.0000	0.0000	-1.759	0.0000	0.0000
Smpdl3a	ENSMUSG00000019872	sphingomyelin phosphodiesterase, acid-like 3A	-2.792	0.0000	0.0000	-2.667	0.0000	0.0000
Smpx	ENSMUSG00000041476	small muscle protein, X-linked	-2.143	0.0000	0.0000	-2.535	0.0000	0.0000
Sms-ps	ENSMUSG00000081752	spermine synthase, pseudogene	-3.169	0.0000	0.0000	-2.970	0.0000	0.0000
Smtn	ENSMUSG00000020439	smoothelin	-2.027	0.0000	0.0000	-1.698	0.0000	0.0000
Smyd4	ENSMUSG00000018809	SET and MYND domain containing 4	-1.575	0.0007	0.0021	-1.629	0.0003	0.0013

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Snai1	ENSMUSG00000042821	snail family zinc finger 1	-3.271	0.0000	0.0000	-1.755	0.0211	0.0499
Snai2	ENSMUSG00000022676	snail family zinc finger 2	-2.182	0.0000	0.0001	-2.073	0.0001	0.0005
Snai3	ENSMUSG00000006587	snail family zinc finger 3	-10.105	0.0000	0.0000	-5.686	0.0000	0.0000
Snap47	ENSMUSG00000009894	synaptosomal-associated protein, 47	-2.463	0.0000	0.0000	-2.151	0.0000	0.0000
Snapc2	ENSMUSG00000011837	small nuclear RNA activating complex, polypeptide 2	-2.118	0.0000	0.0000	-2.112	0.0000	0.0000
Snhg18	ENSMUSG00000096956	small nucleolar RNA host gene 18	-1.799	0.0000	0.0000	-1.870	0.0000	0.0000
Snora17	ENSMUSG00000077192	small nucleolar RNA, H/ACA box 17	-13.250	0.0081	0.0199	-10.088	0.0222	0.0522
Snrpb	ENSMUSG00000027404	small nuclear ribonucleoprotein B	-2.514	0.0000	0.0000	-2.186	0.0000	0.0000
Snu13	ENSMUSG00000063480	SNU13 homolog, small nuclear ribonucleoprotein (U4/U6.U5)	-1.712	0.0000	0.0000	-1.555	0.0000	0.0000
Snx17	ENSMUSG00000029146	sorting nexin 17	-1.769	0.0000	0.0000	-1.502	0.0000	0.0000
Sox18	ENSMUSG00000046470	SRY (sex determining region Y)-box 18	-3.774	0.0000	0.0000	-3.484	0.0000	0.0000
Sp3os	ENSMUSG00000063714	trans-acting transcription factor 3, opposite strand	-1.589	0.0007	0.0022	-1.861	0.0000	0.0001
Spata2	ENSMUSG00000047030	spermatogenesis associated 2	-1.781	0.0000	0.0000	-1.745	0.0000	0.0000
Spata20	ENSMUSG00000020867	spermatogenesis associated 20	-9.654	0.0000	0.0000	-2.440	0.0269	0.0615
Spata24	ENSMUSG00000024352	spermatogenesis associated 24	-1.819	0.0264	0.0558	-1.772	0.0393	0.0849
Spata2l	ENSMUSG00000033594	spermatogenesis associated 2-like	-1.869	0.0006	0.0019	-1.674	0.0045	0.0132
Spats1	ENSMUSG00000023935	spermatogenesis associated, serine-rich 1	-3.638	0.0001	0.0003	-3.104	0.0009	0.0032
Spink4	ENSMUSG00000028415	serine peptidase inhibitor, Kazal type 4	-21.589	0.0019	0.0055	-22.451	0.0016	0.0052
Spns1	ENSMUSG00000030741	spinster homolog 1	-3.503	0.0000	0.0000	-2.800	0.0000	0.0000
Spns3	ENSMUSG00000020798	spinster homolog 3	-14.310	0.0106	0.0253	-9.670	0.0269	0.0616
Sppl2b	ENSMUSG00000035206	signal peptide peptidase like 2B	-2.472	0.0000	0.0000	-2.137	0.0000	0.0000
Spr	ENSMUSG00000033735	sepiapterin reductase	-2.584	0.0000	0.0000	-2.192	0.0000	0.0000
Sprn	ENSMUSG00000045733	shadow of prion protein	-2.976	0.0001	0.0005	-2.068	0.0089	0.0238
Spr-ps1	ENSMUSG00000068303	sepiapterin reductase pseudogene 1	-11.124	0.0000	0.0000	-6.293	0.0000	0.0000
Spryd4	ENSMUSG00000051346	SPRY domain containing 4	-1.924	0.0000	0.0000	-1.886	0.0000	0.0000
Spsb1	ENSMUSG00000039911	splA/ryanodine receptor domain and SOCS box containing 1	-2.150	0.0001	0.0004	-1.913	0.0010	0.0035
Spsb3	ENSMUSG00000024160	splA/ryanodine receptor domain and SOCS box containing 3	-1.622	0.0000	0.0000	-1.558	0.0000	0.0000
Srd5a3	ENSMUSG00000029233	steroid 5 alpha-reductase 3	-2.134	0.0000	0.0000	-2.489	0.0000	0.0000
Srebf1	ENSMUSG00000020538	sterol regulatory element binding transcription factor 1	-3.033	0.0000	0.0000	-2.939	0.0000	0.0000
Srpx	ENSMUSG00000090084	sushi-repeat-containing protein	-2.253	0.0001	0.0003	-2.666	0.0000	0.0000
Srr	ENSMUSG00000001323	serine racemase	-1.695	0.0000	0.0000	-1.792	0.0000	0.0000
Ss18l2	ENSMUSG00000032526	SS18, nBAF chromatin remodeling complex subunit like 2	-2.476	0.0000	0.0000	-2.420	0.0000	0.0000
Ssh3	ENSMUSG00000034616	slingshot protein phosphatase 3	-1.961	0.0001	0.0002	-1.728	0.0012	0.0041
Ssna1	ENSMUSG00000026966	SS nuclear autoantigen 1	-2.733	0.0000	0.0000	-2.648	0.0000	0.0000
Ssu2	ENSMUSG00000034387	ssu-2 homolog (C. elegans)	-1.962	0.0000	0.0000	-1.874	0.0001	0.0002
St6galnac4	ENSMUSG00000079442	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 4	-1.722	0.0000	0.0000	-2.123	0.0000	0.0000
Stab1	ENSMUSG00000042286	stabilin 1	-1.888	0.0000	0.0000	-1.662	0.0004	0.0015
Stap2	ENSMUSG00000038781	signal transducing adaptor family member 2	-1.960	0.0000	0.0000	-1.543	0.0020	0.0064
Stard3	ENSMUSG00000018167	START domain containing 3	-1.610	0.0004	0.0012	-1.519	0.0017	0.0057
Stard8	ENSMUSG00000031216	START domain containing 8	-1.752	0.0000	0.0000	-1.866	0.0000	0.0000
Sting1	ENSMUSG00000024349	stimulator of interferon response cGAMP interactor 1	-2.319	0.0000	0.0000	-1.677	0.0048	0.0140
Stk11ip	ENSMUSG00000026213	serine/threonine kinase 11 interacting protein	-1.574	0.0060	0.0153	-1.686	0.0016	0.0054
Stk19	ENSMUSG00000061207	serine/threonine kinase 19	-2.127	0.0000	0.0000	-1.742	0.0001	0.0005

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Stk25	ENSMUSG00000026277	serine/threonine kinase 25 (yeast)	-1.576	0.0000	0.0000	-1.771	0.0000	0.0000
Stn1	ENSMUSG00000042694	STN1, CST complex subunit	-2.335	0.0000	0.0000	-2.218	0.0000	0.0000
Stradb	ENSMUSG00000026027	STE20-related kinase adaptor beta	-1.768	0.0000	0.0000	-1.639	0.0000	0.0000
Strip2	ENSMUSG00000039629	striatin interacting protein 2	-1.635	0.0000	0.0000	-1.787	0.0000	0.0000
Strit1	ENSMUSG00000103476	small transmembrane regulator of ion transport 1	-2.653	0.0000	0.0000	-2.706	0.0000	0.0000
Stx5a	ENSMUSG00000010110	syntaxin 5A	-1.653	0.0000	0.0001	-1.635	0.0000	0.0002
Sufu	ENSMUSG00000025231	SUFU negative regulator of hedgehog signaling	-2.203	0.0000	0.0000	-1.662	0.0000	0.0000
Sult1a1	ENSMUSG00000030711	sulfotransferase family 1A, phenol-preferring, member 1	-2.406	0.0076	0.0189	-2.001	0.0355	0.0777
Sumf2	ENSMUSG00000025538	sulfatase modifying factor 2	-1.966	0.0000	0.0000	-1.518	0.0000	0.0002
Sun1	ENSMUSG00000036817	Sad1 and UNC84 domain containing 1	-1.545	0.0000	0.0000	-1.501	0.0000	0.0000
Sun3	ENSMUSG00000040985	Sad1 and UNC84 domain containing 3	-5.051	0.0000	0.0000	-1.816	0.0007	0.0025
Supt4a	ENSMUSG00000020485	SPT4A, DSIF elongation factor subunit	-2.227	0.0000	0.0000	-1.793	0.0000	0.0000
Suv39h1	ENSMUSG00000039231	suppressor of variegation 3-9 1	-1.853	0.0000	0.0000	-2.379	0.0000	0.0000
Swi5	ENSMUSG00000044627	SWI5 recombination repair homolog (yeast)	-1.827	0.0000	0.0000	-1.682	0.0000	0.0000
Swsap1	ENSMUSG00000051238	SWIM type zinc finger 7 associated protein 1	-2.630	0.0000	0.0000	-2.760	0.0000	0.0000
Syce2	ENSMUSG00000003824	synaptonemal complex central element protein 2	-10.609	0.0004	0.0013	-3.555	0.0080	0.0217
Syngr2	ENSMUSG00000048277	synaptogyrin 2	-3.364	0.0000	0.0000	-2.443	0.0000	0.0000
Syt3	ENSMUSG00000030731	synaptotagmin III	-2.409	0.0000	0.0000	-2.053	0.0001	0.0005
Syvn1	ENSMUSG00000024807	synovial apoptosis inhibitor 1, synoviolin	-2.447	0.0000	0.0000	-1.817	0.0000	0.0000
Szt2	ENSMUSG00000033253	SZT2 subunit of KICSTOR complex	-2.202	0.0000	0.0000	-1.739	0.0000	0.0000
Tab1	ENSMUSG00000022414	TGF-beta activated kinase 1/MAP3K7 binding protein 1	-1.944	0.0000	0.0000	-2.017	0.0000	0.0000
Tada1	ENSMUSG00000026563	transcriptional adaptor 1	-2.097	0.0000	0.0000	-2.188	0.0000	0.0000
Tafazzin	ENSMUSG00000009995	tafazzin, phospholipid-lysophospholipid transacylase	-1.696	0.0000	0.0000	-1.570	0.0000	0.0000
Tagln2	ENSMUSG00000026547	transgelin 2	-1.777	0.0000	0.0000	-1.725	0.0000	0.0000
Tamm41	ENSMUSG00000030316	TAM41 mitochondrial translocator assembly and maintenance homolog	-1.616	0.0013	0.0038	-1.602	0.0018	0.0057
Tango2	ENSMUSG00000013539	transport and golgi organization 2	-2.593	0.0000	0.0000	-2.139	0.0000	0.0000
Tbc1d10a	ENSMUSG00000034412	TBC1 domain family, member 10a	-1.644	0.0072	0.0179	-2.033	0.0002	0.0007
Tbc1d17	ENSMUSG00000038520	TBC1 domain family, member 17	-2.093	0.0000	0.0000	-1.535	0.0071	0.0195
Tbc1d2	ENSMUSG00000039813	TBC1 domain family, member 2	-2.470	0.0001	0.0003	-2.905	0.0000	0.0000
Tbc1d22a	ENSMUSG00000051864	TBC1 domain family, member 22a	-2.474	0.0000	0.0000	-2.076	0.0000	0.0000
Tbc1d5	ENSMUSG00000023923	TBC1 domain family, member 5	-1.678	0.0000	0.0000	-1.627	0.0000	0.0000
Tbc1d7	ENSMUSG00000021368	TBC1 domain family, member 7	-1.746	0.0000	0.0000	-1.606	0.0000	0.0000
Tbc1d8	ENSMUSG00000003134	TBC1 domain family, member 8	-1.539	0.0000	0.0000	-1.737	0.0000	0.0000
Tbl3	ENSMUSG00000040688	transducin (beta)-like 3	-2.777	0.0000	0.0000	-2.249	0.0000	0.0000
Tbxa2r	ENSMUSG00000034881	thromboxane A2 receptor	-3.275	0.0000	0.0000	-2.347	0.0004	0.0016
Tcf19	ENSMUSG00000050410	transcription factor 19	-2.054	0.0006	0.0020	-1.690	0.0151	0.0377
Tcirg1	ENSMUSG00000001750	T cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 protein A3	-2.540	0.0000	0.0000	-1.749	0.0031	0.0095
Tcn2	ENSMUSG00000020432	transcobalamin 2	-2.291	0.0000	0.0000	-2.049	0.0000	0.0000
Tcp11l2	ENSMUSG00000020034	t-complex 11 (mouse) like 2	-1.846	0.0002	0.0009	-2.064	0.0000	0.0001
Tcta	ENSMUSG00000039461	T cell leukemia translocation altered gene	-2.868	0.0000	0.0000	-2.471	0.0000	0.0000
Tctn3	ENSMUSG00000025008	tectonic family member 3	-2.581	0.0000	0.0000	-2.661	0.0000	0.0000
Tdp1	ENSMUSG00000021177	tyrosyl-DNA phosphodiesterase 1	-1.521	0.0002	0.0006	-1.609	0.0000	0.0002
Tecpr1	ENSMUSG00000066621	tectonin beta-propeller repeat containing 1	-2.061	0.0000	0.0000	-1.588	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tecr	ENSMUSG00000031708	trans-2,3-enoyl-CoA reductase	-1.818	0.0000	0.0000	-1.543	0.0000	0.0000
Tecrl	ENSMUSG00000049537	trans-2,3-enoyl-CoA reductase-like	-2.510	0.0000	0.0000	-2.955	0.0000	0.0000
Tedc2	ENSMUSG00000024118	tubulin epsilon and delta complex 2	-2.340	0.0041	0.0109	-2.112	0.0139	0.0350
Tef	ENSMUSG00000022389	thyrotroph embryonic factor	-2.211	0.0000	0.0001	-1.888	0.0005	0.0018
Ten1	ENSMUSG00000020778	TEN1 telomerase capping complex subunit	-1.603	0.0012	0.0036	-1.509	0.0056	0.0159
Tepsin	ENSMUSG00000025377	TEPSIN, adaptor related protein complex 4 accessory protein	-1.985	0.0000	0.0000	-1.740	0.0000	0.0000
Tfg	ENSMUSG00000022757	Trk-fused gene	-1.870	0.0000	0.0000	-2.121	0.0000	0.0000
Tg	ENSMUSG00000053469	thyroglobulin	-2.383	0.0000	0.0000	-1.945	0.0006	0.0022
Tgfb1i1	ENSMUSG00000030782	transforming growth factor beta 1 induced transcript 1	-2.310	0.0000	0.0000	-1.995	0.0000	0.0000
Tgtp1	ENSMUSG00000078922	T cell specific GTPase 1	-2.070	0.0264	0.0558	-2.939	0.0020	0.0063
Thap7	ENSMUSG00000022760	THAP domain containing 7	-2.762	0.0000	0.0000	-2.590	0.0000	0.0000
Them4	ENSMUSG00000028145	thioesterase superfamily member 4	-1.912	0.0000	0.0000	-1.735	0.0000	0.0001
Thnsl2	ENSMUSG00000054474	threonine synthase-like 2 (bacterial)	-1.625	0.0001	0.0003	-1.573	0.0003	0.0013
Thop1	ENSMUSG00000004929	thimet oligopeptidase 1	-2.183	0.0000	0.0000	-1.550	0.0000	0.0000
Ticam1	ENSMUSG00000047123	toll-like receptor adaptor molecule 1	-3.033	0.0000	0.0000	-3.140	0.0000	0.0000
Timm13	ENSMUSG00000020219	translocase of inner mitochondrial membrane 13	-2.004	0.0000	0.0000	-1.584	0.0000	0.0000
Timm50	ENSMUSG00000003438	translocase of inner mitochondrial membrane 50	-3.079	0.0000	0.0000	-2.579	0.0000	0.0000
Timm9	ENSMUSG00000021079	translocase of inner mitochondrial membrane 9	-2.016	0.0000	0.0000	-2.110	0.0000	0.0000
Tkt	ENSMUSG00000021957	transketolase	-2.668	0.0000	0.0000	-2.431	0.0000	0.0000
Tlcd2	ENSMUSG00000038217	TLC domain containing 2	-2.244	0.0000	0.0001	-1.715	0.0045	0.0132
Tlcd3a	ENSMUSG00000069808	TLC domain containing 3A	-2.140	0.0015	0.0045	-2.344	0.0005	0.0020
Tle6	ENSMUSG00000034758	transducin-like enhancer of split 6	-2.642	0.0000	0.0000	-2.043	0.0000	0.0000
Tlr5	ENSMUSG00000079164	toll-like receptor 5	-1.722	0.0399	0.0797	-2.571	0.0016	0.0054
Tm2d2	ENSMUSG00000031556	TM2 domain containing 2	-2.196	0.0000	0.0000	-1.680	0.0000	0.0000
Tm2d3	ENSMUSG00000078681	TM2 domain containing 3	-1.755	0.0000	0.0000	-1.705	0.0000	0.0000
Tm4sf1	ENSMUSG00000027800	transmembrane 4 superfamily member 1	-1.538	0.0002	0.0006	-1.554	0.0001	0.0005
Tmc6	ENSMUSG00000025572	transmembrane channel-like gene family 6	-2.372	0.0000	0.0000	-1.701	0.0001	0.0005
Tmc8	ENSMUSG00000050106	transmembrane channel-like gene family 8	-1.668	0.0005	0.0017	-1.832	0.0001	0.0003
Tmed1	ENSMUSG00000032180	transmembrane p24 trafficking protein 1	-1.953	0.0000	0.0000	-1.730	0.0000	0.0000
Tmed10-ps	ENSMUSG00000114251	transmembrane p24 trafficking protein 10, pseudogene	-2.155	0.0000	0.0000	-2.191	0.0000	0.0000
Tmed2b	ENSMUSG00000079884	transmembrane p24 trafficking protein 2B	-2.670	0.0003	0.0010	-1.707	0.0437	0.0924
Tmed3	ENSMUSG00000032353	transmembrane p24 trafficking protein 3	-1.829	0.0000	0.0000	-1.575	0.0000	0.0000
Tmem104	ENSMUSG00000045980	transmembrane protein 104	-1.930	0.0000	0.0000	-1.723	0.0000	0.0000
Tmem108	ENSMUSG00000042757	transmembrane protein 108	-2.643	0.0000	0.0000	-2.424	0.0000	0.0000
Tmem120a	ENSMUSG00000039886	transmembrane protein 120A	-2.582	0.0000	0.0000	-2.798	0.0000	0.0000
Tmem120b	ENSMUSG00000054434	transmembrane protein 120B	-1.850	0.0000	0.0000	-1.619	0.0001	0.0003
Tmem126a	ENSMUSG00000030615	transmembrane protein 126A	-4.116	0.0000	0.0000	-4.094	0.0000	0.0000
Tmem128	ENSMUSG00000067365	transmembrane protein 128	-1.564	0.0000	0.0000	-1.561	0.0000	0.0000
Tmem129	ENSMUSG00000019295	transmembrane protein 129	-2.904	0.0000	0.0000	-2.736	0.0000	0.0000
Tmem140	ENSMUSG00000057137	transmembrane protein 140	-1.852	0.0003	0.0010	-1.735	0.0012	0.0041
Tmem143	ENSMUSG00000002781	transmembrane protein 143	-2.172	0.0000	0.0000	-1.834	0.0000	0.0000
Tmem144	ENSMUSG00000027956	transmembrane protein 144	-2.376	0.0000	0.0000	-2.129	0.0000	0.0000
Tmem14a	ENSMUSG00000025933	transmembrane protein 14A	-1.923	0.0007	0.0023	-1.880	0.0015	0.0048

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tmem154	ENSMUSG00000056498	transmembrane protein 154	-1.646	0.0047	0.0124	-2.011	0.0001	0.0006
Tmem175	ENSMUSG00000013495	transmembrane protein 175	-2.379	0.0000	0.0000	-1.959	0.0000	0.0000
Tmem176b	ENSMUSG00000029810	transmembrane protein 176B	-2.531	0.0000	0.0000	-1.567	0.0002	0.0010
Tmem177	ENSMUSG00000036975	transmembrane protein 177	-1.538	0.0000	0.0000	-1.554	0.0000	0.0000
Tmem179b	ENSMUSG00000118346	transmembrane protein 179B	-2.175	0.0000	0.0000	-1.798	0.0000	0.0000
Tmem184b	ENSMUSG00000009035	transmembrane protein 184b	-2.351	0.0000	0.0000	-1.959	0.0000	0.0000
Tmem204	ENSMUSG00000024168	transmembrane protein 204	-1.947	0.0000	0.0000	-1.786	0.0000	0.0000
Tmem205	ENSMUSG00000040883	transmembrane protein 205	-2.133	0.0000	0.0000	-1.747	0.0000	0.0000
Tmem208	ENSMUSG00000014856	transmembrane protein 208	-2.929	0.0000	0.0000	-3.169	0.0000	0.0000
Tmem216	ENSMUSG00000024667	transmembrane protein 216	-2.274	0.0000	0.0000	-1.740	0.0000	0.0001
Tmem219	ENSMUSG00000060538	transmembrane protein 219	-1.733	0.0000	0.0000	-1.627	0.0000	0.0001
Tmem223	ENSMUSG00000117924	transmembrane protein 223	-4.062	0.0000	0.0000	-3.133	0.0000	0.0000
Tmem230	ENSMUSG00000027341	transmembrane protein 230	-1.988	0.0000	0.0001	-3.864	0.0000	0.0000
Tmem241	ENSMUSG00000049411	transmembrane protein 241	-1.594	0.0001	0.0002	-2.108	0.0000	0.0000
Tmem242	ENSMUSG00000004945	transmembrane protein 242	-2.194	0.0000	0.0000	-2.069	0.0000	0.0000
Tmem25	ENSMUSG00000002032	transmembrane protein 25	-1.794	0.0008	0.0026	-1.873	0.0003	0.0013
Tmem254	ENSMUSG00000072676	transmembrane protein 254	-1.592	0.0266	0.0562	-1.597	0.0279	0.0635
Tmem258	ENSMUSG00000036372	transmembrane protein 258	-2.698	0.0000	0.0000	-2.566	0.0000	0.0000
Tmem35b	ENSMUSG00000070737	transmembrane protein 35B	-2.373	0.0011	0.0033	-2.008	0.0084	0.0225
Tmem37	ENSMUSG00000050777	transmembrane protein 37	-6.581	0.0000	0.0000	-6.259	0.0000	0.0000
Tmem41a	ENSMUSG00000022856	transmembrane protein 41a	-1.693	0.0051	0.0133	-1.851	0.0011	0.0039
Tmem41b	ENSMUSG00000047554	transmembrane protein 41B	-1.812	0.0000	0.0000	-1.650	0.0000	0.0000
Tmem41b-ps	ENSMUSG00000096647	transmembrane protein 41B, pseudogene	-3.194	0.0482	0.0937	-3.232	0.0355	0.0777
Tmem42	ENSMUSG00000066233	transmembrane protein 42	-1.522	0.0009	0.0028	-1.654	0.0001	0.0004
Tmem45a	ENSMUSG00000022754	transmembrane protein 45a	-1.788	0.0017	0.0051	-1.509	0.0278	0.0634
Tmem52	ENSMUSG00000023153	transmembrane protein 52	-4.560	0.0000	0.0002	-2.623	0.0092	0.0245
Tmem53	ENSMUSG00000048772	transmembrane protein 53	-1.721	0.0000	0.0000	-1.623	0.0000	0.0000
Tmem59	ENSMUSG00000028618	transmembrane protein 59	-1.776	0.0000	0.0000	-1.730	0.0000	0.0000
Tmem60	ENSMUSG00000045435	transmembrane protein 60	-2.102	0.0000	0.0000	-1.885	0.0000	0.0000
Tmem63a	ENSMUSG00000026519	transmembrane protein 63a	-1.571	0.0000	0.0000	-1.530	0.0000	0.0000
Tmem79	ENSMUSG00000001420	transmembrane protein 79	-2.584	0.0000	0.0001	-3.214	0.0000	0.0000
Tmem81	ENSMUSG00000048174	transmembrane protein 81	-1.654	0.0070	0.0176	-1.606	0.0126	0.0322
Tmem86a	ENSMUSG00000010307	transmembrane protein 86A	-3.127	0.0000	0.0000	-2.317	0.0000	0.0000
Tmem88	ENSMUSG00000045377	transmembrane protein 88	-2.933	0.0000	0.0000	-2.314	0.0000	0.0000
Tmem9	ENSMUSG00000026411	transmembrane protein 9	-1.652	0.0000	0.0001	-1.512	0.0008	0.0028
Tmem94	ENSMUSG00000020747	transmembrane protein 94	-2.020	0.0000	0.0000	-1.872	0.0000	0.0000
Tmem97	ENSMUSG00000037278	transmembrane protein 97	-1.686	0.0011	0.0033	-2.001	0.0000	0.0001
Tmem98	ENSMUSG00000035413	transmembrane protein 98	-1.698	0.0003	0.0011	-1.632	0.0009	0.0033
Tmsb10	ENSMUSG00000079523	thymosin, beta 10	-1.921	0.0004	0.0014	-2.262	0.0000	0.0001
Tnfaip8l1	ENSMUSG00000044469	tumor necrosis factor, alpha-induced protein 8-like 1	-2.433	0.0000	0.0000	-2.009	0.0000	0.0000
Tnfaip8l2	ENSMUSG00000013707	tumor necrosis factor, alpha-induced protein 8-like 2	-4.787	0.0000	0.0000	-8.547	0.0000	0.0000
Tnfrsf12a	ENSMUSG00000023905	tumor necrosis factor receptor superfamily, member 12a	-2.360	0.0000	0.0000	-2.473	0.0000	0.0000
Tnfrsf1a	ENSMUSG00000030341	tumor necrosis factor receptor superfamily, member 1a	-2.167	0.0000	0.0000	-1.775	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Tnfrsf26	ENSMUSG00000045362	tumor necrosis factor receptor superfamily, member 26	-2.280	0.0047	0.0123	-3.162	0.0004	0.0015
Tnfsf9	ENSMUSG00000035678	tumor necrosis factor (ligand) superfamily, member 9	-2.791	0.0246	0.0526	-2.633	0.0379	0.0823
Tnxb	ENSMUSG00000033327	tenascin XB	-1.870	0.0000	0.0000	-1.630	0.0000	0.0002
Tom1	ENSMUSG00000042870	target of myb1 trafficking protein	-3.127	0.0000	0.0000	-2.487	0.0000	0.0000
Tomm5	ENSMUSG00000078713	translocase of outer mitochondrial membrane 5	-1.634	0.0000	0.0000	-1.604	0.0000	0.0000
Tor2a	ENSMUSG00000009563	torsin family 2, member A	-2.284	0.0000	0.0000	-2.022	0.0000	0.0000
Tpd52l1	ENSMUSG00000000296	tumor protein D52-like 1	-1.597	0.0037	0.0099	-1.640	0.0022	0.0070
Tpgs1	ENSMUSG00000020308	tubulin polyglutamylase complex subunit 1	-3.370	0.0000	0.0000	-2.436	0.0000	0.0000
Tpk1	ENSMUSG00000029735	thiamine pyrophosphokinase	-2.314	0.0000	0.0001	-1.687	0.0088	0.0235
Tpp1	ENSMUSG00000030894	tripeptidyl peptidase I	-2.172	0.0000	0.0000	-2.435	0.0000	0.0000
Tpra1	ENSMUSG00000002871	transmembrane protein, adipocyte asscociated 1	-2.569	0.0000	0.0000	-2.160	0.0000	0.0000
Tpst2	ENSMUSG00000029344	protein-tyrosine sulfotransferase 2	-1.782	0.0000	0.0000	-1.786	0.0000	0.0000
Traf7	ENSMUSG00000052752	TNF receptor-associated factor 7	-2.762	0.0000	0.0000	-2.656	0.0000	0.0000
Trappc12	ENSMUSG00000020628	trafficking protein particle complex 12	-1.701	0.0000	0.0000	-1.672	0.0000	0.0000
Trappc4	ENSMUSG00000032112	trafficking protein particle complex 4	-2.067	0.0000	0.0000	-2.229	0.0000	0.0000
Trappc9	ENSMUSG00000047921	trafficking protein particle complex 9	-2.375	0.0000	0.0000	-1.969	0.0000	0.0000
Triap1	ENSMUSG00000029535	TP53 regulated inhibitor of apoptosis 1	-2.030	0.0000	0.0000	-1.902	0.0000	0.0000
Trib3	ENSMUSG00000032715	tribbles pseudokinase 3	-1.871	0.0003	0.0011	-1.716	0.0020	0.0063
Trim32	ENSMUSG00000051675	tripartite motif-containing 32	-1.841	0.0000	0.0000	-1.952	0.0000	0.0000
Trim46	ENSMUSG00000042766	tripartite motif-containing 46	-2.635	0.0003	0.0009	-2.137	0.0047	0.0136
Trim65	ENSMUSG00000054517	tripartite motif-containing 65	-1.766	0.0000	0.0000	-1.690	0.0000	0.0000
Triqk	ENSMUSG00000055963	triple QxxK/R motif containing	-2.079	0.0000	0.0000	-2.334	0.0000	0.0000
Trmt112-ps2	ENSMUSG00000070572	tRNA methyltransferase 11-2, pseudogene 2	-32.846	0.0001	0.0004	-3.114	0.0455	0.0955
Trp53i13	ENSMUSG00000044328	transformation related protein 53 inducible protein 13	-1.775	0.0007	0.0021	-1.878	0.0002	0.0010
Trpt1	ENSMUSG00000047656	tRNA phosphotransferase 1	-3.361	0.0000	0.0000	-2.268	0.0000	0.0000
Trpv4	ENSMUSG00000014158	transient receptor potential cation channel, subfamily V, member 4	-2.268	0.0003	0.0009	-1.812	0.0081	0.0220
Trrap	ENSMUSG00000045482	transformation/transcription domain-associated protein	-1.855	0.0000	0.0000	-1.738	0.0000	0.0000
Trub2	ENSMUSG00000039826	TruB pseudouridine (psi) synthase family member 2	-2.427	0.0000	0.0000	-2.188	0.0000	0.0000
Tsacc	ENSMUSG00000010538	TSSK6 activating co-chaperone	-2.318	0.0154	0.0350	-2.513	0.0156	0.0386
Tsc2	ENSMUSG00000002496	TSC complex subunit 2	-1.833	0.0000	0.0000	-1.555	0.0000	0.0000
Tsen15	ENSMUSG00000014980	tRNA splicing endonuclease subunit 15	-1.799	0.0000	0.0000	-1.928	0.0000	0.0000
Tsen2	ENSMUSG00000042389	tRNA splicing endonuclease subunit 2	-1.542	0.0004	0.0014	-1.525	0.0009	0.0030
Tsku	ENSMUSG00000049580	tsukushi, small leucine rich proteoglycan	-1.610	0.0060	0.0151	-2.018	0.0002	0.0007
Tspan11	ENSMUSG00000030351	tetraspanin 11	-2.487	0.0019	0.0055	-3.066	0.0003	0.0011
Tspan4	ENSMUSG00000025511	tetraspanin 4	-2.166	0.0000	0.0000	-2.520	0.0000	0.0000
Tspo	ENSMUSG00000041736	translocator protein	-4.999	0.0000	0.0000	-6.281	0.0000	0.0000
Ttc30a2	ENSMUSG00000075272	tetratricopeptide repeat domain 30A2	-3.046	0.0136	0.0314	-3.848	0.0037	0.0110
Ttc32	ENSMUSG00000066637	tetratricopeptide repeat domain 32	-2.082	0.0000	0.0000	-1.969	0.0000	0.0000
Ttc38	ENSMUSG00000035944	tetratricopeptide repeat domain 38	-2.404	0.0000	0.0000	-1.535	0.0001	0.0005
Ttc7b	ENSMUSG00000033530	tetratricopeptide repeat domain 7B	-1.580	0.0000	0.0000	-1.671	0.0000	0.0000
Ttll1	ENSMUSG00000022442	tubulin tyrosine ligase-like 1	-3.102	0.0000	0.0000	-2.796	0.0000	0.0000
Tubg1	ENSMUSG00000035198	tubulin, gamma 1	-3.037	0.0000	0.0000	-2.513	0.0000	0.0000
Tubgcp4	ENSMUSG00000027263	tubulin, gamma complex associated protein 4	-1.800	0.0000	0.0000	-1.555	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Twf2	ENSMUSG00000023277	twinfilin actin binding protein 2	-3.748	0.0000	0.0000	-3.098	0.0000	0.0000
Tyk2	ENSMUSG00000032175	tyrosine kinase 2	-2.134	0.0000	0.0000	-1.617	0.0001	0.0003
Tyrobp	ENSMUSG00000030579	TYRO protein tyrosine kinase binding protein	-1.946	0.0015	0.0045	-1.531	0.0437	0.0924
Ubb-ps	ENSMUSG00000044285	ubiquitin B, pseudogene	-3.173	0.0000	0.0000	-1.995	0.0000	0.0001
Ubc	ENSMUSG00000008348	ubiquitin C	-5.528	0.0000	0.0000	-5.938	0.0000	0.0000
Ube2a	ENSMUSG00000016308	ubiquitin-conjugating enzyme E2A	-1.729	0.0000	0.0000	-1.822	0.0000	0.0000
Ube2c	ENSMUSG00000001403	ubiquitin-conjugating enzyme E2C	-2.030	0.0003	0.0009	-2.342	0.0001	0.0002
Ube2d-ps	ENSMUSG00000083844	ubiquitin-conjugating enzyme E2D, pseudogene	-2.152	0.0000	0.0000	-2.002	0.0000	0.0000
Ube2l3	ENSMUSG00000038965	ubiquitin-conjugating enzyme E2L 3	-1.629	0.0000	0.0000	-1.640	0.0000	0.0000
Ube2t	ENSMUSG00000026429	ubiquitin-conjugating enzyme E2T	-2.061	0.0000	0.0001	-2.337	0.0000	0.0000
Ube4bos1	ENSMUSG00000085819	ubiquitination factor E4B, opposite strand 1	-2.117	0.0370	0.0747	-18.260	0.0002	0.0006
Ubiad1	ENSMUSG00000047719	UbiA prenyltransferase domain containing 1	-1.546	0.0001	0.0003	-1.728	0.0000	0.0000
Ubl7	ENSMUSG00000055720	ubiquitin-like 7 (bone marrow stromal cell-derived)	-2.053	0.0000	0.0000	-1.904	0.0000	0.0000
Ubox5	ENSMUSG00000027300	U box domain containing 5	-1.981	0.0000	0.0000	-2.274	0.0000	0.0000
Ubtd1	ENSMUSG00000025171	ubiquitin domain containing 1	-1.850	0.0000	0.0000	-2.109	0.0000	0.0000
Ubxn6	ENSMUSG00000019578	UBX domain protein 6	-2.009	0.0000	0.0000	-1.649	0.0000	0.0000
Uchl1	ENSMUSG00000029223	ubiquitin carboxy-terminal hydrolase L1	-2.061	0.0003	0.0011	-1.710	0.0076	0.0208
Uchl4	ENSMUSG00000035337	ubiquitin carboxyl-terminal esterase L4	-6.014	0.0000	0.0000	-7.485	0.0000	0.0000
Uck1	ENSMUSG00000002550	uridine-cytidine kinase 1	-2.446	0.0000	0.0000	-2.774	0.0000	0.0000
Uckl1	ENSMUSG00000089917	uridine-cytidine kinase 1-like 1	-2.585	0.0000	0.0000	-2.057	0.0000	0.0000
Ugt1a6b	ENSMUSG00000090145	UDP glucuronosyltransferase 1 family, polypeptide A6B	-2.246	0.0343	0.0700	-2.406	0.0327	0.0725
Unc93b1	ENSMUSG00000036908	unc-93 homolog B1, TLR signaling regulator	-2.477	0.0000	0.0000	-2.203	0.0000	0.0000
Upp1	ENSMUSG00000020407	uridine phosphorylase 1	-2.155	0.0000	0.0002	-2.412	0.0000	0.0000
Uqcc2	ENSMUSG00000024208	ubiquinol-cytochrome c reductase complex assembly factor 2	-3.354	0.0000	0.0000	-2.819	0.0000	0.0000
Uqcr10	ENSMUSG00000059534	ubiquinol-cytochrome c reductase, complex III subunit X	-1.842	0.0000	0.0000	-1.815	0.0000	0.0000
Uqcr11	ENSMUSG00000020163	ubiquinol-cytochrome c reductase, complex III subunit XI	-4.343	0.0000	0.0000	-3.632	0.0000	0.0000
Urb1	ENSMUSG00000039929	URB1 ribosome biogenesis 1 homolog (S. cerevisiae)	-1.706	0.0000	0.0000	-1.718	0.0000	0.0000
Urod	ENSMUSG00000028684	uroporphyrinogen decarboxylase	-1.853	0.0000	0.0000	-1.647	0.0000	0.0000
Usp22	ENSMUSG00000042506	ubiquitin specific peptidase 22	-1.943	0.0000	0.0000	-2.248	0.0000	0.0000
Uxt	ENSMUSG00000001134	ubiquitously expressed prefoldin like chaperone	-1.579	0.0000	0.0000	-1.651	0.0000	0.0000
Vegfc	ENSMUSG00000031520	vascular endothelial growth factor C	-1.546	0.0012	0.0037	-1.522	0.0019	0.0062
Vipr2	ENSMUSG00000011171	vasoactive intestinal peptide receptor 2	-1.552	0.0424	0.0840	-1.786	0.0104	0.0271
Vkorc1	ENSMUSG00000096145	vitamin K epoxide reductase complex, subunit 1	-2.594	0.0014	0.0041	-1.908	0.0202	0.0482
Vma21-ps	ENSMUSG00000061619	VMA21 vacuolar H+-ATPase homolog (S. cerevisiae), pseudogene	-25.600	0.0007	0.0022	-25.161	0.0007	0.0025
Vmac	ENSMUSG00000054723	vimentin-type intermediate filament associated coiled-coil protein	-2.111	0.0000	0.0000	-1.711	0.0000	0.0000
Vnn1	ENSMUSG00000037440	vanin 1	-5.511	0.0184	0.0409	-8.380	0.0104	0.0272
Vps35l	ENSMUSG00000030982	VPS35 endosomal protein sorting factor like	-2.268	0.0000	0.0000	-1.901	0.0000	0.0000
Vps51	ENSMUSG00000024797	VPS51 GARP complex subunit	-1.868	0.0000	0.0000	-1.566	0.0000	0.0000
Vrk3	ENSMUSG00000002205	vaccinia related kinase 3	-2.161	0.0000	0.0000	-1.688	0.0000	0.0000
Vtn	ENSMUSG00000017344	vitronectin	-2.891	0.0000	0.0000	-2.616	0.0000	0.0000
Vwa3a	ENSMUSG00000030889	von Willebrand factor A domain containing 3A	-1.834	0.0004	0.0014	-1.832	0.0005	0.0019
Vwa5a	ENSMUSG00000023186	von Willebrand factor A domain containing 5A	-1.992	0.0000	0.0000	-1.986	0.0000	0.0000
Washc5	ENSMUSG00000022350	WASH complex subunit 5	-1.832	0.0000	0.0000	-1.887	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Wbp2	ENSMUSG00000034341	WW domain binding protein 2	-2.482	0.0000	0.0000	-1.949	0.0000	0.0000
Wdr18	ENSMUSG00000035754	WD repeat domain 18	-2.157	0.0000	0.0000	-1.654	0.0000	0.0000
Wdr24	ENSMUSG00000025737	WD repeat domain 24	-1.896	0.0000	0.0000	-1.572	0.0000	0.0000
Wdr45	ENSMUSG00000039382	WD repeat domain 45	-2.176	0.0000	0.0001	-1.869	0.0004	0.0014
Wdr6	ENSMUSG00000066357	WD repeat domain 6	-1.955	0.0000	0.0000	-1.539	0.0000	0.0000
Wdr74	ENSMUSG00000042729	WD repeat domain 74	-2.383	0.0000	0.0000	-1.870	0.0000	0.0000
Wdr83os	ENSMUSG00000059355	WD repeat domain 83 opposite strand	-2.127	0.0000	0.0000	-2.179	0.0000	0.0000
Wdr90	ENSMUSG00000073434	WD repeat domain 90	-2.238	0.0000	0.0001	-1.593	0.0144	0.0361
Wdr91	ENSMUSG00000058486	WD repeat domain 91	-1.882	0.0000	0.0000	-1.535	0.0010	0.0034
Wfdc1	ENSMUSG00000023336	WAP four-disulfide core domain 1	-3.494	0.0000	0.0000	-2.881	0.0000	0.0000
Wfdc2	ENSMUSG00000017723	WAP four-disulfide core domain 2	-27.895	0.0074	0.0183	-15.434	0.0292	0.0660
Wipf3	ENSMUSG00000086040	WAS/WASL interacting protein family, member 3	-1.724	0.0000	0.0000	-1.594	0.0000	0.0000
Wrap73	ENSMUSG00000029029	WD repeat containing, antisense to Trp73	-2.289	0.0000	0.0000	-2.509	0.0000	0.0000
Wscd1	ENSMUSG00000020811	WSC domain containing 1	-1.857	0.0001	0.0004	-1.606	0.0031	0.0095
Xpnpep1	ENSMUSG00000025027	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	-2.142	0.0000	0.0000	-1.863	0.0000	0.0000
Ydjc	ENSMUSG00000041774	YdjC homolog (bacterial)	-2.805	0.0000	0.0001	-3.714	0.0000	0.0000
Yeats2	ENSMUSG00000041215	YEATS domain containing 2	-1.522	0.0019	0.0055	-1.852	0.0000	0.0000
Yif1a	ENSMUSG00000024875	Yip1 interacting factor homolog A (S. cerevisiae)	-2.268	0.0000	0.0000	-2.144	0.0000	0.0000
Yif1b	ENSMUSG00000030588	Yip1 interacting factor homolog B (S. cerevisiae)	-3.857	0.0000	0.0000	-2.486	0.0000	0.0000
Yipf1	ENSMUSG00000057375	Yip1 domain family, member 1	-1.852	0.0000	0.0000	-1.794	0.0000	0.0000
Yipf7	ENSMUSG00000029158	Yip1 domain family, member 7	-1.936	0.0000	0.0000	-1.919	0.0000	0.0000
Zbtb3	ENSMUSG00000071661	zinc finger and BTB domain containing 3	-1.699	0.0018	0.0052	-2.368	0.0000	0.0001
Zbtb45	ENSMUSG00000049600	zinc finger and BTB domain containing 45	-2.256	0.0000	0.0000	-2.339	0.0000	0.0000
Zc3h3	ENSMUSG00000075600	zinc finger CCCH type containing 3	-3.307	0.0000	0.0001	-2.802	0.0002	0.0008
Zdhhc12	ENSMUSG00000015335	zinc finger, DHHC domain containing 12	-4.225	0.0000	0.0000	-3.182	0.0000	0.0000
Zdhhc16	ENSMUSG00000025157	zinc finger, DHHC domain containing 16	-1.733	0.0000	0.0000	-1.635	0.0000	0.0000
Zdhhc4	ENSMUSG00000001844	zinc finger, DHHC domain containing 4	-1.747	0.0000	0.0000	-1.851	0.0000	0.0000
Zer1	ENSMUSG00000039686	zyg-11 related, cell cycle regulator	-1.851	0.0000	0.0000	-1.635	0.0000	0.0000
Zfand2a	ENSMUSG00000053581	zinc finger, AN1-type domain 2A	-1.693	0.0000	0.0000	-1.980	0.0000	0.0000
Zfand2b	ENSMUSG00000026197	zinc finger, AN1 type domain 2B	-1.903	0.0000	0.0000	-1.699	0.0000	0.0001
Zfat	ENSMUSG00000022335	zinc finger and AT hook domain containing	-1.624	0.0004	0.0014	-1.628	0.0005	0.0019
Zfp119a	ENSMUSG00000057835	zinc finger protein 119a	-1.935	0.0000	0.0000	-2.507	0.0000	0.0000
Zfp128	ENSMUSG00000060397	zinc finger protein 128	-1.679	0.0006	0.0021	-1.563	0.0036	0.0107
Zfp142	ENSMUSG00000026135	zinc finger protein 142	-1.601	0.0000	0.0000	-1.595	0.0000	0.0000
Zfp174	ENSMUSG00000054939	zinc finger protein 174	-2.097	0.0000	0.0000	-1.669	0.0001	0.0005
Zfp2	ENSMUSG00000049321	zinc finger protein 2	-1.695	0.0000	0.0001	-2.097	0.0000	0.0000
Zfp213	ENSMUSG00000071256	zinc finger protein 213	-1.838	0.0000	0.0001	-1.703	0.0003	0.0010
Zfp276	ENSMUSG00000001065	zinc finger protein (C2H2 type) 276	-1.946	0.0000	0.0000	-2.115	0.0000	0.0000
Zfp277	ENSMUSG00000055917	zinc finger protein 277	-2.127	0.0000	0.0000	-2.092	0.0000	0.0000
Zfp324	ENSMUSG00000004500	zinc finger protein 324	-1.835	0.0000	0.0001	-1.647	0.0005	0.0017
Zfp335	ENSMUSG00000039834	zinc finger protein 335	-1.825	0.0000	0.0000	-1.859	0.0000	0.0000
Zfp346	ENSMUSG00000021481	zinc finger protein 346	-1.650	0.0000	0.0000	-1.577	0.0000	0.0000
Zfp36l1-ps	ENSMUSG00000080942	zinc finger protein 36, C3H type-like 1, pseudogene	-20.100	0.0000	0.0000	-3.709	0.0028	0.0087

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

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Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zfp41	ENSMUSG00000047003	zinc finger protein 41	-1.831	0.0003	0.0012	-1.657	0.0030	0.0093
Zfp414	ENSMUSG00000073423	zinc finger protein 414	-2.254	0.0000	0.0000	-1.963	0.0000	0.0000
Zfp446	ENSMUSG00000033961	zinc finger protein 446	-2.298	0.0000	0.0000	-1.844	0.0000	0.0000
Zfp455	ENSMUSG00000051037	zinc finger protein 455	-1.603	0.0106	0.0252	-2.013	0.0003	0.0012
Zfp456	ENSMUSG00000078995	zinc finger protein 456	-2.065	0.0112	0.0266	-2.208	0.0064	0.0178
Zfp51	ENSMUSG00000023892	zinc finger protein 51	-1.909	0.0000	0.0000	-1.690	0.0000	0.0000
Zfp511	ENSMUSG00000025470	zinc finger protein 511	-2.024	0.0000	0.0000	-2.062	0.0000	0.0000
Zfp536	ENSMUSG00000043456	zinc finger protein 536	-1.542	0.0092	0.0223	-1.520	0.0125	0.0320
Zfp619	ENSMUSG00000068959	zinc finger protein 619	-1.703	0.0001	0.0005	-1.607	0.0010	0.0036
Zfp637	ENSMUSG00000059689	zinc finger protein 637	-2.571	0.0000	0.0000	-2.189	0.0000	0.0000
Zfp64	ENSMUSG00000027551	zinc finger protein 64	-1.766	0.0000	0.0000	-1.708	0.0000	0.0000
Zfp647	ENSMUSG00000054967	zinc finger protein 647	-4.730	0.0000	0.0000	-3.292	0.0000	0.0002
Zfp653	ENSMUSG00000038895	zinc finger protein 653	-2.489	0.0000	0.0001	-1.592	0.0231	0.0539
Zfp658	ENSMUSG00000056592	zinc finger protein 658	-1.750	0.0315	0.0651	-2.077	0.0086	0.0230
Zfp672	ENSMUSG00000049755	zinc finger protein 672	-2.080	0.0000	0.0000	-2.150	0.0000	0.0000
Zfp688	ENSMUSG00000045251	zinc finger protein 688	-1.690	0.0008	0.0025	-1.644	0.0020	0.0064
Zfp706	ENSMUSG00000062397	zinc finger protein 706	-1.579	0.0002	0.0005	-2.062	0.0000	0.0000
Zfp709	ENSMUSG00000056019	zinc finger protein 709	-1.571	0.0003	0.0011	-1.806	0.0000	0.0000
Zfp712	ENSMUSG00000090641	zinc finger protein 712	-3.273	0.0000	0.0000	-1.635	0.0035	0.0106
Zfp719	ENSMUSG00000030469	zinc finger protein 719	-1.709	0.0001	0.0005	-1.879	0.0000	0.0000
Zfp729b	ENSMUSG00000058093	zinc finger protein 729b	-2.073	0.0000	0.0000	-2.380	0.0000	0.0000
Zfp748	ENSMUSG00000095432	zinc finger protein 748	-2.211	0.0000	0.0000	-2.061	0.0000	0.0000
Zfp781	ENSMUSG00000096718	zinc finger protein 781	-4.605	0.0228	0.0493	-5.159	0.0265	0.0608
Zfp808	ENSMUSG00000074867	zinc finger protein 808	-5.084	0.0000	0.0000	-4.112	0.0000	0.0000
Zfp810	ENSMUSG00000066829	zinc finger protein 810	-1.516	0.0000	0.0000	-1.698	0.0000	0.0000
Zfp85	ENSMUSG00000058331	zinc finger protein 85	-1.625	0.0024	0.0068	-1.996	0.0001	0.0005
Zfp868	ENSMUSG00000060427	zinc finger protein 868	-1.525	0.0000	0.0001	-1.614	0.0000	0.0000
Zfp873	ENSMUSG00000061371	zinc finger protein 873	-1.650	0.0025	0.0071	-1.623	0.0042	0.0123
Zfp874a	ENSMUSG00000069206	zinc finger protein 874a	-1.683	0.0006	0.0018	-1.797	0.0001	0.0005
Zfp874b	ENSMUSG00000059839	zinc finger protein 874b	-1.659	0.0003	0.0010	-1.618	0.0006	0.0022
Zfp9	ENSMUSG00000072623	zinc finger protein 9	-1.894	0.0000	0.0000	-1.874	0.0000	0.0000
Zfp954	ENSMUSG00000062116	zinc finger protein 954	-2.211	0.0000	0.0000	-2.577	0.0000	0.0000
Zfp958	ENSMUSG00000058748	zinc finger protein 958	-2.099	0.0000	0.0000	-2.381	0.0000	0.0000
Zfp97	ENSMUSG00000095990	zinc finger protein 97	-4.269	0.0000	0.0000	-3.090	0.0001	0.0003
Zfp971	ENSMUSG00000074519	zinc finger protein 971	-1.780	0.0000	0.0000	-1.888	0.0000	0.0000
Zfp975	ENSMUSG00000069727	zinc finger protein 975	-1.575	0.0053	0.0138	-1.549	0.0090	0.0239
Zfpl1	ENSMUSG00000024792	zinc finger like protein 1	-1.772	0.0000	0.0000	-2.117	0.0000	0.0000
Zfyve19	ENSMUSG00000068580	zinc finger, FYVE domain containing 19	-2.422	0.0000	0.0000	-2.297	0.0000	0.0000
Zfyve21	ENSMUSG00000021286	zinc finger, FYVE domain containing 21	-2.637	0.0000	0.0000	-1.701	0.0003	0.0013
Zfyve26	ENSMUSG00000066440	zinc finger, FYVE domain containing 26	-1.935	0.0000	0.0000	-1.878	0.0000	0.0000
Zkscan17	ENSMUSG00000020472	zinc finger with KRAB and SCAN domains 17	-2.380	0.0000	0.0000	-2.025	0.0000	0.0001
Znhit2	ENSMUSG00000075227	zinc finger, HIT domain containing 2	-2.555	0.0000	0.0000	-2.488	0.0000	0.0000
Zswim1	ENSMUSG00000017764	zinc finger SWIM-type containing 1	-2.569	0.0000	0.0000	-2.236	0.0000	0.0000

• **Table S5: Differentially expressed transcripts in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

DOWNREGULATED

Gene Symbol	Ensembl Gene ID	Description	mG4H-ON vs. Con-ON			mG4H-OFF vs. Con-OFF		
			Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)
Zswim7	ENSMUSG00000014243	zinc finger SWIM-type containing 7	-1.889	0.0000	0.0000	-2.047	0.0000	0.0000
Zwint	ENSMUSG00000019923	ZW10 interactor	-1.712	0.0000	0.0000	-1.609	0.0000	0.0000
	ENSMUSG00000095041		-1.518	0.0072	0.0180	-1.553	0.0049	0.0142

• **Table S6: Enriched pathways specific to mG4H-ON (Venn Diagram: Group I)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	membrane repolarization during ventricular cardiac muscle cell action potential (GO:0098915)	4/5	0.0005	0.4404	35.2059	267.6232	KCNH2;KCNE1;KCNJ8;KCNQ1
GOBP2021	peptidyl-cysteine S-nitrosylation (GO:0018119)	4/5	0.0005	0.4404	35.2059	267.6232	NOS2;NOS1;S100A9;S100A8
GOBP2021	leukocyte aggregation (GO:0070486)	5/8	0.0005	0.4404	14.6747	112.2449	RAC2;S100A9;JAM2;CD44;S100A8
GOBP2021	regulation of calcium ion transmembrane transport via high voltage-gated calcium channel (GO:1902514)	6/11	0.0003	0.4404	10.5698	84.6768	CACNG6;CACNB1;CAMK2D;NOS1AP;NPPA;NOS1
GOBP2021	peptidyl-cysteine modification (GO:0018198)	5/9	0.0010	0.7212	11.0054	76.2236	NOS2;NOS1;RAB6A;S100A9;S100A8
GOBP2021	regulation of defense response to bacterium (GO:1900424)	4/7	0.0030	1.0000	11.7340	68.3509	GRN;CYBA;SIRT2;FOXP1
GOBP2021	homoserine metabolic process (GO:0009092)	3/5	0.0091	1.0000	13.1950	62.0170	TST;CBS;CTH
GOBP2021	p38MAPK cascade (GO:0038066)	3/5	0.0091	1.0000	13.1950	62.0170	LGALS9;MAPK14;ZFP36L1
GOBP2021	regulation of cytochrome-c oxidase activity (GO:1904959)	3/5	0.0091	1.0000	13.1950	62.0170	SPHK2;COX17;COA8
GOBP2021	regulation of respiratory burst involved in inflammatory response (GO:0060264)	3/5	0.0091	1.0000	13.1950	62.0170	GRN;SLAMF8;LBP
GOBP2021	transsulfuration (GO:0019346)	3/5	0.0091	1.0000	13.1950	62.0170	TST;CBS;CTH
Reactome2016	LRR FLII-interacting protein 1 (LRRFIP1) activates type I IFN production Homo sapiens R-HSA-3134973	3/5	0.0091	1.0000	13.1950	62.0170	IRF3;CTNNB1;LRRFIP1
Reactome2016	Signaling by MST1 Homo sapiens R-HSA-8852405	3/5	0.0091	1.0000	13.1950	62.0170	HPN;SPINT2;MST1R
GOBP2021	positive regulation of T cell apoptotic process (GO:0070234)	5/10	0.0018	0.9719	8.8038	55.6462	PRELID1;CCL5;ZC3H8;LGALS9;IDO1
BioPlanet2019	Lysine catabolism	4/8	0.0054	1.0000	8.8000	45.9011	GCDH;OGDH;DLD;AASS
GOBP2021	ventricular cardiac muscle cell membrane repolarization (GO:0099625)	4/8	0.0054	1.0000	8.8000	45.9011	KCNH2;KCNE1;KCNJ8;KCNQ1
KEGG2019M	Phosphonate and phosphinate metabolism	3/6	0.0168	0.5718	8.7962	35.9377	PCYT1B;PCYT2;SELENOI
GOBP2021	cellular response to lipoteichoic acid (GO:0071223)	3/6	0.0168	1.0000	8.7962	35.9377	LBP;MAPK14;TLR2
GOBP2021	cerebral cortex cell migration (GO:0021795)	3/6	0.0168	1.0000	8.7962	35.9377	RELN;EFHC1;PEX13
GOBP2021	regulation of collagen fibril organization (GO:1904026)	3/6	0.0168	1.0000	8.7962	35.9377	EFEMP2;EMILIN1;AEBP1
GOBP2021	response to lipoteichoic acid (GO:0070391)	3/6	0.0168	1.0000	8.7962	35.9377	LBP;MAPK14;TLR2
GOBP2021	striated muscle hypertrophy (GO:0014897)	3/6	0.0168	1.0000	8.7962	35.9377	CSRP3;MYOC;HTR2B
GOBP2021	valine metabolic process (GO:0006573)	3/6	0.0168	1.0000	8.7962	35.9377	ALDH6A1;BCAT1;BCAT2
Reactome2016	Synthesis of Dolichyl-phosphate Homo sapiens R-HSA-446199	3/6	0.0168	1.0000	8.7962	35.9377	NUS1;DOLK;MVD
GOBP2021	lysine catabolic process (GO:0006554)	5/12	0.0047	1.0000	6.2877	33.6418	GCDH;PHYKPL;OGDH;DLD;AASS
GOBP2021	lysine metabolic process (GO:0006553)	5/12	0.0047	1.0000	6.2877	33.6418	GCDH;PHYKPL;OGDH;DLD;AASS
Reactome2016	Lysine catabolism Homo sapiens R-HSA-71064	5/12	0.0047	1.0000	6.2877	33.6418	GCDH;PHYKPL;OGDH;DLD;AASS
GOBP2021	regulation of calcium ion transmembrane transport (GO:1903169)	8/23	0.0014	0.8861	4.6997	30.8579	CACNG6;CACNB1;CAMK2D;NOS1AP;NPPA;CASQ1;NOS1;CBARP
BioPlanet2019	Sonic Hedgehog (Shh) pathway	6/16	0.0037	1.0000	5.2834	29.6335	GSK3B;PRKAR1B;PRKAR2B;PTCH1;DYRK1A;DYRK1B
GOBP2021	kinetochore organization (GO:0051383)	5/13	0.0071	1.0000	5.5015	27.2427	CENPE;CENPF;CENPH;NUF2;NDC80
GOBP2021	macrophage activation involved in immune response (GO:0002281)	5/13	0.0071	1.0000	5.5015	27.2427	GRN;FER1L5;SBNO2;IFI35;LBP
GOBP2021	positive regulation of toll-like receptor 4 signaling pathway (GO:0034145)	4/10	0.0138	1.0000	5.8660	25.1339	NR1H3;PTPN22;LBP;IFI35
GOBP2021	regulation of neutrophil migration (GO:1902622)	4/10	0.0138	1.0000	5.8660	25.1339	BST1;SLAMF8;RAC2;RHOG
GOBP2021	serine family amino acid catabolic process (GO:0009071)	4/10	0.0138	1.0000	5.8660	25.1339	CBS;SHMT2;SHMT1;DLD
Reactome2016	ADP signalling through P2Y purinoceptor 1 Homo sapiens R-HSA-418592	8/25	0.0026	1.0000	4.1463	24.7138	GNA14;GNA15;GNG10;GNB2;GNB1;GNB3;MAPK14;GNG11
BioPlanet2019	Fas signaling pathway in cardiomyocytes	3/7	0.0272	1.0000	6.5968	23.7763	GSK3B;AKT3;NPPA
GOBP2021	cytochrome complex assembly (GO:0017004)	3/7	0.0272	1.0000	6.5968	23.7763	SURF1;CYBA;COX10
GOBP2021	DNA ligation (GO:0006266)	3/7	0.0272	1.0000	6.5968	23.7763	TOP2A;LIG1;MGMT
GOBP2021	dolichyl diphosphate biosynthetic process (GO:0006489)	3/7	0.0272	1.0000	6.5968	23.7763	NUS1;DOLK;MVD
GOBP2021	dolichyl diphosphate metabolic process (GO:0046465)	3/7	0.0272	1.0000	6.5968	23.7763	NUS1;DOLK;MVD
GOBP2021	negative regulation of double-strand break repair via nonhomologous end joining (GO:2001033)	3/7	0.0272	1.0000	6.5968	23.7763	TFIP11;AUNIP;NUDT16L1
GOBP2021	positive regulation of lymphocyte apoptotic process (GO:0070230)	3/7	0.0272	1.0000	6.5968	23.7763	PRELID1;CCL5;IDO1
GOBP2021	proline metabolic process (GO:0006560)	3/7	0.0272	1.0000	6.5968	23.7763	ALDH4A1;PYCR1;PYCR2
GOBP2021	protein localization to ciliary membrane (GO:1903441)	3/7	0.0272	1.0000	6.5968	23.7763	ARL13B;WDR19;RAB29
Reactome2016	APEX1-Independent Resolution of AP Sites via the Single Nucleotide Replacement Pathway Homo sapiens R-HSA-5649702	3/7	0.0272	1.0000	6.5968	23.7763	NEIL2;PNKP;XRCC1
Reactome2016	Phase 3 - rapid repolarisation Homo sapiens R-HSA-5576890	3/7	0.0272	1.0000	6.5968	23.7763	KCNH2;KCNE1;KCNQ1
GOBP2021	cellular amino acid catabolic process (GO:0009063)	21/90	0.0002	0.4404	2.6910	22.5097	GCDH;GOT1;NOS2;PHYKPL;SHMT2;SHMT1;ABAT;GLS;ALDH4A1;ALDH6A1;ALDH5A1;CBS;DBT;CARNS1;OGDH;NOS1;BCAT1;DLD;AASS;IDO1;BCAT2
GOBP2021	2-oxoglutarate metabolic process (GO:0006103)	5/14	0.0101	1.0000	4.8899	22.4780	GOT1;ADHFE1;TAT;IDH2;OGDH
GOBP2021	protein modification by small protein conjugation or removal (GO:0070647)	5/14	0.0101	1.0000	4.8899	22.4780	SENP6;UBA7;DESI1;DESI2;ATG7
GOBP2021	sodium ion import across plasma membrane (GO:0098719)	6/18	0.0071	1.0000	4.4024	21.7766	HCN4;SLC9A2;SLC9A4;SLC5A1;SLC9A1;TRPM4
BioPlanet2019	Signal amplification	9/31	0.0030	1.0000	3.6052	20.9563	P2RY12;GNA14;GNA15;GNG10;GNB2;GNB1;GNB3;MAPK14;GNG11
KEGG2019M	Arginine and proline metabolism	13/50	0.0012	0.1772	3.0999	20.8230	AMD2;GOT1;NOS2;PYCR1;PYCR2;SRM;AGMAT;ALDH4A1;ALDH1B1;P4HA3;CARNS1;SMS;NOS1
KEGG2019M	Cysteine and methionine metabolism	13/50	0.0012	0.1772	3.0999	20.8230	AMD2;GOT1;TAT;GSS;SRM;TST;MAT2A;CBS;CTH;SMS;KYAT3;BCAT1;BCAT2
GOBP2021	cardiac muscle cell membrane repolarization (GO:0099622)	4/11	0.0199	1.0000	5.0277	19.6875	KCNH2;KCNE1;KCNQ1;ATP1B1
GOBP2021	positive regulation of transforming growth factor beta production (GO:0071636)	4/11	0.0199	1.0000	5.0277	19.6875	LGALS9;CD46;CD34;BMPR1A
GOBP2021	regulation of T cell apoptotic process (GO:0070232)	4/11	0.0199	1.0000	5.0277	19.6875	LGALS3;PRELID1;CCL5;IDO1
GOBP2021	telomere maintenance via recombination (GO:0000722)	4/11	0.0199	1.0000	5.0277	19.6875	RAD50;TEP1;XRCC3;SMC5
WikiPath2019M	SREBF and miR33 in cholesterol and lipid homeostasis WP2084	4/11	0.0199	0.8679	5.0277	19.6875	NR1H3;PPARA;PPARGC1A;SREBF2
Reactome2016	Thromboxane signalling through TP receptor Homo sapiens R-HSA-428930	7/23	0.0065	1.0000	3.8531	19.4203	GNA14;GNA15;GNG10;GNB2;GNB1;GNB3;GNG11
Reactome2016	Signal amplification Homo sapiens R-HSA-392518	9/32	0.0038	1.0000	3.4483	19.2278	P2RY12;GNA14;GNA15;GNG10;GNB2;GNB1;GNB3;MAPK14;GNG11
BioPlanet2019	Glycosaminoglycan degradation	6/19	0.0095	1.0000	4.0635	18.9197	HGSNAT;HEXB;HYAL3;HPSE;ARSB;SGSH
GOBP2021	aspartate family amino acid catabolic process (GO:0009068)	6/19	0.0095	1.0000	4.0635	18.9197	GCDH;GOT1;PHYKPL;OGDH;DLD;AASS
GOBP2021	membrane repolarization during cardiac muscle cell action potential (GO:0086013)	5/15	0.0139	1.0000	4.4007	18.8252	KCNH2;KCNE1;KCNJ8;KCNQ1;ATP1B1
GOBP2021	phosphatidylethanolamine biosynthetic process (GO:0006646)	5/15	0.0139	1.0000	4.4007	18.8252	SLC27A1;PCYT2;ETNK1;SELENOI;LPIN3
GOBP2021	response to muscle stretch (GO:0035994)	5/15	0.0139	1.0000	4.4007	18.8252	CSRP3;GSN;NPPA;CTNNB1;SLC9A1
GOBP2021	axon extension involved in axon guidance (GO:0048846)	3/8	0.0403	1.0000	5.2771	16.9501	NRP2;SLIT1;SLIT3
GOBP2021	cellular response to epinephrine stimulus (GO:0071872)	3/8	0.0403	1.0000	5.2771	16.9501	KCNQ1;SIRT2;SLC9A1
GOBP2021	cysteine metabolic process (GO:0006534)	3/8	0.0403	1.0000	5.2771	16.9501	TST;CBS;CTH
GOBP2021	elastic fiber assembly (GO:0048251)	3/8	0.0403	1.0000	5.2771	16.9501	MFAP4;EFEMP2;EMILIN1
GOBP2021	integrin activation (GO:0033622)	3/8	0.0403	1.0000	5.2771	16.9501	FN1;MZB1;FERMT3
GOBP2021	negative regulation of cAMP-dependent protein kinase activity (GO:2000480)	3/8	0.0403	1.0000	5.2771	16.9501	PKIB;PRKAR1B;PRKAR2B
GOBP2021	negative regulation of chromosome organization (GO:2001251)	3/8	0.0403	1.0000	5.2771	16.9501	TOP2A;ESPL1;SETMAR
GOBP2021	negative regulation of macrophage migration (GO:1905522)	3/8	0.0403	1.0000	5.2771	16.9501	DDT;SLAMF8;EMILIN1
GOBP2021	neuron projection extension involved in neuron projection guidance (GO:1902284)	3/8	0.0403	1.0000	5.2771	16.9501	NRP2;SLIT1;SLIT3
GOBP2021	positive regulation of early endosome to late endosome transport (GO:2000643)	3/8	0.0403	1.0000	5.2771	16.9501	RDX;VPS11;PTPN23
GOBP2021	protein localization to microtubule (GO:0035372)	3/8	0.0403	1.0000	5.2771	16.9501	KIF20B;MAPRE1;MID1
GOBP2021	protein localization to microtubule cytoskeleton (GO:0072698)	3/8	0.0403	1.0000	5.2771	16.9501	KIF20B;MAPRE1;MID1
GOBP2021	regulation of chemokine-mediated signaling pathway (GO:0070099)	3/8	0.0403	1.0000	5.2771	16.9501	EDN1;PADI2;SLIT3
GOBP2021	regulation of nitric oxide metabolic process (GO:0080164)	3/8	0.0403	1.0000	5.2771	16.9501	SELENOS;NOS1AP;TMEM106A
GOBP2021	regulation of proton transport (GO:0010155)	3/8	0.0403	1.0000	5.2771	16.9501	DNAJC30;SPHK2;SLC30A5
GOBP2021	response to epinephrine (GO:0071871)	3/8	0.0403	1.0000	5.2771	16.9501	KCNQ1;SIRT2;SLC9A1
Reactome2016	Axonal growth inhibition (RHOA activation) Homo sapiens R-HSA-193634	3/8	0.0403	1.0000	5.2771	16.9501	NGFR;LINGO1;MAG
Reactome2016	Metabolism of ingested SeMet, Sec, MeSec into H2Se Homo sapiens R-HSA-2408508	3/8	0.0403	1.0000	5.2771	16.9501	CBS;CTH;GNMT
BioPlanet2019	Arginine and proline metabolism	13/54	0.0026	1.0000	2.7968	16.6826	ACY1;GOT1;NOS2;PYCR1;PYCR2;GLS;SRM;AGMAT;ALDH4A1;ALDH1B1;P4HA3;SMS;NOS1
GOBP2021	regulation of double-strand break repair via nonhomologous end joining (GO:2001032)	8/29	0.0071	1.0000	3.3558	16.6158	PNKP;WAS;SETMAR;KMT5B;TFIP11;AUNIP;NUDT16L1;WRAP53

• **Table S6: Enriched pathways specific to mG4H-ON (Venn Diagram: Group I)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
KEGG2019M	Mineral absorption	11/44	0.0039	0.3836	2.9387	16.2795	VDR;TRF;ATP1A3;HMOX1;CYBRD1;SLC30A1;MT2;SLC5A1;MT1;ATP1B1;SLC26A3
GOBP2021	regulation of cholesterol storage (GO:0010885)	5/16	0.0185	1.0000	4.0004	15.9587	SCARB1;NR1H3;PPARA;SREBF2;PPARD
GOBP2021	regulation of fatty acid oxidation (GO:0046320)	5/16	0.0185	1.0000	4.0004	15.9587	SIRT4;PDK4;PRKAG2;PPARA;PPARGC1A
Reactome2016	Metabolism of folate and pterines Homo sapiens R-HSA-196757	5/16	0.0185	1.0000	4.0004	15.9587	ALDH1L1;SHMT2;SHMT1;MTHFS;SLC25A32
GOBP2021	glycine metabolic process (GO:0006544)	4/12	0.0275	1.0000	4.3990	15.8059	SHMT2;SHMT1;DLD;GCAT
GOBP2021	homocysteine metabolic process (GO:0050667)	4/12	0.0275	1.0000	4.3990	15.8059	TST;CBS;CTH;NOX4
GOBP2021	phagolysosome assembly (GO:0001845)	4/12	0.0275	1.0000	4.3990	15.8059	PIKFYVE;RAB34;CORO1A;SYT7
Reactome2016	Hyaluronan uptake and degradation Homo sapiens R-HSA-2160916	4/12	0.0275	1.0000	4.3990	15.8059	HEXB;HYAL3;CD44;SLC9A1
BioPlanet2019	Ovarian infertility genes	8/30	0.0088	1.0000	3.2031	15.1607	EGR1;LHCGR;VDR;GJA4;INHA;BMPR1B;PRLR;ZP2
KEGG2019M	Base excision repair	9/35	0.0072	0.5280	3.0499	15.0440	POLE4;PCNA;NEIL2;LIG1;MPG;TDG;POLE2;XRCC1;POLL
BioPlanet2019	Base excision repair	9/35	0.0072	1.0000	3.0499	15.0440	POLE4;PCNA;NEIL2;LIG1;MPG;TDG;POLE2;XRCC1;POLL
Reactome2016	Base Excision Repair Homo sapiens R-HSA-73884	9/35	0.0072	1.0000	3.0499	15.0440	PCNA;PARG;NEIL2;LIG1;MPG;PNKP;TDG;POLE2;XRCC1
Reactome2016	Resolution of Abasic Sites (AP sites) Homo sapiens R-HSA-73933	9/35	0.0072	1.0000	3.0499	15.0440	PCNA;PARG;NEIL2;LIG1;MPG;PNKP;TDG;POLE2;XRCC1
GOBP2021	glycosaminoglycan catabolic process (GO:0006027)	13/56	0.0036	1.0000	2.6664	14.9951	HGSNAT;CEMIP2;HEXB;BGN;PRELP;SGSH;SLC9A1;HYAL3;GPC2;SDC1;HPSE;CD44;ARSB
KEGG2019M	Glycosaminoglycan degradation	6/21	0.0159	0.5718	3.5213	14.5785	HGSNAT;HEXB;HYAL3;HPSE;ARSB;SGSH
BioPlanet2019	Presynaptic function of kainate receptors	6/21	0.0159	1.0000	3.5213	14.5785	GNG10;GNB2;GNB1;GRIK3;GNB3;GNG11
Reactome2016	Presynaptic function of Kainate receptors Homo sapiens R-HSA-500657	6/21	0.0159	1.0000	3.5213	14.5785	GNG10;GNB2;GNB1;GRIK3;GNB3;GNG11
GOBP2021	response to growth factor (GO:0070848)	10/41	0.0070	1.0000	2.8428	14.0864	URI1;AMHR2;MYC;CTNNB1;LRP2;NOS1;BMPR1B;MAP2K5;ACVR2A;BMPR1A
BioPlanet2019	Stathmin and breast cancer resistance to antimicrotubule agents	8/31	0.0108	1.0000	3.0636	13.8673	CD2;CAMK2D;HSPA5;PRKAR1B;PRKAR2B;TUBB1;CD247;UHMK1
WikiPath2019M	Ovarian Infertility Genes WP273	8/31	0.0108	0.8547	3.0636	13.8673	EGR1;LHCGR;VDR;GJA4;INHA;BMPR1B;PRLR;ZP2
WikiPath2019M	One carbon metabolism and related pathways WP1770	12/52	0.0053	0.8440	2.6451	13.8395	PCYT1B;PCYT2;MAT2A;SHMT2;CBS;SHMT1;GSS;CTH;ETNK1;BCAT1;BCAT2;GNMT
BioPlanet2019	Branched-chain amino acid catabolism	5/17	0.0241	1.0000	3.6668	13.6657	ALDH6A1;DBT;BCAT1;DLD;BCAT2
GOBP2021	positive regulation of heart rate (GO:0010460)	5/17	0.0241	1.0000	3.6668	13.6657	EDN1;KCNQ1;NPPA;SCN3B;TRPM4
Reactome2016	Hyaluronan metabolism Homo sapiens R-HSA-2142845	5/17	0.0241	1.0000	3.6668	13.6657	HEXB;HAS1;HYAL3;CD44;SLC9A1
GOBP2021	regulation of cytoskeleton organization (GO:0051493)	22/112	0.0020	0.9719	2.1599	13.4392	GSK3B;RHOG;PDGFA;RHOF;IQGAP2;RND2;BAIAP2;COR O1A;RND3;P2RX7;SYDE1;CCDC88A;BST1;CAPN6;SH3BP1;KATNBL1;RAC2;MAP6D1;PLXNB1;S100A9;CRK;S100A8
Reactome2016	Glucagon-like Peptide-1 (GLP1) regulates insulin secretion Homo sapiens R-HSA-381676	10/42	0.0084	1.0000	2.7538	13.1551	GNG10;PRKAR1B;PRKAR2B;KCNB1;GNB2;GNB1;GNB3;ITPR3;GNG11;ADCY5
GOBP2021	chromatin organization involved in regulation of transcription (GO:0034401)	4/13	0.0366	1.0000	3.9100	12.9331	SPI1;ZMIZ2;PADI2;ARID1A
GOBP2021	glucose import (GO:0046323)	4/13	0.0366	1.0000	3.9100	12.9331	SLC27A1;SLC2A1;ZDHHC7;SLC5A1
GOBP2021	negative regulation of endoplasmic reticulum unfolded protein response (GO:1900102)	4/13	0.0366	1.0000	3.9100	12.9331	HSPA5;ATF6B;DNAJB9;NCK1
GOBP2021	negative regulation of locomotion (GO:0040013)	4/13	0.0366	1.0000	3.9100	12.9331	WAS;FBLN1;SPINT2;CRK
GOBP2021	positive regulation of purine nucleotide biosynthetic process (GO:1900373)	4/13	0.0366	1.0000	3.9100	12.9331	NOS2;NOS1;PPARA;PPARGC1A
GOBP2021	regulation of actomyosin structure organization (GO:0110020)	4/13	0.0366	1.0000	3.9100	12.9331	PTGER4;FHOD1;WAS;SLC9A1
GOBP2021	regulation of nucleocytoplasmic transport (GO:0046822)	4/13	0.0366	1.0000	3.9100	12.9331	NUP214;RBM4;IFI27;UHMK1
Reactome2016	Signaling by Activin Homo sapiens R-HSA-1502540	4/13	0.0366	1.0000	3.9100	12.9331	SMAD2;FST;ACVR2A;FSTL3
GOBP2021	regulation of voltage-gated calcium channel activity (GO:1901385)	6/22	0.0200	1.0000	3.3010	12.9067	CACNB1;FMR1;NOS1AP;NPPA;STAC2;CBARP
Reactome2016	ADP signalling through P2Y purinoceptor 12 Homo sapiens R-HSA-392170	6/22	0.0200	1.0000	3.3010	12.9067	P2RY12;GNG10;GNB2;GNB1;GNB3;GNG11
GOBP2021	glutamine family amino acid metabolic process (GO:0009064)	9/37	0.0105	1.0000	2.8317	12.8900	ALDH4A1;ALDH5A1;GOT1;TAT;SIRT4;PYCR1;PYCR2;MTHFS;GLS
KEGG2019M	beta-Alanine metabolism	8/32	0.0132	0.5718	2.9358	12.7131	ALDH3B3;ALDH6A1;ALDH1B1;CARNS1;SMS;ABAT;UPB1;SRM
BioPlanet2019	ADP signalling through P2Y purinoceptor 12	7/27	0.0163	1.0000	3.0818	12.6804	P2RY12;GNG10;GNB2;GNB1;GRIK3;GNB3;GNG11
GOBP2021	positive regulation of toll-like receptor signaling pathway (GO:0034123)	7/27	0.0163	1.0000	3.0818	12.6804	NR1H3;PTPN22;CYBA;IFI35;LBP;PJA2;TLR2
BioPlanet2019	Insulin secretion regulation by glucagon-like peptide-1	10/43	0.0100	1.0000	2.6702	12.2992	GNG10;PRKAR1B;PRKAR2B;KCNB1;GNB2;GNB1;GNB3;ITPR3;GNG11;ADCY5
BioPlanet2019	Pre-NOTCH processing in Golgi	5/18	0.0306	1.0000	3.3846	11.8021	B4GALT1;MFNG;ST3GAL4;RFNG;RAB6A
GOBP2021	hyaluronan catabolic process (GO:0030214)	5/18	0.0306	1.0000	3.3846	11.8021	CEMIP2;HEXB;HYAL3;CD44;SLC9A1
GOBP2021	intracellular estrogen receptor signaling pathway (GO:0030520)	5/18	0.0306	1.0000	3.3846	11.8021	RBFOX2;NCOA4;TADA3;PADI2;ARID1A
GOBP2021	negative regulation of cation transmembrane transport (GO:1904063)	5/18	0.0306	1.0000	3.3846	11.8021	KCNH2;CAMK2D;SLC43A1;MMP9;CBARP
GOBP2021	ventricular cardiac muscle cell action potential (GO:0086005)	5/18	0.0306	1.0000	3.3846	11.8021	KCNH2;KCNE1;KCNJ8;KCNQ1;SCN3B
Reactome2016	Pre-NOTCH Processing in Golgi Homo sapiens R-HSA-1912420	5/18	0.0306	1.0000	3.3846	11.8021	B4GALT1;MFNG;ST3GAL4;RFNG;RAB6A
BioPlanet2019	Glucagon signaling in metabolic regulation	8/33	0.0159	1.0000	2.8182	11.6791	GNG10;PRKAR1B;PRKAR2B;GNB2;GNB1;GNB3;GNG11;ADCY5
Reactome2016	Glucagon signaling in metabolic regulation Homo sapiens R-HSA-163359	8/33	0.0159	1.0000	2.8182	11.6791	GNG10;PRKAR1B;PRKAR2B;GNB2;GNB1;GNB3;GNG11;ADCY5
GOBP2021	regulation of small molecule metabolic process (GO:0062012)	7/28	0.0199	1.0000	2.9349	11.4954	NCOR2;ARV1;PDK4;GNB3;RORA;PPARA;PDK1
GOBP2021	hyaluronan metabolic process (GO:0030212)	6/23	0.0248	1.0000	3.1067	11.4811	CEMIP2;HEXB;HAS1;HYAL3;CD44;SLC9A1
GOBP2021	protein alkylation (GO:0008213)	6/23	0.0248	1.0000	3.1067	11.4811	PCMT1;PRMT2;ETF1;EEF1AKMT2;GSPT1;CAMKMT
GOBP2021	respiratory chain complex IV assembly (GO:0008535)	6/23	0.0248	1.0000	3.1067	11.4811	OXA1L;SURF1;FASTKD3;COX17;COA8;COX10
Reactome2016	Branched-chain amino acid catabolism Homo sapiens R-HSA-70895	6/23	0.0248	1.0000	3.1067	11.4811	ALDH6A1;SHMT1;DBT;BCAT1;DLD;BCAT2
GOBP2021	regulation of lipid metabolic process (GO:0019216)	18/92	0.0051	1.0000	2.1469	11.3397	PRKAG2;RORA;EDF1;NR1D2;LSS;SREBF2;ACACA;TM7SF2;TM6SF2;NCOR2;C1QTNF2;TGS1;APOC1;GNB3;MVD;PPARA;PPARD;CERS2
Reactome2016	Regulation of insulin secretion Homo sapiens R-HSA-422356	16/80	0.0064	1.0000	2.2056	11.1346	SYT5;KCNJ11;KCNB1;SLC2A1;ITPR3;GNG11;ADCY5;GNA14;GNA15;GNG10;PRKAR1B;PRKAR2B;GNB2;GNB1;GNB3;SLC25A5
GOBP2021	action potential (GO:0001508)	10/45	0.0138	1.0000	2.5173	10.7843	CHRNA1;KCNH2;CACNA1I;GNA14;KCNE1;GNA15;KCNB1;KCNQ1;KCNMB2;SCN3B
GOBP2021	cardiac muscle contraction (GO:0060048)	8/34	0.0189	1.0000	2.7097	10.7496	KCNH2;CAMK2D;CSRP3;GSN;KCNQ1;MYL3;SCN3B;ATP1B1
BioPlanet2019	Hyaluronan metabolism	4/14	0.0472	1.0000	3.5188	10.7437	HEXB;HAS1;CD44;SLC9A1
BioPlanet2019	Polyamine metabolism	4/14	0.0472	1.0000	3.5188	10.7437	GOT1;SMS;AGMAT;SRM
GOBP2021	membrane repolarization during action potential (GO:0086011)	4/14	0.0472	1.0000	3.5188	10.7437	KCNH2;KCNE1;KCNQ1;ATP1B1
GOBP2021	positive regulation of lymphocyte migration (GO:2000403)	4/14	0.0472	1.0000	3.5188	10.7437	PYCARD;TMEM102;CCL5;JAM2
GOBP2021	regulation of response to endoplasmic reticulum stress (GO:1905897)	4/14	0.0472	1.0000	3.5188	10.7437	NR1H3;NUPR1;CLU;MBTPS2
Reactome2016	CS/DS degradation Homo sapiens R-HSA-2024101	4/14	0.0472	1.0000	3.5188	10.7437	HEXB;HYAL3;BGN;ARSB
Reactome2016	Synthesis of Prostaglandins (PG) and Thromboxanes (TX) Homo sapiens R-HSA-2162123	4/14	0.0472	1.0000	3.5188	10.7437	CBR1;PTGIS;PTGR1;PTGDS
Reactome2016	Regulation of pyruvate dehydrogenase (PDH) complex Homo sapiens R-HSA-204174	4/14	0.0472	1.0000	3.5188	10.7437	PDK4;DLD;PDK1;PPARD
BioPlanet2019	Inhibition of insulin secretion by adrenaline/noradrenaline	7/29	0.0240	1.0000	2.8013	10.4497	GNAO1;GNG10;GNB2;GNB1;GNB3;GNG11;ADCY5
KEGG2019M	Glycine, serine and threonine metabolism	9/40	0.0176	0.5718	2.5573	10.3365	GRHPR;THA1;SHMT2;CBS;SHMT1;CTH;DLD;GCAT;GNMT
KEGG2019M	Arginine biosynthesis	5/19	0.0381	1.0000	3.1426	10.2668	GOT1;ACY1;NOS2;NOS1;GLS
BioPlanet2019	Resolution of abasic sites (AP sites)	5/19	0.0381	1.0000	3.1426	10.2668	PCNA;LIG1;MPG;TDG;XRCC1
GOBP2021	folic acid metabolic process (GO:0046655)	5/19	0.0381	1.0000	3.1426	10.2668	ALDH1L1;SHMT2;SHMT1;MTHFS;SLC25A32
GOBP2021	myeloid cell activation involved in immune response (GO:0002275)	5/19	0.0381	1.0000	3.1426	10.2668	PYCARD;FER1L5;SBNO2;IFI35;LBP
GOBP2021	neural crest cell differentiation (GO:0014033)	5/19	0.0381	1.0000	3.1426	10.2668	TCOF1;HTR2B;FBXL17;KLHL12;LRP6
Reactome2016	Prostacyclin signalling through prostacyclin receptor Homo sapiens R-HSA-392851	5/19	0.0381	1.0000	3.1426	10.2668	GNG10;GNB2;GNB1;GNB3;GNG11
WikiPath2019M	Mitochondrial Gene Expression WP1263	5/19	0.0381	0.8679	3.1426	10.2668	PPP3CA;MTERF1A;TFB2M;POLRMT;PPARGC1A
GOBP2021	base-excision repair, gap-filling (GO:0006287)	8/35	0.0224	1.0000	2.6092	9.9113	PCNA;PARG;LIG1;MPG;PNKP;TDG;XRCC1;POLL

• **Table S6: Enriched pathways specific to mG4H-ON (Venn Diagram: Group I)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	semaphorin-plexin signaling pathway (GO:0071526)	8/35	0.0224	1.0000	2.6092	9.9113	SEMA5A;FARP2;SEMA5B;NRP2;SH3BP1;SEMA3E;PLXNB1;PLXNA3
GOBP2021	smoothened signaling pathway (GO:0007224)	8/35	0.0224	1.0000	2.6092	9.9113	TMEM17;ARL13B;DHH;STK36;TCTN2;PTCH1;PTCH2;GPC2
GOBP2021	inorganic cation import across plasma membrane (GO:0098659)	15/77	0.0104	1.0000	2.1337	9.7400	KCNH2;HCN4;KCNJ10;KCNJ8;KCNJ11;ATP1A3;SLC5A1;ATP1B1;SLC9A1;SLC9A2;SLC8A3;SLC9A4;SLC12A8;SLC12A9;TRPM4
GOBP2021	protein methylation (GO:0006479)	9/41	0.0205	1.0000	2.4772	9.6274	PCMT1;TRMT112;PRMT2;ETF1;RAB6A;EEF1AKMT2;GSPT1;CAMKMT;EZH2
Reactome2016	Histidine, lysine, phenylalanine, tyrosine, proline and tryptophan catabolism Homo sapiens R-HSA-6788656	9/41	0.0205	1.0000	2.4772	9.6274	ALDH4A1;GCDH;PHYKPL;TAT;CARNS1;OGDH;DLD;AASS;IDO1
Reactome2016	Integration of energy metabolism Homo sapiens R-HSA-163685	20/110	0.0076	1.0000	1.9616	9.5654	SYT5;KCNJ11;KCNB1;SLC2A1;PRKAG2;ITPR3;AGPAT1;GNG11;ACACA;ADCY5;GNA14;GNG10;GNA15;PRKAR1B;PPP2R1A;PRKAR2B;GNB2;GNB1;GNB3;SLC25A5
BioPlanet2019	Integration of energy metabolism	22/125	0.0078	1.0000	1.8859	9.1434	SYT5;KCNJ11;KCNB1;SLC2A1;PRKAG2;ITPR3;AGPAT1;GNG11;ACACA;ADCY5;GNAO1;GNA14;GNG10;GNA15;PRKAR1B;PPP2R1A;PRKAR2B;GNB2;GNB1;GNB3;CTNNB1;SLC25A5
GOBP2021	branched-chain amino acid catabolic process (GO:0009083)	5/20	0.0467	1.0000	2.9330	8.9873	ALDH6A1;DBT;BCAT1;DLD;BCAT2
GOBP2021	branched-chain amino acid metabolic process (GO:0009081)	5/20	0.0467	1.0000	2.9330	8.9873	ALDH6A1;DBT;BCAT1;DLD;BCAT2
GOBP2021	cellular modified amino acid biosynthetic process (GO:0042398)	5/20	0.0467	1.0000	2.9330	8.9873	SLC27A1;GSS;MTHFS;CHAC1;OPLAH
GOBP2021	folic acid-containing compound metabolic process (GO:0006760)	5/20	0.0467	1.0000	2.9330	8.9873	ALDH1L1;SHMT2;SHMT1;MTHFS;SLC25A32
GOBP2021	inositol phosphate-mediated signaling (GO:0048016)	5/20	0.0467	1.0000	2.9330	8.9873	PPP3CA;EDN1;HRH1;NFATC2;GPR62
GOBP2021	mitochondrial cytochrome c oxidase assembly (GO:0033617)	5/20	0.0467	1.0000	2.9330	8.9873	OXA1L;SURF1;FASTKD3;COX17;COA8
GOBP2021	positive regulation of heart contraction (GO:0045823)	5/20	0.0467	1.0000	2.9330	8.9873	EDN1;KCNQ1;NPPA;SCN3B;TRPM4
GOBP2021	toll-like receptor 4 signaling pathway (GO:0034142)	5/20	0.0467	1.0000	2.9330	8.9873	TRIL;TNIP3;LBP;LGALS9;PIK3AP1
Reactome2016	G beta:gamma signalling through PLC beta Homo sapiens R-HSA-418217	5/20	0.0467	1.0000	2.9330	8.9873	GNG10;GNB2;GNB1;GNB3;GNG11
GOBP2021	potassium ion import across plasma membrane (GO:1990573)	9/42	0.0238	1.0000	2.4020	8.9769	HCN4;KCNH2;KCNJ10;KCNJ8;KCNJ11;ATP1A3;ATP1B1;SLC12A8;SLC12A9
GOBP2021	base-excision repair (GO:0006284)	10/48	0.0214	1.0000	2.3182	8.9148	USP47;PCNA;PARG;NEIL2;LIG1;MPG;PNKP;TDG;XRCC1;POLL
BioPlanet2019	Inwardly rectifying potassium channels	7/31	0.0338	1.0000	2.5676	8.6974	GNG10;KCNJ10;KCNJ8;KCNJ11;GNB2;GNB1;GNB3
GOBP2021	positive regulation of protein targeting to mitochondrion (GO:1903955)	7/31	0.0338	1.0000	2.5676	8.6974	RNF31;NPEPPS;FZD5;FBXW7;VPS11;RAC2;SREBF2
Reactome2016	Inwardly rectifying K+ channels Homo sapiens R-HSA-1296065	7/31	0.0338	1.0000	2.5676	8.6974	GNG10;KCNJ10;KCNJ8;KCNJ11;GNB2;GNB1;GNB3
WikiPath2019M	Glutathione and one carbon metabolism WP730	7/31	0.0338	0.8679	2.5676	8.6974	SHMT2;CBS;SHMT1;ANPEP;GSS;CTH;OPLAH
Reactome2016	Vasopressin regulates renal water homeostasis via Aquaporins Homo sapiens R-HSA-432040	9/43	0.0275	1.0000	2.3312	8.3791	GNG10;PRKAR1B;PRKAR2B;GNB2;GNB1;GNB3;AQP4;GNG11;ADCY5
BioPlanet2019	PGC-1a regulation	6/26	0.0436	1.0000	2.6402	8.2736	HDAC5;PPP3CA;CAMK2D;PPARA;PPARGC1A;CAMKK1
BioPlanet2019	RXR/VDR pathway	6/26	0.0436	1.0000	2.6402	8.2736	NCOR2;RARG;VDR;NR1H3;PPARA;PPARD
GOBP2021	cellular response to drug (GO:0035690)	6/26	0.0436	1.0000	2.6402	8.2736	KCNH2;MYC;KCNQ1;SLAMF8;PPM1E;RBM22
GOBP2021	meiosis I (GO:0007127)	6/26	0.0436	1.0000	2.6402	8.2736	ZCWPW1;ING2;PTTG1;FOXJ3;MOV10L1;SLC25A31
BioPlanet2019	Glycine, serine and threonine metabolism	7/32	0.0396	1.0000	2.4647	7.9601	SHMT2;CBS;SHMT1;CTH;DLD;GCAT;GNMT
GOBP2021	regulation of intracellular protein transport (GO:0033157)	7/32	0.0396	1.0000	2.4647	7.9601	BCAS3;IFI27;RAB29;ZFAND1;KIF20B;CEP290;UHMK1
Reactome2016	Thrombin signalling through proteinase activated receptors (PARs) Homo sapiens R-HSA-456926	7/32	0.0396	1.0000	2.4647	7.9601	GNA14;GNA15;GNG10;GNB2;GNB1;GNB3;GNG11
BioPlanet2019	Aquaporin-mediated transport	10/50	0.0279	1.0000	2.2021	7.8830	GNG10;PRKAR1B;PRKAR2B;AQP8;GNB2;GNB1;GNB3;AQP4;GNG11;ADCY5
BioPlanet2019	NFAT involvement in hypertrophy of the heart	13/69	0.0213	1.0000	2.0460	7.8734	GSK3B;HDAC5;EDN1;CTF1;NFATC2;MAPK14;CAMKK1;PPP3CA;ACTA1;PRKAR1B;PRKAR2B;NPPA;ADSS
GOBP2021	positive regulation of potassium ion transmembrane transport (GO:1901381)	9/44	0.0315	1.0000	2.2645	7.8288	KCNH2;KCNE1;KCNJ10;KCNQ1;KCNMB2;NPPA;NOS1AP;GNB1;ATP1B1
KEGG2019M	Relaxin signaling pathway	22/131	0.0134	0.5718	1.7815	7.6823	SHC4;SMAD2;EDN1;ATF6B;NOS2;MMP2;VEGFD;MAPK14;RXFP1;GNG11;MMP9;ADCY5;GNAO1;MAPK9;GNG10;GNA15;GNB2;AKT3;GNB1;COL4A6;GNB3;NOS1
GOBP2021	dicarboxylic acid metabolic process (GO:0043648)	11/57	0.0277	1.0000	2.1067	7.5514	ALDH1L1;ALDH5A1;GOT1;SHMT2;TAT;SHMT1;ADHFE1;IDH2;OGDH;MTHFS;SLC25A32
BioPlanet2019	Metabolism of vitamins and cofactors	10/51	0.0316	1.0000	2.1482	7.4203	SLC5A6;MOCS2;RFK;NAPRT;SHMT1;SLC2A1;SLC19A3;SLC25A32;NADSYN1;COASY
GOBP2021	regulation of smoothened signaling pathway (GO:0008589)	10/51	0.0316	1.0000	2.1482	7.4203	STK36;RAB34;PTCH1;PTCH2;ARMC9;FBXL17;RORA;FUZ;UCHL5;GLIS2
Reactome2016	Aquaporin-mediated transport Homo sapiens R-HSA-445717	10/51	0.0316	1.0000	2.1482	7.4203	GNG10;PRKAR1B;PRKAR2B;AQP8;GNB2;GNB1;GNB3;AQP4;GNG11;ADCY5
BioPlanet2019	Pyruvate metabolism and citric acid (TCA) cycle	8/40	0.0466	1.0000	2.2009	6.7504	SLC16A1;ADHFE1;IDH2;PDK4;OGDH;SLC16A8;DLD;PDK1
GOBP2021	regulation of actin filament-based process (GO:0032970)	13/73	0.0326	1.0000	1.9091	6.5373	RHOG;PDGFA;RHOF;RND2;IQGAP2;BAIAP2;RND3;CORO1A;BST1;CCDC88A;SH3BP1;RAC2;CRK
Reactome2016	Platelet homeostasis Homo sapiens R-HSA-418346	15/87	0.0297	1.0000	1.8363	6.4551	NOS2;ITPR3;MAPK14;GNG11;P2RX7;SLC8A3;P2RX6;GNG10;PPP2R5E;PPP2R1A;GNB2;KCNMB2;GNB1;GNB3;NOS1
BioPlanet2019	Delta Np63 pathway	9/47	0.0461	1.0000	2.0854	6.4186	YAP1;TOP2A;SEC14L2;GSK3B;CEBPD;FBXW7;VDR;BDKRB2;FOSL2
Reactome2016	Ca2+ pathway Homo sapiens R-HSA-4086398	11/61	0.0433	1.0000	1.9377	6.0829	GNAO1;PPP3CA;GNG10;FZD5;GNB2;GNB1;GNB3;CTNNB1;ITPR3;GNG11;TNRC6B
BioPlanet2019	Glycosaminoglycan metabolism	18/110	0.0300	1.0000	1.7251	6.0518	B4GALT3;B4GALT1;GLCE;HEXB;BGN;PRELP;HS3ST1;SLC9A1;SGSH;HAS1;UST;ST3GAL4;SDC1;GPC2;HPSE;ST3GAL1;ARSB;CD44
GOBP2021	translational termination (GO:0006415)	16/96	0.0337	1.0000	1.7629	5.9779	MRPS26;MRPS35;MRPS34;MRPL38;MRPL17;MRPL28;MRPL58;MRPL37;GSPT2;MRPL10;GSPT1;MRPL22;MRPL41;TRMT112;OXA1L;ETF1
GOBP2021	positive regulation of inflammatory response (GO:0050729)	15/89	0.0356	1.0000	1.7865	5.9573	SETD4;PTGER4;GRN;IL16;C2CD4B;IFI35;SNX4;DDT;NFKBIZ;CCN4;LBP;NUPR1;S100A9;S100A8;TLR2
GOBP2021	regulation of cell division (GO:0051302)	13/76	0.0435	1.0000	1.8179	5.7010	PLK4;UVRAG;SUSD2;HTR2B;PRPF40A;SIRT2;KLHL9;PRC1;MYC;INSC;EFHC1;TXNIP;RAB11FIP4
Reactome2016	Metabolism of water-soluble vitamins and cofactors Homo sapiens R-HSA-196849	16/98	0.0398	1.0000	1.7197	5.5441	CUBN;ALDH1L1;MOCS2;PTGIS;SHMT2;SHMT1;SLC2A1;MTHFS;NADSYN1;ACACA;COASY;SLC5A6;NAPRT;RFK;SLC19A3;SLC25A32
GOBP2021	positive regulation of tumor necrosis factor production (GO:0032760)	13/77	0.0476	1.0000	1.7894	5.4491	SETD4;FZD5;SPHK2;CYBA;CLU;PYCARD;CD2;DDT;TNFRSF8;LBP;LGALS9;TMEM106A;TLR2
Reactome2016	Glycosaminoglycan metabolism Homo sapiens R-HSA-1630316	19/121	0.0383	1.0000	1.6423	5.3588	B4GALT3;B4GALT1;GLCE;HEXB;BGN;PRELP;HS3ST1;SLC9A1;SGSH;HAS1;UST;HYAL3;ST3GAL4;SDC1;GPC2;HPSE;ST3GAL1;ARSB;CD44
BioPlanet2019	Potassium channels	16/99	0.0431	1.0000	1.6989	5.3399	KCNH2;HCN4;KCNG4;KCNJ10;KCNJ8;KCNJ11;KCNB1;KCNA4;KCNV2;GNG10;KCNQ1;GNB2;KCNMB2;GNB1;GNB3;KCNK1
Reactome2016	Potassium Channels Homo sapiens R-HSA-1296071	16/99	0.0431	1.0000	1.6989	5.3399	KCNH2;HCN4;KCNG4;KCNJ10;KCNJ8;KCNJ11;KCNB1;KCNA4;KCNV2;GNG10;KCNQ1;GNB2;KCNMB2;GNB1;GNB3;KCNK1
GOBP2021	cell-matrix adhesion (GO:0007160)	16/100	0.0467	1.0000	1.6786	5.1437	ITGB4;FN1;PTPRK;L1CAM;MSLN;THSD1;THBS3;ITGA10;ANGPTL3;ITGA7;EMILIN1;ITGB7;HPSE;CD34;CD44;FERMT3
KEGG2019M	Apelin signaling pathway	21/138	0.0412	1.0000	1.5827	5.0475	SMAD2;EGR1;HDAC5;NOS2;SPHK2;PRKAG2;ITPR3;GNG11;GABARAP;SLC9A1;ADCY5;SLC8A3;GNG10;GNB2;AKT3;MYL3;GNB1;GNB3;NOS1;PLIN1;PPARGC1A

• **Table S6: Enriched pathways specific to mG4H-ON (Venn Diagram: Group I)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
BioPlanet2019	Amino acid metabolism	28/195	0.0408	1.0000	1.4795	4.7321	GCDH;PSMD13;SHMT1;TAT;PSMB10;GLS;SRM;MAT2A;CBS;DBT;AASS;GOT1;PYCR1;AZIN1;AGMAT;ALDH4A1;GRHPR;ALDH6A1;PSMA3;TST;CTH;OGDH;SMS;INHA;BCAT1;DLD;IDO1;BCAT2
GOBP2021	regulation of inflammatory response (GO:0050727)	29/206	0.0472	1.0000	1.4456	4.4132	SETD4;PTGER4;GRN;CELF1;RORA;IFI35;USP18;SBNO2;DDT;CCL5;NFKBIZ;CCN4;PTGIS;NR1H3;NR1D2;IL16;MMP9;FOXP1;BST1;SELENOS;BCL6B;TYRO3;PPARA;PIK3AP1;S100A9;S100A8;VAMP3;TLR2;PPARD

• **Table S7: Enriched pathways specific to mG4H-OFF (Venn Diagram: Group II)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
BioPlanet2019	Abacavir metabolism	3/5	0.0024	1.0000	22.0051	133.0539	ADAL;GUK1;PCK1
GOBP2021	glycerol biosynthetic process (GO:0006114)	3/5	0.0024	1.0000	22.0051	133.0539	PDXP;PCK1;PCK2
Reactome2016	Abacavir metabolism Homo sapiens R-HSA-2161541	3/5	0.0024	1.0000	22.0051	133.0539	ADAL;GUK1;PCK1
GOBP2021	chemical homeostasis within a tissue (GO:0048875)	3/7	0.0075	1.0000	11.0014	53.8075	RCN3;NAPSA;CTSH
GOBP2021	surfactant homeostasis (GO:0043129)	3/7	0.0075	1.0000	11.0014	53.8075	RCN3;NAPSA;CTSH
GOBP2021	organophosphate catabolic process (GO:0046434)	4/11	0.0038	1.0000	8.3872	46.6993	PON1;PLBD1;PDXP;NUDT15
GOBP2021	peptidyl-proline hydroxylation to 4-hydroxy-L-proline (GO:0018401)	3/8	0.0115	1.0000	8.8006	39.3330	EGLN1;P4HA1;P4HTM
GOBP2021	regulation of MyD88-independent toll-like receptor signaling pathway (GO:0034127)	3/8	0.0115	1.0000	8.8006	39.3330	IRF7;TLR4;TLR3
GOBP2021	single strand break repair (GO:0000012)	3/8	0.0115	1.0000	8.8006	39.3330	APLF;LIG4;APTX
GOBP2021	axon choice point recognition (GO:0016198)	2/5	0.0359	1.0000	9.7719	32.5133	ROBO2;ROBO1
GOBP2021	chemokine (C-X-C motif) ligand 12 signaling pathway (GO:0038146)	2/5	0.0359	1.0000	9.7719	32.5133	STK39;TREM2
GOBP2021	negative regulation of pinocytosis (GO:0048550)	2/5	0.0359	1.0000	9.7719	32.5133	STX1B;CAV1
GOBP2021	positive regulation of neurotransmitter transport (GO:0051590)	2/5	0.0359	1.0000	9.7719	32.5133	STX1B;DTNBP1
GOBP2021	positive regulation of nucleotide-binding oligomerization domain containing signaling pathway (GO:0070426)	2/5	0.0359	1.0000	9.7719	32.5133	SLC15A4;HSPA1A
GOBP2021	regulation of inward rectifier potassium channel activity (GO:1901979)	2/5	0.0359	1.0000	9.7719	32.5133	CAV1;TREM2
GOBP2021	serotonin metabolic process (GO:0042428)	2/5	0.0359	1.0000	9.7719	32.5133	DDC;RNF180
GOBP2021	negative regulation of cellular metabolic process (GO:0031324)	9/39	0.0006	1.0000	4.4152	32.4581	TFAP2A;SDCBP;ITGB3;BRCA1;APOE;MT3;ANKRD13A;OPTN;PLIN5
GOBP2021	microtubule-based transport (GO:0099111)	4/13	0.0075	1.0000	6.5227	31.9455	CCDC103;HTT;SPA17;CCDC40
GOBP2021	response to nitric oxide (GO:0071731)	4/13	0.0075	1.0000	6.5227	31.9455	EGLN1;KCNC2;MMP3;MT3
BioPlanet2019	Inactivation of Cdc42 and Rac	3/9	0.0164	1.0000	7.3335	30.1556	GPC1;SRGAP3;ROBO1
GOBP2021	cellular response to nitric oxide (GO:0071732)	3/9	0.0164	1.0000	7.3335	30.1556	KCNC2;MMP3;MT3
GOBP2021	cellular response to reactive nitrogen species (GO:1902170)	3/9	0.0164	1.0000	7.3335	30.1556	KCNC2;MMP3;MT3
GOBP2021	epithelial cilium movement involved in determination of left/right asymmetry (GO:0060287)	3/9	0.0164	1.0000	7.3335	30.1556	CCDC103;CFAP53;CCDC40
GOBP2021	ketone body biosynthetic process (GO:0046951)	3/9	0.0164	1.0000	7.3335	30.1556	ACSS3;BDH2;HMGCS2
GOBP2021	mast cell mediated immunity (GO:0002448)	3/9	0.0164	1.0000	7.3335	30.1556	MILR1;SERPINB9;PIK3CG
Reactome2016	Inactivation of Cdc42 and Rac Homo sapiens R-HSA-428543	3/9	0.0164	1.0000	7.3335	30.1556	GPC1;SRGAP3;ROBO1
BioPlanet2019	Abacavir transport and metabolism	3/10	0.0223	1.0000	6.2855	23.9062	ADAL;GUK1;PCK1
GOBP2021	cellular response to oxidised low-density lipoprotein particle stimulus (GO:0140052)	3/10	0.0223	1.0000	6.2855	23.9062	MIA3;TREM2;TLR4
GOBP2021	positive regulation of keratinocyte migration (GO:0051549)	3/10	0.0223	1.0000	6.2855	23.9062	EPB41L4B;FGF7;FGF10
GOBP2021	secretory granule organization (GO:0033363)	3/10	0.0223	1.0000	6.2855	23.9062	SRGN;DTNBP1;F2RL3
Reactome2016	Abacavir transport and metabolism Homo sapiens R-HSA-2161522	3/10	0.0223	1.0000	6.2855	23.9062	ADAL;GUK1;PCK1
GOBP2021	positive regulation of transcription from RNA polymerase II promoter involved in cellular response to chemical stimulus (GO:1901522)	5/21	0.0091	1.0000	4.5882	21.5491	XBP1;BMP2;MT3;RUNX2;NFE2L2
GOBP2021	cellular response to interleukin-2 (GO:0071352)	3/11	0.0292	1.0000	5.4995	19.4286	STAT5A;IL2RB;IL2RG
GOBP2021	interleukin-2-mediated signaling pathway (GO:0038110)	3/11	0.0292	1.0000	5.4995	19.4286	STAT5A;IL2RB;IL2RG
GOBP2021	ketone body metabolic process (GO:1902224)	3/11	0.0292	1.0000	5.4995	19.4286	ACSS3;BDH2;HMGCS2
GOBP2021	peptidyl-proline hydroxylation (GO:0019511)	3/11	0.0292	1.0000	5.4995	19.4286	EGLN1;P4HA1;P4HTM
GOBP2021	positive regulation of voltage-gated potassium channel activity (GO:1903818)	3/11	0.0292	1.0000	5.4995	19.4286	KCNIP2;LRRC38;TREM2
GOBP2021	negative regulation of reactive oxygen species metabolic process (GO:2000378)	5/23	0.0136	1.0000	4.0779	17.5338	TFAP2A;MMP3;BRCA1;MT3;PLIN5
GOBP2021	cellular response to thyroid hormone stimulus (GO:0097067)	3/12	0.0372	1.0000	4.8882	16.0956	CTSH;BRD8;CTSS
GOBP2021	motile cilium assembly (GO:0044458)	3/12	0.0372	1.0000	4.8882	16.0956	RSPH9;SPATA6;CCDC40
GOBP2021	regulation of keratinocyte migration (GO:0051547)	3/12	0.0372	1.0000	4.8882	16.0956	EPB41L4B;FGF7;FGF10
GOBP2021	purine nucleotide metabolic process (GO:0006163)	5/24	0.0163	1.0000	3.8631	15.9117	NT5E;GUK1;NUDT15;DNPH1;GART
GOBP2021	positive regulation of excitatory postsynaptic potential (GO:2000463)	4/18	0.0248	1.0000	4.1920	15.5047	NLGN3;RIMS2;STX1B;SHANK1
GOBP2021	positive regulation of Rho protein signal transduction (GO:0035025)	6/31	0.0125	1.0000	3.5248	15.4408	GPR35;LPAR6;GPR4;GPR18;ROBO1;F2RL3
GOBP2021	liver development (GO:0001889)	6/32	0.0146	1.0000	3.3890	14.3262	XBP1;PCK1;GFER;AURKA;PCK2;CCDC40
GOBP2021	positive regulation of Ras protein signal transduction (GO:0046579)	10/63	0.0063	1.0000	2.7756	14.0442	RASGEF1A;ALS2;GPR35;LPAR6;GPR4;PIK3CG;GPR18;ROBO1;FGF10;F2RL3
GOBP2021	long-term memory (GO:0007616)	4/19	0.0298	1.0000	3.9124	13.7433	CAMK4;SLC2A4;APOE;SHANK1
GOBP2021	cellular response to interleukin-15 (GO:0071350)	3/13	0.0461	1.0000	4.3991	13.5400	STAT5A;IL2RB;IL2RG
GOBP2021	extracellular transport (GO:0006858)	3/13	0.0461	1.0000	4.3991	13.5400	CCDC103;SPA17;CCDC40
GOBP2021	Golgi ribbon formation (GO:0090161)	3/13	0.0461	1.0000	4.3991	13.5400	GOLGA2;OPTN;TMED5
GOBP2021	interleukin-15-mediated signaling pathway (GO:0035723)	3/13	0.0461	1.0000	4.3991	13.5400	STAT5A;IL2RB;IL2RG
GOBP2021	negative regulation of histone methylation (GO:0031061)	3/13	0.0461	1.0000	4.3991	13.5400	DNMT3B;BRCA1;MACROH2A1
GOBP2021	positive regulation of neuron migration (GO:2001224)	3/13	0.0461	1.0000	4.3991	13.5400	SHTN1;SEMA3A;NSMF
GOBP2021	purine nucleotide catabolic process (GO:0006195)	3/13	0.0461	1.0000	4.3991	13.5400	NT5E;NUDT15;DNPH1
GOBP2021	purine-containing compound catabolic process (GO:0072523)	3/13	0.0461	1.0000	4.3991	13.5400	NT5E;NUDT15;DNPH1
GOBP2021	response to thyroid hormone (GO:0097066)	3/13	0.0461	1.0000	4.3991	13.5400	CTSH;BRD8;CTSS
GOBP2021	very long-chain fatty acid metabolic process (GO:0000038)	6/33	0.0169	1.0000	3.2633	13.3166	ELOVL4;ACOX2;ACOT2;PEX2;ACSBG1;HACD2
GOBP2021	epithelial cilium movement involved in extracellular fluid movement (GO:0003351)	4/20	0.0354	1.0000	3.6676	12.2502	CCDC103;SPA17;CFAP53;CCDC40
GOBP2021	modulation of excitatory postsynaptic potential (GO:0098815)	5/27	0.0264	1.0000	3.3358	12.1262	NLGN3;RIMS2;STX1B;CBLN1;SHANK1
GOBP2021	positive regulation of cytosolic calcium ion concentration involved in phospholipase C-activating G protein-coupled signaling pathway (GO:0051482)	5/28	0.0305	1.0000	3.1906	11.1379	GPR35;LPAR6;GPR4;GPR18;F2RL3
GOBP2021	cellular response to inorganic substance (GO:0071241)	4/21	0.0416	1.0000	3.4517	10.9732	KCNC2;MMP3;RTF2;MT3
GOBP2021	positive regulation of nervous system development (GO:0051962)	7/45	0.0231	1.0000	2.7057	10.1919	NLGN3;NUMBL;RASSF10;CLSTN3;CLSTN1;LIG4;EPHB3
GOBP2021	regulation of cation transmembrane transport (GO:1904062)	5/30	0.0398	1.0000	2.9350	9.4618	KCNIP1;KCNIP2;RANGRF;KCNAB1;FGF12
GOBP2021	regulation of synapse assembly (GO:0051963)	7/47	0.0287	1.0000	2.5701	9.1242	NLGN3;ROBO2;CLSTN3;CLSTN1;VPS35;GPC6;EPHB3
GOBP2021	regulation of ion transmembrane transporter activity (GO:0032412)	6/39	0.0360	1.0000	2.6691	8.8699	FHL1;STK39;FXYD7;RANGRF;FGF12;SCN1B
GOBP2021	negative regulation of peptidyl-tyrosine phosphorylation (GO:0050732)	5/31	0.0451	1.0000	2.8220	8.7479	PTPRC;MVP;CAV1;NTF3;SH2B3
GOBP2021	cellular response to hormone stimulus (GO:0032870)	10/76	0.0225	1.0000	2.2274	8.4477	ROBO2;XBP1;CAV1;RARA;CTSH;SERPINB9;NSMF;SOST;BRD8;CTSS
GOBP2021	positive regulation of cation channel activity (GO:2001259)	6/40	0.0402	1.0000	2.5905	8.3261	NLGN3;KCNIP2;LRRC38;HTT;ATPSCKMT;CTSS
WikiPath2019M	Microglia Pathogen Phagocytosis Pathway WP3626	6/41	0.0446	1.0000	2.5164	7.8239	C1QB;NCF2;TREM2;PIK3CG;LAT;SIGLECE
KEGG2019M	Amyotrophic lateral sclerosis (ALS)	7/52	0.0465	0.9999	2.2839	7.0068	GRIN2A;TOMM40;ALS2;CAT;DERL1;NEFL;BAX
GOBP2021	positive regulation of secretion by cell (GO:1903532)	9/72	0.0395	1.0000	2.0988	6.7837	STX1B;BMP2;ANKRD1;DTNBP1;TREM2;ANG;RAB27B;STX1A;BMP6
KEGG2019M	Herpes simplex virus 1 infection	40/433	0.0125	0.9999	1.5056	6.5979	ZFP623;H2-M5;ITGB3;H2-Q6;ZFP944;ZFP948;ZFP947;H2-Q1;ZFP119B;ZFP54;H2-DMB1;ZFP560;ZFP184;ZFP382;ZFP960;ZFP101;EIF2B5;ZFP677;ZFP853;ZFP930;ZFP951;H2-T10;ZFP715;ZFP459;ZFP316;ZFP558;ZFP811;ZFP959;2810021J22RIK;H2-T-PS;POU2F2;ZFP354A;ZFP40;OAS3;ZFP472;IRF7;BAX;ZFP7;ZFP772;TLR3
GOBP2021	regulation of cell cycle G2/M phase transition (GO:1902749)	10/85	0.0444	1.0000	1.9591	6.1026	CEP164;CEP131;CDK1;CEP72;CSNK1E;PCNT;GTSE1;MACROH2A1;HAUS2;AURKA
GOBP2021	regulation of neuron apoptotic process (GO:0043523)	11/98	0.0483	1.0000	1.8581	5.6313	TFAP2A;TOX3;GDNF;NTF3;LIG4;BAX;FAIM2;NSMF;TREM2;APOE;MT3

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	Formation of a pool of free 40S subunits Homo sapiens R-HSA-72689	52/96	0.0000	0.0000	4.3923	118.7493	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;RPL35A;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;EIF3A;RPS24;EIF3B
GOBP2021	snoRNA localization (GO:0048254)	5/6	0.0022	0.2587	18.4286	112.8601	FBL;NOP58;ZNHIT6;PIH1D1;PRPF31
GOBP2021	cytoplasmic translation (GO:0002181)	50/93	0.0000	0.0000	4.3198	110.9571	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;ZC3H15;EIF2B3;TMA7;RPL35A;RPS25;RPS28;EIF3M;RPS27;RPS29;EIF3I;DRG2;RPL22L1;RPS21;RPS24
Reactome2016	Viral mRNA Translation Homo sapiens R-HSA-192823	45/84	0.0000	0.0000	4.2826	99.0031	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;FAU;RPL29;GRSF1;UBA52;RPS21;RPS24
GOBP2021	negative regulation of glycoprotein biosynthetic process (GO:0010561)	7/9	0.0005	0.0692	12.9053	98.5746	BACE2;ACOT8;SLC2A10;ABCA7;JAK3;ITM2A;ITM2C
GOBP2021	protein targeting to ER (GO:0045047)	53/103	0.0000	0.0000	3.9390	97.9993	RPL5;RPL3;RPL32;RPL34;ZFAND2A;RPLP1;ZFAND2B;RPLP0;SRP14;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;SEC61A1;RPS19;RPS18;SEC61G;RPL36;RPL38;RPL37;SEC62;RPS11;GET3;RPS13;RPS12;SEC63;RPS5;RPS6;RPSA;RPL37A;CHMP4B;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;RPL35A;RPS25;RPS28;SPCS2;RPS27;RPS29;RPS21;RPS24
BioPlanet2019	Influenza viral RNA transcription and replication	62/125	0.0000	0.0000	3.6618	97.8421	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;CASC3;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;UPF2;UPF1;HSP90AA1;NCBP1;RPS5;RPS6;RPSA;GTF2F1;RPL37A;RPL27;RPL26;RPL29;UBA52;RBM8A;RPL10;RPL12;RPL11;RPL36A;PPP2CA;RPS15A;POLR2C;POLR2D;RPS3;POLR2E;RPL13;RPS2;POLR2I;POLR2L;UPF3B;RPL35A;UPF3A;RPS25;RPS28;RPS27;RPS29;RNPS1;FAU;GRSF1;RPS21;RPS24;EIF4G1
Reactome2016	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC) Homo sapiens R-HSA-975956	47/89	0.0000	0.0000	4.1546	97.2756	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;UPF1;NCBP1;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;FAU;RPL29;UBA52;RPS21;RPS24;EIF4G1
Reactome2016	Selenocysteine synthesis Homo sapiens R-HSA-2408557	46/87	0.0000	0.0000	4.1647	95.8056	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;EEFSEC;RPS5;RPS6;SARS;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;FAU;RPL29;UBA52;RPS21;RPS24
Reactome2016	Nonsense-Mediated Decay (NMD) Homo sapiens R-HSA-927802	54/106	0.0000	0.0000	3.8594	95.7518	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;CASC3;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;UPF2;UPF1;NCBP1;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RBM8A;RPL10;RPL12;RPL11;RPL36A;PPP2CA;RPS15A;RPS3;RPL13;RPS2;UPF3B;RPL35A;UPF3A;RPS25;RPS28;RPS27;RPS29;RNPS1;FAU;RPS21;RPS24;EIF4G1
Reactome2016	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC) Homo sapiens R-HSA-975957	54/106	0.0000	0.0000	3.8594	95.7518	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;CASC3;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;UPF2;UPF1;NCBP1;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RBM8A;RPL10;RPL12;RPL11;RPL36A;PPP2CA;RPS15A;RPS3;RPL13;RPS2;UPF3B;RPL35A;UPF3A;RPS25;RPS28;RPS27;RPS29;RNPS1;FAU;RPS21;RPS24;EIF4G1
GOBP2021	SRP-dependent cotranslational protein targeting to membrane (GO:0006614)	47/90	0.0000	0.0000	4.0578	92.9488	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;ZFAND2B;RPLP0;RPL11;RPL36A;SRP14;RPL10A;RPL8;RPL9;RPL7;RPS15;SEC61A1;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;SEC63;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;RPL29;UBA52;RPS21;RPS24
Reactome2016	GTP hydrolysis and joining of the 60S ribosomal subunit Homo sapiens R-HSA-72706	54/107	0.0000	0.0000	3.7863	92.1570	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;EIF5B;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;RPL35A;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;RPS24;EIF3A;EIF4G1;EIF3B
BioPlanet2019	Cytoplasmic ribosomal proteins	54/108	0.0000	0.0000	3.7160	88.7303	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS6KA6;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;RPL35A;RPS25;RPS28;RPS27;RPS6KB1;EIF3K;RPS29;EIF3I;RPS6KB2;EIF3H;FAU;EIF3F;GRSF1;RPS21;RPS24;EIF3A;EIF3B
Reactome2016	Peptide chain elongation Homo sapiens R-HSA-156902	44/84	0.0000	0.0000	4.0816	88.4645	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;FAU;RPL29;UBA52;RPS21;RPS24

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	L13a-mediated translational silencing of Ceruloplasmin expression Homo sapiens R-HSA-156827	53/106	0.0000	0.0000	3.7153	87.1842	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;RPL35A;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;RPS24;EIF3A;EIF4G1;EIF3B
Reactome2016	3' -UTR-mediated translational regulation Homo sapiens R-HSA-157279	53/106	0.0000	0.0000	3.7153	87.1842	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;RPL35A;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;RPS24;EIF3A;EIF4G1;EIF3B
Reactome2016	Eukaryotic Translation Termination Homo sapiens R-HSA-72764	45/87	0.0000	0.0000	3.9760	85.8324	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;APEH;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;FAU;RPL29;UBA52;RPS21;RPS24
GOBP2021	nuclear-transcribed mRNA catabolic process, nonsense-mediated decay (GO:0000184)	55/113	0.0000	0.0000	3.5237	80.9006	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;CASC3;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;UPF2;UPF1;NCBP1;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RBM8A;RPL10;RPL12;RPL11;RPL36A;PPP2CA;RPS15A;DHX34;RPS3;RPL13;RPS2;UPF3B;RPL35A;UPF3A;MAGOHB;RPS25;RPS28;RPS27;RPS29;RNPS1;RPS21;RPS24;EIF4G1
Reactome2016	Cap-dependent Translation Initiation Homo sapiens R-HSA-72737	55/114	0.0000	0.0000	3.4638	78.0458	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;EIF5B;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;EIF2B3;RPL35A;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;RPS24;EIF3A;EIF4G1;EIF3B
Reactome2016	Eukaryotic Translation Initiation Homo sapiens R-HSA-72613	55/114	0.0000	0.0000	3.4638	78.0458	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;EIF5B;RPS5;RPS6;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;EIF2B3;RPL35A;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;RPS24;EIF3A;EIF4G1;EIF3B
GOBP2021	cotranslational protein targeting to membrane (GO:0006613)	47/94	0.0000	0.0000	3.7115	77.9126	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;SRP14;RPL10A;RPL8;RPL9;RPL7;RPS15;SEC61A1;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;SEC62;RPS11;RPS13;RPS12;SEC63;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;RPL29;UBA52;RPS21;RPS24
GOBP2021	rRNA processing (GO:0006364)	77/173	0.0000	0.0000	2.9888	76.8014	RPL5;RPL3;RPL32;RPL34;POP4;RPLP1;RRP1;RPLP0;NAT10;THUMPD1;RPL8;RPL10A;RPL9;WDR43;RPL7;RRP9;RPS15;FBL;RPS14;SART1;RPS19;RPL36;RPL38;RPL37;RRP15;PIH1D1;RPS6;WDR74;DDX10;UTP18;NSA2;RPL37A;SBDS;RPL27;SRFBP1;RPL26;RPL29;UBA52;DDX27;RPL10;RPL12;RPL11;MAK16;RPL36A;NOL8;SNU13;NOC4L;EXOSC7;EXOSC5;EXOSC9;BMS1;DHX37;RPL13;RRP36;RPS2;EXOSC3;LYAR;EXOSC2;MDN1;DCAF13;NOP14;NOP58;UTP3;WDR18;RPL35A;RCL1;RPS25;BOP1;TBL3;RPS28;LSM6;RPS27;LAS1L;MPHOSPH10;ESF1;RPS24;MPHOSPH6
Reactome2016	Formation of the ternary complex, and subsequently, the 43S complex Homo sapiens R-HSA-72695	28/50	0.0000	0.0000	4.7101	76.3471	RPS15;RPS14;RPS15A;RPS19;RPS18;RPS3;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;EIF3A;RPS24;EIF3B
GOBP2021	peptide biosynthetic process (GO:0043043)	72/162	0.0000	0.0000	2.9787	71.6459	MRPS17;RPL5;RPL3;MRPS16;RPL32;MRPS14;RPL34;MRPS11;RPLP1;MRPS12;RPLP0;MRPL36;RPL8;RPL10A;MRPL34;RPL9;RPL7;RPS15;RPS14;MRPL3;RPS19;RPS18;RPL36;RPL38;RPL37;MRPL9;RPS11;RPS13;RPS12;RPS5;PABPC4;RPS6;MRPS18B;MRPS18A;RPSA;MRPS7;MRPS5;MRPL43;MRPL52;RPL37A;RPL27;RPL26;RPL29;MRRF;RPL10;MRPL18;RPL12;RPL11;RPL36A;RRBP1;MRPL11;RHD;RPS15A;RPS3;RPL13;RPS2;ABCF1;GGT5;GGT7;MRPL27;RPL35A;MRPL23;RPS25;RPS28;RPS27;RPS29;RPS6KB2;RPS21;RSL24D1;RPS24;EIF4G1;FARSB
GOBP2021	mesonephric duct development (GO:0072177)	4/5	0.0086	0.5590	14.7395	70.0643	OSR1;GPC3;PKD2;PKD1
GOBP2021	positive regulation of endothelial cell chemotaxis by VEGF-activated vascular endothelial growth factor receptor signaling pathway (GO:0038033)	4/5	0.0086	0.5590	14.7395	70.0643	KDR;HSPB1;PRKD2;VEGFA
WikiPath2019M	Aflatoxin B1 metabolism WP1262	4/5	0.0086	0.3664	14.7395	70.0643	AKR7A5;GSTM1;EPHX1;GSTT1
Reactome2016	Eukaryotic Translation Elongation Homo sapiens R-HSA-156842	44/89	0.0000	0.0000	3.6269	70.0092	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPL35A;RPSA;RPS25;RPS28;RPS27;RPS29;RPL37A;RPL27;RPL26;FAU;RPL29;UBA52;RPS21;RPS24
Reactome2016	SRP-dependent cotranslational protein targeting to membrane Homo sapiens R-HSA-1799339	51/107	0.0000	0.0000	3.3814	69.2267	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;SRP14;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;SEC61A1;RPS19;RPS18;SEC61G;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;DDOST;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;SEC11A;SEC11C;RPL35A;RPS25;RPS28;SPCS2;RPS27;RPS29;FAU;RPS21;RPS24

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	rRNA processing Homo sapiens R-HSA-72312	77/180	0.0000	0.0000	2.7845	64.9526	LTV1;RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;NAT10;THUMPD1;RPL8;RPL10A;RPL9;WDR43;RPL7;RRP9;RPS15;FBL;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;UTP18;RPL37A;RPP21;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS27L;NOC4L;HSD17B10;EXOSC7;EXOSC5;RPS15A;EXOSC9;BMS1;DHX37;GAR1;RPS3;RPL13;RRP36;RPS2;EXOSC3;EXOSC2;DCAF13;NOP14;NOP58;UTP3;WDR18;RPP40;RPL35A;RCL1;RPS25;BOP1;TBL3;RPS28;RPS27;LAS1L;RPS29;MPHOSPH10;FAU;RPS21;NOP10;RPS24;MPHOSPH6
Reactome2016	Major pathway of rRNA processing in the nucleolus Homo sapiens R-HSA-6791226	72/166	0.0000	0.0000	2.8512	64.6647	LTV1;RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;WDR43;RPL7;RRP9;RPS15;FBL;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;UTP18;RPL37A;RPP21;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS27L;NOC4L;EXOSC7;EXOSC5;RPS15A;EXOSC9;BMS1;DHX37;RPS3;RPL13;RRP36;RPS2;EXOSC3;EXOSC2;DCAF13;NOP14;NOP58;UTP3;WDR18;RPP40;RPL35A;RCL1;RPS25;BOP1;TBL3;RPS28;RPS27;LAS1L;RPS29;MPHOSPH10;FAU;RPS21;RPS24;MPHOSPH6
Reactome2016	mRNA Splicing Homo sapiens R-HSA-72172	64/144	0.0000	0.0000	2.9749	64.1533	PDCD7;HNRNPU;HNRNPR;CASC3;YBX1;CCAR1;PTBP1;SART1;SNRPD1;SNRNP70;PCF11;SNRNP35;CTNNBL1;BCAS2;NCBP1;ZCRB1;GTF2F1;HNRNPUL1;HNRNPH1;PRPF3;SRSF2;SNRNP27;HNRNPH2;SRSF5;DNAJC8;SNRPB;SRSF9;SF3B4;SF3B5;SF3B2;RBM8A;SF3B6;SRRT;SRSF1;DDX23;PRPF8;PABPN1;FIP1L1;POLR2C;POLR2D;CSTF1;POLR2E;POLR2I;HNRNPA1;SRSF11;POLR2L;HNRNPA0;HSPA8;SF3A1;HNRNPA3;ALYREF;UPF3B;CWC15;HNRNPL;HNRNPM;LSM8;HNRNPK;LSM6;HNRNPA2B1;HNRNPD;RNPS1;PRPF31;SNRNP48;HNRNPC
Reactome2016	mRNA Splicing - Major Pathway Homo sapiens R-HSA-72163	60/134	0.0000	0.0000	3.0134	62.3049	HNRNPU;HNRNPR;CASC3;YBX1;CCAR1;PTBP1;SART1;SNRPD1;SNRNP70;PCF11;CTNNBL1;BCAS2;NCBP1;GTF2F1;HNRNPUL1;HNRNPH1;PRPF3;SRSF2;SNRNP27;HNRNPH2;SRSF5;DNAJC8;SNRPB;SRSF9;SF3B4;SF3B5;SF3B2;RBM8A;SF3B6;SRRT;SRSF1;DDX23;PRPF8;PABPN1;FIP1L1;POLR2C;POLR2D;CSTF1;POLR2E;POLR2I;HNRNPA1;SRSF11;POLR2L;HNRNPA0;HSPA8;SF3A1;HNRNPA3;ALYREF;UPF3B;CWC15;HNRNPL;HNRNPM;LSM8;HNRNPK;LSM6;HNRNPA2B1;HNRNPD;RNPS1;PRPF31;HNRNPC
GOBP2021	rRNA metabolic process (GO:0016072)	70/162	0.0000	0.0000	2.8313	61.9844	TRIR;RPL5;RPL3;RPL32;RPL34;POP4;RPLP1;RRP1;RPLP0;RPL8;RPL10A;RPL9;WDR43;RPL7;RRP9;RPS15;FBL;RPS14;RPS19;RPL36;RPL38;RPL37;PIH1D1;RPS6;WDR74;DDX10;UTP18;RPL37A;SBDS;RPL27;RPL26;RPL29;UBA52;DDX27;RPL10;RPL12;RPL11;RPL36A;NOL8;SNU13;NOC4L;EXOSC7;EXOSC5;EXOSC9;BMS1;DHX37;RPL13;RRP36;RPS2;EXOSC3;LYAR;EXOSC2;MDN1;DCAF13;NOP14;NOP58;UTP3;WDR18;RPL35A;RCL1;RPS25;BOP1;TBL3;RPS28;RPS27;LAS1L;MPHOSPH10;ESF1;RPS24;MPHOSPH6
WikiPath2019M	Cytoplasmic Ribosomal Proteins WP163	44/92	0.0000	0.0000	3.3996	61.2340	RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPS15;RPS14;RPS15A;RPS19;RPS18;RPL36;RPS3;RPL13;RPL38;RPL37;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPL35A;RPSA;RPL34-PS1;RPS25;RPS28;RPS27;RPS29;RPL37A;RPS6KB2;RPL27;RPL26;FAU;RPL29;RPS21;RPS24
Reactome2016	RHO GTPases Activate ROCKs Homo sapiens R-HSA-5627117	11/17	0.0001	0.0052	6.7645	59.9677	PPP1CB;PPP1R12A;ROCK1;ROCK2;MYH14;MYH9;MYH11;MYL9;MYH10;RHOA;MYL12B
GOBP2021	ncRNA processing (GO:0034470)	83/201	0.0000	0.0000	2.6211	59.8886	RPL5;POP7;RPL3;TUT7;RPL32;RPL34;POP4;RPLP1;RRP1;RPLP0;ADAR;RPL8;RPL10A;RPL9;WDR43;RPL7;RRP9;FARS2;THG1L;RPS15;RPS14;FBL;RPS19;RPL36;RPL38;RPL37;PIH1D1;RPS6;WDR74;DDX10;TRPT1;UTP18;RPL37A;RPP21;SBDS;RPL27;RPL26;RPL29;UBA52;DDX27;RPL10;RPL12;RPL11;SRRT;RPL36A;NOL8;SNU13;NOC4L;EXOSC7;EXOSC5;EXOSC9;BMS1;DHX37;RPL13;RRP36;RPS2;EXOSC3;LYAR;EXOSC2;MDN1;DCAF13;SMAD1;NOP14;NOP58;SSB;UTP3;WDR18;RPL35A;RCL1;RPS25;BOP1;TBL3;RPS28;RPS27;LAS1L;PRKRA;HNRNPA2B1;INTS5;MPHOSPH10;ESF1;INTS9;RPS24;MPHOSPH6
KEGG2019M	Ribosome	72/170	0.0000	0.0000	2.7341	58.4549	MRPS17;RPL5;RPL3;MRPS16;RPL32;MRPS14;RPL34;MRPS11;RPLP1;MRPS12;RPLP0;MRPL36;RPL8;RPL10A;MRPL34;RPL9;RPL7;RPS15;MRPL4;RPS14;MRPL3;RPS19;RPS18;RPL36;RPL38;RPL37;MRPL9;RPS11;RPS13;RPS12;RPS5;RPS6;MRPS18A;RPSA;MRPS7;MRPS5;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;MRPL18;RPL12;RPL11;MRPL16;RPL36A;RPS27L;MRPL14;MRPL12;MRPL11;RPS15A;RPS3;RPL13;RPS2;RPL39L;MRPL27;RPL35A;MRPL23;RPL34-PS1;MRPL30;RPS25;RPS28;RPS27;RPS29;MT-RNR1;RPS27RT;RPL22L1;FAU;RPS21;RSL24D1;RPS24
BioPlanet2019	Messenger RNA splicing: major pathway	34/68	0.0000	0.0000	3.7032	57.8252	SF3B5;RBM8A;SF3B6;SRSF1;HNRNPU;HNRNPR;YBX1;CCAR1;PTBP1;PABPN1;PCF11;SNRNP70;CSTF1;HNRNPA1;SRSF11;HNRNPA0;HNRNPA3;ALYREF;UPF3B;SMC1A;HNRNPL;HNRNPM;HNRNPK;HNRNPUL1;HNRNPH1;HNRNPA2B1;SRSF2;HNRNPD;HNRNPH2;RNPS1;DNAJC8;SRSF5;HNRNPC;SRSF9

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377)	99/251	0.0000	0.0000	2.4311	57.7530	PDCD7;HNRNPU;HNRNPR;CASC3;CWC27;CCAR1;PNN;SNRPD1;SNRNP35;IK;ZCRB1;GTF2F1;WBP11;CRNKL1;DDX39B;HNRNPUL1;PRPF3;SRSF2;SNRNP27;GEMIN5;GEMIN6;SRSF5;SNRPB;SRSF9;RBM8A;YTHDC1;SNU13;PRPF8;ZMAT2;DHX35;CSTF1;ZRSR2;HSPA8;ALYREF;NONO;UPF3B;CWC15;MAGOHB;HNRNPL;HNRNPM;LSM8;HNRNPK;SNW1;LSM6;HNRNPD;RNPS1;HNRNPC;DDX46;DDX42;PPWD1;YBX1;PTBP1;SART1;METTL14;SART3;PCF11;SNRNP70;CTNNBL1;BCAS2;RBM6;RBM17;NCBP1;GCFC2;SFPQ;HNRNPH1;SYF2;FRG1;HNRNPH2;HNRNPH3;DNAJC8;SF3B4;SF3B5;SF3B2;SF3B6;SRRT;WBP4;SRSF1;DDX23;RBM15B;PABPN1;FIP1L1;POLR2C;POLR2D;POLR2E;POLR2I;HNRNPA1;SMNDC1;SRSF11;POLR2L;HNRNPA0;SF3A1;HNRNPA3;U2SURP;NOVA2;HNRNPA2B1;PRPF31;BUD13;SNRNP48;PPIL3
GOBP2021	gene expression (GO:0010467)	132/356	0.0000	0.0000	2.2068	57.0519	RPL5;RPL3;NUP107;RPL32;NUP188;RPL34;SCX;HNRNPU;CASC3;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;MRPS18B;MRPS18A;RPSA;THOC2;DDX39B;HNRNPUL1;SARNP;DNAJB11;SRSF2;RPL27;RPL26;SRSF5;RPL29;SRSF9;SLBP;RBM8A;YTHDC1;MRPL18;MRPL11;TPR;TSPAN5;RBPMS;ALYREF;MRPL27;UPF3B;MRPL23;MAGOHB;HNRNPL;NR4A2;RPS25;RPS28;HNRNPK;RPS27;FUBP3;RPS29;BCL3;HNRNPD;MPHOSPH10;RNPS1;MMS19;RPS21;RSL24D1;RPS24;FARSB;EIF4G1;NFKBIB;MRPS17;MRPS16;MRPS14;MRPS11;RPLP1;MRPS12;RPLP0;MRPL36;ADAR;MRPL34;RBM3;MRPL3;MRPL9;RBM6;UPF2;APOBEC1;UPF1;NCBP1;NUP133;TESC;PABPC4;MRPS7;MRPS5;MRPL43;MRPL52;DDX19B;HNRNPH1;RPL37A;HNRNPH3;PTMA;MRRF;RPL10;RPL12;RPL11;SRSF1;RPL36A;RRBP1;LMF2;LMF1;HSPD1;RBM15B;RPS15A;PABPN1;FIP1L1;POLR2C;POLR2D;RPS3;E2F1;POLR2E;RPL13;RPS2;POLR2I;SRSF11;ABCF1;POLR2L;GALNT2;RPL35A;GOLPH3;HNRNPA2B1;TSPAN17;RPS6KB2
GOBP2021	ribosome biogenesis (GO:0042254)	79/192	0.0000	0.0000	2.6035	56.2974	LTV1;RPL5;RPL3;RPL32;RPL34;POP4;RPLP1;RRP1;RPLP0;MRPL36;RPL8;RPL10A;NOC2L;RPL9;WDR43;RPL7;RRP9;RPS15;FBL;RPS14;RPS19;RPL36;RPL38;RPL37;PIH1D1;RPS6;WDR74;GTF3A;DDX10;UTP18;LSG1;RPL37A;SBDS;RPL27;NAF1;RPL26;RPL29;UBA52;DDX27;RPL10;RPL12;RPL11;RPL36A;NOL8;SNU13;NOC4L;MALSU1;EXOSC7;EXOSC5;EXOSC9;BMS1;DHX37;RPL13;RRP36;RPS2;EXOSC3;LYAR;EXOSC2;MDN1;DCAF13;NOP14;NOP58;NPM1;UTP3;WDR18;RPL35A;RCL1;CUL4A;RPS25;BOP1;TBL3;RPS28;RPS27;LAS1L;MPHOSPH10;ESF1;RBIS;RPS24;MPHOSPH6
KEGG2019M	Spliceosome	58/132	0.0000	0.0000	2.9116	55.8283	TCERG1;RBM25;DDX46;DDX42;HNRNPU;SART1;SNRPD1;SNRNP70;ALYREF2;CTNNBL1;BCAS2;RBM17;NCBP1;THOC2;WBP11;CRNKL1;PRPF18;DDX39B;SYF2;PRPF3;SRSF2;SNRNP27;RP9;SRSF5;SNRPB;SRSF9;SF3B4;SF3B5;SF3B2;HNRNPA1L2-PS2;RBM8A;SF3B6;SRSF1;DDX23;SNU13;GM13092;PRPF8;ZMAT2;HNRNPA1;SMNDC1;HSPA8;PRPF38B;SF3A1;HNRNPA3;CCDC12;ALYREF;CWC15;MAGOHB;U2SURP;HNRNPM;LSM8;HNRNPK;LSM6;SNW1;ACIN1;PRPF31;HNRNPC;HSPA1B
Reactome2016	Influenza Life Cycle Homo sapiens R-HSA-168255	59/136	0.0000	0.0000	2.8465	53.7769	RPL5;RPL3;NUP107;RPL32;NUP188;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;HSP90AA1;NUP133;RPS5;RPS6;RPSA;GTF2F1;RPL37A;CANX;RPL27;RPL26;RPL29;UBA52;KPNB1;RPL10;RPL12;RPL11;RPL36A;RPS15A;POLR2C;TPR;POLR2D;RPS3;POLR2E;RPL13;RPS2;POLR2I;POLR2L;RPL35A;RPS25;RPS28;RPS27;RPS29;CALR;FAU;GRSF1;RPS21;RPS24
Reactome2016	Ribosomal scanning and start codon recognition Homo sapiens R-HSA-72702	29/57	0.0000	0.0000	3.8324	53.6563	RPS15;RPS14;RPS15A;RPS19;RPS18;RPS3;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;EIF3A;RPS24;EIF4G1;EIF3B
Reactome2016	Translation initiation complex formation Homo sapiens R-HSA-72649	29/57	0.0000	0.0000	3.8324	53.6563	RPS15;RPS14;RPS15A;RPS19;RPS18;RPS3;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;EIF3A;RPS24;EIF4G1;EIF3B
BioPlanet2019	Influenza infection	61/142	0.0000	0.0000	2.7983	53.2168	RPL5;RPL3;NUP107;RPL32;NUP188;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;HSP90AA1;NUP133;RPS5;RPS6;RPSA;GTF2F1;RPL37A;CANX;RPL27;RPL26;RPL29;UBA52;KPNB1;RPL10;RPL12;RPL11;RPL36A;RPS15A;PABPN1;POLR2C;TPR;POLR2D;RPS3;POLR2E;RPL13;RPS2;POLR2I;POLR2L;TGFB1;RPL35A;RPS25;RPS28;RPS27;RPS29;CALR;FAU;GRSF1;RPS21;RPS24
Reactome2016	Influenza Viral RNA Transcription and Replication Homo sapiens R-HSA-168273	56/128	0.0000	0.0000	2.8883	53.0883	RPL5;RPL3;NUP107;RPL32;NUP188;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;HSP90AA1;NUP133;RPS5;RPS6;RPSA;GTF2F1;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;POLR2C;TPR;POLR2D;RPS3;POLR2E;RPL13;RPS2;POLR2I;POLR2L;RPL35A;RPS25;RPS28;RPS27;RPS29;FAU;GRSF1;RPS21;RPS24
GOBP2021	ribosome assembly (GO:0042255)	26/50	0.0000	0.0005	4.0068	53.0305	RPL5;DDX3X;RPL3;RPL10;MRPS11;RPLP0;RPL11;MPV17L2;RPS27L;RPS15;RPS14;RPS19;DHX37;MDN1;NPM1;MTERF3;RPS5;RPSA;MRPS7;NLE1;TRAF7;BOP1;RPS28;RPS27;SBDS;RSL24D1

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	mRNA processing (GO:0006397)	113/300	0.0000	0.0000	2.2580	53.0017	TCERG1;RAMAC;PDCD7;GEMIN2;HNRNPU;HNRNPR;CASC3;CWC27;CCAR1;PNN;SNRPD1;SNRNP35;CMTR1;IK;THOC2;ZCRB1;GTF2F1;WBP11;CRNKL1;DDX39B;HNRNPUL1;SARNP;PRPF3;SRSF2;SNRNP27;GEMIN5;GEMIN6;SRSF5;AURKAIP1;SNRPB;SRSF9;RBM8A;YTHDC1;SNU13;PRPF8;ZMAT2;DHX35;CSTF1;RPRD1B;ZRSR2;HSPA8;ALYREF;NONO;UPF3B;CWC15;MAGOHB;HNRNPL;HNRNPM;LSM8;HNRNPK;SNW1;LSM6;HNRNPD;RNPS1;HNRNPC;MNAT1;DDX46;DDX42;PPWD1;YBX1;PTBP1;SART1;METTL14;SART3;PCF11;SNRNP70;CTNNBL1;BCAS2;RBM6;RBM17;NCBP1;GCFC2;SFPQ;PRPF18;HNRNPH1;SYF2;FRG1;HNRNPH2;HNRNPH3;DNAJC8;PRMT9;SF3B4;SF3B5;SF3B2;SF3B6;SRRT;WBP4;SRSF1;DDX23;RBM15B;PABPN1;FIP1L1;POLR2C;POLR2D;POLR2E;POLR2I;HNRNPA1;SMNDC1;SRSF11;POLR2L;HNRNPA0;SF3A1;HNRNPA3;GTF2H3;GTF2H4;U2SURP;NOVA2;HNRNPA2B1;ERCC2;PRPF31;BUD13;SNRNP48;PPIL3
Reactome2016	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S Homo sapiens R-HSA-72662	29/58	0.0000	0.0001	3.7000	50.0803	RPS15;RPS14;RPS15A;RPS19;RPS18;RPS3;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPS25;RPS28;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;EIF3A;RPS24;EIF4G1;EIF3B
Reactome2016	Influenza Infection Homo sapiens R-HSA-168254	62/147	0.0000	0.0000	2.7103	49.9965	RPL5;RPL3;NUP107;RPL32;NUP188;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;KPNA2;RPS11;RPS13;RPS12;HSP90AA1;NUP133;RPS5;RPS6;RPSA;GTF2F1;RPL37A;CANX;RPL27;RPL26;RPL29;UBA52;KPNB1;RPL10;RPL12;RPL11;RPL36A;RPS15A;PABPN1;POLR2C;TPR;POLR2D;RPS3;POLR2E;RPL13;RPS2;POLR2I;POLR2L;TGFB1;RPL35A;RPS25;RPS28;RPS27;RPS29;CALR;FAU;GRSF1;RPS21;RPS24
Reactome2016	Selenoamino acid metabolism Homo sapiens R-HSA-2408522	49/111	0.0000	0.0000	2.9318	48.7539	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RARS;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;RPS5;RPS6;SARS;RPSA;RPL37A;RPL27;RPL26;RPL29;UBA52;AHCY;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;EEFSEC;GSR;RPL35A;RPS25;RPS28;RPS27;RPS29;FAU;RPS21;RPS24
BioPlanet2019	Translation	63/151	0.0000	0.0000	2.6602	48.4529	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;SRP14;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;SEC61A1;RPS19;RPS18;SEC61G;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;EIF5B;RPS5;RPS6;RPSA;DDOST;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS27L;RPS15A;RPS3;RPL13;RPS2;SEC11A;SEC11C;EIF2B3;RPL35A;RPS25;RPS28;SPCS2;RPS27;EIF3K;RPS29;EIF3I;EIF3H;RPL22L1;FAU;EIF3F;RPS21;RSL24D1;RPS24;EIF3A;EIF4G1;EIF3B
Reactome2016	Translation Homo sapiens R-HSA-72766	63/151	0.0000	0.0000	2.6602	48.4529	RPL5;RPL3;RPL32;RPL34;RPLP1;RPLP0;APEH;SRP14;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;SEC61A1;RPS19;RPS18;SEC61G;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;EIF5B;RPS5;RPS6;RPSA;DDOST;RPL37A;RPL27;RPL26;RPL29;UBA52;RPL10;RPL12;RPL11;RPL36A;RPS15A;RPS3;RPL13;RPS2;SEC11A;SEC11C;EIF2B3;RPL35A;RPS25;RPS28;SPCS2;EIF3M;RPS27;EIF3K;RPS29;EIF3L;EIF3I;EIF3H;FAU;EIF3F;RPS21;RPS24;EIF3A;EIF4G1;EIF3B
GOBP2021	translation (GO:0006412)	84/214	0.0000	0.0000	2.4066	48.4506	MRPS17;RPL5;RPL3;MRPS16;RPL32;MRPS14;RPL34;MRPS11;RPLP1;MRPS12;RPLP0;MRPL36;RPL8;MRPL34;APEH;RPL10A;RPL9;RPL7;FARS2;RPS15;RPS14;MRPL3;RPS19;RPS18;RPL36;RPL38;RPL37;MRPL9;RPS11;RPS13;RPS12;MRPS28;MRPS24;PABPC4;RPS5;RPS6;MRPS18B;MRPS18A;RPSA;MRPS7;MRPS5;MRPL43;MRPL52;LARS2;SARS2;RPL37A;RPL27;RPL26;RPL29;UBA52;MRRF;RPL10;MRPL18;RPL12;RPL11;MRPL16;RPL36A;RRBP1;MRPL57;MRPL11;RPS15A;RPS3;RPL13;RPS2;ZC3H15;ABCF1;EEFSEC;NDUFA7;TMA7;MRPL27;RPL35A;MRPL23;RPS25;RPS28;RPS27;RPS29;RPS6KB2;DRG2;RPL22L1;RPS21;RSL24D1;RPS24;FARSB;EIF4G1
GOBP2021	SMAD protein complex assembly (GO:0007183)	5/7	0.0063	0.4583	9.2137	46.6757	FKBP1A;SMAD1;EID2;SMAD4;TGFB1
GOBP2021	vascular associated smooth muscle cell development (GO:0097084)	5/7	0.0063	0.4583	9.2137	46.6757	NOTCH1;HEY2;HES1;ENG;VEGFA
GOBP2021	mRNA splicing, via spliceosome (GO:0000398)	101/274	0.0000	0.0000	2.1772	43.0921	PDCD7;GEMIN2;HNRNPU;HNRNPR;CASC3;CWC27;CCAR1;PNN;SNRPD1;SNRNP35;IK;ZCRB1;GTF2F1;WBP11;CRNKL1;DDX39B;HNRNPUL1;PRPF3;SRSF2;SNRNP27;GEMIN5;GEMIN6;SRSF5;SNRPB;SRSF9;RBM8A;YTHDC1;SNU13;PRPF8;ZMAT2;DHX35;CSTF1;ZRSR2;HSPA8;ALYREF;NONO;UPF3B;CWC15;MAGOHB;HNRNPL;HNRNPM;LSM8;HNRNPK;SNW1;LSM6;HNRNPD;RNPS1;HNRNPC;CDK13;DDX46;DDX42;PPWD1;YBX1;PTBP1;SART1;METTL14;SART3;PCF11;SNRNP70;CTNNBL1;BCAS2;RBM6;RBM17;NCBP1;GCFC2;SFPQ;HNRNPH1;SYF2;FRG1;HNRNPH2;HNRNPH3;DNAJC8;SF3B4;SF3B5;SF3B2;SF3B6;SRRT;WBP4;SRSF1;DDX23;RBM15B;PABPN1;FIP1L1;POLR2C;POLR2D;POLR2E;POLR2I;HNRNPA1;SMNDC1;SRSF11;POLR2L;HNRNPA0;SF3A1;HNRNPA3;U2SURP;NOVA2;HNRNPA2B1;PRPF31;BUD13;SNRNP48;PPIL3
BioPlanet2019	Spliceosome	53/127	0.0000	0.0000	2.6574	41.4285	TCERG1;RBM25;DDX46;DDX42;HNRNPU;SART1;SNRPD1;SNRNP70;CTNNBL1;BCAS2;RBM17;NCBP1;THOC2;WBP11;CRNKL1;PRPF18;DDX39B;SYF2;PRPF3;SRSF2;SNRNP27;SRSF5;SNRPB;SRSF9;SF3B4;SF3B5;SF3B2;RBM8A;SF3B6;SRSF1;DDX23;PRPF8;ZMAT2;HNRNPA1;SMNDC1;HSPA8;PRPF38B;SF3A1;HNRNPA3;CCDC12;ALYREF;CWC15;MAGOHB;U2SURP;HNRNPM;LSM8;HNRNPK;LSM6;SNW1;ACIN1;PRPF31;HNRNPC;HSPA1B

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	mitochondrial respirasome assembly (GO:0097250)	6/9	0.0044	0.3562	7.3722	40.0803	COX7A2L;COX7A2;COX7A1;HIGD1B;HIGD2A;RAB5IF
GOBP2021	negative regulation of biomineralization (GO:0110150)	6/9	0.0044	0.3562	7.3722	40.0803	TGFB1;NOTCH1;ROCK1;NOS3;ROCK2;HEY2
Reactome2016	Processing of Capped Intron-Containing Pre-mRNA Homo sapiens R-HSA-72203	74/193	0.0000	0.0000	2.3122	38.8015	NUP107;NUP188;PDCD7;HNRNPU;HNRNPR;CASC3;YBX1;CCAR1;PTBP1;SART1;METTL14;SNRPD1;PCF11;SNRNP70;SNRNP35;CTNNBL1;BCAS2;NCBP1;NUP133;THOC2;ZCRB1;GTF2F1;DDX39B;HNRNPUL1;HNRNPH1;SARNP;PRPF3;SRSF2;SNRNP27;HNRNPH2;SRSF5;DNAJC8;SNRPB;SRSF9;SF3B4;SLBP;SF3B5;SF3B2;RBM8A;SF3B6;SRRT;SRSF1;DDX23;PRPF8;PABPN1;FIP1L1;POLR2C;TPR;POLR2D;CSTF1;POLR2E;POLR2I;HNRNPA1;SRSF11;POLR2L;HNRNPA0;HSPA8;SF3A1;HNRNPA3;WTAP;ALYREF;UPF3B;CWC15;HNRNPL;HNRNPM;LSM8;HNRNPK;LSM6;HNRNPA2B1;HNRNPD;RNPS1;PRPF31;SNRNP48;HNRNPC
BioPlanet2019	Activation of mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	27/57	0.0000	0.0017	3.3282	37.9595	RPS15;RPS14;RPS15A;RPS19;RPS18;RPS3;RPS2;RPS11;RPS13;RPS12;RPS5;RPS6;RPSA;RPS25;RPS28;RPS27;EIF3K;RPS29;EIF3I;EIF3H;FAU;EIF3F;RPS21;EIF3A;RPS24;EIF4G1;EIF3B
GOBP2021	ribosomal small subunit assembly (GO:0000028)	10/17	0.0009	0.1193	5.2695	37.2397	RPS15;RPS14;RPS28;RPS27;RPS19;MRPS11;RPS5;RPS27L;RPSA;MRPS7
GOBP2021	ribosomal small subunit biogenesis (GO:0042274)	20/40	0.0001	0.0134	3.6943	36.0526	LTV1;NOP14;NPM1;MRPS11;RPS5;RPS6;RPS27L;SNU13;RPSA;MRPS7;RPS15;RPS14;RPS25;RPS28;LSM6;RPS27;RPS19;RRP36;SRFBP1;RPS24
GOBP2021	nuclear-transcribed mRNA catabolic process (GO:0000956)	66/171	0.0000	0.0001	2.3348	36.0244	RPL5;RPL3;TUT7;RPL32;RPL34;RPLP1;RPLP0;CASC3;RPL8;RPL10A;RPL9;TENT4B;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;UPF2;UPF1;NCBP1;RPS5;RPS6;RPSA;CSDE1;RPL37A;RPL27;DXO;RPL26;RPL29;UBA52;RBM8A;RPL10;RPL12;RPL11;PARN;RPL36A;EXOSC7;PPP2CA;EXOSC5;RPS15A;DHX34;EXOSC9;POLR2D;RPS3;RPL13;RPS2;UPF3B;RPL35A;UPF3A;MAGOHB;RPS25;RPS28;RPS27;PAN3;CNOT11;RPS29;RNPS1;RPS21;RPS24;EIF4G1
Reactome2016	Respiratory electron transport Homo sapiens R-HSA-611105	38/88	0.0000	0.0002	2.8142	35.4387	NDUFB9;COX7B;NDUFA11;NDUFB6;COX16;UQCRB;NDUFA12;NDUFB11;NDUFB5;COX18;NDUFB3;NDUFB2;NDUFB1;UQCR11;ETFB;UQCR10;COX6A1;COX7C;COX11;COX14;COX8A;NDUFA9;NDUFA7;TIMMDC1;NDUFA5;NDUFA3;ACAD9;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFAF6;SCO2;NDUFS5;NDUFAF3;COX20
BioPlanet2019	Cap-dependent translation initiation	32/73	0.0000	0.0019	2.8876	32.3767	RPL5;RPL3;RPL32;RPL10;RPL34;RPLP1;RPL12;RPLP0;RPL11;RPL36A;RPL10A;RPL8;RPL9;RPL7;RPL36;RPL13;RPL38;RPL37;EIF5B;RPL35A;EIF3K;EIF3I;RPL37A;EIF3H;RPL27;RPL26;EIF3F;RPL29;UBA52;EIF3A;EIF4G1;EIF3B
WikiPath2019M	mRNA processing WP310	147/457	0.0000	0.0000	1.7724	30.3579	LTV1;RPL32;HNRNPU;HNRNPR;MSI1;RPL8;SRP14;RPL9;RPL7;RDM1;RPS14;FBL;SNRPD1;RPL38;EIF2D;RPL37;SNRNP35;RPS11;RPS13;RPS6;CIRBP;PCOLCE;ZCRB1;DDX39B;EWSR1;NCL;PRPF3;SRSF2;RPL26;SRSF5;SREK1;SNRPB;SRSF9;SLBP;ZFP622;ZFP346;HNRNPA1L2-PS2;RBM8A;SNU13;HTATSF1;HNRNPLL;PRPF8;NOP9;MRPL11;FXR2;HNRNPDL;ZMAT2;DND1;SAFB2;CSTF1;SRP54A;ZFP740;RPL39L;ZRSR1;ZRSR2;RBPMS;ALYREF;NONO;MRPL23;PUM3;HNRNPL;CLK1;HNRNPM;LSM8;RPS28;HNRNPK;SLC6A8;RPS27;RPS29;HNRNPD;RNPS1;HNRNPC;CLASRP;GRSF1;RPS24;DAZAP1;RBM25;DDX3X;ADAR;YBX1;RBM3;PTBP1;TMEM223;SART3;SNRNP70;RNPEP;ALYREF2;ILKAP;RBM33;RBM6;MRPS28;RBM17;PABPC4;DDX56;ELMOD3;SMC1A;DDX19B;SFPQ;PRPF18;SLTM;HNRNPH1;OAS2;CSDE1;HNRNPH2;NAA38;DNAJC8;EIF4E2;TLR5;SF3B4;SF3B5;SF3B2;SFSWAP;SF3B6;RPL12;RPL11;SRSF1;MAK16;WBP4;NOL8;PPM1G;EXOSC7;EXOSC5;RBM15B;PABPN1;EXOSC9;SPOP;HNRNPA1;SRSF11;HNRNPA0;SF3A1;PPP1R14B;HNRNPA3;ZFP830;NPM1;SSB;MYEF2;TAF15;RSRC2;HNRNPAB;U2SURP;TNRC6C;HNRNPA2B1;ACIN1;TARDBP;RBM45;PPIL4;EIF3B
GOBP2021	RNA destabilization (GO:0050779)	10/18	0.0016	0.2013	4.6105	29.8204	YTHDF1;METTL14;RIDA;ROCK1;ROCK2;ZC3H18;DXO;MEX3D;RBM24;GIGYF2
BioPlanet2019	Capped intron-containing pre-mRNA processing	53/138	0.0000	0.0006	2.3119	28.9716	NUP107;NUP188;HNRNPU;HNRNPR;YBX1;CCAR1;PTBP1;SNRPD1;SNRNP70;PCF11;NCBP1;NUP133;GTF2F1;SMC1A;HNRNPUL1;HNRNPH1;SRSF2;HNRNPH2;SRSF5;DNAJC8;SNRPB;SRSF9;SF3B4;SLBP;SF3B5;SF3B2;RBM8A;SF3B6;SRSF1;DDX23;PRPF8;PABPN1;POLR2C;TPR;POLR2D;CSTF1;POLR2E;POLR2I;HNRNPA1;SRSF11;POLR2L;HNRNPA0;SF3A1;HNRNPA3;ALYREF;UPF3B;HNRNPL;HNRNPM;HNRNPK;HNRNPA2B1;HNRNPD;RNPS1;HNRNPC
Reactome2016	Mitochondrial translation termination Homo sapiens R-HSA-5419276	35/84	0.0000	0.0009	2.6432	28.4825	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MRPL14;MRPS30;MRPL34;MRPL12;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1;MRRF;MTRF1L
BioPlanet2019	Beta-oxidation of very long chain fatty acids	4/6	0.0215	0.6742	7.3693	28.3008	ACOT8;HSD17B4;ABCD1;CRAT
GOBP2021	embryonic skeletal joint development (GO:0072498)	4/6	0.0215	0.8278	7.3693	28.3008	SLC2A10;OSR1;NOG;WNT9A
GOBP2021	endoplasmic reticulum localization (GO:0051643)	4/6	0.0215	0.8278	7.3693	28.3008	POLR2M;VAPB;MOSPD3;TLE6
GOBP2021	establishment of planar polarity (GO:0001736)	4/6	0.0215	0.8278	7.3693	28.3008	BRSK1;VANGL2;NPHP1;CELSR1
GOBP2021	free ubiquitin chain polymerization (GO:0010994)	4/6	0.0215	0.8278	7.3693	28.3008	RNF135;UBE2C;UBE2S;UBE2K
GOBP2021	mitochondrial ribosome assembly (GO:0061668)	4/6	0.0215	0.8278	7.3693	28.3008	DDX28;DHX30;MTERF3;MPV17L2
GOBP2021	negative regulation of amyloid precursor protein biosynthetic process (GO:0042985)	4/6	0.0215	0.8278	7.3693	28.3008	BACE2;ABCA7;ITM2A;ITM2C

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	nuclear polyadenylation-dependent ncRNA catabolic process (GO:0071046)	4/6	0.0215	0.8278	7.3693	28.3008	EXOSC7;EXOSC9;EXOSC3;EXOSC2
GOBP2021	nuclear polyadenylation-dependent rRNA catabolic process (GO:0071035)	4/6	0.0215	0.8278	7.3693	28.3008	EXOSC7;EXOSC9;EXOSC3;EXOSC2
GOBP2021	nuclear polyadenylation-dependent tRNA catabolic process (GO:0071038)	4/6	0.0215	0.8278	7.3693	28.3008	EXOSC7;EXOSC9;EXOSC3;EXOSC2
GOBP2021	pyrimidine nucleotide-sugar transmembrane transport (GO:0090481)	4/6	0.0215	0.8278	7.3693	28.3008	SLC35A2;SLC35A3;SLC35C2;SLC35B1
GOBP2021	regulation of response to reactive oxygen species (GO:1901031)	4/6	0.0215	0.8278	7.3693	28.3008	HEBP2;GCH1;BMP7;FBLN5
GOBP2021	ruffle assembly (GO:0097178)	4/6	0.0215	0.8278	7.3693	28.3008	INPP5K;RAC1;AIF1;ARF6
GOBP2021	tRNA surveillance (GO:0106354)	4/6	0.0215	0.8278	7.3693	28.3008	EXOSC7;EXOSC9;EXOSC3;EXOSC2
Reactome2016	Scavenging by Class F Receptors Homo sapiens R-HSA-3000484	4/6	0.0215	0.3747	7.3693	28.3008	HSP90AA1;HSPH1;CALR;SCARF1
Reactome2016	Beta-oxidation of very long chain fatty acids Homo sapiens R-HSA-390247	4/6	0.0215	0.3747	7.3693	28.3008	ACOT8;HSD17B4;ABCD1;CRAT
WikiPath2019M	Robo4 and VEGF Signaling Pathways Crosstalk WP3864	4/6	0.0215	0.6088	7.3693	28.3008	ROBO4;KDR;RAC1;VEGFA
GOBP2021	RNA processing (GO:0006396)	65/179	0.0000	0.0008	2.1162	26.9248	TCERG1;TUT7;PDCD7;GEMIN2;HNRNPU;HNRNPR;ADAR;TSEN2;TENT4A;TENT4B;PPP1R9B;RBM3;PTBP1;SNRPD1;KHSRP;SNRNP35;BCAS2;RBM6;APOBEC1;NCBP1;PABPC4;ZCRB1;SFPQ;PRPF18;DDX39B;HNRNPUL1;HNRNPH1;PRPF3;SRSF2;LUC7L3;RP9;PPIG;SRSF5;HNRNPH3;AURKAIP1;PRMT9;SNRPB;SRSF9;SF3B4;TSEN34;SF3B2;RBM8A;WBP4;SRSF1;DDX23;PRPF8;PPP2CA;PABPN1;SRSF11;HNRNPA0;ZRSR2;SF3A1;RBPMS;NONO;MAGOHB;HNRNPL;HNRNPK;LSM6;HNRNPA2B1;HNRNPD;MPHOSPH10;RNPS1;SNRNP48;HNRNPC;TARDBP
GOBP2021	negative regulation of release of sequestered calcium ion into cytosol (GO:0051280)	7/12	0.0057	0.4303	5.1611	26.6279	FKBP1A;GSTM2;GSTO1;FKBP1B;CALM3;PKD2;CALM2
GOBP2021	negative regulation of ryanodine-sensitive calcium-release channel activity (GO:0060315)	7/12	0.0057	0.4303	5.1611	26.6279	FKBP1A;GSTM2;GSTO1;FKBP1B;CALM3;PKD2;CALM2
GOBP2021	regulation of amyloid precursor protein catabolic process (GO:1902991)	7/12	0.0057	0.4303	5.1611	26.6279	FKBP1A;ABCA2;PRNP;ROCK1;ROCK2;RANBP9;ABCA7
BioPlanet2019	Messenger RNA processing	72/203	0.0000	0.0005	2.0410	26.3770	NUP107;NUP188;HNRNPU;HNRNPR;ADAR;YBX1;CCAR1;LSM10;PTBP1;SNRPD1;PCF11;SNRNP70;APOBEC1;RBM17;NCBP1;NUP133;GTF2F1;SMC1A;SFPQ;PRPF18;HNRNPUL1;HNRNPH1;PRPF3;SRSF2;HNRNPH2;SRSF5;SREK1;DNAJC8;SNRPB;SRSF9;SF3B4;SLBP;SF3B5;SF3B2;RBM8A;SFSWAP;SF3B6;SRSF1;DDX23;PRPF8;PPM1G;PABPN1;POLR2C;TPR;POLR2D;CSTF1;SPOP;POLR2E;POLR2I;HNRNPA1;SRSF11;POLR2L;HNRNPA0;SF3A1;HNRNPA3;ALYREF;NONO;UPF3B;GTF2H3;GTF2H4;HNRNPAB;HNRNPL;CLK1;HNRNPM;HNRNPK;HNRNPA2B1;ERCC2;HNRNPD;RNPS1;HNRNPC;CLASRP;MNAT1
KEGG2019M	Riboflavin metabolism	5/8	0.0139	0.4383	6.1421	26.2769	FLAD1;ACP5;BLVRB;ACP2;ACP1
KEGG2019M	Sulfur relay system	5/8	0.0139	0.4383	6.1421	26.2769	MPST;CTU2;NFS1;MOCS3;URM1
GOBP2021	positive regulation of ryanodine-sensitive calcium-release channel activity (GO:0060316)	5/8	0.0139	0.6921	6.1421	26.2769	GSTM2;JPH2;GSTO1;CALM3;CALM2
GOBP2021	protein retention in ER lumen (GO:0006621)	5/8	0.0139	0.6921	6.1421	26.2769	RER1;KDELR1;GPAA1;KDELR2;KDELR3
GOBP2021	U4 snRNA 3'-end processing (GO:0034475)	5/8	0.0139	0.6921	6.1421	26.2769	EXOSC7;EXOSC5;EXOSC9;EXOSC3;EXOSC2
GOBP2021	rRNA 3'-end processing (GO:0031125)	6/10	0.0089	0.5716	5.5288	26.0911	EXOSC7;EXOSC9;ERI3;EXOSC3;RPS21;EXOSC2
GOBP2021	cellular macromolecule biosynthetic process (GO:0034645)	104/314	0.0000	0.0002	1.8438	25.9691	RPL5;RPL3;RPL32;RPL34;SCX;RPL8;RPL10A;RPL9;RPL7;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;LARGE1;RPS13;RPS12;RPS5;RPS6;MRPS18B;MRPS18A;RPSA;TIMELESS;RPL27;RPL26;RPL29;SET;MRPL18;MRPL11;ORC5;ATRIP;EEFSEC;MRPL27;INHBA;MRPL23;NR4A2;RPS25;RPS28;POLA2;RPS27;FUBP3;RPS29;BCL3;RNPS1;MMS19;RPS21;RSL24D1;RPS24;FARSB;EIF4G1;RAD9A;NFKBIB;MRPS17;MRPS16;MRPS14;MCM8;MRPS11;RPLP1;MRPS12;RPLP0;MRPL36;MRPL34;PTMS;ING5;MRPL3;MRPL9;POLE;RFC5;UPF1;PABPC4;MRPS7;MRPS5;MRPL43;MRPL52;DBF4;RPL37A;TOP1;PTMA;MRRF;RPL10;RPL12;RPL11;RPL36A;RRBP1;RPS15A;POLD1;POLR2C;POLD2;POLR2D;RPS3;E2F1;POLR2E;RPL13;RPS2;POLR2I;ABCF1;POLR2L;DONSON;RPL35A;GOLPH3;RPS6KB2
GOBP2021	ribonucleoprotein complex biogenesis (GO:0022613)	26/60	0.0001	0.0219	2.8265	25.8374	LTV1;RPL5;RPL11;MRPL36;MALSU1;NOC2L;RPL7;RPS15;RPS19;DHX37;RRP36;RPL38;NOP14;NPM1;RPS6;WDR74;GTF3A;RPL35A;CUL4A;BOP1;RPS25;RPS28;NAF1;RPL26;RBIS;RPS24
GOBP2021	RNA splicing (GO:0008380)	39/98	0.0000	0.0068	2.4468	25.8357	SF3B4;TCERG1;SF3B2;RBM8A;PDCD7;GEMIN2;WBP4;DDX23;PRPF8;PPP1R9B;PPP2CA;PTBP1;SNRPD1;KHSRP;SNRNP35;SMNDC1;BCAS2;SRSF11;ZRSR2;NCBP1;NONO;ZCRB1;MAGOHB;SFPQ;LSM6;PRPF18;DDX39B;PRPF3;SRSF2;MPHOSPH10;LUC7L3;RNPS1;RP9;SNRNP48;PPIG;HNRNPC;HNRNPH3;TARDBP;SNRPB
GOBP2021	mitochondrial translational termination (GO:0070126)	36/89	0.0000	0.0084	2.5135	25.8156	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MRPL14;MRPS30;MRPL34;MRPL12;MRPL57;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1;MRRF;MTRF1L
Reactome2016	Mitochondrial translation initiation Homo sapiens R-HSA-5368286	34/84	0.0001	0.0022	2.5156	24.6453	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MTIF2;MRPL14;MRPS30;MRPL34;MRPL12;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	Mitochondrial translation Homo sapiens R-HSA-5368287	36/90	0.0000	0.0019	2.4668	24.6383	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MTIF2;MRPL14;MRPS30;MRPL34;MRPL12;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1;MRRF;MTRF1L
Reactome2016	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins. Homo sapiens R-HSA-163200	42/109	0.0000	0.0014	2.3209	23.9955	NDUFB9;COX7B;NDUFA11;COX16;UQCRB;NDUFB6;NDUFA12;NDUFB11;NDUFB5;COX18;NDUFB3;NDUFB2;NDUFB1;UQCR11;ETFB;UQCR10;COX6A1;ATP5O;ATP5G2;COX7C;ATP5L;ATP5D;COX11;COX14;COX8A;NDUFA9;NDUFA7;TIMMDC1;NDUFA5;NDUFA3;ACAD9;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFAF6;NDUFS7;SCO2;NDUFS5;NDUFAF3;COX20
GOBP2021	ribonucleoprotein complex assembly (GO:0022618)	50/136	0.0000	0.0068	2.1540	22.6642	RPL5;RAMAC;RPL3;HSP90AB1;GEMIN2;MRPS11;RPLP0;RPS15;RPS14;SART1;SART3;RPS19;SNRPD1;DENR;RPL38;EIF2D;HSP90AA1;NCBP1;RPS5;RPSA;MRPS7;CRNKL1;TRAF7;GCFC2;PRPF18;DDX39B;GEMIN5;LUC7L3;GEMIN6;NAF1;SRSF5;LUC7L2;SNRPB;SRSF9;RPL10;YTHDC1;RPL11;SRSF1;DDX23;RPS27L;POLR2D;MDN1;ZRSR2;PTGES3;NLE1;BOP1;RPS28;RPS27;RSL24D1;EIF3A
Reactome2016	Infectious disease Homo sapiens R-HSA-5663205	111/348	0.0000	0.0001	1.7436	22.4422	RPL5;RPL3;NUP107;RPL32;NUP188;CCNT1;RPL34;RPL8;RPL10A;RPL9;RPL7;PSMD8;RPS15;RPS14;PSMD7;RPS19;PSMD5;RPS18;RPL36;RPL38;RPL37;RPS11;KPNA2;B2M;RPS13;RPS12;MAP2K2;RPS5;RPS6;AP1B1;RPSA;GTF2F1;ELMO1;CHMP4C;CHMP4B;RPL27;RPL26;RPL29;UBA52;PPIA;KPNB1;PSMD10;PSMD14;GTF2E1;TPR;UBC;PSMF1;MAP2K7;TGFB1;HMGA1;MSRA;RPS25;RPS28;RPS27;RPS29;CALR;MNAT1;GRSF1;RPS21;RPS24;HSP90AB1;RPLP1;RPLP0;PSIP1;AP2A1;RAC1;NELFA;HSP90AA1;NCBP1;NUP133;PSMA5;CANX;RPL37A;VAMP1;CHMP3;CHMP7;VAMP2;GTF2A1;CTDP1;RPL10;RPL12;RPL11;RPL36A;PSMB7;RPS15A;PABPN1;PSMB3;POLR2C;POLR2D;RPS3;POLR2E;RPL13;FYN;RPS2;POLR2I;POLR2L;RANBP1;NPM1;TAF12;TAF13;TAF10;RPL35A;SSRP1;GTF2H3;GTF2H4;ERCC2;CD9;FAU;TAF5;TAF4;TAF3
GOBP2021	mitochondrial ATP synthesis coupled electron transport (GO:0042775)	29/71	0.0002	0.0290	2.5526	22.3435	NDUFB9;COX7B;NDUFA11;NDUFB6;UQCRB;NDUFA12;NDUFB11;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFB1;UQCR11;UQCR10;COX6A1;COX7C;COX6A2;COA6;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;SDHA;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5
GOBP2021	nucleic acid metabolic process (GO:0090304)	29/71	0.0002	0.0290	2.5526	22.3435	HNRNPU;HNRNPR;PTBP1;METTL14;POLR2C;POLR2D;POLR2E;KPNA2;POLR2I;HNRNPA1;POLR2L;HNRNPA0;HNRNPA3;NCBP1;WTAP;WDR74;GTF2F1;HNRNPL;HNRNPM;LSM8;HNRNPK;HNRNPH1;HNRNPA2B1;HNRNPD;HNRNPH2;DXO;MMS19;HNRNPC;DNASE1L2
BioPlanet2019	Smooth muscle contraction	11/22	0.0028	0.2144	3.6886	21.7293	TPM4;TPM3;CALD1;TPM2;TPM1;LMOD1;MYL6B;MYH11;MYL9;MYLK;MYL12B
GOBP2021	chaperone-mediated protein complex assembly (GO:0051131)	11/22	0.0028	0.2886	3.6886	21.7293	MKKS;HSP90AA1;HSP90AB1;HSPA4;PTGES3;PSMG3;LONP1;PSMG2;HOPX;PFDN6;HSPD1
GOBP2021	maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000466)	11/22	0.0028	0.2886	3.6886	21.7293	EXOSC7;NOP14;EXOSC9;RPP40;ERI3;URB1;EXOSC3;RPS21;EXOSC2;NOP9;FTSJ3
GOBP2021	translational termination (GO:0006415)	37/96	0.0001	0.0196	2.3203	21.5543	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MRPL14;MRPS30;MRPL34;APEH;MRPL12;MRPL57;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1;MRRF;MTRF1L
GOBP2021	ribosomal large subunit biogenesis (GO:0042273)	24/57	0.0003	0.0502	2.6870	21.5372	RPL5;NPM1;RPL3;RPL10;RPLP0;RPL11;MAK16;WDR74;GTF3A;RPL35A;SNU13;MALSU1;RPL10A;NOC2L;NLE1;RPL7;TRAF7;BOP1;NSA2;LAS1L;RPL26;RSL24D1;RRP15;MDN1
GOBP2021	cellular response to arsenic-containing substance (GO:0071243)	8/15	0.0065	0.4583	4.2136	21.2422	VCP;DDX3X;GSTO1;HSF1;PPIF;HNRNPA1;CPEB2;MAPK13
Reactome2016	Mitochondrial translation elongation Homo sapiens R-HSA-5389840	33/84	0.0001	0.0052	2.3930	21.2146	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MRPL14;MRPS30;MRPL34;MRPL12;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1
GOBP2021	artery morphogenesis (GO:0048844)	14/30	0.0018	0.2199	3.2287	20.4825	TBX1;PDGFRB;NOTCH1;HPGD;LRP1;FOXF1;NOG;PKD2;TBX2;SMAD7;VEGFA;HEY2;HES1;ENG
GOBP2021	mRNA destabilization (GO:0061157)	17/38	0.0011	0.1440	2.9883	20.4798	UPF1;YTHDF1;TUT7;ROCK1;ROCK2;MEX3D;GIGYF2;ZFP36L2;ZC3H12D;MOV10;METTL14;RIDA;KHSRP;POLR2D;DND1;TARDBP;RBM24
Reactome2016	mRNA Splicing - Minor Pathway Homo sapiens R-HSA-72165	22/52	0.0005	0.0186	2.7087	20.4140	SF3B4;SF3B5;SF3B2;NCBP1;PDCD7;SF3B6;SRSF1;DDX23;YBX1;ZCRB1;GTF2F1;PRPF8;SNRPD1;POLR2C;POLR2D;SRSF2;POLR2E;SNRNP48;SNRNP35;POLR2I;SNRPB;POLR2L
GOBP2021	negative regulation of telomere maintenance via telomerase (GO:0032211)	10/20	0.0043	0.3562	3.6879	20.0970	CTC1;ACD;STN1;TEN1;HNRNPU;NAT10;HNRNPC;TERF1;HNRNPA1;TENT4B
GOBP2021	ribosomal large subunit assembly (GO:0000027)	12/25	0.0028	0.2886	3.4052	20.0547	DDX28;RPL5;DHX30;BOP1;TRAF7;RPL3;RPL10;RPL11;RPLP0;RSL24D1;MDN1;NLE1
GOBP2021	aerobic electron transport chain (GO:0019646)	28/70	0.0003	0.0483	2.4640	19.9159	NDUFB9;COX7B;NDUFA11;NDUFB6;UQCRB;NDUFA12;NDUFB11;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFB1;UQCR11;UQCR10;COX6A1;COX7C;COX6A2;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;SDHA;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5
GOBP2021	endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000479)	7/13	0.0102	0.5827	4.3007	19.7327	RCL1;NOP14;TBL3;BMS1;RPP40;RPS21;NOP9
GOBP2021	negative regulation of stem cell differentiation (GO:2000737)	7/13	0.0102	0.5827	4.3007	19.7327	REST;NOTCH1;TCF15;ESRRB;HNRNPU;HES1;ZFP36L2

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	mitochondrial translational elongation (GO:0070125)	34/89	0.0002	0.0365	2.2862	19.3275	MRPS17;MRPS16;MRPS14;MRPS11;MRPL18;MRPS12;MRPL16;MRPL36;MRPL14;MRPS30;MRPL34;MRPL12;MRPL57;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPS7;MRPL23;MRPS5;MRPL43;MRPL52;MRPL30;MRPL50;AURKAIP1
GOBP2021	mitochondrial translation (GO:0032543)	39/105	0.0002	0.0290	2.1863	19.2002	MRPS17;MRPS16;MRPS14;MRPL18;MRPS11;MRPS12;MRPL16;MRPL14;MRPL36;MTIF2;MRPS30;MRPL12;MRPL34;MRPL57;MRPL54;MRPL11;MRPL4;MRPL3;MRPL9;CHCHD1;MRPS28;NDUFA7;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPL23;MRPS7;MRPS5;MRPL43;MRPL30;MRPL52;LARS2;MRPL50;AURKAIP1;MRRF;MTRF1L
GOBP2021	positive regulation of cellular protein metabolic process (GO:0032270)	38/102	0.0002	0.0305	2.1966	19.0356	RPL5;HDAC2;DDX3X;NAT10;RPS27L;RBM3;METTL14;FXR2;CAPN3;METTL5;BAK1;SOX4;TBC1D10A;DACT1;HSP90AA1;YTHDF1;NPM1;TGFB1;FBXW11;NSUN5;NR1H2;ATG10;CIRBP;UPF3B;UPF3A;INHBA;KLF4;LARP6;AGT;ASPH;RPS6KB1;BCL3;HNRNPD;PLXNB2;RPL26;AURKAIP1;TRIM32;EIF4G1
BioPlanet2019	HIV-1 transcription initiation	17/39	0.0015	0.1311	2.8523	18.5407	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;POLR2L
GOBP2021	mitochondrial respiratory chain complex assembly (GO:0033108)	34/90	0.0003	0.0440	2.2452	18.4254	NDUFB9;NDUFA11;NDUFB6;COX16;NDUFA12;NDUFB11;NDUFB5;COX18;NDUFB3;NDUFB2;NDUFB1;CHCHD4;AIFM1;COX14;NDUFA9;COA3;NDUFA7;TIMMDC1;NDUFA5;PET100;UQCC2;NDUFA3;ACAD9;NDUFAF8;NDUFS8;NDUFS7;NDUFAF6;SCO2;NDUFS5;SDHAF1;TMEM126A;NDUFAF3;SDHAF4;COX20
GOBP2021	pyrimidine nucleoside salvage (GO:0043097)	6/11	0.0161	0.7309	4.4228	18.2583	CDA;UCK2;UCK1;UPP2;UPP1;UCKL1
GOBP2021	pyrimidine-containing compound salvage (GO:0008655)	6/11	0.0161	0.7309	4.4228	18.2583	CDA;UCK2;UCK1;UPP2;UPP1;UCKL1
GOBP2021	regulation of amyloid precursor protein biosynthetic process (GO:0042984)	6/11	0.0161	0.7309	4.4228	18.2583	ABCA2;BACE2;NECAB3;ABCA7;ITM2A;ITM2C
Reactome2016	The citric acid (TCA) cycle and respiratory electron transport Homo sapiens R-HSA-1428517	53/153	0.0001	0.0039	1.9632	18.0801	COX7B;NDUFA11;NDUFA12;ETFB;COX6A1;ATP5G2;COX7C;MPC1;PDK3;SLC16A3;PDK2;COX8A;ACAD9;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;SCO2;NDUFS5;HAGH;NDUFB9;COX16;UQCRB;NDUFB6;NDUFB11;NDUFB5;COX18;NDUFB3;NDUFB2;NDUFB1;UQCR11;UQCR10;PDHB;ATP5O;ATP5L;LDHB;ATP5D;COX11;COX14;NDUFA9;NDUFA7;PDHA1;TIMMDC1;NDUFA5;MDH2;IDH3G;NDUFA3;CS;NDUFAF6;NDUFAF3;COX20
BioPlanet2019	Respiratory electron transport, ATP biosynthesis by chemiosmotic coupling, and heat production by uncoupling proteins	31/81	0.0004	0.0411	2.2920	18.0351	NDUFB9;COX7B;NDUFA11;NDUFB6;UQCRB;NDUFA12;NDUFB11;NDUFB5;NDUFB3;NDUFB2;NDUFB1;UQCR11;ETFB;UQCR10;COX6A1;ATP5O;COX7C;ATP5L;ATP5D;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5
GOBP2021	positive regulation of protein dephosphorylation (GO:0035307)	15/34	0.0024	0.2753	2.9133	17.5331	PDGFRB;HSP90AB1;TGFB1;CD300A;GBA;PPP2R5A;DUSP26;SPPL3;PTBP1;SMPD1;CNEP1R1;PIN1;CALM3;PPIA;CALM2
Reactome2016	EPHA-mediated growth cone collapse Homo sapiens R-HSA-3928663	15/34	0.0024	0.0746	2.9133	17.5331	EPHA7;HSP90AA1;ROCK1;ROCK2;RHOA;MYL12B;VEGFA;EFNA1;KDR;MYH14;MYH9;FYN;MYH11;MYH10;MYL9
GOBP2021	translational elongation (GO:0006414)	38/104	0.0003	0.0440	2.1298	17.4773	MRPS17;MRPS16;MRPS14;MRPL18;MRPS11;MRPS12;MRPL16;MRPL14;MRPL36;MRPS30;MRPL12;MRPL34;MRPL57;MRPL54;MRPL11;MRPL4;MRPL3;RACK1;MRPL9;CHCHD1;EEFSEC;MRPS28;MRPS27;MRPS24;MRPS25;MRPS18B;MRPL27;MRPS18A;MRPL23;MRPS7;MRPS5;MRPL43;MRPL30;MRPL52;MRPL50;MTRES1;NEMF;AURKAIP1
BioPlanet2019	ALK1 pathway	12/26	0.0042	0.2415	3.1618	17.3393	FKBP1A;SMAD1;SMAD4;TGFB1;TGFB3;ID1;CSNK2B;INHBA;ACVR2B;MAPK3;SMAD7;ENG
BioPlanet2019	RNA polymerase II transcription	37/101	0.0003	0.0358	2.1383	17.2924	SLBP;GTF2A1;CTDP1;CCNT1;RBM8A;SRSF1;GTF2E1;LSM10;PABPN1;PCF11;POLR2C;POLR2D;CSTF1;POLR2E;NELFA;POLR2I;SRSF11;POLR2L;NCBP1;TAF12;TAF13;ALYREF;TAF10;UPF3B;SSRP1;GTF2F1;GTF2H3;GTF2H4;ERCC2;SRSF2;RNPS1;SRSF5;TAF5;MNAT1;TAF4;SNRPB;SRSF9
GOBP2021	mRNA metabolic process (GO:0016071)	35/95	0.0004	0.0576	2.1571	16.9317	SF3B4;TCERG1;SLBP;SF3B2;GEMIN2;SRSF1;HNRNPR;PRPF8;ZFP36L2;LSM10;ZC3H12D;PTBP1;RIDA;PCF11;HSF1;SRSF11;HNRNPA0;SF3A1;SSB;NCBP1;NONO;RNASE4;SFPQ;PRPF18;LSM6;PRPF3;HNRNPA2B1;SRSF2;DXO;SRSF5;AURKAIP1;PRMT9;HSPA1B;SNRPB;SRSF9
BioPlanet2019	Pyrimidine salvage reactions	5/9	0.0258	0.7339	4.6063	16.8540	CDA;UCK2;UCK1;UPP2;UPP1
GOBP2021	epithelial to mesenchymal transition involved in endocardial cushion formation (GO:0003198)	5/9	0.0258	0.9024	4.6063	16.8540	NOTCH1;HEY2;SNAI1;SNAI2;ENG
GOBP2021	exonucleolytic trimming involved in rRNA processing (GO:0000459)	5/9	0.0258	0.9024	4.6063	16.8540	EXOSC7;EXOSC9;ERI3;EXOSC3;EXOSC2
GOBP2021	exonucleolytic trimming to generate mature 3'-end of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000467)	5/9	0.0258	0.9024	4.6063	16.8540	EXOSC7;EXOSC9;ERI3;EXOSC3;EXOSC2
GOBP2021	mitral valve morphogenesis (GO:0003183)	5/9	0.0258	0.9024	4.6063	16.8540	EFNA1;NOTCH1;SMAD6;ZFPM1;SOX4
Reactome2016	Pyrimidine salvage reactions Homo sapiens R-HSA-73614	5/9	0.0258	0.3993	4.6063	16.8540	CDA;UCK2;UCK1;UPP2;UPP1
Reactome2016	RHO GTPases activate PAKs Homo sapiens R-HSA-5627123	10/21	0.0067	0.1657	3.3525	16.8050	PPP1CB;PPP1R12A;MYH14;MYH9;MYH11;RAC1;MYL9;MYH10;MYLK;MYL12B
BioPlanet2019	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	8/16	0.0105	0.4456	3.6867	16.7859	FKBP1A;TGFB1;PARD6A;PARD3;UBC;PRKCZ;UBA52;RHOA
GOBP2021	3'-UTR-mediated mRNA destabilization (GO:0061158)	8/16	0.0105	0.5827	3.6867	16.7859	ZC3H12D;UPF1;MOV10;KHSRP;DND1;TARDBP;RBM24;ZFP36L2
GOBP2021	mRNA cis splicing, via spliceosome (GO:0045292)	8/16	0.0105	0.5827	3.6867	16.7859	SART1;SFSWAP;WBP4;DDX23;SRSF1;PSIP1;CWC15;WBP11
Reactome2016	RHO GTPases activate CIT Homo sapiens R-HSA-5625900	8/16	0.0105	0.2261	3.6867	16.7859	MYH14;MYH9;MYH11;RAC1;MYL9;MYH10;RHOA;MYL12B

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition) Homo sapiens R-HSA-2173791	8/16	0.0105	0.2261	3.6867	16.7859	FKBP1A;TGFB1;PARD6A;PARD3;UBC;PRKCZ;UBA52;RHOA
BioPlanet2019	Sema4D in semaphorin signaling	13/29	0.0039	0.2395	2.9974	16.5908	CD72;ROCK1;SEMA4D;ROCK2;RHOA;MYL12B;RRAS;MYH14;MYH9;MYH11;RAC1;MYH10;MYL9
Reactome2016	Complex I biogenesis Homo sapiens R-HSA-6799198	20/49	0.0016	0.0546	2.5463	16.3858	NDUFA9;NDUFB9;NDUFA7;TIMMDC1;NDUFA11;NDUFB6;NDUFA5;NDUFA12;NDUFB11;NDUFB5;NDUFA3;ACAD9;NDUFB3;NDUFB2;NDUFB1;NDUFS8;NDUFS7;NDUFAF6;NDUFS5;NDUFAF3
GOBP2021	cardiac muscle tissue morphogenesis (GO:0055008)	14/32	0.0037	0.3332	2.8696	16.0703	NOTCH1;TGFB1;TNNC1;NOG;TPM1;SMAD7;FKBP1A;ACTC1;TNNT2;MYL2;PKP2;ZFPM1;MYH6;ENG
Reactome2016	Sema4D induced cell migration and growth-cone collapse Homo sapiens R-HSA-416572	11/24	0.0064	0.1624	3.1207	15.7632	ROCK1;SEMA4D;ROCK2;MYH14;MYH9;MYH11;RAC1;MYL9;MYH10;RHOA;MYL12B
BioPlanet2019	Creatine metabolism	4/7	0.0417	0.9439	4.9125	15.6058	GAMT;SLC6A8;CKM;CKB
BioPlanet2019	Viral dsRNA-TLR3-TRIF complex activation of RIP1	4/7	0.0417	0.9439	4.9125	15.6058	RIPK3;CHUK;RIPK1;TICAM1
GOBP2021	atrioventricular valve formation (GO:0003190)	4/7	0.0417	1.0000	4.9125	15.6058	OLFM1;SMAD4;NOTCH1;ZFPM1
GOBP2021	creatine metabolic process (GO:0006600)	4/7	0.0417	1.0000	4.9125	15.6058	GAMT;SLC6A8;CKM;CKB
GOBP2021	negative regulation of cell cycle phase transition (GO:1901988)	4/7	0.0417	1.0000	4.9125	15.6058	RGCC;PTEN;ATF5;ZFP36L2
GOBP2021	negative regulation of protein kinase activity by regulation of protein phosphorylation (GO:0044387)	4/7	0.0417	1.0000	4.9125	15.6058	NPM1;ADAR;DUSP26;CDK5RAP3
GOBP2021	pericardium morphogenesis (GO:0003344)	4/7	0.0417	1.0000	4.9125	15.6058	DLL4;NOTCH1;FLRT3;BMP7
GOBP2021	polyadenylation-dependent snoRNA 3'-end processing (GO:0071051)	4/7	0.0417	1.0000	4.9125	15.6058	EXOSC5;PARN;EXOSC3;EXOSC2
GOBP2021	posttranslational protein targeting to membrane, translocation (GO:0031204)	4/7	0.0417	1.0000	4.9125	15.6058	SEC61A1;SEC61G;SEC62;SEC63
GOBP2021	regulation of extracellular matrix assembly (GO:1901201)	4/7	0.0417	1.0000	4.9125	15.6058	TGFB1;NOTCH1;RGCC;AGT
GOBP2021	regulation of glycogen (starch) synthase activity (GO:2000465)	4/7	0.0417	1.0000	4.9125	15.6058	PPP1R3F;GSK3A;IGF2;INPP5K
GOBP2021	regulation of metallopeptidase activity (GO:1905048)	4/7	0.0417	1.0000	4.9125	15.6058	LRP1;DDRGK1;SVBP;TIMP2
GOBP2021	regulation of transforming growth factor beta activation (GO:1901388)	4/7	0.0417	1.0000	4.9125	15.6058	HSP90AB1;GATA6;LRRC32;LTBP1
GOBP2021	ribosomal small subunit export from nucleus (GO:0000056)	4/7	0.0417	1.0000	4.9125	15.6058	LTV1;RPS15;NPM1;NOP9
Reactome2016	Clearance of Nuclear Envelope Membranes from Chromatin Homo sapiens R-HSA-2993913	4/7	0.0417	0.5243	4.9125	15.6058	LEMD3;EMD;LEMD2;TMPO
WikiPath2019M	Pentose Phosphate Pathway WP63	4/7	0.0417	0.7762	4.9125	15.6058	RPIA;G6PDX;PGLS;TKT
Reactome2016	RNA Polymerase II Transcription Homo sapiens R-HSA-73857	43/124	0.0004	0.0150	1.9642	15.2684	SLBP;GTF2A1;CTDP1;CCNT1;RBM8A;SRSF1;CASC3;GTF2E1;LSM10;PABPN1;FIP1L1;PCF11;POLR2C;POLR2D;CSTF1;POLR2E;NELFA;POLR2I;SRSF11;POLR2L;NCBP1;TAF12;TAF13;ALYREF;TAF10;UPF3B;THOC2;SSRP1;GTF2F1;GTF2H3;GTF2H4;DDX39B;SARNP;ERCC2;SRSF2;RNPS1;SRSF5;TAF5;MNAT1;TAF4;TAF3;SNRPB;SRSF9
Reactome2016	RNA Polymerase II HIV Promoter Escape Homo sapiens R-HSA-167162	18/44	0.0026	0.0746	2.5554	15.1899	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
Reactome2016	RNA Polymerase II Promoter Escape Homo sapiens R-HSA-73776	18/44	0.0026	0.0746	2.5554	15.1899	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
Reactome2016	RNA Polymerase II Transcription Initiation And Promoter Clearance Homo sapiens R-HSA-76042	18/44	0.0026	0.0746	2.5554	15.1899	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
Reactome2016	RNA Polymerase II Transcription Initiation Homo sapiens R-HSA-75953	18/44	0.0026	0.0746	2.5554	15.1899	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
Reactome2016	RNA Polymerase II Transcription Pre-Initiation And Promoter Opening Homo sapiens R-HSA-73779	18/44	0.0026	0.0746	2.5554	15.1899	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
Reactome2016	HIV Transcription Initiation Homo sapiens R-HSA-167161	18/44	0.0026	0.0746	2.5554	15.1899	GTF2A1;TAF12;TAF13;TAF10;GTF2H3;GTF2F1;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
GOBP2021	negative regulation of DNA damage response, signal transduction by p53 class mediator (GO:0043518)	7/14	0.0166	0.7309	3.6860	15.0992	PSMD10;CD74;KDM1A;SNAI1;TWIST1;SNAI2;MIF
GOBP2021	pyrimidine nucleoside biosynthetic process (GO:0046134)	7/14	0.0166	0.7309	3.6860	15.0992	CDA;UCK2;UCK1;UPP2;UPP1;UCKL1;DHODH
Reactome2016	Sema4D in semaphorin signaling Homo sapiens R-HSA-400685	12/27	0.0060	0.1565	2.9508	15.0768	ROCK1;RRAS;SEMA4D;ROCK2;MYH14;MYH9;MYH11;RAC1;MYH10;MYL9;RHOA;MYL12B
KEGG2019M	Thermogenesis	73/231	0.0002	0.0172	1.7132	14.8594	ATF2;COX7B;SMARCB1;NDUFA11;KDM1A;NDUFA12;COX4I2;COX6A1;ATP5G2;COX7C;COX6A2;PRKAG3;ACTG1;LIPE;RPS6KA6;CPT2;CREB3L1;MLST8;HRAS;PRKG1;COA6;MAP3K5;COX8A;SMARCC2;RPS6;TSC2;CPT1C;SDHA;CPT1B;SDHB;COX6B1;CREB3;COX7A2L;NDUFS8;NDUFS7;NDUFS5;NDUFB9;SMARCD3;COX16;UQCRB;NDUFB6;NDUFB11;NDUFB5;COX18;NDUFB3;ADCY4;NDUFA4L2;NDUFB2;UQCR11;COX7A2;UQCR10;ATP5O;COX7A1;ATP5L;SLC25A29;ATP5D;COX11;COX14;SMARCE1;NDUFA9;COA3;NDUFA7;NDUFA5;NDUFA3;SMARCA2;MAPK13;NDUFAF6;RPS6KB1;RHEB;RPS6KB2;NDUFAF3;KRAS;COX20
GOBP2021	maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000462)	13/30	0.0056	0.4303	2.8209	14.6165	NOP14;UTP3;MRPS11;RPP40;NOP9;RPS14;TBL3;RPS19;BMS1;DHX37;RRP36;RPS21;DCAF13

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	cellular protein metabolic process (GO:0044267)	122/417	0.0001	0.0172	1.5379	14.5502	RPL5;APP;RPL3;RPL32;RPL34;UBE2D3;PLOD2;RPL8;RPL10A;RPL9;ZDHHC2;RPL7;UBE2L3;RPS15;RPS14;RPS19;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;CHGB;RPS12;ATG3;CSNK1G3;RPS5;APLP2;RPS6;MRPS18B;MRPS18A;RPSA;PDIA6;RPL27;RPL26;RPL29;UBA52;MRPL18;GATA6;LTBP1;MRPL11;HSP90B1;NCSTN;APH1B;STC2;PENK;ABL2;IGFBP7;RIPK1;LTA4H;ABCA3;SIAH2;MRPL27;IGF2;MRPL23;MSRA;RPS25;RPS28;RPS27;RPS29;UBE2S;HRC;UBA3;CPE;RSL24D1;RPS21;RPS24;FARSB;EIF4G1;UBE2M;MRPS17;MRPS16;MRPS14;RPLP1;MRPS11;RPLP0;MRPS12;MRPL36;IDE;MRPL34;SPPL3;MRPL3;MRPL9;PSENEN;RIPK3;PABPC4;ANO8;MRPS7;RABGGTA;MRPL43;MRPS5;CKAP4;MRPL52;RCN1;RPL37A;MFGE8;MRRF;RPL10;RPL12;RPL11;RPL36A;NEDD8;RRBP1;SPG7;RPS15A;RPS3;GPC3;RPL13;TMEM208;RPS2;SEC11A;SEC11C;ABCF1;LAMB2;MCRS1;RPL35A;UBE2G2;SPCS2;RAB12;QPCT;RPS6KB2;MSRB1
BioPlanet2019	Semaphorin interactions	25/66	0.0016	0.1317	2.2522	14.4940	ITGB1;SEMA7A;HSP90AB1;PLXND1;ROCK1;ROCK2;MYL12B;DPYSL4;RRAS;DPYSL2;DPYSL3;MYH14;MYH11;FYN;RAC1;MYH10;SEMA4A;HSP90AA1;CD72;SEMA4D;RHOA;TYROBP;PLXNB3;MYH9;MYL9
BioPlanet2019	RNA polymerase II promoter escape	10/22	0.0099	0.4455	3.0729	14.1842	GTF2A1;TAF12;TAF13;TAF10;ERCC2;TAF5;GTF2H3;TAF4;GTF2E1;GTF2H4
GOBP2021	heme biosynthetic process (GO:0006783)	10/22	0.0099	0.5827	3.0729	14.1842	SLC25A38;ALAD;PGRMC1;UROD;HMBS;FLVCR1;CPOX;TSPO;FXN;NFE2L1
GOBP2021	negative regulation of phosphate metabolic process (GO:0045936)	10/22	0.0099	0.5827	3.0729	14.1842	CDKN1C;CDA;CDKN2C;ROCK1;PRKRIP1;TESK1;INPP5K;INHBA;DYNLL1;BMP7
BioPlanet2019	Protein metabolism	128/442	0.0001	0.0110	1.5163	14.1824	DPAGT1;RPL5;RPL3;RPL32;RPL34;RPL8;RPL10A;SRP14;RPL9;RPL7;RPS15;CHCHD4;RPS14;C1GALT1C1;RPS19;RPS18;RPL36;FBXO4;RPL38;FBXO6;RPL37;RPS11;RPS13;RPS12;FBXW4;ARSA;ALG8;RPS5;RPS6;PAM16;RPSA;ALG12;ALG1;MUC3A;DPM2;DPM3;RPL27;VDAC1;RPL26;FKBP9;RPL29;UBA52;TIMM50;GRPEL1;GRPEL2;MLEC;ARSG;EDEM3;HSPA9;EIF2B3;TBCC;TIMM44;CS;RPS25;RPS28;RPS27;RPS29;FBXL3;CALR;RPS21;RPS24;EIF4G1;PIGS;B4GALT2;MCFD2;PIGT;PIGO;GPAA1;RPLP1;PIGQ;RPLP0;PIGP;PIGV;B3GNTL1;SEC61A1;TUBA1B;TUBA1A;SEC61G;GMPPA;VKORC1;EIF5B;SUMF2;DDOST;SUMF1;TUBB2A;DAD1;RPL37A;CANX;B3GNT2;PFDN2;PIGF;ST6GALNAC4;FXN;PFDN6;RPL10;RPL12;TIMM9;RPL11;TIMM13;RPL36A;TIMM10;HSPD1;GANAB;RPS15A;RPS3;RPL13;RPS2;SEC11A;SEC11C;TIMM8B;MTX1;IDH3G;GALNT2;GALNT1;RPL35A;DOHH;SPCS2;EIF3K;DOLPP1;EIF3I;TOMM70A;MGAT4B;EIF3H;EIF3F;FAU;EIF3A;TOMM5;EIF3B
GOBP2021	mitochondrial electron transport, NADH to ubiquinone (GO:0006120)	16/39	0.0043	0.3562	2.5670	13.9877	NDUFA9;NDUFB9;NDUFA7;NDUFB6;NDUFA11;NDUFA5;NDUFB11;NDUFA12;NDUFB5;NDUFA3;NDUFB3;NDUFB2;NDUFB1;NDUFS8;NDUFS7;NDUFS5
GOBP2021	establishment of protein localization to mitochondrion (GO:0072655)	19/48	0.0032	0.2994	2.4184	13.9283	TIMM8B;RALA;TIMM9;PAM16;TIMM13;TIMM44;TIMM10;DNAJC15;HSPD1;HK1;TIMM50;CHCHD4;GRPEL1;AIFM1;GRPEL2;DNLZ;TSPO;ROMO1;TOMM5
BioPlanet2019	Messenger RNA splicing: minor pathway	17/42	0.0039	0.2395	2.5095	13.9256	SF3B4;SF3B5;SF3B2;NCBP1;SF3B6;DDX23;SRSF1;GTF2F1;PRPF8;SNRPD1;POLR2C;POLR2D;POLR2E;SRSF2;POLR2I;POLR2L;SNRPB
GOBP2021	mitochondrial gene expression (GO:0140053)	17/42	0.0039	0.3448	2.5095	13.9256	MRPS17;MRPS28;NDUFA7;MRPS16;MRPS24;MRPS14;MRPS11;MRPS12;MRPL16;MRPS18B;MRPS18A;MRPL12;MRPS7;MRPL23;MRPL57;LARS2;TFAM
BioPlanet2019	RNA polymerase III transcription	18/45	0.0035	0.2395	2.4606	13.9090	NFIX;SSB;BRF2;BRF1;POLR3GL;NONO;GTF3A;ADAR;SNAPC5;SFPQ;SNAPC2;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	Semaphorin interactions Homo sapiens R-HSA-373755	25/67	0.0020	0.0680	2.1985	13.6120	ITGB1;SEMA7A;HSP90AB1;PLXND1;ROCK1;ROCK2;MYL12B;DPYSL4;RRAS;DPYSL2;DPYSL3;MYH14;MYH11;FYN;RAC1;MYH10;SEMA4A;HSP90AA1;CD72;SEMA4D;RHOA;TYROBP;PLXNB3;MYH9;MYL9
GOBP2021	ventricular cardiac muscle tissue development (GO:0003229)	11/25	0.0093	0.5790	2.8976	13.5678	FKBP1A;TGFB1;IRX3;TNNC1;TNNT2;MYL2;TPM1;PKP2;HOPX;MYH6;SMAD7
BioPlanet2019	Destabilization of mRNA by KSRP	8/17	0.0162	0.5662	3.2768	13.5046	EXOSC7;EXOSC5;KHSRP;EXOSC9;PARN;EXOSC3;YWHAZ;EXOSC2
GOBP2021	amyloid-beta metabolic process (GO:0050435)	8/17	0.0162	0.7309	3.2768	13.5046	PSENEN;BACE2;NCSTN;ACE;APH1B;ABCA7;IDE;APEH
GOBP2021	aorta morphogenesis (GO:0035909)	8/17	0.0162	0.7309	3.2768	13.5046	TBX1;PDGFRB;DLL4;LRP1;HEY2;TBX2;MYLK;ENG
GOBP2021	mitochondrial electron transport, cytochrome c to oxygen (GO:0006123)	8/17	0.0162	0.7309	3.2768	13.5046	COX8A;COX7B;COX7A2L;COX4I2;COX6A1;COX7C;COX6A2;COX6B1
GOBP2021	ruffle organization (GO:0031529)	8/17	0.0162	0.7309	3.2768	13.5046	CSF1R;PLEKHA1;TPM1;INPP5K;RAC1;AIF1;CORO1B;ARF6
Reactome2016	KSRP (KHSRP) binds and destabilizes mRNA Homo sapiens R-HSA-450604	8/17	0.0162	0.3018	3.2768	13.5046	EXOSC7;EXOSC5;KHSRP;EXOSC9;PARN;EXOSC3;YWHAZ;EXOSC2
BioPlanet2019	Tricarboxylic acid (TCA) cycle and respiratory electron transport	40/117	0.0009	0.0849	1.9212	13.4719	NDUFB9;COX7B;NDUFA11;UQCRB;NDUFB6;NDUFA12;NDUFB11;NDUFB5;NDUFB3;NDUFB2;NDUFB1;UQCR11;ETFB;UQCR10;PDHB;COX6A1;ATP5O;COX7C;ATP5L;LDHB;ATP5D;PDK3;SLC16A3;PDK2;COX8A;NDUFA9;NDUFA7;PDHA1;NDUFA5;MDH2;IDH3G;NDUFA3;SDHA;SDHB;COX6B1;CS;COX7A2L;NDUFS8;NDUFS7;NDUFS5
GOBP2021	carboxylic acid catabolic process (GO:0046395)	6/12	0.0265	0.9024	3.6854	13.3835	BCKDK;ACOT8;GNPDA1;AMDHD2;RENBP;ACOT4
GOBP2021	nucleoside salvage (GO:0043174)	6/12	0.0265	0.9024	3.6854	13.3835	CDA;UCK2;UCK1;UPP2;UPP1;UCKL1
GOBP2021	posttranslational protein targeting to endoplasmic reticulum membrane (GO:0006620)	6/12	0.0265	0.9024	3.6854	13.3835	SEC61A1;SEC61G;CHMP4B;SEC62;GET3;SEC63
GOBP2021	protein insertion into mitochondrial inner membrane (GO:0045039)	6/12	0.0265	0.9024	3.6854	13.3835	TIMM8B;TIMM29;TIMM9;TIMM13;ROMO1;TIMM10
GOBP2021	sno(s)RNA 3'-end processing (GO:0031126)	6/12	0.0265	0.9024	3.6854	13.3835	FBL;EXOSC5;PARN;EXOSC3;TENT4B;EXOSC2
BioPlanet2019	PKB-mediated events	12/28	0.0085	0.4178	2.7662	13.1737	PPM1A;STK11;CAB39;RPS6KB1;RHEB;STRADB;PDE3B;RPS6;MLST8;TSC2;PRKAG3;EIF4G1

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	mitochondrial respiratory chain complex I assembly (GO:0032981)	22/58	0.0029	0.2930	2.2564	13.1680	NDUFA9;NDUFB9;NDUFA7;TIMMDC1;NDUFA11;NDUFB6;NDUFA5;NDUFA12;NDUFB11;NDUFB5;NDUFA3;ACAD9;NDUFB3;NDUFB2;NDUFB1;NDUFAF8;NDUFS8;NDUFS7;NDUFAF6;NDUFS5;TMEM126A;NDUFAF3
GOBP2021	NADH dehydrogenase complex assembly (GO:0010257)	22/58	0.0029	0.2930	2.2564	13.1680	NDUFA9;NDUFB9;NDUFA7;TIMMDC1;NDUFA11;NDUFB6;NDUFA5;NDUFA12;NDUFB11;NDUFB5;NDUFA3;ACAD9;NDUFB3;NDUFB2;NDUFB1;NDUFAF8;NDUFS8;NDUFS7;NDUFAF6;NDUFS5;TMEM126A;NDUFAF3
Reactome2016	rRNA modification in the nucleus Homo sapiens R-HSA-6790901	22/58	0.0029	0.0815	2.2564	13.1680	NOP58;NOP14;UTP3;RPS6;NAT10;NOC4L;THUMPD1;UTP18;WDR43;RRP9;RCL1;FBL;RPS14;TBL3;BMS1;DHX37;GAR1;RRP36;MPHOSPH10;RPS2;DCAF13;NOP10
GOBP2021	interstrand cross-link repair (GO:0036297)	21/55	0.003283207	0.300979509	2.280252397	13.04061433	MUS81;VCP;DCLRE1C;CENPX;POLN;MCM8;XPA;FAAP24;NUCKS1;FANCB;FANCG;UBE2T;ERCC1;UBC;USP1;EXO5;UBA52;ATRIP;FAN1;FAAP100;CENPS
GOBP2021	protein targeting to mitochondrion (GO:0006626)	21/55	0.003283207	0.300979509	2.280252397	13.04061433	MIPEP;TIMM8B;HSP90AA1;TIMM29;HSPA4;TIMM9;PAM16;TIMM13;TIMM44;TIMM10;DNAJC15;TIMM50;HSPD1;CHCHD4;AIFM1;GRPEL1;GRPEL2;DNLZ;TSPO;ROMO1;TOMM5
GOBP2021	negative regulation of response to DNA damage stimulus (GO:2001021)	13/31	0.007814086	0.51934366	2.664031724	12.92542194	PSMD10;CD74;RTEL1;KDM1A;TWIST1;MIF;DDX39B;RPS3;SNAI1;SNAI2;ACKR3;TRIM32;TPT1
GOBP2021	ventricular cardiac muscle tissue morphogenesis (GO:0055010)	14/34	0.00709593	0.477583049	2.582339126	12.77801793	SMAD4;NOTCH1;TGFB1;TNNC1;NOG;TPM1;SMAD7;DLL4;FKBP1A;TNNT2;MYL2;PKP2;MYH6;ENG
KEGG2019M	Cardiac muscle contraction	28/78	0.002234811	0.112112999	2.068727615	12.62668337	COX7B;UQCRB;COX4I2;ATP2A2;UQCR11;COX7A2;UQCR10;COX6A1;COX7C;COX6A2;COX7A1;CACNG7;CACNA1S;COX8A;TPM4;TPM3;TPM2;TNNC1;TPM1;CACNA2D2;ATP1B3;COX6B1;COX7A2L;ACTC1;MYL2;TNNT2;FXYD2;MYH6
GOBP2021	cardiac epithelial to mesenchymal transition (GO:0060317)	9/20	0.015330498	0.730935785	3.016505662	12.60269256	OLFM1;NOTCH1;HEY2;PDCD4;SNAI1;SNAI2;SPRY1;TBX3;ENG
BioPlanet2019	Signaling events mediated by PRL	10/23	0.014206803	0.549756547	2.836335415	12.06586823	ITGB1;PTP4A3;TUBA1B;ROCK1;RAC1;ATF5;RABGGTA;RHOA;AGT;MAPK3
KEGG2019M	Oxidative phosphorylation	44/134	0.001322716	0.099534416	1.808241354	11.98514612	NDUFB9;COX7B;NDUFA11;UQCRB;NDUFB6;NDUFA12;NDUFB11;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFA4L2;COX7A2;UQCR11;TCIRG1;UQCR10;COX6A1;ATP5O;ATP5G2;COX6A2;COX7A1;COX7C;ATP5L;ATP5D;COX11;ATP6V0E2;ATP6V1F;COX8A;NDUFA9;ATP6V1G1;NDUFA7;NDUFA5;NDUFA3;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5;ATP6V1B2;ATP6V0D1;ATP6V0C;ATP6V0E
GOBP2021	mRNA 3'-end processing (GO:0031124)	28/79	0.002767243	0.288636727	2.028034965	11.94493075	APP;SLBP;AHCYL1;RBM8A;SRSF1;CASC3;TENT4B;PABPN1;FIP1L1;PCF11;POLR2D;LEO1;CSTF1;RPRD1B;SRSF11;NCBP1;ALYREF;UPF3B;THOC2;MAGOHB;DDX39B;SARNP;SRSF2;PAF1;RNPS1;SRSF5;GRSF1;SRSF9
BioPlanet2019	Transcription	57/181	0.000911872	0.084864911	1.70173344	11.91215221	CCNT1;LSM10;SNAPC5;PCF11;SNAPC2;UBTF;NELFA;NCBP1;GTF3A;GTF2F1;POLR1B;POLR1C;SRSF2;POLR1D;TFAM;SRSF5;BDP1;SNRPB;SRSF9;SLBP;GTF2A1;NFIX;CTDP1;RBM8A;SRSF1;GTF2E1;PABPN1;POLR2C;TAF1A;POLR2D;CSTF1;POLR2E;POLR2I;SRSF11;MAPK3;POLR2L;SSB;BRF2;BRF1;TAF12;POLR3GL;CBX3;TAF13;ALYREF;TAF10;MBD2;UPF3B;SSRP1;GTF2H3;GTF2H4;POLR3D;ERCC2;POLR3G;RNPS1;TAF5;MNAT1;TAF4
GOBP2021	regulation of aerobic respiration (GO:1903715)	7/15	0.025531806	0.902427467	3.225087925	11.82907528	VCP;COX7A2L;UQCC2;COX7A2;IDE;COX7A1;ABCD1
GOBP2021	tRNA 5'-end processing (GO:0099116)	7/15	0.025531806	0.902427467	3.225087925	11.82907528	SSB;POP7;POP4;RPP40;RPP21;HSD17B10;RPP25L
Reactome2016	Depolymerisation of the Nuclear Lamina Homo sapiens R-HSA-4419969	7/15	0.025531806	0.399289904	3.225087925	11.82907528	CTDNEP1;CNEP1R1;LEMD3;LEMD2;EMD;LMNB1;TMPO
Reactome2016	NRIF signals cell death from the nucleus Homo sapiens R-HSA-205043	7/15	0.025531806	0.399289904	3.225087925	11.82907528	PSENEN;NCSTN;APH1B;UBC;NGF;UBA52;ITGB3BP
GOBP2021	maturation of LSU-rRNA (GO:0000470)	11/26	0.012999416	0.677626444	2.704263475	11.74421282	BOP1;NSA2;LAS1L;ZNHIT6;MAK16;SNU13;URB1;RPL10A;RRP15;RPL7;FTSJ3
GOBP2021	positive regulation of viral transcription (GO:0050434)	11/26	0.012999416	0.677626444	2.704263475	11.74421282	CTDP1;CCNT1;MDFIC;POLR2C;POLR2D;POLR2E;RSF1;NELFA;POLR2I;GTF2F1;POLR2L
Reactome2016	FGFR2 alternative splicing Homo sapiens R-HSA-6803529	11/26	0.012999416	0.266679205	2.704263475	11.74421282	PTBP1;HNRNPM;NCBP1;HNRNPH1;POLR2C;POLR2D;POLR2E;POLR2I;HNRNPA1;GTF2F1;POLR2L
BioPlanet2019	LKB1 signaling events	18/47	0.006029766	0.311761213	2.290598706	11.70735797	YWHAE;BRSK1;HSP90AA1;SMAD4;SMARCD3;CAB39;STK11IP;STRADB;TSC2;YWHAZ;STK11;CDC37;MLST8;SIK2;MARK4;CTSD;MARK2;YWHAH
BioPlanet2019	IKK complex recruitment mediated by RIP1	5/10	0.042598094	0.943919677	3.684790251	11.62899817	CHUK;LY96;RIPK1;CD14;TICAM1
BioPlanet2019	Tetrahydrobiopterin (BH4) biosynthesis, recycling, salvage and regulation	5/10	0.042598094	0.943919677	3.684790251	11.62899817	GCHFR;HSP90AA1;SPR;GCH1;NOS3
GOBP2021	defense response to tumor cell (GO:0002357)	5/10	0.042598094	0.999996358	3.684790251	11.62899817	PRDX2;PLK5;ABI3;LAPTM5;KLF4
GOBP2021	DNA replication-dependent nucleosome assembly (GO:0006335)	5/10	0.042598094	0.999996358	3.684790251	11.62899817	CHAF1A;NASP;ASF1A;IPO4;ASF1B
GOBP2021	DNA replication-dependent nucleosome organization (GO:0034723)	5/10	0.042598094	0.999996358	3.684790251	11.62899817	CHAF1A;NASP;ASF1A;IPO4;ASF1B
GOBP2021	negative regulation of receptor binding (GO:1900121)	5/10	0.042598094	0.999996358	3.684790251	11.62899817	ADAM15;HFE;NOG;ATP2A2;B2M
GOBP2021	nuclear-transcribed mRNA catabolic process, exonucleolytic, 3'-5' (GO:0034427)	5/10	0.042598094	0.999996358	3.684790251	11.62899817	EXOSC7;EXOSC5;EXOSC9;EXOSC3;EXOSC2
GOBP2021	rRNA pseudouridine synthesis (GO:0031118)	5/10	0.042598094	0.999996358	3.684790251	11.62899817	RPUSD1;RPUSD3;GAR1;NAF1;NOP10
Reactome2016	TRIF-mediated programmed cell death Homo sapiens R-HSA-2562578	5/10	0.042598094	0.525879129	3.684790251	11.62899817	RIPK3;LY96;RIPK1;CD14;TICAM1
Reactome2016	Tetrahydrobiopterin (BH4) synthesis, recycling, salvage and regulation Homo sapiens R-HSA-1474151	5/10	0.042598094	0.525879129	3.684790251	11.62899817	GCHFR;HSP90AA1;SPR;GCH1;NOS3
WikiPath2019M	Macrophage markers WP2271	5/10	0.042598094	0.776192516	3.684790251	11.62899817	CD74;CD163;CD83;LYZ2;CD14
GOBP2021	cardiac ventricle morphogenesis (GO:0003208)	17/44	0.006781409	0.462266048	2.323340732	11.60176546	GSK3A;NOTCH1;TGFB1;FOXF1;TNNC1;TPM1;SMAD7;DLL4;FKBP1A;TNNT2;MYL2;HEY2;PKP2;CPE;SOX4;MYH6;ENG
GOBP2021	intracellular protein transmembrane transport (GO:0065002)	17/44	0.006781409	0.462266048	2.323340732	11.60176546	ZFAND2B;PAM16;PEX10;TIMM44;DNAJC15;HSPD1;TIMM50;CHCHD4;SEC61A1;GRPEL1;AIFM1;SEC61G;GRPEL2;DNLZ;ROMO1;SEC62;SEC63
GOBP2021	positive regulation of dephosphorylation (GO:0035306)	12/29	0.011791824	0.633304319	2.603314002	11.55962241	PTBP1;TGFB1;RIPK3;SMPD1;CNEP1R1;GBA;PPP2R5A;PIN1;CALM3;SPPL3;PPIA;CALM2

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	peptide metabolic process (GO:0006518)	29/83	0.002995549	0.294635774	1.983860127	11.52747257	MIPEP;ENPEP;CARNMT1;GSTT2;GSTT1;IDE;ABCB9;APEH;SPPL3;RHD;DNPEP;CPXM1;LTA4H;SEC11A;SEC11C;GSTK1;GSTM2;ACE;GSTM1;GSR;BACE2;SPCS2;GSTA4;ETHE1;DPEP1;CPE;TPP1;THOP1;MMACHC
Reactome2016	RNA Polymerase III Abortive And Retractive Initiation Homo sapiens R-HSA-749476	16/41	0.007615168	0.183157928	2.361353383	11.5177684	NFIX;SSB;BRF2;BRF1;GTF3C6;POLR3GL;GTF3A;SNAPC5;SNAPC2;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	RNA Polymerase III Transcription Homo sapiens R-HSA-74158	16/41	0.007615168	0.183157928	2.361353383	11.5177684	NFIX;SSB;BRF2;BRF1;GTF3C6;POLR3GL;GTF3A;SNAPC5;SNAPC2;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
GOBP2021	7-methylguanosine mRNA capping (GO:0006370)	13/32	0.010630805	0.582721541	2.523658877	11.46750435	RAMAC;NCBP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;POLR2I;MNAT1;CMTR1;POLR2L
GOBP2021	7-methylguanosine RNA capping (GO:0009452)	13/32	0.010630805	0.582721541	2.523658877	11.46750435	RAMAC;NCBP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;POLR2I;MNAT1;CMTR1;POLR2L
GOBP2021	aortic valve morphogenesis (GO:0003180)	13/32	0.010630805	0.582721541	2.523658877	11.46750435	NOTCH1;TGFB1;ROCK1;ROCK2;NOS3;ELN;TWIST1;SMAD6;DLL4;EFNA1;HEY2;SNAI1;SNAI2
GOBP2021	peptidyl-proline modification (GO:0018208)	13/32	0.010630805	0.582721541	2.523658877	11.46750435	FKBP10;PPIL2;PPWD1;CWC27;FKBP1A;NTMT1;FKBP1B;PPIF;PIN1;PPIG;PPIL3;PPIA;PPID
GOBP2021	regulation of mRNA stability (GO:0043488)	47/146	0.001478888	0.196581217	1.756172375	11.44403524	PSMD10;SET;ANP32A;PSMD14;ROCK1;ROCK2;PARN;HNRNPU;HSPB1;YBX1;ZFP36L2;GIGYF2;PSMD8;EXOSC7;PSMB7;METTL14;EXOSC5;RIDA;PSMD7;FXR2;PSMD5;PSMB3;KHSRP;EXOSC9;UBC;DND1;E2F1;PSMF1;EXOSC3;EXOSC2;PAIP1;HSPA8;YTHDF1;NPM1;TAF15;SLC11A1;CIRBP;AXIN2;MEX3D;YWHAZ;PSMA5;CSDC2;SERBP1;HNRNPD;UBA52;RBM24;EIF4G1
GOBP2021	maturation of SSU-rRNA (GO:0030490)	14/35	0.00954123	0.582721541	2.459214028	11.4405904	NOP14;UTP3;MRPS11;NAT10;SNU13;RPS14;RPS28;LSM6;RPS19;BMS1;DHX37;RRP36;SRFBP1;DCAF13
BioPlanet2019	Cardiac muscle contraction	28/80	0.003403805	0.239513204	1.988907417	11.30268523	COX7B;UQCRB;COX4I2;ATP2A2;UQCR11;COX7A2;UQCR10;COX6A1;COX7C;COX6A2;COX7A1;CACNG7;CACNA1S;COX8A;TPM4;TPM3;TPM2;TNNC1;TPM1;CACNA2D2;ATP1B3;COX6B1;COX7A2L;ACTC1;MYL2;TNNT2;FXYD2;MYH6
Reactome2016	Mitochondrial protein import Homo sapiens R-HSA-1268020	20/54	0.006056905	0.156470037	2.171158209	11.08714183	HSPA9;TIMM8B;MTX1;IDH3G;TIMM9;PAM16;TIMM13;TIMM44;TIMM10;TIMM50;HSPD1;CHCHD4;CS;CHCHD2;GRPEL1;TOMM70A;GRPEL2;VDAC1;FXN;TOMM5
GOBP2021	muscle contraction (GO:0006936)	42/129	0.002014308	0.24341075	1.785065623	11.08075882	TRIM72;ROCK1;SMPX;ROCK2;LMOD1;MYL6B;MYL12A;LMOD3;MYLK;MYL12B;LMOD2;GJC1;SGCA;PABPN1;CALD1;MYH11;CACNA1S;EMD;GAMT;TPM4;TPM3;KCNJ12;TPM2;TNNC1;TPM1;PGAM2;SMTN;SLC6A8;ACTC1;ASPH;TNNT1;MYOT;MYL2;TNNT2;FXYD1;TNNT3;HRC;SCN4A;ALDOA;MYL9;CRYAB;MYH6
Reactome2016	RNA Polymerase II Pre-transcription Events Homo sapiens R-HSA-674695	23/64	0.005217044	0.139957236	2.071081287	10.88523943	GTF2A1;CTDP1;CCNT1;NCBP1;TAF12;TAF13;TAF10;SSRP1;GTF2F1;GTF2H3;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
GOBP2021	positive regulation of cellular amide metabolic process (GO:0034250)	28/81	0.004159943	0.356163452	1.95125638	10.69728306	RPL5;GSK3A;DDX3X;ROCK2;NAT10;RPS27L;PLA2G6;RBM3;METTL14;FXR2;RACK1;METTL5;SOX4;ABCA2;YTHDF1;NPM1;NSUN5;CIRBP;UPF3B;UPF3A;LARP6;TNFRSF1A;EFNA1;RPS6KB1;BCL3;HNRNPD;PLXNB2;RPL26
BioPlanet2019	HIV genome transcription	22/61	0.005924478	0.311761213	2.082401207	10.6799334	GTF2A1;CTDP1;CCNT1;NCBP1;TAF12;TAF13;TAF10;SSRP1;GTF2F1;GTF2H3;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;TAF5;POLR2I;MNAT1;TAF4;POLR2L
GOBP2021	negative regulation of peptidyl-serine phosphorylation (GO:0033137)	9/21	0.02183889	0.82940984	2.764954258	10.57335916	GADD45A;PAQR3;PTEN;INPP5J;RACK1;NCK2;INPP5K;GPD1L;SMAD7
GOBP2021	DNA replication-independent nucleosome assembly (GO:0006336)	15/39	0.011181167	0.606635341	2.305614282	10.36033417	CENPT;NPM1;CENPW;CENPX;SMARCA5;RSF1;CENPA;IPO4;CABIN1;NASP;RUVBL1;ASF1A;ITGB3BP;ASF1B;CENPS
BioPlanet2019	Plexin D1 signaling	10/24	0.019781806	0.654025371	2.633572434	10.33148524	ITGB1;SEMA4A;PLXND1;RRAS;ITGA3;ITGA11;PIP5K1B;ITGA5;VEGFA;ARF6
BioPlanet2019	Tumor suppressor Arf inhibits ribosomal biogenesis	10/24	0.019781806	0.654025371	2.633572434	10.33148524	HSP90AA1;POLR1B;POLR1C;E2F1;POLR1D;TWIST1;UBE2A;RAC1;TBX2;NFKBIB
GOBP2021	porphyrin-containing compound biosynthetic process (GO:0006779)	10/24	0.019781806	0.827808582	2.633572434	10.33148524	SLC25A38;ALAD;PGRMC1;UROD;HMBS;FLVCR1;CPOX;TSPO;FXN;NFE2L1
GOBP2021	aortic valve development (GO:0003176)	14/36	0.012601797	0.670037554	2.347282121	10.26681446	NOTCH1;TGFB1;ROCK1;ROCK2;NOS3;ELN;TWIST1;SMAD6;TNFRSF1A;DLL4;EFNA1;HEY2;SNAI1;SNAI2
Reactome2016	RNA Polymerase III Transcription Initiation Homo sapiens R-HSA-76046	14/36	0.012601797	0.266356167	2.347282121	10.26681446	BRF2;BRF1;GTF3C6;POLR3GL;GTF3A;SNAPC5;SNAPC2;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
KEGG2019M	Alzheimer disease	54/175	0.002029433	0.112112999	1.651281991	10.23794612	APP;COX7B;NDUFA11;NDUFA12;COX4I2;ATP2A2;IDE;COX6A1;ATP5G2;COX6A2;COX7C;PPP3CC;COX8A;PSENEN;SDHA;SDHB;COX6B1;TNFRSF1A;BACE2;COX7A2L;NDUFS8;NDUFS7;NDUFS5;NDUFB9;UQCRB;LRP1;NDUFB6;NDUFB11;NDUFB5;NDUFB3;NDUFB2;NDUFA4L2;COX7A2;UQCR11;UQCR10;ATP5O;COX7A1;HSD17B10;RTN4;NCSTN;APH1C;APH1B;ATP5D;CACNA1S;BID;SNCA;MAPK3;NDUFA9;NDUFA7;NDUFA5;NDUFA3;GRIN2D;CALM3;CALM2
GOBP2021	protein peptidyl-prolyl isomerization (GO:0000413)	11/27	0.017784144	0.775067972	2.535085661	10.21499589	FKBP1A;PPIL2;FKBP1B;PPIF;PPWD1;PIN1;PPIG;CWC27;PPIL3;PPIA;PPID
GOBP2021	RNA stabilization (GO:0043489)	13/33	0.014176309	0.692083735	2.397323315	10.20344694	TAF15;SLC11A1;PARN;CIRBP;HNRNPU;YBX1;AXIN2;ZCCHC17;DND1;E2F1;NAF1;RBM24;PAIP1
Reactome2016	Formation of the Early Elongation Complex Homo sapiens R-HSA-113418	13/33	0.014176309	0.278534523	2.397323315	10.20344694	CTDP1;NCBP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
Reactome2016	Formation of the HIV-1 Early Elongation Complex Homo sapiens R-HSA-167158	13/33	0.014176309	0.278534523	2.397323315	10.20344694	CTDP1;NCBP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
Reactome2016	Smooth Muscle Contraction Homo sapiens R-HSA-445355	13/33	0.014176309	0.278534523	2.397323315	10.20344694	TRIM72;TPM4;TPM3;TPM2;TPM1;LMOD1;MYL6B;MYL12A;MYLK;MYL12B;CALD1;MYH11;MYL9
GOBP2021	oligosaccharide-lipid intermediate biosynthetic process (GO:0006490)	6/13	0.040454399	0.999996358	3.158730159	10.13187934	DPAGT1;ALG8;SRD5A3;ALG12;ALG1;MPDU1
GOBP2021	pteridine-containing compound metabolic process (GO:0042558)	6/13	0.040454399	0.999996358	3.158730159	10.13187934	GCHFR;HSP90AA1;GCH1;SPR;NOS3;FPGS

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	regulation of mRNA metabolic process (GO:1903311)	6/13	0.040454399	0.999996358	3.158730159	10.13187934	NCBP1;SLTM;SAFB2;SAFB;CDK11B;IWS1
GOBP2021	tRNA 5'-leader removal (GO:0001682)	6/13	0.040454399	0.999996358	3.158730159	10.13187934	SSB;POP7;POP4;RPP40;RPP21;RPP25L
Reactome2016	Initiation of Nuclear Envelope Reformation Homo sapiens R-HSA-2995383	6/13	0.040454399	0.513035333	3.158730159	10.13187934	PPP2CA;LEMD3;LEMD2;EMD;LMNB1;TMPO
Reactome2016	Nuclear Envelope Reassembly Homo sapiens R-HSA-2995410	6/13	0.040454399	0.513035333	3.158730159	10.13187934	PPP2CA;LEMD3;LEMD2;EMD;LMNB1;TMPO
Reactome2016	p38MAPK events Homo sapiens R-HSA-171007	6/13	0.040454399	0.513035333	3.158730159	10.13187934	RALA;MAPKAPK3;KRAS;HRAS;RALGDS;MAPK13
Reactome2016	Signaling by Activin Homo sapiens R-HSA-1502540	6/13	0.040454399	0.513035333	3.158730159	10.13187934	DRAP1;SMAD4;INHBB;INHBA;ACVR1B;ACVR2B
GOBP2021	DNA-templated transcription, initiation (GO:0006352)	52/168	0.002255983	0.260762209	1.658408237	10.10662086	MAML2;HDAC10;THRA;RSF1;UBTF;TEAD2;TEAD3;GTF2F1;MED27;MED26;MED7;POLR1B;POLR1C;TFAM;GTF2A1;NOTCH1;MAZ;GTF2E1;HDAC7;POLR2C;TAF1A;POLR2D;POLR2E;NRBF2;POLR2I;MAPK3;POLR2L;ESRRA;BRF2;TAF15;CAVIN1;BRF1;TAF12;TAF13;NR1H2;TAF10;ESRRB;SMARCA5;NR2F1;NR1D1;GTF2H3;NR0B2;GTF2H4;NR2F6;NR4A2;NR4A1;SNW1;ERCC2;TAF5;MNAT1;TAF4;TAF3
BioPlanet2019	Mitochondrial protein import	19/52	0.008679572	0.41781663	2.124739043	10.08567534	HSPA9;TIMM8B;MTX1;IDH3G;TIMM9;PAM16;TIMM13;TIMM44;TIMM10;TIMM50;HSPD1;CHCHD4;CS;GRPEL1;TOMM70A;GRPEL2;VDAC1;FXN;TOMM5
WikiPath2019M	TNF-alpha NF-kB Signaling Pathway WP246	57/187	0.002119213	0.120088752	1.622567753	9.989679695	YWHAE;SMARCB1;DDX3X;HSP90AB1;PEBP1;HSPB1;RPL8;FBL;PSMD7;SUMO1;NKIRAS1;NKIRAS2;RACK1;CAPN3;KPNA2;RPS11;RPS13;YWHAH;PIAS3;HSP90AA1;SMARCC2;CSNK2A1;PEG3;RIPK3;CHUK;FBXW11;USP2;COMMD1;YWHAZ;TNFRSF1A;CDC37;POLR1B;CSNK2B;POLR1C;POLR1D;PFDN2;HDAC2;AKAP8;MTIF2;TNFRSF11A;PRKCZ;RELB;PPP2CA;RIPK1;MARK2;SMARCE1;RNF25;PTPN11;CFLAR;COPS3;DAP;RPS6KB1;TNIP2;BCL3;TAB1;MAP3K14;NFKBIB
GOBP2021	transcription, DNA-templated (GO:0006351)	66/221	0.001778789	0.219949278	1.57657724	9.982607574	CCNT1;THRA;SCX;RSF1;YBX2;MED16;SNAPC2;UBTF;ELOB;ELOC;NELFA;NCBP1;GTF3A;GTF2F1;MAF;TFDP1;POLR1C;TFAM;PTMA;GTF2A1;CTDP1;NFIX;CBFB;GTF3C6;MRPL12;GTF2E1;PMF1;IWS1;DEAF1;POLR2C;HSF1;TAF1A;POLR2D;LEO1;E2F1;POLR2E;POLR2I;POLR2L;BTF3;BRF2;TAF15;BRF1;TAF12;POLR3GL;TAF13;TAF10;SMARCA5;DEK;SSRP1;GTF2H3;GTF2H4;NR4A2;DRAP1;FUBP3;BCL3;ERCC2;PAF1;POLR3G;RNPS1;MMS19;TRIP13;TAF5;MNAT1;TAF4;TAF3;NFKBIB
GOBP2021	positive regulation of translation (GO:0045727)	33/100	0.004554564	0.366918447	1.819680789	9.811037238	RPL5;KHDRBS1;TRUB2;DDX3X;MPV17L2;NAT10;RPS27L;YBX3;RBM3;METTL14;FXR2;POLR2D;HABP4;METTL5;SOX4;COA3;YTHDF1;NPM1;MRPS27;UQCC2;NSUN5;CIRBP;UPF3B;UPF3A;LARP6;PKM;RPS6KB1;BCL3;RPUSD3;RPS6KB2;HNRNPD;PLXNB2;RPL26
GOBP2021	regulation of mRNA splicing, via spliceosome (GO:0048024)	30/90	0.005637767	0.430270773	1.846770391	9.563070427	SF3B4;KHDRBS1;RBM25;DAZAP1;KHDRBS3;RBM8A;YTHDC1;SFSWAP;HNRNPU;RBM3;PTBP1;RBM15B;FXR2;SAP18;HNRNPA1;ZBTB7A;NCBP1;WTAP;CIRBP;QKI;HNRNPL;REST;HNRNPK;SNW1;NCL;NOVA2;RNPS1;NSRP1;RBM24;SRSF9
BioPlanet2019	Cleavage of growing transcript in the termination region	16/43	0.012711712	0.507015724	2.186159844	9.543093782	SLBP;RBM8A;NCBP1;ALYREF;SRSF1;UPF3B;LSM10;PABPN1;PCF11;CSTF1;SRSF2;RNPS1;SRSF5;SRSF11;SNRPB;SRSF9
WikiPath2019M	Eukaryotic Transcription Initiation WP567	16/43	0.012711712	0.432198217	2.186159844	9.543093782	TAF12;TAF13;AK6;GTF2H3;GTF2E1;GTF2H4;POLR2C;POLR3D;POLR1B;ERCC2;POLR1C;POLR2E;POLR1D;TAF5;POLR2I;MNAT1
BioPlanet2019	Cell death signaling by NRIF in the nucleus	7/16	0.03719663	0.927258851	2.866562459	9.435396713	PSENEN;NCSTN;APH1B;UBC;NGF;UBA52;ITGB3BP
GOBP2021	positive regulation of collagen biosynthetic process (GO:0032967)	7/16	0.03719663	0.999996358	2.866562459	9.435396713	HDAC2;TGFB1;RGCC;TGFB3;CREB3L1;SCX;LARP6
GOBP2021	regulation of activin receptor signaling pathway (GO:0032925)	7/16	0.03719663	0.999996358	2.866562459	9.435396713	FKBP1A;CSNK2B;LEMD3;ACVR1B;ACVR2B;SMAD7;DACT1
GOBP2021	regulation of oxidative phosphorylation (GO:0002082)	7/16	0.03719663	0.999996358	2.866562459	9.435396713	VCP;COX7A2L;UQCC2;PPIF;COX7A2;COX7A1;ABCD1
GOBP2021	regulation of translation (GO:0006417)	54/178	0.003047765	0.294635774	1.611021888	9.333208301	APP;RPL5;DDX3X;NAT10;HSPB1;YBX2;YBX1;RBM3;METTL14;MTG1;RACK1;SOX4;EIF5B;UPF1;NCBP1;NSUN5;NANOS3;CIRBP;MIF4GD;NEMF;NCL;CSDE1;GEMIN5;MAPKAPK5;RPL26;EIF4E2;RPL10;RPS27L;MTIF2;MALSU1;GIGYF2;RIDA;FXR2;RPS3;METTL5;PAIP1;YTHDF1;NPM1;UPF3B;UPF3A;LARP6;PUM3;EIF1;MTRES1;RPS6KB1;CAPRIN1;BCL3;HNRNPD;PLXNB2;EIF3H;CALR;LSM14A;EIF4G1;EIF3B
BioPlanet2019	MAL role in Rho-mediated activation of SRF	8/19	0.033628505	0.869359135	2.680709534	9.093988633	DIAPH1;MAP2K2;ROCK1;SRF;RAC1;HRAS;RHOA;MAPK3
GOBP2021	aspartate family amino acid metabolic process (GO:0009066)	8/19	0.033628505	0.999996358	2.680709534	9.093988633	MSRA;GOT2;ASPG;MTHFR;ASNS;NAT8L;ASPA;NIT2
GOBP2021	atrioventricular valve morphogenesis (GO:0003181)	8/19	0.033628505	0.999996358	2.680709534	9.093988633	EFNA1;OLFM1;SMAD4;NOTCH1;HEY2;SMAD6;ZFPM1;SOX4
GOBP2021	diol metabolic process (GO:0034311)	8/19	0.033628505	0.999996358	2.680709534	9.093988633	GCHFR;HSP90AA1;GCH1;SPR;NOS3;NAAA;SGPP1;PLPP1
GOBP2021	protein import into mitochondrial matrix (GO:0030150)	8/19	0.033628505	0.999996358	2.680709534	9.093988633	GRPEL1;PAM16;GRPEL2;DNLZ;TIMM44;ROMO1;DNAJC15;TIMM50
GOBP2021	regulation of bicellular tight junction assembly (GO:2000810)	8/19	0.033628505	0.999996358	2.680709534	9.093988633	CLDN5;ROCK1;CBFB;ROCK2;NPHP1;SNAI1;SNAI2;NPHP4
GOBP2021	regulation of mitotic spindle assembly (GO:1901673)	8/19	0.033628505	0.999996358	2.680709534	9.093988633	TPR;CHMP4C;HNRNPU;CHMP3;CHMP4B;CEP97;CCSAP;HSPA1B
Reactome2016	Other semaphorin interactions Homo sapiens R-HSA-416700	8/19	0.033628505	0.47385621	2.680709534	9.093988633	ITGB1;SEMA4A;SEMA7A;CD72;TYROBP;PLXND1;SEMA4D;PLXNB3
Reactome2016	Cleavage of Growing Transcript in the Termination Region Homo sapiens R-HSA-109688	21/60	0.010354909	0.226080011	1.987279011	9.082450528	SLBP;NCBP1;RBM8A;ALYREF;SRSF1;UPF3B;CASC3;THOC2;LSM10;DDX39B;PABPN1;FIP1L1;PCF11;SARNP;SRSF2;CSTF1;RNPS1;SRSF5;SRSF11;SNRPB;SRSF9
Reactome2016	RNA Polymerase II Transcription Termination Homo sapiens R-HSA-73856	21/60	0.010354909	0.226080011	1.987279011	9.082450528	SLBP;NCBP1;RBM8A;ALYREF;SRSF1;UPF3B;CASC3;THOC2;LSM10;DDX39B;PABPN1;FIP1L1;PCF11;SARNP;SRSF2;CSTF1;RNPS1;SRSF5;SRSF11;SNRPB;SRSF9

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	Post-Elongation Processing of the Transcript Homo sapiens R-HSA-76044	21/60	0.010354909	0.226080011	1.987279011	9.082450528	SLBP;NCBP1;RBM8A;ALYREF;SRSF1;UPF3B;CASC3;THOC2;LSM10;DDX39B;PABPN1;FIP1L1;PCF11;SARNP;SRSF2;CSTF1;RNPS1;SRSF5;SRSF11;SNRPB;SRSF9
GOBP2021	negative regulation of osteoblast differentiation (GO:0045668)	12/31	0.021017647	0.827808582	2.328984433	8.99545288	NOTCH1;SEMA4D;SUFU;NOG;TWIST2;CHRD;CRIM1;TWIST1;TMEM64;LIMD1;SMAD6;HDAC7
GOBP2021	cellular response to osmotic stress (GO:0071470)	9/22	0.030109135	0.963672499	2.552103069	8.939829925	DDX3X;CAB39;TRPV4;CAPN3;OXSR1;PKD2;YBX3;AQP1;MYLK
GOBP2021	glutathione derivative biosynthetic process (GO:1901687)	9/22	0.030109135	0.963672499	2.552103069	8.939829925	GSTK1;GSTM2;GSTM1;GSTA4;GSTO1;MGST3;ESD;MGST1;GSTT1
GOBP2021	glutathione derivative metabolic process (GO:1901685)	9/22	0.030109135	0.963672499	2.552103069	8.939829925	GSTK1;GSTM2;GSTM1;GSTA4;GSTO1;MGST3;ESD;MGST1;GSTT1
Reactome2016	Pink/Parkin Mediated Mitophagy Homo sapiens R-HSA-5205685	9/22	0.030109135	0.433012812	2.552103069	8.939829925	MAP1LC3B;MAP1LC3A;MTERF3;TOMM70A;UBC;MFN1;VDAC1;UBA52;TOMM5
Reactome2016	Mitophagy Homo sapiens R-HSA-5205647	9/22	0.030109135	0.433012812	2.552103069	8.939829925	MAP1LC3B;MAP1LC3A;MTERF3;TOMM70A;UBC;MFN1;VDAC1;UBA52;TOMM5
GOBP2021	transcription elongation from RNA polymerase II promoter (GO:0006368)	23/67	0.009724887	0.582721541	1.929502129	8.939512561	ELOF1;CTDP1;CCNT1;NCBP1;ELP4;SSRP1;GTF2F1;GTF2H3;GTF2H4;IWS1;POLR2C;POLR2D;ERCC2;LEO1;POLR2E;PAF1;ELOB;NELFA;ELOC;POLR2I;CDK13;MNAT1;POLR2L
Reactome2016	Transcription of the HIV genome Homo sapiens R-HSA-167172	23/67	0.009724887	0.226080011	1.929502129	8.939512561	GTF2A1;CTDP1;CCNT1;NCBP1;TAF12;TAF13;TAF10;SSRP1;GTF2F1;GTF2H3;GTF2E1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;TAF5;POLR2I;MNAT1;TAF4;TAF3;POLR2L
KEGG2019M	RNA polymerase	11/28	0.023762209	0.5960354	2.385811119	8.922119623	POLR3GL;POLR2C;POLR3D;POLR1B;POLR2D;POLR1C;POLR2E;POLR1D;POLR3G;POLR2I;POLR2L
BioPlanet2019	Messenger RNA capping	11/28	0.023762209	0.705788154	2.385811119	8.922119623	NCBP1;POLR2C;POLR2D;ERCC2;POLR2E;POLR2I;GTF2H3;GTF2F1;MNAT1;GTF2H4;POLR2L
BioPlanet2019	RNA polymerase III transcription initiation From type 3 promoter	11/28	0.023762209	0.705788154	2.385811119	8.922119623	SNAPC5;BRF2;SNAPC2;POLR3GL;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	RNA Polymerase III Transcription Initiation From Type 1 Promoter Homo sapiens R-HSA-76061	11/28	0.023762209	0.395667239	2.385811119	8.922119623	BRF1;GTF3C6;POLR3GL;POLR3D;POLR1C;POLR2E;GTF3A;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	RNA Polymerase III Transcription Initiation From Type 3 Promoter Homo sapiens R-HSA-76071	11/28	0.023762209	0.395667239	2.385811119	8.922119623	SNAPC5;BRF2;SNAPC2;POLR3GL;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	Post-translational modification: synthesis of GPI-anchored proteins Homo sapiens R-HSA-163125	10/25	0.026798682	0.406349575	2.457844517	8.895928802	PIGS;DPM2;DPM3;PIGT;PIGO;GPAA1;PIGQ;PIGP;PIGV;PIGF
Reactome2016	ATF4 activates genes Homo sapiens R-HSA-380994	10/25	0.026798682	0.406349575	2.457844517	8.895928802	EXOSC7;EXOSC5;NFYB;KHSRP;EXOSC9;NFYC;PARN;ASNS;EXOSC3;EXOSC2
GOBP2021	regulation of alternative mRNA splicing, via spliceosome (GO:0000381)	19/54	0.013490226	0.692083735	2.003070102	8.624798956	KHDRBS1;RBM25;KHDRBS3;RBM8A;WTAP;YTHDC1;HNRNPU;HNRNPL;PTBP1;RBM15B;REST;FXR2;NOVA2;SAP18;RNPS1;NSRP1;HNRNPA1;RBM24;ZBTB7A
BioPlanet2019	Oxidative phosphorylation	42/136	0.005875514	0.311761213	1.651395805	8.483157185	NDUFB9;COX7B;NDUFA11;UQCRB;NDUFB6;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFA4L2;NDUFB1;COX7A2;UQCR11;TCIRG1;UQCR10;COX6A1;ATP5O;ATP5G2;COX6A2;COX7A1;COX7C;ATP5L;ATP5D;COX11;ATP6V0E2;ATP6V1F;COX8A;NDUFA9;ATP6V1G1;NDUFA7;NDUFA5;NDUFA3;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5;ATP6V1B2;ATP6V0D1;ATP6V0C
BioPlanet2019	Metabolism of vitamins and cofactors	18/51	0.015410218	0.551606783	2.012437492	8.397347175	PANK4;CYB5A;PANK2;SLC46A1;MOCS3;PANK1;GSTO1;TPK1;MTHFR;NFS1;NMNAT1;FLAD1;FASN;FPGS;PNPO;ACP5;MOCS1;SLC19A1
Reactome2016	mRNA 3'-end processing Homo sapiens R-HSA-72187	18/51	0.015410218	0.294482936	2.012437492	8.397347175	NCBP1;RBM8A;ALYREF;SRSF1;UPF3B;CASC3;THOC2;DDX39B;PABPN1;FIP1L1;PCF11;SARNP;SRSF2;CSTF1;RNPS1;SRSF5;SRSF11;SRSF9
Reactome2016	Post-Elongation Processing of Intron-Containing pre-mRNA Homo sapiens R-HSA-112296	18/51	0.015410218	0.294482936	2.012437492	8.397347175	NCBP1;RBM8A;ALYREF;SRSF1;UPF3B;CASC3;THOC2;DDX39B;PABPN1;FIP1L1;PCF11;SARNP;SRSF2;CSTF1;RNPS1;SRSF5;SRSF11;SRSF9
Reactome2016	Global Genome Nucleotide Excision Repair (GG-NER) Homo sapiens R-HSA-5696399	27/82	0.009965949	0.226080011	1.81248956	8.353005139	INO80B;GPS1;XPA;COPS7A;YY1;TFPT;POLD4;SUMO1;POLD1;RUVBL1;UBC;POLD2;POLE;RFC5;PIAS3;MCRS1;GTF2H3;RAD23B;GTF2H4;CUL4A;COPS3;COPS6;ERCC1;ERCC2;UBE2V2;MNAT1;UBA52
Reactome2016	Glutathione conjugation Homo sapiens R-HSA-156590	14/38	0.020941388	0.374528669	2.151401284	8.317377159	GGT5;GSTK1;GGT7;GSTM2;GSTM1;GSTO1;MGST3;MGST1;GSTT2;GSTT1;GGCT;GCLC;GSTA4;ESD
GOBP2021	RNA metabolic process (GO:0016070)	41/133	0.006657198	0.462266048	1.646943368	8.254573312	DDX3X;PARN;HNRNPU;HNRNPR;ADAR;LAGE3;RBM3;EXOSC7;PTBP1;METTL14;PABPN1;POLR2C;POLR2D;POLR2E;POLR2I;HNRNPA1;RBM6;POLR2L;HNRNPA0;APOBEC1;HNRNPA3;RBPMS;NCBP1;WTAP;PABPC4;WDR74;RNASE4;GTF2F1;HNRNPL;HNRNPM;LSM8;HNRNPK;DDX39B;HNRNPUL1;HNRNPH1;HNRNPA2B1;HNRNPD;MPHOSPH10;HNRNPH2;HNRNPC;HNRNPH3
GOBP2021	chromatin remodeling at centromere (GO:0031055)	12/32	0.027249759	0.911238795	2.212394366	7.970616642	CENPT;NPM1;CENPV;CENPW;CENPX;NASP;RUVBL1;SMARCA5;RSF1;CENPA;ITGB3BP;CENPS
GOBP2021	protein transmembrane import into intracellular organelle (GO:0044743)	12/32	0.027249759	0.911238795	2.212394366	7.970616642	CHCHD4;GRPEL1;AIFM1;GRPEL2;PAM16;DNLZ;ROMO1;PEX10;TIMM44;DNAJC15;HSPD1;TIMM50
GOBP2021	transcription initiation from RNA polymerase I promoter (GO:0006361)	12/32	0.027249759	0.911238795	2.212394366	7.970616642	CAVIN1;POLR1B;TAF1A;ERCC2;POLR1C;POLR2E;UBTF;GTF2H3;MNAT1;GTF2H4;MAPK3;POLR2L
BioPlanet2019	Integrin-linked kinase signaling	16/45	0.020145481	0.654025371	2.035130931	7.946728996	PPP1R14A;GIT2;PPP1R14B;HSP90AA1;PPP1R12A;PARVB;DIAPH1;CCND1;CDC37;RUVBL1;NCK2;SNAI1;ELMO2;RAC1;MYL9;ILKAP
GOBP2021	cellular protein-containing complex assembly (GO:0034622)	50/168	0.006377996	0.458267624	1.566652482	7.919273753	NUP107;HSP90AB1;CLTB;CD3E;CHCHD4;AIFM1;OTUD6B;LONP1;NCK2;RPL38;RAB5IF;MKKS;HSP90AA1;DNAAF2;AXIN1;VAMP8;EID2;COX7A2L;CSNK2B;CHMP4B;VAMP1;CHMP3;VAMP2;PFDN6;TBCEL;ARL6;ARL2;COX7A2;COX7A1;HIGD1B;CENPA;RTN4;HSPD1;TPR;HSF1;SNX9;SNCA;CENPT;SMAD1;SMAD4;TGFB1;CENPW;HSPA4;PTGES3;TBCC;HOPX;HIGD2A;FKBP1A;PSMG3;PSMG2
BioPlanet2019	Shigellosis	21/62	0.015403691	0.551606783	1.890097595	7.887657188	ITGB1;CHUK;ROCK1;FBXW11;ROCK2;ARPC5L;NOD1;ACTG1;MAPK13;MAD2L2;DIAPH1;ARPC2;ARPC3;ELMO1;PFN4;HCLS1;CSK;RAC1;ITGA5;MAPK3;NFKBIB
GOBP2021	I-kappaB kinase/NF-kappaB signaling (GO:0007249)	21/62	0.015403691	0.730935785	1.890097595	7.887657188	CHUK;ROCK1;ROCK2;LY96;NLRC3;TICAM1;TNFRSF1A;RELB;PRDX4;NKIRAS1;NKIRAS2;UBC;BCL3;RIPK1;TBKBP1;RBCK1;CD14;TAB1;UBA52;MAP3K14;FAIM

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	DNA-templated transcription, elongation (GO:0006354)	23/69	0.014187912	0.692083735	1.845375382	7.852745737	ELOF1;CTDP1;CCNT1;NCBP1;ELP4;SSRP1;GTF2F1;GTF2H3;GTF2H4;IWS1;POLR2C;POLR2D;ERCC2;LEO1;POLR2E;PAF1;ELOB;NELFA;ELOC;POLR2I;CDK13;MNAT1;POLR2L
GOBP2021	RNA 3'-end processing (GO:0031123)	23/69	0.014187912	0.692083735	1.845375382	7.852745737	TUT7;NCBP1;RBM8A;ALYREF;SRSF1;UPF3B;CASC3;THOC2;TENT4A;MAGOHB;TENT4B;DDX39B;PABPN1;FIP1L1;PCF11;SARNP;SRSF2;CSTF1;RPRD1B;RNPS1;SRSF5;SRSF11;SRSF9
BioPlanet2019	RNA polymerase	11/29	0.031077452	0.834310056	2.253122637	7.821203191	POLR3GL;POLR2C;POLR3D;POLR1B;POLR2D;POLR1C;POLR2E;POLR1D;POLR3G;POLR2I;POLR2L
GOBP2021	negative regulation of mRNA catabolic process (GO:1902373)	11/29	0.031077452	0.977744449	2.253122637	7.821203191	TAF15;DHX34;SLC11A1;DND1;E2F1;CIRBP;HNRNPU;YBX1;AXIN2;RBM24;PAIP1
Reactome2016	mRNA Capping Homo sapiens R-HSA-72086	11/29	0.031077452	0.442378015	2.253122637	7.821203191	NCBP1;POLR2C;POLR2D;ERCC2;POLR2E;POLR2I;GTF2H3;GTF2F1;MNAT1;GTF2H4;POLR2L
BioPlanet2019	Electron transport chain	33/105	0.01024003	0.44562833	1.692773453	7.755358202	NDUFB9;COX7B;UQCRB;NDUFB6;NDUFA12;NDUFB5;NDUFB3;NDUFB2;NDUFB1;COX7A2;UQCR11;UQCR10;COX6A1;ATP5O;ATP5G2;COX6A2;COX7A1;COX7C;ATP5L;ATP5D;COX11;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5
GOBP2021	regulation of telomere maintenance via telomerase (GO:0032210)	18/52	0.018973505	0.820179907	1.953123704	7.743572442	CTC1;ACD;STN1;NEK7;PARN;NAT10;HNRNPU;TERF1;TENT4B;TEN1;FBXO4;NEK2;MAPKAPK5;NAF1;HNRNPC;MAP2K7;HNRNPA1;MAPK3
GOBP2021	ATP-dependent chromatin remodeling (GO:0043044)	15/42	0.023056488	0.863319329	2.049043406	7.724500408	MBD3;SMARCE1;INO80B;HDAC2;SMARCB1;SMARCC2;MBD2;SMARCA5;CHD4;SMARCA2;GATAD2B;NASP;ANP32E;DMAP1;HNRNPC
GOBP2021	negative regulation of telomere maintenance via telomere lengthening (GO:1904357)	10/26	0.035423232	0.999996358	2.30408259	7.696528478	CTC1;ACD;STN1;TEN1;NAT10;HNRNPU;HNRNPC;HNRNPA1;TERF1;TENT4B
BioPlanet2019	Collagen binding in corneal epithelia mediated by Erk and PI-3 Kinase	9/23	0.040332073	0.943919677	2.369659194	7.608047417	ITGB1;DIAPH1;ROCK1;MYL2;FYN;HRAS;RHOA;MYLK;MAPK3
BioPlanet2019	RNA polymerase III transcription termination	9/23	0.040332073	0.943919677	2.369659194	7.608047417	SSB;NFIX;POLR3GL;POLR3D;POLR1C;POLR1D;POLR2E;POLR3G;POLR2L
GOBP2021	blood vessel endothelial cell migration (GO:0043534)	9/23	0.040332073	0.999996358	2.369659194	7.608047417	EFNB2;NR4A1;SOX18;SRF;ID1;KDR;MYH9;EMP2;VEGFA
GOBP2021	nucleotide-excision repair, DNA damage recognition (GO:0000715)	9/23	0.040332073	0.999996358	2.369659194	7.608047417	CUL4A;COPS3;COPS6;GPS1;UBC;XPA;COPS7A;RAD23B;UBA52
GOBP2021	positive regulation of mRNA processing (GO:0050685)	9/23	0.040332073	0.999996358	2.369659194	7.608047417	SF3B4;RBM3;DAZAP1;SNW1;NCBP1;NCL;CIRBP;LEO1;PAF1
Reactome2016	RNA Polymerase III Transcription Termination Homo sapiens R-HSA-73980	9/23	0.040332073	0.513035333	2.369659194	7.608047417	SSB;NFIX;POLR3GL;POLR3D;POLR1C;POLR1D;POLR2E;POLR3G;POLR2L
Reactome2016	Abortive elongation of HIV-1 transcript in the absence of Tat Homo sapiens R-HSA-167242	9/23	0.040332073	0.513035333	2.369659194	7.608047417	CTDP1;NCBP1;POLR2C;POLR2D;POLR2E;NELFA;GTF2F1;POLR2I;POLR2L
Reactome2016	Metabolism of amino acids and derivatives Homo sapiens R-HSA-71291	92/335	0.004472284	0.122330119	1.402543958	7.587560928	RPL5;RPL3;RPL32;PYCRL;RPL34;RPLP1;RPLP0;APIP;RPL8;RPL10A;RPL9;RPL7;PSMD8;GCSH;RPS15;RPS14;PSMD7;RPS19;PSMD5;RPS18;RARS;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;GAMT;BCKDHA;RPS5;RPS6;BCKDHB;SARS;RPSA;ASRGL1;PSMA5;SLC25A15;ETHE1;IVD;RPL37A;ASPG;RPL27;SLC25A10;RPL26;RPL29;UBA52;ASPA;PSMD10;AHCY;RPL10;PSMD14;RPL12;HDC;RPL11;ODC1;RPL36A;PDHB;OAZ1;HSD17B10;PSMB7;RPS15A;PSMB3;AFMID;RPS3;RPL13;ASL;PSMF1;CKB;RPS2;EEFSEC;PDHA1;CKM;SMOX;GSR;GOT2;ASNS;RPL35A;FAH;SUOX;NMRAL1;BCKDK;RPS25;RPS28;GCLC;RPS27;SLC6A8;RPS29;PAH;ALDH18A1;FAU;RPS21;RPS24
GOBP2021	mesoderm development (GO:0007498)	8/20	0.04582719	0.999996358	2.457160725	7.575126016	TBX1;GDF11;TCF15;BMX;MESD;MEST;TBX3;VEGFA
GOBP2021	nucleobase-containing compound biosynthetic process (GO:0034654)	8/20	0.04582719	0.999996358	2.457160725	7.575126016	CDA;DGUOK;PNP;GMPR2;POLD1;POLD2;ADA;APRT
WikiPath2019M	Glutathione metabolism WP164	8/20	0.04582719	0.776192516	2.457160725	7.575126016	GGT5;GSTM2;GCLC;GPX3;GSR;G6PDX;GSTT2;GSTT1
GOBP2021	nucleotide-excision repair, DNA incision (GO:0033683)	14/39	0.026407118	0.902427467	2.065213715	7.505237969	RFC5;OGG1;XPA;GTF2H3;GTF2H4;CUL4A;POLD4;POLD1;ERCC1;UBC;POLD2;ERCC2;UBA52;FAN1
BioPlanet2019	Muscle contraction	17/49	0.021734269	0.674245319	1.959694477	7.503405698	TPM4;TPM3;TPM2;TNNC1;TPM1;LMOD1;MYL6B;MYLK;MYL12B;TNNT1;CALD1;MYL2;TNNT2;TNNT3;MYH11;MYL9;MYH6
GOBP2021	response to unfolded protein (GO:0006986)	17/49	0.021734269	0.82940984	1.959694477	7.503405698	HSPA9;HSPA8;HSP90AA1;HSP90AB1;HSPA4;RHBDD1;HSPB1;HSPB3;HSPE1;HSPD1;DNAJB2;HSPH1;HSF1;TMBIM6;BAK1;STT3B;HSPA1B
Reactome2016	EPH-Ephrin signaling Homo sapiens R-HSA-2682334	30/95	0.012951579	0.266679205	1.70416712	7.407226343	ROCK1;ROCK2;ITSN1;CLTB;AP2A1;MYL12A;ACTG1;MYL12B;EFNB2;NCSTN;APH1B;KDR;NCK2;MYH14;MYH11;FYN;RAC1;HRAS;MYH10;PSENEN;EPHA7;HSP90AA1;RHOA;DNM1;VEGFA;EFNA1;ARPC2;ARPC3;MYH9;MYL9
GOBP2021	regulation of mRNA processing (GO:0050684)	13/36	0.03026769	0.963672499	2.084230836	7.289960994	KHDRBS1;AHCYL1;KHDRBS3;NCBP1;YTHDC1;SAFB;CDK11B;IWS1;QKI;HNRNPK;PABPN1;SLTM;SAFB2
BioPlanet2019	Toll receptor cascades	47/159	0.009128987	0.424802184	1.55103973	7.284148764	ATF1;ATF2;APP;UNC93B1;UBE2D3;LY96;NOD1;HMGB1;UBE2J2;UBE2L3;HSP90B1;EEA1;PPP2CA;UBE2Q1;UBE2Q2;UBC;RIPK1;CD14;MAP2K7;CTSB;MAPK3;UBE2H;MAP2K2;RIPK3;CHUK;UBE2C;LY86;UBE2E2;UBE2A;IRAK4;UBE2G2;TICAM1;DNM1;DUSP7;SIGIRR;MAPKAPK3;UBE2R2;UBE2S;UBE2T;UBE2V2;TAB1;TLR5;UBA52;UBE2K;MAP3K14;UBE2M;NFKBIB

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
BioPlanet2019	Disease	173/674	0.003699769	0.239513204	1.282758221	7.18278533	RPL5;APP;RPL3;NUP107;RPL32;CCNT1;NUP188;RPL34;RPL8;RPL10A;RPL9;RPL7;PSMD8;RPS15;RPS14;PSMD7;FGF9;RPS19;PSMD5;RPS18;KHSRP;RPL36;RPL38;RPL37;RPS11;B2M;RPS13;RPS12;TSPYL2;SLC30A6;ATP6V1G1;MAP2K2;RPS5;SLC11A1;RPS6;AP1B1;TSC2;RPSA;GTF2F1;HSPG2;PDIA6;PDIA5;PRKAR1A;CDC37;DNAJB11;ELMO1;RPL27;TRIB3;RPL26;KDELR3;RPL29;ATP6V0D1;UBA52;PPIA;KPNB1;PSMD10;PSMD14;PDE1B;FOXO4;GTF2E1;HSP90B1;LDHB;TPR;UBC;FGF20;THEM4;PSMF1;ATP6V1F;TGFB1;IGF2;HMGA1;ASNS;RAB27A;H19;MSRA;RPS25;FGF16;NR4A1;RPS28;RPS27;RPS29;PAH;CPE;TPP1;CALR;MNAT1;GRSF1;RPS21;FGFR3;RPS24;GSK3A;RPLP1;RPLP0;PTEN;PSIP1;AP2A1;TCIRG1;MLST8;NELFA;RAC1;HRAS;HSP90AA1;CHUK;NCBP1;NUP133;EXOC7;PSMA5;RPL37A;CANX;ATP6V1B2;VAMP1;MFGE8;ATP6V0C;VAMP2;GTF2A1;CTDP1;RPL10;RPL12;RPL11;ADCY4;RPL36A;PARN;STX11;EXOSC7;PPP2CA;PSMB7;EXOSC5;RPS15A;PABPN1;PSMB3;POLR2C;EXOSC9;POLR2D;RPS3;POLR2E;RPL13;CSK;FYN;RPS2;POLR2I;EXOSC3;ATP6V0E2;SEC11A;EXOSC2;SEC11C;POLR2L;SNCA;MAPK3;RANBP1;NPM1;TAF12;NFYB;TAF13;NOS3;NFYC;TAF10;SYVN1;RPL35A;PTPN11;SSRP1;GTF2H3;KLF4;GTF2H4;YIF1A;SPCS2;RPS6KB2;ERCC2;HDGF;SPRY1;KRAS;FAU;TAF5;TAF4
Reactome2016	Formation of TC-NER Pre-Incision Complex Homo sapiens R-HSA-6781823	18/53	0.02313856	0.395667239	1.897199275	7.145335825	GPS1;XPA;COPS7A;GTF2H3;GTF2H4;CUL4A;COPS3;COPS6;POLR2C;UBC;POLR2D;ERCC2;POLR2E;POLR2I;MNAT1;UBA52;HMGN1;POLR2L
BioPlanet2019	Global genomic nucleotide excision repair (GG-NER)	12/33	0.034720309	0.881264575	2.106908115	7.080118259	RFC5;POLD4;POLD1;ERCC1;POLD2;ERCC2;XPA;GTF2H3;MNAT1;POLE;RAD23B;GTF2H4
GOBP2021	negative regulation of cell differentiation (GO:0045596)	55/191	0.009101152	0.576081249	1.495278216	7.02684209	PTEN;HNRNPU;LIMD1;TSKU;PTBP1;SPRED2;METTL14;GPER1;SUFU;EID2B;OSR1;WNT5A;NOG;WNT9A;PKP2;TRIB3;SINHCAF;ZFPM1;NOTCH1;TWIST2;CHRD;TWIST1;GPS2;ADIPOR1;ZFP36L2;HDAC7;PPP2CA;E2F1;LEO1;HES1;SUZ12;TBX1;TGFB1;SEMA4D;NR1H2;ESRRB;CRIM1;IGF2;PTPN11;TMEM64;SMAD6;BMP7;HOPX;TBX3;SMAD7;EFNA1;MAD2L2;MEIS1;REST;PDCD4;SNAI2;PAF1;SPRY1;ANP32B;CALR
GOBP2021	glutathione metabolic process (GO:0006749)	15/43	0.028598337	0.938625667	1.975737441	7.022574413	GGT5;GSTK1;GGT7;GSTM2;GSTM1;GSR;GSTT2;GSTT1;GGCT;GCLC;GSTA4;ETHE1;DPEP1;HAGH;MMACHC
GOBP2021	myofibril assembly (GO:0030239)	15/43	0.028598337	0.938625667	1.975737441	7.022574413	PDGFRB;TPM1;LMOD1;CFLAR;LMOD3;LMOD2;CSRP2;ACTC1;TNNT1;TNNT2;MYL2;TNNT3;CAPN3;MYOZ2;MYH6
Reactome2016	HIV Transcription Elongation Homo sapiens R-HSA-167169	15/43	0.028598337	0.419944002	1.975737441	7.022574413	CTDP1;CCNT1;NCBP1;SSRP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
Reactome2016	Tat-mediated elongation of the HIV-1 transcript Homo sapiens R-HSA-167246	15/43	0.028598337	0.419944002	1.975737441	7.022574413	CTDP1;CCNT1;NCBP1;SSRP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
Reactome2016	Formation of HIV-1 elongation complex containing HIV-1 Tat Homo sapiens R-HSA-167200	15/43	0.028598337	0.419944002	1.975737441	7.022574413	CTDP1;CCNT1;NCBP1;SSRP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
GOBP2021	CENP-A containing chromatin organization (GO:0061641)	11/30	0.039860593	0.999996358	2.134401364	6.877824713	CENPT;NPM1;CENPW;CENPX;NASP;RUVBL1;SMARCA5;RSF1;CENPA;ITGB3BP;CENPS
GOBP2021	CENP-A containing nucleosome assembly (GO:0034080)	11/30	0.039860593	0.999996358	2.134401364	6.877824713	CENPT;NPM1;CENPW;CENPX;NASP;RUVBL1;SMARCA5;RSF1;CENPA;ITGB3BP;CENPS
GOBP2021	termination of RNA polymerase I transcription (GO:0006363)	11/30	0.039860593	0.999996358	2.134401364	6.877824713	CAVIN1;POLR1B;TAF1A;ERCC2;POLR1C;POLR2E;UBTF;GTF2H3;MNAT1;GTF2H4;POLR2L
Reactome2016	RNA Polymerase I Promoter Escape Homo sapiens R-HSA-73772	11/30	0.039860593	0.513035333	2.134401364	6.877824713	POLR1B;TAF1A;ERCC2;POLR1C;POLR2E;UBTF;POLR1D;GTF2H3;MNAT1;GTF2H4;POLR2L
BioPlanet2019	Pathogenic Escherichia coli infection	19/57	0.024372084	0.708821445	1.844580296	6.851355762	ITGB1;ROCK1;ROCK2;ARPC5L;LY96;YWHAZ;RHOA;ACTG1;TUBA1B;TUBA1A;TUBB2A;ARPC2;ARPC3;NCL;NCK2;HCLS1;FYN;CD14;TLR5
Reactome2016	Nucleotide Excision Repair Homo sapiens R-HSA-5696398	33/108	0.015830052	0.298417875	1.624751121	6.735966487	INO80B;GPS1;XPA;COPS7A;YY1;TFPT;POLD4;SUMO1;POLD1;POLR2C;RUVBL1;UBC;POLD2;POLR2D;POLR2E;POLR2I;POLE;HMGN1;POLR2L;RFC5;PIAS3;MCRS1;GTF2H3;RAD23B;GTF2H4;CUL4A;COPS3;COPS6;ERCC1;ERCC2;UBE2V2;MNAT1;UBA52
BioPlanet2019	Alzheimer's disease	49/169	0.011581447	0.475520602	1.509179888	6.728453404	APP;COX7B;COX4I2;ATP2A2;IDE;COX6A1;ATP5G2;COX6A2;COX7C;PPP3CC;COX8A;PSENEN;SDHA;SDHB;COX6B1;TNFRSF1A;BACE2;COX7A2L;NDUFS8;NDUFS7;NDUFS5;NDUFB9;UQCRB;LRP1;NDUFB6;NDUFB5;NDUFB3;NDUFB2;NDUFA4L2;NDUFB1;COX7A2;UQCR11;UQCR10;ATP5O;COX7A1;HSD17B10;NCSTN;ATP5D;CACNA1S;BID;SNCA;MAPK3;NDUFA9;NDUFA7;NDUFA5;NDUFA3;GRIN2D;CALM3;CALM2
BioPlanet2019	RNA polymerase III transcription initiation from type 2 promoter	10/27	0.045799175	0.992061408	2.168410302	6.686269737	BRF1;POLR3GL;POLR3D;POLR1C;POLR2E;GTF3A;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	RNA Polymerase III Transcription Initiation From Type 2 Promoter Homo sapiens R-HSA-76066	10/27	0.045799175	0.550774565	2.168410302	6.686269737	BRF1;GTF3C6;POLR3GL;POLR3D;POLR1C;POLR2E;POLR1D;POLR3G;BDP1;POLR2L
Reactome2016	RNA Pol II CTD phosphorylation and interaction with CE Homo sapiens R-HSA-167160	10/27	0.045799175	0.550774565	2.168410302	6.686269737	POLR2C;POLR2D;ERCC2;POLR2E;POLR2I;GTF2H3;GTF2F1;MNAT1;GTF2H4;POLR2L
Reactome2016	RNA Pol II CTD phosphorylation and interaction with CE Homo sapiens R-HSA-77075	10/27	0.045799175	0.550774565	2.168410302	6.686269737	POLR2C;POLR2D;ERCC2;POLR2E;POLR2I;GTF2H3;GTF2F1;MNAT1;GTF2H4;POLR2L
Reactome2016	Unfolded Protein Response (UPR) Homo sapiens R-HSA-381119	27/86	0.019159068	0.347102597	1.689177697	6.680662562	GSK3A;PARN;HSP90B1;EXOSC7;SEC61A1;EXOSC5;KHSRP;SEC61G;EXOSC9;SEC62;EXOSC3;EXOSC2;SEC63;TSPYL2;NFYB;NFYC;SYVN1;ASNS;PDIA6;PDIA5;YIF1A;DNAJB11;HDGF;TPP1;KDELR3;CALR;ATP6V0D1
GOBP2021	regulation of translational initiation (GO:0006446)	22/68	0.023042916	0.863319329	1.764726343	6.65371874	EIF5B;KHDRBS1;CEBPB;YTHDF1;NPM1;DDX3X;NCBP1;HSPB1;MTIF2;MIF4GD;EIF1;RPS6KB1;CSDE1;TPR;POLR2D;RPS6KB2;HABP4;NCK2;EIF3H;PAIP1;EIF4G1;EIF3B
GOBP2021	regulation of DNA binding (GO:0051101)	16/47	0.030491343	0.965014699	1.903589619	6.644122604	ILRUN;CDT1;FOXC1;TGFB1;KDM1A;CEBPG;RSF1;HMGB1;NGF;SUMO1;CSNK2B;BCL3;E2F1;HABP4;HES1;ZBTB7A

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
BioPlanet2019	Parkinson's disease	39/131	0.014570911	0.549756547	1.565864481	6.621615149	NDUFB9;COX7B;UQCRB;NDUFB6;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFA4L2;NDUFB1;COX7A2;UQCR11;UQCR10;COX6A1;UBE2J2;ATP5O;ATP5G2;COX6A2;COX7A1;COX7C;UBE2L3;UCHL1;ATP5D;SNCA;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;UBE2G2;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5;VDAC1;PPID
GOBP2021	positive regulation of DNA biosynthetic process (GO:2000573)	20/61	0.025449009	0.902427467	1.799669596	6.60672835	PDGFRB;RFC5;HSP90AA1;ACD;HSP90AB1;PTGES3;NEK7;PARN;PDGFB;KLF4;RGCC;POLG2;FBXO4;NEK2;MAPKAPK5;NAF1;PRKD2;MAP2K7;HNRNPA1;MAPK3
Reactome2016	Formation of HIV elongation complex in the absence of HIV Tat Homo sapiens R-HSA-167152	15/44	0.035062761	0.479534822	1.90748706	6.391255989	CTDP1;CCNT1;NCBP1;SSRP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
Reactome2016	RNA Polymerase II Transcription Elongation Homo sapiens R-HSA-75955	15/44	0.035062761	0.479534822	1.90748706	6.391255989	CTDP1;CCNT1;NCBP1;SSRP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
Reactome2016	Formation of RNA Pol II elongation complex Homo sapiens R-HSA-112382	15/44	0.035062761	0.479534822	1.90748706	6.391255989	CTDP1;CCNT1;NCBP1;SSRP1;GTF2H3;GTF2F1;GTF2H4;POLR2C;POLR2D;ERCC2;POLR2E;NELFA;POLR2I;MNAT1;POLR2L
GOBP2021	fat cell differentiation (GO:0045444)	19/58	0.029184647	0.951992439	1.797168816	6.351396776	CEBPA;TMEM120B;MKKS;WNT5B;CTBP2;TMEM120A;INHBB;METRNL;GDF6;KLF4;SMAD6;BSCL2;NR4A2;NR4A1;FAM120B;ATF5;ZBTB7A;TRIM32;BBS4
BioPlanet2019	Glutathione metabolism	17/51	0.032116237	0.845929556	1.844183314	6.341028028	GGT5;GSTK1;GSTM2;GGT7;GSTM1;GPX3;GSTO1;MGST3;ODC1;GSR;MGST1;GPX7;GSTT2;GSTT1;GGCT;GCLC;GSTA4
Reactome2016	Transcription-Coupled Nucleotide Excision Repair (TC-NER) Homo sapiens R-HSA-6781827	24/76	0.024392389	0.395667239	1.703172534	6.324704166	RFC5;GPS1;XPA;COPS7A;GTF2H3;GTF2H4;CUL4A;POLD4;COPS3;COPS6;POLD1;POLR2C;ERCC1;UBC;POLD2;POLR2D;ERCC2;POLR2E;POLR2I;MNAT1;POLE;UBA52;HMGN1;POLR2L
KEGG2019M	RNA transport	48/167	0.01456013	0.438259919	1.490546218	6.304217971	POP7;NUP107;NUP188;RBM8A;GEMIN2;POP4;CASC3;PNN;FXR2;SUMO1;TPR;SAP18;EIF3J2;EIF3J1;ALYREF2;PAIP1;UPF2;EIF5B;UPF1;EIF2B3;SAP18B;NCBP1;NUP133;ALYREF;PABPC4;RPP40;ELAC1;UPF3B;UPF3A;THOC2;MAGOHB;RPP25L;EIF1;DDX39B;EIF3I;RPP21;GEMIN5;EIF3H;ACIN1;GEMIN6;RNPS1;EIF3F;EIF1A;EIF4E2;KPNB1;EIF3A;EIF4G1;EIF3B
GOBP2021	positive regulation of telomerase activity (GO:0051973)	12/34	0.043535354	0.999996358	2.011011524	6.30287597	ACD;HSP90AA1;HSP90AB1;PTGES3;NEK7;PARN;NEK2;MAPKAPK5;NAF1;MAP2K7;KLF4;MAPK3
GOBP2021	transcription by RNA polymerase I (GO:0006360)	12/34	0.043535354	0.999996358	2.011011524	6.30287597	CAVIN1;POLR1B;TAF1A;ERCC2;POLR1C;POLR2E;UBTF;GTF2H3;MNAT1;GTF2H4;MAPK3;POLR2L
KEGG2019M	Hepatocellular carcinoma	49/171	0.014498377	0.438259919	1.484249019	6.283892619	SMARCB1;PTEN;ACTG1;FRAT1;FRAT2;PEG12;CCND1;HRAS;APC2;MAP2K2;SMARCC2;WNT5B;GSTO1;WNT5A;AXIN1;AXIN2;WNT9A;SHC3;SMARCD3;MGST3;MGST1;GSTT2;GSTT1;E2F1;BAK1;BRD7;MAPK3;FZD1;SMARCE1;SMAD4;GSTM2;TCF7L1;TGFB1;FZD2;GSTM1;PHF10;TGFB3;GADD45A;FZD7;FZD6;IGF2;FZD8;SMARCA2;GADD45G;GSTA4;RPS6KB1;CDK4;RPS6KB2;KRAS
GOBP2021	transcription initiation from RNA polymerase II promoter (GO:0006367)	41/140	0.01656773	0.730935785	1.529807649	6.272667954	GTF2A1;NOTCH1;MAML2;HDAC10;THRA;MAZ;GTF2E1;HDAC7;POLR2C;POLR2D;POLR2E;NRBF2;POLR2I;TEAD2;TEAD3;POLR2L;ESRRA;TAF15;TAF12;TAF13;NR1H2;TAF10;ESRRB;NR2F1;NR1D1;GTF2F1;MED27;GTF2H3;NR0B2;MED26;GTF2H4;MED7;NR2F6;NR4A2;NR4A1;SNW1;ERCC2;TAF5;MNAT1;TAF4;TAF3
KEGG2019M	Parkinson disease	42/144	0.01656523	0.453284941	1.521095814	6.237176318	NDUFB9;COX7B;NDUFA11;UQCRB;NDUFB6;NDUFA12;NDUFB11;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFA4L2;COX7A2;UQCR11;UQCR10;COX6A1;UBE2J2;ATP5O;ATP5G2;COX6A2;COX7A1;COX7C;UBE2L3;UCHL1;ATP5D;SNCA;GM10705;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;UBE2G2;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5;PPIF;VDAC1
GOBP2021	regulation of protein metabolic process (GO:0051246)	16/48	0.036930066	0.999996358	1.843984962	6.082807141	APP;HSP90AB1;ACE;ROCK2;GBA;ODC1;NEDD8;ABCA7;KLF4;ZDHHC2;KLF2;FKBP1A;PM20D2;SPOP;SPOPL;TMEM9
GOBP2021	nuclear export (GO:0051168)	26/84	0.025382672	0.902427467	1.654376533	6.077664129	NUP188;RBM8A;SRSF1;CASC3;PKD1;TPR;CCHCR1;HNRNPA1;SRSF11;TGFB1;NCBP1;STRADB;ALYREF;RITA1;UPF3B;THOC2;MAGOHB;LSG1;NEMF;DDX39B;SARNP;SRSF2;RNPS1;SRSF5;CALR;SRSF9
Reactome2016	TP53 Regulates Metabolic Genes Homo sapiens R-HSA-5628897	26/84	0.025382672	0.399289904	1.654376533	6.077664129	YWHAE;COX7B;COX16;COX18;PTEN;COX6A1;COX7C;PRKAG3;PRDX2;SESN2;MLST8;COX11;COX14;YWHAH;COX8A;GSR;TSC2;YWHAZ;COX6B1;TNRC6C;MOV10;COX7A2L;SCO2;RHEB;LAMTOR3;COX20
GOBP2021	transcription-coupled nucleotide-excision repair (GO:0006283)	23/73	0.027875117	0.926324995	1.697312309	6.076413434	RFC5;GPS1;XPA;COPS7A;GTF2H3;GTF2H4;CUL4A;POLD4;COPS3;COPS6;POLD1;POLR2C;ERCC1;UBC;POLD2;POLR2D;ERCC2;POLR2E;POLR2I;MNAT1;UBA52;HMGN1;POLR2L
BioPlanet2019	Striated muscle contraction	13/38	0.046559382	0.992061408	1.91724818	5.880251472	TPM4;TPM3;TNNC1;TPM2;TPM1;ACTG1;ACTC1;TNNT1;TNNT2;MYL2;TNNT3;MYL9;MYH6
GOBP2021	histone exchange (GO:0043486)	13/38	0.046559382	0.999996358	1.91724818	5.880251472	CENPT;NPM1;CENPW;CENPX;SMARCA5;RSF1;CENPA;NASP;RUVBL1;ANP32E;DMAP1;ITGB3BP;CENPS
GOBP2021	negative regulation of TOR signaling (GO:0032007)	13/38	0.046559382	0.999996358	1.91724818	5.880251472	GSK3A;SZT2;NPRL2;NPRL3;TSC2;STK11;TMEM127;SESN2;TBC1D7;TNFAIP8L1;SH3BP4;MAPKAPK5;KPTN
Reactome2016	DNA Damage Recognition in GG-NER Homo sapiens R-HSA-5696394	13/38	0.046559382	0.555131088	1.91724818	5.880251472	INO80B;GPS1;MCRS1;COPS7A;RAD23B;YY1;CUL4A;TFPT;COPS3;COPS6;RUVBL1;UBC;UBA52
GOBP2021	fatty acid beta-oxidation (GO:0006635)	17/52	0.038499854	0.999996358	1.791378211	5.834699456	ACOT8;ECHS1;HSD17B4;ETFB;MTLN;HSD17B10;MCAT;HADHB;CPT2;IVD;ECHDC1;ACAD11;ACAD10;ABCD1;ACADS;CRAT;DECR1
BioPlanet2019	TGF-beta regulation of skeletal system development	26/85	0.029341178	0.819205689	1.626232466	5.738589537	ROCK1;ROCK2;CHRD;LTBP1;PPP2CA;E2F4;MAPK3;SMAD1;SMAD4;TGFB1;TGFB3;NOG;INHBB;INHBA;GDF6;SMAD6;BMP7;ACVR2B;RHOA;DCN;SMAD7;TFDP1;RPS6KB1;ID1;RPS6KB2;ID3
Reactome2016	Dual incision in TC-NER Homo sapiens R-HSA-6782135	20/63	0.035658734	0.482950819	1.715745258	5.719884903	RFC5;XPA;GTF2H3;GTF2H4;CUL4A;POLD4;POLD1;POLR2C;ERCC1;UBC;POLD2;POLR2D;ERCC2;POLR2E;POLR2I;MNAT1;POLE;UBA52;HMGN1;POLR2L

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
GOBP2021	cellular response to amino acid starvation (GO:0034198)	23/74	0.03250175	0.999996358	1.663925537	5.701376519	ATF2;SZT2;ATP6V1G1;CEBPB;MIOS;NPRL2;NPRL3;TCIRG1;WDR24;DAP;RHEB;SESN2;MLST8;ATP6V1B2;KPTN;ATP6V0D1;ATP6V0E2;ATP6V0C;LAMTOR3;GCN1;MAP3K5;MAPK3;ATP6V1F
GOBP2021	negative regulation of cell projection organization (GO:0031345)	16/49	0.044297731	0.999996358	1.787992709	5.572854693	RTN4R;PRNP;HDAC2;PAQR3;PTEN;LPAR1;CIB1;RTN4RL2;TSKU;EFNB2;GORASP1;TRPV4;DPYSL3;FYN;YWHAH;ITM2C
GOBP2021	regulation of cellular protein metabolic process (GO:0032268)	16/49	0.044297731	0.999996358	1.787992709	5.572854693	APP;TGFB1;RPL10;NANOS3;NR1H2;GBA;INHBA;KLF4;AGT;PUM3;RBM3;PM20D2;WDR91;GEMIN5;MAPKAPK5;EIF4G1
BioPlanet2019	Eukaryotic transcription initiation	14/42	0.049032148	0.992061408	1.843588539	5.55893402	TAF12;TAF13;GTF2H3;GTF2E1;GTF2H4;POLR2C;POLR3D;POLR1B;ERCC2;POLR2E;POLR1D;TAF5;POLR2I;MNAT1
GOBP2021	nucleic acid-templated transcription (GO:0097659)	14/42	0.049032148	0.999996358	1.843588539	5.55893402	SCX;NR4A2;FUBP3;POLR2C;POLR2D;BCL3;E2F1;POLR2E;RNPS1;MMS19;POLR2I;PTMA;POLR2L;NFKBIB
BioPlanet2019	Neurotrophic factor-mediated Trk receptor signaling	19/60	0.040889905	0.943919677	1.709284121	5.464362645	PRKCI;RGS19;SHC3;MAGED1;PTPN11;NGF;PRKCZ;RHOA;DNM1;RAP1B;RAP1A;CCND1;GIPC1;ELMO1;KRAS;RAC1;HRAS;FAIM;MAPK3
Reactome2016	Organelle biogenesis and maintenance Homo sapiens R-HSA-1852241	86/326	0.016975469	0.311589198	1.325816213	5.404008304	MRPS17;YWHAE;ATF2;MRPS16;C2CD3;TRAF3IP1;MRPS14;MRPS11;MRPS12;MRPL36;MRPL34;PKD2;PKD1;HSPB11;PRKAG3;MRPL4;MRPL3;PCM1;TUBA1A;TCTN3;CEP250;NEK2;MRPL9;CEP97;IFT57;CHCHD1;BBS4;RAB8A;MRPS28;MKKS;HSP90AA1;MRPS27;MRPS24;EXOC7;MRPS25;MRPS18B;MRPS18A;HAUS3;CYS1;TUBG1;MRPS7;DYNLL1;DYNLL2;MRPS5;MRPL43;HAUS1;MRPL52;MRPL50;POLG2;TMEM216;AKAP9;TFAM;CEP63;AURKAIP1;MRRF;MTRF1L;SDCCAG8;SMARCD3;ARL6;MRPL18;SSNA1;MRPL16;MRPL14;MTIF2;MRPS30;MRPL12;MRPL54;MRPL11;KIF3A;NPHP1;PDE6D;NPHP4;MARK4;ESRRA;MRPL27;NR1D1;MRPL23;MRPL30;ATAT1;CARM1;CEP83;IFT27;B9D2;SSBP1;CLUAP1;CEP89
GOBP2021	response to amino acid starvation (GO:1990928)	23/75	0.03768183	0.999996358	1.631822872	5.350057362	ATF2;SZT2;ATP6V1G1;CEBPB;MIOS;NPRL2;NPRL3;TCIRG1;WDR24;DAP;RHEB;SESN2;MLST8;ATP6V1B2;KPTN;ATP6V0D1;ATP6V0E2;ATP6V0C;LAMTOR3;GCN1;MAP3K5;MAPK3;ATP6V1F
GOBP2021	tRNA processing (GO:0008033)	20/64	0.041771132	0.999996358	1.676644146	5.324266994	TSEN34;TRUB1;TRMT10A;PTCD1;POP7;SSB;TSEN15;URM1;RTCB;RPP40;TRPT1;THUMPD1;TSEN2;THG1L;FARS2;ADAT2;CTU2;RPP21;LCMT2;RTRAF
BioPlanet2019	mTOR signaling pathway	33/113	0.030337522	0.830415305	1.522717622	5.322461474	YWHAE;PRR5;CAB39;PTEN;YY1;PPP2CA;STK11;RPS6KA6;MLST8;RAC1;HRAS;PDK2;YWHAH;MAPK3;SREBF1;MAP2K2;FBXW11;RPS6;VEGFB;TSC2;VEGFC;YWHAZ;RHOA;VEGFA;FKBP1A;RPS6KB1;RHEB;RPS6KB2;PDCD4;KRAS;EIF4E2;EIF3A;EIF4G1
GOBP2021	positive regulation of ubiquitin-dependent protein catabolic process (GO:2000060)	24/79	0.038103011	0.999996358	1.609964047	5.26049628	PSMD10;CEBPA;GSK3A;VCP;ZER1;PTEN;AXIN1;LAPTM5;RNF19B;KLHL40;HSPBP1;DDA1;SMAD7;DNAJB2;SUMO1;DDRGK1;RNF217;RACK1;ELOB;TRIB3;ARIH1;CCDC22;CDK5RAP3;HSPA1B
KEGG2019M	TGF-beta signaling pathway	27/91	0.038793065	0.834050907	1.556713781	5.058562873	ROCK1;CHRD;ACVR1B;LTBP1;PPP2CA;E2F4;MAPK3;SMAD1;SMAD4;TGFB1;TGFB3;NOG;INHBB;INHBA;GDF6;SMAD6;BMP7;ACVR2B;RHOA;DCN;SMAD7;TFDP1;RPS6KB1;ID1;RPS6KB2;ID3;NBL1
WikiPath2019M	Electron Transport Chain WP295	30/103	0.038828356	0.776192516	1.516634051	4.926944155	NDUFB9;COX7B;UQCRB;NDUFB6;NDUFA12;NDUFB5;NDUFB3;NDUFB2;COX7A2;UQCR11;UQCR10;COX6A1;ATP5O;ATP5G2;COX6A2;COX7A1;ATP5L;ATP5D;COX8A;NDUFA9;NDUFA7;NDUFA5;NDUFA3;SDHA;SDHB;COX6B1;COX7A2L;NDUFS8;NDUFS7;NDUFS5
GOBP2021	mRNA export from nucleus (GO:0006406)	31/107	0.038730487	0.999996358	1.505392224	4.894223128	SLBP;ENY2;NUP107;NUP188;RBM8A;YTHDC1;SRSF1;CASC3;IWS1;RBM15B;PABPN1;FIP1L1;TPR;POLR2D;SRSF11;UPF2;UPF1;NCBP1;NUP133;ALYREF;UPF3B;THOC2;MAGOHB;DDX19B;DDX39B;SARNP;HNRNPA2B1;SRSF2;RNPS1;SRSF5;SRSF9
GOBP2021	regulation of protein serine/threonine kinase activity (GO:0071900)	32/111	0.038587858	0.999996358	1.495008359	4.865979531	CSF1R;CCNJ;DDX3X;CCNI;CCNT1;CAB39;TESK1;BCCIP;CIB1;PKMYT1;SLC8A2;PPP2CA;CCND1;CDK5RAP3;SNCA;MAP2K2;CDKN2C;GADD45A;PIH1D1;PARP16;CDC25A;GTPBP4;RHOA;FGF16;INCENP;CDC37;CCNG2;TRIB3;CALM3;CAMK1;MNAT1;CALM2
GOBP2021	positive regulation of transmembrane receptor protein serine/threonine kinase signaling pathway (GO:0090100)	27/92	0.044075727	0.999996358	1.532666485	4.784748834	CDKN1C;CRB2;HSP90AB1;NOTCH1;CITED2;HFE;TGFB1I1;ACVR1B;STK11;GDF11;SMAD4;FOXD1;TGFB1;RBPMS;SLC2A10;TGFB3;GDF15;INHBB;FBXL15;INHBA;GDF6;BMP7;ACVR2B;SNW1;GIPC1;CSNK2B;ENG
KEGG2019M	Non-alcoholic fatty liver disease (NAFLD)	42/151	0.035588452	0.824009545	1.422773115	4.745992757	NDUFB9;CEBPA;GSK3A;COX7B;NDUFA11;UQCRB;NDUFB6;NDUFA12;NDUFB11;NDUFB5;COX4I2;NDUFB3;NDUFB2;NDUFA4L2;COX7A2;UQCR11;UQCR10;COX6A1;ADIPOR1;COX6A2;COX7A1;COX7C;PRKAG3;MLX;RAC1;BID;MAP3K5;COX8A;NDUFA9;SREBF1;NDUFA7;TGFB1;NDUFA5;NDUFA3;SDHA;SDHB;COX6B1;TNFRSF1A;COX7A2L;NDUFS8;NDUFS7;NDUFS5
KEGG2019M	mRNA surveillance pathway	28/96	0.044029669	0.844186786	1.519376837	4.744849114	DAZAP1;RBM8A;MSI1;CASC3;PPP1CB;PPP2CA;PNN;PPP1CC;PPP2R3D;PABPN1;FIP1L1;PCF11;CSTF1;SAP18;ALYREF2;UPF2;UPF1;SAP18B;NCBP1;PABPC4;ALYREF;PPP2R5A;UPF3B;UPF3A;MAGOHB;DDX39B;ACIN1;RNPS1

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
Reactome2016	Disease Homo sapiens R-HSA-1643685	177/725	0.024144928	0.395667239	1.197320927	4.458441138	RPL5;RPL3;NUP107;MAML2;RPL32;CCNT1;HDAC10;NUP188;RPL34;RPL8;RPL10A;RPL9;RPL7;PSMD8;RPS15;RPS14;C1GALT1C1;PSMD7;FGF9;RPS19;PSMD5;RPS18;RPL36;RPL38;RPL37;KPNA2;RPS11;B2M;RPS13;RPS12;PDGFRB;MAP2K2;RPS5;RPS6;AP1B1;TSC2;RPSA;GTF2F1;TICAM1;HSPG2;MUC3A;CDC37;ELMO1;CHMP4C;CHMP4B;RPL27;RPL26;RPL29;UBA52;PPIA;KPNB1;MMADHC;PSMD10;VCP;NOTCH1;CTBP2;SDC4;PSMD14;PDGFB;LY96;FOXO4;GTF2E1;NCSTN;APH1B;ADAMTS19;TPR;UBC;FGF20;PSMF1;CD14;MAP2K7;SMAD4;TGFB1;FZD6;HMGA1;FZD8;CDK8;MSRA;RPS25;FGF16;NR4A1;RPS28;RPS27;SNW1;TCN2;RPS29;OGN;CSPG4;CALR;MNAT1;GRSF1;RPS21;FGFR3;RPS24;CD320;NFKBIB;PRR5;GSK3A;HSP90AB1;RPLP1;RPLP0;PSIP1;AP2A1;ADAMTSL5;ADAMTSL4;HEY2;MLST8;NELFA;RAC1;HRAS;PSENEN;HSP90AA1;CHUK;NCBP1;NUP133;ABCC8;AXIN1;PPP2R5A;IRAK4;DCN;PSMA5;RPL37A;CANX;VAMP1;CHMP3;TLR5;CHMP7;VAMP2;GTF2A1;HDAC2;CTDP1;RPL10;RPL12;RPL11;RPL36A;HDAC7;PPP2CA;DLL4;PSMB7;ERLEC1;RPS15A;PABPN1;PSMB3;POLR2C;POLR2D;RPS3;POLR2E;GPC3;RPL13;FYN;HES1;RPS2;GPC4;POLR2I;POLR2L;RANBP1;NPM1;TAF12;TAF13;TAF10;SYVN1;RPL35A;PTPN11;SSRP1;GTF2H3;GTF2H4;MIB1;FKBP1A;RPS6KB2;ERCC2;CD9;KRAS;FAU;TAF5;TAF4;MMACHC;TAF3
BioPlanet2019	Signaling by insulin receptor	31/109	0.048792616	0.992061408	1.466604998	4.429405642	SHC3;CAB39;PDE3B;TCIRG1;PRKAG3;STK11;FGF9;FGF20;MLST8;THEM4;ATP6V0E2;HRAS;ATP6V1F;MAPK3;ATP6V1G1;MAP2K2;STRADB;RPS6;TSC2;PTPN11;FGF16;PPM1A;RPS6KB1;RHEB;ATP6V1B2;TRIB3;KRAS;ATP6V0D1;FGFR3;ATP6V0C;EIF4G1
Reactome2016	Metabolism of proteins Homo sapiens R-HSA-392499	256/1074	0.023921964	0.395667239	1.161904947	4.337342647	RPL5;APP;NUP107;RPL3;CMAS;RPL32;KDELR1;RPL34;SMC6;RPL8;SMC3;ZDHHC2;RPL9;RPL7;RPS15;RPS14;C1GALT1C1;HERC2;TFG;RPS19;RPS18;FBXO4;RPL36;FBXO6;RPL38;RPL37;SEC62;RPS11;B2M;RPS13;SEC63;RPS12;TSPYL2;ARSA;ALG8;COG8;CSNK2A1;LMAN1L;ALG1;HSPG2;ANK1;DYNC1LI2;CSNK2B;KDELR2;RPL27;VDAC1;KDELR3;RPL26;RPL29;ATP6V0D1;UBA52;ENPEP;GATA6;GRPEL1;ADAMTS19;DPH1;GRPEL2;ST3GAL5;MLEC;ARSG;EDEM3;CTSA;PHC2;ACE;ABCA3;SIAH2;IGF2;RAB27A;CS;MSRA;RPS25;RPS28;HNRNPK;RPS27;RPS29;FBXL3;CALR;HNRNPC;RPS21;RPS24;ARF3;PIGS;ACHE;PIGT;PIGO;GPAA1;RPLP1;PIGQ;RPLP0;PIGP;PIGV;B3GNTL1;TUBA1B;TUBA1A;GNGT2;ADAMTSL5;ADAMTSL4;SEC61G;TMED3;CTSD;TMED9;RING1;EXOC7;FN3KRP;COPZ2;DYNLL1;DYNLL2;RENBP;SUMF2;SUMF1;TUBB2A;INCENP;CANX;B3GNT2;MFGE8;PIGF;VAMP2;ARF5;NAPA;RPL10;RPL12;TIMM9;GBA;RPL11;TIMM13;TIMM10;FUOM;EXOSC7;EXOSC5;RPS15A;EXOSC9;RPS3;RPL13;RPS2;EXOSC3;YKT6;EXOSC2;MTX1;NFYB;NFYC;SYVN1;DOHH;YIF1A;AGT;SPCS2;HDGF;FAU;TOMM5;MSRB1;DPAGT1;NUP188;APEH;SRP14;RPL10A;CHCHD4;CHCHD2;KHSRP;SCMH1;NUDT14;FBXW4;PIAS4;PIAS3;SLC30A6;RPS5;RPS6;PAM16;RPSA;ALG12;MUC3A;PDIA6;PDIA5;DPM2;DPM3;TBC1D20;DNAJB11;FKBP9;ARL2;HSP90B1;TIMM50;SPTA1;AMDHD2;TPR;UBC;MPDU1;HSPA9;TRAPPC3;EIF2B3;TRAPPC4;SRD5A3;ASNS;TBCC;TIMM44;INHBB;INHBA;TRAPPC9;CNIH1;PDCL;CPE;TPP1;COPE;EIF4G1;B4GALT2;MCFD2;GSK3A;SEC61A1;SUMO1;GMPPA;EIF5B;NUP133;ADRA2C;SMC1A;DDOST;CKAP4;NSMCE4A;DAD1;TRAPPC6B;GORASP1;RPL37A;PFDN2;TOP1;ST6GALNAC4;SEC22A;FXN;PFDN6;DCTN5;RAB1B;PARN;RPL36A;HDAC7;HSPD1;CANAB;GNG5;GNG7;SEC11A;SEC11C;SNCA;TIMM8B;NOP
GOBP2021	transcription by RNA polymerase II (GO:0006366)	82/320	0.037381809	0.999996358	1.273720944	4.18617443	MAML2;HDAC10;CCNT1;THRA;YBX2;MED16;LSM10;SNAPC5;PCF11;SNAPC2;ELOB;ELOC;NELFA;TEAD2;TEAD3;NCBP1;MED27;GTF2F1;MED26;MED7;MAF;TFDP1;SNRPB;SLBP;GTF2A1;ELOF1;CTDP1;NFIX;NOTCH1;CBFB;SRRT;C5AR1;MAZ;GTF2E1;PMF1;IWS1;HDAC7;PABPN1;FIP1L1;DEAF1;POLR2C;TAF1A;POLR2D;CSTF1;LEO1;POLR2E;RPRD1B;NRBF2;POLR2I;POLR2L;BTF3;ESRRA;TAF15;TAF12;TAF13;NR1H2;TAF10;ESRRB;NR2F1;NR1D1;ELP4;DEK;SSRP1;GTF2H3;NR0B2;ELL2;GTF2H4;NR2F6;NR4A2;DRAP1;NR4A1;SNW1;ERCC2;INTS5;PAF1;TRIP13;TAF5;CDK13;INTS9;MNAT1;TAF4;TAF3
KEGG2019M	Huntington disease	51/192	0.049219097	0.844186786	1.335667156	4.022326359	COX7B;NDUFA11;NDUFA12;COX4I2;CLTB;AP2A1;COX6A1;ATP5G2;COX6A2;COX7C;BBC3;CREB3L1;IFT57;COX8A;SDHA;SDHB;COX6B1;CREB3;COX7A2L;NDUFS8;NDUFS7;NDUFS5;PPIF;TFAM;VDAC1;NDUFB9;HDAC2;UQCRB;NDUFB6;NDUFB11;NDUFB5;NDUFB3;NDUFB2;NDUFA4L2;COX7A2;UQCR11;UQCR10;ATP5O;COX7A1;POLR2C;ATP5D;POLR2D;POLR2E;POLR2I;POLR2L;NDUFA9;NDUFA7;NDUFA5;NDUFA3;REST;TAF4

• **Table S8: Enriched pathways in both mG4H-ON and mG4H-OFF (Venn Diagram: Group III)**

Database	Term	Overlap	*P*-value	Adjusted *P*-value (*Q*-value)	Odds Ratio	Combined Score	Genes
BioPlanet2019	Gene expression	228/968	0.048930092	0.992061408	1.141919962	3.4455867	RPL5;NUP107;RPL3;MAML2;RPL32;RPL34;PARS2;HNRNPU;HNRNPR;RPL8;RPL9;CCAR1;RPL7;LSM10;PSMD8;RPS15;RPS14;PSMD7;RPS19;PSMD5;SNRPD1;RPS18;RPL36;RPL38;RPL37;RPS11;RPS13;RPS12;ZFP2;MED7;LARS2;TFAM;RPL27;RPL26;RPL29;UBA52;SLBP;SET;ANP32A;CSTF1;PSMF1;NRBF2;NR2F1;UPF3B;UPF3A;NR1D1;NR0B2;NR2F6;HNRNPL;HNRNPM;RPS25;RPS28;SNW1;HNRNPK;RPS27;RPS29;HNRNPD;RNPS1;HNRNPC;RPS21;RPS24;FARSB;RPLP1;RPLP0;MED16;FARS2;PCF11;MED10;RARS;SEC61G;NELFA;TEAD2;TEAD3;UPF2;APOBEC1;UPF1;MED27;MED26;PSMA5;MED24;HNRNPH1;HNRNPH2;SF3B4;SF3B5;SF3B2;CTDP1;NFIX;RPL10;SF3B6;RPL12;RPL11;EXOSC7;PPP2CA;PSMB7;EXOSC5;RPS15A;PSMB3;EXOSC9;RPS3;RPL13;RPS2;EXOSC3;EXOSC2;SRSF11;PAIP1;SF3A1;BRF2;BRF1;NR1H2;MBD2;GTF2H3;GTF2H4;SPCS2;HNRNPA2B1;FAU;CCNT1;NUP188;GEMIN2;UBE2D3;CASC3;SRP14;RPL10A;EDC3;EDC4;KHSRP;RPS5;RPS6;GTF3A;SARS;RPSA;GTF2F1;HNRNPUL1;SRSF2;GEMIN5;GEMIN6;SRSF5;SRSF9;SNRPB;PSMD10;NOTCH1;PSMD14;RBM8A;GTF2E1;PRPF8;MED30;TPR;UBC;ESRRA;HSPA8;EIF2B3;SMAD4;POLR3GL;CBX3;ALYREF;ESRRB;SMAD7;NR4A2;CDK8;NR4A1;PAN3;LSM6;CNOT11;MNAT1;EIF4G1;THRA;HSPB1;ADAR;YBX1;SNAPC5;SEC61A1;PTBP1;SNRNP70;SNAPC2;UBTF;EIF5B;NCBP1;NUP133;SMC1A;YWHAZ;DDOST;PPM1A;TFDP1;SARS2;POLR1B;RPL37A;POLR1C;POLR1D;DNAJC8;BDP1;GTF2A1;SMARCD3;SRSF1;DDX23;PARN;RPL36A;PABPN1;POLR2C;TAF1A;POLR2D;POLR2E;E2F4;HNRNPA1;POLR2I;SEC11A;HNRNPA0;SEC11C;POLR2L;MAPK3;HNRNPA3;SSB;TAF12;TAF13;TAF10;RPL35A;SSRP1;TNRC6C;EIF3K;EIF3I;CARM1;POLR3D;ERCC2;EIF3H;POLR3G;EIF3F;TAF5;TAF4;EIF3A;EIF3B

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Rab23	chr1	33759047	mm39_genes_promoters	0.0000	0.0000	-55.396
Gm32229	chr1	33759047	mm39_genes_exonintronboundaries	0.0000	0.0000	-55.396
Gm32229	chr1	33759047	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.396
	chr1	33759047	mm39_cpg_islands	0.0000	0.0000	-55.396
Gm32229	chr1	33759047	mm39_genes_promoters	0.0000	0.0000	-55.396
Rab23	chr1	33759047	mm39_genes_5UTRs	0.0000	0.0000	-55.396
Rab23	chr1	33759047	mm39_genes_exons	0.0000	0.0000	-55.396
Bag2	chr1	33797089	mm39_genes_promoters	0.0000	0.0000	-77.633
	chr1	33797089	mm39_cpg_shores	0.0000	0.0000	-77.633
Mir5103	chr1	34474681	mm39_genes_1to5kb	0.0000	0.0475	45.161
Imp4	chr1	34474681	mm39_genes_1to5kb	0.0000	0.0475	45.161
	chr1	34474681	mm39_cpg_shelves	0.0000	0.0475	45.161
	chr1	34882190	mm39_cpg_islands	0.0000	0.0000	24.494
Fam168b	chr1	34882190	mm39_genes_intronexonboundaries	0.0000	0.0000	24.494
Fam168b	chr1	34882190	mm39_genes_intronexonboundaries	0.0000	0.0000	24.494
Fam168b	chr1	34882190	mm39_genes_intronexonboundaries	0.0000	0.0000	24.494
Fam168b	chr1	34882190	mm39_genes_promoters	0.0000	0.0000	24.494
Fam168b	chr1	34882190	mm39_genes_promoters	0.0000	0.0000	24.494
Fam168b	chr1	34882190	mm39_genes_promoters	0.0000	0.0000	24.494
	chr1	38036457	mm39_cpg_islands	0.0000	0.0000	-57.689
Txndc9	chr1	38036457	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.689
Eif5b	chr1	38036457	mm39_genes_promoters	0.0000	0.0000	-57.689
Txndc9	chr1	38036457	mm39_genes_promoters	0.0000	0.0000	-57.689
Aff3	chr1	38665587	mm39_genes_introns	0.0000	0.0002	-27.000
	chr1	38665587	mm39_cpg_shores	0.0000	0.0002	-27.000
Tgfbrap1	chr1	43132035	mm39_genes_introns	0.0000	0.0110	15.988
Tgfbrap1	chr1	43132035	mm39_genes_promoters	0.0000	0.0110	15.988
	chr1	43132035	mm39_cpg_shores	0.0000	0.0110	15.988
Tgfbrap1	chr1	43132080	mm39_genes_introns	0.0000	0.0000	71.831
Tgfbrap1	chr1	43132080	mm39_genes_promoters	0.0000	0.0000	71.831
	chr1	43132080	mm39_cpg_shores	0.0000	0.0000	71.831
Wdr75	chr1	45835056	mm39_genes_introns	0.0000	0.0013	-79.487
	chr1	45835056	mm39_cpg_shores	0.0000	0.0013	-79.487
	chr1	51868759	mm39_cpg_inter	0.0000	0.0396	46.939
Myo1b	chr1	51868759	mm39_genes_introns	0.0000	0.0396	46.939
Myo1b	chr1	51868759	mm39_genes_introns	0.0000	0.0396	46.939
Myo1b	chr1	51868759	mm39_genes_introns	0.0000	0.0396	46.939
	chr1	55276006	mm39_cpg_shores	0.0000	0.0796	34.609
Mars2	chr1	55276006	mm39_genes_promoters	0.0000	0.0796	34.609
	chr1	55417242	mm39_cpg_inter	0.0000	0.0624	-46.853
	chr1	55417242	mm39_genes_intergenic	0.0000	0.0624	-46.853
Tmem237	chr1	59159071	mm39_genes_introns	0.0000	0.0000	-66.264
Tmem237	chr1	59159071	mm39_genes_introns	0.0000	0.0000	-66.264
Tmem237	chr1	59159071	mm39_genes_intronexonboundaries	0.0000	0.0000	-66.264
Tmem237	chr1	59159071	mm39_genes_exonintronboundaries	0.0000	0.0000	-66.264
Tmem237	chr1	59159071	mm39_genes_promoters	0.0000	0.0000	-66.264
	chr1	59159071	mm39_cpg_islands	0.0000	0.0000	-66.264
Tmem237	chr1	59159071	mm39_genes_intronexonboundaries	0.0000	0.0000	-66.264
	chr1	59803704	mm39_cpg_shores	0.0000	0.0000	-74.836
Bmpr2	chr1	59803704	mm39_genes_exons	0.0000	0.0000	-74.836
Bmpr2	chr1	59803704	mm39_genes_5UTRs	0.0000	0.0000	-74.836

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Bmpr2	chr1	59803704	mm39_genes_exonintronboundaries	0.0000	0.0000	-74.836
	chr1	59803705	mm39_cpg_shores	0.0000	0.0000	58.937
Bmpr2	chr1	59803705	mm39_genes_exons	0.0000	0.0000	58.937
Bmpr2	chr1	59803705	mm39_genes_5UTRs	0.0000	0.0000	58.937
Bmpr2	chr1	59803705	mm39_genes_exonintronboundaries	0.0000	0.0000	58.937
	chr1	59803741	mm39_cpg_shores	0.0000	0.0045	75.000
Bmpr2	chr1	59803741	mm39_genes_exons	0.0000	0.0045	75.000
Bmpr2	chr1	59803741	mm39_genes_5UTRs	0.0000	0.0045	75.000
Bmpr2	chr1	59803741	mm39_genes_exonintronboundaries	0.0000	0.0045	75.000
Raph1	chr1	60605184	mm39_genes_introns	0.0000	0.0000	-73.913
	chr1	60605184	mm39_cpg_shores	0.0000	0.0000	-73.913
	chr1	61645057	mm39_cpg_inter	0.0000	0.0047	-48.296
	chr1	61645057	mm39_genes_intergenic	0.0000	0.0047	-48.296
Klf7	chr1	64159729	mm39_genes_introns	0.0000	0.0000	-72.024
	chr1	64159729	mm39_cpg_shores	0.0000	0.0000	-72.024
Ccnyl1	chr1	64729927	mm39_genes_promoters	0.0000	0.0000	-53.297
2810408I11Rik	chr1	64729927	mm39_genes_intronexonboundaries	0.0000	0.0000	-53.297
	chr1	64729927	mm39_cpg_islands	0.0000	0.0000	-53.297
2810408I11Rik	chr1	64729927	mm39_genes_promoters	0.0000	0.0000	-53.297
	chr1	72251539	mm39_cpg_islands	0.0000	0.0729	-71.429
Mreg	chr1	72251539	mm39_genes_intronexonboundaries	0.0000	0.0729	-71.429
Mreg	chr1	72251539	mm39_genes_intronexonboundaries	0.0000	0.0729	-71.429
Mreg	chr1	72251539	mm39_genes_promoters	0.0000	0.0729	-71.429
Mreg	chr1	72251539	mm39_genes_promoters	0.0000	0.0729	-71.429
Tmem198	chr1	75451873	mm39_genes_1to5kb	0.0000	0.0910	45.559
Chpf	chr1	75451873	mm39_genes_exons	0.0000	0.0910	45.559
Chpf	chr1	75451873	mm39_genes_exons	0.0000	0.0910	45.559
	chr1	75451873	mm39_cpg_islands	0.0000	0.0910	45.559
	chr1	78287272	mm39_cpg_islands	0.0000	0.0256	12.980
Sgpp2	chr1	78287272	mm39_genes_exonintronboundaries	0.0000	0.0256	12.980
Sgpp2	chr1	78287272	mm39_genes_introns	0.0000	0.0256	12.980
	chr1	82702891	mm39_cpg_islands	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_exonintronboundaries	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Mff	chr1	82702891	mm39_genes_introns	0.0000	0.0028	-30.371
Atg16l1	chr1	87683684	mm39_genes_promoters	0.0000	0.0000	-54.838
Atg16l1	chr1	87683684	mm39_genes_promoters	0.0000	0.0000	-54.838
Atg16l1	chr1	87683684	mm39_genes_promoters	0.0000	0.0000	-54.838
Gm33517	chr1	87683684	mm39_genes_promoters	0.0000	0.0000	-54.838
Gm33517	chr1	87683684	mm39_genes_promoters	0.0000	0.0000	-54.838
	chr1	87683684	mm39_cpg_islands	0.0000	0.0000	-54.838
	chr1	87861038	mm39_cpg_inter	0.0000	0.0484	-27.860
Dgkd	chr1	87861038	mm39_genes_introns	0.0000	0.0484	-27.860
	chr1	89871266	mm39_genes_intergenic	0.0000	0.0000	52.196
	chr1	89871266	mm39_cpg_shores	0.0000	0.0000	52.196
Asb18	chr1	89919948	mm39_genes_introns	0.0000	0.0284	-40.090
Asb18	chr1	89919948	mm39_genes_introns	0.0000	0.0284	-40.090
Asb18	chr1	89919948	mm39_genes_introns	0.0000	0.0284	-40.090
	chr1	89919948	mm39_cpg_islands	0.0000	0.0284	-40.090
	chr1	90926769	mm39_cpg_islands	0.0000	0.0066	-28.835
Lrrfip1	chr1	90926769	mm39_genes_exonintronboundaries	0.0000	0.0066	-28.835
Lrrfip1	chr1	90926769	mm39_genes_introns	0.0000	0.0066	-28.835
9430060I03Rik	chr1	92862500	mm39_genes_exons	0.0000	0.0000	-45.238
	chr1	92862500	mm39_cpg_islands	0.0000	0.0000	-45.238
Capn10	chr1	92862500	mm39_genes_exons	0.0000	0.0000	-45.238
Capn10	chr1	92862500	mm39_genes_5UTRs	0.0000	0.0000	-45.238
Mir6902	chr1	93271151	mm39_genes_1to5kb	0.0000	0.0897	-39.746
	chr1	93271151	mm39_cpg_islands	0.0000	0.0897	-39.746
Ppp1r7	chr1	93271151	mm39_genes_promoters	0.0000	0.0897	-39.746
Pask	chr1	93271151	mm39_genes_promoters	0.0000	0.0897	-39.746
St8sia4	chr1	95596039	mm39_genes_promoters	0.0000	0.0253	-56.410
St8sia4	chr1	95596039	mm39_genes_promoters	0.0000	0.0253	-56.410
	chr1	95596039	mm39_cpg_shores	0.0000	0.0253	-56.410
Gm30431	chr1	95596039	mm39_genes_exonintronboundaries	0.0000	0.0253	-56.410
Gm30431	chr1	95596039	mm39_genes_introns	0.0000	0.0253	-56.410
	chr1	103407350	mm39_cpg_inter	0.0000	0.0516	-21.745
	chr1	103407350	mm39_genes_intergenic	0.0000	0.0516	-21.745
	chr1	103407351	mm39_cpg_inter	0.0000	0.0000	-41.300
	chr1	103407351	mm39_genes_intergenic	0.0000	0.0000	-41.300
Kdsr	chr1	106687031	mm39_genes_introns	0.0000	0.0091	-32.768
Kdsr	chr1	106687031	mm39_genes_introns	0.0000	0.0091	-32.768
	chr1	106687031	mm39_cpg_shores	0.0000	0.0091	-32.768
Dsel	chr1	111792593	mm39_genes_5UTRs	0.0000	0.0136	-85.238
Dsel	chr1	111792593	mm39_genes_exons	0.0000	0.0136	-85.238
	chr1	111792593	mm39_cpg_islands	0.0000	0.0136	-85.238
Dsel	chr1	111792593	mm39_genes_intronexonboundaries	0.0000	0.0136	-85.238
	chr1	130491011	mm39_cpg_inter	0.0000	0.0794	68.627
	chr1	130491011	mm39_genes_intergenic	0.0000	0.0794	68.627
	chr1	131725225	mm39_cpg_inter	0.0000	0.0000	49.839

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Pm20d1	chr1	131725225	mm39_genes_exonintronboundaries	0.0000	0.0000	49.839
Pm20d1	chr1	131725225	mm39_genes_exonintronboundaries	0.0000	0.0000	49.839
Pm20d1	chr1	131725225	mm39_genes_exons	0.0000	0.0000	49.839
Pm20d1	chr1	131725225	mm39_genes_exons	0.0000	0.0000	49.839
Nfasc	chr1	132668823	mm39_genes_introns	0.0000	0.0481	20.820
Nfasc	chr1	132668823	mm39_genes_introns	0.0000	0.0481	20.820
	chr1	132668823	mm39_cpg_shores	0.0000	0.0481	20.820
	chr1	135075067	mm39_cpg_islands	0.0000	0.0102	-27.499
Arl8a	chr1	135075067	mm39_genes_introns	0.0000	0.0102	-27.499
	chr1	135614542	mm39_genes_intergenic	0.0000	0.0184	25.673
	chr1	135614542	mm39_cpg_shores	0.0000	0.0184	25.673
Lhx9	chr1	138775142	mm39_genes_1to5kb	0.0000	0.0005	-39.828
Lhx9	chr1	138775142	mm39_genes_1to5kb	0.0000	0.0005	-39.828
Lhx9	chr1	138775142	mm39_genes_intronexonboundaries	0.0000	0.0005	-39.828
	chr1	138775142	mm39_cpg_islands	0.0000	0.0005	-39.828
Lhx9	chr1	138775142	mm39_genes_introns	0.0000	0.0005	-39.828
Lhx9	chr1	138775142	mm39_genes_exonintronboundaries	0.0000	0.0005	-39.828
Lhx9	chr1	138775142	mm39_genes_intronexonboundaries	0.0000	0.0005	-39.828
	chr1	151220761	mm39_cpg_islands	0.0000	0.0000	18.396
Ivns1abp	chr1	151220761	mm39_genes_introns	0.0000	0.0000	18.396
Ivns1abp	chr1	151220761	mm39_genes_introns	0.0000	0.0000	18.396
Ivns1abp	chr1	151220761	mm39_genes_introns	0.0000	0.0000	18.396
Ivns1abp	chr1	151220761	mm39_genes_introns	0.0000	0.0000	18.396
Ivns1abp	chr1	151220761	mm39_genes_introns	0.0000	0.0000	18.396
Edem3	chr1	151631091	mm39_genes_promoters	0.0000	0.0000	24.650
Edem3	chr1	151631091	mm39_genes_promoters	0.0000	0.0000	24.650
Edem3	chr1	151631091	mm39_genes_promoters	0.0000	0.0000	24.650
2810414N06Rik	chr1	151631091	mm39_genes_promoters	0.0000	0.0000	24.650
2810414N06Rik	chr1	151631091	mm39_genes_promoters	0.0000	0.0000	24.650
2810414N06Rik	chr1	151631091	mm39_genes_promoters	0.0000	0.0000	24.650
	chr1	151631091	mm39_cpg_islands	0.0000	0.0000	24.650
	chr1	152642816	mm39_cpg_islands	0.0000	0.0000	17.608
Rgl1	chr1	152642816	mm39_genes_promoters	0.0000	0.0000	17.608
Rgl1	chr1	152642816	mm39_genes_promoters	0.0000	0.0000	17.608
Rgl1	chr1	152642816	mm39_genes_promoters	0.0000	0.0000	17.608
Arpc5	chr1	152642816	mm39_genes_exonintronboundaries	0.0000	0.0000	17.608
Arpc5	chr1	152642816	mm39_genes_introns	0.0000	0.0000	17.608
	chr1	155618269	mm39_cpg_islands	0.0000	0.0011	31.633
Lhx4	chr1	155618269	mm39_genes_promoters	0.0000	0.0011	31.633
	chr1	155688598	mm39_cpg_islands	0.0000	0.0026	-27.385
Qsox1	chr1	155688598	mm39_genes_exons	0.0000	0.0026	-27.385
Qsox1	chr1	155688598	mm39_genes_exons	0.0000	0.0026	-27.385
Qsox1	chr1	155688598	mm39_genes_intronexonboundaries	0.0000	0.0026	-27.385
Qsox1	chr1	155688598	mm39_genes_intronexonboundaries	0.0000	0.0026	-27.385
Qsox1	chr1	155688598	mm39_genes_5UTRs	0.0000	0.0026	-27.385
Qsox1	chr1	155688598	mm39_genes_5UTRs	0.0000	0.0026	-27.385
	chr1	159351793	mm39_cpg_inter	0.0000	0.0000	-35.775
Tnr	chr1	159351793	mm39_genes_exonintronboundaries	0.0000	0.0000	-35.775
Tnr	chr1	159351793	mm39_genes_introns	0.0000	0.0000	-35.775
Dnm3	chr1	162305266	mm39_genes_exonintronboundaries	0.0000	0.0002	-30.236
Dnm3	chr1	162305266	mm39_genes_exonintronboundaries	0.0000	0.0002	-30.236

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr1	162305266	mm39_cpg_islands	0.0000	0.0002	-30.236
Dnm3	chr1	162305266	mm39_genes_exons	0.0000	0.0002	-30.236
Dnm3	chr1	162305266	mm39_genes_exons	0.0000	0.0002	-30.236
Scyl3	chr1	163757518	mm39_genes_introns	0.0000	0.0000	-52.764
Scyl3	chr1	163757518	mm39_genes_5UTRs	0.0000	0.0000	-52.764
Scyl3	chr1	163757518	mm39_genes_5UTRs	0.0000	0.0000	-52.764
Scyl3	chr1	163757518	mm39_genes_5UTRs	0.0000	0.0000	-52.764
Scyl3	chr1	163757518	mm39_genes_exons	0.0000	0.0000	-52.764
Scyl3	chr1	163757518	mm39_genes_exons	0.0000	0.0000	-52.764
Scyl3	chr1	163757518	mm39_genes_exons	0.0000	0.0000	-52.764
	chr1	163757518	mm39_cpg_islands	0.0000	0.0000	-52.764
	chr1	169708136	mm39_cpg_inter	0.0000	0.0000	68.539
	chr1	169708136	mm39_genes_intergenic	0.0000	0.0000	68.539
	chr1	177703818	mm39_cpg_inter	0.0000	0.0010	92.308
Catspere1	chr1	177703818	mm39_genes_introns	0.0000	0.0010	92.308
	chr1	180468247	mm39_cpg_shores	0.0000	0.0005	-33.496
Lin9	chr1	180468247	mm39_genes_promoters	0.0000	0.0005	-33.496
Lin9	chr1	180468247	mm39_genes_promoters	0.0000	0.0005	-33.496
Hlx	chr1	184467416	mm39_genes_1to5kb	0.0000	0.0033	-73.585
	chr1	184467416	mm39_cpg_shelves	0.0000	0.0033	-73.585
C130074G19Rik	chr1	184614796	mm39_genes_introns	0.0000	0.0000	-41.900
C130074G19Rik	chr1	184614796	mm39_genes_exonintronboundaries	0.0000	0.0000	-41.900
	chr1	184614796	mm39_cpg_islands	0.0000	0.0000	-41.900
	chr1	189428529	mm39_cpg_inter	0.0000	0.0005	37.983
	chr1	189428529	mm39_genes_intergenic	0.0000	0.0005	37.983
	chr1	189669059	mm39_cpg_inter	0.0000	0.0375	-51.613
	chr1	189669059	mm39_genes_intergenic	0.0000	0.0375	-51.613
	chr1	191822470	mm39_cpg_islands	0.0000	0.0000	-57.634
Gm10516	chr1	191822470	mm39_genes_introns	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_intronexonboundaries	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_promoters	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_promoters	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_promoters	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_promoters	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_promoters	0.0000	0.0000	-57.634
Rcor3	chr1	191822470	mm39_genes_promoters	0.0000	0.0000	-57.634
	chr1	194610227	mm39_cpg_inter	0.0000	0.0000	-82.500
	chr1	194610227	mm39_genes_intergenic	0.0000	0.0000	-82.500
	chr10	5756082	mm39_cpg_islands	0.0000	0.0712	46.694
Fbxo5	chr10	5756082	mm39_genes_promoters	0.0000	0.0712	46.694
	chr10	34062754	mm39_cpg_inter	0.0000	0.0008	-31.298
Dse	chr10	34062754	mm39_genes_introns	0.0000	0.0008	-31.298
	chr10	39009829	mm39_cpg_shores	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_introns	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_introns	0.0000	0.0000	-78.571
Tube1	chr10	39009829	mm39_genes_promoters	0.0000	0.0000	-78.571

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exonintronboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_intronexonboundaries	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_5UTRs	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exons	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_5UTRs	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_5UTRs	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_5UTRs	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exons	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exons	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exons	0.0000	0.0000	-78.571
Fam229b	chr10	39009829	mm39_genes_exons	0.0000	0.0000	-78.571
	chr10	39245908	mm39_cpg_islands	0.0000	0.0000	-38.101
Gm31616	chr10	39245908	mm39_genes_promoters	0.0000	0.0000	-38.101
Gm31616	chr10	39245908	mm39_genes_promoters	0.0000	0.0000	-38.101
Fyn	chr10	39245908	mm39_genes_5UTRs	0.0000	0.0000	-38.101
Fyn	chr10	39245908	mm39_genes_5UTRs	0.0000	0.0000	-38.101
Fyn	chr10	39245908	mm39_genes_5UTRs	0.0000	0.0000	-38.101
Fyn	chr10	39245908	mm39_genes_exons	0.0000	0.0000	-38.101
Fyn	chr10	39245908	mm39_genes_exons	0.0000	0.0000	-38.101
Fyn	chr10	39245908	mm39_genes_exons	0.0000	0.0000	-38.101
	chr10	39488976	mm39_cpg_inter	0.0000	0.0590	-20.906
Gm16364	chr10	39488976	mm39_genes_introns	0.0000	0.0590	-20.906
Gm16364	chr10	39488976	mm39_genes_introns	0.0000	0.0590	-20.906
Traf3ip2	chr10	39488976	mm39_genes_5UTRs	0.0000	0.0590	-20.906
Traf3ip2	chr10	39488976	mm39_genes_exons	0.0000	0.0590	-20.906
Nr2e1	chr10	42458005	mm39_genes_introns	0.0000	0.0000	-56.988
Gm38491	chr10	42458005	mm39_genes_1to5kb	0.0000	0.0000	-56.988
	chr10	42458005	mm39_cpg_islands	0.0000	0.0000	-56.988
	chr10	46256385	mm39_cpg_inter	0.0000	0.0049	39.254
	chr10	46256385	mm39_genes_intergenic	0.0000	0.0049	39.254
Grik2	chr10	49659026	mm39_genes_introns	0.0000	0.0147	45.563
Grik2	chr10	49659026	mm39_genes_introns	0.0000	0.0147	45.563
Grik2	chr10	49659026	mm39_genes_introns	0.0000	0.0147	45.563
	chr10	49659026	mm39_cpg_shores	0.0000	0.0147	45.563
Lims1	chr10	58159239	mm39_genes_promoters	0.0000	0.0000	-67.233
Lims1	chr10	58159239	mm39_genes_promoters	0.0000	0.0000	-67.233
	chr10	58159239	mm39_cpg_islands	0.0000	0.0000	-67.233
Chst3	chr10	60054201	mm39_genes_introns	0.0000	0.0568	-46.552
	chr10	60054201	mm39_cpg_shores	0.0000	0.0568	-46.552

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr10	61020435	mm39_cpg_inter	0.0000	0.0135	-30.331
Tbata	chr10	61020435	mm39_genes_introns	0.0000	0.0135	-30.331
Tbata	chr10	61020435	mm39_genes_introns	0.0000	0.0135	-30.331
	chr10	61419330	mm39_cpg_inter	0.0000	0.0098	-44.172
	chr10	61419330	mm39_genes_intergenic	0.0000	0.0098	-44.172
Npffr1	chr10	61441794	mm39_genes_introns	0.0000	0.0002	51.781
	chr10	61441794	mm39_cpg_inter	0.0000	0.0002	51.781
	chr10	61801266	mm39_cpg_inter	0.0000	0.0619	-60.104
Col13a1	chr10	61801266	mm39_genes_introns	0.0000	0.0619	-60.104
Col13a1	chr10	61801266	mm39_genes_introns	0.0000	0.0619	-60.104
	chr10	62097568	mm39_cpg_inter	0.0000	0.0060	-33.104
Tacr2	chr10	62097568	mm39_genes_exonintronboundaries	0.0000	0.0060	-33.104
Tacr2	chr10	62097568	mm39_genes_introns	0.0000	0.0060	-33.104
	chr10	67373465	mm39_cpg_islands	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_introns	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_promoters	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_promoters	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_promoters	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_introns	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_5UTRs	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_exons	0.0000	0.0000	-31.610
Egr2	chr10	67373465	mm39_genes_exonintronboundaries	0.0000	0.0000	-31.610
	chr10	68700777	mm39_cpg_inter	0.0000	0.0782	-50.000
	chr10	68700777	mm39_genes_intergenic	0.0000	0.0782	-50.000
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
	chr10	69761312	mm39_cpg_inter	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_introns	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_promoters	0.0000	0.0793	23.775
Ank3	chr10	69761312	mm39_genes_promoters	0.0000	0.0793	23.775
	chr10	73692770	mm39_cpg_inter	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
Pcdh15	chr10	73692770	mm39_genes_introns	0.0000	0.0010	61.111
	chr10	73723717	mm39_cpg_inter	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Pcdh15	chr10	73723717	mm39_genes_introns	0.0000	0.0396	72.414
Rsph14	chr10	74803891	mm39_genes_introns	0.0000	0.0090	50.270
Rsph14	chr10	74803891	mm39_genes_introns	0.0000	0.0090	50.270
Rsph14	chr10	74803891	mm39_genes_introns	0.0000	0.0090	50.270
Rsph14	chr10	74803891	mm39_genes_introns	0.0000	0.0090	50.270
Gnaz	chr10	74803891	mm39_genes_introns	0.0000	0.0090	50.270
Gnaz	chr10	74803891	mm39_genes_introns	0.0000	0.0090	50.270
	chr10	74803891	mm39_cpg_shores	0.0000	0.0090	50.270
Gstt2	chr10	75669115	mm39_genes_introns	0.0000	0.0279	-55.319
	chr10	75669115	mm39_cpg_shelves	0.0000	0.0279	-55.319
Dip2a	chr10	76180656	mm39_genes_introns	0.0000	0.0000	-46.731
	chr10	76180656	mm39_cpg_islands	0.0000	0.0000	-46.731
	chr10	76484923	mm39_cpg_inter	0.0000	0.0563	-28.535
	chr10	76484923	mm39_genes_intergenic	0.0000	0.0563	-28.535
	chr10	78317833	mm39_genes_intergenic	0.0000	0.0000	-78.049
	chr10	78317833	mm39_cpg_islands	0.0000	0.0000	-78.049
Midn	chr10	79981264	mm39_genes_1to5kb	0.0000	0.0479	25.821
Midn	chr10	79981264	mm39_genes_1to5kb	0.0000	0.0479	25.821
Midn	chr10	79981264	mm39_genes_1to5kb	0.0000	0.0479	25.821
	chr10	79981264	mm39_cpg_shelves	0.0000	0.0479	25.821
Midn	chr10	79981264	mm39_genes_1to5kb	0.0000	0.0479	25.821
Atp5d	chr10	79981264	mm39_genes_exonintronboundaries	0.0000	0.0479	25.821
Atp5d	chr10	79981264	mm39_genes_intronexonboundaries	0.0000	0.0479	25.821
Atp5d	chr10	79981264	mm39_genes_intronexonboundaries	0.0000	0.0479	25.821
Atp5d	chr10	79981264	mm39_genes_exons	0.0000	0.0479	25.821
Atp5d	chr10	79981264	mm39_genes_exons	0.0000	0.0479	25.821
	chr10	80736296	mm39_cpg_islands	0.0000	0.0233	-64.846
Timm13	chr10	80736296	mm39_genes_introns	0.0000	0.0233	-64.846
Timm13	chr10	80736296	mm39_genes_exonintronboundaries	0.0000	0.0233	-64.846
Timm13	chr10	80736296	mm39_genes_intronexonboundaries	0.0000	0.0233	-64.846
Timm13	chr10	80736296	mm39_genes_exonintronboundaries	0.0000	0.0233	-64.846
Snord37	chr10	81013006	mm39_genes_1to5kb	0.0000	0.0000	-43.056
Eef2	chr10	81013006	mm39_genes_introns	0.0000	0.0000	-43.056
	chr10	81013006	mm39_cpg_shores	0.0000	0.0000	-43.056
Tjp3	chr10	81126777	mm39_genes_introns	0.0000	0.0558	24.825
Tjp3	chr10	81126777	mm39_genes_introns	0.0000	0.0558	24.825
Pip5k1c	chr10	81126777	mm39_genes_1to5kb	0.0000	0.0558	24.825
Pip5k1c	chr10	81126777	mm39_genes_1to5kb	0.0000	0.0558	24.825
Pip5k1c	chr10	81126777	mm39_genes_1to5kb	0.0000	0.0558	24.825

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Pip5k1c	chr10	81126777	mm39_genes_1to5kb	0.0000	0.0558	24.825
	chr10	81126777	mm39_cpg_shores	0.0000	0.0558	24.825
Tjp3	chr10	81126777	mm39_genes_exonintronboundaries	0.0000	0.0558	24.825
Ankrd24	chr10	81479317	mm39_genes_exons	0.0000	0.0002	-37.135
Ankrd24	chr10	81479317	mm39_genes_exons	0.0000	0.0002	-37.135
	chr10	81479317	mm39_cpg_islands	0.0000	0.0002	-37.135
Btbd11	chr10	85369290	mm39_genes_introns	0.0000	0.0796	-44.000
	chr10	85369290	mm39_cpg_inter	0.0000	0.0796	-44.000
Tmcc3	chr10	94408944	mm39_genes_introns	0.0000	0.0368	-52.174
Tmcc3	chr10	94408944	mm39_genes_introns	0.0000	0.0368	-52.174
	chr10	94408944	mm39_cpg_inter	0.0000	0.0368	-52.174
Tmcc3	chr10	94408944	mm39_genes_introns	0.0000	0.0368	-52.174
Tmcc3	chr10	94408944	mm39_genes_introns	0.0000	0.0368	-52.174
Tmcc3	chr10	94408944	mm39_genes_1to5kb	0.0000	0.0368	-52.174
Tmcc3	chr10	94408944	mm39_genes_1to5kb	0.0000	0.0368	-52.174
	chr10	109700722	mm39_cpg_inter	0.0000	0.0031	-65.195
Nav3	chr10	109700722	mm39_genes_introns	0.0000	0.0031	-65.195
Nav3	chr10	109700722	mm39_genes_introns	0.0000	0.0031	-65.195
	chr10	116984440	mm39_cpg_islands	0.0000	0.0003	-35.424
Frs2	chr10	116984440	mm39_genes_exonintronboundaries	0.0000	0.0003	-35.424
Frs2	chr10	116984440	mm39_genes_intronexonboundaries	0.0000	0.0003	-35.424
Frs2	chr10	116984440	mm39_genes_promoters	0.0000	0.0003	-35.424
	chr10	120712154	mm39_cpg_inter	0.0000	0.0325	73.913
Msrb3	chr10	120712154	mm39_genes_introns	0.0000	0.0325	73.913
Rassf3	chr10	121311609	mm39_genes_introns	0.0000	0.0000	-34.183
	chr10	121311609	mm39_cpg_islands	0.0000	0.0000	-34.183
Ppm1h	chr10	122516481	mm39_genes_introns	0.0000	0.0050	-60.124
Ppm1h	chr10	122516481	mm39_genes_introns	0.0000	0.0050	-60.124
	chr10	122516481	mm39_cpg_shores	0.0000	0.0050	-60.124
Shmt2	chr10	127362767	mm39_genes_1to5kb	0.0000	0.0000	23.170
Shmt2	chr10	127362767	mm39_genes_1to5kb	0.0000	0.0000	23.170
Nxph4	chr10	127362767	mm39_genes_exons	0.0000	0.0000	23.170
	chr10	127362767	mm39_cpg_islands	0.0000	0.0000	23.170
Nxph4	chr10	127362767	mm39_genes_intronexonboundaries	0.0000	0.0000	23.170
	chr11	3143429	mm39_cpg_islands	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exonintronboundaries	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exonintronboundaries	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exonintronboundaries	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exonintronboundaries	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_5UTRs	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_5UTRs	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_5UTRs	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exons	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exons	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exons	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_5UTRs	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_exons	0.0000	0.0000	-28.856
Sfi1	chr11	3143429	mm39_genes_intronexonboundaries	0.0000	0.0000	-28.856
	chr11	3143627	mm39_cpg_islands	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_5UTRs	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_5UTRs	0.0000	0.0000	71.569

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Sfi1	chr11	3143627	mm39_genes_5UTRs	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_exons	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_exons	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_exons	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_intronexonboundaries	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_intronexonboundaries	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_intronexonboundaries	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_intronexonboundaries	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_promoters	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_exonintronboundaries	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_exonintronboundaries	0.0000	0.0000	71.569
Sfi1	chr11	3143627	mm39_genes_exonintronboundaries	0.0000	0.0000	71.569
	chr11	3143637	mm39_cpg_islands	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_5UTRs	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_5UTRs	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_5UTRs	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_exons	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_exons	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_exons	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_intronexonboundaries	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_intronexonboundaries	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_intronexonboundaries	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_intronexonboundaries	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_promoters	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_exonintronboundaries	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_exonintronboundaries	0.0000	0.0000	73.317
Sfi1	chr11	3143637	mm39_genes_exonintronboundaries	0.0000	0.0000	73.317
	chr11	3143660	mm39_cpg_islands	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_5UTRs	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_5UTRs	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_5UTRs	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_exons	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_exons	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_exons	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_intronexonboundaries	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_intronexonboundaries	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_intronexonboundaries	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_intronexonboundaries	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_promoters	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_exonintronboundaries	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_exonintronboundaries	0.0000	0.0000	69.730
Sfi1	chr11	3143660	mm39_genes_exonintronboundaries	0.0000	0.0000	69.730
	chr11	3143672	mm39_cpg_islands	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_5UTRs	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_5UTRs	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_5UTRs	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_exons	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_exons	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_exons	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_intronexonboundaries	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_intronexonboundaries	0.0000	0.0005	63.967

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Sfi1	chr11	3143672	mm39_genes_intronexonboundaries	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_intronexonboundaries	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_promoters	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_exonintronboundaries	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_exonintronboundaries	0.0000	0.0005	63.967
Sfi1	chr11	3143672	mm39_genes_exonintronboundaries	0.0000	0.0005	63.967
	chr11	4393807	mm39_cpg_inter	0.0000	0.0882	-51.852
Hormad2	chr11	4393807	mm39_genes_1to5kb	0.0000	0.0882	-51.852
Ppp3r1	chr11	17109207	mm39_genes_promoters	0.0000	0.0000	-53.846
	chr11	17109207	mm39_cpg_islands	0.0000	0.0000	-53.846
	chr11	22957916	mm39_cpg_shores	0.0000	0.0482	84.615
Fam161a	chr11	22957916	mm39_genes_promoters	0.0000	0.0482	84.615
Fam161a	chr11	22957916	mm39_genes_promoters	0.0000	0.0482	84.615
Fam161a	chr11	22957916	mm39_genes_promoters	0.0000	0.0482	84.615
Gm8098	chr11	30213796	mm39_genes_1to5kb	0.0000	0.0105	-32.274
Gm8098	chr11	30213796	mm39_genes_1to5kb	0.0000	0.0105	-32.274
Gm8098	chr11	30213796	mm39_genes_1to5kb	0.0000	0.0105	-32.274
	chr11	30213796	mm39_cpg_shelves	0.0000	0.0105	-32.274
	chr11	49500701	mm39_cpg_islands	0.0000	0.0016	-34.737
Flt4	chr11	49500701	mm39_genes_exonintronboundaries	0.0000	0.0016	-34.737
Flt4	chr11	49500701	mm39_genes_introns	0.0000	0.0016	-34.737
	chr11	50493910	mm39_cpg_islands	0.0000	0.0515	-22.619
Adamts2	chr11	50493910	mm39_genes_introns	0.0000	0.0515	-22.619
Adamts2	chr11	50493910	mm39_genes_intronexonboundaries	0.0000	0.0515	-22.619
Vdac1	chr11	52251530	mm39_genes_promoters	0.0000	0.0000	30.696
	chr11	52251530	mm39_cpg_islands	0.0000	0.0000	30.696
Vdac1	chr11	52251530	mm39_genes_promoters	0.0000	0.0000	30.696
	chr11	53965516	mm39_cpg_inter	0.0000	0.0178	48.453
	chr11	53965516	mm39_genes_intergenic	0.0000	0.0178	48.453
Tnip1	chr11	54846804	mm39_genes_introns	0.0000	0.0002	-66.294
Tnip1	chr11	54846804	mm39_genes_introns	0.0000	0.0002	-66.294
Tnip1	chr11	54846804	mm39_genes_introns	0.0000	0.0002	-66.294
Tnip1	chr11	54846804	mm39_genes_introns	0.0000	0.0002	-66.294
Tnip1	chr11	54846804	mm39_genes_introns	0.0000	0.0002	-66.294
	chr11	54846804	mm39_cpg_islands	0.0000	0.0002	-66.294
Tnip1	chr11	54846804	mm39_genes_exonintronboundaries	0.0000	0.0002	-66.294
Mrpl22	chr11	58058987	mm39_genes_1to5kb	0.0000	0.0002	-26.910
Mrpl22	chr11	58058987	mm39_genes_1to5kb	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_introns	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_introns	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_introns	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_introns	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_introns	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_exonintronboundaries	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_exonintronboundaries	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_exonintronboundaries	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_exonintronboundaries	0.0000	0.0002	-26.910
Gemin5	chr11	58058987	mm39_genes_exonintronboundaries	0.0000	0.0002	-26.910
	chr11	58058987	mm39_cpg_islands	0.0000	0.0002	-26.910
Gjc2	chr11	59068074	mm39_genes_exons	0.0000	0.0000	-47.826
Gjc2	chr11	59068074	mm39_genes_exons	0.0000	0.0000	-47.826

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr11	59068074	mm39_cpg_islands	0.0000	0.0000	-47.826
	chr11	59855860	mm39_cpg_islands	0.0000	0.0000	-36.929
Rasd1	chr11	59855860	mm39_genes_intronexonboundaries	0.0000	0.0000	-36.929
Rasd1	chr11	59855860	mm39_genes_promoters	0.0000	0.0000	-36.929
	chr11	67081258	mm39_cpg_inter	0.0000	0.0488	29.825
Myh2	chr11	67081258	mm39_genes_intronexonboundaries	0.0000	0.0488	29.825
Myh2	chr11	67081258	mm39_genes_exonintronboundaries	0.0000	0.0488	29.825
Myh2	chr11	67081258	mm39_genes_exons	0.0000	0.0488	29.825
	chr11	69649558	mm39_cpg_islands	0.0000	0.0000	51.119
Polr2a	chr11	69649558	mm39_genes_intronexonboundaries	0.0000	0.0000	51.119
Polr2a	chr11	69649558	mm39_genes_promoters	0.0000	0.0000	51.119
Mir497b	chr11	70128843	mm39_genes_1to5kb	0.0000	0.0034	39.808
	chr11	70128843	mm39_cpg_islands	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_intronexonboundaries	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_intronexonboundaries	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_intronexonboundaries	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_intronexonboundaries	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_intronexonboundaries	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_intronexonboundaries	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_promoters	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_promoters	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_promoters	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_promoters	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_promoters	0.0000	0.0034	39.808
0610010K14Rik	chr11	70128843	mm39_genes_promoters	0.0000	0.0034	39.808
Itgae	chr11	73029102	mm39_genes_introns	0.0000	0.0000	-37.048
Itgae	chr11	73029102	mm39_genes_introns	0.0000	0.0000	-37.048
Haspin	chr11	73029102	mm39_genes_exons	0.0000	0.0000	-37.048
	chr11	73029102	mm39_cpg_islands	0.0000	0.0000	-37.048
Haspin	chr11	73029102	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.048
Itgae	chr11	73029102	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.048
Itgae	chr11	73029102	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.048
Haspin	chr11	73029102	mm39_genes_5UTRs	0.0000	0.0000	-37.048
Scarf1	chr11	75401354	mm39_genes_1to5kb	0.0000	0.0000	-37.314
Rilp	chr11	75401354	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.314
	chr11	75401354	mm39_cpg_islands	0.0000	0.0000	-37.314
Rilp	chr11	75401354	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.314
Rilp	chr11	75401354	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.314
Rilp	chr11	75401354	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.314
Rilp	chr11	75401354	mm39_genes_exons	0.0000	0.0000	-37.314
Myo1c	chr11	75542763	mm39_genes_introns	0.0000	0.0005	-28.538
Myo1c	chr11	75542763	mm39_genes_1to5kb	0.0000	0.0005	-28.538
Myo1c	chr11	75542763	mm39_genes_promoters	0.0000	0.0005	-28.538
	chr11	75542763	mm39_cpg_islands	0.0000	0.0005	-28.538
Myo1c	chr11	75542763	mm39_genes_introns	0.0000	0.0005	-28.538
Ankrd13b	chr11	77384966	mm39_genes_1to5kb	0.0000	0.0001	-30.632
Ankrd13b	chr11	77384966	mm39_genes_1to5kb	0.0000	0.0001	-30.632
Ankrd13b	chr11	77384966	mm39_genes_1to5kb	0.0000	0.0001	-30.632
Git1	chr11	77384966	mm39_genes_introns	0.0000	0.0001	-30.632
Git1	chr11	77384966	mm39_genes_introns	0.0000	0.0001	-30.632
	chr11	77384966	mm39_cpg_shores	0.0000	0.0001	-30.632

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Gm11190	chr11	77822183	mm39_genes_1to5kb	0.0000	0.0000	-51.477
	chr11	77822183	mm39_cpg_islands	0.0000	0.0000	-51.477
Sez6	chr11	77822183	mm39_genes_introns	0.0000	0.0000	-51.477
Sez6	chr11	77822183	mm39_genes_introns	0.0000	0.0000	-51.477
Ccnq	chr11	78642332	mm39_genes_exons	0.0000	0.0005	62.292
	chr11	78642332	mm39_cpg_islands	0.0000	0.0005	62.292
Ccnq	chr11	78642338	mm39_genes_exons	0.0000	0.0001	63.636
	chr11	78642338	mm39_cpg_islands	0.0000	0.0001	63.636
Wsb1	chr11	79144908	mm39_genes_introns	0.0000	0.0000	-50.980
	chr11	79144908	mm39_cpg_islands	0.0000	0.0000	-50.980
Suz12	chr11	79888443	mm39_genes_introns	0.0000	0.0001	49.761
Suz12	chr11	79888443	mm39_genes_introns	0.0000	0.0001	49.761
	chr11	79888443	mm39_cpg_shelves	0.0000	0.0001	49.761
Crlf3	chr11	79971756	mm39_genes_exonintronboundaries	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_exonintronboundaries	0.0000	0.0033	-29.413
	chr11	79971756	mm39_cpg_islands	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_exons	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_exons	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_intronexonboundaries	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_intronexonboundaries	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_5UTRs	0.0000	0.0033	-29.413
Crlf3	chr11	79971756	mm39_genes_5UTRs	0.0000	0.0033	-29.413
	chr11	80193613	mm39_cpg_shores	0.0000	0.0000	-86.408
Rhbdl3	chr11	80193613	mm39_genes_intronexonboundaries	0.0000	0.0000	-86.408
Rhbdl3	chr11	80193613	mm39_genes_exonintronboundaries	0.0000	0.0000	-86.408
Rhbdl3	chr11	80193613	mm39_genes_introns	0.0000	0.0000	-86.408
	chr11	82454967	mm39_cpg_inter	0.0000	0.0513	59.259
	chr11	82454967	mm39_genes_intergenic	0.0000	0.0513	59.259
Lig3	chr11	82671892	mm39_genes_promoters	0.0000	0.0112	27.712
Lig3	chr11	82671892	mm39_genes_promoters	0.0000	0.0112	27.712
Lig3	chr11	82671892	mm39_genes_promoters	0.0000	0.0112	27.712
Lig3	chr11	82671892	mm39_genes_promoters	0.0000	0.0112	27.712
Gm11423	chr11	82671892	mm39_genes_intronexonboundaries	0.0000	0.0112	27.712
Gm11423	chr11	82671892	mm39_genes_intronexonboundaries	0.0000	0.0112	27.712
	chr11	82671892	mm39_cpg_islands	0.0000	0.0112	27.712
Gm11423	chr11	82671892	mm39_genes_promoters	0.0000	0.0112	27.712
Gm11423	chr11	82671892	mm39_genes_promoters	0.0000	0.0112	27.712
	chr11	82880659	mm39_cpg_inter	0.0000	0.0242	42.477
Mir7679	chr11	82880659	mm39_genes_1to5kb	0.0000	0.0242	42.477
Slfn9	chr11	82880659	mm39_genes_introns	0.0000	0.0242	42.477
	chr11	90555497	mm39_cpg_inter	0.0000	0.0709	-26.316
Tom1l1	chr11	90555497	mm39_genes_introns	0.0000	0.0709	-26.316
Tom1l1	chr11	90555497	mm39_genes_introns	0.0000	0.0709	-26.316
Tom1l1	chr11	90555497	mm39_genes_introns	0.0000	0.0709	-26.316
Tom1l1	chr11	90555497	mm39_genes_1to5kb	0.0000	0.0709	-26.316
Car10	chr11	92988484	mm39_genes_1to5kb	0.0000	0.0236	-32.308
	chr11	92988484	mm39_cpg_shores	0.0000	0.0236	-32.308
Car10	chr11	92988484	mm39_genes_promoters	0.0000	0.0236	-32.308
Car10	chr11	92988484	mm39_genes_promoters	0.0000	0.0236	-32.308
B4galnt2	chr11	95806360	mm39_genes_promoters	0.0000	0.0059	-30.248
	chr11	95806360	mm39_cpg_shores	0.0000	0.0059	-30.248

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr11	95984029	mm39_cpg_inter	0.0000	0.0160	-64.286
	chr11	95984029	mm39_genes_intergenic	0.0000	0.0160	-64.286
Gm11538	chr11	96090581	mm39_genes_1to5kb	0.0000	0.0000	-73.077
	chr11	96090581	mm39_cpg_shelves	0.0000	0.0000	-73.077
	chr11	96721147	mm39_cpg_islands	0.0000	0.0281	-26.032
Nfe2l1	chr11	96721147	mm39_genes_promoters	0.0000	0.0281	-26.032
Nfe2l1	chr11	96721147	mm39_genes_promoters	0.0000	0.0281	-26.032
Mllt6	chr11	97555036	mm39_genes_introns	0.0000	0.0000	-32.500
	chr11	97555036	mm39_cpg_shores	0.0000	0.0000	-32.500
	chr11	97886195	mm39_cpg_inter	0.0000	0.0000	-40.000
Arl5c	chr11	97886195	mm39_genes_introns	0.0000	0.0000	-40.000
Arl5c	chr11	97886195	mm39_genes_introns	0.0000	0.0000	-40.000
Cacnb1	chr11	97917953	mm39_genes_1to5kb	0.0000	0.0066	-22.509
Cacnb1	chr11	97917953	mm39_genes_1to5kb	0.0000	0.0066	-22.509
Cacnb1	chr11	97917953	mm39_genes_1to5kb	0.0000	0.0066	-22.509
Cacnb1	chr11	97917953	mm39_genes_1to5kb	0.0000	0.0066	-22.509
Cacnb1	chr11	97917953	mm39_genes_1to5kb	0.0000	0.0066	-22.509
	chr11	97917953	mm39_cpg_islands	0.0000	0.0066	-22.509
Rpl19	chr11	97917953	mm39_genes_introns	0.0000	0.0066	-22.509
Rpl19	chr11	97917953	mm39_genes_exonintronboundaries	0.0000	0.0066	-22.509
Rpl19	chr11	97917953	mm39_genes_introns	0.0000	0.0066	-22.509
	chr11	97965512	mm39_cpg_inter	0.0000	0.0135	-70.909
	chr11	97965512	mm39_genes_intergenic	0.0000	0.0135	-70.909
Hspb9	chr11	100602962	mm39_genes_1to5kb	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_intronexonboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_intronexonboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_intronexonboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_intronexonboundaries	0.0000	0.0000	-75.168
	chr11	100602962	mm39_cpg_shores	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exonintronboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exonintronboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exonintronboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exonintronboundaries	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exons	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exons	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exons	0.0000	0.0000	-75.168
Kat2a	chr11	100602962	mm39_genes_exons	0.0000	0.0000	-75.168
Stat5b	chr11	100741118	mm39_genes_introns	0.0000	0.0001	-34.015
	chr11	100741118	mm39_cpg_islands	0.0000	0.0001	-34.015
Stat5b	chr11	100741118	mm39_genes_exonintronboundaries	0.0000	0.0001	-34.015
	chr11	100972957	mm39_cpg_shores	0.0000	0.0000	76.271
Coasy	chr11	100972957	mm39_genes_promoters	0.0000	0.0000	76.271
Coasy	chr11	100972957	mm39_genes_promoters	0.0000	0.0000	76.271
	chr11	100986382	mm39_cpg_islands	0.0000	0.0000	39.000
Psmc3ip	chr11	100986382	mm39_genes_intronexonboundaries	0.0000	0.0000	39.000
Psmc3ip	chr11	100986382	mm39_genes_promoters	0.0000	0.0000	39.000
	chr11	101224675	mm39_cpg_inter	0.0000	0.0393	68.615
Aoc3	chr11	101224675	mm39_genes_introns	0.0000	0.0393	68.615
	chr11	101675224	mm39_cpg_shores	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_exonintronboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_exonintronboundaries	0.0000	0.0140	-19.161

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Etv4	chr11	101675224	mm39_genes_exonintronboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_intronexonboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_intronexonboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_intronexonboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_exonintronboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_exonintronboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_exonintronboundaries	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_introns	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_introns	0.0000	0.0140	-19.161
Etv4	chr11	101675224	mm39_genes_introns	0.0000	0.0140	-19.161
	chr11	101843178	mm39_cpg_inter	0.0000	0.0588	-46.831
4930417O22Rik	chr11	101843178	mm39_genes_promoters	0.0000	0.0588	-46.831
4930417O22Rik	chr11	101843178	mm39_genes_exonintronboundaries	0.0000	0.0588	-46.831
Mpp2	chr11	101979955	mm39_genes_promoters	0.0000	0.0961	-75.000
	chr11	101979955	mm39_cpg_shores	0.0000	0.0961	-75.000
	chr11	102550661	mm39_cpg_inter	0.0000	0.0000	51.794
	chr11	102550661	mm39_genes_intergenic	0.0000	0.0000	51.794
Fam187a	chr11	102771830	mm39_genes_1to5kb	0.0000	0.0493	10.703
Ccdc103	chr11	102771830	mm39_genes_promoters	0.0000	0.0493	10.703
Ccdc103	chr11	102771830	mm39_genes_promoters	0.0000	0.0493	10.703
Eftud2	chr11	102771830	mm39_genes_exonintronboundaries	0.0000	0.0493	10.703
Eftud2	chr11	102771830	mm39_genes_exonintronboundaries	0.0000	0.0493	10.703
	chr11	102771830	mm39_cpg_islands	0.0000	0.0493	10.703
Eftud2	chr11	102771830	mm39_genes_intronexonboundaries	0.0000	0.0493	10.703
Eftud2	chr11	102771830	mm39_genes_intronexonboundaries	0.0000	0.0493	10.703
Eftud2	chr11	102771830	mm39_genes_promoters	0.0000	0.0493	10.703
Eftud2	chr11	102771830	mm39_genes_promoters	0.0000	0.0493	10.703
Hexim1	chr11	103003090	mm39_genes_1to5kb	0.0000	0.0206	-46.071
Acbd4	chr11	103003090	mm39_genes_exonintronboundaries	0.0000	0.0206	-46.071
	chr11	103003090	mm39_cpg_shelves	0.0000	0.0206	-46.071
	chr11	103062061	mm39_cpg_islands	0.0000	0.0000	-75.179
Fmnl1	chr11	103062061	mm39_genes_exons	0.0000	0.0000	-75.179
Fmnl1	chr11	103062061	mm39_genes_exons	0.0000	0.0000	-75.179
Fmnl1	chr11	103062061	mm39_genes_5UTRs	0.0000	0.0000	-75.179
Fmnl1	chr11	103062061	mm39_genes_5UTRs	0.0000	0.0000	-75.179
Arhgap27	chr11	103251112	mm39_genes_exons	0.0000	0.0000	-80.476
Arhgap27	chr11	103251112	mm39_genes_exonintronboundaries	0.0000	0.0000	-80.476
	chr11	103251112	mm39_cpg_islands	0.0000	0.0000	-80.476
Arhgap27	chr11	103251112	mm39_genes_exons	0.0000	0.0000	-80.476
Arhgap27	chr11	103251113	mm39_genes_exons	0.0000	0.0377	15.385
Arhgap27	chr11	103251113	mm39_genes_exonintronboundaries	0.0000	0.0377	15.385
	chr11	103251113	mm39_cpg_islands	0.0000	0.0377	15.385
Arhgap27	chr11	103251113	mm39_genes_exons	0.0000	0.0377	15.385
Arhgap27	chr11	103251158	mm39_genes_exons	0.0000	0.0000	20.010
Arhgap27	chr11	103251158	mm39_genes_exonintronboundaries	0.0000	0.0000	20.010
	chr11	103251158	mm39_cpg_islands	0.0000	0.0000	20.010
Arhgap27	chr11	103251158	mm39_genes_exons	0.0000	0.0000	20.010
	chr11	103253604	mm39_cpg_shores	0.0000	0.0000	-54.500
Arhgap27	chr11	103253604	mm39_genes_introns	0.0000	0.0000	-54.500
Arhgap27	chr11	103253604	mm39_genes_introns	0.0000	0.0000	-54.500
	chr11	105858389	mm39_cpg_shores	0.0000	0.0623	25.952

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Gm11651	chr11	105858389	mm39_genes_introns	0.0000	0.0623	25.952
Ace	chr11	105858389	mm39_genes_promoters	0.0000	0.0623	25.952
Ace	chr11	105858389	mm39_genes_promoters	0.0000	0.0623	25.952
	chr11	107580086	mm39_cpg_inter	0.0000	0.0886	-19.310
Helz	chr11	107580086	mm39_genes_exons	0.0000	0.0886	-19.310
Helz	chr11	107580086	mm39_genes_exons	0.0000	0.0886	-19.310
Helz	chr11	107580086	mm39_genes_3UTRs	0.0000	0.0886	-19.310
Helz	chr11	107580086	mm39_genes_3UTRs	0.0000	0.0886	-19.310
	chr11	108234797	mm39_cpg_islands	0.0000	0.0000	-56.000
Prkca	chr11	108234797	mm39_genes_intronexonboundaries	0.0000	0.0000	-56.000
Prkca	chr11	108234797	mm39_genes_promoters	0.0000	0.0000	-56.000
	chr11	113689941	mm39_cpg_inter	0.0000	0.0683	-42.424
Sdk2	chr11	113689941	mm39_genes_introns	0.0000	0.0683	-42.424
Slc9a3r1	chr11	115055401	mm39_genes_introns	0.0000	0.0000	-44.773
	chr11	115055401	mm39_cpg_shores	0.0000	0.0000	-44.773
Slc9a3r1	chr11	115055446	mm39_genes_introns	0.0000	0.1000	-14.817
	chr11	115055446	mm39_cpg_shores	0.0000	0.1000	-14.817
	chr11	115213858	mm39_cpg_shores	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_intronexonboundaries	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_intronexonboundaries	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_exonintronboundaries	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_exonintronboundaries	0.0000	0.0959	23.188
Ush1g	chr11	115213858	mm39_genes_1to5kb	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_5UTRs	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_exons	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_5UTRs	0.0000	0.0959	23.188
Otop2	chr11	115213858	mm39_genes_exons	0.0000	0.0959	23.188
	chr11	115311268	mm39_cpg_islands	0.0000	0.0000	-50.419
Atp5h	chr11	115311268	mm39_genes_promoters	0.0000	0.0000	-50.419
Kctd2	chr11	115311268	mm39_genes_exons	0.0000	0.0000	-50.419
Kctd2	chr11	115311268	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.419
Nt5c	chr11	115382623	mm39_genes_exonintronboundaries	0.0000	0.0053	-24.845
Gm11694	chr11	115382623	mm39_genes_exons	0.0000	0.0053	-24.845
	chr11	115382623	mm39_cpg_islands	0.0000	0.0053	-24.845
Nt5c	chr11	115382623	mm39_genes_exons	0.0000	0.0053	-24.845
Nt5c	chr11	115382623	mm39_genes_intronexonboundaries	0.0000	0.0053	-24.845
Nt5c	chr11	115382623	mm39_genes_5UTRs	0.0000	0.0053	-24.845
Galk1	chr11	115903242	mm39_genes_introns	0.0000	0.0018	16.857
Galk1	chr11	115903242	mm39_genes_exonintronboundaries	0.0000	0.0018	16.857
	chr11	115903242	mm39_cpg_islands	0.0000	0.0018	16.857
	chr11	118979590	mm39_cpg_shores	0.0000	0.0003	-33.187
Cbx4	chr11	118979590	mm39_genes_1to5kb	0.0000	0.0003	-33.187
	chr11	118996542	mm39_genes_intergenic	0.0000	0.0003	-56.253
	chr11	118996542	mm39_cpg_inter	0.0000	0.0003	-56.253
	chr11	119144358	mm39_cpg_inter	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_promoters	0.0000	0.0000	-85.938
Ccdc40	chr11	119144358	mm39_genes_exonintronboundaries	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_intronexonboundaries	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_intronexonboundaries	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_intronexonboundaries	0.0000	0.0000	-85.938
Ccdc40	chr11	119144358	mm39_genes_intronexonboundaries	0.0000	0.0000	-85.938

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Ccdc40	chr11	119144358	mm39_genes_introns	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_promoters	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_promoters	0.0000	0.0000	-85.938
Gm35932	chr11	119144358	mm39_genes_promoters	0.0000	0.0000	-85.938
Ccdc40	chr11	119144358	mm39_genes_exonintronboundaries	0.0000	0.0000	-85.938
2900052L18Rik	chr11	120125415	mm39_genes_1to5kb	0.0000	0.0000	-92.429
Bahcc1	chr11	120125415	mm39_genes_introns	0.0000	0.0000	-92.429
	chr11	120125415	mm39_cpg_islands	0.0000	0.0000	-92.429
	chr11	120264920	mm39_cpg_inter	0.0000	0.0638	58.333
Faap100	chr11	120264920	mm39_genes_exons	0.0000	0.0638	58.333
Gm17586	chr11	120523496	mm39_genes_1to5kb	0.0000	0.0242	-26.956
Mafg	chr11	120523496	mm39_genes_introns	0.0000	0.0242	-26.956
	chr11	120523496	mm39_cpg_islands	0.0000	0.0242	-26.956
	chr11	121245184	mm39_cpg_islands	0.0000	0.0009	20.632
Wdr45b	chr11	121245184	mm39_genes_exonintronboundaries	0.0000	0.0009	20.632
Wdr45b	chr11	121245184	mm39_genes_exons	0.0000	0.0009	20.632
Wdr45b	chr11	121245184	mm39_genes_intronexonboundaries	0.0000	0.0009	20.632
Wdr45b	chr11	121245184	mm39_genes_5UTRs	0.0000	0.0009	20.632
	chr11	121245212	mm39_cpg_islands	0.0000	0.0180	32.034
Wdr45b	chr11	121245212	mm39_genes_exonintronboundaries	0.0000	0.0180	32.034
Wdr45b	chr11	121245212	mm39_genes_exons	0.0000	0.0180	32.034
Wdr45b	chr11	121245212	mm39_genes_intronexonboundaries	0.0000	0.0180	32.034
Wdr45b	chr11	121245212	mm39_genes_5UTRs	0.0000	0.0180	32.034
	chr11	121325663	mm39_cpg_inter	0.0000	0.0534	-62.500
Fn3k	chr11	121325663	mm39_genes_promoters	0.0000	0.0534	-62.500
Fn3k	chr11	121325663	mm39_genes_promoters	0.0000	0.0534	-62.500
Hpcal1	chr12	17778242	mm39_genes_introns	0.0000	0.0560	-52.552
Hpcal1	chr12	17778242	mm39_genes_introns	0.0000	0.0560	-52.552
	chr12	17778242	mm39_cpg_inter	0.0000	0.0560	-52.552
	chr12	18135254	mm39_genes_intergenic	0.0000	0.0513	-79.808
	chr12	18135254	mm39_cpg_inter	0.0000	0.0513	-79.808
	chr12	20339191	mm39_genes_intergenic	0.0000	0.0399	-46.065
	chr12	20339191	mm39_cpg_inter	0.0000	0.0399	-46.065
	chr12	22149754	mm39_genes_intergenic	0.0000	0.0000	36.082
	chr12	22149754	mm39_cpg_inter	0.0000	0.0000	36.082
	chr12	23308753	mm39_genes_intergenic	0.0000	0.0002	35.135
	chr12	23308753	mm39_cpg_inter	0.0000	0.0002	35.135
	chr12	31549611	mm39_cpg_islands	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_exonintronboundaries	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_exonintronboundaries	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_exonintronboundaries	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_intronexonboundaries	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_intronexonboundaries	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_intronexonboundaries	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_exons	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_exons	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_exons	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_5UTRs	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_5UTRs	0.0000	0.0024	-32.514
Cbll1	chr12	31549611	mm39_genes_5UTRs	0.0000	0.0024	-32.514
	chr12	37159246	mm39_cpg_inter	0.0000	0.0000	81.034

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Gm29007	chr12	37159246	mm39_genes_1to5kb	0.0000	0.0000	81.034
Gm29007	chr12	37159246	mm39_genes_1to5kb	0.0000	0.0000	81.034
Meox2	chr12	37159246	mm39_genes_exons	0.0000	0.0000	81.034
Meox2	chr12	37159246	mm39_genes_exonintronboundaries	0.0000	0.0000	81.034
Nrcam	chr12	44376919	mm39_genes_introns	0.0000	0.0000	-50.369
Nrcam	chr12	44376919	mm39_genes_introns	0.0000	0.0000	-50.369
	chr12	44376919	mm39_cpg_shores	0.0000	0.0000	-50.369
Foxg1	chr12	49427276	mm39_genes_1to5kb	0.0000	0.0001	42.424
Foxg1	chr12	49427276	mm39_genes_1to5kb	0.0000	0.0001	42.424
	chr12	49427276	mm39_cpg_shelves	0.0000	0.0001	42.424
	chr12	51534606	mm39_cpg_inter	0.0000	0.0005	26.555
	chr12	51534606	mm39_genes_intergenic	0.0000	0.0005	26.555
Nfkbia	chr12	55539808	mm39_genes_promoters	0.0000	0.0000	-79.296
	chr12	55539808	mm39_cpg_shores	0.0000	0.0000	-79.296
9330151L19Rik	chr12	69243786	mm39_genes_promoters	0.0000	0.0000	-45.592
Dnaaf2	chr12	69243786	mm39_genes_exons	0.0000	0.0000	-45.592
	chr12	69243786	mm39_cpg_islands	0.0000	0.0000	-45.592
	chr12	71962754	mm39_cpg_inter	0.0000	0.0081	-32.918
Daam1	chr12	71962754	mm39_genes_exonintronboundaries	0.0000	0.0081	-32.918
Daam1	chr12	71962754	mm39_genes_exonintronboundaries	0.0000	0.0081	-32.918
Daam1	chr12	71962754	mm39_genes_exonintronboundaries	0.0000	0.0081	-32.918
Daam1	chr12	71962754	mm39_genes_introns	0.0000	0.0081	-32.918
Daam1	chr12	71962754	mm39_genes_introns	0.0000	0.0081	-32.918
Daam1	chr12	71962754	mm39_genes_introns	0.0000	0.0081	-32.918
L3hypdh	chr12	72131746	mm39_genes_exons	0.0000	0.0933	-17.984
	chr12	72131746	mm39_cpg_islands	0.0000	0.0933	-17.984
Jkamp	chr12	72131746	mm39_genes_promoters	0.0000	0.0933	-17.984
Jkamp	chr12	72131746	mm39_genes_promoters	0.0000	0.0933	-17.984
	chr12	73085481	mm39_genes_intergenic	0.0000	0.0433	13.924
	chr12	73085481	mm39_cpg_shelves	0.0000	0.0433	13.924
Six4	chr12	73157570	mm39_genes_introns	0.0000	0.0000	-34.118
Six4	chr12	73157570	mm39_genes_introns	0.0000	0.0000	-34.118
	chr12	73157570	mm39_cpg_shores	0.0000	0.0000	-34.118
	chr12	78751692	mm39_cpg_inter	0.0000	0.0264	-58.658
Garin2	chr12	78751692	mm39_genes_introns	0.0000	0.0264	-58.658
Garin2	chr12	78751692	mm39_genes_introns	0.0000	0.0264	-58.658
	chr12	79343007	mm39_cpg_inter	0.0000	0.0008	-29.514
Rad51b	chr12	79343007	mm39_genes_1to5kb	0.0000	0.0008	-29.514
Rad51b	chr12	79343007	mm39_genes_1to5kb	0.0000	0.0008	-29.514
Zfyve26	chr12	79343007	mm39_genes_exonintronboundaries	0.0000	0.0008	-29.514
Zfyve26	chr12	79343007	mm39_genes_intronexonboundaries	0.0000	0.0008	-29.514
Zfyve26	chr12	79343007	mm39_genes_5UTRs	0.0000	0.0008	-29.514
Zfyve26	chr12	79343007	mm39_genes_exons	0.0000	0.0008	-29.514
	chr12	82539491	mm39_cpg_inter	0.0000	0.0138	75.000
	chr12	82539491	mm39_genes_intergenic	0.0000	0.0138	75.000
	chr12	84161167	mm39_cpg_inter	0.0000	0.0018	38.929
Dnal1	chr12	84161167	mm39_genes_exonintronboundaries	0.0000	0.0018	38.929
Dnal1	chr12	84161167	mm39_genes_exonintronboundaries	0.0000	0.0018	38.929
Dnal1	chr12	84161167	mm39_genes_5UTRs	0.0000	0.0018	38.929
Dnal1	chr12	84161167	mm39_genes_exons	0.0000	0.0018	38.929
Dnal1	chr12	84161167	mm39_genes_exons	0.0000	0.0018	38.929

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Dnal1	chr12	84161167	mm39_genes_5UTRs	0.0000	0.0018	38.929
	chr12	84804905	mm39_cpg_inter	0.0000	0.0000	-84.444
Npc2	chr12	84804905	mm39_genes_introns	0.0000	0.0000	-84.444
Esrrb	chr12	86468862	mm39_genes_introns	0.0000	0.0000	-47.826
	chr12	86468862	mm39_cpg_islands	0.0000	0.0000	-47.826
Esrrb	chr12	86468862	mm39_genes_exonintronboundaries	0.0000	0.0000	-47.826
Esrrb	chr12	86468862	mm39_genes_introns	0.0000	0.0000	-47.826
	chr12	95658851	mm39_cpg_shelves	0.0000	0.0000	39.091
Flrt2	chr12	95658851	mm39_genes_promoters	0.0000	0.0000	39.091
	chr12	95658896	mm39_cpg_shelves	0.0000	0.0000	36.341
Flrt2	chr12	95658896	mm39_genes_promoters	0.0000	0.0000	36.341
Flrt2	chr12	95661024	mm39_genes_introns	0.0000	0.0000	-71.045
	chr12	95661024	mm39_cpg_shores	0.0000	0.0000	-71.045
Golga5	chr12	102435890	mm39_genes_promoters	0.0000	0.0778	-22.486
Golga5	chr12	102435890	mm39_genes_introns	0.0000	0.0778	-22.486
	chr12	102435890	mm39_cpg_shores	0.0000	0.0778	-22.486
Tmem251	chr12	102709994	mm39_genes_promoters	0.0000	0.0000	-58.195
Moap1	chr12	102709994	mm39_genes_exonintronboundaries	0.0000	0.0000	-58.195
	chr12	102709994	mm39_cpg_islands	0.0000	0.0000	-58.195
Gm20604	chr12	102709994	mm39_genes_introns	0.0000	0.0000	-58.195
Moap1	chr12	102709994	mm39_genes_intronexonboundaries	0.0000	0.0000	-58.195
Moap1	chr12	102709994	mm39_genes_intronexonboundaries	0.0000	0.0000	-58.195
Tmem251	chr12	102709994	mm39_genes_exonintronboundaries	0.0000	0.0000	-58.195
Moap1	chr12	102709994	mm39_genes_promoters	0.0000	0.0000	-58.195
Moap1	chr12	102709994	mm39_genes_promoters	0.0000	0.0000	-58.195
Tmem251	chr12	102709994	mm39_genes_5UTRs	0.0000	0.0000	-58.195
Tmem251	chr12	102709994	mm39_genes_exons	0.0000	0.0000	-58.195
Ubr7	chr12	102723816	mm39_genes_promoters	0.0000	0.0000	-40.219
	chr12	102723816	mm39_cpg_islands	0.0000	0.0000	-40.219
Gm20604	chr12	102723816	mm39_genes_exonintronboundaries	0.0000	0.0000	-40.219
Gon7	chr12	102723816	mm39_genes_exonintronboundaries	0.0000	0.0000	-40.219
Gm20604	chr12	102723816	mm39_genes_exons	0.0000	0.0000	-40.219
Gon7	chr12	102723816	mm39_genes_exons	0.0000	0.0000	-40.219
	chr12	110365030	mm39_genes_intergenic	0.0000	0.0005	-71.429
	chr12	110365030	mm39_cpg_inter	0.0000	0.0005	-71.429
	chr12	112586275	mm39_cpg_shores	0.0000	0.0000	-80.653
Adssl1	chr12	112586275	mm39_genes_promoters	0.0000	0.0000	-80.653
	chr12	112892946	mm39_cpg_islands	0.0000	0.0000	-37.159
Jag2	chr12	112892946	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.159
Jag2	chr12	112892946	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.159
Jag2	chr12	112892946	mm39_genes_introns	0.0000	0.0000	-37.159
Jag2	chr12	112892946	mm39_genes_intronexonboundaries	0.0000	0.0000	-37.159
	chr13	4954741	mm39_cpg_inter	0.0000	0.0023	-43.396
	chr13	4954741	mm39_genes_intergenic	0.0000	0.0023	-43.396
	chr13	14946033	mm39_cpg_inter	0.0000	0.0159	18.349
	chr13	14946033	mm39_genes_intergenic	0.0000	0.0159	18.349
	chr13	14946067	mm39_cpg_inter	0.0000	0.0039	21.101
	chr13	14946067	mm39_genes_intergenic	0.0000	0.0039	21.101
	chr13	22179850	mm39_cpg_inter	0.0000	0.0006	71.698
	chr13	22179850	mm39_genes_intergenic	0.0000	0.0006	71.698
	chr13	23595945	mm39_genes_intergenic	0.0000	0.0111	-11.082

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr13	23595945	mm39_cpg_inter	0.0000	0.0111	-11.082
	chr13	23630092	mm39_genes_intergenic	0.0000	0.0000	-43.100
	chr13	23630092	mm39_cpg_islands	0.0000	0.0000	-43.100
Aldh5a1	chr13	25121206	mm39_genes_introns	0.0000	0.0999	28.595
9330162012Rik	chr13	25121206	mm39_genes_promoters	0.0000	0.0999	28.595
Aldh5a1	chr13	25121206	mm39_genes_exonintronboundaries	0.0000	0.0999	28.595
	chr13	25121206	mm39_cpg_islands	0.0000	0.0999	28.595
Psmg4	chr13	34347515	mm39_genes_introns	0.0000	0.0406	-68.788
Psmg4	chr13	34347515	mm39_genes_introns	0.0000	0.0406	-68.788
	chr13	34347515	mm39_cpg_shores	0.0000	0.0406	-68.788
Pxdc1	chr13	34835568	mm39_genes_introns	0.0000	0.0000	-50.794
Pxdc1	chr13	34835568	mm39_genes_introns	0.0000	0.0000	-50.794
Pxdc1	chr13	34835568	mm39_genes_introns	0.0000	0.0000	-50.794
Pxdc1	chr13	34835568	mm39_genes_introns	0.0000	0.0000	-50.794
Gm15908	chr13	34835568	mm39_genes_1to5kb	0.0000	0.0000	-50.794
	chr13	34835568	mm39_cpg_shores	0.0000	0.0000	-50.794
Gfod1	chr13	43409629	mm39_genes_introns	0.0000	0.0121	74.126
	chr13	43409629	mm39_cpg_inter	0.0000	0.0121	74.126
	chr13	45023108	mm39_cpg_inter	0.0000	0.0034	-16.607
Jarid2	chr13	45023108	mm39_genes_introns	0.0000	0.0034	-16.607
Jarid2	chr13	45023108	mm39_genes_introns	0.0000	0.0034	-16.607
Jarid2	chr13	45023108	mm39_genes_introns	0.0000	0.0034	-16.607
Jarid2	chr13	45023108	mm39_genes_introns	0.0000	0.0034	-16.607
	chr13	45023111	mm39_cpg_inter	0.0000	0.0949	-14.208
Jarid2	chr13	45023111	mm39_genes_introns	0.0000	0.0949	-14.208
Jarid2	chr13	45023111	mm39_genes_introns	0.0000	0.0949	-14.208
Jarid2	chr13	45023111	mm39_genes_introns	0.0000	0.0949	-14.208
Jarid2	chr13	45023111	mm39_genes_introns	0.0000	0.0949	-14.208
	chr13	45023125	mm39_cpg_inter	0.0000	0.0435	-14.599
Jarid2	chr13	45023125	mm39_genes_introns	0.0000	0.0435	-14.599
Jarid2	chr13	45023125	mm39_genes_introns	0.0000	0.0435	-14.599
Jarid2	chr13	45023125	mm39_genes_introns	0.0000	0.0435	-14.599
Jarid2	chr13	45023125	mm39_genes_introns	0.0000	0.0435	-14.599
	chr13	45023130	mm39_cpg_inter	0.0000	0.0062	-16.320
Jarid2	chr13	45023130	mm39_genes_introns	0.0000	0.0062	-16.320
Jarid2	chr13	45023130	mm39_genes_introns	0.0000	0.0062	-16.320
Jarid2	chr13	45023130	mm39_genes_introns	0.0000	0.0062	-16.320
Jarid2	chr13	45023130	mm39_genes_introns	0.0000	0.0062	-16.320
	chr13	45023167	mm39_cpg_inter	0.0000	0.0000	-61.814
Jarid2	chr13	45023167	mm39_genes_introns	0.0000	0.0000	-61.814
Jarid2	chr13	45023167	mm39_genes_introns	0.0000	0.0000	-61.814
Jarid2	chr13	45023167	mm39_genes_introns	0.0000	0.0000	-61.814
Jarid2	chr13	45023167	mm39_genes_introns	0.0000	0.0000	-61.814
	chr13	45023176	mm39_cpg_inter	0.0000	0.0000	-65.544
Jarid2	chr13	45023176	mm39_genes_introns	0.0000	0.0000	-65.544
Jarid2	chr13	45023176	mm39_genes_introns	0.0000	0.0000	-65.544
Jarid2	chr13	45023176	mm39_genes_introns	0.0000	0.0000	-65.544
Jarid2	chr13	45023176	mm39_genes_introns	0.0000	0.0000	-65.544
	chr13	47259892	mm39_cpg_islands	0.0000	0.0000	-69.767
Dek	chr13	47259892	mm39_genes_intronexonboundaries	0.0000	0.0000	-69.767
Dek	chr13	47259892	mm39_genes_promoters	0.0000	0.0000	-69.767

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr13	49473484	mm39_cpg_inter	0.0000	0.0001	15.928
	chr13	49473484	mm39_genes_intergenic	0.0000	0.0001	15.928
	chr13	51562905	mm39_cpg_islands	0.0000	0.0000	-82.456
S1pr3	chr13	51562905	mm39_genes_5UTRs	0.0000	0.0000	-82.456
S1pr3	chr13	51562905	mm39_genes_exons	0.0000	0.0000	-82.456
S1pr3	chr13	51562905	mm39_genes_exonintronboundaries	0.0000	0.0000	-82.456
Gadd45g	chr13	51999699	mm39_genes_1to5kb	0.0000	0.0166	-21.456
	chr13	51999699	mm39_cpg_islands	0.0000	0.0166	-21.456
Syk	chr13	52736919	mm39_genes_promoters	0.0000	0.0053	24.247
	chr13	52736919	mm39_cpg_islands	0.0000	0.0053	24.247
Nfil3	chr13	53134508	mm39_genes_introns	0.0000	0.0000	46.934
	chr13	53134508	mm39_cpg_islands	0.0000	0.0000	46.934
	chr13	54972032	mm39_cpg_inter	0.0000	0.0001	-41.206
	chr13	54972032	mm39_genes_intergenic	0.0000	0.0001	-41.206
	chr13	55683977	mm39_cpg_shores	0.0000	0.0000	-41.643
Ddx41	chr13	55683977	mm39_genes_intronexonboundaries	0.0000	0.0000	-41.643
Ddx41	chr13	55683977	mm39_genes_introns	0.0000	0.0000	-41.643
Ddx41	chr13	55683977	mm39_genes_exonintronboundaries	0.0000	0.0000	-41.643
	chr13	55985109	mm39_cpg_shores	0.0000	0.0395	-58.615
	chr13	55985109	mm39_genes_intergenic	0.0000	0.0395	-58.615
Naa35	chr13	59733090	mm39_genes_promoters	0.0000	0.0000	-95.161
Naa35	chr13	59733090	mm39_genes_promoters	0.0000	0.0000	-95.161
Naa35	chr13	59733090	mm39_genes_promoters	0.0000	0.0000	-95.161
Naa35	chr13	59733090	mm39_genes_promoters	0.0000	0.0000	-95.161
A230056J06Rik	chr13	59733090	mm39_genes_exonintronboundaries	0.0000	0.0000	-95.161
A230056J06Rik	chr13	59733090	mm39_genes_intronexonboundaries	0.0000	0.0000	-95.161
	chr13	59733090	mm39_cpg_islands	0.0000	0.0000	-95.161
A230056J06Rik	chr13	59733090	mm39_genes_promoters	0.0000	0.0000	-95.161
Naa35	chr13	59733090	mm39_genes_exonintronboundaries	0.0000	0.0000	-95.161
Naa35	chr13	59733090	mm39_genes_exonintronboundaries	0.0000	0.0000	-95.161
Naa35	chr13	59733090	mm39_genes_exonintronboundaries	0.0000	0.0000	-95.161
	chr13	67303466	mm39_cpg_inter	0.0000	0.0910	-27.947
	chr13	67303466	mm39_genes_intergenic	0.0000	0.0910	-27.947
	chr13	67303530	mm39_cpg_inter	0.0000	0.0004	-35.165
	chr13	67303530	mm39_genes_intergenic	0.0000	0.0004	-35.165
	chr13	67303539	mm39_cpg_inter	0.0000	0.0017	-31.868
	chr13	67303539	mm39_genes_intergenic	0.0000	0.0017	-31.868
	chr13	70166783	mm39_cpg_inter	0.0000	0.0887	28.000
1700084F23Rik	chr13	70166783	mm39_genes_introns	0.0000	0.0887	28.000
Gm3772	chr13	70166783	mm39_genes_1to5kb	0.0000	0.0887	28.000
	chr13	72677262	mm39_cpg_inter	0.0000	0.0661	75.000
	chr13	72677262	mm39_genes_intergenic	0.0000	0.0661	75.000
	chr13	74157697	mm39_cpg_islands	0.0000	0.0832	-36.425
Tppp	chr13	74157697	mm39_genes_exonintronboundaries	0.0000	0.0832	-36.425
Gm15912	chr13	74157697	mm39_genes_promoters	0.0000	0.0832	-36.425
Tppp	chr13	74157697	mm39_genes_introns	0.0000	0.0832	-36.425
	chr13	74712017	mm39_cpg_inter	0.0000	0.0242	-21.519
	chr13	74712017	mm39_genes_intergenic	0.0000	0.0242	-21.519
	chr13	75622325	mm39_cpg_inter	0.0000	0.0680	-34.502
	chr13	75622325	mm39_genes_intergenic	0.0000	0.0680	-34.502
	chr13	84338325	mm39_cpg_inter	0.0000	0.0004	26.000

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr13	84338325	mm39_genes_intergenic	0.0000	0.0004	26.000
	chr13	94846374	mm39_genes_intergenic	0.0000	0.0000	35.135
	chr13	94846374	mm39_cpg_shores	0.0000	0.0000	35.135
	chr13	94846419	mm39_genes_intergenic	0.0000	0.0000	31.857
	chr13	94846419	mm39_cpg_shores	0.0000	0.0000	31.857
	chr13	95007354	mm39_cpg_shores	0.0000	0.0070	-63.509
Otp	chr13	95007354	mm39_genes_1to5kb	0.0000	0.0070	-63.509
Polk	chr13	96678427	mm39_genes_introns	0.0000	0.0048	-90.476
	chr13	96678427	mm39_cpg_shores	0.0000	0.0048	-90.476
Cert1	chr13	96678427	mm39_genes_promoters	0.0000	0.0048	-90.476
Cert1	chr13	96678427	mm39_genes_promoters	0.0000	0.0048	-90.476
Fam169a	chr13	97207829	mm39_genes_introns	0.0000	0.0636	20.526
Fam169a	chr13	97207829	mm39_genes_promoters	0.0000	0.0636	20.526
	chr13	97207829	mm39_cpg_islands	0.0000	0.0636	20.526
	chr13	97572633	mm39_cpg_inter	0.0000	0.0004	-66.892
Lncenc1	chr13	97572633	mm39_genes_introns	0.0000	0.0004	-66.892
	chr13	97572705	mm39_cpg_inter	0.0000	0.0000	-81.547
Lncenc1	chr13	97572705	mm39_genes_introns	0.0000	0.0000	-81.547
Shisal2b	chr13	104999932	mm39_genes_introns	0.0000	0.0007	-67.653
	chr13	104999932	mm39_cpg_shores	0.0000	0.0007	-67.653
Shisal2b	chr13	104999932	mm39_genes_exonintronboundaries	0.0000	0.0007	-67.653
	chr13	106673798	mm39_genes_intergenic	0.0000	0.0000	64.524
	chr13	106673798	mm39_cpg_inter	0.0000	0.0000	64.524
	chr13	106673829	mm39_genes_intergenic	0.0000	0.0000	67.857
	chr13	106673829	mm39_cpg_inter	0.0000	0.0000	67.857
Mcidas	chr13	113126280	mm39_genes_1to5kb	0.0000	0.0000	31.730
Ccno	chr13	113126280	mm39_genes_intronexonboundaries	0.0000	0.0000	31.730
Ccno	chr13	113126280	mm39_genes_exons	0.0000	0.0000	31.730
	chr13	113126280	mm39_cpg_islands	0.0000	0.0000	31.730
Mcidas	chr13	113126325	mm39_genes_1to5kb	0.0000	0.0007	86.538
Ccno	chr13	113126325	mm39_genes_exons	0.0000	0.0007	86.538
	chr13	113126325	mm39_cpg_islands	0.0000	0.0007	86.538
	chr13	118405603	mm39_cpg_inter	0.0000	0.0174	26.506
	chr13	118405603	mm39_genes_intergenic	0.0000	0.0174	26.506
Nnt	chr13	119545539	mm39_genes_exonintronboundaries	0.0000	0.0000	-41.915
Nnt	chr13	119545539	mm39_genes_exonintronboundaries	0.0000	0.0000	-41.915
	chr13	119545539	mm39_cpg_islands	0.0000	0.0000	-41.915
Nnt	chr13	119545539	mm39_genes_intronexonboundaries	0.0000	0.0000	-41.915
Nnt	chr13	119545539	mm39_genes_5UTRs	0.0000	0.0000	-41.915
Nnt	chr13	119545539	mm39_genes_exons	0.0000	0.0000	-41.915
Nnt	chr13	119545539	mm39_genes_5UTRs	0.0000	0.0000	-41.915
Nnt	chr13	119545539	mm39_genes_exons	0.0000	0.0000	-41.915
	chr14	4198894	mm39_cpg_islands	0.0000	0.0000	-38.246
Rpl15	chr14	4198894	mm39_genes_exonintronboundaries	0.0000	0.0000	-38.246
Nkiras1	chr14	4198894	mm39_genes_promoters	0.0000	0.0000	-38.246
Nkiras1	chr14	4198894	mm39_genes_promoters	0.0000	0.0000	-38.246
Nkiras1	chr14	4198894	mm39_genes_promoters	0.0000	0.0000	-38.246
Rpl15	chr14	4198894	mm39_genes_exonintronboundaries	0.0000	0.0000	-38.246
Rpl15	chr14	4198894	mm39_genes_exonintronboundaries	0.0000	0.0000	-38.246
Rpl15	chr14	4198894	mm39_genes_introns	0.0000	0.0000	-38.246
Rpl15	chr14	4198894	mm39_genes_introns	0.0000	0.0000	-38.246

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Rpl15	chr14	4198894	mm39_genes_introns	0.0000	0.0000	-38.246
Myoz1	chr14	20711357	mm39_genes_1to5kb	0.0000	0.0000	-54.777
Synpo2l	chr14	20711357	mm39_genes_exons	0.0000	0.0000	-54.777
Synpo2l	chr14	20711357	mm39_genes_exons	0.0000	0.0000	-54.777
Synpo2l	chr14	20711357	mm39_genes_exons	0.0000	0.0000	-54.777
	chr14	20711357	mm39_cpg_islands	0.0000	0.0000	-54.777
	chr14	20745201	mm39_cpg_islands	0.0000	0.0001	49.153
Fut11	chr14	20745201	mm39_genes_exons	0.0000	0.0001	49.153
Dusp13	chr14	21801092	mm39_genes_1to5kb	0.0000	0.0009	14.243
Samd8	chr14	21801092	mm39_genes_promoters	0.0000	0.0009	14.243
Samd8	chr14	21801092	mm39_genes_exonintronboundaries	0.0000	0.0009	14.243
Samd8	chr14	21801092	mm39_genes_introns	0.0000	0.0009	14.243
Samd8	chr14	21801092	mm39_genes_introns	0.0000	0.0009	14.243
	chr14	21801092	mm39_cpg_shores	0.0000	0.0009	14.243
	chr14	25769640	mm39_cpg_shores	0.0000	0.0003	49.536
Zcchc24	chr14	25769640	mm39_genes_intronexonboundaries	0.0000	0.0003	49.536
Zcchc24	chr14	25769640	mm39_genes_promoters	0.0000	0.0003	49.536
Wnt5a	chr14	28225968	mm39_genes_1to5kb	0.0000	0.0010	-52.159
	chr14	28225968	mm39_cpg_shores	0.0000	0.0010	-52.159
Cacna2d3	chr14	29445250	mm39_genes_1to5kb	0.0000	0.0002	50.000
	chr14	29445250	mm39_cpg_shores	0.0000	0.0002	50.000
Cacna2d3	chr14	29445288	mm39_genes_1to5kb	0.0000	0.0002	69.492
	chr14	29445288	mm39_cpg_shores	0.0000	0.0002	69.492
Grid1	chr14	34541078	mm39_genes_1to5kb	0.0000	0.0000	20.980
	chr14	34541078	mm39_cpg_islands	0.0000	0.0000	20.980
	chr14	34541123	mm39_cpg_islands	0.0000	0.0068	14.529
Grid1	chr14	34541123	mm39_genes_promoters	0.0000	0.0068	14.529
	chr14	39195498	mm39_cpg_islands	0.0000	0.0534	59.852
LOC432842	chr14	39195498	mm39_genes_exons	0.0000	0.0534	59.852
Nrg3	chr14	39195498	mm39_genes_promoters	0.0000	0.0534	59.852
Nrg3	chr14	39195498	mm39_genes_promoters	0.0000	0.0534	59.852
Nrg3	chr14	39195498	mm39_genes_promoters	0.0000	0.0534	59.852
Ero1a	chr14	45556277	mm39_genes_promoters	0.0000	0.0196	-22.780
	chr14	45556277	mm39_cpg_shores	0.0000	0.0196	-22.780
	chr14	47326809	mm39_cpg_inter	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_exonintronboundaries	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_exonintronboundaries	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_exonintronboundaries	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_exonintronboundaries	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_introns	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_introns	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_introns	0.0000	0.0993	53.846
Samd4	chr14	47326809	mm39_genes_introns	0.0000	0.0993	53.846
	chr14	47710438	mm39_cpg_islands	0.0000	0.0111	-29.409
Fbxo34	chr14	47710438	mm39_genes_introns	0.0000	0.0111	-29.409
Fbxo34	chr14	47710438	mm39_genes_introns	0.0000	0.0111	-29.409
Fbxo34	chr14	47710438	mm39_genes_introns	0.0000	0.0111	-29.409
Fbxo34	chr14	47710438	mm39_genes_introns	0.0000	0.0111	-29.409
Zfp219	chr14	52258077	mm39_genes_promoters	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_exonintronboundaries	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_exonintronboundaries	0.0000	0.0000	-90.361

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr14	52258077	mm39_cpg_shores	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_5UTRs	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_5UTRs	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_exons	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_exons	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_intronexonboundaries	0.0000	0.0000	-90.361
Zfp219	chr14	52258077	mm39_genes_intronexonboundaries	0.0000	0.0000	-90.361
Zfp219	chr14	52260598	mm39_genes_1to5kb	0.0000	0.0300	-57.955
Zfp219	chr14	52260598	mm39_genes_1to5kb	0.0000	0.0300	-57.955
Zfp219	chr14	52260598	mm39_genes_1to5kb	0.0000	0.0300	-57.955
	chr14	52260598	mm39_cpg_shelves	0.0000	0.0300	-57.955
	chr14	55309471	mm39_cpg_inter	0.0000	0.0015	58.730
Zfhx2os	chr14	55309471	mm39_genes_1to5kb	0.0000	0.0015	58.730
Zfhx2	chr14	55309471	mm39_genes_exonintronboundaries	0.0000	0.0015	58.730
Zfhx2	chr14	55309471	mm39_genes_exons	0.0000	0.0015	58.730
Zfhx2	chr14	55309471	mm39_genes_intronexonboundaries	0.0000	0.0015	58.730
	chr14	55764635	mm39_cpg_inter	0.0000	0.0143	-50.946
Nrl	chr14	55764635	mm39_genes_1to5kb	0.0000	0.0143	-50.946
Nrl	chr14	55764635	mm39_genes_1to5kb	0.0000	0.0143	-50.946
Nrl	chr14	55764635	mm39_genes_1to5kb	0.0000	0.0143	-50.946
Nrl	chr14	55764635	mm39_genes_1to5kb	0.0000	0.0143	-50.946
	chr14	55995342	mm39_cpg_inter	0.0000	0.0718	-50.000
Ltb4r2	chr14	55995342	mm39_genes_1to5kb	0.0000	0.0718	-50.000
Cideb	chr14	55995342	mm39_genes_exonintronboundaries	0.0000	0.0718	-50.000
Cideb	chr14	55995342	mm39_genes_intronexonboundaries	0.0000	0.0718	-50.000
Cideb	chr14	55995342	mm39_genes_exons	0.0000	0.0718	-50.000
Cenpj	chr14	56809074	mm39_genes_introns	0.0000	0.0932	-19.144
Parp4	chr14	56809074	mm39_genes_1to5kb	0.0000	0.0932	-19.144
	chr14	56809074	mm39_cpg_islands	0.0000	0.0932	-19.144
Cenpj	chr14	56809074	mm39_genes_exonintronboundaries	0.0000	0.0932	-19.144
	chr14	60502582	mm39_cpg_shores	0.0000	0.0000	-85.441
Mtmr6	chr14	60502582	mm39_genes_promoters	0.0000	0.0000	-85.441
Gata4	chr14	63485247	mm39_genes_1to5kb	0.0000	0.0778	-14.875
Gata4	chr14	63485247	mm39_genes_1to5kb	0.0000	0.0778	-14.875
	chr14	63485247	mm39_cpg_shores	0.0000	0.0778	-14.875
	chr14	63507072	mm39_genes_intergenic	0.0000	0.0946	-25.414
	chr14	63507072	mm39_cpg_inter	0.0000	0.0946	-25.414
	chr14	65714616	mm39_cpg_inter	0.0000	0.0769	-35.417
	chr14	65714616	mm39_genes_intergenic	0.0000	0.0769	-35.417
Ebf2	chr14	67470878	mm39_genes_1to5kb	0.0000	0.0000	-40.852
Ebf2	chr14	67470878	mm39_genes_5UTRs	0.0000	0.0000	-40.852
Ebf2	chr14	67470878	mm39_genes_5UTRs	0.0000	0.0000	-40.852
Ebf2	chr14	67470878	mm39_genes_exons	0.0000	0.0000	-40.852
Ebf2	chr14	67470878	mm39_genes_exons	0.0000	0.0000	-40.852
	chr14	67470878	mm39_cpg_islands	0.0000	0.0000	-40.852
	chr14	68288919	mm39_cpg_inter	0.0000	0.0000	-58.259
	chr14	68288919	mm39_genes_intergenic	0.0000	0.0000	-58.259
	chr14	70215716	mm39_cpg_inter	0.0000	0.0654	57.588
Pebp4	chr14	70215716	mm39_genes_introns	0.0000	0.0654	57.588
Ccar2	chr14	70390823	mm39_genes_introns	0.0000	0.0000	-59.753
	chr14	70390823	mm39_cpg_islands	0.0000	0.0000	-59.753

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Sorbs3	chr14	70429708	mm39_genes_exonintronboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_exonintronboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_exonintronboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_exonintronboundaries	0.0000	0.0000	-48.038
	chr14	70429708	mm39_cpg_islands	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_intronexonboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_intronexonboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_intronexonboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_intronexonboundaries	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_introns	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_introns	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_introns	0.0000	0.0000	-48.038
Sorbs3	chr14	70429708	mm39_genes_promoters	0.0000	0.0000	-48.038
	chr14	76075769	mm39_cpg_inter	0.0000	0.0001	-39.456
	chr14	76075769	mm39_genes_intergenic	0.0000	0.0001	-39.456
	chr14	76470717	mm39_cpg_inter	0.0000	0.0182	84.211
	chr14	76470717	mm39_genes_intergenic	0.0000	0.0182	84.211
	chr14	76867764	mm39_cpg_inter	0.0000	0.0780	-47.826
	chr14	76867764	mm39_genes_intergenic	0.0000	0.0780	-47.826
Enox1	chr14	77471957	mm39_genes_introns	0.0000	0.0442	-77.056
Enox1	chr14	77471957	mm39_genes_introns	0.0000	0.0442	-77.056
	chr14	77471957	mm39_cpg_inter	0.0000	0.0442	-77.056
	chr14	89847106	mm39_cpg_inter	0.0000	0.0587	64.564
	chr14	89847106	mm39_genes_intergenic	0.0000	0.0587	64.564
	chr14	99142554	mm39_cpg_inter	0.0000	0.0117	-52.941
	chr14	99142554	mm39_genes_intergenic	0.0000	0.0117	-52.941
	chr14	104953253	mm39_cpg_inter	0.0000	0.0616	-13.175
D130009I18Rik	chr14	104953253	mm39_genes_introns	0.0000	0.0616	-13.175
	chr14	106132420	mm39_cpg_shores	0.0000	0.0000	-35.506
Spry2	chr14	106132420	mm39_genes_introns	0.0000	0.0000	-35.506
	chr14	106132465	mm39_cpg_shores	0.0000	0.0502	-26.253
Spry2	chr14	106132465	mm39_genes_introns	0.0000	0.0502	-26.253
	chr14	113656093	mm39_cpg_inter	0.0000	0.0007	61.364
	chr14	113656093	mm39_genes_intergenic	0.0000	0.0007	61.364
	chr14	122712901	mm39_cpg_islands	0.0000	0.0662	-19.768
2610035F20Rik	chr14	122712901	mm39_genes_promoters	0.0000	0.0662	-19.768
Zic2	chr14	122712901	mm39_genes_exons	0.0000	0.0662	-19.768
Zic2	chr14	122712901	mm39_genes_5UTRs	0.0000	0.0662	-19.768
	chr15	7427926	mm39_cpg_islands	0.0000	0.0196	-32.520
Egflam	chr15	7427926	mm39_genes_intronexonboundaries	0.0000	0.0196	-32.520
Egflam	chr15	7427926	mm39_genes_intronexonboundaries	0.0000	0.0196	-32.520
Egflam	chr15	7427926	mm39_genes_intronexonboundaries	0.0000	0.0196	-32.520
Egflam	chr15	7427926	mm39_genes_promoters	0.0000	0.0196	-32.520
Egflam	chr15	7427926	mm39_genes_promoters	0.0000	0.0196	-32.520
Egflam	chr15	7427926	mm39_genes_promoters	0.0000	0.0196	-32.520
	chr15	8950843	mm39_cpg_inter	0.0000	0.0001	-44.737
	chr15	8950843	mm39_genes_intergenic	0.0000	0.0001	-44.737
	chr15	9914616	mm39_cpg_inter	0.0000	0.0474	39.412
	chr15	9914616	mm39_genes_intergenic	0.0000	0.0474	39.412
Rai14	chr15	10715472	mm39_genes_1to5kb	0.0000	0.0000	-37.078
Rai14	chr15	10715472	mm39_genes_promoters	0.0000	0.0000	-37.078

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
4930556M19Rik	chr15	10715472	mm39_genes_introns	0.0000	0.0000	-37.078
4930556M19Rik	chr15	10715472	mm39_genes_introns	0.0000	0.0000	-37.078
4930556M19Rik	chr15	10715472	mm39_genes_introns	0.0000	0.0000	-37.078
	chr15	10715472	mm39_cpg_shores	0.0000	0.0000	-37.078
Rai14	chr15	10715472	mm39_genes_1to5kb	0.0000	0.0000	-37.078
	chr15	12439199	mm39_cpg_inter	0.0000	0.0011	-35.056
Pdzd2	chr15	12439199	mm39_genes_introns	0.0000	0.0011	-35.056
Gm32618	chr15	32779351	mm39_genes_exons	0.0000	0.0000	-73.529
	chr15	32779351	mm39_cpg_islands	0.0000	0.0000	-73.529
	chr15	36016025	mm39_cpg_inter	0.0000	0.0261	-66.667
Rgs22	chr15	36016025	mm39_genes_intronexonboundaries	0.0000	0.0261	-66.667
Rgs22	chr15	36016025	mm39_genes_introns	0.0000	0.0261	-66.667
	chr15	58744557	mm39_cpg_islands	0.0000	0.0000	-48.811
Trmt12	chr15	58744557	mm39_genes_exons	0.0000	0.0000	-48.811
Trmt12	chr15	58744557	mm39_genes_5UTRs	0.0000	0.0000	-48.811
	chr15	59546125	mm39_cpg_inter	0.0000	0.0000	-47.273
	chr15	59546125	mm39_genes_intergenic	0.0000	0.0000	-47.273
	chr15	68130907	mm39_cpg_islands	0.0000	0.0843	-24.314
Zfat	chr15	68130907	mm39_genes_promoters	0.0000	0.0843	-24.314
Zfat	chr15	68130907	mm39_genes_promoters	0.0000	0.0843	-24.314
Zfat	chr15	68130907	mm39_genes_promoters	0.0000	0.0843	-24.314
Gpaa1	chr15	76211421	mm39_genes_1to5kb	0.0000	0.0359	-22.131
Exosc4	chr15	76211421	mm39_genes_promoters	0.0000	0.0359	-22.131
	chr15	76211421	mm39_cpg_islands	0.0000	0.0359	-22.131
	chr15	76497163	mm39_cpg_inter	0.0000	0.0523	-42.393
Slc39a4	chr15	76497163	mm39_genes_intronexonboundaries	0.0000	0.0523	-42.393
Slc39a4	chr15	76497163	mm39_genes_introns	0.0000	0.0523	-42.393
Cyhr1	chr15	76545327	mm39_genes_1to5kb	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_1to5kb	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_promoters	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_promoters	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_promoters	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_1to5kb	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_1to5kb	0.0000	0.0253	-22.705
Cyhr1	chr15	76545327	mm39_genes_1to5kb	0.0000	0.0253	-22.705
	chr15	76545327	mm39_cpg_shores	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_exonintronboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_exonintronboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_exonintronboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_exonintronboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_exonintronboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_intronexonboundaries	0.0000	0.0253	-22.705

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Kifc2	chr15	76545327	mm39_genes_introns	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_introns	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_introns	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_introns	0.0000	0.0253	-22.705
Kifc2	chr15	76545327	mm39_genes_introns	0.0000	0.0253	-22.705
Arhgap39	chr15	76703110	mm39_genes_promoters	0.0000	0.0303	-52.941
Arhgap39	chr15	76703110	mm39_genes_promoters	0.0000	0.0303	-52.941
	chr15	76703110	mm39_cpg_shores	0.0000	0.0303	-52.941
Eif3d	chr15	77855458	mm39_genes_promoters	0.0000	0.0011	-55.556
	chr15	77855458	mm39_cpg_shores	0.0000	0.0011	-55.556
	chr15	78074919	mm39_cpg_inter	0.0000	0.0664	49.428
	chr15	78074919	mm39_genes_intergenic	0.0000	0.0664	49.428
	chr15	79501719	mm39_cpg_inter	0.0000	0.0646	53.488
Fam227a	chr15	79501719	mm39_genes_introns	0.0000	0.0646	53.488
Fam227a	chr15	79501719	mm39_genes_exonintronboundaries	0.0000	0.0646	53.488
	chr15	82128976	mm39_cpg_islands	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_promoters	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_exonintronboundaries	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_exonintronboundaries	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_intronexonboundaries	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_intronexonboundaries	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_promoters	0.0000	0.0334	58.824
Cenpm	chr15	82128976	mm39_genes_promoters	0.0000	0.0334	58.824
	chr15	84016412	mm39_cpg_inter	0.0000	0.0628	-52.381
	chr15	84016412	mm39_genes_intergenic	0.0000	0.0628	-52.381
	chr15	85518760	mm39_genes_intergenic	0.0000	0.0000	-85.246
	chr15	85518760	mm39_cpg_islands	0.0000	0.0000	-85.246
	chr15	85530666	mm39_genes_intergenic	0.0000	0.0073	32.609
	chr15	85530666	mm39_cpg_shores	0.0000	0.0073	32.609
	chr15	85568568	mm39_genes_intergenic	0.0000	0.0000	-35.615
	chr15	85568568	mm39_cpg_inter	0.0000	0.0000	-35.615
	chr15	88615112	mm39_cpg_shelves	0.0000	0.0781	-50.000
Brd1	chr15	88615112	mm39_genes_introns	0.0000	0.0781	-50.000
Brd1	chr15	88621836	mm39_genes_1to5kb	0.0000	0.0968	-67.117
	chr15	88621836	mm39_cpg_shelves	0.0000	0.0968	-67.117
	chr15	93021078	mm39_cpg_inter	0.0000	0.0853	-15.973
	chr15	93021078	mm39_genes_intergenic	0.0000	0.0853	-15.973
Prickle1	chr15	93417267	mm39_genes_introns	0.0000	0.0000	19.399
	chr15	93417267	mm39_cpg_islands	0.0000	0.0000	19.399
Prickle1	chr15	93417267	mm39_genes_exonintronboundaries	0.0000	0.0000	19.399
Prickle1	chr15	93417267	mm39_genes_5UTRs	0.0000	0.0000	19.399
Prickle1	chr15	93417267	mm39_genes_exons	0.0000	0.0000	19.399
Prickle1	chr15	93417267	mm39_genes_intronexonboundaries	0.0000	0.0000	19.399
Prickle1	chr15	93417312	mm39_genes_introns	0.0000	0.0002	89.474
	chr15	93417312	mm39_cpg_islands	0.0000	0.0002	89.474
Prickle1	chr15	93417312	mm39_genes_exonintronboundaries	0.0000	0.0002	89.474
Prickle1	chr15	93417312	mm39_genes_5UTRs	0.0000	0.0002	89.474
Prickle1	chr15	93417312	mm39_genes_exons	0.0000	0.0002	89.474
Prickle1	chr15	93417312	mm39_genes_intronexonboundaries	0.0000	0.0002	89.474
Ano6	chr15	95688387	mm39_genes_promoters	0.0000	0.0022	48.485
Ano6	chr15	95688387	mm39_genes_promoters	0.0000	0.0022	48.485

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr15	95688387	mm39_cpg_islands	0.0000	0.0022	48.485
Arid2	chr15	96183393	mm39_genes_1to5kb	0.0000	0.0000	-59.098
	chr15	96183393	mm39_cpg_islands	0.0000	0.0000	-59.098
Ddx23	chr15	98560343	mm39_genes_introns	0.0000	0.0001	51.899
	chr15	98560343	mm39_cpg_shores	0.0000	0.0001	51.899
Dhh	chr15	98792769	mm39_genes_exonintronboundaries	0.0000	0.0654	-58.261
Dhh	chr15	98792769	mm39_genes_exons	0.0000	0.0654	-58.261
	chr15	98792769	mm39_cpg_islands	0.0000	0.0654	-58.261
Dhh	chr15	98792769	mm39_genes_intronexonboundaries	0.0000	0.0654	-58.261
Bcdin3d	chr15	99372339	mm39_genes_exonintronboundaries	0.0000	0.0000	-44.911
	chr15	99372339	mm39_cpg_islands	0.0000	0.0000	-44.911
Bcdin3d	chr15	99372339	mm39_genes_exons	0.0000	0.0000	-44.911
	chr15	99920943	mm39_cpg_inter	0.0000	0.0087	-60.000
	chr15	99920943	mm39_genes_intergenic	0.0000	0.0087	-60.000
	chr16	3151117	mm39_cpg_inter	0.0000	0.0566	-30.923
	chr16	3151117	mm39_genes_intergenic	0.0000	0.0566	-30.923
	chr16	3726525	mm39_cpg_shores	0.0000	0.0000	67.294
Cluap1	chr16	3726525	mm39_genes_promoters	0.0000	0.0000	67.294
Gm41410	chr16	3726525	mm39_genes_exonintronboundaries	0.0000	0.0000	67.294
1700037C18Rik	chr16	3726525	mm39_genes_exons	0.0000	0.0000	67.294
Gm41410	chr16	3726525	mm39_genes_intronexonboundaries	0.0000	0.0000	67.294
1700037C18Rik	chr16	3726525	mm39_genes_5UTRs	0.0000	0.0000	67.294
1700037C18Rik	chr16	3726525	mm39_genes_intronexonboundaries	0.0000	0.0000	67.294
Gm41410	chr16	3726525	mm39_genes_promoters	0.0000	0.0000	67.294
Coro7	chr16	4497219	mm39_genes_introns	0.0000	0.0000	-94.737
Dnaja3	chr16	4497219	mm39_genes_1to5kb	0.0000	0.0000	-94.737
Dnaja3	chr16	4497219	mm39_genes_1to5kb	0.0000	0.0000	-94.737
	chr16	4497219	mm39_cpg_islands	0.0000	0.0000	-94.737
Coro7	chr16	4497219	mm39_genes_exonintronboundaries	0.0000	0.0000	-94.737
Rogdi	chr16	4831672	mm39_genes_promoters	0.0000	0.0001	15.480
	chr16	4831672	mm39_cpg_shores	0.0000	0.0001	15.480
	chr16	9811930	mm39_cpg_islands	0.0000	0.0282	43.441
Grin2a	chr16	9811930	mm39_genes_exonintronboundaries	0.0000	0.0282	43.441
Grin2a	chr16	9811930	mm39_genes_intronexonboundaries	0.0000	0.0282	43.441
Grin2a	chr16	9811930	mm39_genes_5UTRs	0.0000	0.0282	43.441
Grin2a	chr16	9811930	mm39_genes_exons	0.0000	0.0282	43.441
	chr16	9812777	mm39_cpg_islands	0.0000	0.0087	-56.277
Grin2a	chr16	9812777	mm39_genes_exonintronboundaries	0.0000	0.0087	-56.277
Grin2a	chr16	9812777	mm39_genes_5UTRs	0.0000	0.0087	-56.277
Grin2a	chr16	9812777	mm39_genes_exons	0.0000	0.0087	-56.277
	chr16	10952744	mm39_cpg_islands	0.0000	0.0000	-83.286
Txndc11	chr16	10952744	mm39_genes_promoters	0.0000	0.0000	-83.286
Prkdc	chr16	15455685	mm39_genes_promoters	0.0000	0.0001	-71.907
	chr16	15455685	mm39_cpg_islands	0.0000	0.0001	-71.907
Mcm4	chr16	15455685	mm39_genes_promoters	0.0000	0.0001	-71.907
Pi4ka	chr16	17223918	mm39_genes_introns	0.0000	0.0453	-28.437
Pi4ka	chr16	17223918	mm39_genes_intronexonboundaries	0.0000	0.0453	-28.437
	chr16	17223918	mm39_cpg_islands	0.0000	0.0453	-28.437
Pi4ka	chr16	17223918	mm39_genes_promoters	0.0000	0.0453	-28.437
Snap29	chr16	17223918	mm39_genes_exons	0.0000	0.0453	-28.437
Snap29	chr16	17223918	mm39_genes_5UTRs	0.0000	0.0453	-28.437

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Klhl22	chr16	17578077	mm39_genes_1to5kb	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_1to5kb	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_1to5kb	0.0000	0.0000	-86.980
	chr16	17578077	mm39_cpg_islands	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_exons	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_5UTRs	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_5UTRs	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_exons	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_introns	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_introns	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_introns	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_introns	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_exonintronboundaries	0.0000	0.0000	-86.980
Klhl22	chr16	17578077	mm39_genes_exonintronboundaries	0.0000	0.0000	-86.980
	chr16	17615460	mm39_cpg_islands	0.0000	0.0003	-88.679
Scarf2	chr16	17615460	mm39_genes_exonintronboundaries	0.0000	0.0003	-88.679
Scarf2	chr16	17615460	mm39_genes_introns	0.0000	0.0003	-88.679
	chr16	20046501	mm39_cpg_inter	0.0000	0.0081	-66.667
Yeats2	chr16	20046501	mm39_genes_intronexonboundaries	0.0000	0.0081	-66.667
Yeats2	chr16	20046501	mm39_genes_intronexonboundaries	0.0000	0.0081	-66.667
Yeats2	chr16	20046501	mm39_genes_exons	0.0000	0.0081	-66.667
Yeats2	chr16	20046501	mm39_genes_exons	0.0000	0.0081	-66.667
Yeats2	chr16	20046501	mm39_genes_exonintronboundaries	0.0000	0.0081	-66.667
Yeats2	chr16	20046501	mm39_genes_exonintronboundaries	0.0000	0.0081	-66.667
Eef1ece2	chr16	20439955	mm39_genes_introns	0.0000	0.0011	64.706
Eef1ece2	chr16	20439955	mm39_genes_introns	0.0000	0.0011	64.706
	chr16	20439955	mm39_cpg_islands	0.0000	0.0011	64.706
Camk2n2	chr16	20439955	mm39_genes_exonintronboundaries	0.0000	0.0011	64.706
Camk2n2	chr16	20439955	mm39_genes_exons	0.0000	0.0011	64.706
Camk2n2	chr16	20439955	mm39_genes_intronexonboundaries	0.0000	0.0011	64.706
Camk2n2	chr16	20439955	mm39_genes_5UTRs	0.0000	0.0011	64.706
Etv5	chr16	22258137	mm39_genes_introns	0.0000	0.0000	-55.469
	chr16	22258137	mm39_cpg_islands	0.0000	0.0000	-55.469
Etv5	chr16	22258137	mm39_genes_exonintronboundaries	0.0000	0.0000	-55.469
Etv5	chr16	22258137	mm39_genes_1to5kb	0.0000	0.0000	-55.469
Etv5	chr16	22258137	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.469
Dlg1	chr16	31482351	mm39_genes_promoters	0.0000	0.0001	38.214
Dlg1	chr16	31482351	mm39_genes_promoters	0.0000	0.0001	38.214
Dlg1	chr16	31482351	mm39_genes_promoters	0.0000	0.0001	38.214
Dlg1	chr16	31482351	mm39_genes_promoters	0.0000	0.0001	38.214
Dlg1	chr16	31482351	mm39_genes_promoters	0.0000	0.0001	38.214
Dlg1	chr16	31482351	mm39_genes_exonintronboundaries	0.0000	0.0001	38.214
Dlg1	chr16	31482351	mm39_genes_introns	0.0000	0.0001	38.214
	chr16	31482351	mm39_cpg_islands	0.0000	0.0001	38.214
	chr16	51807646	mm39_cpg_inter	0.0000	0.0677	-48.387
Gm29686	chr16	51807646	mm39_genes_exonintronboundaries	0.0000	0.0677	-48.387
Gm29686	chr16	51807646	mm39_genes_intronexonboundaries	0.0000	0.0677	-48.387
Gm29686	chr16	51807646	mm39_genes_exons	0.0000	0.0677	-48.387
	chr16	59720474	mm39_cpg_inter	0.0000	0.0048	-36.924
Epha6	chr16	59720474	mm39_genes_introns	0.0000	0.0048	-36.924
	chr16	61596559	mm39_cpg_inter	0.0000	0.0658	-44.377

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr16	61596559	mm39_genes_intergenic	0.0000	0.0658	-44.377
	chr16	74208622	mm39_cpg_inter	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_introns	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_introns	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_introns	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_exons	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_exons	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_5UTRs	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_5UTRs	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_intronexonboundaries	0.0000	0.0000	-62.368
Robo2	chr16	74208622	mm39_genes_intronexonboundaries	0.0000	0.0000	-62.368
Eva1c	chr16	90627853	mm39_genes_introns	0.0000	0.0252	-15.769
	chr16	90627853	mm39_cpg_islands	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_exons	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_exons	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_exons	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_exons	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_exons	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_5UTRs	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_5UTRs	0.0000	0.0252	-15.769
Eva1c	chr16	90627853	mm39_genes_5UTRs	0.0000	0.0252	-15.769
	chr16	91022931	mm39_cpg_shores	0.0000	0.0000	-57.005
Olig2	chr16	91022931	mm39_genes_introns	0.0000	0.0000	-57.005
	chr16	91261752	mm39_cpg_shores	0.0000	0.0170	42.857
A930006K02Rik	chr16	91261752	mm39_genes_promoters	0.0000	0.0170	42.857
Gm10785	chr16	91485533	mm39_genes_promoters	0.0000	0.0000	-49.596
	chr16	91485533	mm39_cpg_islands	0.0000	0.0000	-49.596
Donson	chr16	91485533	mm39_genes_exons	0.0000	0.0000	-49.596
Donson	chr16	91485533	mm39_genes_intronexonboundaries	0.0000	0.0000	-49.596
Vps26c	chr16	94326877	mm39_genes_introns	0.0000	0.0177	-56.875
	chr16	94326877	mm39_cpg_shores	0.0000	0.0177	-56.875
Lca5l	chr16	95992390	mm39_genes_introns	0.0000	0.0098	-60.907
	chr16	95992390	mm39_cpg_shores	0.0000	0.0098	-60.907
	chr17	5542933	mm39_cpg_islands	0.0000	0.0001	14.484
Zdhhc14	chr17	5542933	mm39_genes_exons	0.0000	0.0001	14.484
Zdhhc14	chr17	5542933	mm39_genes_5UTRs	0.0000	0.0001	14.484
	chr17	8453368	mm39_cpg_inter	0.0000	0.0702	-34.664
Ccr6	chr17	8453368	mm39_genes_1to5kb	0.0000	0.0702	-34.664
Prkn	chr17	11059119	mm39_genes_promoters	0.0000	0.0000	-55.590
Prkn	chr17	11059119	mm39_genes_promoters	0.0000	0.0000	-55.590
Pacrg	chr17	11059119	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.590
	chr17	11059119	mm39_cpg_islands	0.0000	0.0000	-55.590
Pacrg	chr17	11059119	mm39_genes_promoters	0.0000	0.0000	-55.590
	chr17	12337701	mm39_cpg_inter	0.0000	0.0000	-92.857
Agpat4	chr17	12337701	mm39_genes_promoters	0.0000	0.0000	-92.857
	chr17	14807283	mm39_cpg_inter	0.0000	0.0007	31.250
	chr17	14807283	mm39_genes_intergenic	0.0000	0.0007	31.250
	chr17	22128662	mm39_cpg_inter	0.0000	0.0821	28.788
Zfp995	chr17	22128662	mm39_genes_exonintronboundaries	0.0000	0.0821	28.788
Zfp995	chr17	22128662	mm39_genes_5UTRs	0.0000	0.0821	28.788
Zfp995	chr17	22128662	mm39_genes_exons	0.0000	0.0821	28.788

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr17	24769537	mm39_cpg_islands	0.0000	0.0000	-33.671
Pkd1	chr17	24769537	mm39_genes_exonintronboundaries	0.0000	0.0000	-33.671
Pkd1	chr17	24769537	mm39_genes_introns	0.0000	0.0000	-33.671
	chr17	25704776	mm39_genes_intergenic	0.0000	0.0235	-61.290
	chr17	25704776	mm39_cpg_inter	0.0000	0.0235	-61.290
1700022N22Rik	chr17	26204670	mm39_genes_promoters	0.0000	0.0000	17.266
1700022N22Rik	chr17	26204670	mm39_genes_promoters	0.0000	0.0000	17.266
1700022N22Rik	chr17	26204670	mm39_genes_promoters	0.0000	0.0000	17.266
	chr17	26204670	mm39_cpg_islands	0.0000	0.0000	17.266
Capn15	chr17	26204670	mm39_genes_5UTRs	0.0000	0.0000	17.266
Capn15	chr17	26204670	mm39_genes_exons	0.0000	0.0000	17.266
Capn15	chr17	26204670	mm39_genes_exons	0.0000	0.0000	17.266
Capn15	chr17	26204670	mm39_genes_intronexonboundaries	0.0000	0.0000	17.266
Capn15	chr17	26204670	mm39_genes_intronexonboundaries	0.0000	0.0000	17.266
Fam234a	chr17	26462936	mm39_genes_introns	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_introns	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_introns	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_introns	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_exonintronboundaries	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_exonintronboundaries	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_exonintronboundaries	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_exonintronboundaries	0.0000	0.0100	-25.339
	chr17	26462936	mm39_cpg_islands	0.0000	0.0100	-25.339
Fam234a	chr17	26462936	mm39_genes_intronexonboundaries	0.0000	0.0100	-25.339
	chr17	27247637	mm39_cpg_inter	0.0000	0.0000	17.525
Ggnbp1	chr17	27247637	mm39_genes_introns	0.0000	0.0000	17.525
Ggnbp1	chr17	27247637	mm39_genes_promoters	0.0000	0.0000	17.525
Bak1	chr17	27247637	mm39_genes_intronexonboundaries	0.0000	0.0000	17.525
Bak1	chr17	27247637	mm39_genes_intronexonboundaries	0.0000	0.0000	17.525
Bak1	chr17	27247637	mm39_genes_promoters	0.0000	0.0000	17.525
Bak1	chr17	27247637	mm39_genes_promoters	0.0000	0.0000	17.525
Anks1	chr17	28144491	mm39_genes_introns	0.0000	0.0090	47.368
Anks1	chr17	28144491	mm39_genes_introns	0.0000	0.0090	47.368
Anks1	chr17	28144491	mm39_genes_introns	0.0000	0.0090	47.368
Anks1	chr17	28144491	mm39_genes_introns	0.0000	0.0090	47.368
	chr17	28144491	mm39_cpg_inter	0.0000	0.0090	47.368
Mir5098	chr17	28361703	mm39_genes_introns	0.0000	0.0157	-57.143
Scube3	chr17	28361703	mm39_genes_exonintronboundaries	0.0000	0.0157	-57.143
Scube3	chr17	28361703	mm39_genes_exonintronboundaries	0.0000	0.0157	-57.143
	chr17	28361703	mm39_cpg_shores	0.0000	0.0157	-57.143
Scube3	chr17	28361703	mm39_genes_introns	0.0000	0.0157	-57.143
Scube3	chr17	28361703	mm39_genes_introns	0.0000	0.0157	-57.143
	chr17	30107112	mm39_cpg_islands	0.0000	0.0000	-50.426
Mdga1	chr17	30107112	mm39_genes_exons	0.0000	0.0000	-50.426
Mdga1	chr17	30107112	mm39_genes_5UTRs	0.0000	0.0000	-50.426
Mdga1	chr17	30107112	mm39_genes_promoters	0.0000	0.0000	-50.426
Slc37a1	chr17	31515058	mm39_genes_promoters	0.0000	0.0000	-45.085
Slc37a1	chr17	31515058	mm39_genes_introns	0.0000	0.0000	-45.085
	chr17	31515058	mm39_cpg_islands	0.0000	0.0000	-45.085
Ndufv3	chr17	31739340	mm39_genes_exonintronboundaries	0.0000	0.0031	40.660
Ndufv3	chr17	31739340	mm39_genes_exonintronboundaries	0.0000	0.0031	40.660

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Ndufv3	chr17	31739340	mm39_genes_introns	0.0000	0.0031	40.660
Ndufv3	chr17	31739340	mm39_genes_introns	0.0000	0.0031	40.660
	chr17	31739340	mm39_cpg_shores	0.0000	0.0031	40.660
Kank3	chr17	34037025	mm39_genes_introns	0.0000	0.0016	65.725
Kank3	chr17	34037025	mm39_genes_exons	0.0000	0.0016	65.725
	chr17	34037025	mm39_cpg_islands	0.0000	0.0016	65.725
	chr17	34139160	mm39_cpg_islands	0.0000	0.0100	-26.144
Tapbp	chr17	34139160	mm39_genes_exonintronboundaries	0.0000	0.0100	-26.144
Tapbp	chr17	34139160	mm39_genes_exonintronboundaries	0.0000	0.0100	-26.144
Gm19412	chr17	34139160	mm39_genes_exonintronboundaries	0.0000	0.0100	-26.144
Tapbp	chr17	34139160	mm39_genes_intronexonboundaries	0.0000	0.0100	-26.144
Tapbp	chr17	34139160	mm39_genes_intronexonboundaries	0.0000	0.0100	-26.144
Tapbp	chr17	34139160	mm39_genes_introns	0.0000	0.0100	-26.144
Tapbp	chr17	34139160	mm39_genes_introns	0.0000	0.0100	-26.144
Gm19412	chr17	34139160	mm39_genes_exons	0.0000	0.0100	-26.144
Vps52	chr17	34170503	mm39_genes_1to5kb	0.0000	0.0000	-35.188
Vps52	chr17	34170503	mm39_genes_1to5kb	0.0000	0.0000	-35.188
Vps52	chr17	34170503	mm39_genes_1to5kb	0.0000	0.0000	-35.188
Vps52	chr17	34170503	mm39_genes_1to5kb	0.0000	0.0000	-35.188
Vps52	chr17	34170503	mm39_genes_1to5kb	0.0000	0.0000	-35.188
	chr17	34170503	mm39_cpg_islands	0.0000	0.0000	-35.188
B3galt4	chr17	34170503	mm39_genes_intronexonboundaries	0.0000	0.0000	-35.188
B3galt4	chr17	34170503	mm39_genes_promoters	0.0000	0.0000	-35.188
Ppt2	chr17	34852111	mm39_genes_1to5kb	0.0000	0.0132	67.500
	chr17	34852111	mm39_cpg_shores	0.0000	0.0132	67.500
Prrt1	chr17	34852111	mm39_genes_exonintronboundaries	0.0000	0.0132	67.500
Prrt1	chr17	34852111	mm39_genes_exonintronboundaries	0.0000	0.0132	67.500
Prrt1	chr17	34852111	mm39_genes_exonintronboundaries	0.0000	0.0132	67.500
Prrt1	chr17	34852111	mm39_genes_exonintronboundaries	0.0000	0.0132	67.500
	chr17	35445660	mm39_cpg_inter	0.0000	0.0534	-47.195
Nfkbil1	chr17	35445660	mm39_genes_introns	0.0000	0.0534	-47.195
Nfkbil1	chr17	35445660	mm39_genes_introns	0.0000	0.0534	-47.195
	chr17	36542184	mm39_genes_intergenic	0.0000	0.0000	7.514
	chr17	36542184	mm39_cpg_islands	0.0000	0.0000	7.514
	chr17	36542187	mm39_genes_intergenic	0.0000	0.0000	7.056
	chr17	36542187	mm39_cpg_islands	0.0000	0.0000	7.056
	chr17	36542211	mm39_genes_intergenic	0.0000	0.0000	8.174
	chr17	36542211	mm39_cpg_islands	0.0000	0.0000	8.174
	chr17	36542220	mm39_genes_intergenic	0.0000	0.0000	7.909
	chr17	36542220	mm39_cpg_islands	0.0000	0.0000	7.909
Rn18s	chr17	40154258	mm39_genes_1to5kb	0.0000	0.0001	9.869
Rn45s	chr17	40154258	mm39_genes_exons	0.0000	0.0001	9.869
	chr17	40154258	mm39_cpg_islands	0.0000	0.0001	9.869
Rn18s	chr17	40154261	mm39_genes_1to5kb	0.0000	0.0489	5.513
Rn45s	chr17	40154261	mm39_genes_exons	0.0000	0.0489	5.513
	chr17	40154261	mm39_cpg_islands	0.0000	0.0489	5.513
Rn18s	chr17	40154277	mm39_genes_1to5kb	0.0000	0.0423	5.606
Rn45s	chr17	40154277	mm39_genes_exons	0.0000	0.0423	5.606
	chr17	40154277	mm39_cpg_islands	0.0000	0.0423	5.606
Rn18s	chr17	40154594	mm39_genes_1to5kb	0.0000	0.0000	7.347
Rn45s	chr17	40154594	mm39_genes_exons	0.0000	0.0000	7.347

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr17	40154594	mm39_cpg_islands	0.0000	0.0000	7.347
Rn18s	chr17	40154616	mm39_genes_1to5kb	0.0000	0.0000	7.771
Rn45s	chr17	40154616	mm39_genes_exons	0.0000	0.0000	7.771
	chr17	40154616	mm39_cpg_islands	0.0000	0.0000	7.771
Rn18s	chr17	40154618	mm39_genes_1to5kb	0.0000	0.0000	8.021
Rn45s	chr17	40154618	mm39_genes_exons	0.0000	0.0000	8.021
	chr17	40154618	mm39_cpg_islands	0.0000	0.0000	8.021
Rn18s	chr17	40154717	mm39_genes_1to5kb	0.0000	0.0000	8.798
Rn45s	chr17	40154717	mm39_genes_exons	0.0000	0.0000	8.798
	chr17	40154717	mm39_cpg_islands	0.0000	0.0000	8.798
Rn18s	chr17	40154807	mm39_genes_1to5kb	0.0000	0.0000	9.328
Rn45s	chr17	40154807	mm39_genes_exons	0.0000	0.0000	9.328
	chr17	40154807	mm39_cpg_islands	0.0000	0.0000	9.328
Rn18s	chr17	40154818	mm39_genes_1to5kb	0.0000	0.0988	5.770
Rn45s	chr17	40154818	mm39_genes_exons	0.0000	0.0988	5.770
	chr17	40154818	mm39_cpg_islands	0.0000	0.0988	5.770
Rn18s	chr17	40155705	mm39_genes_1to5kb	0.0000	0.0000	-6.112
Rn45s	chr17	40155705	mm39_genes_exons	0.0000	0.0000	-6.112
	chr17	40155705	mm39_cpg_islands	0.0000	0.0000	-6.112
Rn18s	chr17	40155716	mm39_genes_1to5kb	0.0000	0.0000	-6.484
Rn45s	chr17	40155716	mm39_genes_exons	0.0000	0.0000	-6.484
	chr17	40155716	mm39_cpg_islands	0.0000	0.0000	-6.484
Rn18s	chr17	40155721	mm39_genes_1to5kb	0.0000	0.0000	-6.901
Rn45s	chr17	40155721	mm39_genes_exons	0.0000	0.0000	-6.901
	chr17	40155721	mm39_cpg_islands	0.0000	0.0000	-6.901
Rn18s	chr17	40155725	mm39_genes_1to5kb	0.0000	0.0000	-6.946
Rn45s	chr17	40155725	mm39_genes_exons	0.0000	0.0000	-6.946
	chr17	40155725	mm39_cpg_islands	0.0000	0.0000	-6.946
Rn18s	chr17	40155734	mm39_genes_1to5kb	0.0000	0.0000	-7.649
Rn45s	chr17	40155734	mm39_genes_exons	0.0000	0.0000	-7.649
	chr17	40155734	mm39_cpg_islands	0.0000	0.0000	-7.649
Rn18s	chr17	40155737	mm39_genes_1to5kb	0.0000	0.0000	-6.850
Rn45s	chr17	40155737	mm39_genes_exons	0.0000	0.0000	-6.850
	chr17	40155737	mm39_cpg_islands	0.0000	0.0000	-6.850
Rn18s	chr17	40155740	mm39_genes_1to5kb	0.0000	0.0000	-7.415
Rn45s	chr17	40155740	mm39_genes_exons	0.0000	0.0000	-7.415
	chr17	40155740	mm39_cpg_islands	0.0000	0.0000	-7.415
Rn18s	chr17	40155832	mm39_genes_1to5kb	0.0000	0.0000	6.438
Rn45s	chr17	40155832	mm39_genes_exons	0.0000	0.0000	6.438
	chr17	40155832	mm39_cpg_islands	0.0000	0.0000	6.438
Rn18s	chr17	40155838	mm39_genes_1to5kb	0.0000	0.0000	6.738
Rn45s	chr17	40155838	mm39_genes_exons	0.0000	0.0000	6.738
	chr17	40155838	mm39_cpg_islands	0.0000	0.0000	6.738
Rn18s	chr17	40155846	mm39_genes_1to5kb	0.0000	0.0000	5.448
Rn45s	chr17	40155846	mm39_genes_exons	0.0000	0.0000	5.448
	chr17	40155846	mm39_cpg_islands	0.0000	0.0000	5.448
Rn18s	chr17	40155976	mm39_genes_1to5kb	0.0000	0.0951	7.604
Rn45s	chr17	40155976	mm39_genes_exons	0.0000	0.0951	7.604
	chr17	40155976	mm39_cpg_islands	0.0000	0.0951	7.604
Rn18s	chr17	40155996	mm39_genes_1to5kb	0.0000	0.0000	5.467
Rn45s	chr17	40155996	mm39_genes_exons	0.0000	0.0000	5.467

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr17	40155996	mm39_cpg_islands	0.0000	0.0000	5.467
Rn18s	chr17	40155998	mm39_genes_1to5kb	0.0000	0.0000	5.567
Rn45s	chr17	40155998	mm39_genes_exons	0.0000	0.0000	5.567
	chr17	40155998	mm39_cpg_islands	0.0000	0.0000	5.567
Rn45s	chr17	40156673	mm39_genes_exons	0.0000	0.0000	-21.178
	chr17	40156673	mm39_cpg_islands	0.0000	0.0000	-21.178
Rn18s	chr17	40156673	mm39_genes_promoters	0.0000	0.0000	-21.178
Rn45s	chr17	40156676	mm39_genes_exons	0.0000	0.0000	-19.228
	chr17	40156676	mm39_cpg_islands	0.0000	0.0000	-19.228
Rn18s	chr17	40156676	mm39_genes_promoters	0.0000	0.0000	-19.228
Rn45s	chr17	40156721	mm39_genes_exons	0.0000	0.0000	-59.392
	chr17	40156721	mm39_cpg_islands	0.0000	0.0000	-59.392
Rn18s	chr17	40156721	mm39_genes_promoters	0.0000	0.0000	-59.392
Rn45s	chr17	40157426	mm39_genes_exons	0.0000	0.0257	-34.747
	chr17	40157426	mm39_cpg_shores	0.0000	0.0257	-34.747
Rn18s	chr17	40157426	mm39_genes_exons	0.0000	0.0257	-34.747
Rn45s	chr17	40157430	mm39_genes_exons	0.0000	0.0069	-37.301
	chr17	40157430	mm39_cpg_shores	0.0000	0.0069	-37.301
Rn18s	chr17	40157430	mm39_genes_exons	0.0000	0.0069	-37.301
Rn45s	chr17	40157446	mm39_genes_exons	0.0000	0.0008	-41.372
	chr17	40157446	mm39_cpg_shores	0.0000	0.0008	-41.372
Rn18s	chr17	40157446	mm39_genes_exons	0.0000	0.0008	-41.372
Rn45s	chr17	40157576	mm39_genes_exons	0.0000	0.0000	-17.176
	chr17	40157576	mm39_cpg_shores	0.0000	0.0000	-17.176
Rn18s	chr17	40157576	mm39_genes_exons	0.0000	0.0000	-17.176
Rn45s	chr17	40158228	mm39_genes_exons	0.0000	0.0000	11.366
	chr17	40158228	mm39_cpg_shores	0.0000	0.0000	11.366
Rn18s	chr17	40158228	mm39_genes_exons	0.0000	0.0000	11.366
Rn45s	chr17	40158235	mm39_genes_exons	0.0000	0.0000	13.232
	chr17	40158235	mm39_cpg_shores	0.0000	0.0000	13.232
Rn18s	chr17	40158235	mm39_genes_exons	0.0000	0.0000	13.232
Rn45s	chr17	40158245	mm39_genes_exons	0.0000	0.0000	12.937
	chr17	40158245	mm39_cpg_shores	0.0000	0.0000	12.937
Rn18s	chr17	40158245	mm39_genes_exons	0.0000	0.0000	12.937
Rn45s	chr17	40158413	mm39_genes_exons	0.0000	0.0000	7.936
	chr17	40158413	mm39_cpg_shores	0.0000	0.0000	7.936
Rn18s	chr17	40158413	mm39_genes_exons	0.0000	0.0000	7.936
Rn45s	chr17	40158456	mm39_genes_exons	0.0000	0.0000	6.256
	chr17	40158456	mm39_cpg_shores	0.0000	0.0000	6.256
Rn18s	chr17	40158456	mm39_genes_exons	0.0000	0.0000	6.256
Rn45s	chr17	40158485	mm39_genes_exons	0.0000	0.0000	7.624
	chr17	40158485	mm39_cpg_shores	0.0000	0.0000	7.624
Rn18s	chr17	40158485	mm39_genes_exons	0.0000	0.0000	7.624
Rn45s	chr17	40158677	mm39_genes_exons	0.0000	0.0101	6.818
	chr17	40158677	mm39_cpg_shores	0.0000	0.0101	6.818
Rn18s	chr17	40158677	mm39_genes_exons	0.0000	0.0101	6.818
Rn45s	chr17	40158764	mm39_genes_exons	0.0000	0.0112	5.424
	chr17	40158764	mm39_cpg_shores	0.0000	0.0112	5.424
Rn18s	chr17	40158764	mm39_genes_exons	0.0000	0.0112	5.424
Rn45s	chr17	40158815	mm39_genes_exons	0.0000	0.0000	-40.586
	chr17	40158815	mm39_cpg_shores	0.0000	0.0000	-40.586

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Rn18s	chr17	40158815	mm39_genes_exons	0.0000	0.0000	-40.586
Rn45s	chr17	40159239	mm39_genes_exons	0.0000	0.0036	-26.190
Rn18s	chr17	40159239	mm39_genes_exonintronboundaries	0.0000	0.0036	-26.190
	chr17	40159239	mm39_cpg_islands	0.0000	0.0036	-26.190
Rn45s	chr17	40159298	mm39_genes_exons	0.0000	0.0176	-5.699
	chr17	40159298	mm39_cpg_islands	0.0000	0.0176	-5.699
Hsp90ab1	chr17	45883544	mm39_genes_introns	0.0000	0.0001	-27.654
	chr17	45883544	mm39_cpg_islands	0.0000	0.0001	-27.654
	chr17	47093736	mm39_cpg_inter	0.0000	0.0000	-73.171
Rpl7l1	chr17	47093736	mm39_genes_exonintronboundaries	0.0000	0.0000	-73.171
Rpl7l1	chr17	47093736	mm39_genes_intronexonboundaries	0.0000	0.0000	-73.171
Rpl7l1	chr17	47093736	mm39_genes_promoters	0.0000	0.0000	-73.171
	chr17	47784684	mm39_genes_intergenic	0.0000	0.0762	-30.078
	chr17	47784684	mm39_cpg_inter	0.0000	0.0762	-30.078
Oard1	chr17	48716702	mm39_genes_promoters	0.0000	0.0213	-26.015
Oard1	chr17	48716702	mm39_genes_promoters	0.0000	0.0213	-26.015
Oard1	chr17	48716702	mm39_genes_promoters	0.0000	0.0213	-26.015
Oard1	chr17	48716702	mm39_genes_promoters	0.0000	0.0213	-26.015
	chr17	48716702	mm39_cpg_islands	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_exonintronboundaries	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_exonintronboundaries	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_exonintronboundaries	0.0000	0.0213	-26.015
Oard1	chr17	48716702	mm39_genes_promoters	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_intronexonboundaries	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_intronexonboundaries	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_intronexonboundaries	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_5UTRs	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_5UTRs	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_exons	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_exons	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_5UTRs	0.0000	0.0213	-26.015
Nfya	chr17	48716702	mm39_genes_exons	0.0000	0.0213	-26.015
	chr17	49735946	mm39_cpg_shores	0.0000	0.0000	-49.294
Mocs1	chr17	49735946	mm39_genes_introns	0.0000	0.0000	-49.294
Mocs1	chr17	49735946	mm39_genes_introns	0.0000	0.0000	-49.294
Kat2b	chr17	53874147	mm39_genes_exons	0.0000	0.0958	-27.713
Kat2b	chr17	53874147	mm39_genes_exons	0.0000	0.0958	-27.713
Kat2b	chr17	53874147	mm39_genes_5UTRs	0.0000	0.0958	-27.713
	chr17	53874147	mm39_cpg_islands	0.0000	0.0958	-27.713
Stap2	chr17	56316599	mm39_genes_1to5kb	0.0000	0.0010	-29.678
	chr17	56316599	mm39_cpg_islands	0.0000	0.0010	-29.678
Stap2	chr17	56316599	mm39_genes_1to5kb	0.0000	0.0010	-29.678
Mpnd	chr17	56316599	mm39_genes_exonintronboundaries	0.0000	0.0010	-29.678
Mpnd	chr17	56316599	mm39_genes_introns	0.0000	0.0010	-29.678
Micos13	chr17	56920366	mm39_genes_1to5kb	0.0000	0.0000	13.953
Rpl36	chr17	56920366	mm39_genes_promoters	0.0000	0.0000	13.953
Rpl36	chr17	56920366	mm39_genes_exonintronboundaries	0.0000	0.0000	13.953
	chr17	56920366	mm39_cpg_islands	0.0000	0.0000	13.953
	chr17	57138400	mm39_cpg_islands	0.0000	0.0256	-46.071
Rfx2	chr17	57138400	mm39_genes_promoters	0.0000	0.0256	-46.071
Rfx2	chr17	57138400	mm39_genes_promoters	0.0000	0.0256	-46.071

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr17	63189078	mm39_cpg_islands	0.0000	0.0000	47.917
Efna5	chr17	63189078	mm39_genes_promoters	0.0000	0.0000	47.917
Efna5	chr17	63189078	mm39_genes_promoters	0.0000	0.0000	47.917
	chr17	63189123	mm39_cpg_islands	0.0000	0.0000	20.599
Efna5	chr17	63189123	mm39_genes_promoters	0.0000	0.0000	20.599
Efna5	chr17	63189123	mm39_genes_promoters	0.0000	0.0000	20.599
	chr17	66508807	mm39_cpg_inter	0.0000	0.0022	40.785
	chr17	66508807	mm39_genes_intergenic	0.0000	0.0022	40.785
Mtcl1	chr17	66755442	mm39_genes_exonintronboundaries	0.0000	0.0000	-52.378
Mtcl1	chr17	66755442	mm39_genes_exonintronboundaries	0.0000	0.0000	-52.378
Mtcl1	chr17	66755442	mm39_genes_exons	0.0000	0.0000	-52.378
Mtcl1	chr17	66755442	mm39_genes_exons	0.0000	0.0000	-52.378
	chr17	66755442	mm39_cpg_islands	0.0000	0.0000	-52.378
Mtcl1	chr17	66757418	mm39_genes_promoters	0.0000	0.0069	24.654
Mtcl1	chr17	66757418	mm39_genes_promoters	0.0000	0.0069	24.654
	chr17	66757418	mm39_cpg_shores	0.0000	0.0069	24.654
Epb41l3	chr17	69464525	mm39_genes_introns	0.0000	0.0000	26.371
Epb41l3	chr17	69464525	mm39_genes_1to5kb	0.0000	0.0000	26.371
Epb41l3	chr17	69464525	mm39_genes_1to5kb	0.0000	0.0000	26.371
Epb41l3	chr17	69464525	mm39_genes_1to5kb	0.0000	0.0000	26.371
Epb41l3	chr17	69464525	mm39_genes_1to5kb	0.0000	0.0000	26.371
	chr17	69464525	mm39_cpg_islands	0.0000	0.0000	26.371
Epb41l3	chr17	69464525	mm39_genes_introns	0.0000	0.0000	26.371
	chr17	74189279	mm39_cpg_inter	0.0000	0.0000	-63.235
	chr17	74189279	mm39_genes_intergenic	0.0000	0.0000	-63.235
	chr17	80787500	mm39_cpg_islands	0.0000	0.0308	13.951
Sos1	chr17	80787500	mm39_genes_exons	0.0000	0.0308	13.951
Sos1	chr17	80787500	mm39_genes_5UTRs	0.0000	0.0308	13.951
Zfp36l2	chr17	84493840	mm39_genes_exons	0.0000	0.0387	-23.540
Gm41640	chr17	84493840	mm39_genes_1to5kb	0.0000	0.0387	-23.540
	chr17	84493840	mm39_cpg_islands	0.0000	0.0387	-23.540
	chr17	85793596	mm39_genes_intergenic	0.0000	0.0000	-79.622
	chr17	85793596	mm39_cpg_shores	0.0000	0.0000	-79.622
	chr17	87510041	mm39_cpg_inter	0.0000	0.0008	53.846
	chr17	87510041	mm39_genes_intergenic	0.0000	0.0008	53.846
Mcfd2	chr17	87573557	mm39_genes_intronexonboundaries	0.0000	0.0000	-30.072
Mcfd2	chr17	87573557	mm39_genes_intronexonboundaries	0.0000	0.0000	-30.072
	chr17	87573557	mm39_cpg_shores	0.0000	0.0000	-30.072
Mcfd2	chr17	87573557	mm39_genes_promoters	0.0000	0.0000	-30.072
Mcfd2	chr17	87573557	mm39_genes_promoters	0.0000	0.0000	-30.072
	chr17	91044279	mm39_cpg_inter	0.0000	0.0505	36.667
Nrxn1	chr17	91044279	mm39_genes_introns	0.0000	0.0505	36.667
Nrxn1	chr17	91044279	mm39_genes_introns	0.0000	0.0505	36.667
Nrxn1	chr17	91044279	mm39_genes_introns	0.0000	0.0505	36.667
	chr18	5162290	mm39_genes_intergenic	0.0000	0.0008	-44.830
	chr18	5162290	mm39_cpg_shores	0.0000	0.0008	-44.830
	chr18	6676299	mm39_cpg_inter	0.0000	0.0008	70.000
	chr18	6676299	mm39_genes_intergenic	0.0000	0.0008	70.000
	chr18	9214732	mm39_cpg_islands	0.0000	0.0009	-70.531
Fzd8	chr18	9214732	mm39_genes_exons	0.0000	0.0009	-70.531
Thoc1	chr18	9958089	mm39_genes_promoters	0.0000	0.0000	-37.669

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr18	9958089	mm39_cpg_islands	0.0000	0.0000	-37.669
Thoc1	chr18	9958089	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.669
4930563E18Rik	chr18	10706409	mm39_genes_promoters	0.0000	0.0000	-66.109
Abhd3	chr18	10706409	mm39_genes_introns	0.0000	0.0000	-66.109
	chr18	10706409	mm39_cpg_islands	0.0000	0.0000	-66.109
Abhd3	chr18	10706409	mm39_genes_exonintronboundaries	0.0000	0.0000	-66.109
4930563E18Rik	chr18	10706410	mm39_genes_promoters	0.0000	0.0000	31.609
Abhd3	chr18	10706410	mm39_genes_introns	0.0000	0.0000	31.609
	chr18	10706410	mm39_cpg_islands	0.0000	0.0000	31.609
Abhd3	chr18	10706410	mm39_genes_exonintronboundaries	0.0000	0.0000	31.609
Gata6	chr18	11049475	mm39_genes_1to5kb	0.0000	0.0007	-65.362
Gata6os	chr18	11049475	mm39_genes_introns	0.0000	0.0007	-65.362
	chr18	11049475	mm39_cpg_shores	0.0000	0.0007	-65.362
	chr18	20890556	mm39_cpg_inter	0.0000	0.0069	-50.000
	chr18	20890556	mm39_genes_intergenic	0.0000	0.0069	-50.000
	chr18	25190322	mm39_cpg_inter	0.0000	0.0396	38.710
Fhod3	chr18	25190322	mm39_genes_introns	0.0000	0.0396	38.710
Fhod3	chr18	25190322	mm39_genes_introns	0.0000	0.0396	38.710
Fhod3	chr18	25190322	mm39_genes_introns	0.0000	0.0396	38.710
	chr18	27201417	mm39_genes_intergenic	0.0000	0.0826	64.286
	chr18	27201417	mm39_cpg_inter	0.0000	0.0826	64.286
	chr18	32064571	mm39_cpg_inter	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_introns	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_exonintronboundaries	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_exonintronboundaries	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_5UTRs	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_exons	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_exons	0.0000	0.0204	-20.536
Lims2	chr18	32064571	mm39_genes_5UTRs	0.0000	0.0204	-20.536
Epb41l4aos	chr18	33927830	mm39_genes_promoters	0.0000	0.0001	-83.939
Epb41l4aos	chr18	33927830	mm39_genes_promoters	0.0000	0.0001	-83.939
	chr18	33927830	mm39_cpg_islands	0.0000	0.0001	-83.939
Dnajc18	chr18	35835843	mm39_genes_introns	0.0000	0.0000	-53.841
	chr18	35835843	mm39_cpg_shores	0.0000	0.0000	-53.841
Dnajc18	chr18	35836037	mm39_genes_introns	0.0000	0.0000	41.026
	chr18	35836037	mm39_cpg_shores	0.0000	0.0000	41.026
Dnajc18	chr18	35836037	mm39_genes_exonintronboundaries	0.0000	0.0000	41.026
Dnajc18	chr18	35836037	mm39_genes_intronexonboundaries	0.0000	0.0000	41.026
	chr18	36969634	mm39_genes_intergenic	0.0000	0.0039	-24.528
	chr18	36969634	mm39_cpg_inter	0.0000	0.0039	-24.528
	chr18	38158889	mm39_cpg_inter	0.0000	0.0110	37.500
	chr18	38158889	mm39_genes_intergenic	0.0000	0.0110	37.500
	chr18	38158890	mm39_cpg_inter	0.0000	0.0266	-62.012
	chr18	38158890	mm39_genes_intergenic	0.0000	0.0266	-62.012
	chr18	38627955	mm39_cpg_inter	0.0000	0.0071	-21.622
	chr18	38627955	mm39_genes_intergenic	0.0000	0.0071	-21.622
Spry4	chr18	38733872	mm39_genes_introns	0.0000	0.0255	-48.718
	chr18	38733872	mm39_cpg_islands	0.0000	0.0255	-48.718
	chr18	40352372	mm39_cpg_islands	0.0000	0.0000	-38.246
Yipf5	chr18	40352372	mm39_genes_exonintronboundaries	0.0000	0.0000	-38.246
Yipf5	chr18	40352372	mm39_genes_intronexonboundaries	0.0000	0.0000	-38.246

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Yipf5	chr18	40352372	mm39_genes_5UTRs	0.0000	0.0000	-38.246
Yipf5	chr18	40352372	mm39_genes_exons	0.0000	0.0000	-38.246
	chr18	59308953	mm39_cpg_islands	0.0000	0.0000	-54.362
Chsy3	chr18	59308953	mm39_genes_exons	0.0000	0.0000	-54.362
	chr18	61201366	mm39_cpg_inter	0.0000	0.0960	32.057
Pdgfrb	chr18	61201366	mm39_genes_intronexonboundaries	0.0000	0.0960	32.057
Pdgfrb	chr18	61201366	mm39_genes_intronexonboundaries	0.0000	0.0960	32.057
Pdgfrb	chr18	61201366	mm39_genes_exonintronboundaries	0.0000	0.0960	32.057
Pdgfrb	chr18	61201366	mm39_genes_exonintronboundaries	0.0000	0.0960	32.057
Pdgfrb	chr18	61201366	mm39_genes_introns	0.0000	0.0960	32.057
Pdgfrb	chr18	61201366	mm39_genes_introns	0.0000	0.0960	32.057
	chr18	63055831	mm39_cpg_islands	0.0000	0.0506	-23.898
Apcdd1	chr18	63055831	mm39_genes_exonintronboundaries	0.0000	0.0506	-23.898
Apcdd1	chr18	63055831	mm39_genes_introns	0.0000	0.0506	-23.898
	chr18	68825205	mm39_cpg_inter	0.0000	0.0283	-6.677
	chr18	68825205	mm39_genes_intergenic	0.0000	0.0283	-6.677
	chr18	73755917	mm39_genes_intergenic	0.0000	0.0063	-26.744
	chr18	73755917	mm39_cpg_shores	0.0000	0.0063	-26.744
	chr18	73760201	mm39_genes_intergenic	0.0000	0.0002	14.764
	chr18	73760201	mm39_cpg_shelves	0.0000	0.0002	14.764
	chr18	75500814	mm39_cpg_islands	0.0000	0.0000	-57.547
Gm20544	chr18	75500814	mm39_genes_promoters	0.0000	0.0000	-57.547
Smad7	chr18	75500814	mm39_genes_exons	0.0000	0.0000	-57.547
Smad7	chr18	75500814	mm39_genes_5UTRs	0.0000	0.0000	-57.547
Tshz1	chr18	84104064	mm39_genes_introns	0.0000	0.0003	-68.966
Tshz1	chr18	84104064	mm39_genes_introns	0.0000	0.0003	-68.966
Zadh2	chr18	84104064	mm39_genes_1to5kb	0.0000	0.0003	-68.966
	chr18	84104064	mm39_cpg_islands	0.0000	0.0003	-68.966
Tshz1	chr18	84104064	mm39_genes_exons	0.0000	0.0003	-68.966
Tshz1	chr18	84104064	mm39_genes_5UTRs	0.0000	0.0003	-68.966
Tshz1	chr18	84104064	mm39_genes_exonintronboundaries	0.0000	0.0003	-68.966
	chr19	4253363	mm39_cpg_shores	0.0000	0.0097	-33.278
Rad9a	chr19	4253363	mm39_genes_1to5kb	0.0000	0.0097	-33.278
Mus81	chr19	5541386	mm39_genes_1to5kb	0.0000	0.0000	15.231
Mus81	chr19	5541386	mm39_genes_1to5kb	0.0000	0.0000	15.231
Mus81	chr19	5541386	mm39_genes_1to5kb	0.0000	0.0000	15.231
	chr19	5541386	mm39_cpg_islands	0.0000	0.0000	15.231
Cfl1	chr19	5541386	mm39_genes_introns	0.0000	0.0000	15.231
	chr19	6127169	mm39_cpg_inter	0.0000	0.0000	-44.052
Tmem262	chr19	6127169	mm39_genes_1to5kb	0.0000	0.0000	-44.052
Vps51	chr19	6127169	mm39_genes_exonintronboundaries	0.0000	0.0000	-44.052
Vps51	chr19	6127169	mm39_genes_exons	0.0000	0.0000	-44.052
Vps51	chr19	6127169	mm39_genes_intronexonboundaries	0.0000	0.0000	-44.052
Bad	chr19	6929341	mm39_genes_exonintronboundaries	0.0000	0.0122	-27.377
Bad	chr19	6929341	mm39_genes_exonintronboundaries	0.0000	0.0122	-27.377
	chr19	6929341	mm39_cpg_islands	0.0000	0.0122	-27.377
	chr19	6929341	mm39_genes_intergenic	0.0000	0.0122	-27.377
Spindoc	chr19	7359764	mm39_genes_introns	0.0000	0.0018	-35.487
Spindoc	chr19	7359764	mm39_genes_introns	0.0000	0.0018	-35.487
1700105P06Rik	chr19	7359764	mm39_genes_promoters	0.0000	0.0018	-35.487
	chr19	7359764	mm39_cpg_islands	0.0000	0.0018	-35.487

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr19	8780060	mm39_cpg_inter	0.0000	0.0000	-45.495
Polr2g	chr19	8780060	mm39_genes_1to5kb	0.0000	0.0000	-45.495
Zbtb3	chr19	8780060	mm39_genes_exonintronboundaries	0.0000	0.0000	-45.495
Zbtb3	chr19	8780060	mm39_genes_exonintronboundaries	0.0000	0.0000	-45.495
Zbtb3	chr19	8780060	mm39_genes_introns	0.0000	0.0000	-45.495
Zbtb3	chr19	8780060	mm39_genes_introns	0.0000	0.0000	-45.495
Ganab	chr19	8875404	mm39_genes_promoters	0.0000	0.0000	-57.212
Ganab	chr19	8875404	mm39_genes_promoters	0.0000	0.0000	-57.212
Ints5	chr19	8875404	mm39_genes_exonintronboundaries	0.0000	0.0000	-57.212
	chr19	8875404	mm39_cpg_islands	0.0000	0.0000	-57.212
Ganab	chr19	8875404	mm39_genes_exonintronboundaries	0.0000	0.0000	-57.212
Ganab	chr19	8875404	mm39_genes_exonintronboundaries	0.0000	0.0000	-57.212
	chr19	25352372	mm39_cpg_inter	0.0000	0.0804	-26.970
Kank1	chr19	25352372	mm39_genes_introns	0.0000	0.0804	-26.970
Kank1	chr19	25352372	mm39_genes_introns	0.0000	0.0804	-26.970
D930032P07Rik	chr19	28657114	mm39_genes_introns	0.0000	0.0002	-77.701
Glis3	chr19	28657114	mm39_genes_exonintronboundaries	0.0000	0.0002	-77.701
Glis3	chr19	28657114	mm39_genes_exonintronboundaries	0.0000	0.0002	-77.701
Glis3	chr19	28657114	mm39_genes_5UTRs	0.0000	0.0002	-77.701
Glis3	chr19	28657114	mm39_genes_5UTRs	0.0000	0.0002	-77.701
Glis3	chr19	28657114	mm39_genes_exons	0.0000	0.0002	-77.701
Glis3	chr19	28657114	mm39_genes_exons	0.0000	0.0002	-77.701
	chr19	28657114	mm39_cpg_islands	0.0000	0.0002	-77.701
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
Cdc37l1	chr19	28967670	mm39_genes_promoters	0.0000	0.0000	18.930
	chr19	28967670	mm39_cpg_islands	0.0000	0.0000	18.930
Slc16a12	chr19	34724248	mm39_genes_introns	0.0000	0.0008	-76.923
	chr19	34724248	mm39_cpg_shores	0.0000	0.0008	-76.923
Fgfbp3	chr19	36896057	mm39_genes_exons	0.0000	0.0000	-60.000
	chr19	36896057	mm39_cpg_islands	0.0000	0.0000	-60.000
Kif11	chr19	37365140	mm39_genes_exonintronboundaries	0.0000	0.0146	41.791
	chr19	37365140	mm39_cpg_shores	0.0000	0.0146	41.791
Kif11	chr19	37365140	mm39_genes_introns	0.0000	0.0146	41.791
E030044B06Rik	chr19	40861919	mm39_genes_introns	0.0000	0.0001	55.556
	chr19	40861919	mm39_cpg_islands	0.0000	0.0001	55.556
Frat2	chr19	41839686	mm39_genes_1to5kb	0.0000	0.0095	-32.593
	chr19	41839686	mm39_cpg_shelves	0.0000	0.0095	-32.593
Lzts2	chr19	45005977	mm39_genes_introns	0.0000	0.0000	-41.690
Lzts2	chr19	45005977	mm39_genes_introns	0.0000	0.0000	-41.690
	chr19	45005977	mm39_cpg_shores	0.0000	0.0000	-41.690
Lzts2	chr19	45005977	mm39_genes_promoters	0.0000	0.0000	-41.690
	chr19	46678360	mm39_cpg_islands	0.0000	0.0381	65.909
Borcs7	chr19	46678360	mm39_genes_exonintronboundaries	0.0000	0.0381	65.909
Borcs7	chr19	46678360	mm39_genes_exons	0.0000	0.0381	65.909
Borcs7	chr19	46678360	mm39_genes_5UTRs	0.0000	0.0381	65.909

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr19	46678403	mm39_cpg_islands	0.0000	0.0000	43.112
Borcs7	chr19	46678403	mm39_genes_exonintronboundaries	0.0000	0.0000	43.112
Borcs7	chr19	46678403	mm39_genes_exons	0.0000	0.0000	43.112
Xpnpep1	chr19	53026838	mm39_genes_introns	0.0000	0.0000	23.521
Xpnpep1	chr19	53026838	mm39_genes_introns	0.0000	0.0000	23.521
	chr19	53026838	mm39_cpg_islands	0.0000	0.0000	23.521
Xpnpep1	chr19	53026838	mm39_genes_exonintronboundaries	0.0000	0.0000	23.521
Xpnpep1	chr19	53026838	mm39_genes_exonintronboundaries	0.0000	0.0000	23.521
Xpnpep1	chr19	53026838	mm39_genes_intronexonboundaries	0.0000	0.0000	23.521
	chr19	53839136	mm39_cpg_inter	0.0000	0.0024	-62.069
Rbm20	chr19	53839136	mm39_genes_introns	0.0000	0.0024	-62.069
Shoc2	chr19	53932694	mm39_genes_promoters	0.0000	0.0000	-85.691
Bbip1	chr19	53932694	mm39_genes_introns	0.0000	0.0000	-85.691
Shoc2	chr19	53932694	mm39_genes_promoters	0.0000	0.0000	-85.691
Shoc2	chr19	53932694	mm39_genes_promoters	0.0000	0.0000	-85.691
	chr19	53932694	mm39_cpg_islands	0.0000	0.0000	-85.691
Bbip1	chr19	53932694	mm39_genes_exonintronboundaries	0.0000	0.0000	-85.691
Bbip1	chr19	53932694	mm39_genes_5UTRs	0.0000	0.0000	-85.691
Bbip1	chr19	53932694	mm39_genes_exons	0.0000	0.0000	-85.691
Shoc2	chr19	53932694	mm39_genes_exonintronboundaries	0.0000	0.0000	-85.691
Bbip1	chr19	53932694	mm39_genes_exonintronboundaries	0.0000	0.0000	-85.691
Dclre1a	chr19	56537288	mm39_genes_promoters	0.0000	0.0005	-27.907
Dclre1a	chr19	56537288	mm39_genes_promoters	0.0000	0.0005	-27.907
Dclre1a	chr19	56537288	mm39_genes_promoters	0.0000	0.0005	-27.907
Dclre1a	chr19	56537288	mm39_genes_promoters	0.0000	0.0005	-27.907
Dclre1a	chr19	56537288	mm39_genes_promoters	0.0000	0.0005	-27.907
Dclre1a	chr19	56537288	mm39_genes_promoters	0.0000	0.0005	-27.907
Nhlrc2	chr19	56537288	mm39_genes_exons	0.0000	0.0005	-27.907
	chr19	56537288	mm39_cpg_islands	0.0000	0.0005	-27.907
Nhlrc2	chr19	56537288	mm39_genes_exonintronboundaries	0.0000	0.0005	-27.907
Adrb1	chr19	56712714	mm39_genes_exons	0.0000	0.0024	-70.952
Adrb1	chr19	56712714	mm39_genes_3UTRs	0.0000	0.0024	-70.952
	chr19	56712714	mm39_cpg_shores	0.0000	0.0024	-70.952
	chr19	57186018	mm39_cpg_inter	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_introns	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_introns	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_introns	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_introns	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_exons	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_exons	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_exons	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_5UTRs	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_5UTRs	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_5UTRs	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.814
Ablim1	chr19	57186018	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.814
	chr2	5719600	mm39_cpg_islands	0.0000	0.0000	-73.732
Camk1d	chr2	5719600	mm39_genes_intronexonboundaries	0.0000	0.0000	-73.732
Camk1d	chr2	5719600	mm39_genes_intronexonboundaries	0.0000	0.0000	-73.732
Camk1d	chr2	5719600	mm39_genes_intronexonboundaries	0.0000	0.0000	-73.732

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Camk1d	chr2	5719600	mm39_genes_promoters	0.0000	0.0000	-73.732
Camk1d	chr2	5719600	mm39_genes_promoters	0.0000	0.0000	-73.732
Camk1d	chr2	5719600	mm39_genes_promoters	0.0000	0.0000	-73.732
	chr2	6511608	mm39_cpg_inter	0.0000	0.0061	51.786
	chr2	6511608	mm39_genes_intergenic	0.0000	0.0061	51.786
4930412O13Rik	chr2	9883610	mm39_genes_1to5kb	0.0000	0.0000	-77.660
	chr2	9883610	mm39_cpg_shores	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_intronexonboundaries	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_intronexonboundaries	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_intronexonboundaries	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_intronexonboundaries	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_promoters	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_promoters	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_promoters	0.0000	0.0000	-77.660
Gata3	chr2	9883610	mm39_genes_promoters	0.0000	0.0000	-77.660
	chr2	11304367	mm39_cpg_inter	0.0000	0.0116	-53.846
Prkcq	chr2	11304367	mm39_genes_exonintronboundaries	0.0000	0.0116	-53.846
Prkcq	chr2	11304367	mm39_genes_introns	0.0000	0.0116	-53.846
Plxdc2	chr2	16361814	mm39_genes_exons	0.0000	0.0923	14.148
Plxdc2	chr2	16361814	mm39_genes_5UTRs	0.0000	0.0923	14.148
	chr2	16361814	mm39_cpg_shores	0.0000	0.0923	14.148
Zmynd19	chr2	24840138	mm39_genes_promoters	0.0000	0.0000	-43.466
	chr2	24840138	mm39_cpg_islands	0.0000	0.0000	-43.466
Zmynd19	chr2	24840138	mm39_genes_exonintronboundaries	0.0000	0.0000	-43.466
Zmynd19	chr2	24840138	mm39_genes_introns	0.0000	0.0000	-43.466
Ndor1	chr2	25146041	mm39_genes_promoters	0.0000	0.0737	-16.552
Ndor1	chr2	25146041	mm39_genes_promoters	0.0000	0.0737	-16.552
Ndor1	chr2	25146041	mm39_genes_promoters	0.0000	0.0737	-16.552
Tmem203	chr2	25146041	mm39_genes_exons	0.0000	0.0737	-16.552
	chr2	25146041	mm39_cpg_shores	0.0000	0.0737	-16.552
Camsap1	chr2	25872726	mm39_genes_introns	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_introns	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_introns	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_introns	0.0000	0.0000	-50.208
	chr2	25872726	mm39_cpg_islands	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.208
Camsap1	chr2	25872726	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.208
Camsap1	chr2	25872771	mm39_genes_introns	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_introns	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_introns	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_introns	0.0000	0.0000	-33.380
	chr2	25872771	mm39_cpg_islands	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_exonintronboundaries	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_exonintronboundaries	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_exonintronboundaries	0.0000	0.0000	-33.380
Camsap1	chr2	25872771	mm39_genes_exonintronboundaries	0.0000	0.0000	-33.380
Lhx3	chr2	26096717	mm39_genes_introns	0.0000	0.0000	-33.530
Lhx3	chr2	26096717	mm39_genes_intronexonboundaries	0.0000	0.0000	-33.530
Lhx3	chr2	26096717	mm39_genes_promoters	0.0000	0.0000	-33.530

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr2	26096717	mm39_cpg_shores	0.0000	0.0000	-33.530
Snapc4	chr2	26270442	mm39_genes_introns	0.0000	0.0032	65.574
Snapc4	chr2	26270442	mm39_genes_introns	0.0000	0.0032	65.574
	chr2	26270442	mm39_cpg_islands	0.0000	0.0032	65.574
Snapc4	chr2	26270442	mm39_genes_exonintronboundaries	0.0000	0.0032	65.574
Snapc4	chr2	26270442	mm39_genes_exonintronboundaries	0.0000	0.0032	65.574
	chr2	26270661	mm39_cpg_islands	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_exonintronboundaries	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_exonintronboundaries	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_intronexonboundaries	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_intronexonboundaries	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_5UTRs	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_5UTRs	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_exons	0.0000	0.0236	-45.833
Snapc4	chr2	26270661	mm39_genes_exons	0.0000	0.0236	-45.833
	chr2	26754172	mm39_cpg_inter	0.0000	0.0610	-40.000
Abo	chr2	26754172	mm39_genes_introns	0.0000	0.0610	-40.000
Abo	chr2	26754172	mm39_genes_introns	0.0000	0.0610	-40.000
Barhl1	chr2	28802597	mm39_genes_introns	0.0000	0.0000	-72.058
Barhl1	chr2	28802597	mm39_genes_introns	0.0000	0.0000	-72.058
Barhl1	chr2	28802597	mm39_genes_introns	0.0000	0.0000	-72.058
	chr2	28802597	mm39_cpg_shores	0.0000	0.0000	-72.058
Barhl1	chr2	28802597	mm39_genes_exonintronboundaries	0.0000	0.0000	-72.058
Barhl1	chr2	28802597	mm39_genes_intronexonboundaries	0.0000	0.0000	-72.058
Barhl1	chr2	28802597	mm39_genes_promoters	0.0000	0.0000	-72.058
	chr2	29510137	mm39_cpg_islands	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_introns	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_introns	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_introns	0.0000	0.0000	-37.815
Rapgef1	chr2	29510137	mm39_genes_introns	0.0000	0.0000	-37.815
	chr2	30306197	mm39_cpg_islands	0.0000	0.0000	-50.598
Crat	chr2	30306197	mm39_genes_promoters	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_exons	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_exons	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_exons	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_5UTRs	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_5UTRs	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_5UTRs	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.598
Ptpa	chr2	30306197	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.598
Hmcn2	chr2	31205257	mm39_genes_introns	0.0000	0.0073	-49.027
	chr2	31205257	mm39_cpg_shores	0.0000	0.0073	-49.027
	chr2	31974345	mm39_cpg_islands	0.0000	0.0000	-51.114
Fam78a	chr2	31974345	mm39_genes_promoters	0.0000	0.0000	-51.114
Fam78a	chr2	31974345	mm39_genes_exonintronboundaries	0.0000	0.0000	-51.114
Fam78a	chr2	31974345	mm39_genes_exons	0.0000	0.0000	-51.114

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Dnm1	chr2	32202089	mm39_genes_introns	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_introns	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_introns	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_introns	0.0000	0.0010	-27.806
	chr2	32202089	mm39_cpg_islands	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_exonintronboundaries	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_exonintronboundaries	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_exonintronboundaries	0.0000	0.0010	-27.806
Dnm1	chr2	32202089	mm39_genes_exonintronboundaries	0.0000	0.0010	-27.806
	chr2	32203172	mm39_cpg_shores	0.0000	0.0379	-61.538
Dnm1	chr2	32203172	mm39_genes_introns	0.0000	0.0379	-61.538
Dnm1	chr2	32203172	mm39_genes_introns	0.0000	0.0379	-61.538
Dnm1	chr2	32203172	mm39_genes_introns	0.0000	0.0379	-61.538
Dnm1	chr2	32203172	mm39_genes_introns	0.0000	0.0379	-61.538
Gsn	chr2	35158312	mm39_genes_introns	0.0000	0.0012	-82.353
	chr2	35158312	mm39_cpg_inter	0.0000	0.0012	-82.353
Gsn	chr2	35158312	mm39_genes_introns	0.0000	0.0012	-82.353
Gsn	chr2	35158312	mm39_genes_introns	0.0000	0.0012	-82.353
Gsn	chr2	35158312	mm39_genes_introns	0.0000	0.0012	-82.353
Gsn	chr2	35158312	mm39_genes_introns	0.0000	0.0012	-82.353
Gsn	chr2	35158312	mm39_genes_introns	0.0000	0.0012	-82.353
	chr2	44262587	mm39_cpg_inter	0.0000	0.0250	-85.714
Arhgap15	chr2	44262587	mm39_genes_introns	0.0000	0.0250	-85.714
Arhgap15	chr2	44262587	mm39_genes_introns	0.0000	0.0250	-85.714
Arhgap15	chr2	44262587	mm39_genes_introns	0.0000	0.0250	-85.714
Arhgap15	chr2	44262587	mm39_genes_introns	0.0000	0.0250	-85.714
Galnt13	chr2	54326223	mm39_genes_promoters	0.0000	0.0170	-29.391
	chr2	54326223	mm39_cpg_islands	0.0000	0.0170	-29.391
	chr2	54891144	mm39_cpg_inter	0.0000	0.0064	-27.705
Galnt13	chr2	54891144	mm39_genes_introns	0.0000	0.0064	-27.705
	chr2	60185595	mm39_cpg_inter	0.0000	0.0965	-20.339
Ly75	chr2	60185595	mm39_genes_introns	0.0000	0.0965	-20.339
Ly75	chr2	60185595	mm39_genes_exonintronboundaries	0.0000	0.0965	-20.339
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
Tank	chr2	61423966	mm39_genes_introns	0.0000	0.0001	-36.212
	chr2	61423966	mm39_cpg_shores	0.0000	0.0001	-36.212
	chr2	65136765	mm39_cpg_inter	0.0000	0.0173	75.000
	chr2	65136765	mm39_genes_intergenic	0.0000	0.0173	75.000
	chr2	68207234	mm39_cpg_inter	0.0000	0.0036	-29.004
Stk39	chr2	68207234	mm39_genes_introns	0.0000	0.0036	-29.004
Gorasp2	chr2	70491753	mm39_genes_promoters	0.0000	0.0488	-16.667
Gorasp2	chr2	70491753	mm39_genes_promoters	0.0000	0.0488	-16.667
	chr2	70491753	mm39_cpg_islands	0.0000	0.0488	-16.667
	chr2	71617323	mm39_cpg_islands	0.0000	0.0289	-49.932

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Itga6	chr2	71617323	mm39_genes_exons	0.0000	0.0289	-49.932
Itga6	chr2	71617323	mm39_genes_exons	0.0000	0.0289	-49.932
Itga6	chr2	71617323	mm39_genes_5UTRs	0.0000	0.0289	-49.932
Itga6	chr2	71617323	mm39_genes_5UTRs	0.0000	0.0289	-49.932
	chr2	71617327	mm39_cpg_islands	0.0000	0.0011	-58.604
Itga6	chr2	71617327	mm39_genes_exons	0.0000	0.0011	-58.604
Itga6	chr2	71617327	mm39_genes_exons	0.0000	0.0011	-58.604
Itga6	chr2	71617327	mm39_genes_5UTRs	0.0000	0.0011	-58.604
Itga6	chr2	71617327	mm39_genes_5UTRs	0.0000	0.0011	-58.604
	chr2	71617338	mm39_cpg_islands	0.0000	0.0211	-51.626
Itga6	chr2	71617338	mm39_genes_exons	0.0000	0.0211	-51.626
Itga6	chr2	71617338	mm39_genes_exons	0.0000	0.0211	-51.626
Itga6	chr2	71617338	mm39_genes_5UTRs	0.0000	0.0211	-51.626
Itga6	chr2	71617338	mm39_genes_5UTRs	0.0000	0.0211	-51.626
	chr2	72258035	mm39_cpg_inter	0.0000	0.0080	80.000
Map3k20	chr2	72258035	mm39_genes_introns	0.0000	0.0080	80.000
Hoxd10	chr2	74518015	mm39_genes_1to5kb	0.0000	0.0023	15.386
	chr2	74518015	mm39_cpg_islands	0.0000	0.0023	15.386
Hnrnpa3	chr2	75490576	mm39_genes_introns	0.0000	0.0002	46.797
Hnrnpa3	chr2	75490576	mm39_genes_introns	0.0000	0.0002	46.797
Hnrnpa3	chr2	75490576	mm39_genes_introns	0.0000	0.0002	46.797
Hnrnpa3	chr2	75490576	mm39_genes_introns	0.0000	0.0002	46.797
Gm39859	chr2	75490576	mm39_genes_1to5kb	0.0000	0.0002	46.797
Gm39859	chr2	75490576	mm39_genes_1to5kb	0.0000	0.0002	46.797
	chr2	75490576	mm39_cpg_shores	0.0000	0.0002	46.797
Pjvk	chr2	76478702	mm39_genes_1to5kb	0.0000	0.0000	26.316
	chr2	76478702	mm39_cpg_islands	0.0000	0.0000	26.316
Prkra	chr2	76478702	mm39_genes_promoters	0.0000	0.0000	26.316
Zfp385b	chr2	77647958	mm39_genes_promoters	0.0000	0.0000	34.528
	chr2	77647958	mm39_cpg_shores	0.0000	0.0000	34.528
	chr2	82237487	mm39_cpg_inter	0.0000	0.0162	-65.909
	chr2	82237487	mm39_genes_intergenic	0.0000	0.0162	-65.909
	chr2	83704123	mm39_cpg_inter	0.0000	0.0000	-38.409
Fam171b	chr2	83704123	mm39_genes_introns	0.0000	0.0000	-38.409
	chr2	90411156	mm39_cpg_islands	0.0000	0.0002	-67.941
Ptprj	chr2	90411156	mm39_genes_promoters	0.0000	0.0002	-67.941
	chr2	91274931	mm39_cpg_inter	0.0000	0.0000	79.070
Cstpp1	chr2	91274931	mm39_genes_exonintronboundaries	0.0000	0.0000	79.070
Cstpp1	chr2	91274931	mm39_genes_exonintronboundaries	0.0000	0.0000	79.070
Cstpp1	chr2	91274931	mm39_genes_intronexonboundaries	0.0000	0.0000	79.070
Cstpp1	chr2	91274931	mm39_genes_intronexonboundaries	0.0000	0.0000	79.070
Cstpp1	chr2	91274931	mm39_genes_exons	0.0000	0.0000	79.070
Cstpp1	chr2	91274931	mm39_genes_exons	0.0000	0.0000	79.070
	chr2	92430806	mm39_cpg_islands	0.0000	0.0000	-28.439
Chst1	chr2	92430806	mm39_genes_promoters	0.0000	0.0000	-28.439
Chst1	chr2	92430806	mm39_genes_introns	0.0000	0.0000	-28.439
Chst1	chr2	92430806	mm39_genes_introns	0.0000	0.0000	-28.439
	chr2	92937827	mm39_cpg_inter	0.0000	0.0430	-59.211
	chr2	92937827	mm39_genes_intergenic	0.0000	0.0430	-59.211
Hsd17b12	chr2	93987844	mm39_genes_introns	0.0000	0.0512	-22.009
	chr2	93987844	mm39_cpg_shores	0.0000	0.0512	-22.009

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr2	98492946	mm39_cpg_inter	0.0000	0.0595	-15.317
	chr2	98492946	mm39_genes_intergenic	0.0000	0.0595	-15.317
	chr2	98497436	mm39_cpg_inter	0.0000	0.0000	28.543
	chr2	98497436	mm39_genes_intergenic	0.0000	0.0000	28.543
	chr2	98497494	mm39_cpg_inter	0.0000	0.0033	21.160
	chr2	98497494	mm39_genes_intergenic	0.0000	0.0033	21.160
Depdc7	chr2	104573411	mm39_genes_promoters	0.0000	0.0000	-50.870
	chr2	104573411	mm39_cpg_shores	0.0000	0.0000	-50.870
	chr2	105443976	mm39_cpg_inter	0.0000	0.0473	-33.560
Pax6os1	chr2	105443976	mm39_genes_introns	0.0000	0.0473	-33.560
Bdnf	chr2	109507618	mm39_genes_introns	0.0000	0.0082	44.636
Bdnf	chr2	109507618	mm39_genes_introns	0.0000	0.0082	44.636
Bdnf	chr2	109507618	mm39_genes_introns	0.0000	0.0082	44.636
Bdnf	chr2	109507618	mm39_genes_introns	0.0000	0.0082	44.636
Bdnf	chr2	109507618	mm39_genes_exonintronboundaries	0.0000	0.0082	44.636
	chr2	109507618	mm39_cpg_islands	0.0000	0.0082	44.636
Bdnf	chr2	109507618	mm39_genes_introns	0.0000	0.0082	44.636
Slc12a6	chr2	112095995	mm39_genes_promoters	0.0000	0.0000	25.114
Slc12a6	chr2	112095995	mm39_genes_promoters	0.0000	0.0000	25.114
	chr2	112095995	mm39_cpg_islands	0.0000	0.0000	25.114
	chr2	112198366	mm39_cpg_islands	0.0000	0.0079	-27.569
Emc4	chr2	112198366	mm39_genes_exons	0.0000	0.0079	-27.569
Emc4	chr2	112198366	mm39_genes_intronexonboundaries	0.0000	0.0079	-27.569
Emc4	chr2	112198366	mm39_genes_5UTRs	0.0000	0.0079	-27.569
Aqr	chr2	114005309	mm39_genes_introns	0.0000	0.0511	51.724
Aqr	chr2	114005309	mm39_genes_introns	0.0000	0.0511	51.724
	chr2	114005309	mm39_cpg_shores	0.0000	0.0511	51.724
	chr2	118058368	mm39_cpg_inter	0.0000	0.0128	42.500
Fsip1	chr2	118058368	mm39_genes_introns	0.0000	0.0128	42.500
Fsip1	chr2	118058368	mm39_genes_introns	0.0000	0.0128	42.500
Rhov	chr2	119101679	mm39_genes_exons	0.0000	0.0000	-41.053
	chr2	119101679	mm39_cpg_islands	0.0000	0.0000	-41.053
Rhov	chr2	119101679	mm39_genes_intronexonboundaries	0.0000	0.0000	-41.053
Rhov	chr2	119101679	mm39_genes_5UTRs	0.0000	0.0000	-41.053
	chr2	119505396	mm39_cpg_shores	0.0000	0.0080	18.427
Rtf1	chr2	119505396	mm39_genes_promoters	0.0000	0.0080	18.427
Rtf1	chr2	119505423	mm39_genes_promoters	0.0000	0.0005	26.296
	chr2	119505423	mm39_cpg_islands	0.0000	0.0005	26.296
Tyro3	chr2	119630543	mm39_genes_introns	0.0000	0.0000	-63.333
	chr2	119630543	mm39_cpg_islands	0.0000	0.0000	-63.333
Tyro3	chr2	119630543	mm39_genes_exonintronboundaries	0.0000	0.0000	-63.333
Tyro3	chr2	119630543	mm39_genes_introns	0.0000	0.0000	-63.333
Duoxa2	chr2	122128194	mm39_genes_1to5kb	0.0000	0.0070	-44.179
	chr2	122128194	mm39_cpg_shores	0.0000	0.0070	-44.179
Duox2	chr2	122128194	mm39_genes_intronexonboundaries	0.0000	0.0070	-44.179
Duox2	chr2	122128194	mm39_genes_exonintronboundaries	0.0000	0.0070	-44.179
Duox2	chr2	122128194	mm39_genes_introns	0.0000	0.0070	-44.179
Duox2	chr2	122128194	mm39_genes_intronexonboundaries	0.0000	0.0070	-44.179
	chr2	126707325	mm39_cpg_inter	0.0000	0.0018	-86.667
Trpm7	chr2	126707325	mm39_genes_introns	0.0000	0.0018	-86.667
Trpm7	chr2	126707325	mm39_genes_introns	0.0000	0.0018	-86.667

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr2	128809609	mm39_cpg_islands	0.0000	0.0772	-75.455
Zc3h6	chr2	128809609	mm39_genes_exons	0.0000	0.0772	-75.455
Zc3h6	chr2	128809609	mm39_genes_5UTRs	0.0000	0.0772	-75.455
Zc3h6	chr2	128809609	mm39_genes_exonintronboundaries	0.0000	0.0772	-75.455
	chr2	130406050	mm39_cpg_islands	0.0000	0.0000	-39.579
4930473A02Rik	chr2	130406050	mm39_genes_promoters	0.0000	0.0000	-39.579
Mrps26	chr2	130406050	mm39_genes_exonintronboundaries	0.0000	0.0000	-39.579
Mrps26	chr2	130406050	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.579
Mrps26	chr2	130406050	mm39_genes_exonintronboundaries	0.0000	0.0000	-39.579
Mrps26	chr2	130406050	mm39_genes_exons	0.0000	0.0000	-39.579
Mrps26	chr2	130406050	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.579
Ubox5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
Ubox5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
Ubox5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_introns	0.0000	0.0000	-50.989
	chr2	130471696	mm39_cpg_islands	0.0000	0.0000	-50.989
Ubox5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
Ubox5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
Ubox5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
Fastkd5	chr2	130471696	mm39_genes_exonintronboundaries	0.0000	0.0000	-50.989
	chr2	131194693	mm39_cpg_islands	0.0000	0.0093	-30.534
Rnf24	chr2	131194693	mm39_genes_exonintronboundaries	0.0000	0.0093	-30.534
Rnf24	chr2	131194693	mm39_genes_intronexonboundaries	0.0000	0.0093	-30.534
Rnf24	chr2	131194693	mm39_genes_5UTRs	0.0000	0.0093	-30.534
Rnf24	chr2	131194693	mm39_genes_exons	0.0000	0.0093	-30.534
	chr2	133394395	mm39_cpg_islands	0.0000	0.0011	20.133
Bmp2	chr2	133394395	mm39_genes_5UTRs	0.0000	0.0011	20.133
Bmp2	chr2	133394395	mm39_genes_exons	0.0000	0.0011	20.133
Ovol2	chr2	144172726	mm39_genes_introns	0.0000	0.0000	-51.908
Ovol2	chr2	144172726	mm39_genes_introns	0.0000	0.0000	-51.908
	chr2	144172726	mm39_cpg_islands	0.0000	0.0000	-51.908
Ovol2	chr2	144172726	mm39_genes_exonintronboundaries	0.0000	0.0000	-51.908
Ovol2	chr2	144172726	mm39_genes_exonintronboundaries	0.0000	0.0000	-51.908
	chr2	145994977	mm39_cpg_inter	0.0000	0.0498	35.294
Cfap61	chr2	145994977	mm39_genes_introns	0.0000	0.0498	35.294
Nkx2-2os	chr2	147036211	mm39_genes_introns	0.0000	0.0001	-38.933
	chr2	147036211	mm39_cpg_islands	0.0000	0.0001	-38.933
	chr2	147880754	mm39_genes_intergenic	0.0000	0.0000	-44.753
	chr2	147880754	mm39_cpg_shores	0.0000	0.0000	-44.753
	chr2	148522755	mm39_cpg_shores	0.0000	0.0000	-38.686
Gzf1	chr2	148522755	mm39_genes_promoters	0.0000	0.0000	-38.686
Gzf1	chr2	148522755	mm39_genes_promoters	0.0000	0.0000	-38.686
E130215H24Rik	chr2	150510283	mm39_genes_introns	0.0000	0.0001	14.348
Acss1	chr2	150510283	mm39_genes_intronexonboundaries	0.0000	0.0001	14.348
Acss1	chr2	150510283	mm39_genes_promoters	0.0000	0.0001	14.348

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
E130215H24Rik	chr2	150510283	mm39_genes_intronexonboundaries	0.0000	0.0001	14.348
	chr2	150510283	mm39_cpg_shores	0.0000	0.0001	14.348
	chr2	152299687	mm39_cpg_inter	0.0000	0.0228	47.895
	chr2	152299687	mm39_genes_intergenic	0.0000	0.0228	47.895
	chr2	152511153	mm39_cpg_shores	0.0000	0.0214	-46.743
H13	chr2	152511153	mm39_genes_promoters	0.0000	0.0214	-46.743
H13	chr2	152511153	mm39_genes_promoters	0.0000	0.0214	-46.743
H13	chr2	152511153	mm39_genes_promoters	0.0000	0.0214	-46.743
H13	chr2	152511153	mm39_genes_promoters	0.0000	0.0214	-46.743
	chr2	154862578	mm39_cpg_inter	0.0000	0.0002	46.752
a	chr2	154862578	mm39_genes_introns	0.0000	0.0002	46.752
	chr2	155907488	mm39_cpg_islands	0.0000	0.0001	-37.814
Spag4	chr2	155907488	mm39_genes_exons	0.0000	0.0001	-37.814
Spag4	chr2	155907488	mm39_genes_exonintronboundaries	0.0000	0.0001	-37.814
Lpin3	chr2	160727259	mm39_genes_introns	0.0000	0.0509	-55.814
Lpin3	chr2	160727259	mm39_genes_1to5kb	0.0000	0.0509	-55.814
	chr2	160727259	mm39_cpg_shelves	0.0000	0.0509	-55.814
Jph2	chr2	163205083	mm39_genes_introns	0.0000	0.0886	-53.125
Jph2	chr2	163205083	mm39_genes_introns	0.0000	0.0886	-53.125
	chr2	163205083	mm39_cpg_inter	0.0000	0.0886	-53.125
	chr2	166499486	mm39_cpg_inter	0.0000	0.0001	-37.444
Prex1	chr2	166499486	mm39_genes_introns	0.0000	0.0001	-37.444
Gm14261	chr2	168609200	mm39_genes_exons	0.0000	0.0702	-49.702
Sall4	chr2	168609200	mm39_genes_intronexonboundaries	0.0000	0.0702	-49.702
Sall4	chr2	168609200	mm39_genes_intronexonboundaries	0.0000	0.0702	-49.702
Sall4	chr2	168609200	mm39_genes_intronexonboundaries	0.0000	0.0702	-49.702
	chr2	168609200	mm39_cpg_shores	0.0000	0.0702	-49.702
Sall4	chr2	168609200	mm39_genes_promoters	0.0000	0.0702	-49.702
Sall4	chr2	168609200	mm39_genes_promoters	0.0000	0.0702	-49.702
Sall4	chr2	168609200	mm39_genes_promoters	0.0000	0.0702	-49.702
Fam210b	chr2	172187940	mm39_genes_exonintronboundaries	0.0000	0.0000	-65.822
Fam210b	chr2	172187940	mm39_genes_introns	0.0000	0.0000	-65.822
	chr2	172187940	mm39_cpg_shores	0.0000	0.0000	-65.822
Pmepa1	chr2	173117591	mm39_genes_introns	0.0000	0.0014	-31.602
	chr2	173117591	mm39_cpg_islands	0.0000	0.0014	-31.602
Nelfcd	chr2	174257869	mm39_genes_exonintronboundaries	0.0000	0.0000	-54.595
Nelfcd	chr2	174257869	mm39_genes_introns	0.0000	0.0000	-54.595
	chr2	174257869	mm39_cpg_shores	0.0000	0.0000	-54.595
	chr2	179813446	mm39_cpg_islands	0.0000	0.0002	72.031
Adrm1	chr2	179813446	mm39_genes_exonintronboundaries	0.0000	0.0002	72.031
Adrm1	chr2	179813446	mm39_genes_5UTRs	0.0000	0.0002	72.031
Adrm1	chr2	179813446	mm39_genes_exons	0.0000	0.0002	72.031
	chr2	179813491	mm39_cpg_islands	0.0000	0.0000	21.525
Adrm1	chr2	179813491	mm39_genes_exonintronboundaries	0.0000	0.0000	21.525
Adrm1	chr2	179813491	mm39_genes_introns	0.0000	0.0000	21.525
Dido1	chr2	180351109	mm39_genes_introns	0.0000	0.0008	-24.071
Dido1	chr2	180351109	mm39_genes_introns	0.0000	0.0008	-24.071
Dido1	chr2	180351109	mm39_genes_exons	0.0000	0.0008	-24.071
Gid8	chr2	180351109	mm39_genes_1to5kb	0.0000	0.0008	-24.071
Gid8	chr2	180351109	mm39_genes_1to5kb	0.0000	0.0008	-24.071
	chr2	180351109	mm39_cpg_shores	0.0000	0.0008	-24.071

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Gid8	chr2	180351109	mm39_genes_promoters	0.0000	0.0008	-24.071
	chr3	3593280	mm39_cpg_inter	0.0000	0.0334	72.727
Hnf4g	chr3	3593280	mm39_genes_introns	0.0000	0.0334	72.727
	chr3	5925767	mm39_cpg_inter	0.0000	0.0020	-26.556
	chr3	5925767	mm39_genes_intergenic	0.0000	0.0020	-26.556
	chr3	5925774	mm39_cpg_inter	0.0000	0.0356	-23.268
	chr3	5925774	mm39_genes_intergenic	0.0000	0.0356	-23.268
Snx16	chr3	10504587	mm39_genes_introns	0.0000	0.0275	-21.053
Snx16	chr3	10504587	mm39_genes_introns	0.0000	0.0275	-21.053
	chr3	10504587	mm39_cpg_islands	0.0000	0.0275	-21.053
Ralyl	chr3	13538246	mm39_genes_introns	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_introns	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_introns	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_introns	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_exons	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_exons	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_5UTRs	0.0000	0.0000	-36.910
Ralyl	chr3	13538246	mm39_genes_5UTRs	0.0000	0.0000	-36.910
	chr3	13538246	mm39_cpg_islands	0.0000	0.0000	-36.910
	chr3	14495861	mm39_cpg_inter	0.0000	0.0541	50.208
	chr3	14495861	mm39_genes_intergenic	0.0000	0.0541	50.208
	chr3	18372734	mm39_cpg_inter	0.0000	0.0886	36.957
	chr3	18372734	mm39_genes_intergenic	0.0000	0.0886	36.957
Hps3	chr3	20089273	mm39_genes_exonintronboundaries	0.0000	0.0000	-31.966
Hps3	chr3	20089273	mm39_genes_exonintronboundaries	0.0000	0.0000	-31.966
Hps3	chr3	20089273	mm39_genes_exonintronboundaries	0.0000	0.0000	-31.966
	chr3	20089273	mm39_cpg_islands	0.0000	0.0000	-31.966
Hps3	chr3	20089273	mm39_genes_exons	0.0000	0.0000	-31.966
Hps3	chr3	20089273	mm39_genes_exons	0.0000	0.0000	-31.966
Hps3	chr3	20089273	mm39_genes_exons	0.0000	0.0000	-31.966
	chr3	26838398	mm39_cpg_inter	0.0000	0.0761	-57.721
Spata16	chr3	26838398	mm39_genes_introns	0.0000	0.0761	-57.721
Spata16	chr3	26838398	mm39_genes_introns	0.0000	0.0761	-57.721
	chr3	26838399	mm39_cpg_inter	0.0000	0.0002	-83.333
Spata16	chr3	26838399	mm39_genes_introns	0.0000	0.0002	-83.333
Spata16	chr3	26838399	mm39_genes_introns	0.0000	0.0002	-83.333
	chr3	27993178	mm39_cpg_islands	0.0000	0.0000	-56.993
Pld1	chr3	27993178	mm39_genes_introns	0.0000	0.0000	-56.993
	chr3	27993223	mm39_cpg_islands	0.0000	0.0000	-45.863
Pld1	chr3	27993223	mm39_genes_introns	0.0000	0.0000	-45.863
Tnik	chr3	28317568	mm39_genes_exons	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_exons	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_exons	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_exons	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_5UTRs	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_5UTRs	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_5UTRs	0.0000	0.0032	-30.303
Tnik	chr3	28317568	mm39_genes_5UTRs	0.0000	0.0032	-30.303
	chr3	28317568	mm39_cpg_islands	0.0000	0.0032	-30.303
	chr3	30820035	mm39_cpg_inter	0.0000	0.0598	-52.821
Samd7	chr3	30820035	mm39_genes_exons	0.0000	0.0598	-52.821

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Samd7	chr3	30820035	mm39_genes_exons	0.0000	0.0598	-52.821
Samd7	chr3	30820035	mm39_genes_3UTRs	0.0000	0.0598	-52.821
Sox2ot	chr3	34702228	mm39_genes_introns	0.0000	0.0459	37.931
Sox2	chr3	34702228	mm39_genes_1to5kb	0.0000	0.0459	37.931
	chr3	34702228	mm39_cpg_shores	0.0000	0.0459	37.931
	chr3	36120149	mm39_cpg_islands	0.0000	0.0000	-36.842
Acad9	chr3	36120149	mm39_genes_exons	0.0000	0.0000	-36.842
Acad9	chr3	36120149	mm39_genes_5UTRs	0.0000	0.0000	-36.842
	chr3	47072930	mm39_cpg_inter	0.0000	0.0170	54.094
	chr3	47072930	mm39_genes_intergenic	0.0000	0.0170	54.094
	chr3	51096079	mm39_cpg_inter	0.0000	0.0573	-42.000
	chr3	51096079	mm39_genes_intergenic	0.0000	0.0573	-42.000
	chr3	56122978	mm39_cpg_inter	0.0000	0.0019	-48.641
	chr3	56122978	mm39_genes_intergenic	0.0000	0.0019	-48.641
	chr3	58277276	mm39_cpg_inter	0.0000	0.0519	-56.183
	chr3	58277276	mm39_genes_intergenic	0.0000	0.0519	-56.183
Dhx36	chr3	62414306	mm39_genes_exonintronboundaries	0.0000	0.0456	-27.688
	chr3	62414306	mm39_cpg_islands	0.0000	0.0456	-27.688
Dhx36	chr3	62414306	mm39_genes_exons	0.0000	0.0456	-27.688
Dhx36	chr3	62414306	mm39_genes_intronexonboundaries	0.0000	0.0456	-27.688
Etfdh	chr3	79534930	mm39_genes_introns	0.0000	0.0027	-67.463
4930579G24Rik	chr3	79534930	mm39_genes_1to5kb	0.0000	0.0027	-67.463
	chr3	79534930	mm39_cpg_shores	0.0000	0.0027	-67.463
	chr3	84122751	mm39_cpg_inter	0.0000	0.0843	25.041
Trim2	chr3	84122751	mm39_genes_introns	0.0000	0.0843	25.041
Trim2	chr3	84122751	mm39_genes_introns	0.0000	0.0843	25.041
Trim2	chr3	84122751	mm39_genes_introns	0.0000	0.0843	25.041
Trim2	chr3	84122751	mm39_genes_introns	0.0000	0.0843	25.041
Trim2	chr3	84122751	mm39_genes_1to5kb	0.0000	0.0843	25.041
	chr3	85094352	mm39_cpg_inter	0.0000	0.0553	-29.075
	chr3	85094352	mm39_genes_intergenic	0.0000	0.0553	-29.075
Lmna	chr3	88399768	mm39_genes_introns	0.0000	0.0000	-75.499
Lmna	chr3	88399768	mm39_genes_introns	0.0000	0.0000	-75.499
Lmna	chr3	88399768	mm39_genes_introns	0.0000	0.0000	-75.499
	chr3	88399768	mm39_cpg_inter	0.0000	0.0000	-75.499
	chr3	88433368	mm39_cpg_inter	0.0000	0.0400	-63.410
	chr3	88433368	mm39_genes_intergenic	0.0000	0.0400	-63.410
Trim46	chr3	89153938	mm39_genes_promoters	0.0000	0.0000	-42.791
Trim46	chr3	89153938	mm39_genes_1to5kb	0.0000	0.0000	-42.791
Trim46	chr3	89153938	mm39_genes_1to5kb	0.0000	0.0000	-42.791
Krtcap2	chr3	89153938	mm39_genes_exonintronboundaries	0.0000	0.0000	-42.791
	chr3	89153938	mm39_cpg_islands	0.0000	0.0000	-42.791
Krtcap2	chr3	89153938	mm39_genes_exonintronboundaries	0.0000	0.0000	-42.791
Krtcap2	chr3	89153938	mm39_genes_introns	0.0000	0.0000	-42.791
Krtcap2	chr3	89153938	mm39_genes_intronexonboundaries	0.0000	0.0000	-42.791
Krtcap2	chr3	89153938	mm39_genes_intronexonboundaries	0.0000	0.0000	-42.791
Krtcap2	chr3	89153938	mm39_genes_introns	0.0000	0.0000	-42.791
	chr3	89256731	mm39_cpg_shores	0.0000	0.0000	-86.792
Adam15	chr3	89256731	mm39_genes_introns	0.0000	0.0000	-86.792
Adam15	chr3	89256731	mm39_genes_introns	0.0000	0.0000	-86.792
Lor	chr3	91988828	mm39_genes_exons	0.0000	0.0000	18.533

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr3	91988828	mm39_cpg_islands	0.0000	0.0000	18.533
Vps72	chr3	95014187	mm39_genes_1to5kb	0.0000	0.0001	69.667
	chr3	95014187	mm39_cpg_islands	0.0000	0.0001	69.667
Pip5k1a	chr3	95014187	mm39_genes_exons	0.0000	0.0001	69.667
Pip5k1a	chr3	95014187	mm39_genes_exons	0.0000	0.0001	69.667
Pip5k1a	chr3	95014187	mm39_genes_5UTRs	0.0000	0.0001	69.667
Pip5k1a	chr3	95014187	mm39_genes_5UTRs	0.0000	0.0001	69.667
Pip5k1a	chr3	95014187	mm39_genes_intronexonboundaries	0.0000	0.0001	69.667
Pip5k1a	chr3	95014187	mm39_genes_intronexonboundaries	0.0000	0.0001	69.667
	chr3	95190535	mm39_cpg_shores	0.0000	0.0076	-17.554
Mindy1	chr3	95190535	mm39_genes_5UTRs	0.0000	0.0076	-17.554
Mindy1	chr3	95190535	mm39_genes_5UTRs	0.0000	0.0076	-17.554
Mindy1	chr3	95190535	mm39_genes_exons	0.0000	0.0076	-17.554
Mindy1	chr3	95190535	mm39_genes_exons	0.0000	0.0076	-17.554
Prune1	chr3	95190535	mm39_genes_1to5kb	0.0000	0.0076	-17.554
	chr3	95726894	mm39_cpg_islands	0.0000	0.0008	-72.000
Rprd2	chr3	95726894	mm39_genes_promoters	0.0000	0.0008	-72.000
Rprd2	chr3	95726894	mm39_genes_promoters	0.0000	0.0008	-72.000
Rprd2	chr3	95726894	mm39_genes_promoters	0.0000	0.0008	-72.000
Rprd2	chr3	95726894	mm39_genes_promoters	0.0000	0.0008	-72.000
Rprd2	chr3	95726894	mm39_genes_promoters	0.0000	0.0008	-72.000
Rprd2	chr3	95726894	mm39_genes_promoters	0.0000	0.0008	-72.000
Acp6	chr3	97066344	mm39_genes_exons	0.0000	0.0000	-86.842
Acp6	chr3	97066344	mm39_genes_5UTRs	0.0000	0.0000	-86.842
	chr3	97066344	mm39_cpg_islands	0.0000	0.0000	-86.842
	chr3	101070228	mm39_cpg_inter	0.0000	0.0822	-27.665
	chr3	101070228	mm39_genes_intergenic	0.0000	0.0822	-27.665
	chr3	104713046	mm39_cpg_inter	0.0000	0.0998	-28.947
Mov10	chr3	104713046	mm39_genes_introns	0.0000	0.0998	-28.947
Mov10	chr3	104713046	mm39_genes_introns	0.0000	0.0998	-28.947
Mov10	chr3	104713046	mm39_genes_introns	0.0000	0.0998	-28.947
Kcnd3os	chr3	105359720	mm39_genes_introns	0.0000	0.0000	-55.093
	chr3	105359720	mm39_cpg_islands	0.0000	0.0000	-55.093
Kcnd3	chr3	105359720	mm39_genes_5UTRs	0.0000	0.0000	-55.093
Kcnd3	chr3	105359720	mm39_genes_5UTRs	0.0000	0.0000	-55.093
Kcnd3	chr3	105359720	mm39_genes_exons	0.0000	0.0000	-55.093
Kcnd3	chr3	105359720	mm39_genes_exons	0.0000	0.0000	-55.093
Kcnd3os	chr3	105359720	mm39_genes_exonintronboundaries	0.0000	0.0000	-55.093
	chr3	107241241	mm39_cpg_islands	0.0000	0.0054	16.547
Rbm15	chr3	107241241	mm39_genes_promoters	0.0000	0.0054	16.547
	chr3	107490823	mm39_genes_intergenic	0.0000	0.0001	-88.406
	chr3	107490823	mm39_cpg_shores	0.0000	0.0001	-88.406
Ahcyl1	chr3	107603338	mm39_genes_introns	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_introns	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_5UTRs	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_exons	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_5UTRs	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_5UTRs	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_exons	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_exons	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_intronexonboundaries	0.0000	0.0000	-88.785

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P* -value	Adjusted *P* -value (*Q* -value)	Methylation difference (%)
Ahcyl1	chr3	107603338	mm39_genes_intronexonboundaries	0.0000	0.0000	-88.785
	chr3	107603338	mm39_cpg_islands	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_exonintronboundaries	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_exonintronboundaries	0.0000	0.0000	-88.785
Ahcyl1	chr3	107603338	mm39_genes_intronexonboundaries	0.0000	0.0000	-88.785
Vav3	chr3	109274177	mm39_genes_introns	0.0000	0.0445	-16.364
Vav3	chr3	109274177	mm39_genes_introns	0.0000	0.0445	-16.364
	chr3	109274177	mm39_cpg_inter	0.0000	0.0445	-16.364
	chr3	112998191	mm39_cpg_inter	0.0000	0.0334	50.000
	chr3	112998191	mm39_genes_intergenic	0.0000	0.0334	50.000
	chr3	121084889	mm39_cpg_shores	0.0000	0.0409	-54.545
Alg14	chr3	121084889	mm39_genes_promoters	0.0000	0.0409	-54.545
Alg14	chr3	121084889	mm39_genes_promoters	0.0000	0.0409	-54.545
	chr3	121220266	mm39_cpg_islands	0.0000	0.0922	-14.094
Cnn3	chr3	121220266	mm39_genes_exons	0.0000	0.0922	-14.094
Cnn3	chr3	121220266	mm39_genes_5UTRs	0.0000	0.0922	-14.094
	chr3	122086771	mm39_genes_intergenic	0.0000	0.0000	-50.199
	chr3	122086771	mm39_cpg_shores	0.0000	0.0000	-50.199
Prss12	chr3	123241299	mm39_genes_exonintronboundaries	0.0000	0.0036	24.723
	chr3	123241299	mm39_cpg_shores	0.0000	0.0036	24.723
Prss12	chr3	123241299	mm39_genes_introns	0.0000	0.0036	24.723
	chr3	127419050	mm39_genes_intergenic	0.0000	0.0143	-29.849
	chr3	127419050	mm39_cpg_islands	0.0000	0.0143	-29.849
	chr3	133187542	mm39_cpg_inter	0.0000	0.0001	62.429
Tet2	chr3	133187542	mm39_genes_introns	0.0000	0.0001	62.429
Tet2	chr3	133187542	mm39_genes_introns	0.0000	0.0001	62.429
	chr3	138351112	mm39_cpg_inter	0.0000	0.0756	-54.203
	chr3	138351112	mm39_genes_intergenic	0.0000	0.0756	-54.203
	chr3	148694658	mm39_genes_intergenic	0.0000	0.0000	31.356
	chr3	148694658	mm39_cpg_islands	0.0000	0.0000	31.356
	chr4	5211545	mm39_cpg_inter	0.0000	0.0000	-61.255
	chr4	5211545	mm39_genes_intergenic	0.0000	0.0000	-61.255
	chr4	9150832	mm39_genes_intergenic	0.0000	0.0038	72.475
	chr4	9150832	mm39_cpg_inter	0.0000	0.0038	72.475
	chr4	19333147	mm39_cpg_inter	0.0000	0.0738	-78.571
Cngb3	chr4	19333147	mm39_genes_introns	0.0000	0.0738	-78.571
	chr4	20042108	mm39_cpg_islands	0.0000	0.0098	-22.173
Ggh	chr4	20042108	mm39_genes_exons	0.0000	0.0098	-22.173
Ggh	chr4	20042108	mm39_genes_5UTRs	0.0000	0.0098	-22.173
Ggh	chr4	20042108	mm39_genes_exonintronboundaries	0.0000	0.0098	-22.173
	chr4	20042153	mm39_cpg_islands	0.0000	0.0543	-19.491
Ggh	chr4	20042153	mm39_genes_exons	0.0000	0.0543	-19.491
Ggh	chr4	20042153	mm39_genes_5UTRs	0.0000	0.0543	-19.491
Ggh	chr4	20042153	mm39_genes_exonintronboundaries	0.0000	0.0543	-19.491
Fbxl4	chr4	22370780	mm39_genes_introns	0.0000	0.0000	80.491
Fbxl4	chr4	22370780	mm39_genes_introns	0.0000	0.0000	80.491
Fbxl4	chr4	22370780	mm39_genes_introns	0.0000	0.0000	80.491
Fbxl4	chr4	22370780	mm39_genes_introns	0.0000	0.0000	80.491
	chr4	22370780	mm39_cpg_inter	0.0000	0.0000	80.491
	chr4	22498608	mm39_genes_intergenic	0.0000	0.0000	-92.857
	chr4	22498608	mm39_cpg_shores	0.0000	0.0000	-92.857

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Manea	chr4	26346410	mm39_genes_introns	0.0000	0.0002	-33.665
Manea	chr4	26346410	mm39_genes_exonintronboundaries	0.0000	0.0002	-33.665
	chr4	26346410	mm39_cpg_islands	0.0000	0.0002	-33.665
	chr4	28176846	mm39_cpg_inter	0.0000	0.0000	-66.922
	chr4	28176846	mm39_genes_intergenic	0.0000	0.0000	-66.922
	chr4	28765683	mm39_cpg_inter	0.0000	0.0577	66.667
	chr4	28765683	mm39_genes_intergenic	0.0000	0.0577	66.667
	chr4	28765693	mm39_cpg_inter	0.0000	0.0577	66.667
	chr4	28765693	mm39_genes_intergenic	0.0000	0.0577	66.667
	chr4	40143523	mm39_cpg_islands	0.0000	0.0000	-57.174
Aco1	chr4	40143523	mm39_genes_5UTRs	0.0000	0.0000	-57.174
Aco1	chr4	40143523	mm39_genes_exons	0.0000	0.0000	-57.174
Aco1	chr4	40143523	mm39_genes_exonintronboundaries	0.0000	0.0000	-57.174
	chr4	41712214	mm39_cpg_shores	0.0000	0.0591	-60.526
Rpp25l	chr4	41712214	mm39_genes_exons	0.0000	0.0591	-60.526
Rpp25l	chr4	41712214	mm39_genes_3UTRs	0.0000	0.0591	-60.526
Rgp1	chr4	43577258	mm39_genes_1to5kb	0.0000	0.0040	82.353
Gba2	chr4	43577258	mm39_genes_introns	0.0000	0.0040	82.353
	chr4	43577258	mm39_cpg_shores	0.0000	0.0040	82.353
	chr4	46188115	mm39_cpg_inter	0.0000	0.0168	35.484
Xpa	chr4	46188115	mm39_genes_introns	0.0000	0.0168	35.484
	chr4	49434423	mm39_cpg_inter	0.0000	0.0796	63.158
	chr4	49434423	mm39_genes_intergenic	0.0000	0.0796	63.158
	chr4	59783064	mm39_cpg_shores	0.0000	0.0000	-42.454
Inip	chr4	59783064	mm39_genes_introns	0.0000	0.0000	-42.454
	chr4	62008738	mm39_cpg_inter	0.0000	0.0482	85.714
Mup3	chr4	62008738	mm39_genes_1to5kb	0.0000	0.0482	85.714
Mup3	chr4	62008738	mm39_genes_1to5kb	0.0000	0.0482	85.714
	chr4	62501351	mm39_cpg_shores	0.0000	0.0000	-42.985
Rgs3	chr4	62501351	mm39_genes_introns	0.0000	0.0000	-42.985
	chr4	68132447	mm39_cpg_inter	0.0000	0.0884	49.690
	chr4	68132447	mm39_genes_intergenic	0.0000	0.0884	49.690
	chr4	82415634	mm39_cpg_inter	0.0000	0.0691	-16.327
Nfib	chr4	82415634	mm39_genes_introns	0.0000	0.0691	-16.327
Nfib	chr4	82415634	mm39_genes_introns	0.0000	0.0691	-16.327
Nfib	chr4	82415634	mm39_genes_introns	0.0000	0.0691	-16.327
Nfib	chr4	82415634	mm39_genes_introns	0.0000	0.0691	-16.327
Nfib	chr4	82415634	mm39_genes_introns	0.0000	0.0691	-16.327
Elavl2	chr4	91269530	mm39_genes_introns	0.0000	0.0000	-32.897
Elavl2	chr4	91269530	mm39_genes_introns	0.0000	0.0000	-32.897
Elavl2	chr4	91269530	mm39_genes_1to5kb	0.0000	0.0000	-32.897
Elavl2	chr4	91269530	mm39_genes_1to5kb	0.0000	0.0000	-32.897
Elavl2	chr4	91269530	mm39_genes_1to5kb	0.0000	0.0000	-32.897
Elavl2	chr4	91269530	mm39_genes_1to5kb	0.0000	0.0000	-32.897
	chr4	91269530	mm39_cpg_inter	0.0000	0.0000	-32.897
	chr4	103171176	mm39_cpg_islands	0.0000	0.0319	15.404
Oma1	chr4	103171176	mm39_genes_exonintronboundaries	0.0000	0.0319	15.404
Oma1	chr4	103171176	mm39_genes_introns	0.0000	0.0319	15.404
	chr4	105014031	mm39_cpg_shores	0.0000	0.0000	66.283
Plpp3	chr4	105014031	mm39_genes_promoters	0.0000	0.0000	66.283
Pars2	chr4	106508129	mm39_genes_promoters	0.0000	0.0226	-21.916

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Pars2	chr4	106508129	mm39_genes_promoters	0.0000	0.0226	-21.916
Pars2	chr4	106508129	mm39_genes_promoters	0.0000	0.0226	-21.916
Pars2	chr4	106508129	mm39_genes_promoters	0.0000	0.0226	-21.916
	chr4	106508129	mm39_cpg_islands	0.0000	0.0226	-21.916
Pars2	chr4	106508129	mm39_genes_exonintronboundaries	0.0000	0.0226	-21.916
Pars2	chr4	106508129	mm39_genes_exonintronboundaries	0.0000	0.0226	-21.916
Lrp8	chr4	107659900	mm39_genes_promoters	0.0000	0.0000	-37.622
	chr4	107659900	mm39_cpg_islands	0.0000	0.0000	-37.622
Lrp8os3	chr4	107659900	mm39_genes_promoters	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_introns	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_introns	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_introns	0.0000	0.0000	-37.622
Lrp8	chr4	107659900	mm39_genes_introns	0.0000	0.0000	-37.622
Dmrta2	chr4	109832929	mm39_genes_1to5kb	0.0000	0.0010	23.440
	chr4	109832929	mm39_cpg_shores	0.0000	0.0010	23.440
Dmrta2	chr4	109834815	mm39_genes_promoters	0.0000	0.0000	19.745
	chr4	109834815	mm39_cpg_islands	0.0000	0.0000	19.745
	chr4	109835386	mm39_cpg_islands	0.0000	0.0482	10.857
Dmrta2	chr4	109835386	mm39_genes_5UTRs	0.0000	0.0482	10.857
Dmrta2	chr4	109835386	mm39_genes_exons	0.0000	0.0482	10.857
Dmrta2	chr4	109835386	mm39_genes_exonintronboundaries	0.0000	0.0482	10.857
Trabd2b	chr4	114263711	mm39_genes_promoters	0.0000	0.0000	26.531
	chr4	114263711	mm39_cpg_islands	0.0000	0.0000	26.531
Pik3r3	chr4	116078537	mm39_genes_1to5kb	0.0000	0.0013	-23.434
Pik3r3	chr4	116078537	mm39_genes_promoters	0.0000	0.0013	-23.434
Pik3r3	chr4	116078537	mm39_genes_promoters	0.0000	0.0013	-23.434
Pik3r3	chr4	116078537	mm39_genes_promoters	0.0000	0.0013	-23.434
	chr4	116078537	mm39_cpg_islands	0.0000	0.0013	-23.434
Ebna1bp2	chr4	118477949	mm39_genes_promoters	0.0000	0.0000	49.476
Cfap57	chr4	118477949	mm39_genes_exonintronboundaries	0.0000	0.0000	49.476
Cfap57	chr4	118477949	mm39_genes_intronexonboundaries	0.0000	0.0000	49.476
Cfap57	chr4	118477949	mm39_genes_5UTRs	0.0000	0.0000	49.476
Cfap57	chr4	118477949	mm39_genes_exons	0.0000	0.0000	49.476
	chr4	118477949	mm39_cpg_islands	0.0000	0.0000	49.476
Kcnq4	chr4	120587602	mm39_genes_introns	0.0000	0.0030	-67.647
	chr4	120587602	mm39_cpg_shores	0.0000	0.0030	-67.647
Bmp8b	chr4	122998951	mm39_genes_promoters	0.0000	0.0443	52.865
	chr4	122998951	mm39_cpg_islands	0.0000	0.0443	52.865
Gm2164	chr4	124540667	mm39_genes_introns	0.0000	0.0329	-17.647
	chr4	124540667	mm39_cpg_inter	0.0000	0.0329	-17.647
	chr4	126503814	mm39_cpg_islands	0.0000	0.0038	-32.811
5730409E04Rik	chr4	126503814	mm39_genes_exonintronboundaries	0.0000	0.0038	-32.811
5730409E04Rik	chr4	126503814	mm39_genes_exonintronboundaries	0.0000	0.0038	-32.811
5730409E04Rik	chr4	126503814	mm39_genes_introns	0.0000	0.0038	-32.811
5730409E04Rik	chr4	126503814	mm39_genes_introns	0.0000	0.0038	-32.811
C77080	chr4	129133017	mm39_genes_introns	0.0000	0.0029	16.060
C77080	chr4	129133017	mm39_genes_introns	0.0000	0.0029	16.060

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr4	129133017	mm39_cpg_islands	0.0000	0.0029	16.060
C77080	chr4	129133017	mm39_genes_intronexonboundaries	0.0000	0.0029	16.060
C77080	chr4	129133017	mm39_genes_promoters	0.0000	0.0029	16.060
Fabp3	chr4	130202917	mm39_genes_introns	0.0000	0.0760	21.491
	chr4	130202917	mm39_cpg_shores	0.0000	0.0760	21.491
Zcchc17	chr4	130253386	mm39_genes_introns	0.0000	0.0013	-66.667
Zcchc17	chr4	130253386	mm39_genes_introns	0.0000	0.0013	-66.667
Zcchc17	chr4	130253386	mm39_genes_introns	0.0000	0.0013	-66.667
Zcchc17	chr4	130253386	mm39_genes_introns	0.0000	0.0013	-66.667
Zcchc17	chr4	130253386	mm39_genes_introns	0.0000	0.0013	-66.667
	chr4	130253386	mm39_cpg_shores	0.0000	0.0013	-66.667
Snrnp40	chr4	130253386	mm39_genes_promoters	0.0000	0.0013	-66.667
	chr4	131031999	mm39_genes_intergenic	0.0000	0.0463	-59.091
	chr4	131031999	mm39_cpg_inter	0.0000	0.0463	-59.091
Epb41	chr4	131801548	mm39_genes_introns	0.0000	0.0000	-68.571
	chr4	131801548	mm39_cpg_shores	0.0000	0.0000	-68.571
Epb41	chr4	131801548	mm39_genes_1to5kb	0.0000	0.0000	-68.571
Ahdc1	chr4	132776503	mm39_genes_introns	0.0000	0.0796	28.219
	chr4	132776503	mm39_cpg_inter	0.0000	0.0796	28.219
	chr4	132967990	mm39_cpg_shores	0.0000	0.0153	58.190
Map3k6	chr4	132967990	mm39_genes_promoters	0.0000	0.0153	58.190
	chr4	134262626	mm39_cpg_islands	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_exonintronboundaries	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_exonintronboundaries	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_intronexonboundaries	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_intronexonboundaries	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_promoters	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_intronexonboundaries	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_5UTRs	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_exons	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_promoters	0.0000	0.0001	-35.123
Mtfr1l	chr4	134262626	mm39_genes_promoters	0.0000	0.0001	-35.123
	chr4	134298260	mm39_cpg_inter	0.0000	0.0804	-46.984
Mir6403	chr4	134298260	mm39_genes_1to5kb	0.0000	0.0804	-46.984
Man1c1	chr4	134298260	mm39_genes_introns	0.0000	0.0804	-46.984
Runx3	chr4	134879878	mm39_genes_introns	0.0000	0.0000	-56.842
	chr4	134879878	mm39_cpg_islands	0.0000	0.0000	-56.842
Runx3	chr4	134879878	mm39_genes_exons	0.0000	0.0000	-56.842
Runx3	chr4	134879878	mm39_genes_5UTRs	0.0000	0.0000	-56.842
Runx3	chr4	134879923	mm39_genes_introns	0.0000	0.0000	-52.841
	chr4	134879923	mm39_cpg_islands	0.0000	0.0000	-52.841
Runx3	chr4	134879923	mm39_genes_exons	0.0000	0.0000	-52.841
Runx3	chr4	134879923	mm39_genes_5UTRs	0.0000	0.0000	-52.841
Runx3	chr4	134879923	mm39_genes_intronexonboundaries	0.0000	0.0000	-52.841
	chr4	134985540	mm39_cpg_inter	0.0000	0.0000	-53.825
Clic4	chr4	134985540	mm39_genes_introns	0.0000	0.0000	-53.825
	chr4	135555992	mm39_cpg_inter	0.0000	0.0003	20.712
	chr4	135555992	mm39_genes_intergenic	0.0000	0.0003	20.712
	chr4	135556037	mm39_cpg_inter	0.0000	0.0064	17.859
	chr4	135556037	mm39_genes_intergenic	0.0000	0.0064	17.859
Ephb2	chr4	136553068	mm39_genes_introns	0.0000	0.0001	15.070

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Ephb2	chr4	136553068	mm39_genes_introns	0.0000	0.0001	15.070
	chr4	136553068	mm39_cpg_inter	0.0000	0.0001	15.070
	chr4	138894885	mm39_cpg_inter	0.0000	0.0045	65.854
	chr4	138894885	mm39_genes_intergenic	0.0000	0.0045	65.854
	chr4	138920496	mm39_cpg_islands	0.0000	0.0860	38.712
Capzb	chr4	138920496	mm39_genes_exonintronboundaries	0.0000	0.0860	38.712
Capzb	chr4	138920496	mm39_genes_exonintronboundaries	0.0000	0.0860	38.712
Capzb	chr4	138920496	mm39_genes_introns	0.0000	0.0860	38.712
Capzb	chr4	138920496	mm39_genes_introns	0.0000	0.0860	38.712
Capzb	chr4	138920496	mm39_genes_promoters	0.0000	0.0860	38.712
	chr4	140338346	mm39_cpg_inter	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_introns	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_introns	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_introns	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_introns	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.614
Arhgef10l	chr4	140338346	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.614
	chr4	140805717	mm39_cpg_islands	0.0000	0.0000	-56.134
Necap2	chr4	140805717	mm39_genes_exonintronboundaries	0.0000	0.0000	-56.134
Necap2	chr4	140805717	mm39_genes_exonintronboundaries	0.0000	0.0000	-56.134
Necap2	chr4	140805717	mm39_genes_intronexonboundaries	0.0000	0.0000	-56.134
Necap2	chr4	140805717	mm39_genes_intronexonboundaries	0.0000	0.0000	-56.134
Necap2	chr4	140805717	mm39_genes_promoters	0.0000	0.0000	-56.134
Necap2	chr4	140805717	mm39_genes_promoters	0.0000	0.0000	-56.134
	chr4	141391607	mm39_cpg_islands	0.0000	0.0000	15.752
Plekhm2	chr4	141391607	mm39_genes_intronexonboundaries	0.0000	0.0000	15.752
Plekhm2	chr4	141391607	mm39_genes_intronexonboundaries	0.0000	0.0000	15.752
Plekhm2	chr4	141391607	mm39_genes_promoters	0.0000	0.0000	15.752
Plekhm2	chr4	141391607	mm39_genes_promoters	0.0000	0.0000	15.752
	chr4	148012324	mm39_cpg_inter	0.0000	0.0000	-78.205
Plod1	chr4	148012324	mm39_genes_introns	0.0000	0.0000	-78.205
	chr4	148483921	mm39_cpg_inter	0.0000	0.0163	45.388
	chr4	148483921	mm39_genes_intergenic	0.0000	0.0163	45.388
	chr4	148683732	mm39_cpg_inter	0.0000	0.0183	-74.702
Masp2	chr4	148683732	mm39_genes_1to5kb	0.0000	0.0183	-74.702
Masp2	chr4	148683732	mm39_genes_1to5kb	0.0000	0.0183	-74.702
	chr4	148809252	mm39_genes_intergenic	0.0000	0.0349	48.148
	chr4	148809252	mm39_cpg_shores	0.0000	0.0349	48.148
Rere	chr4	150399929	mm39_genes_introns	0.0000	0.0628	-67.863
	chr4	150399929	mm39_cpg_inter	0.0000	0.0628	-67.863
Rere	chr4	150399938	mm39_genes_introns	0.0000	0.0595	-68.030
	chr4	150399938	mm39_cpg_inter	0.0000	0.0595	-68.030
Rere	chr4	150399961	mm39_genes_introns	0.0000	0.0737	-67.273
	chr4	150399961	mm39_cpg_inter	0.0000	0.0737	-67.273
Slc45a1	chr4	150736478	mm39_genes_introns	0.0000	0.0011	-32.293
Slc45a1	chr4	150736478	mm39_genes_introns	0.0000	0.0011	-32.293
Slc45a1	chr4	150736478	mm39_genes_exonintronboundaries	0.0000	0.0011	-32.293
Slc45a1	chr4	150736478	mm39_genes_exonintronboundaries	0.0000	0.0011	-32.293
	chr4	150736478	mm39_cpg_islands	0.0000	0.0011	-32.293

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P* -value	Adjusted *P* -value (*Q* -value)	Methylation difference (%)
Slc45a1	chr4	150736478	mm39_genes_intronexonboundaries	0.0000	0.0011	-32.293
Slc45a1	chr4	150736478	mm39_genes_intronexonboundaries	0.0000	0.0011	-32.293
Camta1	chr4	151193182	mm39_genes_introns	0.0000	0.0211	-25.775
	chr4	151193182	mm39_cpg_islands	0.0000	0.0211	-25.775
Camta1	chr4	151214225	mm39_genes_introns	0.0000	0.0772	35.294
	chr4	151214225	mm39_cpg_shores	0.0000	0.0772	35.294
	chr4	155120731	mm39_cpg_inter	0.0000	0.0814	33.891
	chr4	155120731	mm39_genes_intergenic	0.0000	0.0814	33.891
	chr4	155515880	mm39_cpg_inter	0.0000	0.0017	77.143
Cfap74	chr4	155515880	mm39_genes_introns	0.0000	0.0017	77.143
Cfap74	chr4	155515880	mm39_genes_introns	0.0000	0.0017	77.143
	chr4	156282381	mm39_cpg_islands	0.0000	0.0005	-24.772
Agrn	chr4	156282381	mm39_genes_promoters	0.0000	0.0005	-24.772
Agrn	chr4	156282381	mm39_genes_promoters	0.0000	0.0005	-24.772
	chr5	15108640	mm39_cpg_inter	0.0000	0.0473	-21.980
	chr5	15108640	mm39_genes_intergenic	0.0000	0.0473	-21.980
	chr5	24978749	mm39_cpg_inter	0.0000	0.0073	-46.992
	chr5	24978749	mm39_genes_intergenic	0.0000	0.0073	-46.992
	chr5	25305009	mm39_cpg_islands	0.0000	0.0000	-91.476
Prkag2	chr5	25305009	mm39_genes_exonintronboundaries	0.0000	0.0000	-91.476
2900005J15Rik	chr5	25305009	mm39_genes_promoters	0.0000	0.0000	-91.476
Prkag2	chr5	25305009	mm39_genes_exons	0.0000	0.0000	-91.476
1700096K18Rik	chr5	25734888	mm39_genes_promoters	0.0000	0.0002	-53.544
	chr5	25734888	mm39_cpg_islands	0.0000	0.0002	-53.544
	chr5	28363372	mm39_cpg_inter	0.0000	0.0100	-30.287
	chr5	28363372	mm39_genes_intergenic	0.0000	0.0100	-30.287
	chr5	29639988	mm39_cpg_islands	0.0000	0.0147	-24.877
Nom1	chr5	29639988	mm39_genes_exons	0.0000	0.0147	-24.877
Nom1	chr5	29639988	mm39_genes_exons	0.0000	0.0147	-24.877
Nom1	chr5	29639988	mm39_genes_exons	0.0000	0.0147	-24.877
	chr5	31078973	mm39_cpg_islands	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_exons	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_exons	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_exons	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_exons	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_5UTRs	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_5UTRs	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_5UTRs	0.0000	0.0085	-30.833
Khk	chr5	31078973	mm39_genes_5UTRs	0.0000	0.0085	-30.833
Slc30a3	chr5	31250681	mm39_genes_introns	0.0000	0.0000	-94.118
	chr5	31250681	mm39_cpg_islands	0.0000	0.0000	-94.118
Slc30a3	chr5	31250681	mm39_genes_exonintronboundaries	0.0000	0.0000	-94.118
Slc30a3	chr5	31250681	mm39_genes_exons	0.0000	0.0000	-94.118
Slc30a3	chr5	31250681	mm39_genes_intronexonboundaries	0.0000	0.0000	-94.118
Babam2	chr5	31855392	mm39_genes_promoters	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_promoters	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_promoters	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_promoters	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_promoters	0.0000	0.0005	-70.096
	chr5	31855392	mm39_cpg_islands	0.0000	0.0005	-70.096
Rbks	chr5	31855392	mm39_genes_promoters	0.0000	0.0005	-70.096

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Babam2	chr5	31855392	mm39_genes_exonintronboundaries	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_exonintronboundaries	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_exonintronboundaries	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_exonintronboundaries	0.0000	0.0005	-70.096
Babam2	chr5	31855392	mm39_genes_exonintronboundaries	0.0000	0.0005	-70.096
	chr5	32290369	mm39_cpg_shores	0.0000	0.0000	-43.283
Fosl2	chr5	32290369	mm39_genes_1to5kb	0.0000	0.0000	-43.283
	chr5	32307798	mm39_cpg_inter	0.0000	0.0219	-42.045
Fosl2	chr5	32307798	mm39_genes_intronexonboundaries	0.0000	0.0219	-42.045
Fosl2	chr5	32307798	mm39_genes_exonintronboundaries	0.0000	0.0219	-42.045
Fosl2	chr5	32307798	mm39_genes_exons	0.0000	0.0219	-42.045
	chr5	32660299	mm39_cpg_inter	0.0000	0.0001	-42.695
	chr5	32660299	mm39_genes_intergenic	0.0000	0.0001	-42.695
	chr5	32917544	mm39_cpg_inter	0.0000	0.0462	38.095
Pisd	chr5	32917544	mm39_genes_introns	0.0000	0.0462	38.095
	chr5	33432594	mm39_cpg_islands	0.0000	0.0019	-29.997
Ctbp1	chr5	33432594	mm39_genes_promoters	0.0000	0.0019	-29.997
Ctbp1	chr5	33432594	mm39_genes_promoters	0.0000	0.0019	-29.997
Ctbp1	chr5	33432594	mm39_genes_promoters	0.0000	0.0019	-29.997
Ctbp1	chr5	33432594	mm39_genes_promoters	0.0000	0.0019	-29.997
Ctbp1	chr5	33432594	mm39_genes_promoters	0.0000	0.0019	-29.997
	chr5	33591054	mm39_cpg_islands	0.0000	0.0000	-33.613
Nkx1-1	chr5	33591054	mm39_genes_exonintronboundaries	0.0000	0.0000	-33.613
Nkx1-1	chr5	33591054	mm39_genes_exons	0.0000	0.0000	-33.613
Hmx1	chr5	35557196	mm39_genes_intronexonboundaries	0.0000	0.0000	-52.018
Hmx1	chr5	35557196	mm39_genes_exons	0.0000	0.0000	-52.018
	chr5	35557196	mm39_cpg_islands	0.0000	0.0000	-52.018
Hmx1	chr5	35557196	mm39_genes_3UTRs	0.0000	0.0000	-52.018
Grpel1	chr5	36622330	mm39_genes_promoters	0.0000	0.0110	-29.545
2210406O10Rik	chr5	36622330	mm39_genes_intronexonboundaries	0.0000	0.0110	-29.545
2210406O10Rik	chr5	36622330	mm39_genes_intronexonboundaries	0.0000	0.0110	-29.545
2210406O10Rik	chr5	36622330	mm39_genes_intronexonboundaries	0.0000	0.0110	-29.545
	chr5	36622330	mm39_cpg_islands	0.0000	0.0110	-29.545
2210406O10Rik	chr5	36622330	mm39_genes_promoters	0.0000	0.0110	-29.545
2210406O10Rik	chr5	36622330	mm39_genes_promoters	0.0000	0.0110	-29.545
2210406O10Rik	chr5	36622330	mm39_genes_promoters	0.0000	0.0110	-29.545
	chr5	37980721	mm39_cpg_shores	0.0000	0.0366	45.238
Msx1	chr5	37980721	mm39_genes_introns	0.0000	0.0366	45.238
	chr5	50855632	mm39_cpg_inter	0.0000	0.0250	-56.000
	chr5	50855632	mm39_genes_intergenic	0.0000	0.0250	-56.000
4932441J04Rik	chr5	57874824	mm39_genes_introns	0.0000	0.0000	52.570
Pcdh7	chr5	57874824	mm39_genes_promoters	0.0000	0.0000	52.570
Pcdh7	chr5	57874824	mm39_genes_promoters	0.0000	0.0000	52.570
Pcdh7	chr5	57874824	mm39_genes_promoters	0.0000	0.0000	52.570
Pcdh7	chr5	57874824	mm39_genes_promoters	0.0000	0.0000	52.570
	chr5	57874824	mm39_cpg_islands	0.0000	0.0000	52.570
0610040J01Rik	chr5	63984350	mm39_genes_introns	0.0000	0.0951	54.861
	chr5	63984350	mm39_cpg_inter	0.0000	0.0951	54.861
	chr5	64317822	mm39_cpg_islands	0.0000	0.0006	37.353
Tbc1d1	chr5	64317822	mm39_genes_5UTRs	0.0000	0.0006	37.353
Tbc1d1	chr5	64317822	mm39_genes_5UTRs	0.0000	0.0006	37.353

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Tbc1d1	chr5	64317822	mm39_genes_exons	0.0000	0.0006	37.353
Tbc1d1	chr5	64317822	mm39_genes_exons	0.0000	0.0006	37.353
Tbc1d1	chr5	64317822	mm39_genes_exonintronboundaries	0.0000	0.0006	37.353
Tbc1d1	chr5	64317822	mm39_genes_exonintronboundaries	0.0000	0.0006	37.353
Smim14	chr5	65650263	mm39_genes_introns	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_introns	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_introns	0.0000	0.0000	-35.419
	chr5	65650263	mm39_cpg_islands	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_exonintronboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_exonintronboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_exonintronboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_intronexonboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_intronexonboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_intronexonboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_promoters	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_exonintronboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_intronexonboundaries	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_promoters	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_promoters	0.0000	0.0000	-35.419
Smim14	chr5	65650263	mm39_genes_promoters	0.0000	0.0000	-35.419
	chr5	80188150	mm39_cpg_inter	0.0000	0.0126	-64.752
	chr5	80188150	mm39_genes_intergenic	0.0000	0.0126	-64.752
	chr5	82202717	mm39_cpg_inter	0.0000	0.0329	-30.887
	chr5	82202717	mm39_genes_intergenic	0.0000	0.0329	-30.887
Cox18	chr5	90372273	mm39_genes_promoters	0.0000	0.0212	-66.667
Cox18	chr5	90372273	mm39_genes_promoters	0.0000	0.0212	-66.667
Cox18	chr5	90372273	mm39_genes_promoters	0.0000	0.0212	-66.667
	chr5	90372273	mm39_cpg_shores	0.0000	0.0212	-66.667
Septin11	chr5	93240965	mm39_genes_promoters	0.0000	0.0000	-90.741
Septin11	chr5	93240965	mm39_genes_promoters	0.0000	0.0000	-90.741
Septin11	chr5	93240965	mm39_genes_promoters	0.0000	0.0000	-90.741
Septin11	chr5	93240965	mm39_genes_promoters	0.0000	0.0000	-90.741
	chr5	93240965	mm39_cpg_islands	0.0000	0.0000	-90.741
Rasgef1b	chr5	99400400	mm39_genes_introns	0.0000	0.0000	-44.676
Rasgef1b	chr5	99400400	mm39_genes_introns	0.0000	0.0000	-44.676
	chr5	99400400	mm39_cpg_islands	0.0000	0.0000	-44.676
Rasgef1b	chr5	99400400	mm39_genes_exonintronboundaries	0.0000	0.0000	-44.676
Rasgef1b	chr5	99400400	mm39_genes_exonintronboundaries	0.0000	0.0000	-44.676
	chr5	101913177	mm39_cpg_islands	0.0000	0.0993	-22.833
Cds1	chr5	101913177	mm39_genes_exons	0.0000	0.0993	-22.833
Cds1	chr5	101913177	mm39_genes_5UTRs	0.0000	0.0993	-22.833
Cds1	chr5	101913177	mm39_genes_exonintronboundaries	0.0000	0.0993	-22.833
Pcgf3	chr5	108609716	mm39_genes_introns	0.0000	0.0087	-48.154
Pcgf3	chr5	108609716	mm39_genes_introns	0.0000	0.0087	-48.154
Pcgf3	chr5	108609716	mm39_genes_introns	0.0000	0.0087	-48.154
	chr5	108609716	mm39_cpg_shores	0.0000	0.0087	-48.154
Gm42151	chr5	108840300	mm39_genes_introns	0.0000	0.0000	-54.456
Fgfrl1	chr5	108840300	mm39_genes_1to5kb	0.0000	0.0000	-54.456
Fgfrl1	chr5	108840300	mm39_genes_1to5kb	0.0000	0.0000	-54.456
Gm42151	chr5	108840300	mm39_genes_introns	0.0000	0.0000	-54.456
Gm42151	chr5	108840300	mm39_genes_introns	0.0000	0.0000	-54.456

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr5	108840300	mm39_cpg_shores	0.0000	0.0000	-54.456
	chr5	109992923	mm39_cpg_inter	0.0000	0.0011	-69.658
	chr5	109992923	mm39_genes_intergenic	0.0000	0.0011	-69.658
	chr5	110071837	mm39_cpg_inter	0.0000	0.0000	-75.240
Gm26808	chr5	110071837	mm39_genes_promoters	0.0000	0.0000	-75.240
	chr5	110144700	mm39_cpg_inter	0.0000	0.0001	-68.085
Zfp932	chr5	110144700	mm39_genes_introns	0.0000	0.0001	-68.085
Zfp932	chr5	110144700	mm39_genes_introns	0.0000	0.0001	-68.085
Pole	chr5	110434004	mm39_genes_promoters	0.0000	0.0000	20.904
Pxmp2	chr5	110434004	mm39_genes_exons	0.0000	0.0000	20.904
	chr5	110434004	mm39_cpg_islands	0.0000	0.0000	20.904
Pxmp2	chr5	110434004	mm39_genes_intronexonboundaries	0.0000	0.0000	20.904
Pxmp2	chr5	110434004	mm39_genes_5UTRs	0.0000	0.0000	20.904
Pole	chr5	110434049	mm39_genes_promoters	0.0000	0.0000	20.669
	chr5	110434049	mm39_cpg_islands	0.0000	0.0000	20.669
Pxmp2	chr5	110434049	mm39_genes_intronexonboundaries	0.0000	0.0000	20.669
Pxmp2	chr5	110434049	mm39_genes_promoters	0.0000	0.0000	20.669
	chr5	110596273	mm39_cpg_islands	0.0000	0.0000	-48.921
Fbrsl1	chr5	110596273	mm39_genes_exons	0.0000	0.0000	-48.921
Fbrsl1	chr5	110596273	mm39_genes_exons	0.0000	0.0000	-48.921
Fbrsl1	chr5	110596273	mm39_genes_5UTRs	0.0000	0.0000	-48.921
Fbrsl1	chr5	110596273	mm39_genes_5UTRs	0.0000	0.0000	-48.921
Fbrsl1	chr5	110596273	mm39_genes_intronexonboundaries	0.0000	0.0000	-48.921
Fbrsl1	chr5	110596273	mm39_genes_intronexonboundaries	0.0000	0.0000	-48.921
Ttc28	chr5	111167401	mm39_genes_introns	0.0000	0.0050	-52.941
	chr5	111167401	mm39_cpg_inter	0.0000	0.0050	-52.941
Ficd	chr5	113873739	mm39_genes_promoters	0.0000	0.0001	46.338
	chr5	113873739	mm39_cpg_islands	0.0000	0.0001	46.338
Svop	chr5	114229392	mm39_genes_exonintronboundaries	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_exonintronboundaries	0.0000	0.0028	-74.915
	chr5	114229392	mm39_cpg_islands	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_5UTRs	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_exons	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_exons	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_intronexonboundaries	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_intronexonboundaries	0.0000	0.0028	-74.915
Svop	chr5	114229392	mm39_genes_5UTRs	0.0000	0.0028	-74.915
	chr5	114581735	mm39_cpg_shores	0.0000	0.0078	48.884
Mmab	chr5	114581735	mm39_genes_introns	0.0000	0.0078	48.884
Mmab	chr5	114581735	mm39_genes_introns	0.0000	0.0078	48.884
Mvk	chr5	114581735	mm39_genes_promoters	0.0000	0.0078	48.884
Mvk	chr5	114581735	mm39_genes_promoters	0.0000	0.0078	48.884
	chr5	115296604	mm39_cpg_islands	0.0000	0.0000	-26.499
Mlec	chr5	115296604	mm39_genes_promoters	0.0000	0.0000	-26.499
	chr5	115553607	mm39_genes_intergenic	0.0000	0.0001	45.330
	chr5	115553607	mm39_cpg_inter	0.0000	0.0001	45.330
Rab35	chr5	115769859	mm39_genes_promoters	0.0000	0.0000	-61.447
1110006O24Rik	chr5	115769859	mm39_genes_exons	0.0000	0.0000	-61.447
	chr5	115769859	mm39_cpg_islands	0.0000	0.0000	-61.447
1110006O24Rik	chr5	115769859	mm39_genes_intronexonboundaries	0.0000	0.0000	-61.447
	chr5	120419481	mm39_cpg_inter	0.0000	0.0002	-31.081

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr5	120419481	mm39_genes_intergenic	0.0000	0.0002	-31.081
Gm27199	chr5	120565690	mm39_genes_introns	0.0000	0.0000	-46.154
Lhx5	chr5	120565690	mm39_genes_1to5kb	0.0000	0.0000	-46.154
	chr5	120565690	mm39_cpg_islands	0.0000	0.0000	-46.154
	chr5	121484382	mm39_cpg_inter	0.0000	0.0959	-41.304
Hectd4	chr5	121484382	mm39_genes_introns	0.0000	0.0959	-41.304
Kdm2b	chr5	123039177	mm39_genes_introns	0.0000	0.0140	-52.369
Kdm2b	chr5	123039177	mm39_genes_introns	0.0000	0.0140	-52.369
Kdm2b	chr5	123039177	mm39_genes_promoters	0.0000	0.0140	-52.369
Kdm2b	chr5	123039177	mm39_genes_promoters	0.0000	0.0140	-52.369
Kdm2b	chr5	123039177	mm39_genes_promoters	0.0000	0.0140	-52.369
	chr5	123039177	mm39_cpg_shores	0.0000	0.0140	-52.369
	chr5	123153361	mm39_cpg_islands	0.0000	0.0000	-57.839
Orai1	chr5	123153361	mm39_genes_exons	0.0000	0.0000	-57.839
	chr5	123153362	mm39_cpg_islands	0.0000	0.0001	22.059
Orai1	chr5	123153362	mm39_genes_exons	0.0000	0.0001	22.059
	chr5	123153405	mm39_cpg_islands	0.0000	0.0001	22.163
Orai1	chr5	123153405	mm39_genes_exons	0.0000	0.0001	22.163
	chr5	123250717	mm39_cpg_inter	0.0000	0.0110	-27.530
Tmem120b	chr5	123250717	mm39_genes_introns	0.0000	0.0110	-27.530
Rilpl1	chr5	124667023	mm39_genes_introns	0.0000	0.0932	8.939
	chr5	124667023	mm39_cpg_shores	0.0000	0.0932	8.939
	chr5	125466183	mm39_cpg_shores	0.0000	0.0002	-29.032
Ubc	chr5	125466183	mm39_genes_introns	0.0000	0.0002	-29.032
	chr5	128940776	mm39_cpg_inter	0.0000	0.0343	-51.082
Rimbp2	chr5	128940776	mm39_genes_introns	0.0000	0.0343	-51.082
Rimbp2	chr5	128940776	mm39_genes_introns	0.0000	0.0343	-51.082
Rimbp2	chr5	128940776	mm39_genes_introns	0.0000	0.0343	-51.082
	chr5	130406671	mm39_cpg_inter	0.0000	0.0016	-66.667
Caln1	chr5	130406671	mm39_genes_introns	0.0000	0.0016	-66.667
Auts2	chr5	131566068	mm39_genes_introns	0.0000	0.0002	-34.437
	chr5	131566068	mm39_cpg_islands	0.0000	0.0002	-34.437
Auts2	chr5	131566903	mm39_genes_introns	0.0000	0.0039	23.969
	chr5	131566903	mm39_cpg_islands	0.0000	0.0039	23.969
	chr5	135518829	mm39_cpg_inter	0.0000	0.0115	-68.182
Hip1	chr5	135518829	mm39_genes_introns	0.0000	0.0115	-68.182
Hip1	chr5	135518829	mm39_genes_promoters	0.0000	0.0115	-68.182
Hip1	chr5	135518829	mm39_genes_promoters	0.0000	0.0115	-68.182
Mdh2	chr5	135807121	mm39_genes_promoters	0.0000	0.0049	-70.833
	chr5	135807121	mm39_cpg_islands	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exonintronboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exonintronboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exonintronboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exonintronboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exonintronboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_intronexonboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_intronexonboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_5UTRs	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_5UTRs	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exons	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exons	0.0000	0.0049	-70.833

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Styxl1	chr5	135807121	mm39_genes_intronexonboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_intronexonboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_intronexonboundaries	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_5UTRs	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_5UTRs	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_5UTRs	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exons	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exons	0.0000	0.0049	-70.833
Styxl1	chr5	135807121	mm39_genes_exons	0.0000	0.0049	-70.833
Mir3470a	chr5	137061860	mm39_genes_introns	0.0000	0.0000	-50.068
	chr5	137061860	mm39_cpg_islands	0.0000	0.0000	-50.068
Vgf	chr5	137061860	mm39_genes_exons	0.0000	0.0000	-50.068
Vgf	chr5	137061860	mm39_genes_3UTRs	0.0000	0.0000	-50.068
Mir3470a	chr5	137260163	mm39_genes_introns	0.0000	0.0457	-19.090
	chr5	137260163	mm39_cpg_inter	0.0000	0.0457	-19.090
	chr5	139019824	mm39_cpg_inter	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
Prkar1b	chr5	139019824	mm39_genes_introns	0.0000	0.0012	47.850
3110082I17Rik	chr5	139366105	mm39_genes_introns	0.0000	0.0021	18.780
	chr5	139366105	mm39_cpg_shores	0.0000	0.0021	18.780
Gpr146	chr5	139366105	mm39_genes_introns	0.0000	0.0021	18.780
Gpr146	chr5	139366105	mm39_genes_promoters	0.0000	0.0021	18.780
	chr5	142449768	mm39_cpg_islands	0.0000	0.0682	-27.264
Ap5z1	chr5	142449768	mm39_genes_exons	0.0000	0.0682	-27.264
Ap5z1	chr5	142449768	mm39_genes_5UTRs	0.0000	0.0682	-27.264
Ap5z1	chr5	142449768	mm39_genes_exonintronboundaries	0.0000	0.0682	-27.264
Mmd2	chr5	142594740	mm39_genes_promoters	0.0000	0.0000	-82.456
	chr5	142594740	mm39_cpg_shores	0.0000	0.0000	-82.456
	chr5	142723982	mm39_cpg_inter	0.0000	0.0822	-60.714
Tnrc18	chr5	142723982	mm39_genes_introns	0.0000	0.0822	-60.714
Tnrc18	chr5	142798522	mm39_genes_introns	0.0000	0.0002	-54.348
Tnrc18	chr5	142798522	mm39_genes_introns	0.0000	0.0002	-54.348
	chr5	142798522	mm39_cpg_shelves	0.0000	0.0002	-54.348
Zfp316	chr5	143239656	mm39_genes_exons	0.0000	0.0000	-49.159
	chr5	143239656	mm39_cpg_islands	0.0000	0.0000	-49.159
Daglb	chr5	143450684	mm39_genes_exonintronboundaries	0.0000	0.0000	-90.411
Daglb	chr5	143450684	mm39_genes_introns	0.0000	0.0000	-90.411
	chr5	143450684	mm39_cpg_shores	0.0000	0.0000	-90.411
Gsx1	chr5	147125479	mm39_genes_promoters	0.0000	0.0000	24.129
	chr5	147125479	mm39_cpg_islands	0.0000	0.0000	24.129
	chr5	147125525	mm39_cpg_islands	0.0000	0.0000	-58.316
Gsx1	chr5	147125525	mm39_genes_exons	0.0000	0.0000	-58.316
Gsx1	chr5	147125525	mm39_genes_5UTRs	0.0000	0.0000	-58.316
	chr5	147236180	mm39_cpg_inter	0.0000	0.0659	-42.222
	chr5	147236180	mm39_genes_intergenic	0.0000	0.0659	-42.222
	chr6	3201534	mm39_cpg_inter	0.0000	0.0115	-41.973

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr6	3201534	mm39_genes_intergenic	0.0000	0.0115	-41.973
	chr6	3201540	mm39_cpg_inter	0.0000	0.0053	-42.222
	chr6	3201540	mm39_genes_intergenic	0.0000	0.0053	-42.222
	chr6	3201555	mm39_cpg_inter	0.0000	0.0000	-48.638
	chr6	3201555	mm39_genes_intergenic	0.0000	0.0000	-48.638
	chr6	3201558	mm39_cpg_inter	0.0000	0.0004	-46.183
	chr6	3201558	mm39_genes_intergenic	0.0000	0.0004	-46.183
	chr6	3201577	mm39_cpg_inter	0.0000	0.0010	-43.888
	chr6	3201577	mm39_genes_intergenic	0.0000	0.0010	-43.888
	chr6	5613771	mm39_cpg_inter	0.0000	0.0002	-35.015
	chr6	5613771	mm39_genes_intergenic	0.0000	0.0002	-35.015
	chr6	5613813	mm39_cpg_inter	0.0000	0.0000	-39.516
	chr6	5613813	mm39_genes_intergenic	0.0000	0.0000	-39.516
Nxph1	chr6	8948920	mm39_genes_1to5kb	0.0000	0.0000	26.468
	chr6	8948920	mm39_cpg_islands	0.0000	0.0000	26.468
	chr6	13272541	mm39_cpg_inter	0.0000	0.0050	88.000
	chr6	13272541	mm39_genes_intergenic	0.0000	0.0050	88.000
	chr6	13871111	mm39_cpg_inter	0.0000	0.0614	30.000
1110019D14Rik	chr6	13871111	mm39_genes_promoters	0.0000	0.0614	30.000
Smim30	chr6	13871111	mm39_genes_exonintronboundaries	0.0000	0.0614	30.000
Smim30	chr6	13871111	mm39_genes_intronexonboundaries	0.0000	0.0614	30.000
Smim30	chr6	13871111	mm39_genes_5UTRs	0.0000	0.0614	30.000
Smim30	chr6	13871111	mm39_genes_exons	0.0000	0.0614	30.000
	chr6	30205930	mm39_genes_intergenic	0.0000	0.0377	-29.890
	chr6	30205930	mm39_cpg_islands	0.0000	0.0377	-29.890
	chr6	31168693	mm39_cpg_inter	0.0000	0.0539	-57.143
Lncpint	chr6	31168693	mm39_genes_introns	0.0000	0.0539	-57.143
Lncpint	chr6	31168693	mm39_genes_introns	0.0000	0.0539	-57.143
Lncpint	chr6	31168693	mm39_genes_introns	0.0000	0.0539	-57.143
Chchd3	chr6	33037323	mm39_genes_intronexonboundaries	0.0000	0.0366	-18.563
Chchd3	chr6	33037323	mm39_genes_intronexonboundaries	0.0000	0.0366	-18.563
Chchd3	chr6	33037323	mm39_genes_promoters	0.0000	0.0366	-18.563
Chchd3	chr6	33037323	mm39_genes_promoters	0.0000	0.0366	-18.563
	chr6	33037323	mm39_cpg_shores	0.0000	0.0366	-18.563
	chr6	43219204	mm39_cpg_inter	0.0000	0.0000	-74.194
	chr6	43219204	mm39_genes_intergenic	0.0000	0.0000	-74.194
	chr6	47628180	mm39_genes_intergenic	0.0000	0.0000	-32.939
	chr6	47628180	mm39_cpg_islands	0.0000	0.0000	-32.939
Skap2	chr6	51989444	mm39_genes_exonintronboundaries	0.0000	0.0000	-74.242
	chr6	51989444	mm39_cpg_islands	0.0000	0.0000	-74.242
Skap2	chr6	51989444	mm39_genes_exons	0.0000	0.0000	-74.242
Skap2	chr6	51989444	mm39_genes_intronexonboundaries	0.0000	0.0000	-74.242
Skap2	chr6	51989444	mm39_genes_5UTRs	0.0000	0.0000	-74.242
	chr6	52081309	mm39_cpg_inter	0.0000	0.0305	-26.786
Halr1	chr6	52081309	mm39_genes_introns	0.0000	0.0305	-26.786
LOC115490409	chr6	52168962	mm39_genes_introns	0.0000	0.0000	-51.364
Hoxa3	chr6	52168962	mm39_genes_introns	0.0000	0.0000	-51.364
	chr6	52168962	mm39_cpg_islands	0.0000	0.0000	-51.364
Hoxa4	chr6	52168962	mm39_genes_promoters	0.0000	0.0000	-51.364
	chr6	52203292	mm39_cpg_islands	0.0000	0.0001	-36.842
Hoxa9	chr6	52203292	mm39_genes_exons	0.0000	0.0001	-36.842

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P* -value	Adjusted *P* -value (*Q* -value)	Methylation difference (%)
Hoxa9	chr6	52203292	mm39_genes_exons	0.0000	0.0001	-36.842
Hoxa9	chr6	52203292	mm39_genes_5UTRs	0.0000	0.0001	-36.842
	chr6	53825570	mm39_cpg_inter	0.0000	0.0968	48.148
	chr6	53825570	mm39_genes_intergenic	0.0000	0.0968	48.148
	chr6	55303621	mm39_cpg_inter	0.0000	0.0037	-62.500
	chr6	55303621	mm39_genes_intergenic	0.0000	0.0037	-62.500
	chr6	59252997	mm39_genes_intergenic	0.0000	0.0847	65.158
	chr6	59252997	mm39_cpg_inter	0.0000	0.0847	65.158
	chr6	68926117	mm39_cpg_inter	0.0000	0.0000	28.070
	chr6	68926117	mm39_genes_intergenic	0.0000	0.0000	28.070
	chr6	69573002	mm39_cpg_inter	0.0000	0.0116	23.326
	chr6	69573002	mm39_genes_intergenic	0.0000	0.0116	23.326
	chr6	71027961	mm39_genes_intergenic	0.0000	0.0303	51.259
	chr6	71027961	mm39_cpg_inter	0.0000	0.0303	51.259
Usp39	chr6	72324869	mm39_genes_1to5kb	0.0000	0.0032	30.000
0610030E20Rik	chr6	72324869	mm39_genes_exonintronboundaries	0.0000	0.0032	30.000
	chr6	72324869	mm39_cpg_shores	0.0000	0.0032	30.000
0610030E20Rik	chr6	72324869	mm39_genes_introns	0.0000	0.0032	30.000
	chr6	78496256	mm39_cpg_inter	0.0000	0.0175	-48.577
	chr6	78496256	mm39_genes_intergenic	0.0000	0.0175	-48.577
Eva1a	chr6	82018853	mm39_genes_5UTRs	0.0000	0.0002	-71.429
Eva1a	chr6	82018853	mm39_genes_exons	0.0000	0.0002	-71.429
Eva1a	chr6	82018853	mm39_genes_exonintronboundaries	0.0000	0.0002	-71.429
	chr6	82018853	mm39_cpg_islands	0.0000	0.0002	-71.429
	chr6	83048340	mm39_cpg_islands	0.0000	0.0000	-46.062
Tlx2	chr6	83048340	mm39_genes_1to5kb	0.0000	0.0000	-46.062
Vax2	chr6	83694322	mm39_genes_introns	0.0000	0.0131	-59.289
	chr6	83694322	mm39_cpg_inter	0.0000	0.0131	-59.289
Cyp26b1	chr6	84567180	mm39_genes_introns	0.0000	0.0005	-65.217
Cyp26b1	chr6	84567180	mm39_genes_introns	0.0000	0.0005	-65.217
	chr6	84567180	mm39_cpg_shores	0.0000	0.0005	-65.217
Sfxn5	chr6	85309692	mm39_genes_introns	0.0000	0.0000	-58.553
	chr6	85309692	mm39_cpg_islands	0.0000	0.0000	-58.553
Fbxo41	chr6	85461840	mm39_genes_exons	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_exons	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_exons	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_intronexonboundaries	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_intronexonboundaries	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_intronexonboundaries	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_5UTRs	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_5UTRs	0.0000	0.0062	-22.395
Fbxo41	chr6	85461840	mm39_genes_5UTRs	0.0000	0.0062	-22.395
	chr6	85461840	mm39_cpg_shores	0.0000	0.0062	-22.395
	chr6	88171091	mm39_cpg_islands	0.0000	0.0000	-58.597
Gata2	chr6	88171091	mm39_genes_1to5kb	0.0000	0.0000	-58.597
Gata2	chr6	88171091	mm39_genes_exonintronboundaries	0.0000	0.0000	-58.597
Gata2	chr6	88171091	mm39_genes_introns	0.0000	0.0000	-58.597
Sec61a1	chr6	88495702	mm39_genes_exonintronboundaries	0.0000	0.0003	15.327
	chr6	88495702	mm39_cpg_islands	0.0000	0.0003	15.327
Sec61a1	chr6	88495702	mm39_genes_intronexonboundaries	0.0000	0.0003	15.327
Sec61a1	chr6	88495702	mm39_genes_exons	0.0000	0.0003	15.327

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Sec61a1	chr6	88495702	mm39_genes_5UTRs	0.0000	0.0003	15.327
	chr6	97594525	mm39_cpg_islands	0.0000	0.0000	-38.776
Frmd4b	chr6	97594525	mm39_genes_5UTRs	0.0000	0.0000	-38.776
Frmd4b	chr6	97594525	mm39_genes_exons	0.0000	0.0000	-38.776
Frmd4b	chr6	97594525	mm39_genes_intronexonboundaries	0.0000	0.0000	-38.776
Foxp1	chr6	99007229	mm39_genes_introns	0.0000	0.0021	62.963
Foxp1	chr6	99007229	mm39_genes_introns	0.0000	0.0021	62.963
Foxp1	chr6	99007229	mm39_genes_introns	0.0000	0.0021	62.963
	chr6	99007229	mm39_cpg_shores	0.0000	0.0021	62.963
Foxp1	chr6	99007229	mm39_genes_1to5kb	0.0000	0.0021	62.963
	chr6	100856734	mm39_cpg_inter	0.0000	0.0023	-70.000
	chr6	100856734	mm39_genes_intergenic	0.0000	0.0023	-70.000
	chr6	101643105	mm39_cpg_inter	0.0000	0.0899	-46.429
	chr6	101643105	mm39_genes_intergenic	0.0000	0.0899	-46.429
	chr6	108433857	mm39_cpg_inter	0.0000	0.0000	77.551
Itpr1	chr6	108433857	mm39_genes_introns	0.0000	0.0000	77.551
	chr6	113259203	mm39_cpg_shores	0.0000	0.0010	-32.696
Cpne9	chr6	113259203	mm39_genes_promoters	0.0000	0.0010	-32.696
	chr6	115951224	mm39_cpg_inter	0.0000	0.0036	-29.091
Plxnd1	chr6	115951224	mm39_genes_introns	0.0000	0.0036	-29.091
	chr6	119177025	mm39_cpg_inter	0.0000	0.0737	46.875
Cacna1c	chr6	119177025	mm39_genes_1to5kb	0.0000	0.0737	46.875
Cacna1c	chr6	119177025	mm39_genes_1to5kb	0.0000	0.0737	46.875
Cacna1c	chr6	119177025	mm39_genes_1to5kb	0.0000	0.0737	46.875
Cacna1c	chr6	119177025	mm39_genes_1to5kb	0.0000	0.0737	46.875
Dcp1b	chr6	119177025	mm39_genes_introns	0.0000	0.0737	46.875
Hdhd5	chr6	120507953	mm39_genes_introns	0.0000	0.0054	-26.230
	chr6	120507953	mm39_cpg_islands	0.0000	0.0054	-26.230
Hdhd5	chr6	120507953	mm39_genes_exonintronboundaries	0.0000	0.0054	-26.230
Cops7a	chr6	124942493	mm39_genes_exonintronboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_exonintronboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_exonintronboundaries	0.0000	0.0000	-55.168
	chr6	124942493	mm39_cpg_islands	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_intronexonboundaries	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
Cops7a	chr6	124942493	mm39_genes_promoters	0.0000	0.0000	-55.168
	chr6	128508294	mm39_cpg_inter	0.0000	0.0566	52.795
Pzp	chr6	128508294	mm39_genes_1to5kb	0.0000	0.0566	52.795
	chr6	129910046	mm39_cpg_inter	0.0000	0.0564	-38.534

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr6	129910046	mm39_genes_intergenic	0.0000	0.0564	-38.534
	chr6	130826709	mm39_cpg_inter	0.0000	0.0000	88.889
	chr6	130826709	mm39_genes_intergenic	0.0000	0.0000	88.889
	chr6	136805065	mm39_cpg_islands	0.0000	0.0000	13.966
Wbp11	chr6	136805065	mm39_genes_exonintronboundaries	0.0000	0.0000	13.966
BC049715	chr6	136805065	mm39_genes_promoters	0.0000	0.0000	13.966
Wbp11	chr6	136805065	mm39_genes_intronexonboundaries	0.0000	0.0000	13.966
Wbp11	chr6	136805065	mm39_genes_5UTRs	0.0000	0.0000	13.966
Wbp11	chr6	136805065	mm39_genes_exons	0.0000	0.0000	13.966
Ptpro	chr6	137229532	mm39_genes_exons	0.0000	0.0000	-43.271
Ptpro	chr6	137229532	mm39_genes_exons	0.0000	0.0000	-43.271
Ptpro	chr6	137229532	mm39_genes_5UTRs	0.0000	0.0000	-43.271
Ptpro	chr6	137229532	mm39_genes_5UTRs	0.0000	0.0000	-43.271
	chr6	137229532	mm39_cpg_islands	0.0000	0.0000	-43.271
	chr6	146710399	mm39_cpg_inter	0.0000	0.0019	45.946
Arntl2	chr6	146710399	mm39_genes_introns	0.0000	0.0019	45.946
Arntl2	chr6	146710399	mm39_genes_introns	0.0000	0.0019	45.946
Arntl2	chr6	146710399	mm39_genes_introns	0.0000	0.0019	45.946
Arntl2	chr6	146710399	mm39_genes_introns	0.0000	0.0019	45.946
	chr6	147241835	mm39_cpg_inter	0.0000	0.0000	41.170
	chr6	147241835	mm39_genes_intergenic	0.0000	0.0000	41.170
	chr6	148797807	mm39_cpg_islands	0.0000	0.0000	-90.244
Caprin2	chr6	148797807	mm39_genes_intronexonboundaries	0.0000	0.0000	-90.244
Caprin2	chr6	148797807	mm39_genes_intronexonboundaries	0.0000	0.0000	-90.244
Caprin2	chr6	148797807	mm39_genes_promoters	0.0000	0.0000	-90.244
Caprin2	chr6	148797807	mm39_genes_promoters	0.0000	0.0000	-90.244
Epn1	chr7	5083871	mm39_genes_introns	0.0000	0.0853	-52.211
Epn1	chr7	5083871	mm39_genes_introns	0.0000	0.0853	-52.211
Epn1	chr7	5083871	mm39_genes_introns	0.0000	0.0853	-52.211
	chr7	5083871	mm39_cpg_shores	0.0000	0.0853	-52.211
	chr7	6159120	mm39_cpg_islands	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_intronexonboundaries	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
Zfp787	chr7	6159120	mm39_genes_promoters	0.0000	0.0000	-39.860
	chr7	7362267	mm39_cpg_inter	0.0000	0.0522	-25.599
	chr7	7362267	mm39_genes_intergenic	0.0000	0.0522	-25.599
	chr7	16134274	mm39_cpg_islands	0.0000	0.0711	-16.854
Zc3h4	chr7	16134274	mm39_genes_promoters	0.0000	0.0711	-16.854

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Hif3a	chr7	16790594	mm39_genes_exonintronboundaries	0.0000	0.0000	-79.412
Hif3a	chr7	16790594	mm39_genes_introns	0.0000	0.0000	-79.412
Hif3a	chr7	16790594	mm39_genes_intronexonboundaries	0.0000	0.0000	-79.412
	chr7	16790594	mm39_cpg_shores	0.0000	0.0000	-79.412
Hif3a	chr7	16790594	mm39_genes_exons	0.0000	0.0000	-79.412
Hif3a	chr7	16790594	mm39_genes_5UTRs	0.0000	0.0000	-79.412
Ercc1	chr7	19079024	mm39_genes_exonintronboundaries	0.0000	0.0000	-30.724
Ercc1	chr7	19079024	mm39_genes_exonintronboundaries	0.0000	0.0000	-30.724
	chr7	19079024	mm39_cpg_islands	0.0000	0.0000	-30.724
Ercc1	chr7	19079024	mm39_genes_5UTRs	0.0000	0.0000	-30.724
Ercc1	chr7	19079024	mm39_genes_5UTRs	0.0000	0.0000	-30.724
Ercc1	chr7	19079024	mm39_genes_exons	0.0000	0.0000	-30.724
Ercc1	chr7	19079024	mm39_genes_exons	0.0000	0.0000	-30.724
Ppp1r13l	chr7	19092810	mm39_genes_1to5kb	0.0000	0.0000	-35.322
Cd3eap	chr7	19092810	mm39_genes_introns	0.0000	0.0000	-35.322
	chr7	19092810	mm39_cpg_shores	0.0000	0.0000	-35.322
	chr7	19523989	mm39_cpg_inter	0.0000	0.0043	-41.043
Cblc	chr7	19523989	mm39_genes_introns	0.0000	0.0043	-41.043
Cblc	chr7	19523989	mm39_genes_introns	0.0000	0.0043	-41.043
Ltbp4	chr7	27034096	mm39_genes_introns	0.0000	0.0000	-81.690
	chr7	27034096	mm39_cpg_islands	0.0000	0.0000	-81.690
Ltbp4	chr7	27034096	mm39_genes_exonintronboundaries	0.0000	0.0000	-81.690
Ltbp4	chr7	27034096	mm39_genes_1to5kb	0.0000	0.0000	-81.690
Ltbp4	chr7	27034096	mm39_genes_1to5kb	0.0000	0.0000	-81.690
Akt2	chr7	27292119	mm39_genes_1to5kb	0.0000	0.0035	-60.000
Akt2	chr7	27292119	mm39_genes_introns	0.0000	0.0035	-60.000
	chr7	27292119	mm39_cpg_shores	0.0000	0.0035	-60.000
	chr7	28187467	mm39_genes_intergenic	0.0000	0.0935	-16.484
	chr7	28187467	mm39_cpg_inter	0.0000	0.0935	-16.484
	chr7	28938017	mm39_cpg_islands	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_introns	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_exonintronboundaries	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_exonintronboundaries	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_exonintronboundaries	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_exonintronboundaries	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_introns	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_introns	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_exons	0.0000	0.0015	52.000
Yif1b	chr7	28938017	mm39_genes_introns	0.0000	0.0015	52.000
	chr7	29518408	mm39_cpg_inter	0.0000	0.0007	-64.725
Zfp790	chr7	29518408	mm39_genes_introns	0.0000	0.0007	-64.725
Zfp790	chr7	29518408	mm39_genes_introns	0.0000	0.0007	-64.725
	chr7	29894209	mm39_cpg_shores	0.0000	0.0000	-91.045
Capns1	chr7	29894209	mm39_genes_introns	0.0000	0.0000	-91.045
	chr7	35096189	mm39_cpg_inter	0.0000	0.0003	41.246
Cep89	chr7	35096189	mm39_genes_promoters	0.0000	0.0003	41.246
Cep89	chr7	35096189	mm39_genes_promoters	0.0000	0.0003	41.246
Faap24	chr7	35096189	mm39_genes_exons	0.0000	0.0003	41.246
Faap24	chr7	35096189	mm39_genes_5UTRs	0.0000	0.0003	41.246
Faap24	chr7	35096189	mm39_genes_intronexonboundaries	0.0000	0.0003	41.246
	chr7	37067096	mm39_genes_intergenic	0.0000	0.0039	-47.059

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr7	37067096	mm39_cpg_inter	0.0000	0.0039	-47.059
	chr7	40547752	mm39_cpg_shores	0.0000	0.0009	-28.986
A230077H06Rik	chr7	40547752	mm39_genes_exonintronboundaries	0.0000	0.0009	-28.986
A230077H06Rik	chr7	40547752	mm39_genes_intronexonboundaries	0.0000	0.0009	-28.986
Vstm2b	chr7	40547752	mm39_genes_promoters	0.0000	0.0009	-28.986
A230077H06Rik	chr7	40547752	mm39_genes_promoters	0.0000	0.0009	-28.986
	chr7	43531960	mm39_cpg_inter	0.0000	0.0064	80.000
Klk4	chr7	43531960	mm39_genes_introns	0.0000	0.0064	80.000
Clec11a	chr7	43954120	mm39_genes_exons	0.0000	0.0447	19.050
	chr7	43954120	mm39_cpg_islands	0.0000	0.0447	19.050
Pold1	chr7	44197975	mm39_genes_introns	0.0000	0.0003	16.484
	chr7	44197975	mm39_cpg_islands	0.0000	0.0003	16.484
Fuz	chr7	44542083	mm39_genes_1to5kb	0.0000	0.0000	54.795
	chr7	44542083	mm39_cpg_islands	0.0000	0.0000	54.795
Med25	chr7	44542083	mm39_genes_promoters	0.0000	0.0000	54.795
Med25	chr7	44542083	mm39_genes_promoters	0.0000	0.0000	54.795
Med25	chr7	44542083	mm39_genes_promoters	0.0000	0.0000	54.795
Med25	chr7	44542083	mm39_genes_promoters	0.0000	0.0000	54.795
Rasip1	chr7	45281957	mm39_genes_exons	0.0000	0.0000	-52.043
	chr7	45281957	mm39_cpg_islands	0.0000	0.0000	-52.043
Gm2788	chr7	48530926	mm39_genes_promoters	0.0000	0.0000	47.379
E2f8	chr7	48530926	mm39_genes_introns	0.0000	0.0000	47.379
	chr7	48530926	mm39_cpg_islands	0.0000	0.0000	47.379
E2f8	chr7	48530926	mm39_genes_intronexonboundaries	0.0000	0.0000	47.379
E2f8	chr7	48530926	mm39_genes_promoters	0.0000	0.0000	47.379
	chr7	48608937	mm39_cpg_inter	0.0000	0.0037	14.509
Nav2	chr7	48608937	mm39_genes_exonintronboundaries	0.0000	0.0037	14.509
Nav2	chr7	48608937	mm39_genes_introns	0.0000	0.0037	14.509
Cyfip1	chr7	55493014	mm39_genes_introns	0.0000	0.0028	-69.580
Cyfip1	chr7	55493014	mm39_genes_introns	0.0000	0.0028	-69.580
Cyfip1	chr7	55493014	mm39_genes_introns	0.0000	0.0028	-69.580
	chr7	55493014	mm39_cpg_shores	0.0000	0.0028	-69.580
Gm9962	chr7	57036575	mm39_genes_promoters	0.0000	0.0000	-37.505
Gabrg3	chr7	57036575	mm39_genes_exonintronboundaries	0.0000	0.0000	-37.505
	chr7	57036575	mm39_cpg_islands	0.0000	0.0000	-37.505
Gabrg3	chr7	57036575	mm39_genes_exons	0.0000	0.0000	-37.505
Gabrg3	chr7	57036575	mm39_genes_5UTRs	0.0000	0.0000	-37.505
Gm32061	chr7	62070007	mm39_genes_introns	0.0000	0.0808	17.491
Mkrn3	chr7	62070007	mm39_genes_intronexonboundaries	0.0000	0.0808	17.491
	chr7	62070007	mm39_cpg_shores	0.0000	0.0808	17.491
Mkrn3	chr7	62070007	mm39_genes_promoters	0.0000	0.0808	17.491
	chr7	63405213	mm39_cpg_shelves	0.0000	0.0000	56.000
Otud7a	chr7	63405213	mm39_genes_introns	0.0000	0.0000	56.000
	chr7	67680638	mm39_cpg_inter	0.0000	0.0447	31.644
Igf1r	chr7	67680638	mm39_genes_introns	0.0000	0.0447	31.644
	chr7	69017172	mm39_cpg_inter	0.0000	0.0711	14.271
	chr7	69017172	mm39_genes_intergenic	0.0000	0.0711	14.271
Gm29683	chr7	69984546	mm39_genes_introns	0.0000	0.0134	14.005
Gm29683	chr7	69984546	mm39_genes_introns	0.0000	0.0134	14.005
	chr7	69984546	mm39_cpg_shelves	0.0000	0.0134	14.005
	chr7	70873919	mm39_cpg_inter	0.0000	0.0953	48.106

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P* -value	Adjusted *P* -value (*Q* -value)	Methylation difference (%)
	chr7	70873919	mm39_genes_intergenic	0.0000	0.0953	48.106
	chr7	72449466	mm39_cpg_inter	0.0000	0.0005	79.167
	chr7	72449466	mm39_genes_intergenic	0.0000	0.0005	79.167
Slco3a1	chr7	74179356	mm39_genes_introns	0.0000	0.0781	-35.185
Slco3a1	chr7	74179356	mm39_genes_introns	0.0000	0.0781	-35.185
	chr7	74179356	mm39_cpg_inter	0.0000	0.0781	-35.185
Det1	chr7	78497111	mm39_genes_intronexonboundaries	0.0000	0.0019	-25.316
Det1	chr7	78497111	mm39_genes_promoters	0.0000	0.0019	-25.316
	chr7	78497111	mm39_cpg_shores	0.0000	0.0019	-25.316
	chr7	78751668	mm39_cpg_inter	0.0000	0.0474	21.234
Acan	chr7	78751668	mm39_genes_introns	0.0000	0.0474	21.234
Acan	chr7	78751668	mm39_genes_introns	0.0000	0.0474	21.234
Gm31510	chr7	78923210	mm39_genes_promoters	0.0000	0.0086	26.256
Gm31510	chr7	78923210	mm39_genes_promoters	0.0000	0.0086	26.256
Abhd2	chr7	78923210	mm39_genes_exonintronboundaries	0.0000	0.0086	26.256
	chr7	78923210	mm39_cpg_islands	0.0000	0.0086	26.256
Abhd2	chr7	78923210	mm39_genes_introns	0.0000	0.0086	26.256
	chr7	79013346	mm39_cpg_inter	0.0000	0.0012	-28.135
	chr7	79013346	mm39_genes_intergenic	0.0000	0.0012	-28.135
Mir9-3hg	chr7	79175854	mm39_genes_introns	0.0000	0.0588	20.199
	chr7	79175854	mm39_cpg_inter	0.0000	0.0588	20.199
Mir9-3hg	chr7	79175854	mm39_genes_introns	0.0000	0.0588	20.199
Mir9-3hg	chr7	79175854	mm39_genes_introns	0.0000	0.0588	20.199
Mir9-3hg	chr7	79175854	mm39_genes_introns	0.0000	0.0588	20.199
	chr7	80338553	mm39_cpg_islands	0.0000	0.0000	-51.697
Crtc3	chr7	80338553	mm39_genes_exonintronboundaries	0.0000	0.0000	-51.697
Crtc3	chr7	80338553	mm39_genes_exons	0.0000	0.0000	-51.697
Crtc3	chr7	80338553	mm39_genes_intronexonboundaries	0.0000	0.0000	-51.697
Crtc3	chr7	80338553	mm39_genes_5UTRs	0.0000	0.0000	-51.697
Sec11a	chr7	80597279	mm39_genes_exonintronboundaries	0.0000	0.0807	23.193
	chr7	80597279	mm39_cpg_islands	0.0000	0.0807	23.193
Sec11a	chr7	80597279	mm39_genes_intronexonboundaries	0.0000	0.0807	23.193
Sec11a	chr7	80597279	mm39_genes_exons	0.0000	0.0807	23.193
Sec11a	chr7	80597279	mm39_genes_5UTRs	0.0000	0.0807	23.193
	chr7	95044105	mm39_cpg_inter	0.0000	0.0016	85.294
	chr7	95044105	mm39_genes_intergenic	0.0000	0.0016	85.294
Wnt11	chr7	98484655	mm39_genes_1to5kb	0.0000	0.0012	-26.779
Wnt11	chr7	98484655	mm39_genes_1to5kb	0.0000	0.0012	-26.779
Wnt11	chr7	98484655	mm39_genes_exonintronboundaries	0.0000	0.0012	-26.779
Wnt11	chr7	98484655	mm39_genes_exonintronboundaries	0.0000	0.0012	-26.779
	chr7	98484655	mm39_cpg_shores	0.0000	0.0012	-26.779
Wnt11	chr7	98484655	mm39_genes_introns	0.0000	0.0012	-26.779
Wnt11	chr7	98484655	mm39_genes_introns	0.0000	0.0012	-26.779
	chr7	101899736	mm39_cpg_shores	0.0000	0.0005	53.872
Rhog	chr7	101899736	mm39_genes_promoters	0.0000	0.0005	53.872
	chr7	101917138	mm39_cpg_islands	0.0000	0.0034	31.915
Stim1	chr7	101917138	mm39_genes_exons	0.0000	0.0034	31.915
Stim1	chr7	101917138	mm39_genes_exons	0.0000	0.0034	31.915
Stim1	chr7	101917138	mm39_genes_exons	0.0000	0.0034	31.915
Stim1	chr7	101917138	mm39_genes_5UTRs	0.0000	0.0034	31.915
Stim1	chr7	101917138	mm39_genes_5UTRs	0.0000	0.0034	31.915

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Stim1	chr7	101917138	mm39_genes_5UTRs	0.0000	0.0034	31.915
	chr7	110225663	mm39_cpg_inter	0.0000	0.0027	-48.148
Adm	chr7	110225663	mm39_genes_1to5kb	0.0000	0.0027	-48.148
	chr7	111769717	mm39_cpg_inter	0.0000	0.0482	-55.430
	chr7	111769717	mm39_genes_intergenic	0.0000	0.0482	-55.430
	chr7	115638761	mm39_cpg_inter	0.0000	0.0229	-64.856
Sox6	chr7	115638761	mm39_genes_promoters	0.0000	0.0229	-64.856
	chr7	118993875	mm39_cpg_inter	0.0000	0.0155	-32.170
	chr7	118993875	mm39_genes_intergenic	0.0000	0.0155	-32.170
Uqcrc2	chr7	120234316	mm39_genes_promoters	0.0000	0.0000	-87.640
	chr7	120234316	mm39_cpg_islands	0.0000	0.0000	-87.640
Rbbp6	chr7	122569709	mm39_genes_promoters	0.0000	0.0012	82.051
Rbbp6	chr7	122569709	mm39_genes_promoters	0.0000	0.0012	82.051
	chr7	122569709	mm39_cpg_islands	0.0000	0.0012	82.051
4930413G21Rik	chr7	122569709	mm39_genes_intronexonboundaries	0.0000	0.0012	82.051
4930413G21Rik	chr7	122569709	mm39_genes_promoters	0.0000	0.0012	82.051
	chr7	122723295	mm39_cpg_islands	0.0000	0.0004	14.636
Tnrc6a	chr7	122723295	mm39_genes_exons	0.0000	0.0004	14.636
Tnrc6a	chr7	122723295	mm39_genes_5UTRs	0.0000	0.0004	14.636
Kdm8	chr7	125043779	mm39_genes_promoters	0.0000	0.0000	-34.564
Kdm8	chr7	125043779	mm39_genes_exonintronboundaries	0.0000	0.0000	-34.564
	chr7	125043779	mm39_cpg_islands	0.0000	0.0000	-34.564
	chr7	126362308	mm39_cpg_inter	0.0000	0.0703	-23.740
Gdpd3	chr7	126362308	mm39_genes_1to5kb	0.0000	0.0703	-23.740
Mapk3	chr7	126362308	mm39_genes_intronexonboundaries	0.0000	0.0703	-23.740
Mapk3	chr7	126362308	mm39_genes_exonintronboundaries	0.0000	0.0703	-23.740
Mapk3	chr7	126362308	mm39_genes_exons	0.0000	0.0703	-23.740
Mylpf	chr7	126806868	mm39_genes_1to5kb	0.0000	0.0000	-31.862
	chr7	126806868	mm39_cpg_shores	0.0000	0.0000	-31.862
Mylpf	chr7	126806868	mm39_genes_1to5kb	0.0000	0.0000	-31.862
Tbc1d10b	chr7	126806868	mm39_genes_exons	0.0000	0.0000	-31.862
	chr7	127994609	mm39_cpg_inter	0.0000	0.0523	65.000
Rgs10	chr7	127994609	mm39_genes_introns	0.0000	0.0523	65.000
	chr7	131378068	mm39_cpg_inter	0.0000	0.0998	-25.021
	chr7	131378068	mm39_genes_intergenic	0.0000	0.0998	-25.021
	chr7	133827018	mm39_cpg_islands	0.0000	0.0001	-27.910
Adam12	chr7	133827018	mm39_genes_intronexonboundaries	0.0000	0.0001	-27.910
Adam12	chr7	133827018	mm39_genes_promoters	0.0000	0.0001	-27.910
Ebf3	chr7	136910971	mm39_genes_introns	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_introns	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_introns	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_exonintronboundaries	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_exonintronboundaries	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_exonintronboundaries	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_intronexonboundaries	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_intronexonboundaries	0.0000	0.0445	-9.201
Ebf3	chr7	136910971	mm39_genes_intronexonboundaries	0.0000	0.0445	-9.201
	chr7	136910971	mm39_cpg_islands	0.0000	0.0445	-9.201
	chr7	136912228	mm39_cpg_islands	0.0000	0.0059	-28.975
Ebf3	chr7	136912228	mm39_genes_introns	0.0000	0.0059	-28.975
Ebf3	chr7	136912228	mm39_genes_introns	0.0000	0.0059	-28.975

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Ebf3	chr7	136912228	mm39_genes_introns	0.0000	0.0059	-28.975
	chr7	140774934	mm39_cpg_islands	0.0000	0.0001	58.824
Lrrc56	chr7	140774934	mm39_genes_promoters	0.0000	0.0001	58.824
Lrrc56	chr7	140774934	mm39_genes_introns	0.0000	0.0001	58.824
Lrrc56	chr7	140774934	mm39_genes_introns	0.0000	0.0001	58.824
Lrrc56	chr7	140774934	mm39_genes_exonintronboundaries	0.0000	0.0001	58.824
Lrrc56	chr7	140774934	mm39_genes_introns	0.0000	0.0001	58.824
Hras	chr7	140774934	mm39_genes_1to5kb	0.0000	0.0001	58.824
Hras	chr7	140774934	mm39_genes_1to5kb	0.0000	0.0001	58.824
Hras	chr7	140774934	mm39_genes_1to5kb	0.0000	0.0001	58.824
Lrrc56	chr7	140774934	mm39_genes_exonintronboundaries	0.0000	0.0001	58.824
R74862	chr7	142606576	mm39_genes_introns	0.0000	0.0000	-71.957
R74862	chr7	142606576	mm39_genes_introns	0.0000	0.0000	-71.957
R74862	chr7	142606576	mm39_genes_introns	0.0000	0.0000	-71.957
	chr7	142606576	mm39_cpg_islands	0.0000	0.0000	-71.957
Cd81	chr7	142606576	mm39_genes_exons	0.0000	0.0000	-71.957
Cd81	chr7	142606576	mm39_genes_5UTRs	0.0000	0.0000	-71.957
R74862	chr7	142606576	mm39_genes_exonintronboundaries	0.0000	0.0000	-71.957
R74862	chr7	142606576	mm39_genes_exonintronboundaries	0.0000	0.0000	-71.957
R74862	chr7	142606576	mm39_genes_exonintronboundaries	0.0000	0.0000	-71.957
R74862	chr7	142606634	mm39_genes_introns	0.0000	0.0064	-27.940
R74862	chr7	142606634	mm39_genes_introns	0.0000	0.0064	-27.940
R74862	chr7	142606634	mm39_genes_introns	0.0000	0.0064	-27.940
	chr7	142606634	mm39_cpg_islands	0.0000	0.0064	-27.940
Cd81	chr7	142606634	mm39_genes_exons	0.0000	0.0064	-27.940
Cd81	chr7	142606634	mm39_genes_5UTRs	0.0000	0.0064	-27.940
R74862	chr7	142606634	mm39_genes_exonintronboundaries	0.0000	0.0064	-27.940
R74862	chr7	142606634	mm39_genes_exonintronboundaries	0.0000	0.0064	-27.940
R74862	chr7	142606634	mm39_genes_exonintronboundaries	0.0000	0.0064	-27.940
Cd81	chr7	142606634	mm39_genes_exonintronboundaries	0.0000	0.0064	-27.940
	chr7	143014074	mm39_cpg_islands	0.0000	0.0013	-78.571
Cdkn1c	chr7	143014074	mm39_genes_exons	0.0000	0.0013	-78.571
Cdkn1c	chr7	143014074	mm39_genes_exons	0.0000	0.0013	-78.571
Cdkn1c	chr7	143014074	mm39_genes_exons	0.0000	0.0013	-78.571
	chr7	144024126	mm39_cpg_inter	0.0000	0.0000	-52.203
Cttn	chr7	144024126	mm39_genes_introns	0.0000	0.0000	-52.203
Cttn	chr7	144024126	mm39_genes_introns	0.0000	0.0000	-52.203
Cttn	chr7	144024126	mm39_genes_introns	0.0000	0.0000	-52.203
	chr7	144392711	mm39_cpg_islands	0.0000	0.0000	-38.750
Fgf3	chr7	144392711	mm39_genes_exonintronboundaries	0.0000	0.0000	-38.750
Fgf3	chr7	144392711	mm39_genes_introns	0.0000	0.0000	-38.750
Fgf3	chr7	144393566	mm39_genes_introns	0.0000	0.0000	-70.833
	chr7	144393566	mm39_cpg_shores	0.0000	0.0000	-70.833
	chr8	4027868	mm39_cpg_inter	0.0000	0.0031	65.000
	chr8	4027868	mm39_genes_intergenic	0.0000	0.0031	65.000
	chr8	4276982	mm39_cpg_inter	0.0000	0.0027	22.472
Lrrc8e	chr8	4276982	mm39_genes_exonintronboundaries	0.0000	0.0027	22.472
Lrrc8e	chr8	4276982	mm39_genes_5UTRs	0.0000	0.0027	22.472
Lrrc8e	chr8	4276982	mm39_genes_exons	0.0000	0.0027	22.472
Elavl1	chr8	4374878	mm39_genes_introns	0.0000	0.0000	-51.649
Ccl25	chr8	4374878	mm39_genes_promoters	0.0000	0.0000	-51.649

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr8	4374878	mm39_cpg_islands	0.0000	0.0000	-51.649
Elavl1	chr8	4374878	mm39_genes_exonintronboundaries	0.0000	0.0000	-51.649
	chr8	8711885	mm39_cpg_islands	0.0000	0.0000	-56.571
Efnb2	chr8	8711885	mm39_genes_promoters	0.0000	0.0000	-56.571
Efnb2	chr8	8711885	mm39_genes_promoters	0.0000	0.0000	-56.571
	chr8	11891804	mm39_cpg_inter	0.0000	0.0029	86.364
Tex29	chr8	11891804	mm39_genes_introns	0.0000	0.0029	86.364
Cdc16	chr8	13807518	mm39_genes_promoters	0.0000	0.0000	-38.696
Cdc16	chr8	13807518	mm39_genes_promoters	0.0000	0.0000	-38.696
	chr8	13807518	mm39_cpg_islands	0.0000	0.0000	-38.696
Potefam3b	chr8	20143170	mm39_genes_introns	0.0000	0.0161	11.731
	chr8	20143170	mm39_cpg_shores	0.0000	0.0161	11.731
6820431F20Rik	chr8	20143170	mm39_genes_promoters	0.0000	0.0161	11.731
	chr8	22614972	mm39_cpg_inter	0.0000	0.0156	37.101
Nek5	chr8	22614972	mm39_genes_introns	0.0000	0.0156	37.101
Nek5	chr8	22614972	mm39_genes_introns	0.0000	0.0156	37.101
Nek5	chr8	22614972	mm39_genes_exonintronboundaries	0.0000	0.0156	37.101
Nek5	chr8	22614972	mm39_genes_exonintronboundaries	0.0000	0.0156	37.101
Nek5	chr8	22614972	mm39_genes_intronexonboundaries	0.0000	0.0156	37.101
Nek5	chr8	22614972	mm39_genes_intronexonboundaries	0.0000	0.0156	37.101
Vdac3	chr8	23083434	mm39_genes_introns	0.0000	0.0000	86.538
Vdac3	chr8	23083434	mm39_genes_introns	0.0000	0.0000	86.538
	chr8	23083434	mm39_cpg_islands	0.0000	0.0000	86.538
	chr8	23349711	mm39_cpg_islands	0.0000	0.0000	42.574
Kat6a	chr8	23349711	mm39_genes_exonintronboundaries	0.0000	0.0000	42.574
Kat6a	chr8	23349711	mm39_genes_exonintronboundaries	0.0000	0.0000	42.574
Kat6a	chr8	23349711	mm39_genes_introns	0.0000	0.0000	42.574
Kat6a	chr8	23349711	mm39_genes_introns	0.0000	0.0000	42.574
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Ank1	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Mir3107	chr8	23637605	mm39_genes_1to5kb	0.0000	0.0286	35.027
	chr8	23637605	mm39_cpg_shelves	0.0000	0.0286	35.027
Gm15816	chr8	23637605	mm39_genes_exonintronboundaries	0.0000	0.0286	35.027
Gm15816	chr8	23637605	mm39_genes_intronexonboundaries	0.0000	0.0286	35.027
Gm15816	chr8	23637605	mm39_genes_introns	0.0000	0.0286	35.027
Zfp703	chr8	27466945	mm39_genes_promoters	0.0000	0.0000	-40.013
Zfp703	chr8	27466945	mm39_genes_promoters	0.0000	0.0000	-40.013
	chr8	27466945	mm39_cpg_islands	0.0000	0.0000	-40.013
	chr8	34293753	mm39_cpg_inter	0.0000	0.0000	-37.615
Rbpms	chr8	34293753	mm39_genes_introns	0.0000	0.0000	-37.615
Rbpms	chr8	34293753	mm39_genes_introns	0.0000	0.0000	-37.615
Rbpms	chr8	34293753	mm39_genes_introns	0.0000	0.0000	-37.615

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr8	36750933	mm39_cpg_inter	0.0000	0.0855	-24.113
	chr8	36750933	mm39_genes_intergenic	0.0000	0.0855	-24.113
	chr8	45811422	mm39_cpg_inter	0.0000	0.0005	-81.385
Fam149a	chr8	45811422	mm39_genes_introns	0.0000	0.0005	-81.385
	chr8	45908835	mm39_cpg_inter	0.0000	0.0001	78.000
	chr8	45908835	mm39_genes_intergenic	0.0000	0.0001	78.000
	chr8	46749332	mm39_cpg_shores	0.0000	0.0000	-84.946
Helt	chr8	46749332	mm39_genes_1to5kb	0.0000	0.0000	-84.946
	chr8	51444812	mm39_genes_intergenic	0.0000	0.0000	-26.289
	chr8	51444812	mm39_cpg_inter	0.0000	0.0000	-26.289
	chr8	57786163	mm39_cpg_inter	0.0000	0.0006	66.667
Hdnr	chr8	57786163	mm39_genes_introns	0.0000	0.0006	66.667
Palld	chr8	62002889	mm39_genes_introns	0.0000	0.0772	30.664
	chr8	62002889	mm39_cpg_islands	0.0000	0.0772	30.664
Palld	chr8	62002889	mm39_genes_exons	0.0000	0.0772	30.664
Palld	chr8	62002889	mm39_genes_exons	0.0000	0.0772	30.664
Palld	chr8	62002889	mm39_genes_exons	0.0000	0.0772	30.664
	chr8	68514726	mm39_genes_intergenic	0.0000	0.0000	-35.947
	chr8	68514726	mm39_cpg_shores	0.0000	0.0000	-35.947
Tssk6	chr8	70354422	mm39_genes_promoters	0.0000	0.0004	-68.750
	chr8	70354422	mm39_cpg_islands	0.0000	0.0004	-68.750
Ndufa13	chr8	70354422	mm39_genes_intronexonboundaries	0.0000	0.0004	-68.750
Ndufa13	chr8	70354422	mm39_genes_intronexonboundaries	0.0000	0.0004	-68.750
Ndufa13	chr8	70354422	mm39_genes_exonintronboundaries	0.0000	0.0004	-68.750
Ndufa13	chr8	70354422	mm39_genes_introns	0.0000	0.0004	-68.750
Ndufa13	chr8	70354422	mm39_genes_introns	0.0000	0.0004	-68.750
Ndufa13	chr8	70354422	mm39_genes_exonintronboundaries	0.0000	0.0004	-68.750
	chr8	71111891	mm39_cpg_shores	0.0000	0.0000	-44.326
Pgpep1	chr8	71111891	mm39_genes_introns	0.0000	0.0000	-44.326
	chr8	71359044	mm39_cpg_islands	0.0000	0.0028	-30.570
Map1s	chr8	71359044	mm39_genes_introns	0.0000	0.0028	-30.570
	chr8	71922210	mm39_cpg_islands	0.0000	0.0000	-31.050
Dda1	chr8	71922210	mm39_genes_introns	0.0000	0.0000	-31.050
Dda1	chr8	71922210	mm39_genes_introns	0.0000	0.0000	-31.050
Dda1	chr8	71922210	mm39_genes_introns	0.0000	0.0000	-31.050
Dda1	chr8	71922210	mm39_genes_introns	0.0000	0.0000	-31.050
Dda1	chr8	71922210	mm39_genes_introns	0.0000	0.0000	-31.050
	chr8	72635470	mm39_cpg_shores	0.0000	0.0010	-85.714
Zfp709	chr8	72635470	mm39_genes_promoters	0.0000	0.0010	-85.714
Zfp617	chr8	72676544	mm39_genes_promoters	0.0000	0.0000	-58.537
	chr8	72676544	mm39_cpg_islands	0.0000	0.0000	-58.537
	chr8	73373040	mm39_cpg_inter	0.0000	0.0332	26.667
Nwd1	chr8	73373040	mm39_genes_promoters	0.0000	0.0332	26.667
	chr8	78450921	mm39_cpg_inter	0.0000	0.0000	-90.123
Ednra	chr8	78450921	mm39_genes_exonintronboundaries	0.0000	0.0000	-90.123
Ednra	chr8	78450921	mm39_genes_5UTRs	0.0000	0.0000	-90.123
Ednra	chr8	78450921	mm39_genes_exons	0.0000	0.0000	-90.123
Ednra	chr8	78450921	mm39_genes_intronexonboundaries	0.0000	0.0000	-90.123
	chr8	79146489	mm39_cpg_inter	0.0000	0.0001	-67.647
	chr8	79146489	mm39_genes_intergenic	0.0000	0.0001	-67.647
	chr8	79276745	mm39_cpg_inter	0.0000	0.0234	-21.950

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Slc10a7	chr8	79276745	mm39_genes_introns	0.0000	0.0234	-21.950
Slc10a7	chr8	79276745	mm39_genes_introns	0.0000	0.0234	-21.950
Slc10a7	chr8	79276745	mm39_genes_introns	0.0000	0.0234	-21.950
Slc10a7	chr8	79276745	mm39_genes_introns	0.0000	0.0234	-21.950
Slc10a7	chr8	79276745	mm39_genes_introns	0.0000	0.0234	-21.950
	chr8	79900534	mm39_cpg_inter	0.0000	0.0284	40.105
Zfp827	chr8	79900534	mm39_genes_introns	0.0000	0.0284	40.105
Zfp827	chr8	79900534	mm39_genes_introns	0.0000	0.0284	40.105
	chr8	84448630	mm39_cpg_inter	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_exonintronboundaries	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_exonintronboundaries	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_exonintronboundaries	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_exonintronboundaries	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_introns	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_introns	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_introns	0.0000	0.0273	-80.000
Ddx39a	chr8	84448630	mm39_genes_introns	0.0000	0.0273	-80.000
	chr8	84603062	mm39_genes_intergenic	0.0000	0.0008	37.775
	chr8	84603062	mm39_cpg_islands	0.0000	0.0008	37.775
Palm3	chr8	84747935	mm39_genes_promoters	0.0000	0.0000	-77.966
	chr8	84747935	mm39_cpg_islands	0.0000	0.0000	-77.966
Nfix	chr8	85511035	mm39_genes_introns	0.0000	0.0000	-60.499
Nfix	chr8	85511035	mm39_genes_introns	0.0000	0.0000	-60.499
Nfix	chr8	85511035	mm39_genes_introns	0.0000	0.0000	-60.499
Nfix	chr8	85511035	mm39_genes_1to5kb	0.0000	0.0000	-60.499
Nfix	chr8	85511035	mm39_genes_1to5kb	0.0000	0.0000	-60.499
	chr8	85511035	mm39_cpg_islands	0.0000	0.0000	-60.499
Nfix	chr8	85511036	mm39_genes_introns	0.0000	0.0000	32.055
Nfix	chr8	85511036	mm39_genes_introns	0.0000	0.0000	32.055
Nfix	chr8	85511036	mm39_genes_introns	0.0000	0.0000	32.055
Nfix	chr8	85511036	mm39_genes_1to5kb	0.0000	0.0000	32.055
Nfix	chr8	85511036	mm39_genes_1to5kb	0.0000	0.0000	32.055
	chr8	85511036	mm39_cpg_islands	0.0000	0.0000	32.055
Nfix	chr8	85511081	mm39_genes_introns	0.0000	0.0003	62.821
Nfix	chr8	85511081	mm39_genes_introns	0.0000	0.0003	62.821
Nfix	chr8	85511081	mm39_genes_introns	0.0000	0.0003	62.821
Nfix	chr8	85511081	mm39_genes_1to5kb	0.0000	0.0003	62.821
Nfix	chr8	85511081	mm39_genes_1to5kb	0.0000	0.0003	62.821
	chr8	85511081	mm39_cpg_islands	0.0000	0.0003	62.821
	chr8	88750203	mm39_genes_intergenic	0.0000	0.0013	-28.295
	chr8	88750203	mm39_cpg_inter	0.0000	0.0013	-28.295
	chr8	104873099	mm39_genes_intergenic	0.0000	0.0000	-86.486
	chr8	104873099	mm39_cpg_shelves	0.0000	0.0000	-86.486
	chr8	105762337	mm39_cpg_inter	0.0000	0.0000	-51.746
	chr8	105762337	mm39_genes_intergenic	0.0000	0.0000	-51.746
Fbxl8	chr8	105991236	mm39_genes_promoters	0.0000	0.0035	34.709
Tradd	chr8	105991236	mm39_genes_exonintronboundaries	0.0000	0.0035	34.709
Tradd	chr8	105991236	mm39_genes_intronexonboundaries	0.0000	0.0035	34.709
	chr8	105991236	mm39_cpg_islands	0.0000	0.0035	34.709
Fbxl8	chr8	105991236	mm39_genes_exonintronboundaries	0.0000	0.0035	34.709
Tradd	chr8	105991236	mm39_genes_promoters	0.0000	0.0035	34.709

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Tradd	chr8	105996136	mm39_genes_1to5kb	0.0000	0.0000	-75.817
	chr8	105996136	mm39_cpg_islands	0.0000	0.0000	-75.817
Hsf4	chr8	105996136	mm39_genes_promoters	0.0000	0.0000	-75.817
Hsf4	chr8	105996136	mm39_genes_promoters	0.0000	0.0000	-75.817
Hsf4	chr8	105996136	mm39_genes_promoters	0.0000	0.0000	-75.817
Hsf4	chr8	105996136	mm39_genes_promoters	0.0000	0.0000	-75.817
Fbxl8	chr8	105996136	mm39_genes_exonintronboundaries	0.0000	0.0000	-75.817
Plekhg4	chr8	106101398	mm39_genes_promoters	0.0000	0.0899	-32.554
Plekhg4	chr8	106101398	mm39_genes_intronexonboundaries	0.0000	0.0899	-32.554
	chr8	106101398	mm39_cpg_islands	0.0000	0.0899	-32.554
Plekhg4	chr8	106101398	mm39_genes_exonintronboundaries	0.0000	0.0899	-32.554
Plekhg4	chr8	106101398	mm39_genes_exons	0.0000	0.0899	-32.554
	chr8	106252002	mm39_cpg_inter	0.0000	0.0147	37.430
Atp6v0d1	chr8	106252002	mm39_genes_intronexonboundaries	0.0000	0.0147	37.430
Atp6v0d1	chr8	106252002	mm39_genes_exonintronboundaries	0.0000	0.0147	37.430
Atp6v0d1	chr8	106252002	mm39_genes_intronexonboundaries	0.0000	0.0147	37.430
Atp6v0d1	chr8	106252002	mm39_genes_exons	0.0000	0.0147	37.430
Cdh3	chr8	107238508	mm39_genes_introns	0.0000	0.0006	-22.368
Cdh3	chr8	107238508	mm39_genes_introns	0.0000	0.0006	-22.368
	chr8	107238508	mm39_cpg_shores	0.0000	0.0006	-22.368
Has3	chr8	107598954	mm39_genes_introns	0.0000	0.0073	-24.752
Has3	chr8	107598954	mm39_genes_introns	0.0000	0.0073	-24.752
	chr8	107598954	mm39_cpg_shores	0.0000	0.0073	-24.752
	chr8	111572694	mm39_cpg_shores	0.0000	0.0990	-48.759
Sf3b3	chr8	111572694	mm39_genes_introns	0.0000	0.0990	-48.759
Cog4	chr8	111572694	mm39_genes_promoters	0.0000	0.0990	-48.759
Cog4	chr8	111572694	mm39_genes_promoters	0.0000	0.0990	-48.759
Tmem170	chr8	112602864	mm39_genes_introns	0.0000	0.0168	-49.074
	chr8	112602864	mm39_cpg_shores	0.0000	0.0168	-49.074
Chst5	chr8	112625451	mm39_genes_introns	0.0000	0.0000	-45.669
	chr8	112625451	mm39_cpg_inter	0.0000	0.0000	-45.669
	chr8	115886788	mm39_cpg_inter	0.0000	0.0000	-84.314
Wwox	chr8	115886788	mm39_genes_introns	0.0000	0.0000	-84.314
Klhl36	chr8	120589300	mm39_genes_exonintronboundaries	0.0000	0.0000	-92.000
Klhl36	chr8	120589300	mm39_genes_introns	0.0000	0.0000	-92.000
	chr8	120589300	mm39_cpg_shores	0.0000	0.0000	-92.000
	chr8	120956494	mm39_cpg_islands	0.0000	0.0000	-44.555
A330074K22Rik	chr8	120956494	mm39_genes_1to5kb	0.0000	0.0000	-44.555
	chr8	121699545	mm39_cpg_inter	0.0000	0.0047	-76.000
	chr8	121699545	mm39_genes_intergenic	0.0000	0.0047	-76.000
	chr8	123328925	mm39_cpg_inter	0.0000	0.0614	26.268
Galns	chr8	123328925	mm39_genes_introns	0.0000	0.0614	26.268
Galns	chr8	123328925	mm39_genes_introns	0.0000	0.0614	26.268
Nrp1	chr8	129083481	mm39_genes_1to5kb	0.0000	0.0024	-49.143
Nrp1	chr8	129083481	mm39_genes_1to5kb	0.0000	0.0024	-49.143
Nrp1	chr8	129083481	mm39_genes_1to5kb	0.0000	0.0024	-49.143
Mir1903	chr8	129083481	mm39_genes_1to5kb	0.0000	0.0024	-49.143
	chr8	129083481	mm39_cpg_islands	0.0000	0.0024	-49.143
Nrp1	chr8	129083812	mm39_genes_1to5kb	0.0000	0.0000	-56.181
Nrp1	chr8	129083812	mm39_genes_1to5kb	0.0000	0.0000	-56.181
Nrp1	chr8	129083812	mm39_genes_1to5kb	0.0000	0.0000	-56.181

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Mir1903	chr8	129083812	mm39_genes_1to5kb	0.0000	0.0000	-56.181
	chr8	129083812	mm39_cpg_islands	0.0000	0.0000	-56.181
	chr8	129089958	mm39_cpg_shelves	0.0000	0.0000	-70.066
Nrp1	chr8	129089958	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.066
Nrp1	chr8	129089958	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.066
Nrp1	chr8	129089958	mm39_genes_exonintronboundaries	0.0000	0.0000	-70.066
Nrp1	chr8	129089958	mm39_genes_introns	0.0000	0.0000	-70.066
Nrp1	chr8	129089958	mm39_genes_introns	0.0000	0.0000	-70.066
Nrp1	chr8	129089958	mm39_genes_introns	0.0000	0.0000	-70.066
Fat3	chr9	16413450	mm39_genes_intronexonboundaries	0.0000	0.0000	-50.906
	chr9	16413450	mm39_cpg_islands	0.0000	0.0000	-50.906
Fat3	chr9	16413450	mm39_genes_promoters	0.0000	0.0000	-50.906
Fdx2	chr9	20984818	mm39_genes_exons	0.0000	0.0000	-32.080
	chr9	20984818	mm39_cpg_islands	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exonintronboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exonintronboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exonintronboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exons	0.0000	0.0000	-32.080
Gm38431	chr9	20984818	mm39_genes_introns	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_intronexonboundaries	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exons	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exons	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_exons	0.0000	0.0000	-32.080
Fdx2	chr9	20984818	mm39_genes_5UTRs	0.0000	0.0000	-32.080
Pde4a	chr9	21095778	mm39_genes_introns	0.0000	0.0080	29.507
Pde4a	chr9	21095778	mm39_genes_exons	0.0000	0.0080	29.507
Pde4a	chr9	21095778	mm39_genes_exonintronboundaries	0.0000	0.0080	29.507
	chr9	21095778	mm39_cpg_shores	0.0000	0.0080	29.507
S1pr5	chr9	21159878	mm39_genes_exonintronboundaries	0.0000	0.0000	-53.474
S1pr5	chr9	21159878	mm39_genes_intronexonboundaries	0.0000	0.0000	-53.474
	chr9	21159878	mm39_cpg_islands	0.0000	0.0000	-53.474
S1pr5	chr9	21159878	mm39_genes_promoters	0.0000	0.0000	-53.474
	chr9	21176595	mm39_cpg_islands	0.0000	0.0005	-33.059
Atg4d	chr9	21176595	mm39_genes_exons	0.0000	0.0005	-33.059
Atg4d	chr9	21176595	mm39_genes_5UTRs	0.0000	0.0005	-33.059
Ap1m2	chr9	21223470	mm39_genes_introns	0.0000	0.0523	45.227
Ap1m2	chr9	21223470	mm39_genes_introns	0.0000	0.0523	45.227
Ap1m2	chr9	21223470	mm39_genes_exonintronboundaries	0.0000	0.0523	45.227
Ap1m2	chr9	21223470	mm39_genes_exonintronboundaries	0.0000	0.0523	45.227
	chr9	21223470	mm39_cpg_islands	0.0000	0.0523	45.227
Ap1m2	chr9	21223470	mm39_genes_intronexonboundaries	0.0000	0.0523	45.227
Ap1m2	chr9	21223470	mm39_genes_intronexonboundaries	0.0000	0.0523	45.227
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702
Dnm2	chr9	21336819	mm39_genes_introns	0.0000	0.0000	-24.702
	chr9	21336819	mm39_cpg_shores	0.0000	0.0000	-24.702
	chr9	24692452	mm39_genes_intergenic	0.0000	0.0000	-59.540
	chr9	24692452	mm39_cpg_islands	0.0000	0.0000	-59.540
Pknox2	chr9	37057981	mm39_genes_introns	0.0000	0.0000	-41.819
Pknox2	chr9	37057981	mm39_genes_introns	0.0000	0.0000	-41.819
	chr9	37057981	mm39_cpg_islands	0.0000	0.0000	-41.819
	chr9	42739332	mm39_cpg_inter	0.0000	0.0185	-59.091
Grik4	chr9	42739332	mm39_genes_introns	0.0000	0.0185	-59.091
	chr9	43150992	mm39_cpg_islands	0.0000	0.0003	15.034
Oaf	chr9	43150992	mm39_genes_exons	0.0000	0.0003	15.034
Oaf	chr9	43150992	mm39_genes_5UTRs	0.0000	0.0003	15.034
Oaf	chr9	43150992	mm39_genes_intronexonboundaries	0.0000	0.0003	15.034
H2ax	chr9	44247165	mm39_genes_exons	0.0000	0.0000	-27.171
H2ax	chr9	44247165	mm39_genes_3UTRs	0.0000	0.0000	-27.171
	chr9	44247165	mm39_cpg_shores	0.0000	0.0000	-27.171
Scn4b	chr9	45057344	mm39_genes_introns	0.0000	0.0000	-37.713
	chr9	45057344	mm39_cpg_inter	0.0000	0.0000	-37.713
	chr9	48406979	mm39_cpg_islands	0.0000	0.0000	19.445
Rbm7	chr9	48406979	mm39_genes_promoters	0.0000	0.0000	19.445
Rbm7	chr9	48406979	mm39_genes_promoters	0.0000	0.0000	19.445
Rbm7	chr9	48406979	mm39_genes_promoters	0.0000	0.0000	19.445
Rbm7	chr9	48406979	mm39_genes_promoters	0.0000	0.0000	19.445
Rbm7	chr9	48406979	mm39_genes_promoters	0.0000	0.0000	19.445
Gm5617	chr9	48406979	mm39_genes_exons	0.0000	0.0000	19.445
	chr9	50632752	mm39_cpg_inter	0.0000	0.0606	-50.286
Dixdc1	chr9	50632752	mm39_genes_introns	0.0000	0.0606	-50.286
Dixdc1	chr9	50632752	mm39_genes_introns	0.0000	0.0606	-50.286
Dixdc1	chr9	50632752	mm39_genes_introns	0.0000	0.0606	-50.286
	chr9	53295353	mm39_cpg_islands	0.0000	0.0124	63.235
Poglut3	chr9	53295353	mm39_genes_exons	0.0000	0.0124	63.235
Poglut3	chr9	53295353	mm39_genes_5UTRs	0.0000	0.0124	63.235
Idh3a	chr9	54493650	mm39_genes_promoters	0.0000	0.0000	-84.722
	chr9	54493650	mm39_cpg_islands	0.0000	0.0000	-84.722
Idh3a	chr9	54493650	mm39_genes_exonintronboundaries	0.0000	0.0000	-84.722
	chr9	55234368	mm39_cpg_shores	0.0000	0.0000	-76.161
Tmem266	chr9	55234368	mm39_genes_exonintronboundaries	0.0000	0.0000	-76.161
Tmem266	chr9	55234368	mm39_genes_exonintronboundaries	0.0000	0.0000	-76.161
Tmem266	chr9	55234368	mm39_genes_introns	0.0000	0.0000	-76.161
Tmem266	chr9	55234368	mm39_genes_introns	0.0000	0.0000	-76.161
	chr9	55299872	mm39_cpg_inter	0.0000	0.0202	-19.259
Tmem266	chr9	55299872	mm39_genes_introns	0.0000	0.0202	-19.259
Tmem266	chr9	55299872	mm39_genes_introns	0.0000	0.0202	-19.259
	chr9	55450178	mm39_cpg_islands	0.0000	0.0000	-41.520
Isl2	chr9	55450178	mm39_genes_introns	0.0000	0.0000	-41.520
Isl2	chr9	55452746	mm39_genes_intronexonboundaries	0.0000	0.0000	-41.625
Isl2	chr9	55452746	mm39_genes_exons	0.0000	0.0000	-41.625
	chr9	55452746	mm39_cpg_islands	0.0000	0.0000	-41.625
Sin3a	chr9	56979850	mm39_genes_1to5kb	0.0000	0.0018	-28.372
Sin3a	chr9	56979850	mm39_genes_1to5kb	0.0000	0.0018	-28.372

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Sin3a	chr9	56979850	mm39_genes_1to5kb	0.0000	0.0018	-28.372
Gm10658	chr9	56979850	mm39_genes_promoters	0.0000	0.0018	-28.372
Sin3a	chr9	56979850	mm39_genes_introns	0.0000	0.0018	-28.372
	chr9	56979850	mm39_cpg_islands	0.0000	0.0018	-28.372
Sin3a	chr9	56980108	mm39_genes_1to5kb	0.0000	0.0000	-44.348
Sin3a	chr9	56980108	mm39_genes_1to5kb	0.0000	0.0000	-44.348
Sin3a	chr9	56980108	mm39_genes_1to5kb	0.0000	0.0000	-44.348
Gm10658	chr9	56980108	mm39_genes_promoters	0.0000	0.0000	-44.348
Sin3a	chr9	56980108	mm39_genes_introns	0.0000	0.0000	-44.348
	chr9	56980108	mm39_cpg_islands	0.0000	0.0000	-44.348
	chr9	59394214	mm39_cpg_islands	0.0000	0.0003	18.210
Arih1	chr9	59394214	mm39_genes_promoters	0.0000	0.0003	18.210
Celf6	chr9	59493882	mm39_genes_introns	0.0000	0.0691	-43.333
	chr9	59493882	mm39_cpg_inter	0.0000	0.0691	-43.333
Celf6	chr9	59493882	mm39_genes_1to5kb	0.0000	0.0691	-43.333
Celf6	chr9	59493882	mm39_genes_1to5kb	0.0000	0.0691	-43.333
	chr9	60425771	mm39_genes_intergenic	0.0000	0.0826	-60.455
	chr9	60425771	mm39_cpg_shelves	0.0000	0.0826	-60.455
Lrrc49	chr9	60595269	mm39_genes_promoters	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_promoters	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_exonintronboundaries	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_exonintronboundaries	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_exons	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_exons	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_5UTRs	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_5UTRs	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_intronexonboundaries	0.0000	0.0005	31.304
Lrrc49	chr9	60595269	mm39_genes_intronexonboundaries	0.0000	0.0005	31.304
	chr9	60595269	mm39_cpg_islands	0.0000	0.0005	31.304
Tle3	chr9	61281641	mm39_genes_introns	0.0000	0.0000	-50.018
Tle3	chr9	61281641	mm39_genes_introns	0.0000	0.0000	-50.018
Tle3	chr9	61281641	mm39_genes_introns	0.0000	0.0000	-50.018
Tle3	chr9	61281641	mm39_genes_intronexonboundaries	0.0000	0.0000	-50.018
Tle3	chr9	61281641	mm39_genes_intronexonboundaries	0.0000	0.0000	-50.018
Tle3	chr9	61281641	mm39_genes_intronexonboundaries	0.0000	0.0000	-50.018
	chr9	61281641	mm39_cpg_shores	0.0000	0.0000	-50.018
	chr9	63509730	mm39_cpg_shores	0.0000	0.0000	-77.931
Aagab	chr9	63509730	mm39_genes_promoters	0.0000	0.0000	-77.931
Aagab	chr9	63509730	mm39_genes_promoters	0.0000	0.0000	-77.931
Aagab	chr9	63509730	mm39_genes_promoters	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_exonintronboundaries	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_exonintronboundaries	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_intronexonboundaries	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_intronexonboundaries	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_exons	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_exons	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_5UTRs	0.0000	0.0000	-77.931
Iqch	chr9	63509730	mm39_genes_5UTRs	0.0000	0.0000	-77.931
	chr9	64513556	mm39_cpg_inter	0.0000	0.0014	-71.795
Megf11	chr9	64513556	mm39_genes_introns	0.0000	0.0014	-71.795
Megf11	chr9	64513556	mm39_genes_introns	0.0000	0.0014	-71.795

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr9	64645082	mm39_cpg_islands	0.0000	0.0000	-44.803
Rab11a	chr9	64645082	mm39_genes_intronexonboundaries	0.0000	0.0000	-44.803
Rab11a	chr9	64645082	mm39_genes_promoters	0.0000	0.0000	-44.803
Kbtbd13	chr9	65297993	mm39_genes_exons	0.0000	0.0812	34.872
	chr9	65297993	mm39_cpg_islands	0.0000	0.0812	34.872
	chr9	69667905	mm39_cpg_islands	0.0000	0.0000	-62.365
B230323A14Rik	chr9	69667905	mm39_genes_promoters	0.0000	0.0000	-62.365
Foxb1	chr9	69667905	mm39_genes_exonintronboundaries	0.0000	0.0000	-62.365
Foxb1	chr9	69667905	mm39_genes_5UTRs	0.0000	0.0000	-62.365
Foxb1	chr9	69667905	mm39_genes_exons	0.0000	0.0000	-62.365
	chr9	72019139	mm39_cpg_islands	0.0000	0.0119	-21.843
Tcf12	chr9	72019139	mm39_genes_promoters	0.0000	0.0119	-21.843
Tcf12	chr9	72019139	mm39_genes_intronexonboundaries	0.0000	0.0119	-21.843
Tcf12	chr9	72019139	mm39_genes_intronexonboundaries	0.0000	0.0119	-21.843
Tcf12	chr9	72019139	mm39_genes_promoters	0.0000	0.0119	-21.843
Tcf12	chr9	72019139	mm39_genes_promoters	0.0000	0.0119	-21.843
Mns1	chr9	72345931	mm39_genes_exonintronboundaries	0.0000	0.0109	21.143
Mns1	chr9	72345931	mm39_genes_exons	0.0000	0.0109	21.143
Mns1	chr9	72345931	mm39_genes_5UTRs	0.0000	0.0109	21.143
	chr9	72345931	mm39_cpg_shores	0.0000	0.0109	21.143
Eef1a1	chr9	78388353	mm39_genes_introns	0.0000	0.0000	-51.172
	chr9	78388353	mm39_cpg_islands	0.0000	0.0000	-51.172
	chr9	85209719	mm39_cpg_islands	0.0000	0.0820	35.714
Tent5a	chr9	85209719	mm39_genes_promoters	0.0000	0.0820	35.714
Tent5a	chr9	85209719	mm39_genes_promoters	0.0000	0.0820	35.714
	chr9	85210218	mm39_cpg_shores	0.0000	0.0034	66.667
Tent5a	chr9	85210218	mm39_genes_1to5kb	0.0000	0.0034	66.667
Tent5a	chr9	85210218	mm39_genes_1to5kb	0.0000	0.0034	66.667
Dop1a	chr9	86346990	mm39_genes_1to5kb	0.0000	0.0000	21.220
	chr9	86346990	mm39_cpg_islands	0.0000	0.0000	21.220
Ube2cbp	chr9	86346990	mm39_genes_exonintronboundaries	0.0000	0.0000	21.220
Ube2cbp	chr9	86346990	mm39_genes_intronexonboundaries	0.0000	0.0000	21.220
Ube2cbp	chr9	86346990	mm39_genes_promoters	0.0000	0.0000	21.220
Rwdd2a	chr9	86453888	mm39_genes_promoters	0.0000	0.0565	-27.783
Rwdd2a	chr9	86453888	mm39_genes_promoters	0.0000	0.0565	-27.783
Rwdd2a	chr9	86453888	mm39_genes_promoters	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_exonintronboundaries	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_exonintronboundaries	0.0000	0.0565	-27.783
	chr9	86453888	mm39_cpg_islands	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_intronexonboundaries	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_intronexonboundaries	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_5UTRs	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_5UTRs	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_exons	0.0000	0.0565	-27.783
Pgm3	chr9	86453888	mm39_genes_exons	0.0000	0.0565	-27.783
Syncrip	chr9	88365292	mm39_genes_promoters	0.0000	0.0007	-25.798
Syncrip	chr9	88365292	mm39_genes_promoters	0.0000	0.0007	-25.798
Syncrip	chr9	88365292	mm39_genes_promoters	0.0000	0.0007	-25.798
Syncrip	chr9	88365292	mm39_genes_promoters	0.0000	0.0007	-25.798
	chr9	88365292	mm39_cpg_shores	0.0000	0.0007	-25.798
Syncrip	chr9	88365293	mm39_genes_promoters	0.0000	0.0224	12.495

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Syncrip	chr9	88365293	mm39_genes_promoters	0.0000	0.0224	12.495
Syncrip	chr9	88365293	mm39_genes_promoters	0.0000	0.0224	12.495
Syncrip	chr9	88365293	mm39_genes_promoters	0.0000	0.0224	12.495
	chr9	88365293	mm39_cpg_shores	0.0000	0.0224	12.495
	chr9	96601534	mm39_cpg_shores	0.0000	0.0312	-66.667
Zbtb38	chr9	96601534	mm39_genes_introns	0.0000	0.0312	-66.667
Zbtb38	chr9	96601534	mm39_genes_introns	0.0000	0.0312	-66.667
Zbtb38	chr9	96601534	mm39_genes_exonintronboundaries	0.0000	0.0312	-66.667
Zbtb38	chr9	96601534	mm39_genes_intronexonboundaries	0.0000	0.0312	-66.667
Zbtb38	chr9	96601534	mm39_genes_promoters	0.0000	0.0312	-66.667
Slc25a36	chr9	96992865	mm39_genes_introns	0.0000	0.0000	-39.326
	chr9	96992865	mm39_cpg_islands	0.0000	0.0000	-39.326
Slc25a36	chr9	96992865	mm39_genes_exonintronboundaries	0.0000	0.0000	-39.326
	chr9	105205995	mm39_cpg_inter	0.0000	0.0007	-53.423
Nek11	chr9	105205995	mm39_genes_introns	0.0000	0.0007	-53.423
6430571L13Rik	chr9	107215631	mm39_genes_1to5kb	0.0000	0.0003	14.735
Hemk1	chr9	107215631	mm39_genes_exonintronboundaries	0.0000	0.0003	14.735
	chr9	107215631	mm39_cpg_islands	0.0000	0.0003	14.735
Hemk1	chr9	107215631	mm39_genes_intronexonboundaries	0.0000	0.0003	14.735
Hemk1	chr9	107215631	mm39_genes_promoters	0.0000	0.0003	14.735
Rnf123	chr9	107931320	mm39_genes_introns	0.0000	0.0081	66.667
Rnf123	chr9	107931320	mm39_genes_introns	0.0000	0.0081	66.667
Amigo3	chr9	107931320	mm39_genes_exons	0.0000	0.0081	66.667
	chr9	107931320	mm39_cpg_inter	0.0000	0.0081	66.667
	chr9	108359190	mm39_cpg_inter	0.0000	0.0226	28.275
Lamb2	chr9	108359190	mm39_genes_intronexonboundaries	0.0000	0.0226	28.275
Lamb2	chr9	108359190	mm39_genes_exons	0.0000	0.0226	28.275
Lamb2	chr9	108359190	mm39_genes_exonintronboundaries	0.0000	0.0226	28.275
Lamb2	chr9	108359190	mm39_genes_intronexonboundaries	0.0000	0.0226	28.275
	chr9	118729693	mm39_cpg_inter	0.0000	0.0445	46.667
Itga9	chr9	118729693	mm39_genes_exons	0.0000	0.0445	46.667
Itga9	chr9	118729693	mm39_genes_exons	0.0000	0.0445	46.667
Itga9	chr9	118729693	mm39_genes_3UTRs	0.0000	0.0445	46.667
Itga9	chr9	118729693	mm39_genes_3UTRs	0.0000	0.0445	46.667
	chr9	118756109	mm39_cpg_islands	0.0000	0.0000	-27.957
Ctdspl	chr9	118756109	mm39_genes_exonintronboundaries	0.0000	0.0000	-27.957
Ctdspl	chr9	118756109	mm39_genes_introns	0.0000	0.0000	-27.957
	chr9	118917228	mm39_cpg_inter	0.0000	0.0001	-36.264
Plcd1	chr9	118917228	mm39_genes_introns	0.0000	0.0001	-36.264
Plcd1	chr9	118917228	mm39_genes_introns	0.0000	0.0001	-36.264
Plcd1	chr9	118917228	mm39_genes_exonintronboundaries	0.0000	0.0001	-36.264
Plcd1	chr9	118917228	mm39_genes_intronexonboundaries	0.0000	0.0001	-36.264
Plcd1	chr9	118917228	mm39_genes_exons	0.0000	0.0001	-36.264
Csrnp1	chr9	119812731	mm39_genes_introns	0.0000	0.0000	-27.832
Csrnp1	chr9	119812731	mm39_genes_introns	0.0000	0.0000	-27.832
	chr9	119812731	mm39_cpg_islands	0.0000	0.0000	-27.832
Csrnp1	chr9	119812731	mm39_genes_promoters	0.0000	0.0000	-27.832
Csrnp1	chr9	119812731	mm39_genes_exonintronboundaries	0.0000	0.0000	-27.832
Csrnp1	chr9	119812731	mm39_genes_intronexonboundaries	0.0000	0.0000	-27.832
Csrnp1	chr9	119812731	mm39_genes_5UTRs	0.0000	0.0000	-27.832
Csrnp1	chr9	119812731	mm39_genes_exons	0.0000	0.0000	-27.832

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
	chr9	121589651	mm39_cpg_islands	0.0000	0.0000	-52.061
E530011L22Rik	chr9	121589651	mm39_genes_promoters	0.0000	0.0000	-52.061
Zfp651	chr9	121589651	mm39_genes_introns	0.0000	0.0000	-52.061
	chr9	123721605	mm39_genes_intergenic	0.0000	0.0002	66.667
	chr9	123721605	mm39_cpg_shores	0.0000	0.0002	66.667
	chr9	123721630	mm39_genes_intergenic	0.0000	0.0073	54.545
	chr9	123721630	mm39_cpg_shores	0.0000	0.0073	54.545
	chrM	135	mm39_genes_intergenic	0.0000	0.0000	-12.361
	chrM	135	mm39_cpg_inter	0.0000	0.0000	-12.361
	chrM	1429	mm39_genes_intergenic	0.0000	0.0023	-17.365
	chrM	1429	mm39_cpg_inter	0.0000	0.0023	-17.365
	chrM	5727	mm39_genes_intergenic	0.0000	0.0000	-55.233
	chrM	5727	mm39_cpg_inter	0.0000	0.0000	-55.233
	chrM	6114	mm39_genes_intergenic	0.0000	0.0000	-8.200
	chrM	6114	mm39_cpg_inter	0.0000	0.0000	-8.200
Kdm6a	chrX	18029475	mm39_genes_introns	0.0000	0.0000	-65.093
Kdm6a	chrX	18029475	mm39_genes_introns	0.0000	0.0000	-65.093
Kdm6a	chrX	18029475	mm39_genes_intronexonboundaries	0.0000	0.0000	-65.093
Kdm6a	chrX	18029475	mm39_genes_intronexonboundaries	0.0000	0.0000	-65.093
Kdm6a	chrX	18029475	mm39_genes_exonintronboundaries	0.0000	0.0000	-65.093
Kdm6a	chrX	18029475	mm39_genes_exonintronboundaries	0.0000	0.0000	-65.093
	chrX	18029475	mm39_cpg_islands	0.0000	0.0000	-65.093
	chrX	56963313	mm39_genes_intergenic	0.0000	0.0171	69.856
	chrX	56963313	mm39_cpg_inter	0.0000	0.0171	69.856
	chrX	57061456	mm39_genes_intergenic	0.0000	0.0019	-77.273
	chrX	57061456	mm39_cpg_shelves	0.0000	0.0019	-77.273
Vma21	chrX	70859940	mm39_genes_promoters	0.0000	0.0001	-89.130
Vma21	chrX	70859940	mm39_genes_promoters	0.0000	0.0001	-89.130
Vma21	chrX	70859940	mm39_genes_5UTRs	0.0000	0.0001	-89.130
Vma21	chrX	70859940	mm39_genes_exons	0.0000	0.0001	-89.130
Vma21	chrX	70859940	mm39_genes_intronexonboundaries	0.0000	0.0001	-89.130
Vma21	chrX	70859940	mm39_genes_exonintronboundaries	0.0000	0.0001	-89.130
	chrX	70859940	mm39_cpg_shores	0.0000	0.0001	-89.130
Pls3	chrX	74918571	mm39_genes_promoters	0.0000	0.0000	-39.971
Pls3	chrX	74918571	mm39_genes_introns	0.0000	0.0000	-39.971
Pls3	chrX	74918571	mm39_genes_introns	0.0000	0.0000	-39.971
Pls3	chrX	74918571	mm39_genes_exonintronboundaries	0.0000	0.0000	-39.971
Pls3	chrX	74918571	mm39_genes_exonintronboundaries	0.0000	0.0000	-39.971
	chrX	74918571	mm39_cpg_inter	0.0000	0.0000	-39.971
Cldn34d	chrX	75642188	mm39_genes_introns	0.0000	0.0000	-83.347
	chrX	75642188	mm39_cpg_inter	0.0000	0.0000	-83.347
Tbl1x	chrX	76554773	mm39_genes_promoters	0.0000	0.0000	-51.111
Tbl1x	chrX	76554773	mm39_genes_exonintronboundaries	0.0000	0.0000	-51.111
	chrX	76554773	mm39_cpg_islands	0.0000	0.0000	-51.111
Prrg1	chrX	77557580	mm39_genes_introns	0.0000	0.0033	37.692
Prrg1	chrX	77557580	mm39_genes_introns	0.0000	0.0033	37.692
Prrg1	chrX	77557580	mm39_genes_introns	0.0000	0.0033	37.692
	chrX	77557580	mm39_cpg_inter	0.0000	0.0033	37.692
Amer1	chrX	94488037	mm39_genes_introns	0.0000	0.0012	-82.979
	chrX	94488037	mm39_cpg_inter	0.0000	0.0012	-82.979
Pja1	chrX	98514270	mm39_genes_5UTRs	0.0000	0.0012	-59.375

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Pja1	chrX	98514270	mm39_genes_5UTRs	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_5UTRs	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_5UTRs	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exons	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exons	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exons	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exons	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_intronexonboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_intronexonboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_intronexonboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_intronexonboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exonintronboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exonintronboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exonintronboundaries	0.0000	0.0012	-59.375
Pja1	chrX	98514270	mm39_genes_exonintronboundaries	0.0000	0.0012	-59.375
	chrX	98514270	mm39_cpg_islands	0.0000	0.0012	-59.375
	chrX	109460808	mm39_genes_intergenic	0.0000	0.0004	-18.001
	chrX	109460808	mm39_cpg_inter	0.0000	0.0004	-18.001
	chrX	110276988	mm39_genes_intergenic	0.0000	0.0796	66.667
	chrX	110276988	mm39_cpg_inter	0.0000	0.0796	66.667
Mir7646	chrX	134643502	mm39_genes_1to5kb	0.0000	0.0145	-48.564
Armcx5	chrX	134643502	mm39_genes_5UTRs	0.0000	0.0145	-48.564
Gprasp1	chrX	134643502	mm39_genes_5UTRs	0.0000	0.0145	-48.564
Gprasp1	chrX	134643502	mm39_genes_5UTRs	0.0000	0.0145	-48.564
Gprasp1	chrX	134643502	mm39_genes_5UTRs	0.0000	0.0145	-48.564
Armcx5	chrX	134643502	mm39_genes_exons	0.0000	0.0145	-48.564
Gprasp1	chrX	134643502	mm39_genes_exons	0.0000	0.0145	-48.564
Gprasp1	chrX	134643502	mm39_genes_exons	0.0000	0.0145	-48.564
Gprasp1	chrX	134643502	mm39_genes_exons	0.0000	0.0145	-48.564
	chrX	134643502	mm39_cpg_islands	0.0000	0.0145	-48.564
Tmem29	chrX	149242158	mm39_genes_promoters	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_promoters	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_promoters	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_promoters	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_intronexonboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_intronexonboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_intronexonboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_intronexonboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_exonintronboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_exonintronboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_exonintronboundaries	0.0000	0.0004	-85.714
Tmem29	chrX	149242158	mm39_genes_exonintronboundaries	0.0000	0.0004	-85.714
	chrX	149242158	mm39_cpg_islands	0.0000	0.0004	-85.714
Sat1	chrX	153999508	mm39_genes_promoters	0.0000	0.0232	-47.545
Sat1	chrX	153999508	mm39_genes_promoters	0.0000	0.0232	-47.545
Sat1	chrX	153999508	mm39_genes_intronexonboundaries	0.0000	0.0232	-47.545
Sat1	chrX	153999508	mm39_genes_intronexonboundaries	0.0000	0.0232	-47.545
	chrX	153999508	mm39_cpg_islands	0.0000	0.0232	-47.545
Msl3	chrX	167456507	mm39_genes_promoters	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161

• **Table S9: Differentially methylated loci in mG4H-OFF vs. Con-OFF**

Gene Symbol	Chromosome	Location	Regulatory Groups	*P*-value	Adjusted *P*-value (*Q*-value)	Methylation difference (%)
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
Msl3	chrX	167456507	mm39_genes_introns	0.0000	0.0000	-87.161
	chrX	167456507	mm39_cpg_islands	0.0000	0.0000	-87.161
	chrY	2408123	mm39_genes_intergenic	0.0000	0.0899	34.024
	chrY	2408123	mm39_cpg_inter	0.0000	0.0899	34.024
	chrY	5879097	mm39_genes_intergenic	0.0000	0.0000	85.657
	chrY	5879097	mm39_cpg_inter	0.0000	0.0000	85.657
	chrY	6886099	mm39_genes_intergenic	0.0000	0.0003	65.143
	chrY	6886099	mm39_cpg_inter	0.0000	0.0003	65.143
	chrY	6999495	mm39_genes_intergenic	0.0000	0.0004	72.131
	chrY	6999495	mm39_cpg_inter	0.0000	0.0004	72.131

• **Table S10: Potential target genes that are differentially expressed, methylated, and inversely regulated at least in mG4H-OFF**

Gene Symbol	Ensembl ID	Description	Regulatory Groups	RNA sequencing			DNA methylation sequencing		
				Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	meth.diff	*P*-value	Adjusted *P*-value (*Q*-value)
1110019D14Rik	ENSMUSG00000097616	RIKEN cDNA 1110019D14 gene	mm39_genes_promoters	-8.030	0.0000	0.0001	30.000	0.0000	0.0614
1700022N22Rik	ENSMUSG00000097523	RIKEN cDNA 1700022N22 gene	mm39_genes_promoters	-17.537	0.0063	0.0176	17.266	0.0000	0.0000
2900005J15Rik	ENSMUSG00000043833	RIKEN cDNA 2900005J15 gene	mm39_genes_promoters	4.676	0.0001	0.0002	-91.476	0.0000	0.0000
5730409E04Rik	ENSMUSG00000073755	RIKEN cDNA 5730409E04Rik gene	mm39_genes_exonintronboundaries	1.953	0.0000	0.0000	-32.811	0.0000	0.0038
Ace	ENSMUSG00000020681	angiotensin I converting enzyme (peptidyl-dipeptidase A) 1	mm39_genes_promoters	-1.744	0.0007	0.0025	25.952	0.0000	0.0623
Adrb1	ENSMUSG00000035283	adrenergic receptor, beta 1	mm39_genes_exons	2.727	0.0000	0.0000	-70.952	0.0000	0.0024
Adrm1	ENSMUSG00000039041	adhesion regulating molecule 1	mm39_genes_exonintronboundaries	-1.500	0.0008	0.0027	72.031	0.0000	0.0002
Adrm1	ENSMUSG00000039041	adhesion regulating molecule 1	mm39_genes_exonintronboundaries	-1.500	0.0008	0.0027	21.525	0.0000	0.0000
Adssl1	ENSMUSG00000011148	adenylosuccinate synthetase like 1	mm39_genes_promoters	1.781	0.0000	0.0000	-80.653	0.0000	0.0000
Agpat4	ENSMUSG00000023827	1-acylglycerol-3-phosphate O-acyltransferase 4 (lysophosphatidic acid acyltransferase, delta)	mm39_genes_promoters	1.553	0.0001	0.0003	-92.857	0.0000	0.0000
Ahcyl1	ENSMUSG00000027893	S-adenosylhomocysteine hydrolase-like 1	mm39_genes_introns	1.851	0.0000	0.0000	-88.785	0.0000	0.0000
Amigo3	ENSMUSG00000032593	adhesion molecule with Ig like domain 3	mm39_genes_exons	-2.911	0.0026	0.0080	66.667	0.0000	0.0081
Arl8a	ENSMUSG00000026426	ADP-ribosylation factor-like 8A	mm39_genes_introns	2.852	0.0000	0.0000	-27.499	0.0000	0.0102
Arntl2	ENSMUSG00000040187	aryl hydrocarbon receptor nuclear translocator-like 2	mm39_genes_introns	-6.734	0.0245	0.0567	45.946	0.0000	0.0019
Atp5d	ENSMUSG00000003072	ATP synthase, H+ transporting, mitochondrial F1 complex, delta subunit	mm39_genes_exonintronboundaries	-3.150	0.0000	0.0000	25.821	0.0000	0.0479
Atp6v0d1	ENSMUSG00000013160	ATPase, H+ transporting, lysosomal V0 subunit D1	mm39_genes_intronexonboundaries	-2.713	0.0000	0.0000	37.430	0.0000	0.0147
Bak1	ENSMUSG00000057789	BCL2-antagonist/killer 1	mm39_genes_intronexonboundaries	-2.354	0.0000	0.0000	17.525	0.0000	0.0000
Bmp2	ENSMUSG00000027358	bone morphogenetic protein 2	mm39_genes_5UTRs	-1.615	0.0122	0.0312	20.133	0.0000	0.0011
C130074G19Rik	ENSMUSG00000039349	RIKEN cDNA C130074G19 gene	mm39_genes_introns	2.178	0.0000	0.0000	-41.900	0.0000	0.0000
Ccdc103	ENSMUSG00000020930	coiled-coil domain containing 103	mm39_genes_promoters	-4.949	0.0282	0.0641	10.703	0.0000	0.0493
Ccnq	ENSMUSG00000049489	cyclin Q	mm39_genes_exons	-1.719	0.0000	0.0000	62.292	0.0000	0.0005
Ccnq	ENSMUSG00000049489	cyclin Q	mm39_genes_exons	-1.719	0.0000	0.0000	63.636	0.0000	0.0001
Cdkn1c	ENSMUSG00000037664	cyclin-dependent kinase inhibitor 1C (P57)	mm39_genes_exons	3.382	0.0000	0.0000	-78.571	0.0000	0.0013
Cds1	ENSMUSG00000029330	CDP-diacylglycerol synthase 1	mm39_genes_exons	2.363	0.0000	0.0000	-22.833	0.0000	0.0993
Chsy3	ENSMUSG00000058152	chondroitin sulfate synthase 3	mm39_genes_exons	2.655	0.0058	0.0164	-54.362	0.0000	0.0000
Cideb	ENSMUSG00000022219	cell death-inducing DNA fragmentation factor, alpha subunit-like effector B	mm39_genes_exonintronboundaries	1.727	0.0082	0.0220	-50.000	0.0000	0.0718
Col13a1	ENSMUSG00000058806	collagen, type XIII, alpha 1	mm39_genes_introns	2.516	0.0015	0.0051	-60.104	0.0000	0.0619
Cstpp1	ENSMUSG00000040591	centriolar satellite-associated tubulin polyglutamylase complex regulator 1	mm39_genes_exonintronboundaries	-1.722	0.0000	0.0001	79.070	0.0000	0.0000
Cyhr1	ENSMUSG00000053929	cysteine and histidine rich 1	mm39_genes_1to5kb	1.774	0.0000	0.0000	-22.705	0.0000	0.0253
Dcp1b	ENSMUSG00000041477	decapping mRNA 1B	mm39_genes_introns	-1.737	0.0008	0.0028	46.875	0.0000	0.0737
Dek	ENSMUSG00000021377	DEK proto-oncogene (DNA binding)	mm39_genes_intronexonboundaries	1.892	0.0000	0.0000	-69.767	0.0000	0.0000
Dnm1	ENSMUSG00000026825	dynamin 1	mm39_genes_introns	2.112	0.0000	0.0000	-27.806	0.0000	0.0010
Dnm1	ENSMUSG00000026825	dynamin 1	mm39_genes_introns	2.112	0.0000	0.0000	-61.538	0.0000	0.0379
Donson	ENSMUSG00000022960	downstream neighbor of SON	mm39_genes_exons	1.784	0.0010	0.0036	-49.596	0.0000	0.0000
Dop1a	ENSMUSG00000034973	DOP1 leucine zipper like protein A	mm39_genes_1to5kb	-1.848	0.0000	0.0000	21.220	0.0000	0.0000
Dusp13	ENSMUSG00000021768	dual specificity phosphatase 13	mm39_genes_1to5kb	-5.422	0.0251	0.0580	14.243	0.0000	0.0009
E130215H24Rik	ENSMUSG00000087406	RIKEN cDNA E130215H24 gene	mm39_genes_introns	-4.740	0.0171	0.0417	14.348	0.0000	0.0001
Efnb2	ENSMUSG00000001300	ephrin B2	mm39_genes_promoters	1.744	0.0000	0.0000	-56.571	0.0000	0.0000
Eif5b	ENSMUSG00000026083	eukaryotic translation initiation factor 5B	mm39_genes_promoters	2.657	0.0000	0.0000	-57.689	0.0000	0.0000
Faap100	ENSMUSG00000025384	Fanconi anemia core complex associated protein 100	mm39_genes_exons	-3.403	0.0000	0.0000	58.333	0.0000	0.0638
Faap24	ENSMUSG00000030493	Fanconi anemia core complex associated protein 24	mm39_genes_exons	-1.579	0.0324	0.0720	41.246	0.0000	0.0003
Fgfbp3	ENSMUSG00000047632	fibroblast growth factor binding protein 3	mm39_genes_exons	2.329	0.0000	0.0000	-60.000	0.0000	0.0000
Ficd	ENSMUSG00000053334	FIC domain containing	mm39_genes_promoters	-1.868	0.0000	0.0000	46.338	0.0000	0.0001
Frat2	ENSMUSG00000047604	frequently rearranged in advanced T cell lymphomas 2	mm39_genes_1to5kb	4.685	0.0000	0.0000	-32.593	0.0000	0.0095

• **Table S10: Potential target genes that are differentially expressed, methylated, and inversely regulated at least in mG4H-OFF**

Gene Symbol	Ensembl ID	Description	Regulatory Groups	RNA sequencing			DNA methylation sequencing		
				Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	meth.diff	*P*-value	Adjusted *P*-value (*Q*-value)
Fyn	ENSMUSG00000019843	Fyn proto-oncogene	mm39_genes_5UTRs	3.018	0.0000	0.0000	-38.101	0.0000	0.0000
Fzd8	ENSMUSG00000036904	frizzled class receptor 8	mm39_genes_exons	1.641	0.0018	0.0058	-70.531	0.0000	0.0009
Galns	ENSMUSG00000015027	galactosamine (N-acetyl)-6-sulfate sulfatase	mm39_genes_introns	-1.769	0.0000	0.0001	26.268	0.0000	0.0614
Gata6	ENSMUSG00000005836	GATA binding protein 6	mm39_genes_1to5kb	1.664	0.0002	0.0007	-65.362	0.0000	0.0007
Ggnbp1	ENSMUSG00000048731	gametogenetin binding protein 1	mm39_genes_introns	-1.892	0.0000	0.0000	17.525	0.0000	0.0000
Gm20544	ENSMUSG00000092569	predicted gene 20544	mm39_genes_promoters	2.651	0.0000	0.0000	-57.547	0.0000	0.0000
Gm29686	ENSMUSG00000116725	predicted gene, 29686	mm39_genes_exonintronboundaries	2.613	0.0114	0.0294	-48.387	0.0000	0.0677
Gm5617	ENSMUSG00000042293	predicted gene 5617	mm39_genes_exons	-2.926	0.0000	0.0000	19.445	0.0000	0.0000
Gm8098	ENSMUSG00000073073	predicted gene 8098	mm39_genes_1to5kb	3.455	0.0002	0.0007	-32.274	0.0000	0.0105
Gon7	ENSMUSG00000091931	GON7 subunit of KEOPS complex	mm39_genes_exonintronboundaries	1.570	0.0053	0.0151	-40.219	0.0000	0.0000
Gpr146	ENSMUSG00000044197	G protein-coupled receptor 146	mm39_genes_introns	-1.864	0.0000	0.0000	18.780	0.0000	0.0021
Grin2a	ENSMUSG00000059003	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	mm39_genes_exonintronboundaries	-4.517	0.0214	0.0506	43.441	0.0000	0.0282
Grin2a	ENSMUSG00000059003	glutamate receptor, ionotropic, NMDA2A (epsilon 1)	mm39_genes_exonintronboundaries	-4.517	0.0214	0.0506	-56.277	0.0000	0.0087
Hoxa3	ENSMUSG00000079560	homeobox A3	mm39_genes_introns	1.978	0.0043	0.0127	-51.364	0.0000	0.0000
Hoxa4	ENSMUSG00000000942	homeobox A4	mm39_genes_promoters	8.845	0.0000	0.0000	-51.364	0.0000	0.0000
Hsp90ab1	ENSMUSG00000023944	heat shock protein 90 alpha (cytosolic), class B member 1	mm39_genes_introns	2.304	0.0000	0.0000	-27.654	0.0000	0.0001
Jph2	ENSMUSG00000017817	junctophilin 2	mm39_genes_introns	2.242	0.0000	0.0001	-53.125	0.0000	0.0886
Kcnd3os	ENSMUSG00000074346	potassium voltage-gated channel, Shal-related family, member 3, opposite strand	mm39_genes_introns	2.239	0.0027	0.0083	-55.093	0.0000	0.0000
Kctd2	ENSMUSG00000016940	potassium channel tetramerisation domain containing 2	mm39_genes_exons	3.250	0.0000	0.0000	-50.419	0.0000	0.0000
Lamb2	ENSMUSG00000052911	laminin, beta 2	mm39_genes_intronexonboundaries	-1.652	0.0000	0.0000	28.275	0.0000	0.0226
Lrrc49	ENSMUSG00000047766	leucine rich repeat containing 49	mm39_genes_promoters	-1.748	0.0000	0.0001	31.304	0.0000	0.0005
Lrrc56	ENSMUSG00000038637	leucine rich repeat containing 56	mm39_genes_promoters	-2.006	0.0004	0.0015	58.824	0.0000	0.0001
Ly75	ENSMUSG00000026980	lymphocyte antigen 75	mm39_genes_introns	1.506	0.0060	0.0169	-20.339	0.0000	0.0965
Mkrn3	ENSMUSG00000070527	makorin, ring finger protein, 3	mm39_genes_intronexonboundaries	-2.670	0.0314	0.0701	17.491	0.0000	0.0808
Mlec	ENSMUSG00000048578	malectin	mm39_genes_promoters	1.594	0.0000	0.0000	-26.499	0.0000	0.0000
Mllt6	ENSMUSG00000038437	myeloid/lymphoid or mixed-lineage leukemia; translocated to, 6	mm39_genes_introns	1.540	0.0000	0.0000	-32.500	0.0000	0.0000
Mpnd	ENSMUSG00000003199	MPN domain containing	mm39_genes_exonintronboundaries	2.548	0.0000	0.0000	-29.678	0.0000	0.0010
Mreg	ENSMUSG00000039395	melanoregulin	mm39_genes_intronexonboundaries	2.409	0.0000	0.0000	-71.429	0.0000	0.0729
Msl3	ENSMUSG00000031358	MSL complex subunit 3	mm39_genes_promoters	1.929	0.0012	0.0039	-87.161	0.0000	0.0000
Msx1	ENSMUSG00000048450	msh homeobox 1	mm39_genes_introns	-2.152	0.0006	0.0021	45.238	0.0000	0.0366
Mtcl1	ENSMUSG00000052105	microtubule crosslinking factor 1	mm39_genes_exonintronboundaries	2.565	0.0000	0.0000	-52.378	0.0000	0.0000
Mtcl1	ENSMUSG00000052105	microtubule crosslinking factor 1	mm39_genes_promoters	2.565	0.0000	0.0000	24.654	0.0000	0.0069
Mus81	ENSMUSG00000024906	MUS81 structure-specific endonuclease subunit	mm39_genes_1to5kb	-2.045	0.0000	0.0000	15.231	0.0000	0.0000
Nfe2l1	ENSMUSG00000038615	nuclear factor, erythroid derived 2,-like 1	mm39_genes_promoters	1.710	0.0000	0.0000	-26.032	0.0000	0.0281
Nfix	ENSMUSG00000001911	nuclear factor I/X	mm39_genes_introns	2.155	0.0000	0.0000	-60.499	0.0000	0.0000
Nfix	ENSMUSG00000001911	nuclear factor I/X	mm39_genes_introns	2.155	0.0000	0.0000	32.055	0.0000	0.0000
Nfix	ENSMUSG00000001911	nuclear factor I/X	mm39_genes_introns	2.155	0.0000	0.0000	62.821	0.0000	0.0003
Nkiras1	ENSMUSG00000021772	NFKB inhibitor interacting Ras-like protein 1	mm39_genes_promoters	1.969	0.0000	0.0000	-38.246	0.0000	0.0000
Npc2	ENSMUSG00000021242	NPC intracellular cholesterol transporter 2	mm39_genes_introns	1.614	0.0000	0.0000	-84.444	0.0000	0.0000
Orai1	ENSMUSG00000049686	ORAI calcium release-activated calcium modulator 1	mm39_genes_exons	3.550	0.0000	0.0000	-57.839	0.0000	0.0000
Orai1	ENSMUSG00000049686	ORAI calcium release-activated calcium modulator 1	mm39_genes_exons	3.550	0.0000	0.0000	22.059	0.0000	0.0001
Orai1	ENSMUSG00000049686	ORAI calcium release-activated calcium modulator 1	mm39_genes_exons	3.550	0.0000	0.0000	22.163	0.0000	0.0001
Palm3	ENSMUSG00000047986	paralemmin 3	mm39_genes_promoters	5.170	0.0000	0.0000	-77.966	0.0000	0.0000
Pcgf3	ENSMUSG00000033623	polycomb group ring finger 3	mm39_genes_introns	1.747	0.0000	0.0000	-48.154	0.0000	0.0087
Pdgfrb	ENSMUSG00000024620	platelet derived growth factor receptor, beta polypeptide	mm39_genes_intronexonboundaries	-1.741	0.0000	0.0000	32.057	0.0000	0.0960

• **Table S10: Potential target genes that are differentially expressed, methylated, and inversely regulated at least in mG4H-OFF**

Gene Symbol	Ensembl ID	Description	Regulatory Groups	RNA sequencing			DNA methylation sequencing		
				Fold-Change	*P*-value	Adjusted *P*-value (*Q*-value)	meth.diff	*P*-value	Adjusted *P*-value (*Q*-value)
Pmepa1	ENSMUSG00000038400	prostate transmembrane protein, androgen induced 1	mm39_genes_introns	1.563	0.0000	0.0000	-31.602	0.0000	0.0014
Pold1	ENSMUSG00000038644	polymerase (DNA directed), delta 1, catalytic subunit	mm39_genes_introns	-1.524	0.0000	0.0002	16.484	0.0000	0.0003
Pole	ENSMUSG00000007080	polymerase (DNA directed), epsilon	mm39_genes_promoters	-1.751	0.0065	0.0180	20.904	0.0000	0.0000
Pole	ENSMUSG00000007080	polymerase (DNA directed), epsilon	mm39_genes_promoters	-1.751	0.0065	0.0180	20.669	0.0000	0.0000
Prkra	ENSMUSG00000002731	protein kinase, interferon inducible double stranded RNA dependent activator	mm39_genes_promoters	-1.711	0.0000	0.0000	26.316	0.0000	0.0000
Pxdc1	ENSMUSG00000021411	PX domain containing 1	mm39_genes_introns	2.978	0.0000	0.0000	-50.794	0.0000	0.0000
Pzp	ENSMUSG00000030359	PZP, alpha-2-macroglobulin like	mm39_genes_1to5kb	-2.234	0.0245	0.0569	52.795	0.0000	0.0566
Rassf3	ENSMUSG00000025795	Ras association (RalGDS/AF-6) domain family member 3	mm39_genes_introns	2.081	0.0000	0.0000	-34.183	0.0000	0.0000
Rbpms	ENSMUSG00000031586	RNA binding protein gene with multiple splicing	mm39_genes_introns	3.197	0.0000	0.0000	-37.615	0.0000	0.0000
Rhbdl3	ENSMUSG00000017692	rhomboid like 3	mm39_genes_intronexonboundaries	3.447	0.0000	0.0000	-86.408	0.0000	0.0000
Rnf123	ENSMUSG00000041528	ring finger protein 123	mm39_genes_introns	-1.504	0.0000	0.0000	66.667	0.0000	0.0081
Robo2	ENSMUSG00000052516	roundabout guidance receptor 2	mm39_genes_introns	2.125	0.0021	0.0067	-62.368	0.0000	0.0000
Rpl36	ENSMUSG00000057863	ribosomal protein L36	mm39_genes_promoters	-4.184	0.0000	0.0000	13.953	0.0000	0.0000
Runx3	ENSMUSG00000070691	runt related transcription factor 3	mm39_genes_introns	2.080	0.0071	0.0194	-56.842	0.0000	0.0000
Runx3	ENSMUSG00000070691	runt related transcription factor 3	mm39_genes_introns	2.080	0.0071	0.0194	-52.841	0.0000	0.0000
S1pr5	ENSMUSG00000045087	sphingosine-1-phosphate receptor 5	mm39_genes_exonintronboundaries	2.044	0.0002	0.0009	-53.474	0.0000	0.0000
Sall4	ENSMUSG00000027547	spalt like transcription factor 4	mm39_genes_intronexonboundaries	1.728	0.0100	0.0264	-49.702	0.0000	0.0702
Scarf2	ENSMUSG00000012017	scavenger receptor class F, member 2	mm39_genes_exonintronboundaries	2.699	0.0000	0.0000	-88.679	0.0000	0.0003
Sec61a1	ENSMUSG00000030082	Sec61 alpha 1 subunit (S. cerevisiae)	mm39_genes_exonintronboundaries	-1.607	0.0000	0.0000	15.327	0.0000	0.0003
Shoc2	ENSMUSG00000024976	Shoc2, leucine rich repeat scaffold protein	mm39_genes_promoters	1.652	0.0000	0.0000	-85.691	0.0000	0.0000
Skap2	ENSMUSG00000059182	src family associated phosphoprotein 2	mm39_genes_exonintronboundaries	1.853	0.0000	0.0000	-74.242	0.0000	0.0000
Smad7	ENSMUSG00000025880	SMAD family member 7	mm39_genes_exons	3.717	0.0000	0.0000	-57.547	0.0000	0.0000
Spindoc	ENSMUSG00000024970	spindlin interactor and repressor of chromatin binding	mm39_genes_introns	1.573	0.0001	0.0005	-35.487	0.0000	0.0018
Stk39	ENSMUSG00000027030	serine/threonine kinase 39	mm39_genes_introns	1.768	0.0000	0.0000	-29.004	0.0000	0.0036
Tmem251	ENSMUSG00000046675	transmembrane protein 251	mm39_genes_promoters	1.922	0.0000	0.0000	-58.195	0.0000	0.0000
Tnrc18	ENSMUSG00000039477	trinucleotide repeat containing 18	mm39_genes_introns	1.719	0.0000	0.0000	-60.714	0.0000	0.0822
Tnrc18	ENSMUSG00000039477	trinucleotide repeat containing 18	mm39_genes_introns	1.719	0.0000	0.0000	-54.348	0.0000	0.0002
Tom1l1	ENSMUSG00000020541	target of myb1-like 1 (chicken)	mm39_genes_introns	1.545	0.0000	0.0000	-26.316	0.0000	0.0709
Vstm2b	ENSMUSG00000039257	V-set and transmembrane domain containing 2B	mm39_genes_promoters	4.233	0.0055	0.0156	-28.986	0.0000	0.0009
Wnt5a	ENSMUSG00000021994	wingless-type MMTV integration site family, member 5A	mm39_genes_1to5kb	1.942	0.0000	0.0002	-52.159	0.0000	0.0010
Wsb1	ENSMUSG00000017677	WD repeat and SOCS box-containing 1	mm39_genes_introns	1.616	0.0000	0.0001	-50.980	0.0000	0.0000
Xpnpep1	ENSMUSG00000025027	X-prolyl aminopeptidase (aminopeptidase P) 1, soluble	mm39_genes_introns	-1.863	0.0000	0.0000	23.521	0.0000	0.0000
Yif1b	ENSMUSG00000030588	Yip1 interacting factor homolog B (S. cerevisiae)	mm39_genes_introns	-2.486	0.0000	0.0000	52.000	0.0000	0.0015
Zc3h6	ENSMUSG00000042851	zinc finger CCCH type containing 6	mm39_genes_exons	1.715	0.0001	0.0005	-75.455	0.0000	0.0772
Zcchc17	ENSMUSG00000028772	zinc finger, CCHC domain containing 17	mm39_genes_introns	1.834	0.0000	0.0000	-66.667	0.0000	0.0013
Zfp316	ENSMUSG00000046658	zinc finger protein 316	mm39_genes_exons	1.643	0.0000	0.0000	-49.159	0.0000	0.0000
Zfp36l2	ENSMUSG00000045817	zinc finger protein 36, C3H type-like 2	mm39_genes_exons	2.073	0.0000	0.0002	-23.540	0.0000	0.0387
Zfp703	ENSMUSG00000085795	zinc finger protein 703	mm39_genes_promoters	1.560	0.0279	0.0636	-40.013	0.0000	0.0000
Zfp787	ENSMUSG00000046792	zinc finger protein 787	mm39_genes_intronexonboundaries	1.574	0.0001	0.0005	-39.860	0.0000	0.0000
Zfp995	ENSMUSG00000078546	zinc finger protein 995	mm39_genes_exonintronboundaries	-2.199	0.0221	0.0519	28.788	0.0000	0.0821
Zmynd19	ENSMUSG00000026974	zinc finger, MYND domain containing 19	mm39_genes_promoters	2.200	0.0000	0.0000	-43.466	0.0000	0.0000

Table S11. Echocardiographic measurements of systolic function in mG4H-OFF mice 8 weeks after TAC, related to Fig. 6.

Parameter	Con-OFF-Sham (M)	Con-OFF-TAC (M)	mG4H-OFF-Sham (M)	mG4H-OFF-TAC (M)	Con-OFF-Sham (F)	Con-OFF-TAC (F)	mG4H-OFF-Sham (F)	mG4H-OFF-TAC (F)
No. of mice	12	15	5	10	9	14	9	15
IVS;d (mm)	0.78 ± 0.11	1.03 ± 0.22*	0.7 ± 0.15	1.09 ± 0.25*	0.79 ± 0.16	1 ± 0.22*	0.75 ± 0.08	0.97 ± 0.13*
IVS;s (mm)	0.99 ± 0.19	1.13 ± 0.27	0.93 ± 0.17	1.12 ± 0.26	1.01 ± 0.21	1.25 ± 0.22*	1.03 ± 0.15	1.16 ± 0.16
LVID;d (mm)	3.98 ± 0.18	4.17 ± 0.4	3.94 ± 0.4	3.94 ± 0.35	3.82 ± 0.16	3.71 ± 0.26	3.79 ± 0.17	3.78 ± 0.2
LVID;s (mm)	2.64 ± 0.21	2.98 ± 0.41	2.42 ± 0.32	3.03 ± 0.43*	2.4 ± 0.33	2.4 ± 0.37	2.29 ± 0.21	2.51 ± 0.31
LVPW;d (mm)	0.98 ± 0.16	1.16 ± 0.25	1.17 ± 0.46	1.52 ± 0.34‡	0.85 ± 0.18	1.15 ± 0.29*	0.89 ± 0.15	1.08 ± 0.27
LVPW;s (mm)	1.33 ± 0.15	1.5 ± 0.28	1.4 ± 0.4	1.74 ± 0.29	1.24 ± 0.16	1.54 ± 0.31*	1.32 ± 0.15	1.52 ± 0.29
LVESD (mm)	2.62 ± 0.17	2.91 ± 0.39	2.45 ± 0.22	2.92 ± 0.39	2.39 ± 0.33	2.42 ± 0.35	2.33 ± 0.2	2.53 ± 0.26
LVEDD (mm)	3.95 ± 0.23	4.15 ± 0.39	3.89 ± 0.4	3.97 ± 0.32	3.77 ± 0.26	3.72 ± 0.3	3.8 ± 0.22	3.79 ± 0.22
ESV (μL)	25.2 ± 4.13	33.37 ± 11.56	21.51 ± 4.62	33.63 ± 11.39	20.55 ± 7.42	21.19 ± 7.53	18.98 ± 3.96	23.33 ± 5.71
EDV (μL)	68.43 ± 9.6	77.35 ± 17.24	66.41 ± 16.51	69.56 ± 13.19	61.18 ± 10.51	59.62 ± 11.51	62.1 ± 8.79	61.97 ± 8.27
SV (μL)	43.23 ± 7.61	43.98 ± 8.88	44.89 ± 13.74	35.94 ± 5.79	40.63 ± 5.49	38.43 ± 5.44	43.12 ± 6.59	38.63 ± 4.17
CO (mL/min)	18.55 ± 2.42	20.11 ± 4.04	19.23 ± 5.67	15.8 ± 3.38‡	17.88 ± 2.76	16.44 ± 2.82	16.77 ± 3.29	17.59 ± 2.52
EF (%)	62.48 ± 7.34	55.2 ± 8.61	69.66 ± 4.37	46.66 ± 11.67*	67.51 ± 8.91	65.3 ± 8.2	70.8 ± 4.64	62.91 ± 8.92
FS (%)	33.5 ± 5.14	28.64 ± 5.48	38.78 ± 3.37	23.3 ± 6.74*	37.38 ± 6.94	35.52 ± 6.29	39.66 ± 3.89	33.82 ± 6.36
LV Mass (mg)	106.21 ± 14.01	159.09 ± 49.93*	114.66 ± 34.88	191.13 ± 69.35*	90.46 ± 11.46	128.78 ± 36.81*	88.92 ± 10.1	122.51 ± 25.55*
LV Vol;d (μL)	69.35 ± 7.46	78.38 ± 17.86	68.55 ± 16.33	68.41 ± 14.4	62.92 ± 6.26	58.89 ± 10.11	61.67 ± 6.8	61.55 ± 7.38
LV Vol;s (μL)	25.91 ± 5.05	35.49 ± 12.54	21.09 ± 6.67	36.9 ± 13.31	20.72 ± 7.07	20.95 ± 7.63	18.13 ± 4.2	23.1 ± 6.75

IVS, interventricular septum thickness; LVID, left ventricular internal dimension; LVPW, left ventricular posterior wall; d, at diastole; s, at systole; LVESD, left ventricular end-systolic diameter; LVEDD, left ventricular end-diastolic diameter; ESV, end-systolic volume; EDV, end-diastolic volume; SV, stroke volume; CO, cardiac output; EF, ejection fraction; FS, fractional shortening; LV Vol, left ventricular volume. Quantitative data are mean ± SD. Statistical significance was based on two-way ANOVA followed by Tukey's multiple comparisons test, * $P < 0.05$ vs. surgery-matched control (Sham), ‡ $P < 0.05$ vs. transgene-matched control (Con-OFF).

Figure S1; related to Figure 1

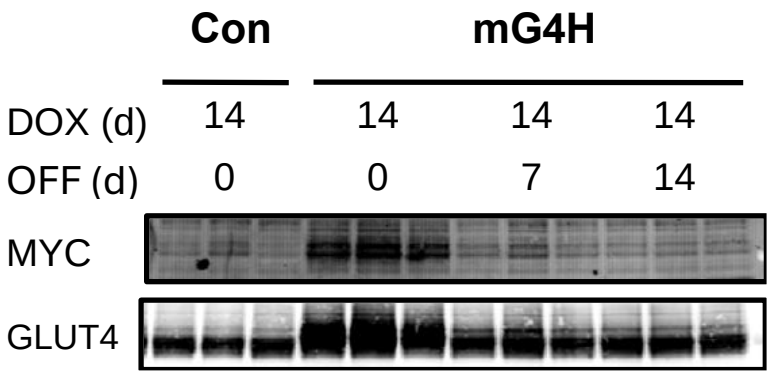

Figure S1. Confirmation of inducible yet reversible cardiomyocyte specific GLUT4 expression. Whole cell extracts subjected to immunoblot analysis for transgene regulation show evidence of inducible GLUT4 expression, which reverts after one week of DOX removal and is completely reversible after two weeks. *DOX: Doxycycline. OFF: Reversal of transgene induction.*

Figure S2; related to Figure 5

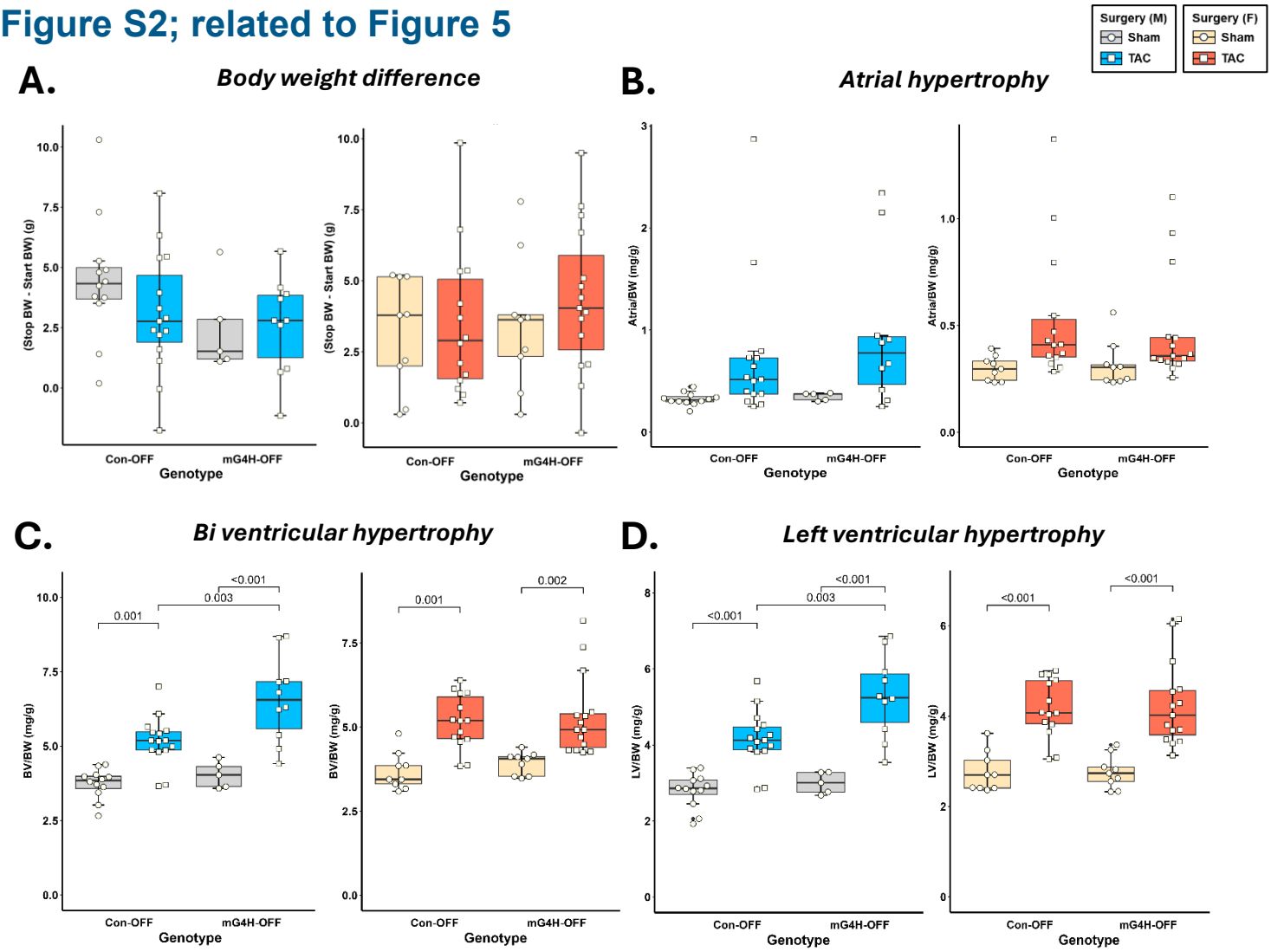

Figure S2. Phenotypic characteristics of mice with a previous memory of enhanced glucose uptake upon TAC. A, Difference in body weight before and after TAC surgery in male (left) and female (right) mice of all groups. **B,** Ratio of atrial weight to body weight in male (left) and female (right) mice of all groups. **C,** Ratio of both ventricular weight to body weight in male (left) and female (right) mice of all groups. **D,** Ratio of left ventricular weight to body weight in male (left) and female (right) mice of all groups. Statistical significance was calculated based on two-way ANOVA followed by Tukey's honestly significant difference test and only significant comparisons were visualized with brackets and associated *P*-value. *BV: Bi-ventricle, LV: Left Ventricle, BW: Body weight.*

Figure S3; related to Figure 6

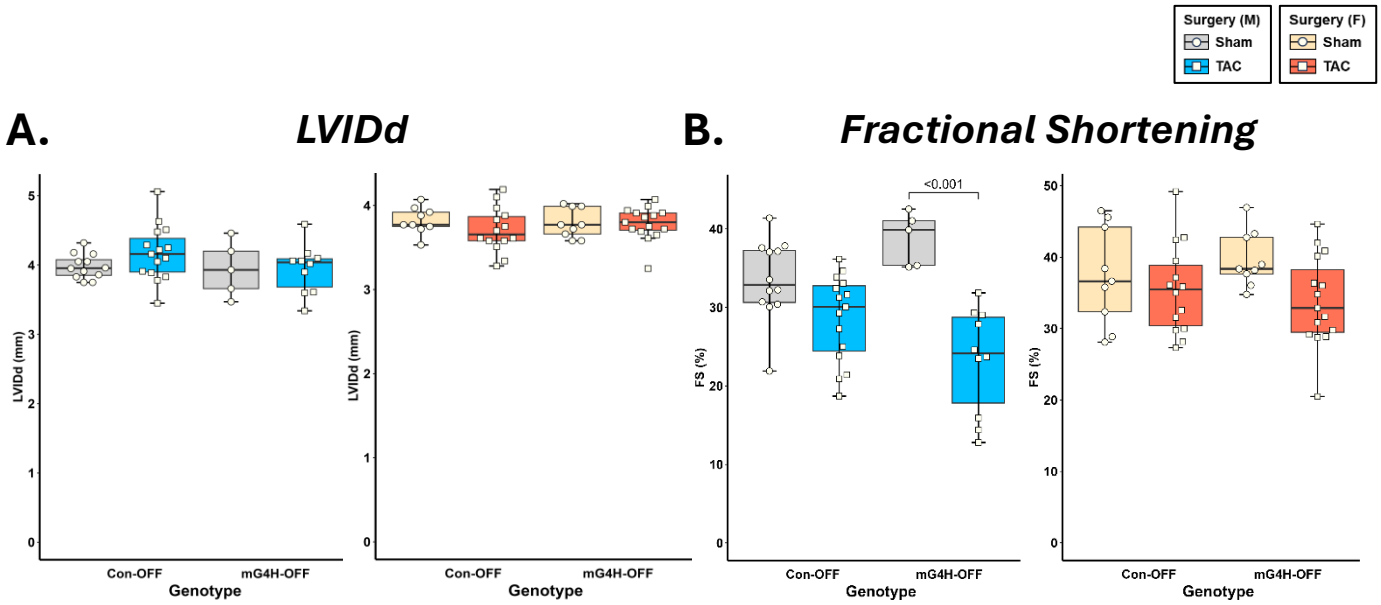

Figure S3. Functional characteristics in mice upon TAC with a history of transiently enhanced cellular glucose. Echocardiographic analysis of cardiac dimensions and function in mG4H-OFF mice with matched controls 8 weeks after TAC. Measures at diastole for left ventricular internal diameter (LVIDd, **A**), and cardiac systolic function (presented as fractional shortening, **B**) in both male (left) and female (right) mice of all groups. Statistical significance was calculated based on two-way ANOVA followed by Tukey's honestly significant difference test and only significant comparisons were visualized with brackets and associated *P*-value.