EnrichmentHsSymbolsFile2 Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_KERATINIZATION	−0.15192254	206	5.956e−14	3.868e−10	KRTAP4−8:105 LCE2D:142 KRTAP13−1:161 TGM1:176 KRTAP6−1:196 KRT77:206
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.07236738	664	2.344e−10	7.612e−07	KIAA0825:10 SPAG5:13 DLGAP5:14 NCAPD2:17 FANCG:19 KNL1:42
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	−0.29023319	37	1.003e−09	2.170e−06	GPER1:68 SNX8:154 INTS1:211 CHST12:307 FBXL18:474 ADAP1:644
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.16560682	112	1.433e−09	2.326e−06	ECSIT:4 TIMMDC1:9 LRPPRC:28 TMEM126B:49 TMEM186:192 NDUFAF1:197
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.17816195	90	5.224e−09	6.785e−06	ECSIT:4 TIMMDC1:9 LRPPRC:28 TMEM126B:49 TMEM186:192 NDUFAF1:197
FISCHER_DREAM_TARGETS	0.05443862	921	2.525e−08	2.697e−05	SPAG5:13 DLGAP5:14 NCAPD2:17 FANCG:19 ARL13B:22 KNL1:42
WONG_MITOCHONDRIA_GENE_MODULE	0.11013262	214	2.908e−08	2.697e−05	LRPPRC:28 NDUFAF1:197 MRPS15:330 COX7C:360 TOMM7:442 NDUFB1:503
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	−0.09561569	265	8.741e−08	7.096e−05	SSTR4:14 PTH1R:35 TAAR6:38 GABRA5:43 MC4R:50 CHRNA7:66
REACTOME_SIGNALING_BY_GPCR	−0.05912227	684	1.510e−07	8.170e−05	ADCY1:4 SSTR4:14 PTH1R:35 ARHGEF4:37 TAAR6:38 MC4R:50
REACTOME_GPCR_LIGAND_BINDING	−0.07300445	450	1.186e−07	8.170e−05	SSTR4:14 PTH1R:35 TAAR6:38 MC4R:50 GPER1:68 VIPR1:78
REACTOME_MITOCHONDRIAL_TRANSLATION	0.15796675	93	1.417e−07	8.170e−05	PTCD3:55 MTIF2:61 MRPS23:79 MRPS35:157 MRPS15:330 MRPS31:347
KEGG_OXIDATIVE_PHOSPHORYLATION	0.14251984	114	1.487e−07	8.170e−05	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593
REACTOME_TRANSLATION	0.09271378	269	1.722e−07	8.600e−05	PTCD3:55 MTIF2:61 MRPS23:79 MRPS35:157 MRPS15:330 RARS1:333
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	−0.08371856	324	2.318e−07	1.075e−04	SSTR4:14 TAAR6:38 MC4R:50 GPER1:68 GPR17:99 OPN3:148
WP_GPCRS_CLASS_A_RHODOPSINLIKE	−0.09400043	251	3.024e−07	1.227e−04	SSTR4:14 MC4R:50 GPER1:68 GPR17:99 OPN3:148 MAS1:216
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.21626531	47	2.912e−07	1.227e−04	ECSIT:4 TIMMDC1:9 TMEM126B:49 TMEM186:192 NDUFAF1:197 NDUFS1:384
REACTOME_NEURONAL_SYSTEM	−0.07517959	391	3.540e−07	1.344e−04	ADCY1:4 GABRR3:25 KCNV1:29 CACNA1B:31 APBA2:32 GABRA5:43
MOOTHA_VOXPHOS	0.15860306	86	3.725e−07	1.344e−04	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 GATB:549 NDUFA8:570
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.15360786	89	5.525e−07	1.888e−04	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	−0.06010626	576	8.889e−07	2.886e−04	KCNV1:29 APBA2:32 PCNX2:40 GABRA5:43 SLC35F3:69 NETO1:70
REACTOME_COMPLEX_I_BIOGENESIS	0.20224244	48	1.253e−06	3.698e−04	ECSIT:4 TIMMDC1:9 TMEM126B:49 TMEM186:192 NDUFAF1:197 NDUFS1:384
JOHNSTONE_PARVB_TARGETS_3_DN	0.05092821	793	1.204e−06	3.698e−04	CCPG1:7 SPAG5:13 DLGAP5:14 CEP350:88 UBAP2:90 RAD51AP1:116
KEGG_PARKINSONS_DISEASE	0.13029560	110	2.371e−06	6.693e−04	COX7C:360 NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593
WP_OXIDATIVE_PHOSPHORYLATION	0.18522252	51	4.753e−06	1.286e−03	NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593 NDUFA11:701
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	−0.11686870	126	5.955e−06	1.487e−03	LCE2D:142 TGM1:176 KRT77:206 PKP1:210 KRT5:260 LCE2A:386
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.05428397	602	5.779e−06	1.487e−03	NEDD4:1 CCPG1:7 AGGF1:11 DLGAP5:14 LRPPRC:28 KNL1:42
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.10052860	162	1.025e−05	2.244e−03	ECSIT:4 TIMMDC1:9 LRPPRC:28 TMEM126B:49 TMEM186:192 NDUFAF1:197
REACTOME_RRNA_PROCESSING	0.09472127	183	1.007e−05	2.244e−03	TRMT10C:62 NOL6:152 DDX52:174 PRORP:201 UTP20:316 RIOK1:350
REACTOME_SENSORY_PERCEPTION	−0.05312837	598	9.710e−06	2.244e−03	SCN9A:7 SCN2A:60 OR9G1:61 OR10D3:137 RLBP1:191 OR9G4:200
KEGG_HUNTINGTONS_DISEASE	0.10140597	159	1.037e−05	2.244e−03	COX7C:360 NDUFS1:384 CREB3L3:445 NDUFB1:503 ATP5PO:519 TFAM:522
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_I	0.09198856	174	2.883e−05	6.040e−03	SPAG5:13 FANCG:19 KNL1:42 ATAD5:59 CDC25C:205 PGPEP1:234
NIKOLSKY_BREAST_CANCER_22Q13_AMPLICON	−0.29098611	17	3.267e−05	6.630e−03	MLC1:208 PLXNB2:268 TTLL8:379 PANX2:669 MOV10L1:753 TRABD:1082
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	−0.06918268	298	4.098e−05	7.827e−03	ADCY1:4 SSTR4:14 GPER1:68 GPR17:99 OPN3:148 GRM8:178
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.03447634	1273	4.053e−05	7.827e−03	NEDD4:1 TIMMDC1:9 SPAG5:13 DLGAP5:14 FANCG:19 LRPPRC:28
FERREIRA_EWINGS_SARCOMA_UNSTABLE_VS_STAB	0.09586257	152	4.575e−05	8.253e−03	DLGAP5:14 NCAPD2:17 KNL1:42 ATAD5:59 FANCM:89 PIGS:231
PEDERSEN_METASTASIS_BY_ERBB2_ISOFORM_1	−0.17391181	46	4.493e−05	8.253e−03	RASD1:33 GEM:65 EPHA2:439 RASGEF1A:507 CAPN8:521 ADGRG6:598
MARTENS_TRETINOIN_RESPONSE_UP	−0.04245969	784	5.680e−05	9.969e−03	TRIM29:24 PTH1R:35 IGFBP3:49 ACTL7B:56 OR9G1:61 GEM:65
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	−0.06301062	340	6.728e−05	1.150e−02	BNC1:11 GABRA5:43 VIPR1:78 KCNK1:100 PAX1:120 LAD1:185
KORKOLA_EMBRYONAL_CARCINOMA_UP	0.18100080	40	7.466e−05	1.243e−02	RAD51AP1:116 NANOG:186 GDF3:292 LRP6:430 TEAD4:628 EMG1:730
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SY	−0.07236192	250	8.315e−05	1.338e−02	ADCY1:4 GABRR3:25 CACNA1B:31 GABRA5:43 CHRNA7:66 KCNJ12:157

DisGeNET Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Autism Spectrum Disorders	−0.07024872	517	5.616e−08	5.514e−04	ZNF423:5 EHMT1:10 SSTR4:14 APBA2:32 HERC2:39 GABRA5:43
Mitochondrial Diseases	0.07825820	363	3.433e−07	1.686e−03	ECSIT:4 LRPPRC:28 TMEM126B:49 TRMT10C:62 MRPS23:79 MTPAP:153
Autistic Disorder	−0.05488036	637	2.753e−06	9.012e−03	EHMT1:10 ATF6:13 APBA2:32 DOCK4:42 GABRA5:43 IGFBP3:49
HIV Infections	−0.05066071	718	4.627e−06	1.136e−02	SSTR4:14 HSPH1:41 GEM:65 TMEM132D:72 KCNH2:73 VIPR1:78
Infection	−0.06125344	466	6.667e−06	1.309e−02	PTH1R:35 VIPR1:78 APOC1:96 BCL2L11:226 SLC2A1:272 CALCA:288
Increased CSF lactate	0.17244364	56	8.150e−06	1.334e−02	TIMMDC1:9 LRPPRC:28 TMEM126B:49 TRMT10C:62 NDUFAF1:197 NDUFS1:384
Hypertensive disease	−0.03832918	1199	1.094e−05	1.535e−02	ZFAT:8 SSTR4:14 GALNT2:30 GCK:34 IGFBP3:49 MC4R:50
Primary microcephaly	0.11963364	110	1.495e−05	1.836e−02	FANCG:19 KNL1:42 STIL:82 FANCM:89 TRMT10A:125 CENPJ:241
Schizophrenia	−0.03138579	1727	2.311e−05	2.522e−02	ADCY1:4 EHMT1:10 SSTR4:14 GABRR3:25 GALNT2:30 CACNA1B:31
Bipolar Disorder	−0.04412458	757	4.296e−05	4.219e−02	ADCY1:4 SSTR4:14 GABRR3:25 CACNA1B:31 TAAR6:38 GABRA5:43
Lung diseases	−0.06224887	362	5.130e−05	4.580e−02	SSTR4:14 PTH1R:35 COL3A1:82 SEC14L2:248 ADORA1:252 SLC2A1:272
Obesity	−0.02882536	1786	8.027e−05	6.507e−02	EHMT1:10 ATF6:13 SSTR4:14 CDHR1:19 GALNT2:30 GCK:34
Withdrawal Symptoms	−0.13680040	69	8.614e−05	6.507e−02	ADCY1:4 SSTR4:14 CHRNA7:66 ADORA1:252 CHRNA4:368 CRP:382
Eczema	−0.05467004	420	1.319e−04	8.264e−02	TRPM1:45 IL37:59 APOC1:96 EFL1:147 TGM1:176 MAS1:216
Endometriosis	−0.04266543	691	1.515e−04	8.264e−02	NSD2:6 IGFBP3:49 IL37:59 GPER1:68 SYNE1:133 SLC22A23:146
Increased serum lactate	0.11178543	99	1.234e−04	8.264e−02	LRPPRC:28 TRMT10C:62 TWNK:254 TRMT5:482 GFM1:532 POLG2:534
Lactic acidemia	0.09930189	123	1.457e−04	8.264e−02	TIMMDC1:9 LRPPRC:28 TMEM126B:49 TRMT10C:62 NDUFAF1:197 NDUFS1:384
Myocardial Infarction	−0.03787722	891	1.502e−04	8.264e−02	GPER1:68 COL3A1:82 APOC1:96 GPR17:99 CDCP1:104 ARC:110
Color vision defect, severe	−0.17121482	39	2.167e−04	8.867e−02	ATF6:13 CDHR1:19 RLBP1:191 CNGB3:199 PDE6C:328 ELOVL4:577
Abnormal color vision	−0.17121482	39	2.167e−04	8.867e−02	ATF6:13 CDHR1:19 RLBP1:191 CNGB3:199 PDE6C:328 ELOVL4:577
Heart failure	−0.04065824	732	2.070e−04	8.867e−02	KCNH2:73 APOC1:96 GPR17:99 ARC:110 HTT:128 MAS1:216
Loss in color vision	−0.17121482	39	2.167e−04	8.867e−02	ATF6:13 CDHR1:19 RLBP1:191 CNGB3:199 PDE6C:328 ELOVL4:577
Mood Disorders	−0.06093403	318	1.982e−04	8.867e−02	ADCY1:4 TAAR6:38 GABRA5:43 HTT:128 PPP1R13B:156 VSX1:253
Pain	−0.05122460	452	2.060e−04	8.867e−02	SCN9A:7 SSTR4:14 SCN2A:60 ASAP1:136 GRM8:178 ERBB4:246
Epidermolysis Bullosa Simplex	−0.21871893	23	2.828e−04	1.111e−01	KRT5:260 VIM:352 PLEC:500 BHLHE23:626 TGM5:830 KRT17:1301
Depressive Symptoms	−0.08905646	139	2.957e−04	1.117e−01	NKPD1:126 HTT:128 TGFB1:290 EGFR:335 CRP:382 IFNA13:502
Addictive Behavior	−0.07495692	189	3.917e−04	1.329e−01	MET:167 BCL2L11:226 ERBB4:246 TGFB1:290 EGFR:335 CHRNA4:368
Arteriosclerosis	−0.03327913	984	4.872e−04	1.329e−01	EHMT1:10 OSBP:22 GCK:34 MC4R:50 SLC17A4:55 IL37:59
Atherosclerosis	−0.03272716	1027	4.683e−04	1.329e−01	EHMT1:10 OSBP:22 GCK:34 IGFBP3:49 MC4R:50 SLC17A4:55
Borderline Personality Disorder	−0.09976691	104	4.459e−04	1.329e−01	SCN9A:7 APBA2:32 ERBB4:246 ANGPT1:278 EGFR:335 HTR1B:391
Chronic Obstructive Airway Disease	−0.04216855	609	4.218e−04	1.329e−01	EHMT1:10 CHRNA7:66 VIPR1:78 CRYGC:90 KCNK1:100 ENTPD1:127
Congestive heart failure	−0.03739489	793	3.945e−04	1.329e−01	KCNH2:73 COL3A1:82 APOC1:96 GPR17:99 ARC:110 HTT:128
Coronary Arteriosclerosis	−0.03949428	704	4.029e−04	1.329e−01	EHMT1:10 GALNT2:30 GCK:34 GPER1:68 NDST4:80 COL3A1:82
Dermatologic disorders	−0.05314122	370	4.757e−04	1.329e−01	APBA2:32 GEM:65 TGM1:176 ZNF267:229 ALOX12B:234 TRPV6:259
Hyperinsulinism	−0.05377551	360	4.849e−04	1.329e−01	EHMT1:10 CDHR1:19 GCK:34 HERC2:39 IGFBP3:49 MC4R:50
Inflammatory Bowel Diseases	−0.03688113	810	4.155e−04	1.329e−01	ATF6:13 IGFBP3:49 IL37:59 GPER1:68 VIPR1:78 REG1B:113
Cardiovascular Diseases	−0.03815857	721	5.455e−04	1.422e−01	EHMT1:10 ATF6:13 IGFBP3:49 SCN2A:60 DCLK1:63 GPER1:68
Drug Withdrawal Symptoms	−0.13857430	52	5.501e−04	1.422e−01	ADCY1:4 CHRNA7:66 ADORA1:252 CRP:382 CRH:743 CHRNA5:774
Acute Coronary Syndrome	−0.06392929	239	6.878e−04	1.535e−01	GEM:65 COL3A1:82 F5:205 CLU:289 TGFB1:290 EGFR:335
Age related macular degeneration	−0.05322420	351	6.475e−04	1.535e−01	CDHR1:19 TRPM1:45 ZBTB41:52 GEM:65 CNGB3:199 FLT1:245

customGeneSet Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	0.06950067	13	4.367e−01	6.550e−01	SLC39A8:1779 LCT:2540 AS3MT:9689 GPX1:9689 GPX3:9689 CELF1:9689
NAFLDGWAS	−0.09636364	15	2.552e−01	6.550e−01	PNPLA3:494 FTO:936 APOE:1541 PNPLA2:1556 GID4:1673 GPAM:1865
expressionDirectionalSelection	0.02380952	42	7.371e−01	7.371e−01	TLR10:882 TLR6:1223 HSD17B8:2871 ZBTB12:2936 HLA−DQB1:9689 HLA−DRB1:9689
NA	NA	NA	NA	NA	NA NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA NA
NA.26	NA	NA	NA	NA	NA NA NA NA NA NA
NA.27	NA	NA	NA	NA	NA NA NA NA NA NA
NA.28	NA	NA	NA	NA	NA NA NA NA NA NA
NA.29	NA	NA	NA	NA	NA NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA NA
NA.35	NA	NA	NA	NA	NA NA NA NA NA NA
NA.36	NA	NA	NA	NA	NA NA NA NA NA NA

GO_Biological_Process_2023 Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Mitochondrial Gene Expression (GO:014005	0.17372477	102	1.401e−09	7.576e−06	POLRMT:21 FASTKD1:38 PTCD3:55 MRPS23:79 TFB2M:115 TEFM:146
NADH Dehydrogenase Complex Assembly (GO:	0.22613934	49	4.407e−08	5.957e−05	ECSIT:4 TMEM126B:49 TMEM126A:181 TMEM186:192 NDUFAF1:197 NDUFS1:384
Mitochondrial Respiratory Chain Complex	0.22613934	49	4.407e−08	5.957e−05	ECSIT:4 TMEM126B:49 TMEM126A:181 TMEM186:192 NDUFAF1:197 NDUFS1:384
Mitochondrial Translation (GO:0032543)	0.16383219	97	2.550e−08	5.957e−05	PTCD3:55 MTIF2:61 MRPS23:79 MTRF1:198 MRPS15:330 MRPS31:347
Aerobic Electron Transport Chain (GO:001	0.19210325	64	1.089e−07	9.810e−05	NDUFAF1:197 COX7C:360 NDUFS1:384 NDUFB1:503 NDUFA8:570 NDUFB7:593
Mitochondrial Respiratory Chain Complex	0.17084585	82	9.131e−08	9.810e−05	ECSIT:4 TMEM126B:49 TMEM126A:181 TMEM186:192 NDUFAF1:197 NDUFS1:384
Mitochondrial ATP Synthesis Coupled Elec	0.18314722	65	3.345e−07	2.584e−04	NDUFAF1:197 COX7C:360 NDUFS1:384 NDUFB1:503 NDUFA8:570 NDUFB7:593
Translation (GO:0006412)	0.10209894	208	4.140e−07	2.798e−04	PTCD3:55 MRPS23:79 FTSJ1:212 MRPS15:330 RARS1:333 MRPS31:347
Adenylate Cyclase−Modulating G Protein−C	−0.11638624	158	4.685e−07	2.815e−04	ADCY1:4 PTH1R:35 MC4R:50 GPER1:68 VIPR1:78 GRM8:178
Mitochondrial RNA Metabolic Process (GO:	0.32147611	20	6.473e−07	3.500e−04	POLRMT:21 FASTKD1:38 TFB2M:115 TEFM:146 FASTKD5:253 TWNK:254
Oxidative Phosphorylation (GO:0006119)	0.18263174	59	1.241e−06	6.098e−04	TEFM:146 NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593
Cellular Respiration (GO:0045333)	0.13799059	82	1.591e−05	6.772e−03	COX7C:360 NDUFS1:384 NDUFB1:503 NDUFA8:570 NDUFB7:593 UQCRFS1:699
Proton Motive Force−Driven Mitochondrial	0.17585665	50	1.710e−05	6.772e−03	NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593 NDUFA11:701
tRNA Modification (GO:0006400)	0.15181511	67	1.753e−05	6.772e−03	THADA:5 TRMT10A:125 FTSJ1:212 DTWD1:487 TYW1B:572 PUS10:750
Positive Regulation Of Mitochondrial Tra	0.32695370	14	2.280e−05	8.219e−03	TRMT10C:62 NGRN:180 RCC1L:461 RPUSD3:718 FASTKD2:931 FASTKD3:1117
Mitochondrial Electron Transport, NADH T	0.21158979	33	2.606e−05	8.806e−03	NDUFAF1:197 NDUFS1:384 NDUFB1:503 NDUFA8:570 NDUFB7:593 NDUFB10:927
Regulation Of Mitochondrial Translation	0.25587808	22	3.266e−05	1.039e−02	LRPPRC:28 TRMT10C:62 NGRN:180 RCC1L:461 RPUSD3:718 FASTKD2:931
Proton Motive Force−Driven ATP Synthesis	0.16114076	54	4.242e−05	1.274e−02	NDUFS1:384 NDUFB1:503 ATP5PO:519 NDUFA8:570 NDUFB7:593 NDUFA11:701
Ribosomal Small Subunit Biogenesis (GO:0	0.13580823	75	4.842e−05	1.378e−02	NOL6:152 DDX52:174 UTP20:316 SRFBP1:319 RIOK1:350 RIOK2:389
Centromere Complex Assembly (GO:0034508)	0.31222772	14	5.238e−05	1.416e−02	DLGAP5:14 HJURP:323 CENPF:362 CENPT:459 NASP:656 CENPC:748
Aerobic Respiration (GO:0009060)	0.15336227	57	6.266e−05	1.540e−02	TEFM:146 NDUFS1:384 NDUFB1:503 NDUFA8:570 NDUFB7:593 NDUFA11:701
Mitochondrial RNA Processing (GO:0000963	0.38576142	9	6.136e−05	1.540e−02	FASTKD1:38 TRMT10C:62 FASTKD5:253 SUPV3L1:490 FASTKD2:931 FASTKD3:1117
Adenylate Cyclase−Activating G Protein−C	−0.11274898	104	7.247e−05	1.704e−02	ADCY1:4 PTH1R:35 MC4R:50 GPER1:68 GPR161:242 CALCA:288
Intermediate Filament Organization (GO:0	−0.14139398	65	8.164e−05	1.766e−02	BFSP2:28 KRT77:206 PKP1:210 KRT5:260 VIM:352 BFSP1:364
Mitochondrial Transcription (GO:0006390)	0.32888382	12	7.988e−05	1.766e−02	POLRMT:21 TFB2M:115 TEFM:146 TWNK:254 TFAM:522 MTERF1:660
Positive Regulation Of Calcium Ion Trans	−0.17531729	41	1.032e−04	2.147e−02	GPER1:68 PPP3R2:134 P2RX3:472 CAPN3:802 P2RX7:919 CX3CL1:1010
Potassium Ion Transmembrane Transport (G	−0.09411406	135	1.636e−04	3.276e−02	KCNV1:29 KCNH2:73 KCNK1:100 KCNK13:135 KCNJ12:157 KCNF1:292
Peptide Biosynthetic Process (GO:0043043	0.09237117	137	1.940e−04	3.746e−02	MRPS15:330 RPS17:528 TNIP1:637 MRPS6:737 MRPS5:752 RPL4:781
Sensory Perception Of Smell (GO:0007608)	−0.07445466	207	2.305e−04	4.298e−02	OR10D3:137 OR9G4:200 OR2L8:267 OR2M2:410 OR2L3:431 NXNL2:460
Visual Perception (GO:0007601)	−0.10685880	99	2.427e−04	4.373e−02	ATF6:13 TRPM1:45 VAX2:48 CRYBA4:62 CRYGC:90 CRYBB1:124
Potassium Ion Transport (GO:0006813)	−0.09639627	121	2.551e−04	4.450e−02	KCNV1:29 KCNH2:73 KCNK1:100 KCNK13:135 KCNJ12:157 KCNF1:292
tRNA Methylation (GO:0030488)	0.17346104	36	3.176e−04	5.366e−02	THADA:5 TRMT10C:62 TRMT10A:125 FTSJ1:212 TRMT5:482 TRMT61B:541
Lymphocyte Activation Involved In Immune	−0.21637593	23	3.286e−04	5.385e−02	IFNA5:393 F2RL1:534 IFNA1:820 IFNA4:962 IFNA21:983 IFNA6:1398
DNA Repair (GO:0006281)	0.06177301	281	3.844e−04	5.927e−02	FANCG:19 STON1:48 MLH3:85 FANCM:89 MBD4:106 RAD51AP1:116
Calcium Ion Import Across Plasma Membran	−0.17565077	34	3.948e−04	5.927e−02	SCN9A:7 CACNA1B:31 TRPM1:45 SCN1A:57 SCN2A:60 TRPV6:259
Chemical Synaptic Transmission (GO:00072	−0.06355560	263	4.056e−04	5.927e−02	GABRR3:25 CACNA1B:31 APBA2:32 GABRA5:43 CHRNA7:66 EXOC4:79
Protein Localization To Microtubule Orga	0.26489487	15	3.825e−04	5.927e−02	SPAG5:13 C2CD3:26 STIL:82 CEP192:110 CEP250:479 PIBF1:613
Calcium Ion Transport (GO:0006816)	−0.09691286	110	4.533e−04	6.023e−02	TRPM1:45 CHRNA7:66 TRPV6:259 SLC8A3:282 CLU:289 ATP2A2:321
Double−Strand Break Repair (GO:0006302)	0.08012838	161	4.627e−04	6.023e−02	STON1:48 RAD51AP1:116 UIMC1:127 RNF168:160 EYA3:259 RMI1:288
Inorganic Cation Transmembrane Transport	−0.06107921	280	4.574e−04	6.023e−02	SCN9A:7 KCNV1:29 TRPM1:45 SCN2A:60 KCNH2:73 KCNK1:100

MGI_Mammalian_Phenotype_Level_4 Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003252 abnormal bile duct	0.21267463	25	2.379e−04	1.132e−01	PKHD1:63 CYP8B1:277 ABCB11:478 ABCG5:776 MAP3K14:1341 ATXN2:1537
MP0001970 abnormal pain threshold	−0.08162940	152	5.863e−04	1.395e−01	ADCY1:4 SSTR4:14 CACNA1B:31 PTPRZ1:108 TSHZ3:144 GABRR1:186
MP0004085 abnormal heartbeat	−0.07558663	160	1.100e−03	1.451e−01	CACNA1B:31 KCNH2:73 SYNE1:133 ERBB4:246 CALCA:288 ATP2A2:321
MP0005551 abnormal eye electrophysiolog	−0.07727509	144	1.524e−03	1.451e−01	CDHR1:19 TRPM1:45 GABRR1:186 CNGB3:199 GJA10:202 RBP3:217
MP0002085 abnormal embryonic tissue	0.03814621	654	1.505e−03	1.451e−01	ECSIT:4 ARL13B:22 CUBN:23 C2CD3:26 STIL:82 TRPM6:103
MP0002398 abnormal bone marrow	0.03398642	813	1.928e−03	1.530e−01	NEDD4:1 JAK3:33 THPO:65 HPS3:70 AIRE:75 NFATC3:83
MP0005253 abnormal eye physiology	−0.08935214	95	2.784e−03	1.656e−01	BFSP2:28 TRPM1:45 CRYGC:90 RLBP1:191 CNGB3:199 CSTB:555
MP0003635 abnormal synaptic transmissio	−0.04368387	425	2.721e−03	1.656e−01	ADCY1:4 SCN9A:7 CACNA1B:31 GABRA5:43 SCN1A:57 CHRNA7:66
MP0005388 respiratory system phenotype	−0.07320463	130	4.276e−03	2.035e−01	SSTR4:14 TOM1L2:92 SYNE1:133 TSHZ3:144 DBNL:212 CYLD:302
MP0002133 abnormal respiratory system	−0.07320463	130	4.276e−03	2.035e−01	SSTR4:14 TOM1L2:92 SYNE1:133 TSHZ3:144 DBNL:212 CYLD:302
MP0009745 abnormal behavioral response	−0.05654969	205	5.919e−03	2.561e−01	EHMT1:10 CACNA1B:31 GABRA5:43 SCN1A:57 CHRNA7:66 CALCA:288
MP0002084 abnormal developmental patter	0.04144554	364	8.107e−03	2.968e−01	ECSIT:4 ARL13B:22 CUBN:23 C2CD3:26 STIL:82 INTU:161
MP0002932 abnormal joint morphology	0.07300942	112	8.068e−03	2.968e−01	FBN2:29 PHC2:303 LRP6:430 ZEB1:728 GDF5:810 RARG:834
MP0002113 abnormal skeleton development	0.03938338	385	9.818e−03	3.338e−01	FBN2:29 DMP1:67 TRPM6:103 NBR1:133 DNMT3B:287 LRP6:430
MP0002572 abnormal emotion/affect behav	−0.04398558	287	1.195e−02	3.694e−01	ADCY1:4 EHMT1:10 CACNA1B:31 APBA2:32 CHRNA7:66 TOM1L2:92
MP0000689 abnormal spleen morphology	0.03185191	551	1.398e−02	3.694e−01	JAK3:33 PKHD1:63 FOXN1:91 PARL:164 LAMP2:170 SIGLEC1:224
MP0002080 prenatal lethality	0.02218168	1335	1.442e−02	3.694e−01	NEDD4:1 ECSIT:4 ARL13B:22 CUBN:23 C2CD3:26 NFKBIZ:41
MP0002272 abnormal nervous system	−0.05218516	196	1.294e−02	3.694e−01	CACNA1B:31 SCN1A:57 ARC:110 GABRR1:186 ADORA1:252 CHRNA4:368
MP0001177 atelectasis	−0.09373224	57	1.475e−02	3.694e−01	SYNE1:133 TSHZ3:144 CYLD:302 EGFR:335 TRPS1:583 DOCK1:685
MP0009765 abnormal xenobiotic induced	0.07104009	95	1.742e−02	3.948e−01	APOD:232 BCHE:298 SKIL:315 MTF1:376 KCNK2:863 FAIM:903
MP0005620 abnormal muscle contractility	−0.04863976	208	1.713e−02	3.948e−01	LIMS2:106 ENTPD1:127 ERBB4:246 ATP2B1:265 CLU:289 NBEA:296
MP0010329 abnormal lipoprotein level	−0.07181021	90	1.926e−02	4.114e−01	SEC14L2:248 SCARB1:395 APOA4:556 GPIHBP1:765 PLTP:868 FTO:936
MP0006138 congestive heart failure	−0.09745820	48	1.988e−02	4.114e−01	ATP2A2:321 EGFR:335 SOX9:437 IGF1R:1098 E2F3:1246 EPAS1:1475
MP0005535 abnormal body temperature	−0.05995931	124	2.221e−02	4.218e−01	APBA2:32 ADORA1:252 HRH3:399 CBL:517 SLC18A2:628 PRLR:1053
MP0002429 abnormal blood cell	0.02124681	1241	2.234e−02	4.218e−01	NEDD4:1 JAK3:33 PTPN13:64 THPO:65 HPS3:70 AIRE:75
MP0002114 abnormal axial skeleton	0.03290925	431	2.304e−02	4.218e−01	TRPM6:103 PARL:164 DNMT3B:287 BUB1B:301 PHC2:303 LRP6:430
MP0000716 abnormal immune system	0.02231814	1014	2.605e−02	4.428e−01	NEDD4:1 JAK3:33 PTPN13:64 AIRE:75 NFATC3:83 FOXN1:91
MP0002063 abnormal learning/memory/cond	−0.03526532	357	2.558e−02	4.428e−01	ADCY1:4 EHMT1:10 CACNA1B:31 APBA2:32 GABRA5:43 CHRNA7:66
MP0005220 abnormal exocrine pancreas	0.09305177	46	2.948e−02	4.840e−01	PKHD1:63 INVS:682 SERPINI2:704 PTF1A:1014 SERPINF1:1162 ONECUT1:1274
MP0000432 abnormal head morphology	0.03575228	321	3.127e−02	4.961e−01	DMP1:67 TRPM6:103 HESX1:272 DNMT3B:287 LRP6:430 INPPL1:456
MP0005584 abnormal enzyme/coenzyme acti	−0.05269133	139	3.361e−02	5.161e−01	ADCY1:4 IGFBP3:49 PDE8A:257 CYLD:302 GZMB:443 CBL:517
MP0001501 abnormal sleep pattern	−0.09929271	37	3.706e−02	5.513e−01	CACNA1B:31 KCNC2:1128 FOS:1151 CHRM3:1488 SLC6A4:1529 PER3:1619
MP0002135 abnormal kidney morphology	0.02925421	453	3.875e−02	5.590e−01	CUBN:23 TRPV1:24 PKHD1:63 TET2:151 AMHR2:486 PTCD2:562
MP0003942 abnormal urinary system	0.06593428	81	4.131e−02	5.784e−01	AMHR2:486 PYGO1:706 GPC3:744 CBS:973 FGFR1:1039 FAT4:1245
MP0003935 abnormal craniofacial develop	0.03777614	246	4.483e−02	6.096e−01	DMP1:67 TRPM6:103 HESX1:272 DLC1:359 LRP6:430 SUPV3L1:490
MP0002169 no abnormal phenotype	0.01874309	1181	4.775e−02	6.136e−01	SPAG5:13 TMPRSS2:20 PKHD1:63 NFATC3:83 FOXN1:91 NFE2L3:107
MP0008058 abnormal DNA repair	0.08506735	44	5.156e−02	6.136e−01	POLK:202 ALKBH2:494 BAZ1B:767 NHEJ1:970 XRCC4:1144 BRCA2:1208
MP0005646 abnormal pituitary gland	−0.12720123	20	4.920e−02	6.136e−01	DRD2:1115 ARNT2:1466 APOE:1541 GAL:1859 PRL:2003 PDPK1:2529
MP0002064 seizures	−0.03605829	255	5.140e−02	6.136e−01	SCN9A:7 SCN1A:57 CHRNA7:66 NETO1:70 HTT:128 DBNL:212
MP0002873 normal phenotype	0.01872340	1186	4.764e−02	6.136e−01	SPAG5:13 TMPRSS2:20 PKHD1:63 NFATC3:83 FOXN1:91 NFE2L3:107

tissue_specific Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
EBV.lymphocyte	0.052158721	750	2.448e−06	1.322e−04	DLGAP5:14 NCAPD2:17 SFMBT2:40 KNL1:42 ATAD5:59 STIL:82
pancreas	0.093073635	117	5.364e−04	1.448e−02	TMED6:72 CELA3A:78 ERP27:104 CELA3B:262 G6PC2:312 MATN4:375
suprapubic.skin	−0.054892496	257	2.706e−03	4.871e−02	BNC1:11 IL37:59 NKPD1:126 LCE2D:142 PARD6G:153 KRT77:206
Brodmann.area.9	−0.062289055	183	3.908e−03	5.276e−02	KCNV1:29 SCN1A:57 DCLK1:63 NETO1:70 TMEM132D:72 MAS1:216
leg.skin	−0.044896497	286	9.794e−03	1.058e−01	BNC1:11 CDHR1:19 TRIM29:24 TRPM1:45 IL37:59 NKPD1:126
cerebral.cortex	−0.064873516	109	1.980e−02	1.782e−01	MAS1:216 C1QL2:238 KCNF1:292 SHC3:492 KCNB2:548 CSMD1:590
putamen	−0.139262186	17	4.694e−02	3.621e−01	GRM3:920 RGS9:1969 PDE10A:2020 KCNH4:2245 SLC18A3:2247 CORT:2466
amygdala	−0.098342016	9	3.071e−01	7.686e−01	PTPRZ1:108 TNR:2618 BCAN:8869 LHFPL3:8869 NEUROD2:8869 NEUROD6:8869
C1.spinal.cord	−0.019270184	194	3.584e−01	7.686e−01	HEPACAM:76 TTYH2:149 PDE6B:219 SEC14L5:225 MMD2:243 CDH20:357
cerebellar.hemisphere	−0.011567536	536	3.701e−01	7.686e−01	ADCY1:4 SSTR4:14 APBA2:32 MYT1:47 VAX2:48 SCN2A:60
cerebellum	−0.017211039	407	2.412e−01	7.686e−01	SSTR4:14 CACNA1B:31 PCNX2:40 MYT1:47 RNF112:164 DOCK3:166
cortex.kidney	0.023615090	131	3.531e−01	7.686e−01	CUBN:23 PKHD1:63 CLCNKB:77 KIF12:295 SLC4A9:397 ENAM:518
endocervix	−0.036386228	76	2.741e−01	7.686e−01	NXNL2:460 ELFN1:574 PRSS12:627 SLC18A2:628 TACR1:1291 LUM:1335
esophagus.mucosa	−0.027542545	261	1.295e−01	7.686e−01	BNC1:11 CDCP1:104 TGM1:176 LAD1:185 PKP1:210 KRT5:260
esophagus.muscularis.mucosa	0.063593453	28	2.446e−01	7.686e−01	PRUNE2:6 KCNMB1:978 CCDC69:998 CYSLTR1:2146 RGMB:2209 SMTN:2304
fallopian.tube	0.057676944	60	1.231e−01	7.686e−01	ATP8B4:217 ADGRG4:264 CCDC17:291 BCHE:298 ADAMTS3:419 CCDC198:523
hypothalamus	−0.042897311	78	1.916e−01	7.686e−01	SCN9A:7 MC4R:50 GABRG3:305 RAB3C:312 PNMA6F:464 PNMA5:665
liver	0.015034081	397	3.116e−01	7.686e−01	THPO:65 NUGGC:66 PBLD:73 AFP:105 SERPINA7:145 CYP8B1:277
minor.salivary.gland	−0.029897546	91	3.259e−01	7.686e−01	TFCP2L1:237 KRT5:260 SOX9:437 CLDN8:487 KRT81:1058 MMP3:1105
nucleus.accumbens	−0.029633054	104	2.983e−01	7.686e−01	GABRA5:43 JAKMIP1:366 INSYN2A:397 KCNA4:420 CPNE5:543 COCH:571
peyers.patch	−0.021327100	199	3.034e−01	7.686e−01	SLC17A4:55 UGT2B17:338 APOA4:556 KRT12:562 ADGRG7:682 PHGR1:797
skeletal.muscle	−0.017107742	258	3.490e−01	7.686e−01	LMOD2:88 SLC8A3:282 ATP2A2:321 TTN:387 SMYD1:411 GLRX:505
testis	0.010359515	1639	1.947e−01	7.686e−01	SPAG5:13 KNL1:42 MANSC4:43 UMODL1:44 GPR156:54 DMP1:67
uterus	0.034240713	62	3.522e−01	7.686e−01	DENND2B:169 MEIS3:547 ATP2B4:554 ADAMTS19:565 PTK7:649 CLEC4F:918
vagina	−0.026875052	118	3.155e−01	7.686e−01	BNC1:11 PKP1:210 KRT5:260 CSTB:555 IL36RN:578 SLC18A2:628
eye.development	0.031801832	69	3.622e−01	7.686e−01	FZD6:815 PTF1A:1014 ONECUT1:1274 TBX5:1347 BMP4:1462 PITX2:1805
aorta	0.019346583	156	4.072e−01	7.853e−01	HMCN1:18 KCNK15:92 FILIP1L:119 SCUBE3:149 FOXS1:235 GGTA1:854
transformed.skin.fibroblast	−0.014966394	276	3.973e−01	7.853e−01	BNC1:11 CLMP:23 COL3A1:82 OPN3:148 ATP2B1:265 ANGPT1:278
blood	−0.011266493	345	4.782e−01	8.904e−01	PLXNC1:355 PHOSPHO1:405 GZMB:443 NBEAL2:529 NTNG2:560 AGTRAP:619
ovary	0.017388705	118	5.160e−01	9.237e−01	NRK:139 PLIN5:329 OBSL1:391 UBXN8:589 IGSF10:823 FFAR1:1026
subcutaneous.adipose	0.020109205	82	5.303e−01	9.237e−01	GPBAR1:71 SIGLEC1:224 LVRN:642 CSN1S1:1024 MEOX1:1092 EDN1:1263
atrium.auricle	0.016252046	95	5.854e−01	9.281e−01	TNNI3K:12 CCDC141:131 RPL3L:1167 HAMP:1173 TBX5:1347 SMCO1:1464
breast	−0.032166812	20	6.187e−01	9.281e−01	KRT5:260 TNN:285 SCGB2A2:1900 ADIPOQ:8869 ALX4:8869 CIDEC:8869
Brodmann.area.24	0.026042963	33	6.050e−01	9.281e−01	OSTN:1380 FAM107A:1473 DOK6:1826 NTRK2:2159 SLC39A12:2217 CNTN5:2233
caudate.nucleus	−0.028836768	27	6.043e−01	9.281e−01	RLBP1:191 MLC1:208 GRM3:920 GPR37L1:927 SLC1A2:1872 HS3ST5:8869
tibial.artery	0.014222278	114	6.015e−01	9.281e−01	SCUBE3:149 RERGL:381 SYTL2:418 TRABD2B:790 LPP:816 GGTA1:854
hippocampus.proper	0.032819749	13	6.821e−01	9.731e−01	CNIH2:1096 CTXND1:1900 NEUROD2:9689 NEUROD6:9689 SLC17A7:9689 HRK:9689
lung	−0.009329334	161	6.848e−01	9.731e−01	VIPR1:78 ADAMTS8:168 RHOBTB2:423 BPIFA1:524 XAGE2:705 COL6A5:757
bladder	−0.013588145	29	8.003e−01	9.821e−01	PADI3:1222 RD3:1278 TPSD1:2055 WFDC13:2650 SLC14A1:2662 ABCC4:8869
esophagogastric.junction	0.031078585	9	7.469e−01	9.821e−01	RTL3:2685 F2RL2:2761 ADCY5:9689 BARX1:9689 COL4A5:9689 GADL1:9689