Geneset	stat	num.genes	pval	p.adj	gene.vals
NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	-0.32785611	21	1.979e-07	1.285e-03	PCSK6:244 TARS3:497 LYSMD4:547 ARRDC4:710 LRRK1:766 SNRPA1:828
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.03993861	1274	1.974e-06	6.410e-03	NUP133:7 APOC1:19 NUP205:22 GALNT2:30 NUP155:34 NSD2:82
ZHANG_BREAST_CANCER_PROGENITORS_UP	-0.06207104	414	1.538e-05	2.497e-02	MET:5 PRPS2:26 TRPS1:28 NUP155:34 BCLAF3:48 PAXBP1:109
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	-0.03602415	1306	1.430e-05	2.497e-02	MET:5 EHMT1:14 ZNF274:29 ZIM2:49 ZNF211:50 WWP1:52
KEGG_CYTOKINE_CYTOKINE_RECEPTOR_INTERACT	-0.07605665	258	2.661e-05	3.456e-02	MET:5 PRL:92 TGFB1:97 TSLP:117 TNF:254 FLT1:312
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.03604673	1189	3.215e-05	3.479e-02	HERC2:1 MET:5 LTN1:15 SCN2A:16 ARHGEF4:32 ATP2B1:56
NIKOLSKY_BREAST_CANCER_1Q21_AMPLICON	0.20294201	34	4.219e-05	3.914e-02	THBS3:14 ADAM15:60 DCST1:98 ZBTB7B:226 PYGO2:259 RUSC1:318
BRIDEAU_IMPRINTED_GENES	-0.15143650	58	6.650e-05	5.398e-02	ATP10A:20 IGF2:105 UBE3A:201 CNTN3:224 MAGEL2:234 CALCR:314
REACTOME_PROLACTIN_RECEPTOR_SIGNALING	-0.28533212	15	1.300e-04	9.383e-02	PRL:92 PRLR:805 JAK2:812 GH2:821 CSH1:835 GH1:982
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	-0.13786708	63	1.544e-04	1.003e-01	HERC2:1 GABRA5:2 ATP10A:20 MDM4:85 GABRG3:148 OCA2:170
WP_PHOTODYNAMIC_THERAPYINDUCED_AP1_SURVI	-0.15599790	48	1.849e-04	1.092e-01	FOS:169 TNF:254 BAX:283 BCL2L11:379 CCNE1:466 MAPK8:494
REACTOME_FORMATION_OF_SENESCENCE_ASSOCIA	-0.25942608	17	2.127e-04	1.151e-01	H1-4:172 H1-1:374 UBN1:478 H1-3:720 CABIN1:741 EP400:919
WP_OVERVIEW_OF_PROINFLAMMATORY_AND_PROFI	-0.09259063	126	3.341e-04	1.669e-01	AREG:95 TGFB1:97 TSLP:117 IL33:146 TNF:254 IL18:321
EACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.06463052	253	4.072e-04	1.889e-01	NUP133:7 NUP205:22 NUP155:34 SYMPK:68 U2AF1L4:300 THOC5:364
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.04199629	602	4.518e-04	1.956e-01	NUP155:34 MPHOSPH10:43 E2F5:57 GPSM2:174 ORC6:193 NETO2:221
BIOCARTA_PEPI_PATHWAY	0.34902846	8	6.288e-04	2.149e-01	CELA1:27 CELA2B:468 SLPI:511 CELA3B:611 CELA2A:778 ELANE:1483
HOLLERN_EMT_BREAST_TUMOR_DN	0.09143831	118	6.055e-04	2.149e-01	CLIC3:156 SDR42E1:230 EVPL:297 ENDOU:328 POF1B:391 PTPRF:425
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.08905522	126	5.599e-04	2.149e-01	KRT39:139 KRT84:170 SPRR2A:204 EVPL:297 KRT20:322 KRT72:474
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	-0.03896305	673	5.952e-04	2.149e-01	COL7A1:25 MPHOSPH10:43 CNOT1:55 ATP2B1:56 CDH2:87 AREG:95
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.08674749	127	7.404e-04	2.193e-01	RBM12B:35 ZBTB10:118 SNX16:134 RALYL:200 PIP4P2:213 MMP16:242
REACTOME_CELL_SURFACE_INTERACTIONS_AT_TH	-0.08374567	137	7.190e-04	2.193e-01	TGFB1:97 GRB14:223 PIK3CA:308 GYPC:378 SIRPA:485 JAML:489
KEGG_P53_SIGNALING_PATHWAY	-0.11919283	67	7.431e-04	2.193e-01	MDM4:85 IGFBP3:111 SHISA5:132 BAX:283 CHEK1:369 CCNE1:466
MILI_PSEUDOPODIA_HAPTOTAXIS_UP	-0.04310826	496	1.044e-03	2.635e-01	LTN1:15 CAMSAP2:47 BCLAF3:48 WWP1:52 SNX16:134 ZNF131:149
DANG_BOUND_BY_MYC	-0.03081833	1010	9.878e-04	2.635e-01	MET:5 ZNF134:6 PRPS2:26 ZNF274:29 NUP155:34 SYMPK:68
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.04259597	517	9.485e-04	2.635e-01	GABRA5:2 CAMSAP2:47 ATP2B1:56 CHL1:62 SARS1:121 DCTN1:147
PID_E2F_PATHWAY	-0.11405483	69	1.055e-03	2.635e-01	E2F5:57 RBL2:80 CASP7:131 CDC25A:150 MYBL2:391 CCNE1:466
REACTOME_TP53_REGULATES_TRANSCRIPTION_OF	-0.13697975	47	1.160e-03	2.660e-01	CNOT1:55 RBL2:80 BAX:283 CCNE1:466 CDK1:852 CNOT11:946
JOHNSTONE_PARVB_TARGETS_3_DN	-0.03414968	793	1.133e-03	2.660e-01	PRPS2:26 SETD2:27 ZNF274:29 UAP1:71 MDM4:85 ZNF22:119
BLUM_RESPONSE_TO_SALIRASIB_DN	-0.05231851	326	1.188e-03	2.660e-01	GALNT2:30 CDC25A:150 FOS:169 GPSM2:174 ORC6:193 PBK:361
SHEN_SMARCA2_TARGETS_UP	-0.04639322	410	1.300e-03	2.814e-01	HERC2:1 NUP133:7 PSMF1:206 CAPN7:287 NPTN:376 WDR11:503
KEGG_GRAFT_VERSUS_HOST_DISEASE	-0.14999908	37	1.593e-03	3.336e-01	TNF:254 HLA-DOB:384 HLA-DQA1:502 GZMB:550 KIR3DL2:680 CD28:931
REACTOME_CYTOKINE_SIGNALING_IN_IMMUNE_SY	-0.03504975	698	1.670e-03	3.388e-01	NUP133:7 NUP205:22 NUP155:34 PRL:92 TGFB1:97 HERC5:108
REACTOME_SPERM_MOTILITY_AND_TAXES	-0.30130682	9	1.746e-03	3.435e-01	CATSPERD:91 CATSPER2:191 CATSPER3:529 CATSPERB:652 KCNU1:1747 CATSPER1:206
OYLANCE_BREAST_CANCER_16Q_COPY_NUMBER_D	-0.18622521	23	1.990e-03	3.565e-01	ORC6:193 NETO2:221 GPT2:885 VPS35:1402 ITFG1:1428 SHCBP1:1476
MIKKELSEN_ES_ICP_WITH_H3K4ME3	0.03468095	684	2.068e-03	3.565e-01	THBS3:14 DGLUCY:37 AKR1E2:57 LSG1:101 GDF3:105 RNF186:121
REACTOME_TRAIL_SIGNALING	-0.31340549	8	2.141e-03	3.565e-01	CASP8:1005 TNFSF10:1172 CFLAR:1345 CASP10:1595 TNFRSF10B:1687 TNFRSF10D:227
REACTOME_UPTAKE_OF_DIETARY_COBALAMINS_IN	0.28216944	10	2.001e-03	3.565e-01	CBLIF:48 TCN1:414 CTRB1:608 CUBN:751 PRSS1:1148 CTRB2:1245
SCHLOSSER_SERUM_RESPONSE_DN	-0.03532171	655	2.122e-03	3.565e-01	PDE8A:41 TDRD7:46 E2F5:57 RBL2:80 IGF2:105 ARSL:139
NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON	0.23697885	14	2.139e-03	3.565e-01	YBEY:812 PCNT:914 FTCD:1210 COL6A1:1379 POFUT2:1546 DIP2A:1953

DisGeNET Top pathways by non-permulation

2.238e-03 3.624e-01

0.07738365

MIKKELSEN_ES_LCP_WITH_H3K4ME3

Neuroblastoma

Oncocytic Neoplasm

Partial chromosome Y deletion

NA.35

NA

NA

NA

NA

-0.02309536

-0.12687192

-0.37276775

GLMP:10 GGT6:64 PRTN3:92 SLC12A8:122 KLHDC7A:161 ARHGEF11:284

HERC2:1 MET:5 SETD2:27 CYLD:42 KNG1:45 CNOT1:55

PRL:92 ZFP42:123 MST1:329 CLDN8:651 PTGS2:964 CD9:1033 DAZ1:567 DAZ4:714 DAZ3:851 DAZ2:997 USP9Y:1817 DDX3Y:9284.5

NA NA NA NA NA NA

NA NA NA NA NA

Geneset	stat	num.genes	pval	p.adj	gene.vals
Adenocarcinoma in Situ	-0.22462139	29	2.842e-05	2.791e-01	CDH2:87 ASAP1:488 DPYD:507 SEC14L2:664 PAPOLA:918 STS:1054
Carcinosarcoma	-0.17316279	43	8.589e-05	4.217e-01	MET:5 TGFB1:97 IGF2:105 PHB2:199 PIK3CA:308 SOX9:515
Allergic Reaction	-0.12627535	61	6.522e-04	6.250e-01	KNG1:45 TGFB1:97 TNF:254 IL18:321 HLA-DQA1:502 CX3CL1:625
Anal squamous cell carcinoma	-0.28741944	12	5.659e-04	6.250e-01	PIK3CA:308 MDM2:757 DCC:1247 NELFE:1264 TP53:1339 CDKN2A:1536
Cataract	-0.04542582	484	6.695e-04	6.250e-01	CNGB3:8 COL7A1:25 TDRD7:46 ATP2B1:56 SUMF1:76 RBP3:83
Cervical Squamous Intraepithelial Neopla	-0.14195945	47	7.638e-04	6.250e-01	MET:5 TGFB1:97 TNF:254 LAMB2:286 HMGB1:551 MTHFR:662
Hepatitis C	-0.03838935	677	7.359e-04	6.250e-01	MET:5 APOA1:13 APOC1:19 TGFB1:97 CLU:101 IGF2:105
insulinoma	-0.08206995	164	2.953e-04	6.250e-01	MET:5 EHMT1:14 PRL:92 TGFB1:97 IGF2:105 SDS:173
Liver carcinoma	-0.02026726	3047	6.026e-04	6.250e-01	MET:5 APOA1:13 SETD2:27 GALNT2:30 CYLD:42 KNG1:45
Prader-Willi Syndrome	-0.10739578	88	5.035e-04	6.250e-01	HERC2:1 GABRA5:2 ATP10A:20 ZNF274:29 GABRG3:148 OCA2:170
Stable angina	-0.12132354	70	4.525e-04	6.250e-01	APOA1:13 TGFB1:97 IGF2:105 IL33:146 TNF:254 CX3CL1:625
Tumor Immunity	-0.09083163	122	5.398e-04	6.250e-01	AREG:95 IL33:146 FOS:169 HAVCR1:198 TNF:254 TLR8:267
Leukemia, Myelocytic, Acute	-0.02567732	1494	1.152e-03	6.286e-01	MET:5 SETD2:27 TRPS1:28 CHL1:62 ZNF331:74 MDM4:85
Bilateral cataracts (disorder)	-0.09453982	104	8.768e-04	6.286e-01	TDRD7:46 BFSP2:93 TGFB1:97 MGST1:207 AKR1B1:212 EPHA2:356
Cervical Intraepithelial Neoplasia	-0.06942076	187	1.089e-03	6.286e-01	MET:5 TGFB1:97 SYCP3:196 TNF:254 BAX:283 LAMB2:286
Cholestasis in newborn	0.10161197	87	1.064e-03	6.286e-01	GPBAR1:31 PEX1:73 HAMP:271 SLC10A2:273 LIPA:287 MPI:288
Influenza	-0.04241087	508	1.150e-03	6.286e-01	CYLD:42 TDRD7:46 ARSF:79 AREG:95 TGFB1:97 HERC5:108
Myasthenia Gravis	-0.07707270	156	9.131e-04	6.286e-01	TGFB1:97 TSLP:117 CRK:137 TNF:254 CALCR:314 HLA-DQA1:502
CATARACT, AUTOSOMAL DOMINANT	-0.29751104	9	1.997e-03	6.674e-01	BFSP2:93 CRYBB1:214 CRYAA2:956 STS:1054 GJA8:1582 MIP:2175
Tuberculosis, Pulmonary	-0.07405264	150	1.779e-03	6.674e-01	TGFB1:97 CRK:137 PHB2:199 PDE6B:247 TNF:254 TLR8:267
Acute inflammatory demyelinating polyneu	-0.32422268	7	2.971e-03	6.674e-01	TNF:254 PTGDS:302 TNFRSF1A:858 ALB:1419 PMP22:1499 HLA-DRB1:9284.5
Adenovirus Infections	-0.09567072	85	2.318e-03	6.674e-01	TRPS1:28 MDM4:85 CDC25A:150 TNF:254 BAX:283 CHEK1:369
Anasarca	-0.16972994	26	2.743e-03	6.674e-01	APOA1:13 KNG1:45 TNF:254 VIP:917 PTGS2:964 CASP8:1005
Anti-Basement Membrane Glomerulonephriti	-0.15029550	36	1.810e-03	6.674e-01	CLU:101 TNF:254 MAPK8:494 CX3CL1:625 ITGA4:1477 PTK2B:1508
Carcinoma of bladder	-0.02953013	1013	1.710e-03	6.674e-01	MET:5 SETD6:24 KNG1:45 MDM4:85 CDH2:87 TGFB1:97
Central neuroblastoma	-0.02391509	1507	2.374e-03	6.674e-01	HERC2:1 SETD2:27 CYLD:42 KNG1:45 CNOT1:55 CHL1:62
Cervix carcinoma	-0.02923264	943	2.668e-03	6.674e-01	MET:5 SETD2:27 CYLD:42 CHL1:62 NSD2:82 TGFB1:97
Choriocarcinoma	-0.05287199	279	2.456e-03	6.674e-01	MDM4:85 TGFB1:97 IGF2:105 PHB2:199 CRH:215 INSR:231
Epithelial ovarian cancer	-0.02650156	1150	2.852e-03	6.674e-01	MET:5 SETD2:27 KNG1:45 RBL2:80 MDM4:85 PRL:92
Extramedullary Plasmacytoma	-0.24780234	12	2.956e-03	6.674e-01	PECAM1:679 ANGPT1:1132 ENG:1334 TP53:1339 CDKN2A:1536 PRM3:1703
Generalized hypopigmentation	-0.23851841	14	2.002e-03	6.674e-01	HERC2:1 MAGEL2:234 NDN:1164 OCRL:1727 MKRN3:2059 LEMD3:2181
Glioblastoma	-0.02250462	1686	2.672e-03	6.674e-01	MET:5 APOA1:13 SETD2:27 CD109:31 CNOT1:55 RBL2:80
HIV Infections	-0.03300997	717	2.856e-03	6.674e-01	ZNF134:6 APOA1:13 CYLD:42 CNOT1:55 CDH2:87 TGFB1:97
Human metapneumovirus infection	-0.32969415	7	2.521e-03	6.674e-01	TSLP:117 TNF:254 NCR1:424 PPIP5K1:903 ISYNA1:1940 SCT:9284.5
Hyperinsulinism	-0.04804065	359	1.854e-03	6.674e-01	HERC2:1 EHMT1:14 APOC1:19 MC4R:61 RBP3:83 PRL:92
Infection	-0.04332542	463	1.494e-03	6.674e-01	APOA1:13 APOC1:19 CYLD:42 TGFB1:97 IGF2:105 IL33:146
Male sterility due to Y-chromosome delet	-0.37276775	6	1.566e-03	6.674e-01	DAZ1:567 DAZ4:714 DAZ3:851 DAZ2:997 USP9Y:1817 DDX3Y:9284.5

customGeneSet Top pathways by non-permulation

2.990e-03 6.674e-01

2.631e-03 6.674e-01

1.566e-03 6.674e-01

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	0.05735493	13	5.210e-01	7.814e-01	SLC39A8:2409 LCT:9221.5 AS3MT:9221.5 GPX3:9221.5 CELF1:9221.5 SEPSECS:9221.5
NAFLDGWAS	-0.06787879	15	4.228e-01	7.814e-01	INSR:231 TOR1B:959 GID4:1220 FTO:1677 GPAM:1954 PNPLA3:9284.5
expressionDirectionalSelection	0.01147959	42	8.714e-01	8.714e-01	DEF8:2262 HLA-DRB1:9221.5 FADS1:9221.5 POU5F1:9221.5 HLA-DRB5:9221.5 KAT8:9221.5
NA	NA	NA	NA	NA	NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA
NA.26	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.29	NA	NA	NA	NA	NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA NA

GO_Biological_Process_2023 Top pathways by non-permulation

Geneset stat Positive Regulation Of Tyrosine Phosphor -0.149635 Regulation Of Tyrosine Phosphorylation O -0.132919 'De Novo' AMP Biosynthetic Process (GO:0 -0.002399 'De Novo' Post-Translational Protein Fol -0.015235 2-Oxoglutarate Metabolic Process (GO:000 0.003545 3'-UTR-mediated mRNA Destabilization (GO 0.0606200 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625373 5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005757 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0046033) 0.0425410 ATF6-mediated Unfolded Protein Response 0.2065814 ATP Biosynthetic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 AV Node Cell Action Potential (GO:008601 0.1198584	3617 65 3080 6 075 30 870 14 322 15 2774 18 042 14 3552 5 1952 5 881 2	1.248e-04 2.127e-04 9.838e-01 7.728e-01 9.634e-01 4.163e-01 6.292e-02 4.179e-01 1.795e-01	5.751e-01 9.999e-01 9.999e-01 9.999e-01 9.999e-01 9.999e-01	gene.vals TSLP:117 TNF:254 IL18:321 CSH2:345 CSHL1:400 LIF:612 TSLP:117 TNF:254 IL18:321 CSH2:345 CSHL1:400 LIF:612 GART:367 PAICS:9284.5 ATIC:9284.5 ADSS1:9284.5 ADSS2:9284.5 PFAS:17849 HSPA1A:347 UGGT1:770 HSPA1B:1321 SDF2L1:9284.5 HSPA9:9284.5 CCT2:9284.5 PHYH:91 IDH1:9221.5 GOT2:9221.5 MRPS36:9221.5 GOT1:9221.5 IDH2:9221.5 ZC3H12A:350 PLEKHN1:661 ZFP36L1:1503 UPF1:9221.5 TRIM71:9221.5 RC3H1:9221.5 DAZ1:567 DAZ4:714 DAZ3:851 DAZL:896 DAZ2:997 ZFP36:9284.5
Regulation Of Tyrosine Phosphorylation O 'De Novo' AMP Biosynthetic Process (GO:0 -0.002399) 'De Novo' Post-Translational Protein Fol -0.015235 2-Oxoglutarate Metabolic Process (GO:000 0.0035457) 3'-UTR-mediated mRNA Destabilization (GO 0.0606200) 3'-UTR-mediated mRNA Stabilization (GO:0 -0.126629) 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625370 5''S Class rRNA Transcription By RNA Polym -0.1733200 7-Methylguanosine RNA Capping (GO:000945 -0.1875310) 7-Methylguanosine Cap Hypermethylation (0.00057500) 7-Methylguanosine mRNA Capping (GO:00063 -0.1875310) ADP Transport (GO:0015866) -0.0514020 AMP Biosynthetic Process (GO:0006167) 0.0545029 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.0874590 ATP Transport (GO:0015867) 0.0035408	3617 65 3080 6 075 30 870 14 322 15 2774 18 042 14 3552 5 1952 5 881 2	2.127e-04 9.838e-01 7.728e-01 9.634e-01 4.163e-01 6.292e-02 4.179e-01 1.795e-01	5.751e-01 9.999e-01 9.999e-01 9.999e-01 9.999e-01 9.999e-01	TSLP:117 TNF:254 IL18:321 CSH2:345 CSHL1:400 LIF:612 GART:367 PAICS:9284.5 ATIC:9284.5 ADSS1:9284.5 ADSS2:9284.5 PFAS:17849 HSPA1A:347 UGGT1:770 HSPA1B:1321 SDF2L1:9284.5 HSPA9:9284.5 CCT2:9284.5 PHYH:91 IDH1:9221.5 GOT2:9221.5 MRPS36:9221.5 GOT1:9221.5 IDH2:9221.5 ZC3H12A:350 PLEKHN1:661 ZFP36L1:1503 UPF1:9221.5 TRIM71:9221.5 RC3H1:9221.5
'De Novo' AMP Biosynthetic Process (GO:0 -0.002399) 'De Novo' Post-Translational Protein Fol -0.015235 2-Oxoglutarate Metabolic Process (GO:000 0.0035456) 3'-UTR-mediated mRNA Destabilization (GO 0.0606200) 3'-UTR-mediated mRNA Stabilization (GO:0 -0.126629) 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625370 5S Class rRNA Transcription By RNA Polym -0.1733200 7-Methylguanosine RNA Capping (GO:000945 -0.1875310) 7-Methylguanosine Cap Hypermethylation (0.0005750) 7-Methylguanosine mRNA Capping (GO:00063 -0.1875310) ADP Transport (GO:0015866) -0.0514020 AMP Biosynthetic Process (GO:0006167) 0.0545020 AMP Metabolic Process (GO:0046033) 0.0425410 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.0874590 ATP Transport (GO:0015867) 0.0035408	8080 6 075 30 870 14 322 15 2774 18 042 14 8552 5 1952 5 881 2	9.838e-01 7.728e-01 9.634e-01 4.163e-01 6.292e-02 4.179e-01 1.795e-01	9.999e-01 9.999e-01 9.999e-01 9.999e-01 9.999e-01	GART:367 PAICS:9284.5 ATIC:9284.5 ADSS1:9284.5 ADSS2:9284.5 PFAS:17849 HSPA1A:347 UGGT1:770 HSPA1B:1321 SDF2L1:9284.5 HSPA9:9284.5 CCT2:9284.5 PHYH:91 IDH1:9221.5 GOT2:9221.5 MRPS36:9221.5 GOT1:9221.5 IDH2:9221.5 ZC3H12A:350 PLEKHN1:661 ZFP36L1:1503 UPF1:9221.5 TRIM71:9221.5 RC3H1:9221.5
'De Novo' Post-Translational Protein Fol -0.015235 2-Oxoglutarate Metabolic Process (GO:000 0.0035457 3'-UTR-mediated mRNA Destabilization (GO 0.0606200 3'-UTR-mediated mRNA Stabilization (GO:0 -0.126629 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625373 5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005757 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408	075 30 870 14 322 15 2774 18 042 14 3552 5 1952 5 881 2	7.728e-01 9.634e-01 4.163e-01 6.292e-02 4.179e-01 1.795e-01	9.999e-01 9.999e-01 9.999e-01 9.999e-01	HSPA1A:347 UGGT1:770 HSPA1B:1321 SDF2L1:9284.5 HSPA9:9284.5 CCT2:9284.5 PHYH:91 IDH1:9221.5 GOT2:9221.5 MRPS36:9221.5 GOT1:9221.5 IDH2:9221.5 ZC3H12A:350 PLEKHN1:661 ZFP36L1:1503 UPF1:9221.5 TRIM71:9221.5 RC3H1:9221.5
2-Oxoglutarate Metabolic Process (GO:000 0.0035457 3'-UTR-mediated mRNA Destabilization (GO 0.0606200 3'-UTR-mediated mRNA Stabilization (GO:0 -0.126629 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625373 5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005757 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408	870 14 322 15 2774 18 042 14 3552 5 1952 5 881 2	9.634e-01 4.163e-01 6.292e-02 4.179e-01 1.795e-01	9.999e-01 9.999e-01 9.999e-01	PHYH:91 IDH1:9221.5 GOT2:9221.5 MRPS36:9221.5 GOT1:9221.5 IDH2:9221.5 ZC3H12A:350 PLEKHN1:661 ZFP36L1:1503 UPF1:9221.5 TRIM71:9221.5 RC3H1:9221.5
3'-UTR-mediated mRNA Destabilization (GO 0.0606200 3'-UTR-mediated mRNA Stabilization (GO:0 -0.126629 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625373 5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005753 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408	322 15 2774 18 042 14 8552 5 1952 5 881 2	4.163e-01 6.292e-02 4.179e-01 1.795e-01	9.999e-01 9.999e-01	ZC3H12A:350 PLEKHN1:661 ZFP36L1:1503 UPF1:9221.5 TRIM71:9221.5 RC3H1:9221.5
3'-UTR-mediated mRNA Stabilization (GO:0 -0.126629 3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625373 5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005753 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408	2774 18 042 14 3552 5 1952 5 881 2	6.292e-02 4.179e-01 1.795e-01	9.999e-01	
3'-Phosphoadenosine 5'-Phosphosulfate Me 0.0625373 5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005757 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATF6-mediated Unfolded Protein Response 0.2065814 ATP Biosynthetic Process (GO:0046034) -0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408	042 14 8552 5 1952 5 881 2	4.179e-01 1.795e-01		
5S Class rRNA Transcription By RNA Polym -0.173320 7-Methylguanosine RNA Capping (GO:000945 -0.187531 7-Methylguanosine Cap Hypermethylation (0.0005753 7-Methylguanosine mRNA Capping (GO:00063 -0.187531 ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATF6-mediated Unfolded Protein Response 0.2065814 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408	5552 5 1952 5 881 2	1.795e-01	0.0000	ENPP1:163 BPNT1:2259 PAPSS1:9221.5 PAPSS2:9221.5 SULT1C4:9221.5 SULT1A2:9221.5
7-Methylguanosine RNA Capping (GO:000945 7-Methylguanosine Cap Hypermethylation (0.0005757 7-Methylguanosine mRNA Capping (GO:00063 ADP Transport (GO:0015866) AMP Biosynthetic Process (GO:0006167) AMP Metabolic Process (GO:0046033) ATF6-mediated Unfolded Protein Response ATP Biosynthetic Process (GO:0006754) ATP Metabolic Process (GO:0046034) ATP Synthesis Coupled Electron Transport ATP Transport (GO:0015867) -0.0035405	1952 5 881 2		9 999e-01	GTF3C4:1012 GTF3C3:1444 GTF3C2:9284.5 GTF3C5:9284.5 GTF3C6:9284.5 NA
7-Methylguanosine Cap Hypermethylation (7-Methylguanosine mRNA Capping (GO:00063 -0.187531. ADP Transport (GO:0015866) -0.051402. AMP Biosynthetic Process (GO:0006167) 0.0545029. AMP Metabolic Process (GO:0046033) 0.0425410. ATF6-mediated Unfolded Protein Response 0.2065814. ATP Biosynthetic Process (GO:0006754) 0.0027970. ATP Metabolic Process (GO:0046034) -0.009608. ATP Synthesis Coupled Electron Transport -0.087459. ATP Transport (GO:0015867) 0.0035408	881 2	1 464e-01	9.999e-01	RNMT:372 RAMAC:761 RNGTT:9284.5 NCBP1:9284.5 CMTR2:9284.5 NA
7-Methylguanosine mRNA Capping (GO:00063			9.999e-01	SNRPD2:9221.5 TGS1:9221.5 NA NA NA
ADP Transport (GO:0015866) -0.051402 AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATF6-mediated Unfolded Protein Response 0.2065814 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408			9.999e-01	RNMT:372 RAMAC:761 RNGTT:9284.5 NCBP1:9284.5 CMTR2:9284.5 NA
AMP Biosynthetic Process (GO:0006167) 0.0545029 AMP Metabolic Process (GO:0046033) 0.0425410 ATF6-mediated Unfolded Protein Response 0.2065814 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408			9.999e-01	SLC25A25:2552 SLC25A4:9284.5 SLC25A42:9284.5 SLC25A41:9284.5 SLC25A24:9284.5 SLC25A5:9284.5
AMP Metabolic Process (GO:0046033) 0.0425410 ATF6-mediated Unfolded Protein Response 0.2065814 ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408			9.999e-01	PFAS:657 NUDT2:932 PAICS:9221.5 ATIC:9221.5 ADSS1:9221.5 ADSS2:9221.5
ATF6-mediated Unfolded Protein Response ATP Biosynthetic Process (GO:0006754) ATP Metabolic Process (GO:0046034) ATP Synthesis Coupled Electron Transport ATP Transport (GO:0015867) 0.2065814 0.0027970 0.0027970 0.0035409			9.999e-01	NUDT2:932 AMPD1:1014 ADSS1:9221.5 ADSS2:9221.5 NT5C1A:9221.5 AMPD2:9221.5
ATP Biosynthetic Process (GO:0006754) 0.0027970 ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408		7.969e-02		DDIT3:418 MBTPS2:1927 MBTPS1:2474 XBP1:9221.5 ATF6B:9221.5 CREBZF:9221.5
ATP Metabolic Process (GO:0046034) -0.009608 ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035408			9.999e-01	SLC25A13:587 NUDT2:932 VPS9D1:9221.5 ATP5PF:9221.5 ATP5PD:9221.5 ATP5PB:9221.5
ATP Synthesis Coupled Electron Transport -0.087459 ATP Transport (GO:0015867) 0.0035405			9.999e-01	TGFB1:97 HSPA1A:347 ATP1B1:1174 NT5E:1263 HSPA1B:1321 PRKAG2:2356
ATP Transport (GO:0015867) 0.0035405			9.999e-01	NDUFA12:1131 NDUFB6:9284.5 NDUFS2:9284.5 NDUFV3:9284.5 NDUFV1:9284.5 NA
		9.647e-01		CALHM1:89 CALHM3:2522 SLC25A4:9221.5 SLC25A42:9221.5 SLC25A41:9221.5 SLC25A24:9221.5
AV 11006 CEII ACIIOITT OIETIIIAI 130.000001			9.999e-01	CACNA1G:303 TRPM4:2468 SCN5A:2580 CACNB2:9221.5 SCN4B:9221.5 SCN10A:18349
AV Node Cell To Bundle Of His Cell Commu 0.210037	970 6	7.479e-02		GJC3:536 GJD3:1334 SCN5A:2580 CXADR:9221.5 GJC1:9221.5 GJA5:9221.5
Arp2/3 Complex–Mediated Actin Nucleation 0.0523929	592 15	4.824e-01	9.999e-01	WHAMM:1030 WIPF3:1539 JMY:1654 TRIM27:2519 ACTR3:9221.5 ARPC1B:9221.5
B Cell Activation (GO:0042113) -0.002605	3386 89	9.324e-01		PHB2:199 CR2:655 FLT3:853 FCRLA:978 CASP8:1005 IFNK:1068
B Cell Activation Involved In Immune Res 0.0636950	213 14		9.999e-01	GPR183:555 LIG4:606 CD40LG:1224 IFNB1:9221.5 C17ORF99:9221.5 CD180:9221.5
B Cell Chemotaxis (GO:0035754) 0.0787344	324 5	5.420e-01	9.999e-01	HSD3B7:2000 PIK3CD:9221.5 CXCL13:9221.5 CYP7B1:9221.5 GAS6:9221.5 NA
B Cell Differentiation (GO:0030183) -0.003913	8675 66	9.125e-01	9.999e-01	CR2:655 FLT3:853 IFNK:1068 DCAF1:1231 VCAM1:1260 ITGA4:1477
B Cell Homeostasis (GO:0001782) 0.0005760	783 9	9.952e-01	9.999e-01	MEF2C:9221.5 GAPT:9221.5 DOCK11:9221.5 LYN:9221.5 DOCK10:9221.5 TNFRSF13B:9221.5
B Cell Mediated Immunity (GO:0019724) 0.0600675	078 14	4.365e-01	9.999e-01	SLA2:529 CD74:1137 IL21R:1639 CD70:9221.5 FCGR2B:9221.5 CD19:9221.5
B Cell Proliferation (GO:0042100) -0.013511	31	7.946e-01	9.999e-01	CR2:655 IFNK:1068 IFNA4:1801 IFNA7:2248 IL10:9284.5 CD70:9284.5
B Cell Receptor Signaling Pathway (GO:00 0.0373077	305 32	4.653e-01	9.999e-01	BTK:447 PLCG2:960 NFAM1:1463 BCAR1:1497 LCK:1704 BCL2:2418
BMP Signaling Pathway (GO:0030509) 0.0172347	396 61	6.418e-01	9.999e-01	GDF3:105 AMHR2:378 INHBA:618 RGMB:790 SLC39A5:888 HIVEP1:1190
C-terminal Protein Amino Acid Modificati -0.006016	9575 11	9.449e-01	9.999e-01	ATG5:992 AGBL5:9284.5 GPLD1:9284.5 ICMT:9284.5 AGTPBP1:9284.5 ATG16L1:9284.5
C-terminal Protein Deglutamylation (GO:0 0.0943438	670 4	5.134e-01	9.999e-01	FOLH1:2278 AGBL5:9221.5 AGTPBP1:9221.5 AGBL4:9221.5 NA NA
C-terminal Protein Lipidation (GO:000650 -0.111314	0656 4	4.407e-01	9.999e-01	ATG5:992 GPLD1:9284.5 ATG16L1:9284.5 ATG7:9284.5 NA NA
C4-dicarboxylate Transport (GO:0015740) 0.1173923	221 12	1.591e-01	9.999e-01	LRRC8E:158 SLC25A13:587 SLC25A18:644 SLC1A6:1113 SLC13A2:9221.5 SLC13A5:9221.5
CD4-positive, Alpha-Beta T Cell Activati -0.227882	9542 4	1.144e-01	9.999e-01	HMGB1:551 TNFSF4:1083 STOML2:9284.5 NKG7:9284.5 NA NA
CD40 Signaling Pathway (GO:0023035) -0.120773	3910 7	2.685e-01	9.999e-01	PHB2:199 CD86:1566 RNF31:2310 ITGB1:9284.5 TNIP2:9284.5 ITGA5:9284.5
CENP-A Containing Chromatin Assembly (GO 0.0918226	542 6	4.360e-01	9.999e-01	HJURP:95 NASP:1138 CENPW:9221.5 CENPI:9221.5 OIP5:9221.5 MIS18A:16349
COPI Coating Of Golgi Vesicle (GO:004820 -0.152328	J	2.381e-01		

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pvai	p.aaj	gene.vais
MP0008875 abnormal xenobiotic pharmacok	0.176566733	20	6.330e-03	9.112e-01	ADH7:223 ABCC3:298 AHR:321 POR:705 ABCC2:841 SLC47A1:991
MP0002086 abnormal extraembryonic tissu	-0.035487163	487	9.569e-03	9.112e-01	MET:5 SETD2:27 CDH2:87 TGFB1:97 IGF2:105 FGG:135
MP0002080 prenatal lethality	-0.024703358	1338	6.387e-03	9.112e-01	HERC2:1 MET:5 NUP133:7 EHMT1:14 LTN1:15 SETD2:27
MP0003252 abnormal bile duct	0.149938539	25	9.572e-03	9.112e-01	MAP3K14:281 AHR:321 PKHD1:341 CYP8B1:371 ABCG5:428 ABCB4:563
MP0001666 abnormal nutrient absorption	0.126160722	46	3.162e-03	9.112e-01	TREH:166 SLC2A4:180 SLC10A2:273 CYP8B1:371 ABCG5:428 NPC1L1:553
MP0008438 abnormal cutaneous collagen	-0.064579574	15	3.869e-01	9.188e-01	FBN1:658 DCN:782 TNXB:2241 PLOD3:9284.5 THBS2:9284.5 COL3A1:9284.5
MP0002909 abnormal adrenal gland	-0.059922063	23	3.205e-01	9.188e-01	LRRK2:64 KCNK3:1348 DRD5:1952 CHGB:9284.5 FOXA1:9284.5 CHGA:9284.5
MP0001730 embryonic growth arrest	-0.019075390	182	3.807e-01	9.188e-01	NUP133:7 RBL2:80 DCTN1:147 PIK3CA:308 FLT1:312 CHD8:530
MP0001731 abnormal postnatal growth	-0.007862130	592	5.311e-01	9.188e-01	MET:5 LTN1:15 COL7A1:25 SUMF1:76 AREG:95 IGF2:105
MP0002210 abnormal sex determination	-0.034019461	349	3.308e-02	9.188e-01	SPAG16:103 OCA2:170 TAF4B:175 SYCP3:196 UBE3A:201 SLC14A1:228
MP0000598 abnormal liver morphology	-0.016970750	482	2.175e-01	9.188e-01	MET:5 APOA1:13 TGFB1:97 F11:106 OCA2:170 ASAH1:211
MP0005334 abnormal fat pad	-0.035393033	152	1.361e-01	9.188e-01	IGFBP3:111 OCA2:170 INSR:231 IL18:321 GPR12:423 HDC:471
MP0005330 cardiomyopathy	-0.049576922	70		9.188e-01	MYOZ2:209 HEXIM1:834 IGF1R:878 MCOLN1:1079 CAV1:1483 ERBB4:1484
MP0001765 abnormal ion homeostasis	-0.034197306	110	2.187e-01		PTH1R:307 CALCR:314 SLC24A2:505 PTGER4:537 FGF23:693 PRLR:805
MP0004043 abnormal pH regulation	-0.070367133	13		9.188e-01	SLC26A7:819 SLC4A4:1153 SLC4A10:1779 HIF1AN:9284.5 SOD2:9284.5 ERCC1:9284
MP0002837 dystrophic cardiac calcinosis	0.192311544	9	4.585e-02		SLC2A4:180 MYBPC3:1006 MMP9:1239 SCG5:2193 GSTZ1:9221.5 DNM1L:9221.5
MP0002066 abnormal motor capabilities/c	-0.009175861	1087		9.188e-01	HERC2:1 GABRA5:2 MET:5 EHMT1:14 LTN1:15 GIGYF2:39
MP0005248 abnormal Harderian gland	-0.059567316	16		9.188e-01	PRLR:805 ALDH1A3:1117 RXRA:1467 MITF:2635 RARA:9284.5 CDKN1A:9284.5
MP0004133 heterotaxia	0.042533937	32		9.188e-01	LAMA5:1018 TGIF1:1058 PITX2:1799 CFC1:2075 DAND5:2179 PKD2:2310
MP0001529 abnormal vocalization	0.042333937	19		9.188e-01	CHRM5:706 PLP1:1637 MKKS:1837 FZD3:1865 DRD2:9221.5 DHCR7:9221.5
MP0004134 abnormal chest morphology	-0.091543291	28	9.420e-02		FBN1:658 UNCX:1175 CACNA1S:1612 COL1A1:1730 CBFB:2044 NF1:2190
, ,,		508		9.188e-01	IRAK2:36 PTAFR:50 BIRC3:67 FOXN1:78 PHYH:91 FFAR2:115
MP0004026 charmal muscle relevation	0.009797878				
MP0004036 abnormal muscle relaxation	0.055103557 -0.021796266	41 68		9.188e-01 9.188e-01	CASQ1:219 MYLK:345 ATP2A3:517 MYBPC3:1006 PRKG1:1059 CLCN1:1983 MET:5 RBL2:80 PAX1:291 IGF1R:878 LATS2:1019 TWIST1:1253
MP000733 abnormal muscle development					ATP1A2:1235 DSCAM:1700 TAS1R2:1772 TAS1R1:2219 L1CAM:9221.5 SLC12A5:922
MP0005423 abnormal somatic nervous	0.111644756	11		9.188e-01	NUP133:7 EHMT1:14 SETD2:27 RAD54L2:63 MDM4:85 CDH2:87
MP0003984 embryonic growth retardation	-0.029609923	337	6.803e-02		CDK5R1:411 BDKRB1:626 MRGPRD:792 TRPV3:948 NMUR2:1044 MMP24:1273
MP0002733 abnormal thermal nociception	0.030577074	94		9.188e-01	
MP0005387 immune system phenotype	0.044820200	98		9.188e-01	FOXN1:78 SIGLEC1:260 MAP3K14:281 AHR:321 JAK3:352 BTK:447
MP0005386 behavior/neurological phenoty	0.034880860	96		9.188e-01	ACACB:513 CHRM5:706 BHLHE22:769 CCKAR:915 TMIE:1320 PPARGC1A:1375
MP0005385 cardiovascular system phenoty	-0.020032249	181		9.188e-01	CDH2:87 F11:106 DDAH1:183 MYOZ2:209 SOX9:515 VAV3:520
MP0001544 abnormal cardiovascular syste	-0.020032249	181		9.188e-01	CDH2:87 F11:106 DDAH1:183 MYOZ2:209 SOX9:515 VAV3:520
MP0005380 embryogenesis phenotype	-0.022571088	418	1.243e-01		NUP133:7 EHMT1:14 SETD2:27 RAD54L2:63 MDM4:85 CDH2:87
MP0008995 early reproductive senescence	0.049889460	16	4.900e-01		PER2:174 AMHR2:378 CYP17A1:1114 PER1:1958 SFTPC:2394 ESR1:9221.5
MP0005389 reproductive system phenotype	-0.048281653	70		9.188e-01	HOXA10:243 BAX:283 CCNE1:466 LHX9:571 FGF23:693 PRLR:805
MP0005388 respiratory system phenotype	-0.030709699	130		9.188e-01	TRPS1:28 CYLD:42 F11:106 CRH:215 PTGER4:537 HMGB1:551
MP0000428 abnormal craniofacial morphol	-0.044288778	79	1.758e-01	9.188e-01	SUMF1:76 SOX9:515 LTBP3:637 OTX2:1372 ITGA4:1477 FOXG1:1623
MP0005636 abnormal mineral homeostasis	-0.021119457	141	3.911e-01	9.188e-01	ACO1:263 PTH1R:307 CALCR:314 NME2:396 ATOX1:726 PRLR:805
MP0009703 decreased birth body	-0.040321797	125	1.226e-01	9.188e-01	CYLD:42 IGF2:105 INSR:231 HSPA1A:347 NIPBL:610 YY1:787
MP0002163 abnormal gland morphology	0.104645445	11		9.188e-01	ZEB1:634 SCG5:2193 CCR7:2222 CFTR:2557 FAS:9221.5 PAX7:9221.5
MP0002161 abnormal fertility/fecundity	-0.014217376	862	1.839e-01	9.188e-01	HERC2:1 MC4R:61 SPAG16:103 ADCY10:122 FGG:135 OCA2:170

Geneset	stat	num.genes	pval	p.adj	gene.vals
testis	-0.03601205	1632	6.813e-06	3.679e-04	CNGB3:8 CRISP1:10 SCN9A:11 NAA80:21 FSIP2:23 PRPS2:26
leg.skin	0.06168184	286	3.874e-04	1.046e-02	PSAPL1:41 A2ML1:42 ARHGAP40:46 GGT6:64 FOXN1:78 LAMB4:107
peyers.patch	0.06437525	196	2.045e-03	3.681e-02	ACY3:13 REG4:23 RNF186:121 TREH:166 TMEM236:191 APOBEC1:236
esophagus.mucosa	0.04834662	261	7.784e-03	1.051e-01	A2ML1:42 FOXN1:78 RAB11FIP1:138 CLIC3:156 ADGRF1:189 SPRR2A:204
stomach	0.07349060	99	1.183e-02	1.277e-01	PGC:25 PSAPL1:41 CBLIF:48 CHIA:55 AKR7L:192 PGA4:333
suprapubic.skin	0.04405487	257	1.608e-02	1.448e-01	PSAPL1:41 A2ML1:42 GGT6:64 FOXN1:78 LAMB4:107 KRT39:139
vagina	0.06069207	118	2.340e-02	1.805e-01	A2ML1:42 FOXN1:78 ALOX15B:96 CRYBG2:222 EVPL:297 ENDOU:328
Brodmann.area.9	-0.04767114	184	2.682e-02	1.810e-01	PLPPR5:115 B3GALT2:203 DCLK1:261 KCNV1:355 ATRNL1:392 KCNC2:443
EBV.lymphocyte	-0.01874747	751	9.016e-02	5.410e-01	BFSP2:93 CDC25A:150 TAF4B:175 ORC6:193 ZGRF1:220 NETO2:221
cerebellar.hemisphere	-0.01805609	532	1.633e-01	6.090e-01	SCN2A:16 GPRIN1:78 OLFM3:104 APBA2:107 SPRN:129 MAP7D2:164
cortex.kidney	0.03698149	131	1.459e-01	6.090e-01	RNF186:121 KLHDC7A:161 PKHD1:341 SLC4A9:401 TINAG:448 KIF12:561
hypothalamus	-0.04399431	78	1.805e-01	6.090e-01	SCN9A:11 MC4R:61 GABRG3:148 CALCB:205 MAGEL2:234 CALCR:314
liver	0.02333994	396	1.167e-01	6.090e-01	SERPINA7:129 THPO:182 CPN2:186 CP:202 HAMP:271 SHBG:278
pancreas	0.03666506	117	1.727e-01	6.090e-01	RNF186:121 CUZD1:412 CELA2B:468 ERP27:535 CTRB1:608 CELA3B:611
sigmoid.colon	0.06027260	51	1.372e-01	6.090e-01	MYLK:345 TACR2:348 PDE9A:376 GUCY1A1:464 PLA2G2C:497 MRGPRD:792
transverse.colon	0.03162656	168	1.600e-01	6.090e-01	LRRC31:97 RXFP4:114 RNF186:121 TMEM236:191 KRT20:322 AGR3:349
left.ventricle	0.04536001	69	1.938e-01	6.097e-01	MYZAP:541 MYH7B:574 TNNI3K:760 MYBPC3:1006 RPL3L:1068 XIRP1:1324
spleen	0.01975573	362	2.032e-01	6.097e-01	SPNS3:45 CROCC2:49 ARHGAP4:62 GDF3:105 LIPA:287 RUBCNL:364
aorta	0.02664415	156	2.537e-01	6.639e-01	MYH10:28 ERG:228 C1QTNF8:336 SUSD5:351 HMCN1:578 KALRN:739
blood	0.01803789	342	2.582e-01	6.639e-01	BPI:44 PTAFR:50 PRTN3:92 FFAR2:115 SHKBP1:118 VNN2:123
subcutaneous.adipose	0.03698513	81	2.513e-01	6.639e-01	GPBAR1:31 SIGLEC1:260 ACACB:513 LGALS12:802 FOLR2:910 LIPE:987
skeletal.muscle	0.01930471	258	2.906e-01	6.902e-01	SVIL:103 SLC2A4:180 TXLNB:215 CASQ1:219 FLNC:389 ANKRD23:477
uterus	-0.03862606	62	2.940e-01	6.902e-01	HOXA10:243 MOXD1:533 SSC5D:771 TRPC4:984 HOXA11:1528 WT1:1698
C1.spinal.cord	-0.02139661	194	3.078e-01	6.926e-01	PCSK6:244 PDE6B:247 UGT8:269 SEC14L5:290 VXN:500 SLC24A2:505
atrium.auricle	0.02471295	95	4.069e-01	7.324e-01	ALPK2:56 TBX5:150 HAMP:271 CCDC141:543 METTL7B:747 TNNI3K:760
cerebellum	-0.01279336	403	3.859e-01	7.324e-01	CLEC4G:60 SPRN:129 CACNA1B:151 CATSPER2:191 ZNF781:346 TRIM73:351
esophagus.muscularis.mucosa	0.05012469	28	3.591e-01	7.324e-01	PRUNE2:2 KCNMB1:438 RGMB:790 CYSLTR1:2116 PGM5:2373 CHRM3:9221.5
ovary	0.02262915	118	3.980e-01	7.324e-01	TSHZ2:143 LRRC17:485 NR4A1:757 FHL2:849 ANGPTL5:869 TENM4:1017
tibial.artery	0.02444233	114	3.694e-01	7.324e-01	TNC:22 TMTC1:253 SUSD5:351 HRCT1:406 TRABD2B:439 SYTL2:501
transformed.skin.fibroblast	-0.01554050	276	3.795e-01	7.324e-01	ADAMTS6:9 CD109:31 ATP2B1:56 ADAM12:181 CNTN3:224 SEC24D:257
bladder	-0.04047284	29	4.511e-01	7.690e-01	SLC14A1:228 WFDC13:483 TPSD1:928 AKR1B10:1799 ACER2:1955 ABCC4:9284.5
lung	0.01676052	158	4.699e-01	7.690e-01	SLC22A31:59 SHROOM4:93 HIGD1B:151 GPC3:193 ROS1:197 NKD2:363
substantia.nigra	0.06362618	11	4.651e-01	7.690e-01	CHRM5:706 SLC6A3:2331 DBX2:9221.5 FOXB1:9221.5 KCNE5:9221.5 KLHL1:9221.5
endocervix	0.01962956	76	5.552e-01	8.038e-01	LAMC3:127 PTPRU:137 STRA6:266 SNCAIP:274 PAMR1:413 XKR5:492
fallopian.tube	0.02323590	60	5.345e-01	8.038e-01	ADGRG4:1 CROCC2:49 ADAMTS3:429 VNN3:698 MRGPRD:792 HOXC5:1015
greater.omentum	0.02685459	38	5.673e-01	8.038e-01	RBP7:1527 ATF3:1732 ITLN1:1737 UPK3B:1868 ALOX15:1906 BARX1:2358
hippocampus.proper	0.04552200	13	5.700e-01	8.038e-01	CTXND1:1898 CABP7:2518 NEUROD2:9221.5 NEUROD6:9221.5 SLC17A7:9221.5 HRK:9221

NCDN:205 DACH2:282 SV2C:493 PTPN5:584 MINDY4B:633 WNT10B:1130

PRL:92 OR10AD1:180 CALCB:205 SAMD11:218 SPAG6:277 CRYBA2:327

ELF3:452 SOX9:515 FOXE3:639 LUM:975 OTX2:1372 FOXC1:1457

nucleus.accumbens

pituitary.gland

eye.development

0.01569460

-0.01021308

-0.01871307

104

232

5.818e-01 8.038e-01

5.954e-01 8.038e-01

5.919e-01 8.038e-01