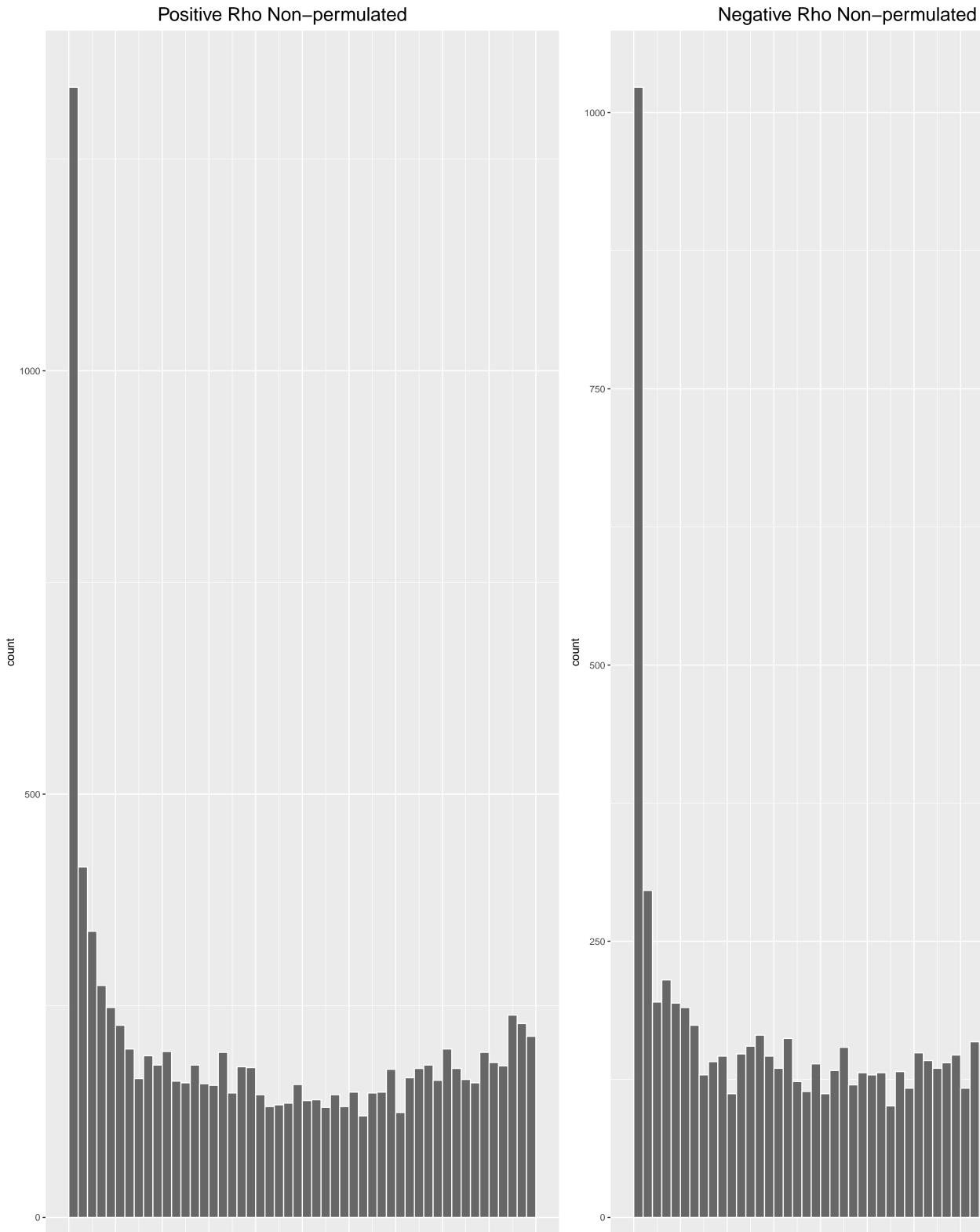
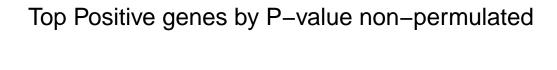
Gene	Rho	P	p.adj	qValueNoperm
CCPG1	-8.061186	7.555777e-16	1.417e-11	2.658e-07
MRGPRE	7.612440	2.689700e-14	2.266e-10	1.345e-06
PER2	7.573814	3.624238e-14	2.266e-10	1.345e-06
SHANK2	7.505582	6.115605e-14	2.868e-10	1.345e-06
AFDN	7.246365	4.281049e-13	1.439e-09	4.498e-06
SORL1	7.236534	4.602958e-13	1.439e-09	4.498e-06
USP43	7.180193	6.961293e-13	1.865e-09	4.998e-06
TET1	-7.106627	1.189133e-12	2.712e-09	5.510e-06
TMEM126B	-7.094171	1.301296e-12	2.712e-09	5.510e-06
TET2	-7.068486	1.566336e-12	2.938e-09	5.510e-06
TRANK1	6.898544	5.253838e-12	8.958e-09	1.527e-05
PKP1	6.790265	1.119281e-11	1.645e-08	2.373e-05
SLC17A4	6.787609	1.140073e-11	1.645e-08	2.373e-05
MKI67	6.700218	2.081088e-11	2.724e-08	3.285e-05
UBAP2	-6.693525	2.178578e-11	2.724e-08	3.285e-05
MYH2	6.679935	2.390477e-11	2.802e-08	3.285e-05
FAM13B	-6.617648	3.649594e-11	4.027e-08	4.220e-05
GPR37L1	6.608339	3.886546e-11	4.050e-08	4.220e-05
TRPM5	6.583262	4.602355e-11	4.543e-08	4.308e-05
FAAP100	6.573197	4.924612e-11	4.618e-08	4.308e-05
PLEC	6.559438	5.401105e-11	4.824e-08	4.308e-05
SPATA2L	6.495394	8.281643e-11	7.060e-08	5.835e-05
SMIM26	-6.486677	8.774997e-11	7.156e-08	5.835e-05
ADAMTS20	-6.441540	1.182676e-10	8.873e-08	6.605e-05
SRFBP1	-6.445909	1.149095e-10	8.873e-08	6.605e-05
J	3		2.0.00	3.0000 00







_{0.5} p Values

1000	_										
750											
count											
8 ₅₀₀											
250											
0	_										

Top Negative genes by P-value non-permulated

0.5 p Values

0.4

0.3

0.0

Gene	Rho	Р	p.adj	qValueNoperm
MRGPRE	7.612440	2.689700e-14	2.266e-10	1.345e-06
PER2	7.573814	3.624238e-14	2.266e-10	1.345e-06
SHANK2	7.505582	6.115605e-14	2.868e-10	1.345e-06
AFDN	7.246365	4.281049e-13	1.439e-09	4.498e-06
SORL1	7.236534	4.602958e-13	1.439e-09	4.498e-06
USP43	7.180193	6.961293e-13	1.865e-09	4.998e-06
TRANK1	6.898544	5.253838e-12	8.958e-09	1.527e-05
PKP1	6.790265	1.119281e-11	1.645e-08	2.373e-05
SLC17A4	6.787609	1.140073e-11	1.645e-08	2.373e-05
MKI67	6.700218	2.081088e-11	2.724e-08	3.285e-05

CCPG1	-8.061186	7.555777e-16	1.417e-11	2.658e-07
TET1	-7.106627	1.189133e-12	2.712e-09	5.510e-06
TMEM126B	-7.094171	1.301296e-12	2.712e-09	5.510e-06
TET2	-7.068486	1.566336e-12	2.938e-09	5.510e-06
UBAP2	-6.693525	2.178578e-11	2.724e-08	3.285e-05
FAM13B	-6.617648	3.649594e-11	4.027e-08	4.220e-05
SMIM26	-6.486677	8.774997e-11	7.156e-08	5.835e-05
ADAMTS20	-6.441540	1.182676e-10	8.873e-08	6.605e-05
SRFBP1	-6.445909	1.149095e-10	8.873e-08	6.605e-05
DLGAP5	-6.411111	1.444629e-10	1.004e-07	6.605e-05

Gene Rho P p.adj qValueNoperm

Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO:	-0.34082393	49	1.587e-16	4.290e-13	TMEM126B:3 NDUFA11:49 ECSIT:63 NDUFAF1:73 NDUFB8:148 NDUFB5:190
Mitochondrial Respiratory Chain Complex	-0.34082393	49	1.587e-16	4.290e-13	TMEM126B:3 NDUFA11:49 ECSIT:63 NDUFAF1:73 NDUFB8:148 NDUFB5:190
Mitochondrial Gene Expression (GO:014005	-0.23505441	102	2.542e-16	4.582e-13	TFAM:14 TEFM:93 POLRMT:101 TFB2M:112 TWNK:217 MRPS14:376
Mitochondrial Translation (GO:0032543)	-0.22711501	97	1.150e-14	1.555e-11	MRPS14:376 GADD45GIP1:477 FASTKD2:485 MRPS9:488 MRPS5:509 MRPL22:559
Mitochondrial ATP Synthesis Coupled Elec	-0.27220331	65	3.343e-14	3.615e-11	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Aerobic Electron Transport Chain (GO:001	-0.27107537	64	6.639e-14	5.983e-11	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Mitochondrial Respiratory Chain Complex	-0.23698959	82	1.244e-13	9.608e-11	TMEM126B:3 NDUFA11:49 ECSIT:63 NDUFAF1:73 NDUFB8:148 NDUFB5:190
Intermediate Filament Organization (GO:0	0.25637844	65	9.107e-13	6.155e-10	PKP1:8 DSP:30 KRT17:105 KRT80:119 KRT20:129 DES:220
Monoatomic Cation Transmembrane Transpor	0.12346999	277	1.821e-12	1.094e-09	TRPM5:13 TRPV6:31 SLC24A3:125 KCNQ3:126 CACNA1S:152 SLC24A4:169
Oxidative Phosphorylation (GO:0006119)	-0.26105936	59	4.166e-12	2.252e-09	NDUFA11:49 TEFM:93 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422
Proton Motive Force-Driven Mitochondrial	-0.27879639	50	9.319e-12	4.581e-09	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Translation (GO:0006412)	-0.13473174	208	2.376e-11	1.071e-08	MRPS14:376 ZAR1:424 HBS1L:440 GADD45GIP1:477 FASTKD2:485 MRPS9:488
Mitochondrial Electron Transport, NADH T	-0.32843823	33	6.670e-11	2.774e-08	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Proton Motive Force–Driven ATP Synthesis	-0.25205853	55	1.030e-10	3.976e-08	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Chemical Synaptic Transmission (GO:00072	0.11476942	263	1.697e-10	6.118e-08	KCNQ3:126 HRH2:130 CACNA1E:166 GRIK4:236 HTR5A:246 SLC18A3:251
Inorganic Cation Transmembrane Transport	0.11013440	280	2.622e-10	8.860e-08	TRPM5:13 TRPV6:31 SLC24A3:125 KCNQ3:126 CACNA1S:152 SLC24A4:169
Cilium Organization (GO:0044782)	-0.12170787	221	5.042e-10	1.604e-07	KIAA0586:44 KIF27:46 ARL13B:87 GBF1:126 CENPJ:149 IQCG:231
tRNA Modification (GO:0006400)	-0.21526005	67	1.137e-09	3.416e-07	MTO1:174 TYW5:244 PUS10:301 TRMT10A:361 METTL8:364 DTWD1:394
Cilium Assembly (GO:0060271)	-0.11396835	232	2.474e-09	7.040e-07	TBC1D32:31 KIAA0586:44 KIF27:46 ARL13B:87 GBF1:126 CENPJ:149
Muscle Contraction (GO:0006936)	0.17646929	91	6.161e-09	1.666e-06	MYH2:11 MYH13:54 MYOF:127 CACNA1S:152 DES:220 MYH1:239
Cellular Respiration (GO:0045333)	-0.18370358	82	9.167e-09	2.360e-06	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Aerobic Respiration (GO:0009060)	-0.21956862	57	1.001e-08	2.460e-06	NDUFA11:49 TEFM:93 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422
Calcium Ion Transmembrane Import Into Cy	0.18574261	79	1.180e-08	2.774e-06	TRPV6:31 CACNA1I:148 CACNA1S:152 CACNA1E:166 SLC24A4:169 CACNA1G:287
Calcium Ion Transport (GO:0006816)	0.15520251	110	1.950e-08	4.393e-06	TRPM5:13 TRPV6:31 SLC24A3:125 CACNA1S:152 SLC24A4:169 CACNA1G:287
Sensory Perception Of Smell (GO:0007608)	0.11040761	208	4.383e-08	9.481e-06	SLC24A4:169 OR10A2:211 OR2H2:369 OR10D3:475 DRD2:522 OR10C1:636
Potassium Ion Transmembrane Transport (G	0.13547872	135	5.751e-08	1.196e-05	SLC24A3:125 KCNQ3:126 SLC24A4:169 KCNK10:225 KCNJ12:259 KCNH2:365
Potassium Ion Transport (GO:0006813)	0.13631751	121	2.319e-07	4.645e-05	SLC24A3:125 KCNQ3:126 SLC24A4:169 KCNK10:225 KCNJ12:259 KCNH2:365
Positive Regulation Of DNA Metabolic Pro	-0.14608275	104	2.729e-07	5.269e-05	RNF168:52 STON1:61 SMCHD1:136 ABRAXAS1:141 DNA2:193 UIMC1:291
Response To Calcium Ion (GO:0051592)	0.14622412	100	4.487e-07	8.365e-05	SYT2:18 TRPV6:31 ADCY1:32 SYT8:179 RASGRP2:240 SYT6:275
Neuron Projection Morphogenesis (GO:0048	0.12392007	139	4.761e-07	8.582e-05	ADGRB1:39 NRCAM:96 CTTN:149 TRIO:200 FLRT1:218 TNN:252
DNA Repair (GO:0006281)	-0.08740794	281	5.052e-07	8.811e-05	RNF168:52 STON1:61 USP44:64 TOPBP1:123 ABRAXAS1:141 DNA2:193
Cardiac Conduction (GO:0061337)	0.21419307	45	6.722e-07	1.136e-04	DSP:30 DSG2:104 CACNA1G:287 KCNH2:365 DSC2:569 CACNB2:890
Regulation Of Heart Rate By Cardiac Cond	0.22627703	40	7.413e-07	1.215e-04	DSP:30 DSG2:104 CACNA1G:287 KCNH2:365 DSC2:569 CACNB2:890
tRNA Methylation (GO:0030488)	-0.23693916	36	8.735e-07	1.389e-04	MTO1:174 TRMT61B:285 TRMT10C:293 TRMT10A:361 METTL8:364 FTSJ1:505
Anterograde Trans-Synaptic Signaling (GO	0.10311036	190	1.010e-06	1.560e-04	KCNQ3:126 HRH2:130 CACNA1E:166 GRIK4:236 HTR5A:246 SLC18A3:251
Modulation Of Chemical Synaptic Transmis	0.12903473	118	1.332e-06	2.001e-04	MYOF:127 TRIO:200 GRIK4:236 OTOF:272 GRM2:438 DRD2:522
Calcium Ion Transmembrane Transport (GO:	0.15800063	78	1.434e-06	2.095e-04	TRPM5:13 TRPV6:31 SLC24A3:125 CACNA1S:152 SLC24A4:169 CACNA1G:287
Cellular Response To Calcium Ion (GO:007	0.16811948	67	1.980e-06	2.818e-04	SYT2:18 ADCY1:32 SYT8:179 RASGRP2:240 SYT6:275 CAPN3:448
Metal Ion Transport (GO:0030001)	0.10488688	169	2.671e-06	3.702e-04	SLC17A4:9 TRPV6:31 CACNA1S:152 KCNJ12:259 CHRNA4:393 ITPR1:416
Mitochondrial RNA Metabolic Process (GO:	-0.29839148	20	3.852e-06	5.207e-04	TFAM:14 TEFM:93 POLRMT:101 TFB2M:112 TWNK:217 FASTKD1:431

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_KERATINIZATION	0.22485940	214	9.785e-30	6.355e-26	PKP1:8 DSP:30 KRTAP6-1:34 KRTAP10-1:83 KRTAP10-3:84 DSG2:104
FISCHER_DREAM_TARGETS	-0.10069796	924	5.494e-25	1.784e-21	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 CEP192:39 SGO2:62
JOHNSTONE_PARVB_TARGETS_3_DN	-0.09707511	794	2.019e-20	4.369e-17	CCPG1:1 UBAP2:5 FAM13B:6 SRFBP1:8 DLGAP5:10 TFAM:14
MARSON_BOUND_BY_E2F4_UNSTIMULATED	-0.10201173	664	4.108e-19	6.670e-16	UBAP2:5 DLGAP5:10 PARPBP:29 LRRC40:33 SGO2:62 DNMT1:74
REACTOME_NEURONAL_SYSTEM	0.13056085	394	6.861e-19	8.911e-16	SHANK2:3 SYT2:18 PPFIA1:23 ADCY1:32 GJA10:91 PPFIA4:107
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.22527613	128	1.407e-18	1.522e-15	PKP1:8 DSP:30 DSG2:104 KRT17:105 KRT80:119 KRT20:129
REACTOME_SENSORY_PERCEPTION	0.10279761	603	8.354e-18	7.750e-15	TRPM5:13 RGS9:52 MYO15A:68 OR10A2:211 OR51E2:230 OTOF:272
HAMAI_APOPTOSIS_VIA_TRAIL_UP	-0.09519660	625	5.595e-16	4.542e-13	FAM13B:6 DLGAP5:10 CEP350:22 ATAD2:27 PARPBP:29 KIF18A:30
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.09655581	601	7.640e-16	5.513e-13	CCPG1:1 DLGAP5:10 LRPPRC:13 TFAM:14 ATAD2:27 PARPBP:29
MARTENS_TRETINOIN_RESPONSE_UP	0.08438836	788	1.041e-15	5.647e-13	SHANK2:3 CEP170B:19 TRIM29:35 AXIN2:98 JAG2:138 RNF186:139
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	-0.24471771	90	1.043e-15	5.647e-13	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 ECSIT:63 NDUFAF1:73
DODD_NASOPHARYNGEAL_CARCINOMA_DN	-0.06723991	1278	1.042e-15	5.647e-13	TET1:2 DLGAP5:10 LRPPRC:13 TFAM:14 MTPAP:25 ATAD2:27
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	-0.33691063	47	1.345e-15	6.720e-13	TMEM126B:3 TIMMDC1:56 ECSIT:63 NDUFAF1:73 TMEM70:95 NDUFB8:148
REACTOME_DEVELOPMENTAL_BIOLOGY	0.07004333	1097	7.012e-15	3.253e-12	PKP1:8 DSP:30 KRTAP6-1:34 SEMA7A:58 KRTAP10-1:83 KRTAP10-3:84
REACTOME_MITOCHONDRIAL_TRANSLATION	-0.23115179	93	1.344e-14	5.820e-12	MRPS35:322 MRPS14:376 GADD45GIP1:477 MRPS9:488 MRPS5:509 MRPL22:559
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	-0.20979641	112	1.764e-14	6.737e-12	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 ECSIT:63 NDUFAF1:73
REACTOME_COMPLEX_I_BIOGENESIS	-0.31996423	48	1.739e-14	6.737e-12	TMEM126B:3 NDUFA11:49 TIMMDC1:56 ECSIT:63 NDUFAF1:73 NDUFB8:148
REACTOME_SIGNALING_BY_GPCR	0.08400692	687	7.518e-14	2.712e-11	GPR37L1:12 TAAR6:28 ADCY1:32 RGS9:52 CALCA:63 TIAM1:111
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.13432814	253	2.006e-13	6.856e-11	GPR37L1:12 HRH2:130 FFAR2:150 GPR68:174 GPER1:188 GPR35:205
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	0.11476644	340	3.870e-13	1.256e-10	SYT2:18 BNC1:26 ADGRB1:39 LAD1:42 SEMA7A:58 JAG2:138
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	0.08850454	577	4.363e-13	1.349e-10	ADGRB1:39 LAD1:42 DSG2:104 KCNQ3:126 HRH2:130 JAG2:138
REACTOME_CELL_CYCLE	-0.08305517	652	5.582e-13	1.648e-10	DAXX:12 KIF18A:30 CEP192:39 SYNE2:43 RNF168:52 SGO2:62
KEGG_CALCIUM_SIGNALING_PATHWAY	0.15946070	168	1.036e-12	2.925e-10	ADCY1:32 HRH2:130 CACNA1I:148 CACNA1S:152 CACNA1E:166 HTR5A:246
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	0.10049285	426	1.263e-12	3.419e-10	SYT2:18 ADGRB1:39 SEMA7A:58 ZBTB16:76 KCNQ3:126 CLMP:143
BENPORATH_ES_WITH_H3K27ME3	0.06463374	1063	1.462e-12	3.797e-10	PKP1:8 PLEC:15 BNC1:26 PHLDB1:45 RGS9:52 CALCA:63
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	-0.06071051	1204	1.845e-12	4.608e-10	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 LARP4:38 SGO2:62
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.33247509	37	2.593e-12	6.233e-10	INTS1:109 GPER1:188 ZFAND2A:199 SNX8:387 MAD1L1:459 AP5Z1:508
REACTOME_MUSCLE_CONTRACTION	0.14500232	196	2.687e-12	6.233e-10	MYBPC2:144 MME:145 CASQ1:147 CACNA1I:148 DES:220 KCNK10:225
REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.10246751	390	4.139e-12	9.269e-10	OR10A2:211 OR51E2:230 OR4K15:315 OR2H2:369 OR9K2:400 OR10D3:475
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_U	-0.08599122	558	4.358e-12	9.433e-10	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 CEP192:39 KIAA0586:44
YOSHIMURA_MAPK8_TARGETS_UP	0.05905172	1226	4.813e-12	1.008e-09	AFDN:4 SYT2:18 ADH7:37 ARC:49 RGS9:52 CALCA:63
KEGG_OLFACTORY_TRANSDUCTION	0.10253300	377	8.933e-12	1.813e-09	OR10A2:211 OR51E2:230 OR4K15:315 OR2H2:369 OR9K2:400 OR6B3:501
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	-0.14435381	186	1.170e-11	2.302e-09	DLGAP5:10 PARPBP:29 KIF18A:30 SGO2:62 KIF22:90 KIF2C:108
WP_2Q37_COPY_NUMBER_VARIATION_SYNDROME	0.17186962	129	1.613e-11	3.080e-09	PER2:2 CALCA:63 PASK:65 KIF1A:161 GPR35:205 PPP1R7:244
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_I	-0.14567517	175	3.083e-11	5.720e-09	KIF2C:108 SPAG5:163 NEXN:164 GCNT3:201 FANCG:202 KIF20A:251
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	0.10550387	335	3.454e-11	6.230e-09	SYT2:18 BNC1:26 ADGRB1:39 LAD1:42 JAG2:138 LMX1A:306
REACTOME_CELL_CYCLE_CHECKPOINTS	-0.11719376	270	3.598e-11	6.315e-09	KIF18A:30 RNF168:52 SGO2:62 CENPC:70 CENPT:71 KIF2C:108
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	0.11650318	265	7.010e-11	1.198e-08	TAAR6:28 HRH2:130 GPR35:205 GRIK4:236 HTR5A:246 ADORA2A:269
MD FLECTBON TRANSPORT OUALN OVERLOOD OVERT	0.40070004	00	0.000 44	4 500 00	NDUEDO-440 NDUEDE-400 NDUEDA-440 NDUEGE-400 NDUEDO-454 NDUEDA-500

DisGeNET Top pathways by non-permulation

3.619e-10 5.875e-08

9.209e-11 1.533e-08 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451 NDUFB4:502

DLGAP5:10 LRPPRC:13 MTPAP:25 ATAD2:27 PARPBP:29 KIF18A:30

WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE -0.19876994

SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6 -0.08756792

Arthrogryposis Bipolar Disorder O.06 Increased CSF lactate Charcot-Marie-Tooth Disease NADH:Q(1) Oxidoreductase deficiency Primary microcephaly Autism Spectrum Disorders Autistic Disorder Mitochondrial Diseases Reflex, Deep Tendon, Absent Absent reflex Congenital myopathy (disorder) O.06 O.07 O.17 O.17 O.18 O.19 O.1	05648410 09909345 06247038 .21571940 09819164 .30491833 .14646853 06649237 06024552 .07909509 12974571 12974571 14018054	1731 298 755 56 268 25 110 516 637 363 129 129	2.403e-14 4.549e-09 7.235e-09 2.394e-08 3.482e-08 1.317e-07 1.154e-07 2.808e-07 2.642e-07 2.566e-07	2.233e-05 2.368e-05 5.876e-05 6.837e-05 1.847e-04 1.847e-04 2.757e-04	SHANK2:3 SORL1:5 TRANK1:7 PLEC:15 NAV1:17 TAAR6:28 MYH2:11 PLEC:15 SYT2:18 OFD1:121 COL6A1:158 IGHMBP2:176 PER2:2 SORL1:5 TRANK1:7 TAAR6:28 TRPV6:31 ADCY1:32 TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 TRMT10C:293 SYT2:18 DSP:30 SBF1:33 PRKN:57 MYO15A:68 DSG2:104 TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451 CENPJ:149 DNA2:193 FANCG:202 STIL:219 XRCC4:255 KNL1:350 SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80 SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Bipolar Disorder 0.06 Increased CSF lactate -0.2 Charcot-Marie-Tooth Disease 0.09 NADH:Q(1) Oxidoreductase deficiency -0.3 Primary microcephaly -0.1 Autism Spectrum Disorders 0.06 Autistic Disorder 0.06 Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.06247038 .21571940 .09819164 .30491833 .14646853 .06649237 .06024552 .07909509 .12974571 .12974571 .14018054	755 56 268 25 110 516 637 363 129	7.235e-09 2.394e-08 3.482e-08 1.317e-07 1.154e-07 2.808e-07 2.642e-07 2.566e-07	2.368e-05 5.876e-05 6.837e-05 1.847e-04 1.847e-04 2.757e-04 2.757e-04	PER2:2 SORL1:5 TRANK1:7 TAAR6:28 TRPV6:31 ADCY1:32 TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 TRMT10C:293 SYT2:18 DSP:30 SBF1:33 PRKN:57 MYO15A:68 DSG2:104 TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451 CENPJ:149 DNA2:193 FANCG:202 STIL:219 XRCC4:255 KNL1:350 SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80 SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Increased CSF lactate -0.2 Charcot-Marie-Tooth Disease 0.09 NADH:Q(1) Oxidoreductase deficiency -0.3 Primary microcephaly -0.1 Autism Spectrum Disorders 0.00 Autistic Disorder 0.00 Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.21571940 .09819164 .30491833 .14646853 .06649237 .06024552 .07909509 .12974571 .12974571 .14018054	56 268 25 110 516 637 363 129	2.394e-08 3.482e-08 1.317e-07 1.154e-07 2.808e-07 2.642e-07 2.566e-07	5.876e-05 6.837e-05 1.847e-04 1.847e-04 2.757e-04 2.757e-04	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 TRMT10C:293
Charcot-Marie-Tooth Disease 0.09 NADH:Q(1) Oxidoreductase deficiency -0.3 Primary microcephaly -0.1 Autism Spectrum Disorders 0.00 Autistic Disorder 0.00 Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.09819164 .30491833 .14646853 .06649237 .06024552 .07909509 .12974571 .12974571 .14018054	268 25 110 516 637 363 129	3.482e-08 1.317e-07 1.154e-07 2.808e-07 2.642e-07 2.566e-07	6.837e-05 1.847e-04 1.847e-04 2.757e-04 2.757e-04	SYT2:18 DSP:30 SBF1:33 PRKN:57 MYO15A:68 DSG2:104 TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451 CENPJ:149 DNA2:193 FANCG:202 STIL:219 XRCC4:255 KNL1:350 SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80 SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
NADH:Q(1) Oxidoreductase deficiency -0.3 Primary microcephaly -0.1 Autism Spectrum Disorders 0.06 Autistic Disorder 0.06 Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.30491833 .14646853 .06649237 .06024552 .07909509 .12974571 .12974571 .14018054	25 110 516 637 363 129	1.317e-07 1.154e-07 2.808e-07 2.642e-07 2.566e-07	1.847e-04 1.847e-04 2.757e-04 2.757e-04	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451 CENPJ:149 DNA2:193 FANCG:202 STIL:219 XRCC4:255 KNL1:350 SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80 SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Primary microcephaly -0.1 Autism Spectrum Disorders 0.06 Autistic Disorder 0.06 Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.14646853 .06649237 .06024552 .07909509 .12974571 .12974571 .14018054	110 516 637 363 129	1.154e-07 2.808e-07 2.642e-07 2.566e-07	1.847e-04 2.757e-04 2.757e-04	CENPJ:149 DNA2:193 FANCG:202 STIL:219 XRCC4:255 KNL1:350 SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80 SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Autism Spectrum Disorders O.06 Autistic Disorder Mitochondrial Diseases Congenital myopathy (disorder) O.06 Autism Spectrum Disorders O.06 Autism Spectrum Disorders O.06 O.07 O.08 O.09	.06649237 .06024552 .07909509 .12974571 .12974571 .14018054	516 637 363 129	2.808e-07 2.642e-07 2.566e-07	2.757e-04 2.757e-04	SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80 SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Autistic Disorder 0.06 Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.06024552 .07909509 12974571 12974571 14018054	637 363 129	2.642e-07 2.566e-07	2.757e-04	SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Mitochondrial Diseases -0.0 Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.07909509 .12974571 .12974571 .14018054	363 129	2.566e-07		
Reflex, Deep Tendon, Absent 0.12 Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.12974571 .12974571 .14018054	129		2.757e-04	
Absent reflex 0.12 Congenital myopathy (disorder) 0.14	.12974571 .14018054	-	3 7/80 07		TMEM126B:3 LRPPRC:13 MTPAP:25 NDUFA11:49 ECSIT:63 NDUFAF1:73
Congenital myopathy (disorder) 0.14	.14018054	129	J. / 406-0/	3.067e-04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
			3.748e-07	3.067e-04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Absent tendon reflex 0.12	12000100	109	4.416e-07	3.335e-04	MYH2:11 CASQ1:147 CACNA1S:152 COL6A1:158 IGHMBP2:176 DES:220
	.12988190	126	4.964e-07	3.482e-04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Mood Disorders 0.07	.07987856	319	1.029e-06	6.735e-04	ZHX3:24 TAAR6:28 ADCY1:32 HTT:46 PPP1R13B:64 ADARB1:157
MITOCHONDRIAL COMPLEX I DEFICIENCY -0.2	.27270922	26	1.491e-06	9.151e-04	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB3:451 FOXRED1:619
Congenital pes cavus 0.12	.12653047	120	1.745e-06	9.517e-04	SYT2:18 ANOS1:77 MME:145 HSD17B4:320 L1CAM:326 INF2:410
Unipolar Depression 0.00	.06365788	487	1.737e-06	9.517e-04	ZHX3:24 HTT:46 ZBTB16:76 ACSL4:92 ADARB1:157 TRIO:200
Ciliopathies -0.1	.10474399	174	1.969e-06	1.018e-03	TBC1D32:31 KIAA0586:44 ARL13B:87 NME8:273 NPHP3:306 BUB1B:318
Gait, Drop Foot 0.29	.25007073	30	2.142e-06	1.052e-03	IGHMBP2:176 L1CAM:326 INF2:410 MPZ:602 GNE:649 TTN:825
Abnormal mitochondria in muscle tissue -0.2	.27011667	25	2.950e-06	1.379e-03	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451
Acute necrotizing encephalopathy -0.3	.30034987	20	3.327e-06	1.485e-03	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB3:451 FOXRED1:619
Myopathy 0.07	.07025291	358	5.469e-06	2.335e-03	MYH2:11 PLEC:15 CASQ1:147 COL6A1:158 IGHMBP2:176 DES:220
Abnormal behavior 0.0	.07148187	341	6.270e-06	2.565e-03	SHANK2:3 HTT:46 NRCAM:96 ADARB1:157 HTR5A:246 HDAC4:291
Myocardial Infarction 0.04	.04480251	896	6.918e-06	2.717e-03	SBF1:33 ARC:49 ALMS1:103 PC:185 GPER1:188 NDST1:204
Congestive heart failure 0.04	.04714750	791	8.074e-06	2.936e-03	DSP:30 TRPV6:31 HTT:46 ARC:49 AIMP2:74 ALMS1:103
Spasmodic torticollis 0.20	.26362179	24	7.827e-06	2.936e-03	COL6A1:158 KCTD17:368 DRD2:522 PNKD:561 CACNA1B:716 SCP2:1254
Mental Depression 0.09	.05666113	534	8.616e-06	3.022e-03	PER2:2 ADCY1:32 HTT:46 ACSL4:92 KRT20:129 GRIK4:236
Foot–drop 0.20	.20237383	40	9.539e-06	3.122e-03	MME:145 IGHMBP2:176 DES:220 INF2:410 MPZ:602 GNE:649
Heart failure 0.04	.04858939	732	9.225e-06	3.122e-03	DSP:30 HTT:46 ARC:49 AIMP2:74 ALMS1:103 MME:145
Chromosome Breakage -0.2	.20190579	40	1.000e-05	3.168e-03	FANCG:202 XRCC4:255 BRCA1:300 FANCM:414 DNMT3B:780 IL4:927
Alzheimer's Disease 0.03	.03187802	1795	1.231e-05	3.777e-03	PER2:2 SHANK2:3 SORL1:5 HTT:46 ARC:49 LGR6:51
nervous system disorder 0.00	.06332214	407	1.294e-05	3.850e-03	SHANK2:3 HTT:46 CALCA:63 ACKR3:254 NOTCH1:258 ATP7B:273
Distal muscle weakness 0.14	.14617587	74	1.397e-05	4.023e-03	SYT2:18 COL6A1:158 IGHMBP2:176 DES:220 INF2:410 MPZ:602
Torticollis 0.24	.24585795	26	1.434e-05	4.023e-03	COL6A1:158 KCTD17:368 DRD2:522 PNKD:561 CACNA1B:716 DNM2:1182
Depressive disorder 0.04	.04914697	678	1.522e-05	4.150e-03	PER2:2 TAAR6:28 ADCY1:32 HTT:46 AIMP2:74 ANOS1:77
Distal sensory impairment 0.19	.15060127	68	1.774e-05	4.709e-03	SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 PIK3R5:363 INF2:410
Major Depressive Disorder 0.09	.05651225	486	2.226e-05	5.670e-03	TAAR6:28 HTT:46 ZBTB16:76 ADARB1:157 GRIK4:236 ACKR3:254
Pervasive Development Disorder 0.1	.11216959	120	2.252e-05	5.670e-03	SHANK2:3 HTT:46 PRKN:57 KMT5B:61 TRIO:200 KMT2C:227
Distal limb muscle weakness due to perip 0.14	.14125547	75	2.376e-05	5.832e-03	SYT2:18 COL6A1:158 IGHMBP2:176 DES:220 INF2:410 MPZ:602

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003635 abnormal synaptic transmissio	0.09019531	425	6.037e-10	2.874e-07	SYT2:18 ADCY1:32 ARC:49 NRCAM:96 ADARB1:157 CACNA1E:166
MP0001929 abnormal gametogenesis	-0.08306070	470	2.406e-09	5.727e-07	ARID4A:86 FGD2:145 ADCY10:173 FANCG:202 SYCP1:216 EIF4G3:234
MP0003698 abnormal male reproductive	-0.06637641	521	5.859e-07	9.296e-05	CATSPER2:41 CLGN:84 ADCY10:173 FANCG:202 SYCP1:216 EIF4G3:234
MP0002066 abnormal motor capabilities/c	0.04659325	1087	1.822e-06	1.497e-04	PER2:2 SYT2:18 HTT:46 NRCAM:96 HRH2:130 CACNA1S:152
MP0002063 abnormal learning/memory/cond	0.07591129	356	1.590e-06	1.497e-04	PER2:2 ADCY1:32 HTT:46 ARC:49 NRCAM:96 HTR5A:246
MP0009745 abnormal behavioral response	0.09790641	205	1.887e-06	1.497e-04	PER2:2 CALCA:63 SLC18A3:251 ADORA2A:269 CACNA1G:287 UPP1:377
MP0010094 abnormal chromosome stability	-0.16744916	65	3.340e-06	2.271e-04	FANCG:202 XRCC4:255 BRCA1:300 MBD1:313 BUB1B:318 CENPE:392
MP0002085 abnormal embryonic tissue	-0.05180204	655	1.610e-05	9.580e-04	ADAMTS20:9 CUBN:11 DAXX:12 TFAM:14 NSD1:24 ECSIT:63
MP0002067 abnormal sensory capabilities	0.07410385	267	4.273e-05	2.034e-03	HTT:46 CACNA1S:152 CACNA1E:166 IGHMBP2:176 GRIK4:236 HDAC4:291
MP0002064 seizures	0.07614848	255	3.886e-05	2.034e-03	HTT:46 KCNQ3:126 HRH2:130 ADARB1:157 GRIK4:236 SLC18A3:251
MP0003077 abnormal cell cycle	-0.09570616	153	5.262e-05	2.129e-03	ITGB1:152 RIF1:179 MED1:208 BRCA1:300 BUB1B:318 CENPE:392
MP0002572 abnormal emotion/affect behav	0.07068146	287	5.366e-05	2.129e-03	ADCY1:32 HTT:46 ARC:49 ULK2:155 CACNA1E:166 HTR5A:246
MP0002210 abnormal sex determination	-0.06338802	350		2.564e-03	FANCG:202 SYCP1:216 EIF4G3:234 BRCA1:300 MAGEL2:373 RNF17:386
MP0005620 abnormal muscle contractility	0.08102015	206		2.579e-03	CASQ1:147 CACNA1S:152 COL6A1:158 DES:220 TNNT2:380 APOE:461
MP0000653 abnormal sex gland	-0.05226620	523		2.579e-03	AFP:53 ARID4A:86 FANCG:202 SYCP1:216 EIF4G3:234 BRCA1:300
MP0002429 abnormal blood cell	-0.03635617	1240	9.287e-05	2.763e-03	SPIC:40 ARID4A:86 NR2C1:99 IL23R:113 PTPN12:131 ITGB1:152
MP0002272 abnormal nervous system	0.08022435	197	1.279e-04	3.581e-03	PLEC:15 ARC:49 NRCAM:96 KCNQ3:126 GRIK4:236 CACNA1G:287
MP0002086 abnormal extraembryonic tissu	-0.05156409	486	1.690e-04	4.469e-03	DLGAP5:10 CUBN:11 DAXX:12 NSD1:24 NANOG:65 BPTF:66
MP0000689 abnormal spleen morphology	-0.04830224	552	1.911e-04	4.548e-03	SPIC:40 DNMT1:74 ARID4A:86 GRB14:153 IKZF3:256 SERPINI2:302
MP0000313 abnormal cell death	-0.05242775	463	1.831e-04	4.548e-03	DAXX:12 TFAM:14 DNMT1:74 CTH:116 UBR5:127 ITGB1:152
MP0000749 muscle degeneration	0.17594437	36	2.677e-04	6.067e-03	PLEC:15 MYOF:127 CACNA1S:152 IGHMBP2:176 DES:220 PFKM:388
MP0000598 abnormal liver morphology	-0.04992233	482		6.180e-03	XIRP2:26 ARID4A:86 CTH:116 PTPN12:131 ITGB1:152 GRB14:153
MP0001119 abnormal female reproductive	-0.06010604	295		1.039e-02	AFP:53 ARID4A:86 SMCHD1:136 FANCG:202 SYCP1:216 BRCA1:300
MP0000716 abnormal immune system	-0.03467999	1013		1.082e-02	SPIC:40 ARID4A:86 IL23R:113 PTPN12:131 NFATC3:156 CRLF2:158
MP0001145 abnormal male reproductive	-0.04806045	457		1.240e-02	FANCG:202 SYCP1:216 EIF4G3:234 BRCA1:300 AGTPBP1:324 RNF17:386
MP0001970 abnormal pain threshold	0.07835581	152		1.770e-02	ADCY1:32 CALCA:63 HOXB13:88 KIF1A:161 ADORA2A:269 HDAC4:291
MP0002723 abnormal immune serum	-0.03886331	649		2.237e-02	IL23R:113 PTPN12:131 CRLF2:158 IL27RA:197 GCNT3:201 IKZF3:256
MP0002135 abnormal kidney morphology	-0.04537609	455		2.237e-02	TET2:4 CUBN:11 ARID4A:86 IKZF3:256 BRCA1:300 NPHP3:306
MP0001800 abnormal humoral immune	-0.05077512	333		3.053e-02	CRLF2:158 GCNT3:201 IKZF3:256 GABPB2:346 SH2D3C:405 REV3L:416
MP0004957 abnormal blastocyst morpholog	-0.09936407	82		3.138e-02	NANOG:65 ITGB1:152 CHD8:367 AHCTF1:402 NUSAP1:429 LAMA1:434
MP0002084 abnormal developmental patter	-0.04782237	366		3.366e-02	CUBN:11 DAXX:12 NSD1:24 ECSIT:63 NANOG:65 BPTF:66
MP0001486 abnormal startle reflex	0.08896226	96		4.042e-02	LOXHD1:128 OTOF:272 APOE:461 NTSR1:518 DRD2:522 CACNA1B:716
MP0002876 abnormal thyroid physiology	-0.19828553	19		4.042e-02	MED1:208 GHR:499 CGA:1054 AIRE:1447 GLIS3:1571 GFRA4:2849
MP0002080 prenatal lethality	-0.02699920	1335		4.057e-02	CUBN:11 DAXX:12 TFAM:14 NSD1:24 SPIC:40 ECSIT:63
MP0004085 abnormal heartbeat	0.06806791	160			CALCA:63 IGHMBP2:176 HIRA:237 ADORA2A:269 CACNA1G:287 KCNH2:36
MP0003693 abnormal embryo hatching	-0.17361362	24		4.353e-02	VEZT:103 KIF11:475 RBBP8:507 CDC25A:1235 CDCA8:1236 PARG:2207
MP000579 abnormal nail morphology	0.18433457	21		4.497e-02	KRT17:105 ITGB4:223 L1CAM:326 EGFR:686 KRT75:977 KRT6A:1248
MP0003121 genomic imprinting	-0.15587105	29		4.497e=02 4.556e=02	DNMT1:74 ARID4A:86 SMCHD1:136 MAGEL2:373 PLAGL1:420 PEG10:836
MP0003121 genomic imprinting MP0002971 abnormal brown adipose	0.09686093	76		4.556e-02	CACNA1S:152 GPR68:174 APOE:461 MOGAT2:737 RPTOR:1013 C3:1147
MP0002161 abnormal fertility/fecundity	-0.03068056	865	4.0796-03	4.854e-02	DLGAP5:10 CATSPER2:41 AFP:53 DNMT1:74 CLGN:84 ARID4A:86

tissue_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
testis	-0.13832981	1678	1.777e-68	9.598e-67	CCDC148:15 MTPAP:25 ZBBX:28 ZYG11A:34 KIF27:46 CT55:48
leg.skin	0.13887164	288	1.077e-15	2.909e-14	PKP1:8 INAVA:22 BNC1:26 DSP:30 TRIM29:35 PSAPL1:67
EBV.lymphocyte	-0.08265165	753	7.214e-14	1.298e-12	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 KIF2C:108 IL23R:113
suprapubic.skin	0.12212317	259	2.103e-11	2.839e-10	PKP1:8 BNC1:26 PSAPL1:67 AADACL2:89 NKPD1:99 KRT17:105
cerebellar.hemisphere	0.07787661	542	1.300e-09	1.404e-08	SYT2:18 ADCY1:32 ARHGAP44:90 MYT1:100 PPFIA4:107 TIAM1:111
cerebral.cortex	0.14936925	110	7.057e-08	6.351e-07	ADGRB1:39 KIF1A:161 DPYSL4:262 POU6F2:425 HECW1:551 MCHR1:581
cerebellum	0.07260181	409	7.177e-07	5.234e-06	TRANK1:7 SYT2:18 GLRA4:73 MYT1:100 PPFIA4:107 TIAM1:111
skeletal.muscle	0.09025646	258	7.753e-07	5.234e-06	MYH2:11 MYBPC2:144 CASQ1:147 CACNA1S:152 MYH1:239 PYGM:292
Brodmann.area.9	0.09778598	185	5.253e-06	3.152e-05	NRCAM:96 KCNQ3:126 NECAB1:198 OLFM1:356 POU6F2:425 GPR26:479
esophagus.mucosa	0.07743980	263	1.875e-05	1.012e-04	PKP1:8 BNC1:26 ADH7:37 LAD1:42 FAM83H:124 RNF222:194
pancreas	-0.09460248	118	4.097e-04	2.011e-03	TMED6:188 CATSPERB:246 SERPINI2:302 ERP27:332 FBXW12:345 G6PC2:555
nucleus.accumbens	0.09733599	105	5.980e-04	2.484e-03	INSYN2A:113 CACNA1E:166 OTOF:272 JAKMIP1:276 SV2C:414 ARPP21:654
vagina	0.09205920	119	5.542e-04	2.484e-03	PKP1:8 BNC1:26 RNF222:194 SLURP1:253 LCE3D:304 NOD2:312
putamen	0.17511245	17	1.248e-02	4.813e-02	RGS9:52 SLC18A3:251 DIPK1C:623 OPALIN:1651 CORT:2933 LRRC10B:3207
endocervix	0.07506821	79	2.145e-02	7.723e-02	MRGPRE:1 ELFN1:41 KIF26A:66 ZNF516:93 SPON2:286 MLPH:417
greater.omentum	0.10652372	38	2.325e-02	7.848e-02	BNC1:26 AADACL4:383 ITLN1:422 THRSP:630 ADAMTS4:779 FAM89A:952
hypothalamus	0.07156423	78	2.935e-02	9.322e-02	SYT6:275 PNMA6F:477 PNMA5:688 RTL1:782 KISS1R:879 DNER:975
tibial.artery	0.05582169	113	4.124e-02	1.237e-01	SDK1:20 PPP1R12B:142 ADARB1:157 OR51E2:230 TNC:303 INHBA:349
amygdala	0.18028731	9	6.114e-02	1.572e-01	TNR:440 PTPRZ1:493 PCDH15:3256 NEUROD6:6152 SLC17A7:6846 SLC38A8:714
C1.spinal.cord	0.03971908	194	5.831e-02	1.572e-01	ACSBG1:114 CDH20:208 MAGEC3:436 CHADL:562 TTYH2:589 PLAAT3:591
sigmoid.colon	0.07755972	51	5.580e-02	1.572e-01	DES:220 HDAC4:291 TACR2:335 MRGPRD:367 NTSR1:518 GREM2:812
left.ventricle	0.06413733	68	6.810e-02	1.672e-01	MYL3:256 LMOD2:328 TNNT2:380 MYOM2:769 TENM2:1212 CKMT2:1281
peyers.patch	0.03553920	199	8.630e-02	1.970e-01	SLC17A4:9 TRPM5:13 MGAM2:118 KRT20:129 TREH:131 EPS8L3:133
transverse.colon	0.03834125	169	8.754e-02	1.970e-01	SLC17A4:9 DSG2:104 KRT20:129 EPS8L3:133 RNF186:139 MUC2:192
fallopian.tube	-0.06111042	60	1.023e-01	2.126e-01	BCHE:150 ATP8B4:268 ADAMTS3:295 CCDC17:460 TUBA4B:463 CCDC198:863
prostate	-0.06637422	52	9.841e-02	2.126e-01	CPAMD8:58 TTC6:330 SHROOM1:445 MSMB:568 TNFSF15:946 MKX:970
blood	0.02271908	347	1.515e-01	3.029e-01	HRH2:130 FFAR2:150 STX11:214 FUT7:224 TUBB1:332 PIK3R5:363
esophagogastric.junction	-0.12399366	9	1.978e-01	3.815e-01	F2RL2:1282 RTL3:2797 NKX6-1:4194 GADL1:5652 ADCY5:6799 COL4A5:7006
stomach	0.03546474	99	2.244e-01	4.040e-01	MYH13:54 PSAPL1:67 EPS8L3:133 CAPN8:171 VWA2:372 TM4SF5:379
eye.development	0.04254519	69	2.229e-01	4.040e-01	NOTCH1:258 TKT:523 BMP7:1078 TBX5:1425 CRX:1446 FGFR2:1635
hippocampus.proper	0.09538935	13	2.339e-01	4.074e-01	GRP:928 LCN1:1666 CTXND1:1693 NEUROD6:6152 OLIG2:6296 CABP7:6700
caudate.nucleus	0.06345781	28	2.456e-01	4.144e-01	GPR37L1:12 MLC1:40 TAC1:1761 PDE1B:2622 LRRC10B:3207 VAX1:3381
subcutaneous.adipose	0.03595714	82	2.618e-01	4.284e-01	GPD1:282 FASN:514 THRSP:630 F13A1:684 ACACB:896 PRG2:1036

Brodmann.area.24 0.05357897 33 2.873e-01 4.564e-01 DOK6:1564 UPP2:2270 MT3:2809 FAM189A1:2974 SHANK1:3151 GRIN3A:3627 bladder 0.05376583 30 3.086e-01 4.761e-01 UGT1A6:1295 PSCA:1571 PADI3:1835 KRT13:2204 ACSM6:2275 ABCC4:2898

3.833e-01 5.594e-01 CCDC69:740 F2RL2:1282 PRUNE2:1425 COL4A6:2457 CST5:3622 CNTNAP3:4029

NAV1:17 LGR6:51 MTUS2:243 CYP4X1:330 PDGFA:635 GABRR1:637

SLC24A4:169 ITGB4:223 ENTPD2:298 MYOC:389 INF2:410 OR6B3:501

TNN:252 THRSP:630 KRT5:1910 NPY2R:2176 PLIN1:3226 ADIPOQ:3410

transformed.skin.fibroblast 0.01656334 276 3.488e-01 5.232e-01 BNC1:26 ZNF281:81 MYOF:127 CLMP:143 MME:145 COL6A1:158

4.410e-01 6.266e-01

4.739e-01 6.561e-01

5.191e-01 6.663e-01

esophagus.muscularis.mucosa -0.04764841

aorta

tibial.nerve

breast

0.01798357

0.01462615

0.04166667

156

205

20