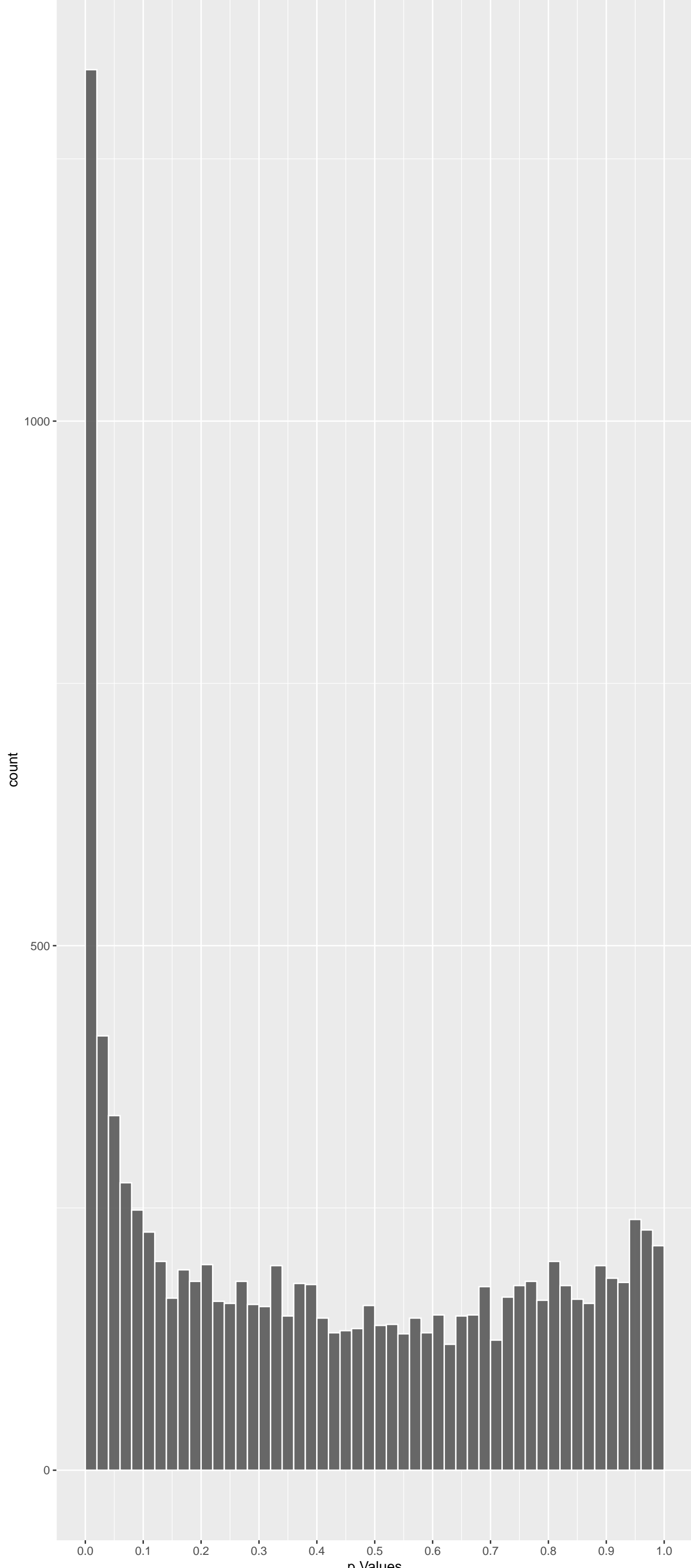


Top genes by P-value non-permuted

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

Positive Rho Non-permuted



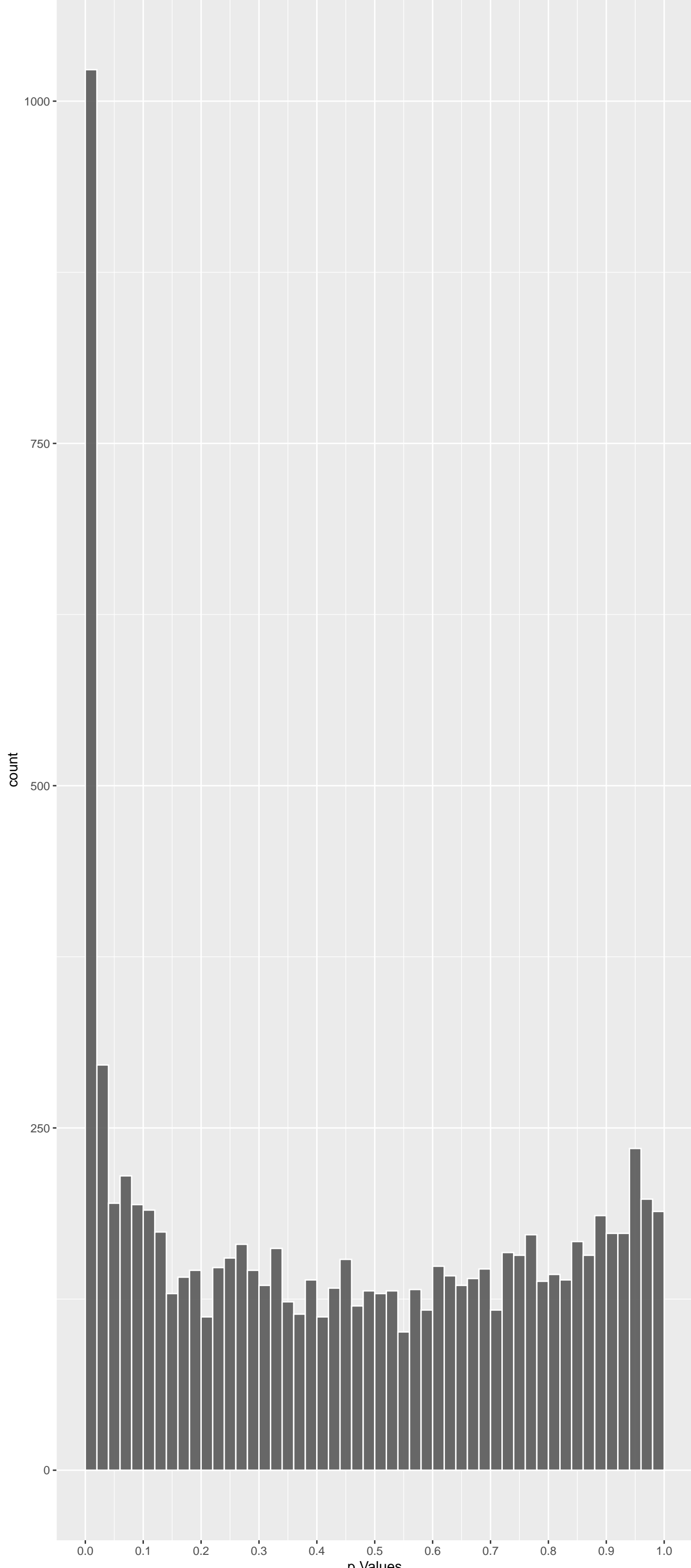
Top Positive genes by P-value non-permuted

Gene	Rho	P	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

Top genes by Q-Value non-permuted

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
TET2	-7.068486	1.566336e-12	2.938e-09	5.510e-06
TMEM126B	-7.094171	1.301296e-12	2.712e-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
MYH2	6.679935	2.390477e-11	2.802e-08	3.285e-05
UBAP2	-6.693525	2.178578e-11	2.724e-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
FAAP100	6.573197	4.924612e-11	4.618e-08	4.308e-05
PLEC	6.559438	5.401105e-11	4.824e-08	4.308e-05
TRPM5	6.583262	4.602355e-11	4.543e-08	4.308e-05
SMIM26	-6.486677	8.774997e-11	7.156e-08	5.835e-05
SPATA2L	6.495394	8.281643e-11	7.060e-08	5.835e-05
ADAMTS20	-6.441540	1.182676e-10	8.873e-08	6.605e-05
CEP170B	6.355277	2.080511e-10	1.207e-07	6.605e-05

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
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

GO_Biological_Process_2023 Top pathways by non-permutation

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	6.582e-13	TFAM:14 TEFM:93 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFB5:422
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 NDUFB5:422 NDUFB3:451
Aerobic Electron Transport Chain (GO:0001	-0.27107537	64	6.639e-14	5.983e-11	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFB5:422 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 NDUFB5:422
Proton Motive Force-Driven Mitochondrial	-0.27879639	50	9.319e-12	4.581e-09	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFB5:422 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 NDUFB5:422 NDUFB3:451
Proton Motive Force-Driven ATP Synthesis	-0.25205953	55	1.030e-10	3.976e-08	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFB5:422 NDUFB3:451
Chemical Synaptic Transmission (GO:00072	0.11476942	263	1.697e-10	6.118e-08	KCNQ3:126 HRH2:130 CACNA1E:166 GRK4:236 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)	-0.12107077	221	5.042e-10	1.604e-07	KIAA0586:44 KIF27:46 ARL13B:87 GBF1:126 CENPJ:149 IQCC: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 NDUFB5:422 NDUFB3:451
Aerobic Respiration (GO:0009060)	-0.21958662	57	1.001e-08	2.460e-06	NDUFA11:49 TEFM:93 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFB5:422
Calcium ion Transmembrane Import Into Cy	0.18574261	79	1.180e-08	2.774e-06	TRPV6:31 CACNA11:148 CACNA1S:152 CACNA1E:166 SLC24A4:169 CACNA1G:287
Calcium ion Transport (GO:0006816)	0.11502051	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)	0.15404761	208	4.383e-08	9.481e-06	SLC24A4:169 OR10A2:211 OR2H2:369 OR10D3:33 SGO2:62 DNMT1:74
Potassium ion Transmembrane Transport (G	0.15504762	135	5.751e-08	1.196e-05	SLC24A3:125 KCNQ3:126 SLC24A4:169 KCNQ10:225 KCNJ12:259 KCNH2:365
Potassium ion Transport (GO:0006813)	0.13631751	121	2.319e-07	4.645e-05	SLC24A3:125 KCNQ3:126 SLC24A4:169 KCNQ10:225 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 UTM1:291
Response To Calcium Ion (GO:0051592)	0.14621422	100	4.487e-07	8.365e-05	SYT2:18 TRPV6:31 ADCY1:32 SYT8:179 RASGRP2:240 SYTE:275 CACNA1G:287
Neuron Projection Morphogenesis (GO:0048	-0.12892007	139	4.761e-07	8.582e-05	ADGRB1:39 NRCAM:66 CTTN:149 TRIO:200 FLRT1:218 TNN:252
DNA Repair (GO:0006281)	0.03470794	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
RNA 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 GRK4:236 HTR5A:246 SLC18A3:251
Modulation Of Chemical Synaptic Transmis	0.12903743	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 SYTE:275 CACNA1G:287
Metal Ion Transport (GO:0030001)	0.10488688	169	2.671e-06	3.702e-04	SLC17A4:9 TRPV6:31 CACNA1S:152 KCNJ12:259 CHRNA4:393 TPR1:416
Mitochondrial RNA Metabolic Process (GO:	-0.29839148	20	3.852e-06	5.207e-04	TFAM:14 TEFM:93 POLRMT:101 TFB2M:112 TNNK:217 FASTKD1:431

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

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 LRRCA40:33 SGO2:62 DNMT1:74
REACTOME_NEURONAL_SYSTEM	0.13056085	394	6.861e-19	9.811e-16	SHANK2:3 SYT2:18 PPPIA:1:23 ADCY1:32 GJA10:91 PPPIA4:107
REACTOME_FORMATION_OF_THE_CORNFIED_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 GAD45GIP1:477 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	GRP37L1:12 TAAR6:28 ADCY1:32 RGS9:52 CALCA:63 TIAM1:111
WP_GPCRS_CLASS_A_RHODOPINLIKE	0.13432814	253	2.006e-13	6.856e-11	GRP37L1:12 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_CALCIIUM_SIGNALING_PATHWAY	0.15946070	168	1.036e-12	2.925e-10	ADCY1:32 HRH2:130 CACNA11:148 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 PHLD1:145 RGS9:52 CALCA:63
KINSEY_TARGETS_OF_EWSR1_FUJI_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 APSZ1:508
REACTOME_MUSCLE_CONTRACTION	0.145600232	196	2.687e-12	6.233e-10	MYBP2C:144 MME:145 CASQ1:147 CACNA11:148 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:104
WP_QQ37_COPY_NUMBER_VARIATION_SYNDROME	0.17186962	129	1.613e-11	3.080e-09	PER2:2 CALCA:63 PASK:65 KIF1A:161 GPR35:205 PPP1R7:248
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_I	-0.14562117	175	3.083e-11	5.720e-09	KIF2C:108 SPAG5:163 NEXN:1:64 GNT3:201 FANGC: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	0.116650318	265	7.010e-11	1.198e-08	TAAR6:28 HRH2:130 GPR35:205 GRIK4:236 HTR5A:246 ADORA2A:269
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	-0.19876994	89	9.209e-11	1.533e-08	NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFB5:422 NDUFB3:451 NDUFB4:502
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	-0.08756792	438	3.619e-10	5.875e-08	DLGAP5:10 LRPPRC:13 MTPAP:25 ATAD2:27 PARPBP:29 KIF18A:30

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Schizophrenia	0.05648410	1731	2.403e-14	2.359e-10	SHANK2:3 SORL1:5 TRANK1:7 PLEC:15 NAV1:17 TAAR6:28
Arthrogryposis	0.09909345	298	4.549e-09	2.233e-05	MYH2:11 PLEC:15 SYT2:18 OFD1:121 COL6A1:158 IGHMBP2:176
Bipolar Disorder	0.06247038	755	7.235e-09	2.368e-05	PER2:2 SORL1:5 TRANK1:7 TAAR6:28 TRPV6:31 ADCY1:32
Increased CSF lactate	-0.21571940	56	2.394e-08	5.876e-05	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 TRMT10C:293
Charcot-Marie-Tooth Disease	0.09819164	268	3.482e-08	6.837e-05	SYT2:18 DSP:30 SBF1:33 PRKN:57 MYO15A:68 DSG2:104
NADH-Q(1) Oxidoreductase deficiency	-0.30491833	25	1.317e-07	1.847e-04	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451
Primary microcephaly	-0.14646853	110	1.154e-07	1.847e-04	CENPJ:149 DNA2:193 FANGC:202 STL:219 XRCC4:255 KNL1:350
Autism Spectrum Disorders	0.06649237	516	2.808e-07	2.757e-04	SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80
Autistic Disorder	0.06024552	637	2.642e-07	2.757e-04	SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Mitochondrial Diseases	-0.07909509	363	2.566e-07	2.757e-04	TMEM126B:3 LRPPRC:13 MTPAP:25 NDUFA11:49 ECSIT:63 NDUFAF1:73
Reflex, Deep Tendon, Absent	0.12974571	129	3.748e-07	3.067e-04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Absent reflex	0.12974571	129	3.748e-07	3.067e-04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Congenital myopathy (disorder)	0.14018054	109	4.416e-07	3.335e-04	MYH2:11 CASQ1:147 CACNA1S:152 COL6A1:158 IGHMBP2:176 DES:220
Absent tendon reflex	0.12988190	126	4.964e-07	3.482e-04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Mood Disorders	0.07987856	319	1.029e-06	6.735e-04	ZHX3:24 TAAR6:28 ADCY1:32 HTT:46 PPP1R13B:64 ADARB1:157
MITOCHONDRIAL COMPLEX I DEFICIENCY	-0.27270922	26	1.491e-06	9.151e-04	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB3:451 FOXRED1:619
Congenital pes cavus	0.12653047	120	1.745e-06	9.517e-04	SYT2:18 ANOS1:77 MME:145 HSD17B4:320 LC1AM:326 INF2:410
Unipolar Depression	0.06365788	487	1.737e-06	9.517e-04	ZHX3:24 HTT:46 ZBTB18:76 ACSL4:92 ADARB1:157 TRIO:200
Ciliopathies	-0.10474399	174	1.969e-06	1.018e-03	TBC1D32:31 KIAA0586:44 ARL13B:87 NME8:273 NPH3:306 BUB1B:318
Gait, Drop Foot	0.25007073	30	2.142e-06	1.052e-03	IGHMBP2:176 LC1AM:326 INF2:410 MPZ:602 GNE:649 TTN:825
Abnormal mitochondrial in muscle tissue	-0.27011667	25	2.950e-06	1.379e-03	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451
Acute necrotizing encephalopathy	-0.30034987	20	3.327e-06	1.485e-03	TMEM126B:3 NDUFA11: