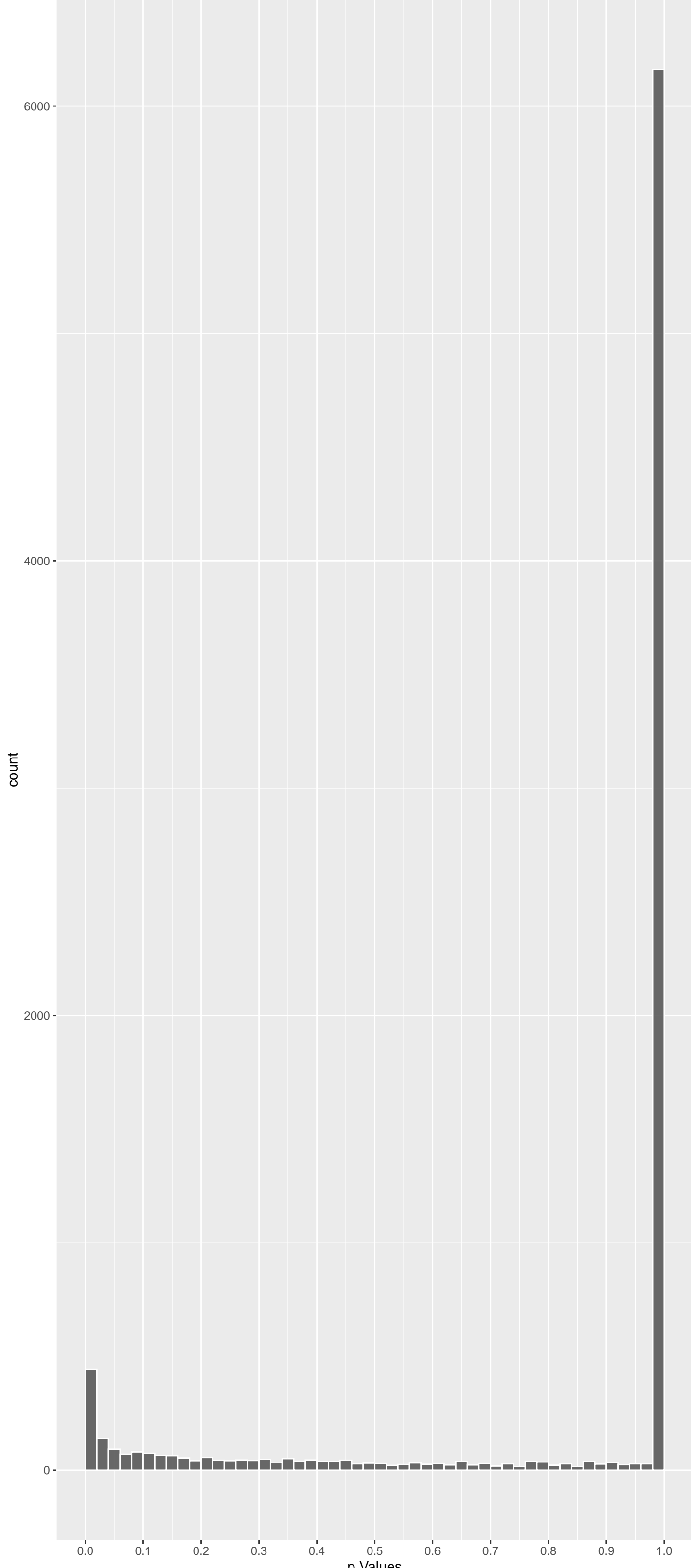


Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
BCLAF3	-7.533746	2.958306e-13	4.776e-09	5.097e-05
THADA	7.364298	1.068487e-12	8.626e-09	5.097e-05
NAV1	-7.297458	1.759527e-12	9.470e-09	5.097e-05
ZBTB41	-7.008288	1.447507e-11	5.843e-08	2.098e-04
MMP16	-6.962093	2.011525e-11	6.496e-08	2.098e-04
DDX59	-6.817231	5.568727e-11	1.284e-07	2.963e-04
SCN9A	-6.824117	5.308058e-11	1.284e-07	2.963e-04
PPP1R12B	-6.753589	8.653910e-11	1.747e-07	3.525e-04
KDM5B	-6.640724	1.872871e-10	3.360e-07	5.883e-04
LOXHD1	-6.607795	2.340518e-10	3.779e-07	5.883e-04
KIAA0825	6.584929	2.730625e-10	4.008e-07	5.883e-04
DPY19L3	-6.424309	7.948193e-10	1.069e-06	9.849e-04
DENND1B	-6.395972	9.571764e-10	1.189e-06	9.849e-04
MUC20	6.380131	1.061617e-09	1.224e-06	9.849e-04
CYP4X1	-6.358992	1.218491e-09	1.230e-06	9.849e-04
ZSCAN29	6.365717	1.166281e-09	1.230e-06	9.849e-04
NSD2	-6.345877	1.326970e-09	1.260e-06	9.849e-04
PIGG	-6.337002	1.405678e-09	1.261e-06	9.849e-04
BPTF	6.324699	1.522362e-09	1.294e-06	9.849e-04
PTPN13	6.316415	1.606200e-09	1.297e-06	9.849e-04
PPFIA4	-6.295575	1.837570e-09	1.349e-06	9.849e-04
CEP192	6.295732	1.835719e-09	1.349e-06	9.849e-04
WWP1	-6.271818	2.141134e-09	1.503e-06	9.849e-04
PTCD3	6.248656	2.483998e-09	1.671e-06	9.849e-04
AKAP9	6.239050	2.641410e-09	1.706e-06	9.849e-04

Positive Rho Non-permuted



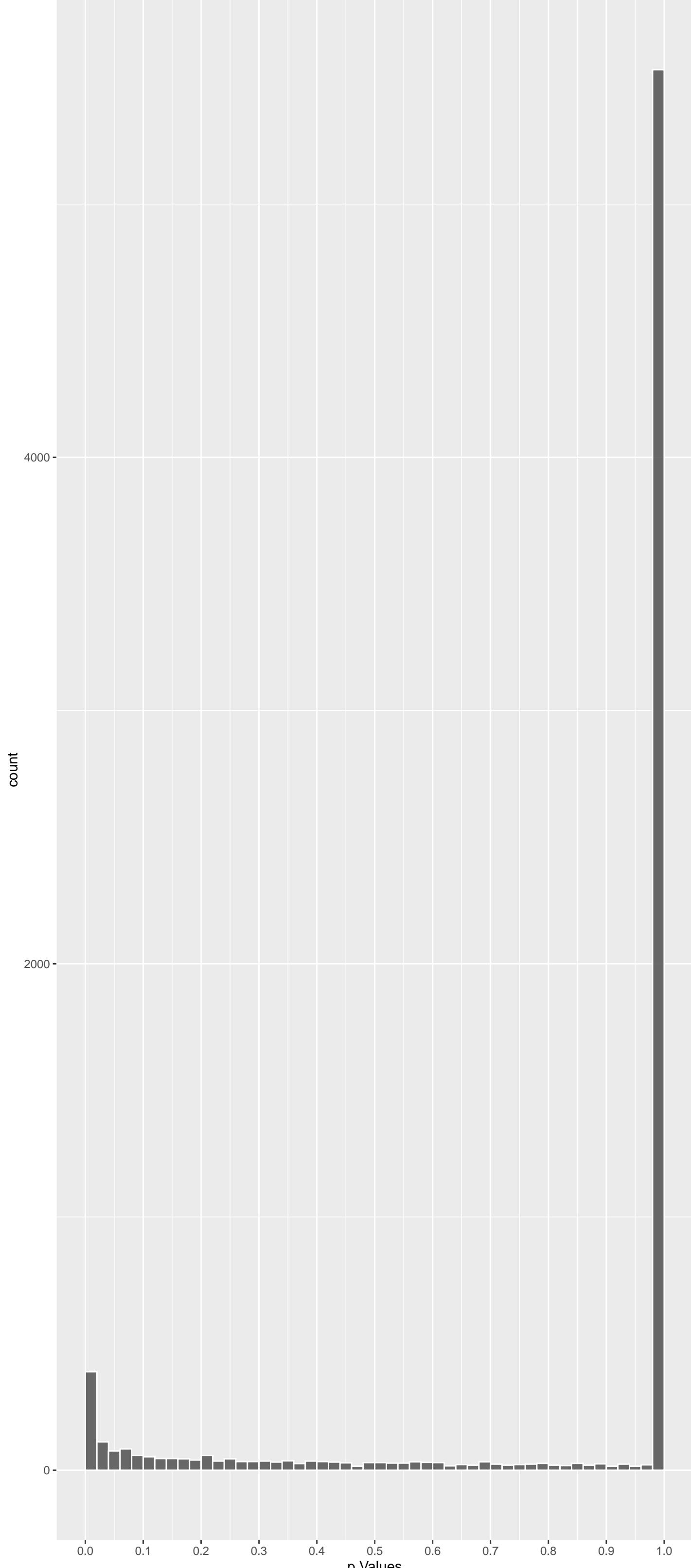
Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
THADA	7.364298	1.068487e-12	8.626e-09	5.097e-05
KIAA0825	6.584929	2.730625e-10	4.008e-07	5.883e-04
MUC20	6.380131	1.061617e-09	1.224e-06	9.849e-04
ZSCAN29	6.365717	1.166281e-09	1.230e-06	9.849e-04
BPTF	6.324699	1.522362e-09	1.294e-06	9.849e-04
PTPN13	6.316415	1.606200e-09	1.297e-06	9.849e-04
CEP192	6.295732	1.835719e-09	1.349e-06	9.849e-04
PTCD3	6.248656	2.483998e-09	1.671e-06	9.849e-04
AKAP9	6.239050	2.641410e-09	1.706e-06	9.849e-04
MBD4	6.221432	2.955821e-09	1.708e-06	9.849e-04

Top genes by Q-Value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
NAV1	-7.297458	1.759527e-12	9.470e-09	5.097e-05
BCLAF3	-7.533746	2.958306e-13	4.776e-09	5.097e-05
THADA	7.364298	1.068487e-12	8.626e-09	5.097e-05
MMP16	-6.962093	2.011525e-11	6.496e-08	2.098e-04
ZBTB41	-7.008288	1.447507e-11	5.843e-08	2.098e-04
DDX59	-6.817231	5.568727e-11	1.284e-07	2.963e-04
SCN9A	-6.824117	5.308058e-11	1.284e-07	2.963e-04
PPP1R12B	-6.753589	8.653910e-11	1.747e-07	3.525e-04
KDM5B	-6.640724	1.872871e-10	3.360e-07	5.883e-04
LOXHD1	-6.607795	2.340518e-10	4.008e-07	5.883e-04
KIAA0825	6.584929	2.730625e-10	3.779e-07	5.883e-04
MBD4	6.221432	2.955821e-09	1.708e-06	9.849e-04
PTCD3	6.248656	2.483998e-09	1.671e-06	9.849e-04
BLMH	-6.221112	2.961858e-09	1.708e-06	9.849e-04
KCNT2	-6.225867	2.873409e-09	1.708e-06	9.849e-04
MUC20	6.380131	1.061617e-09	1.224e-06	9.849e-04
BPTF	6.324699	1.522362e-09	1.294e-06	9.849e-04
AKAP9	6.239050	2.641410e-09	1.706e-06	9.849e-04
PPFIA4	-6.295575	1.837570e-09	1.349e-06	9.849e-04
CYP4X1	-6.358992	1.218491e-09	1.230e-06	9.849e-04
ZSCAN29	6.365717	1.166281e-09	1.230e-06	9.849e-04
PTPN13	6.316415	1.606200e-09	1.297e-06	9.849e-04
PIGG	-6.337002	1.405678e-09	1.261e-06	9.849e-04
CEP192	6.295732	1.835719e-09	1.349e-06	9.849e-04
NSD2	-6.345877	1.326970e-09	1.260e-06	9.849e-04

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
BCLAF3	-7.533746	2.958306e-13	4.776e-09	5.097e-05
NAV1	-7.297458	1.759527e-12	9.470e-09	5.097e-05
ZBTB41	-7.008288	1.447507e-11	5.843e-08	2.098e-04
MMP16	-6.962093	2.011525e-11	6.496e-08	2.098e-04
DDX59	-6.817231	5.568727e-11	1.284e-07	2.963e-04
SCN9A	-6.824117	5.308058e-11	1.284e-07	2.963e-04
PPP1R12B	-6.753589	8.653910e-11	1.747e-07	3.525e-04
KDM5B	-6.640724	1.872871e-10	3.360e-07	5.883e-04
LOXHD1	-6.607795	2.340518e-10	3.779e-07	5.883e-04
DPY19L3	-6.424309	7.948193e-10	1.069e-06	9.849e-04

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Schizophrenia	-0.05642985	1625	1.744e-13	1.711e-09	NAV1:2 MMP16:4 NDST3:19 CSMD1:23 NOS1AP:25 HERC2:34
Autism Spectrum Disorders	-0.08636153	483	1.116e-10	4.921e-07	MMP16:4 CSMD1:23 RYR2:32 HERC2:34 LRNN3:41 EHMT1:44
Autistic Disorder	-0.07640121	615	1.505e-10	4.921e-07	ATF6:26 RYR2:32 DOCK4:35 EHMT1:44 CNTN3:51 CHL1:57
Epilepsy, Temporal Lobe	-0.11544030	164	3.612e-07	7.821e-04	KCNQ3:69 GRM2:88 GABRB3:124 PAG1:141 SLC2A1:290 GRIK1:297
Alzheimer's Disease	-0.03842108	1666	3.986e-07	7.821e-04	BLMH:18 CSMD1:23 RYR2:32 F13B:39 EHMT1:44 SORL1:47
Alcoholic intoxication, Chronic	-0.07554291	376	5.742e-07	9.390e-04	ADCY1:53 GRM2:88 CNTN4:91 HTR1B:114 GABRR1:123 GABRB3:124
Channelopathies	-0.20441645	48	9.747e-07	1.366e-03	SCN9A:5 RYR2:32 ANK2:42 CACNA1S:100 CNGB3:169 SHANK3:171
Generalized seizures	-0.12186189	120	4.172e-06	4.539e-03	HTR1B:114 GABRB3:124 SYNJ1:179 CHRMT1:287 SLC2A1:290 GRIK1:297
Mood Disorders	-0.07745801	303	3.925e-06	4.539e-03	ADCY1:53 CHL1:57 VIPR2:58 GRM2:88 HTR1B:114 TAC1:150
nervous system disorder	-0.06868849	382	4.626e-06	4.539e-03	EHMT1:44 SETX:190 SHANK2:201 SLC2A1:290 GRIK1:297 PON1:314
Diabetes Mellitus, Non-Insulin-Dependent	-0.03786013	1350	5.123e-06	4.569e-03	NOS1AP:25 ATF6:26 RYR2:32 PCNX2:40 ANK2:42 EHMT1:44
Mental Depression	-0.05859171	509	7.183e-06	5.873e-03	NOS1AP:25 ADCY1:53 CHL1:57 VIPR2:58 HTR1B:114 GABRB3:124
Neuralgia	-0.14089322	83	9.335e-06	7.045e-03	SCN9A:5 GRM2:88 TAC1:150 TRPM8:167 DRD2:333 TACR1:365
Aura	-0.16468777	59	1.265e-05	8.275e-03	GABRB3:124 CHRMT1:287 SCN2A:306 HCN1:405 TSC1:478 SLC12A5:555
Awakening Epilepsy	-0.16446877	59	1.265e-05	8.275e-03	GABRB3:124 CHRMT1:287 SCN2A:306 HCN1:405 TSC1:478 SLC12A5:555
Bipolar Disorder	-0.04804988	724	1.354e-05	8.305e-03	DPY19L3:10 NDST3:19 CSMD1:23 NOS1AP:25 SORL1:47 ADCY1:53
Seizures, Focal	-0.11256480	123	1.625e-05	8.390e-03	SCN9A:5 KCNQ3:69 HTR1B:114 CHRMT1:287 SLC2A1:290 GRIK1:297
HIV Infections	-0.05060780	639	1.558e-05	8.390e-03	VIPR1:62 IL16:103 TMEM132D:126 GEM1:134 CYLD:137 TAC1:150
Mental disorders	-0.07524544	282	1.498e-05	8.390e-03	CSMD1:23 NOS1AP:25 MYT1:86 HTR1B:114 PLPPR4:128 SHANK3:171
Depressive disorder	-0.04937112	646	2.270e-05	1.113e-02	NOS1AP:25 ADCY1:53 CHL1:57 VIPR2:58 HTR1B:114 WDR11:120
Major Depressive Disorder	-0.05774971	460	2.517e-05	1.176e-02	VIPR2:58 GRM2:88 HTR1B:114 TAC1:150 MCTP2:158 DDC:200
Epilepsy, Cryptogenic	-0.15397051	61	3.242e-05	1.210e-02	GABRB3:124 CHRMT1:287 SCN2A:306 HCN1:405 TSC1:478 SLC12A5:555
Increased CSF lactate	0.16456012	53	3.453e-05	1.210e-02	LRPPRC:39 TIMMDC1:438 NDUFA9:570 TMEM126B:644 NDUFA1:891 GFMI1:1036
Mitochondrial Diseases	0.06506242	347	3.451e-05	1.210e-02	LRPPRC:39 ECSIT:52 GF2M:86 MTPAP:121 POLG2:122 COXA1:124
Obesity	-0.03166200	1647	3.219e-05	1.210e-02	ATF6:26 HERC2:34 EHMT1:44 SORL1:47 LGR:68 CNTN4:91
Psychotic Disorders	-0.07299263	276	3.247e-05	1.210e-02	LMOD2:56 GRM2:88 HTR1B:114 DDC:200 GABRG3:240 KIDINS220:281
Tonic Seizures	-0.12221321	98	2.981e-05	1.210e-02	HTR1B:114 CHRMT1:287 SLC2A1:290 GRIK1:297 SCN2A:306 DRD2:333
Unipolar Depression	-0.05712210	463	2.908e-05	1.210e-02	CSMD1:23 HTR1B:114 MCTP2:158 DDC:200 SELP:203 EGFR:230
Neuroblastoma	-0.03299064	1453	4.067e-05	1.376e-02	KDM5B:8 HERC2:34 DOCK4:35 URGCP:37 LRNN3:41 ANK2:42
Abnormal behavior	-0.06536177	331	4.782e-05	1.564e-02	CSMD1:23 NOS1AP:25 GRM2:88 HTR1B:114 PLPPR4:128 TAC1:150
Absence Seizures	-0.10966078	115	5.005e-05	1.584e-02	SCN9A:5 EHMT1:44 HTR1B:114 CHRMT1:287 SLC2A1:290 GRIK1:297
Complex partial seizures	-0.11173103	110	5.302e-05	1.626e-02	HTR1B:114 CHRMT1:287 SLC2A1:290 GRIK1:297 DRD2:333 HCN1:405
Andersen Syndrome	-0.24630530	22	6.377e-05	1.896e-02	RYR2:32 ANK2:42 KCNJ12:195 PON1:314 KCNJ5:546 MTHFR:655
NADH(Q)1 Oxidoreductase deficiency	0.22933561	25	7.242e-05	2.090e-02	TIMMDC1:438 TMEM126B:644 NDUFA1:891 NDUFA6:1067 NDUFS3:1122 NDUFB10:1293
Alzheimer's Disease, Focal Onset	-0.13234083	74	8.417e-05	2.204e-02	BLMH:18 SORL1:47 ARC:202 BAX:309 IGF1R:363 BIN1:382
Acute Confusional Senile Dementia	-0.13234083	74	8.417e-05	2.204e-02	BLMH:18 SORL1:47 ARC:202 BAX:309 IGF1R:363 BIN1:382
Asthma	-0.03626775	1061	8.841e-05	2.204e-02	PPP1R12B:7 DENND1B:11 CSMD1:23 ATF6:26 RYR2:32 HERC2:34
Central neuroblastoma	-0.03189942	1414	8.821e-05	2.204e-02	KDM5B:8 HERC2:34 DOCK4:35 URGCP:37 LRNN3:41 ANK2:42
Hypertensive disease	-0.03567892	1108	8.375e-05	2.204e-02	CSMD1:23 MOV10:31 RYR2:32 SORL1:47 SLC22A6:59 CNTN4:91
Tonic - clonic seizures	-0.09410443	146	8.987e-05	2.204e-02	SCN9A:5 KCNQ3:69 HTR1B:114 GABRB3:124 SYNJ1:179 CHRMT1:287

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.09301802	555	8.918e-14	2.893e-10	CSMD1:23 RYR2:32 UGT8:36 PCNX2:40 KCNQ3:69 IKZF1:76
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.13514559	259	7.904e-14	2.893e-10	VIPR2:58 VIPR1:62 GRM2:88 HTR1B:114 HRH2:118 GABRR1:123
REACTOME_NEURONAL_SYSTEM	-0.10806347	385	4.027e-13	8.709e-10	PPFIA4:15 ADCY1:53 KCNQ3:69 APBA2:85 KCNV1:90 KCNF1:98
BENPORATH_ES_WITH_H3K27ME3	-0.06539734	983	6.091e-12	9.879e-09	LMOD1:20 CSMD1:23 SYTE:45 BRINP:66 KCNQ3:69 HSF4:70
REACTOME_SIGNALING_BY_GPCR	-0.07888953	629	1.874e-11	2.432e-08	ADCY1:53 GPR37L1:54 VIPR2:58 VIPR1:62 GRM2:88 HTR1B:114
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.19077763	100	4.472e-11	4.836e-08	PGAP6:197 SPBS3:489 ZNF213:564 PRSS27:587 DECR2:649 WDR24:837
REACTOME_GPCR_LIGAND_BINDING	-0.08938534	396	1.175e-09	1.089e-06	GPR37L1:54 VIPR2:58 VIPR1:62 GRM2:88 HTR1B:114 HRH2:118
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	-0.09588533	331	2.244e-09	1.820e-06	RYR2:32 VIPR1:62 ZNF536:136 PTGFRN:140 BNC1:181 KCNK1:187
BENPORATH_SUZ12_TARGETS	-0.05813332	918	3.200e-09	2.307e-06	CYP4X1:12 CSMD1:23 SYTE:45 VIPR2:58 BRINP:66 KCNQ3:69
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.27105765	38	7.424e-09	4.491e-06	CHST12:160 ADAP1:380 INTS1:436 SUN1:487 TMEM184A:758 TTYH3:850
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.09818012	294	7.614e-09	4.491e-06	GPR37L1:54 HTR1B:114 HRH2:118 PLPPR4:128 TAC1:150 S1PR1:222
REACTOME_POTASSIUM_CHANNELS	-0.17178428	91	1.513e-08	7.550e-06	KCNQ3:69 KCNV1:90 KCNF1:98 KCNU14:149 KCNA10:185 KCNK1:187
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.23914035	47	1.423e-08	7.550e-06	ECSIT:52 COA1:124 TIMMDC1:438 DMAC2:510 TMEM126B:644 TMEM186:753
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.11406410	206	1.763e-08	8.169e-06	GPR37L1:54 HTR1B:114 HRH2:118 OPN3:250 GPR17:279 CHRMT1:287
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	-0.07791280	419	5.021e-08	2.172e-05	PCNX2:40 SYTE:45 KCNV1:90 HS3ST2:53 SLC35F3:144 CLM1:208
REACTOME_COMPLEX_I_BIOGENESIS	0.22501657	48	6.968e-08	2.825e-05	ECSIT:52 COA1:124 TIMMDC1:438 NDUFA9:570 TMEM126B:644 TMEM186:753
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNEL	-0.23936212	42	8.035e-08	3.067e-05	KCNQ3:69 KCNV1:90 KCNF1:98 KCNA10:185 KCNA4:216 KCNAB1:236
REACTOME_G_ALPHA_1_SIGNALING_EVENTS	-0.09487304	269	9.097e-08	3.279e-05	ADCY1:53 GPR37L1:54 GRM2:88 HTR1B:114 ITPR1:186 OPN3:250
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.06759978	528	1.224e-07	4.181e-05	CAMSA2:21 RYR2:32 DOCK4:35 SORL1:47 CHL1:57 VIPR1:62
REACTOME_MUSCLE_CONTRACTION	-0.11095553	190	1.395e-07	4.526e-05	SCN9A:5 LMOD1:20 RYR2:32 KCNJ14:149 NEB:157 ITPR1:186
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.14868490	101	2.476e-07	7.650e-05	LRPPRC:39 ECSIT:52 COA1:124 TIMMDC1:438 NDUFA9:570 TMEM126B:644
WP_CALCIIUM_REGULATION_IN_CARDIAC_CELLS	-0.12656194	137	3.237e-07	9.546e-05	RYR2:32 ADCY1:53 CACNA1S:100 CACNA1B:152 ITPR1:186 GJC2:258
BENPORATH_EED_TARGETS	-0.04937037	928	4.325e-07	1.220e-04	CSMD1:23 VIPR2:58 BRINP:66 KCNQ3:69 HSF4:70 GPR88:72
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.05786627	661	4.552e-07	1.231e-04	KIAA0825:2 DLGAP5:12 KIF24:18 UBAP2:22 TBCCD3:135 PARPB7:47
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	-0.07963433	331	6.844e-07	1.708e-04	RYR2:32 VIPR1:62 HECW1:67 IKZF1:76 ZNF536:136 BNC1:181
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SY	-0.09225929	246	6.584e-07	1.708e-04	PPFIA4:15 ADCY1:53 GABRR1:123 GABRB3:124 CACNA1B:152 KCNJ12:195
REACTOME_MITOCHONDRIAL_TRANSLATION	0.14944352	92	7.390e-07	1.776e-04	PTCD3:8 GF2M:86 GADD45GIP1:199 MRPS31:244 MRP535:413 MTF12:429
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.15771680	81	9.375e-07	2.172e-04	LRPPRC:39 ECSIT:52 COA1:124 TIMMDC1:438 NDUFA9:570 TMEM126B:644
WP_OXIDATIVE_PHOSPHORYLATION	0.20731567	46	1.153e-06	2.580e-04	ATP6AF2:408 NDUFA9:570 ATP5PD:747 NDUVF3:952 ATP5PO:1120 NDUFS3:1122
REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-0.05495853	665	1.593e-06	3.445e-04	WWP1:16 RYR2:32 TRPM1:49 ADCY1:53 SLC22A6:59 ATP11C:63
HAMA_APOPTOSIS_VIA_TRAIL_UP	0.05693541	594	2.413e-06	5.051e-04	BPTF:5 PTPN13:6 CEP192:7 MBD4:10 DLGAP5:12 BDP1:16
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04088708	1165	3.285e-06	6.660e-04	NETO2:24 NOS1AP:25 HERC2:34 LRNN3:41 CHL1:57 UAP1:65
FISCHER_DREAM_TARGETS	0.04627947	882	3.730e-06	7.333e-04	CEP192:7 DLGAP5:12 LCORL1:14 KIF24:18 PARPB7:47 ATAD5:61
MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27	-0.09580381	199	3.895e-06	7.433e-04	CSMD1:23 ELFN1:46 GPR88:72 PTGFRN:140 KCNF1:98 KCNK1:187 CDHR1:234
YOSHIMURA_MAPK8_TARGETS_UP	-0.04133177	1108	4.233e-06	8.014e-04	SCN9A:5 KCNQ3:69 AQPF6:73 APBA2:85 RNF112:93 CACNA1S:100
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.06252872	452	5.667e-06	1.021e-03	BPTF:5 AKAP9:9 ZNF292:19 C2CD3:30 LRPPRC:39 MDN1:62
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR	-0.10141779	166	6.718e-06	1.178e-03	GPR37L1:54 TAC1:150 MCAR:361 TACR1:365 CCR1:517 UTS2R:538
LEE_TARGETS_OF_PTCH1_AND_SUFU_DN	-0.14131846	83	8.666e-06	1.480e-03	ITPR1:186 KCNK1:187 CALB1:271 CAMK2D:334 PRKCG:375 SEZ6L2:396
LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS	-0.03663151	1337	9.052e-06	1.506e-03	MMP16:4 SCN9A:5 KCNT2:17 LMOD1:20 CSMD1:23 DOCK4:35
REACTOME_CARDIAC_CONDUCTION	-0.11669499	121	9.448e-06	1.532e-03	SCN9A:5 RYR2:32 KCNJ14:149 ITPR1:186 KCNK1:187 KCNJ12:195

GO\_Biological\_Process\_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Chemical Synaptic Transmission (GO:00072	-0.12125643	256	2.892e-11	1.558e-07	KCNQ3:69 APBA2:85 GRM2:88 HTR1B:114 HRH2:118 GABRR1:123
Potassium Ion Transmembrane Transport (G	-0.15637176	132	5.992e-10	1.614e-06	KCNT2:17 KCNQ3:69 KCNV1:90 KCNF1:98 KCNJ14:149 KCNA10:185
NADH Dehydrogenase Complex Assembly (GO:	0.25216054	48	1.540e-09	1.801e-06	ECSIT:52 COA1:124 TMEM126A:202 DMAC2:510 NDUFA9:570 TMEM126B:644
Mitochondrial Respiratory Chain Complex	0.25216054	48	1.540e-09	1.801e-06	ECSIT:52 COA1:124 TMEM126A:202 DMAC2:510 NDUFA9:570 TMEM126B:644
Monoatomic Cation Transmembrane Transpor	-0.10645981	273	1.672e-09	1.801e-06	SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:98 CACNA1S:100
Metal Ion Transport (GO:0030001)	-0.13900836	156	2.274e-09	2.042e-06	SCN9A:5 RYR2:32 SLC17A4:43 KCNV1:90 KCNF1:98 CACNA1S:100
Modulation Of Chemical Synaptic Transmis	-0.15560987	118	5.613e-09	4.320e-06	GRM2:88 PLPPR4:128 CACNA1B:152 MCTP2:158 CDH2:188 DLGAP2:248
Mitochondrial Gene Expression (GO:0140005	0.16759059	100	7.500e-09	5.052e-06	PTCD3:8 POLRMT:53 FASTKD1:72 FASTKD5:74 GF2M:86 GADD45GIP1:199
Anterograde Trans-Synaptic Signaling (GO:	-0.12313147	182	1.113e-08	6.666e-06	KCNQ3:69 APBA2:85 GRM2:88 HTR1B:114 HRH2:118 GABRR1:123
Potassium Ion Transport (GO:0008613)	-0.14994468	120	1.490e-08	8.030e-06	KCNQ3:69 KCNV1:90 KCNF1:98 KCNA10:185 KCNK1:187 KCNJ12:195
Inorganic Cation Transmembrane Transport	-0.09821523	276	2.272e-08	1.113e-05	SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:98 CACNA1S:100
Regulation Of Synaptic Transmission, Glu	-0.21829470	54	2.944e-08	1.322e-05	TSZH3:55 GRM2:88 PLPPR4:128 SHANK3:171 CDH2:188 PTKB2:192
Mitochondrial Translation (GO:0032543)	0.15922756	96	7.303e-08	3.027e-05	PTCD3:8 GF2M:86 GADD45GIP1:199 MRPS31:244 MTF12:429 MTRF1:545
Mitochondrial Respiratory Chain Complex	0.17184681	77	1.914e-07	7.365e-05	ECSIT:52 COA1:124 TMEM126A:202 FASTKD3:330 DMAC2:510 NDUFA9:570
Calcium Ion Import Across Plasma Membran	-0.25595096	33	3.647e-07	1.310e-04	SCN9A:5 TRPM1:49 CACNA1S:100 CACNA1B:152 SCN2A:306 CLU:446
Mitochondrial RNA Metabolic Process (GO:	0.31571013	19	1.904e-06	6.412e-04	POLRMT:53 FASTKD1:72 FASTKD5:74 FASTKD3:330 TFB2M:636 TFM4:700
Inorganic Cation Import Across Plasma Me	-0.13968113	96	2.251e-06	7.135e-04	SCN9A:5 TRPM1:49 CACNA1S:100 KCNJ14:149 CACNA1B:152 KCNJ12:195
Proton Motive Force-Driven Mitochondrial	0.19598948	47	3.387e-06	1.014e-03	NDUFA9:570 ATP5PD:747 NDUVF3:952 ATP5PO:1120 NDUFS3:1122 NDUFB10:1293
Positive Regulation Of Synaptic Transmis	-0.15876183	71	3.821e-06	1.029e-03	TSZH3:55 SHANK3:171 PTKB2:192 SHANK2:201 PLK2:204 RIMS1:559
RNA Modification (GO:0006400)	0.16488193	66	3.695e-06	1.029e-03	THADA:1 TRMT10A:41 TDDVD1:103 TRDMT1:302 KTI12:333 CTU2:448
Proton Motive Force-Driven ATP Synthesis	0.18590640	51	4.441e-06	1.139e-03	NDUFA9:570 ATP5PD:747 NDUVF3:952 ATP5PO:1120 NDUFS3:1122 NDUFB10:1293
Calcium Ion Transport (GO:0006816)	-0.12854594	105	5.527e-06	1.354e-03	RYR2:32 TRPM1:49 CACNA1S:100 TRPM6:167 TRPCA:169 ITPR1:186
RNA Methylation (GO:0030488)	0.21744950	36	6.392e-06	1.498e-03	THADA:1 TRMT10A:41 TRMT5:217 TRDMT1:302 TRMT10B:378 TRMT61B:471
Cardiac Conduction (GO:0081337)	-0.19474479	44	7.936e-06	1.782e-03	ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546
Oxidative Phosphorylation (GO:0006119)	0.17330010	55	8.898e-06	1.918e-03	NDUFA9:570 ATP5PD:747 TEFM:789 NDUVF3:952 ATP5PO:1120 NDUFS3:1122
Learning (GO:0007612)	0.19496651	41	9.977e-06	2.067e-03	GP8R872 SHANK3:171 SYNU1:179 SHANK2:201 DRD2:333 MAPK8IP2:400
Adenylate Cyclase-Inhibiting G Protein-C	-0.18493473	46	1.445e-05	2.894e-03	GP8R73L:54 HTR1B:114 CHRMT:287 DRD2:333 GRM5:588 HTR1A:675
Regulation Of Heart Rate By Cardiac Con	-0.19735113	39	2.021e-05	3.888e-03	ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546
Mitochondrial Electron Transport, NADH T	0.21927465	31	2.402e-05	4.314e-03	NDUFA9:570 NDUFA1:891 NDUVF3:952 NDUFS3:1122 NDUFB10:1293 NDUFB9:1483
Regulation Of Cold-Induced Thermogenesis	-0.10437128	138	2.402e-05	4.314e-03	EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGFR:363
Regulation Of Monoatomic Cation Transmem	-0.19560449	38	3.039e-05	5.282e-03	KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BIP1A:626 HCN4:861
Membrane Organization (GO:0061024)	-0.09533025	155	4.412e-05	7.087e-03	ANK2:42 SYNU1:179 EGF2R:230 BIN1:382 LMNB1:415 ACE2A:496
Positive Regulation Of Metabolic Process	-0.11741028	101	4.682e-05	7.087e-03	EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGFR:363 CD36:408
Regulation Of DNA-templated Transcriptio	0.03124259	1647	4.213e-05	7.087e-03	ZSCAN29:4 BPTF:5 LCOLR:14 ZNF292:19 ZFP90:32 NSD1:65
Regulation Of Monoatomic Ion Transmemba	-0.14952550	62	4.735e-05	7.087e-03	ANK2:42 PTKB2:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606
Regulation Of Neurotransmitter Receptor	-0.18857046	39	4.642e-05	7.087e-03	NETO1:87 PTKB2:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:846
Regulation Of Potassium Ion Transport (G	-0.21519344	29	6.082e-05	8.857e-03	ANK2:42 PTKB2:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688
Positive Regulation Of Cold-Induced Ther	-0.11965058	93	6.828e-05	9.681e-03	EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGFR:363 CD36:408
Sister Chromatid Segregation (GO:0000819	0.19978480	33	7.178e-05	9.917e-03	SPAG5:63 SG01:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681
Aerobic Respiration (GO:0009606)	0.15425124	54	8.927e-05	1.203e-02	MTFR2:407 NDUFA9:570 TEFM:789 NDUVF3:952 NDUFS3:1122 NDUFB10:1293