

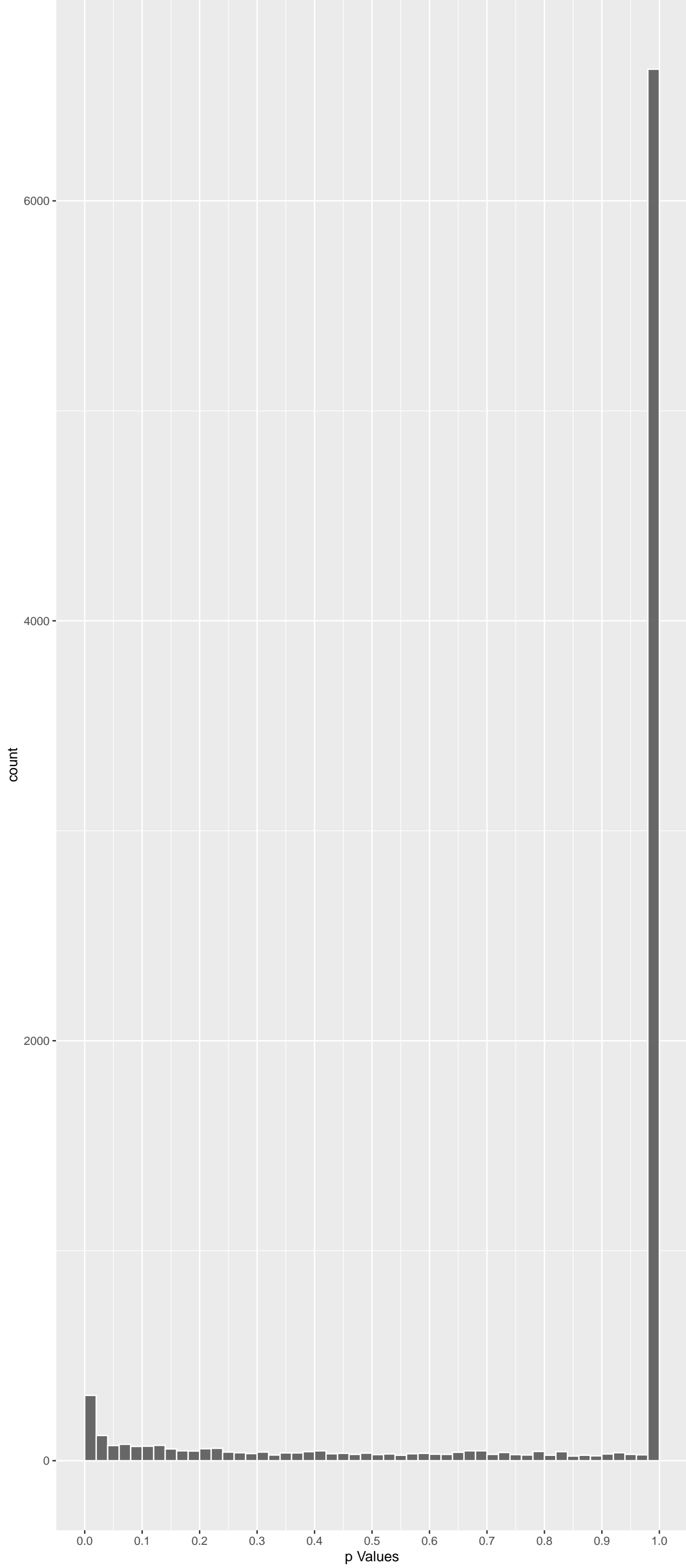
Top genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
WNK4	6.642342	1.852427e-10	1.334e-06	7.181e-03
ADGRV1	6.599271	2.479106e-10	1.334e-06	7.181e-03
FGD5	6.702983	1.225244e-10	1.334e-06	7.181e-03
UAP1	-6.498508	4.867240e-10	1.965e-06	7.930e-03
NOS1AP	-6.395693	9.589227e-10	3.097e-06	7.991e-03
ANK1	6.296786	1.823285e-09	3.959e-06	7.991e-03
PGC	6.303983	1.740550e-09	3.959e-06	7.991e-03
TRPM1	-6.285429	1.961696e-09	3.959e-06	7.991e-03
ATF6	-6.209910	3.180903e-09	5.707e-06	1.024e-02
LOXHD1	-6.132459	5.191875e-09	8.383e-06	1.194e-02
DDX20	-6.113669	5.841981e-09	8.575e-06	1.194e-02
LRRN3	-6.091125	6.727194e-09	9.051e-06	1.194e-02
ZNF292	6.066572	7.840154e-09	9.737e-06	1.194e-02
TSHZ3	-6.044811	8.975105e-09	1.035e-05	1.194e-02
SHISA4	-6.003277	1.160244e-08	1.249e-05	1.276e-02
C2CD2L	-5.990806	1.252824e-08	1.264e-05	1.276e-02
ADGRF1	5.915210	1.988709e-08	1.889e-05	1.794e-02
ARHGEF12	-5.893931	2.262691e-08	2.030e-05	1.821e-02
CNTN3	-5.872755	2.571674e-08	2.185e-05	1.832e-02
PRTG	5.853431	2.889203e-08	2.332e-05	1.832e-02
IDO2	5.840149	3.129242e-08	2.406e-05	1.832e-02
KIAA0825	5.826244	3.401318e-08	2.496e-05	1.832e-02
RAVER2	5.806816	3.820328e-08	2.682e-05	1.883e-02
MCF2L	5.777441	4.550723e-08	3.061e-05	2.060e-02
NCAN	5.762856	4.962134e-08	3.205e-05	2.070e-02

Top genes by Q-Value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
WNK4	6.642342	1.852427e-10	1.334e-06	7.181e-03
ADGRV1	6.599271	2.479106e-10	1.334e-06	7.181e-03
FGD5	6.702983	1.225244e-10	1.334e-06	7.181e-03
UAP1	-6.498508	4.867240e-10	1.965e-06	7.930e-03
ANK1	6.296786	1.823285e-09	3.959e-06	7.991e-03
NOS1AP	-6.395693	9.589227e-10	3.097e-06	7.991e-03
PGC	6.303983	1.740550e-09	3.959e-06	7.991e-03
TRPM1	-6.285429	1.961696e-09	3.959e-06	7.991e-03
ATF6	-6.209910	3.180903e-09	5.707e-06	1.024e-02
TSHZ3	-6.044811	8.975105e-09	1.035e-05	1.194e-02
ZNF292	6.066572	7.840154e-09	9.737e-06	1.194e-02
DDX20	-6.113669	5.841981e-09	8.575e-06	1.194e-02
LRRN3	-6.091125	6.727194e-09	9.051e-06	1.194e-02
LOXHD1	-6.132459	5.191875e-09	8.383e-06	1.194e-02
C2CD2L	-5.990806	1.252824e-08	1.264e-05	1.276e-02
SHISA4	-6.003277	1.160244e-08	1.249e-05	1.276e-02
ADGRF1	5.915210	1.988709e-08	1.889e-05	1.794e-02
ARHGEF12	-5.893931	2.262691e-08	2.030e-05	1.821e-02
CNTN3	-5.872755	2.571674e-08	2.185e-05	1.832e-02
PRTG	5.853431	2.889203e-08	2.332e-05	1.832e-02
IDO2	5.840149	3.129242e-08	2.406e-05	1.832e-02
KIAA0825	5.826244	3.401318e-08	2.496e-05	1.832e-02
RAVER2	5.806816	3.820328e-08	2.682e-05	1.883e-02
MCF2L	5.777441	4.550723e-08	3.061e-05	2.060e-02
NCAN	5.762856	4.962134e-08	3.205e-05	2.070e-02

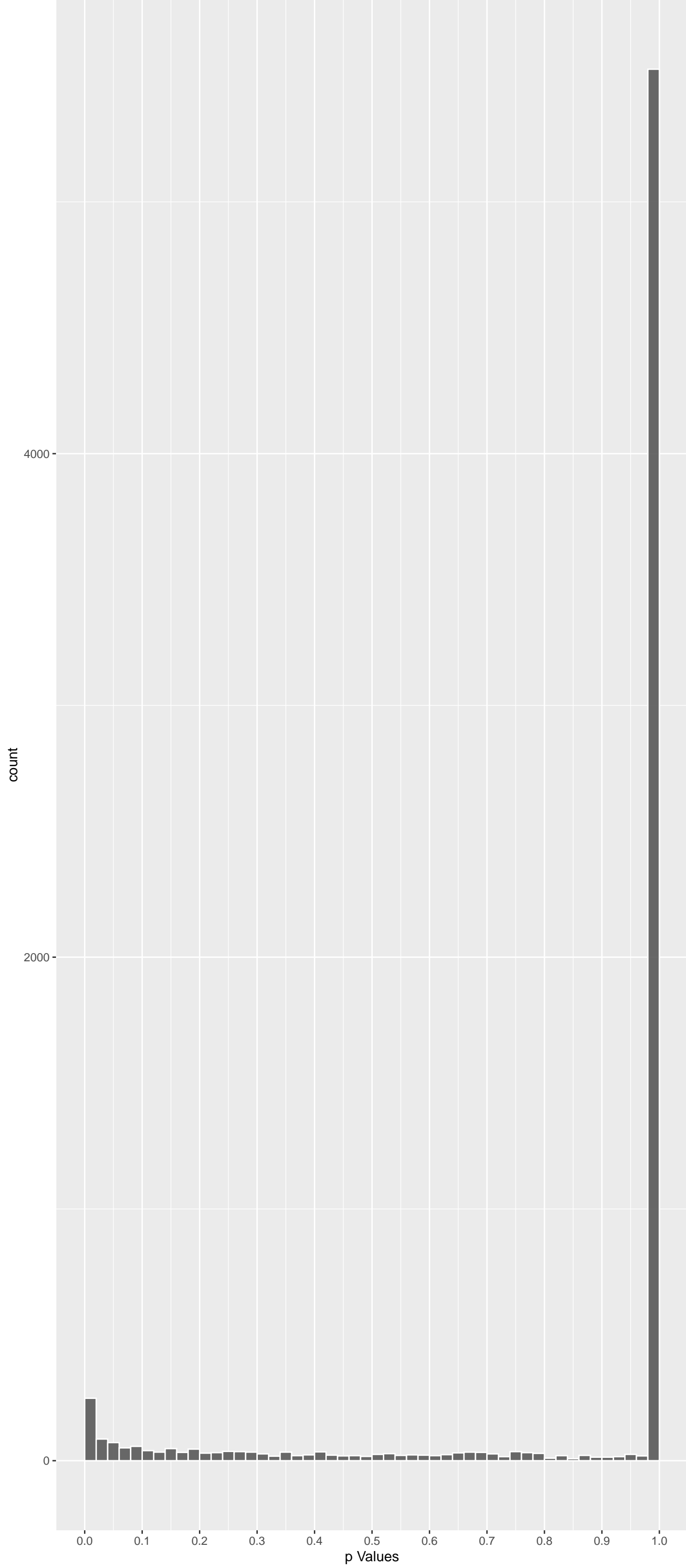
Positive Rho Non-permuted



Top Positive genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
WNK4	6.642342	1.852427e-10	1.334e-06	7.181e-03
ADGRV1	6.599271	2.479106e-10	1.334e-06	7.181e-03
FGD5	6.702983	1.225244e-10	1.334e-06	7.181e-03
ANK1	6.296786	1.823285e-09	3.959e-06	7.991e-03
PGC	6.303983	1.740550e-09	3.959e-06	7.991e-03
ZNF292	6.066572	7.840154e-09	9.737e-06	1.194e-02
ADGRF1	5.915210	1.988709e-08	1.889e-05	1.794e-02
PRTG	5.853431	2.889203e-08	2.332e-05	1.832e-02
IDO2	5.840149	3.129242e-08	2.406e-05	1.832e-02
KIAA0825	5.826244	3.401318e-08	2.496e-05	1.832e-02

Negative Rho Non-permuted



Top Negative genes by P-value non-permuted

Gene	Rho	P	p.adj	qValueNoperm
UAP1	-6.498508	4.867240e-10	1.965e-06	7.930e-03
NOS1AP	-6.395693	9.589227e-10	3.097e-06	7.991e-03
TRPM1	-6.285429	1.961696e-09	3.959e-06	7.991e-03
ATF6	-6.209910	3.180903e-09	5.707e-06	1.024e-02
LOXHD1	-6.132459	5.191875e-09	8.383e-06	1.194e-02
DDX20	-6.113669	5.841981e-09	8.575e-06	1.194e-02
LRRN3	-6.091125	6.727194e-09	9.051e-06	1.194e-02
TSHZ3	-6.044811	8.975105e-09	1.035e-05	1.194e-02
SHISA4	-6.003277	1.160244e-08	1.249e-05	1.276e-02
C2CD2L	-5.990806	1.252824e-08	1.264e-05	1.276e-02

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Autism Spectrum Disorders	-0.07395350	483	3.320e-08	1.629e-04	LRRN3:7 TSHZ3:8 HERC2:13 CNTN4:26 RYR2:32 CARMIL1:55
Schizophrenia	-0.04257165	1625	2.731e-08	1.629e-04	NOS1AP:2 TRPM1:3 HERC2:13 NDS3:22 CNTN4:26 ADCY1:43
Channelpathies	-0.21401913	48	2.949e-07	9.643e-04	ANK2:15 RYR2:32 SCN9A:44 CNGB3:105 CACNA1S:355 HCN1:381
Autistic Disorder	-0.05612765	615	2.535e-06	5.818e-03	ATF6:4 CNTN3:12 CNTN4:26 RYR2:32 ZNF277:35 CHL1:76
HIV Infections	-0.05482550	639	2.863e-06	5.818e-03	VIPR1:24 CYLD:45 CXCR5:46 APOA1:73 IL16:113 SAMHD1:114
Andersen Syndrome	-0.28378140	22	4.089e-06	6.687e-03	ANK2:15 RYR2:32 MTHFR:123 KCNJ12:139 SCN5A:698 PON1:810
Alzheimer's Disease	-0.03247652	1666	1.825e-05	2.558e-02	IREB2:29 RYR2:32 SYNJ1:34 F13B:39 CSF1:51 RNF1:12:59
nervous system disorder	-0.06119901	382	4.473e-05	5.486e-02	MTHFR:123 SETX:194 GLUL:266 DRD2:296 SLC2A1:308 SHANK2:364
CATARACT_AUTOSOMAL DOMINANT	-0.36549345	10	6.279e-05	6.845e-02	GJA8:142 MIP:344 CRYAA2:346 BFSPP:2412 CRYAA:480 CRYBB1:865
Seizures, Focal	-0.10086988	123	1.150e-04	8.056e-02	SCN9A:44 KCNQ3:168 DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387
Complex partial seizures	-0.1114e-04	110	1.114e-04	8.056e-02	VPS11:270 DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416
Generalized seizures	-0.10370761	120	8.968e-05	8.056e-02	SYNJ1:34 DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416
Myocardial Ischemia	-0.05866438	376	1.033e-04	8.056e-02	ANK2:15 RYR2:32 APOA1:73 ACE2:87 SELP:93 MTHFR:123
Sinus Node Dysfunction (disorder)	-0.27046641	17	1.132e-04	8.056e-02	ANK2:15 SCN3B:279 HCNA:375 SCN5A:698 TGFBI:704 CACNA1D:778
Cataract, Central Saccular, With Sutral	-0.44370818	6	1.672e-04	1.035e-01	GJA8:142 MIP:344 BFSPP:2412 CRYBA1:682 CRYGS:349 CRYBB2:2266
Absence Seizures	-0.10105926	115	1.860e-04	1.035e-01	SCN9A:44 DRD2:296 SLC2A1:308 EHMT1:376 HCN1:381 CHRNA3:387
Nicotine Dependence	-0.10345162	110	1.823e-04	1.035e-01	CHRM2:144 CYP2E1:254 DRD2:296 RPTOR:337 CHRNA3:387 DRD5:418
Torsades de Pointes	-0.26951156	16	1.900e-04	1.035e-01	ANK2:15 SCN5A:698 KCNQ1:892 ADRB1:909 KCNH2:958 KCNA4:966
Neuralgia	-0.11767184	83	2.143e-04	1.106e-01	SCN9A:44 CXCR5:46 GRM2:63 TAC1:132 DRD2:296 HCN1:381
Asthma	-0.03345590	1061	2.987e-04	1.127e-01	ATF6:4 HERC2:13 SYNPO2:28 RYR2:32 SFSWAP:58 CSMD1:62
Atrial Fibrillation	-0.06748397	244	2.983e-04	1.127e-01	ANK2:15 RYR2:32 LYST:64 ACE2:87 MTHFR:123 TAC1:132
Hypocalcemia	0.15649098	45	2.834e-04	1.127e-01	RREB1:68 CLDN16:100 VDR:318 GCM2:403 IFT122:424 SLC4A1:490
Psychotic Disorders	-0.06414030	276	2.608e-04	1.127e-01	GRM2:63 MTHFR:123 LMOD2:154 BCL9:226 KIDINS220:248 GLUL:266
Renal salt wasting	0.26297700	16	2.710e-04	1.127e-01	CYP11A1:170 CLCNKB:282 STAR:288 CLCNKA:301 SCN1A:737 CYP21A2:855
Severe myopia	-0.11068269	91	2.679e-04	1.127e-01	TRPM1:3 ATF6:4 CNGB3:105 GRM6:148 IGFBP3:234 PDE6B:258
Tonic Seizures	-0.10655463	98	2.726e-04	1.127e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRMI:420
Mammary Neoplasms	-0.02516443	2000	3.389e-04	1.146e-01	CNTN3:12 HERC2:13 VIPR1:24 KDM5B:27 CXCR5:46 CSF1:51
Nuclear cataract	-0.18389498	32	3.195e-04	1.146e-01	HSF4:19 GJA8:142 MIP:344 FTO:457 KCNAB1:469 CRYAA:480
Tetany	0.22631056	21	3.313e-04	1.146e-01	RREB1:68 CLDN16:100 GCM2:403 JMD1C:910 TRPM6:979 SLC12A1:1014
Alcoholic Intoxication, Chronic	-0.05931246	376	4.381e-04	1.249e-01	CNTN4:26 ADCY1:43 GRM2:63 DSCAML1:98 MTHFR:123 TAC1:132
Diabetes Mellitus, Non-Insulin-Dependent	-0.02303266	1350	4.713e-04	1.249e-01	NOS1AP:2 TRPM1:3 ATF6:4 ARHGEF12:11 ANK2:15 VIPR1:24
Epilepsy, Cryptogenic	-0.12779625	61	5.621e-04	1.249e-01	CHRM2:144 HCN1:381 CHRM1:420 SCN1A:450 SLC12A5:519 GABRB3:630
Epilepsy, Temporal Lobe	-0.07614066	164	7.893e-04	1.249e-01	GRM2:63 KCNQ3:168 ACOT7:240 BIN1:256 GULUL:266 SLC2A1:308
Seizures, Auditory	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRMI:420
Seizures, Clonic	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRMI:420
Seizures, Sensory	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRMI:420
Seizures, Somatosensory	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRMI:420
Ventricular tachycardia, polymorphic	-0.34365553	8	7.628e-04	1.249e-01	RYR2:32 HCNA:375 SCN5A:698 KCNQ1:892 KCNH2:958 CASQ2:1815
Atonic Absence Seizures	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRMI:420
Aura	-0.13113566	59	4.992e-04	1.249e-01	CHRM2:144 HCN1:381 CHRMI:420 SCN1A:450 SLC12A5:519 GABRB3:630

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_SIGNALING_BY_GPCR	-0.07377460	629	3.384e-10	2.195e-06	ARHGEF12:11 VIPR1:24 ADCY1:43 CXCR5:46 GRM2:63 FGD3:77
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.09093491	294	5.641e-09	1.088e-05	CXCR5:46 TAC1:132 CHRM2:144 PLPPR4:152 NTSR1:153 UTS2R:167
REACTOME_MUSCLE_CONTRACTION	-0.12223484	190	6.586e-09	1.088e-05	RYR2:32 SCN9A:44 LMOD1:57 HIPK1:60 ITPR1:117 ITGA1:119
REACTOME_GPCR_LIGAND_BINDING	-0.08525270	396	6.537e-09	1.088e-05	VIPR1:24 CXCR5:46 GRM2:63 TAC1:132 CHRM2:144 GRM6:148
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.10117404	259	2.233e-08	2.885e-05	VIPR1:24 GRM2:63 CHRM2:144 GRM6:148 NTSR1:153 UTS2R:167
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.06859299	555	3.837e-08	4.149e-05	CNTN4:26 RYR2:32 CSMD1:62 UGT8:65 APBA2:91 DSCAML1:98
REACTOME_NEURONAL_SYSTEM	-0.08049448	385	6.522e-08	6.045e-05	ADCY1:43 KCNA10:79 APBA2:91 KCNJ12:139 KCNV2:151 KCNJ14:158
REACTOME_CARDIAC_CONDUCTION	-0.14046100	121	9.739e-08	7.898e-05	RYR2:32 SCN9A:44 HIPK1:60 ITPR1:117 KCNJ12:139 KCNJ14:158
NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON	0.20371628	52	3.769e-07	2.717e-04	ANK1:5 IDO2:9 RAB11FIP1:79 ADAM9:124 ADGRA2:251 STAR:288
WP_GPCRS_CLASS_A_RHODOPSNLIKE	-0.00937392	206	6.180e-07	4.010e-04	CXCR5:46 CHRM2:144 NTSR1:153 MAS1:228 DRD2:296 DRD5:418
REACTOME_POTASSIUM_CHANNELS	-0.14989331	91	7.741e-07	4.566e-04	KCNA10:79 KCNJ12:139 KCNV2:151 KCNJ14:158 KCNQ3:168 KCNF1:320
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR	-0.10943447	166	1.184e-06	6.401e-04	CXCR5:46 TAC1:132 NTSR1:153 UTS2R:167 QRFP:223 NPS:388
BENPORATH_ES_WITH_H3K27ME3	-0.04565189	983	1.579e-06	7.089e-04	HSF4:19 CSF1:51 PHLD81:53 LMOD1:57 CSMD1:62 SYT6:71
REACTOME_G_ALPHA_1_SIGNALLING_EVENTS	-0.08546827	269	1.478e-06	7.089e-04	ADCY1:43 CXCR5:46 GRM2:63 ITPR1:117 CHRM2:144 GRM6:148
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04212956	1165	1.639e-06	7.089e-04	UAP1:1 NOS1AP:2 LRRN3:7 HERC2:13 SYNJ1:34 CHL1:76
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	-0.07198866	331	7.157e-06	2.902e-03	VIPR1:24 RYR2:32 TMEM132E:97 DSCAML1:98 ZNF536:112 BNC1:192
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.12789472	100	1.005e-05	3.834e-03	PGAP6:283 ZNF213:465 SPSB3:474 EME2:495 RHBDL1:560 WDR90:796
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.05625354	528	1.073e-05	3.867e-03	VIPR1:24 CAMSAP2:30 RYR2:32 SYNJ1:34 CHL1:76 SORL1:89
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNEL	-0.18802724	42	2.493e-05	8.087e-03	KCNA10:79 KCNV2:151 KCNQ3:168 KCNJ12:139 KCNAB1:469 KCNV1:509
WP_CALCIUM_REGULATION_IN_CARDIAC_CELLS	-0.10464872	137	2.395e-05	8.087e-03	RYR2:32 ADCY1:43 ITPR1:117 GJA8:142 CHRM2:144 CAMK2D:163
BENPORATH_SUZ12_TARGETS	-0.04087393	918	3.140e-05	9.700e-03	HSF4:19 CSF1:51 PHLD81:53 CSMD1:62 SYT6:71 BRINP3:94
CHEN_LIVER_METABOLISM_QTL_CIS	-0.13079141	84	3.454e-05	1.018e-02	UAP1:1 DDR2:31 NAV1:52 CEP170:51 ADAMTS4:135 CDH19:171
REACTOME_TRNA_MODIFICATION_IN_THE_NUCLEU	0.19064602	39	3.804e-05	1.073e-02	THADA:106 TRMT10A:155 TRMT1:376 TRMT5:391 CTU2:427 TYW1:468
REACTOME_NERVOUS_SYSTEM_DEVELOPMENT	-0.05038394	550	5.794e-05	1.566e-02	ARHGEF12:11 ANK2:15 KCNA10:79 CHL1:76 DNMB3:181 DSCAML1:98
REACTOME_PHASE_0_RAPID_DEPOLARISATION	-0.20537962	31	7.583e-05	1.968e-02	SCN9A:44 CAMK2D:163 CAMK2B:230 SCN3B:279 SCN2B:436 SCN1A:450
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE	-0.05087542	503	1.007e-04	2.513e-02	DNMB3:181 BAIAP2:100 ITPR1:117 WWP1:125 PTKB2:136 ARC:143
STARIK_HYPOCAAMPUS_22Q11_DELETION_UP	-0.15684704	49	1.202e-04	2.805e-02	OLFM2L2B:102 FXJ1:129 NETO1:180 EPAS1:922 CNTNAP1:957
MIKKELSEN_MCV8_HCP_WITH_H3K27ME3	-0.05494735	419	1.211e-04	2.805e-02	SYT6:71 TMEM132E:97 PCNX2:115 HS3ST2:118 NTSR1:153 KCNQ3:168
BENPORATH_EED_TARGETS	-0.03714603	928	1.432e-04	3.000e-02	HSF4:19 CSMD1:62 SORCS2:69 BRINP3:94 TMEM132E:97 DSCAML1:98
LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS	-0.03142787	1337	1.400e-04	3.000e-02	LRRN3:7 TSHZ3:8 CNTN3:12 CNTN4:26 SYNPO2:28 DDR2:31
REACTOME_G_ALPHA_3_SIGNALLING_EVENTS	-0.09522959	134	1.434e-04	3.000e-02	VIPR1:24 ADCY1:43 NPS:388 DRD5:418 VIPR2:427 CRHR1:549
NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON	-0.24486438	20	1.501e-04	3.043e-02	ARRDC4:38 SYNM:253 CHSY1:419 PCSK6:530 ALDH1A3:538 IGFBP1:621
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER	-0.04207277	704	1.571e-04	3.089e-02	CHL1:76 SORL1:89 APBA2:91 DOCK4:96 TAC1:132 PP1A4:214
SERVITJA_ISLET_HNF1A_TARGETS_UP	-0.11337943	149	2.225e-04	4.246e-02	CSF1:51 CHL1:76 DNMB3:181 ZFH4:147 ACOT7:240 COL3A1:287
DAZARD_RESPONSE_TO_UV_NHEK_DN	0.06356511	284	2.359e-04	4.373e-02	DST:57 BPTF:69 GSE1:115 TMEM131L:163 AKAP9:181 ASXL1:206
KEGG_PURINE_METABOLISM	-0.08623413	149	2.845e-04	5.128e-02	ADCY1:43 PDE5A:220 PDE6B:258 PDE1C:306 ALLC:425 CANT1:446
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	-0.09258674	128	3.018e-04	5.292e-02	MYT1:37 NTSR1:153 RTEL1:221 PHACTR3:280 ZBTB46:400 TFAP2C:490
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	-0.05773962	331	3.177e-04	5.424e-02	VIPR1:24 RYR2:32 TMEM132E:97 NTSR1:153 ZNF536:112 BNC1:192
NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON	-0.09404219	122	3.381e-04	5.584e-02	TMEM64:20 MMP16:95 RBM12B:138 ZFH4:147 NCEAB1:215 OSGIN2:242
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	-0.13833289	56	3.442e-04	5.584e-02	HERC2:13 GABRR1:342 GABRA5:416 GABRB3:630 UBE3A:689 GABRG3:740

GO_Biological_Process_2023 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cardiac Conduction (GO:0061337)	-0.21969546	44	4.675e-07	2.021e-03	ANK2:15 CAMK2D:163 BIN1:256 SCN3B:279 HCNA:375 HCN1:381
Chemical Synaptic Transmission (GO:00072)	-0.08867750	256	1.146e-06	2.021e-03	GRM2:63 APBA2:91 CHRM2:144 NTSR1:153 KCNQ3:168 CACNA1B:173
Metal Ion Transport (GO:0030001)	-0.11290351	156	1.207e-06	2.021e-03	RYR2:32 SCN9A:44 SLC17A4:50 KCNA10:79 ITPR1:117 KCNJ12:139
Regulation Of Heart Rate By Cardiac Cond	-0.22087595	39	1.836e-06	2.021e-03	ANK2:15 CAMK2D:163 BIN1:256 SCN3B:279 HCNA:375 HCN1:381
Regulation Of Synaptic Transmission, Glu	-0.18765103	54	1.875e-06	2.021e-03	TSHZ3:8 GRM2:63 PTKB2:136 GRM6:148 PLPPR4:152 DRD2:296
Regulation Of Monoatomic Ion Transmembra	-0.17125026	62	3.171e-06	2.848e-03	ANK2:15 PTKB2:136 SCN3B:279 HCNA:375 HCN1:381 SCN2B:436
Anterograde Trans-Synaptic Signaling (GO	-0.09580404	182	8.803e-06	5.270e-03	GRM2:63 APBA2:91 CHRM2:144 NTSR1:153 KCNQ3:168 CACNA1B:173
Calcium Ion Import Across Plasma Membran	-0.22438541	33	8.227e-06	5.270e-03	TRPM1:3 SCN9A:44 CACNA1B:173 CACNA1S:355 SCN1A:450 SLC8A3:561
Potassium Ion Transmembrane Transport (G	-0.11337585	132	7.174e-06	5.270e-03	KCNA10:79 KCNJ12:139 KCNV2:151 KCNJ14:158 KCNQ3:168 KCNT2:186
tRNA Modification (GO:0006400)	0.15599749	66	1.195e-05	6.439e-03	THADA:106 TRMT10A:155 DTWD1:185 TRMO:256 TRMT1:376 TYW1B:421
Potassium Ion Transport (GO:0006813)	-0.11397943	120	1.674e-05	8.200e-03	KCNA10:79 KCNJ12:139 KCNV2:151 KCNQ3:168 KCNF1:320 KCNJ14:158
Monoatomic Cation Transmembrane Transpor	-0.07392258	273	2.853e-05	1.281e-02	TRPM1:3 SCN9A:44 KCNA10:79 CNGB3:105 KCNV2:151 KCNQ3:168
Adenylate Cyclase-Inhibiting G Protein-C	-0.17555523	46	3.840e-05	1.591e-02	CHRM2:144 DRD2:296 CHRM1:420 HTR1B:467 HTR1A:522 CHRN3:593
Mitochondrial Gene Expression (GO:014005	0.11811212	100	4.599e-05	1.770e-02	GFM2:227 GATB:336 GADD45GIP1:346 FASTKD1:517 POLRMT:584 PTCB3:767
Ventricular Cardiac Muscle Cell Action P	-0.28209781	16	9.375e-05	3.367e-02	RYR2:32 SCN3B:279 KCNA4:550 SCN5A:698 KCNQ1:892 KCNH2:958
Cardiac Muscle Cell Action Potential Inv	-0.20967751	28	1.235e-04	3.825e-02	RYR2:32 SCN3B:279 SCN2B:436 SCN1A:450 KCNE4:550 SCN5A:698
Inorganic Cation Import Across Plasma Me	-0.11300681	96	1.330e-04	3.825e-02	TRPM1:3 SCN9A:44 KCNJ12:139 KCNA1B:173 CACNA1S:355
Regulation Of Monoatomic Cation Transmem	-0.17981898	38	1.261e-04	3.825e-02	DPP6:247 HCNA:375 HCN1:381 KCNAB1:469 SCN5A:698 CACNA1D:778
Somatic Recombination Of Immunoglobulin	0.38974552	8	1.349e-04	3.825e-02	MSH3:291 TCF3:428 PRKDC:1130 NHEJ1:1232 LIG4:1556 MSH6:2026
Positive Regulation Of DNA Metabolic Pro	0.10824944	103	1.507e-04	4.059e-02	SLX4:84 STON1:252 ATAD5:262 EGF:273 ERCC6:287 BABAM1:344
Mitochondrial Translation (GO:0032543)	0.11052885	96	1.862e-04	4.463e-02	GFM2:227 GATB:336 GADD45GIP1:346 MTRF1:687 PTCB3:767 MRPS25:940
Regulation Of Neurotransmitter Receptor	-0.17225620	39	1.988e-04	4.463e-02	PTKB2:136 NETO1:180 DLGAP2:257 NPTX1:474 CRH:791 SHISA9:919
Sister Chromatid Segregation (GO:0000819	0.18744238	33	1.953e-04	4.463e-02	CHAMP1:126 ESPL1:162 SMC4:313 SGO1:476 SPAG5:731 WAPL:775
Visual Perception (GO:0007601)	-0.11231277	93	1.855e-04	4.463e-02	TRPM1:3 ATF6:4 GRM6:148 GNAT2:199 NXN2:199