

Geneset	stat	num_genes	pval	p.adj	gene.vals
Schizophrenia	0.03671360	1612	1.810e-06	1.767e-02	RGS2.9 NDUFV1.10 CLDN1.15 PPIA.17 CIB2.27 MAGI1.42
Ventricular Septal Defects	-0.09263182	212	3.602e-06	1.767e-02	ARHGAP31.42 P300.31 LRP5.153 CCCD22.210 EXT2.48 FBN2.352
Autistic Disorder	0.05441537	606	5.929e-06	1.939e-02	EIF3A.12 SPD1.30 HYDIN.46 CADPS2.58 NTS.75 TGF1.81
Alcoholic Intoxication, Chronic	0.06429785	375	2.144e-05	3.113e-02	NTS.75 AVP.182 HTR1B.191 HDAC2.212 MTHFR.266 GHI.270
Hyperinsulinism	0.06843016	336	1.806e-05	3.113e-02	TSC22D3.11 CIB2.27 LECT2.56 CAV1.65 FAIM2.67 IDE.99
Neuroblastoma	0.03481667	1436	1.662e-05	3.113e-02	STAT5B.26 CAV1.65 FAIM2.67 BIN1.73 NTS.75 FOXP1.81
Pain	0.06117556	414	2.221e-05	3.113e-02	NTS.75 P2RY1.138 RAB7B.140 AVP.182 ADRA2C.197 TBP1.1240
Renal salt wasting	-0.30085310	16	3.100e-05	3.802e-02	BSND.294 SLC12A1.403 CLCNKA.501 CYP11A1.770 CLCNKB.916 HSD3B2.950
Depressive disorder	0.04730531	642	5.201e-05	5.689e-02	NTS.75 TLE1.168 AVP.182 M6PR.186 HTR1B.191 ADRA2C.197
Atrial Fibrillation	0.07302871	243	9.393e-05	5.759e-02	CAV1.65 NDUFS4.152 NEURL1.178 ADRA2C.197 SCNSA.231 TIMP2.238
Central neuroblastoma	0.03204628	1398	8.958e-05	5.759e-02	STAT5B.26 CAV1.65 FAIM2.67 BIN1.73 NTS.75 FOXP1.81
Channelopathies	0.16887401	47	6.254e-05	5.759e-02	SCNSA.231 TBP1.1240 HCN1.255 KCNJ3.352 KCNJ5.618 CNGA3.682
Decreased platelet count	-0.09650374	139	8.866e-05	5.759e-02	GP9.246 ERCC4.511 SLX.4.462 ABCD4.528 SH2D1A.534 NHEJ1.692
Mental Depression	0.05146355	505	8.629e-05	5.759e-02	NTS.75 TLE1.168 AVP.182 M6PR.186 HTR1B.191 ADRA2C.197
Polyhydramnios	-0.10836526	111	8.230e-05	5.759e-02	EP300.131 BSND.294 SLC12A1.403 MYOD1.433 SPINT2.459 CLCNKA.501
Thrombocytopenia	-0.06704423	292	8.747e-05	5.759e-02	GP9.246 NR1I2.289 NAAA.410 ERCC4.411 F8.439 SLX4.462
Autism Spectrum Disorders	0.05134411	480	1.319e-04	6.813e-02	NDUFV1.10 SND1.30 CADPS2.58 FOXP1.81 TTC25.164 AVP.182
Kartagener Syndrome	0.11487333	93	1.299e-04	6.813e-02	FOXJ1.25 HYDIN.46 CCCD65.52 DNAB6.54 CDR2.100 TTC25.164
Post-Traumatic Stress Disorder	0.11397734	95	1.282e-04	6.813e-02	TSC22D3.11 STAT5B.26 OPRM1.517 NOS1.623 ENDOL.641 SGK1.985
Amino Acid Metabolism, Inherited Disorde	-0.31634197	12	1.481e-04	7.266e-02	ARG1.333 D2HGDH.969 PRODH.1361 GAIT.1846 MAT1A.1685 ETCISBP2.2017
Diabetes Mellitus, Insulin-Dependent	0.03961672	739	2.932e-04	1.027e-01	SKIVL2.7 RGS2.9 STAT5B.26 IL37.74 IDE.99 SELENOS.172
Epilepsy, Temporal Lobe	0.08387025	160	2.694e-04	1.027e-01	GNAI4.5 BIN1.73 AVP.182 HCN1.255 SLC12A2.319 LGI1.369
Achromatopsia 1	0.30268889	12	2.830e-04	1.027e-01	FRMD7.160 CNGA3.682 PAX6.919 PNPLA6.926 GNAT2.139 PDE6C.1325
Emotional Stress	0.35083785	9	2.678e-04	1.027e-01	AVP.182 DRD2.562 MSH2.1160 OXT.1518 RCAN1.2569 HTR2C.2725
Hodgkin Disease	0.04822342	493	2.760e-04	1.027e-01	STAT5B.26 SND1.30 FOXP1.81 EBF1.156 TIMP2.238 MTHFR.266
Hypernatruria	-0.43261385	6	2.427e-04	1.027e-01	BSND.294 CLCNKA.501 CYP11A1.770 CLCNKB.916 HSD3B2.950 AVPR2.3198
Psychotic Disorders	0.06387430	274	2.912e-04	1.027e-01	NTS.75 CHN2.130 NDUFS4.152 AVP.182 HTR1B.191 HDAC2.212
Recurrent major depressive episodes	0.20679516	26	2.634e-04	1.027e-01	AVP.182 MTHFR.266 SYNE1.552 GRM7.968 CHR22.1096 APOA4.1536
Diabetes Mellitus, Non-Insulin-Dependent	0.03003733	1346	3.051e-04	1.032e-01	LINGO2.2 PPIA.17 STAT5B.26 CAV1.65 FAIM2.67 IL37.74
Otitis Media	-0.11382635	84	3.160e-04	1.033e-01	CTSB.95 TGIF1.116 CYBB.325 TBS1.607 ADAMTS13.719 PHF.739
Familial migraine	0.39144377	7	3.351e-04	1.060e-01	HTR1B.191 KCNJ3.358 KCNK1.8.57 CSNK1D.1811 SLC4A.2287 ATP1A2.2499
AIDS Dementia Complex	0.16888839	37	3.895e-04	1.061e-01	KCNK1.269 IGF1.408 OPRM1.517 SLC8A1.535 KCNA3.788 NEFL.1196
Mental disorders	0.06230147	281	3.466e-04	1.061e-01	MAGI1.42 CADPS2.58 HTR1B.191 MTHFR.266 EPHB2.470 SLITRK1.497
Neuralgia	0.1295157	83	3.809e-04	1.061e-01	PRKCG.215 HCN1.255 MDH2.290 OPRM1.517 KCNA3.788 DRD2.954
Retinal pigment epithelial mottling	0.36414744	8	3.616e-04	1.061e-01	PRPH2.148 ERCC8.342 ABCA4.914 CACNA2D4.1113 CTNS.1449 ELOVL4.1535
Tracheoesophageal Fistula	-0.15647788	43	3.876e-04	1.061e-01	CYBB.325 ERCC4.411 SLC4.462 ITGA8.504 USB1.751 FANCG.898
Bilateral cataracts (disorder)	0.10053937	103	4.311e-04	1.122e-01	CRYBA4.59 CRYBA1.297 CLP.646 BFPSP1.556 EPHA2.657 MIP.799
Hepatomegaly	-0.05647693	332	4.347e-04	1.122e-01	GFMT1.37 CYP1A1.44 LRP5.153 ALG1.205 AMACR.232 ACOKX1.247
Cataract, Central Sacular, With Sutaral	0.41027343	6	5.008e-04	1.198e-01	CRYBA1.297 MIP.799 CRYGS.82 GJA8.832 BFPSP2.1310 CRYBB2.4533
Andersen Syndrome	0.21440978	22	5.003e-04	1.198e-01	SCNSA.231 MTHFR.266 KCNJ3.358 KCNA3.788 KCNJ3.352 KCNJ5.618

EnrichmentHsSymbolsFile2 Top pathways by permutation

Geneset	stat	num_genes	pval	p.adj	gene.vals
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	-0.306656540	99	6.110e-26	3.964e-22	DEC2R.5 RPU5D1.15 WFKKK1.28 P3A6P.45 MCRIP2.84 TRAF7.102
BENPORATH_ES_WITH_H3K27ME3	0.06650595	982	2.787e-12	8.976e-09	GNAI4.5 FOXJ1.25 TCEA3.47 KCNAB1.49 SLC26A5.55 CLIP4.107
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	0.12319896	261	8.105e-12	1.753e-08	GP9R83.38 P2RY1.138 GLRB.162 HTR1B.191 ADRA2C.197 GHI.270
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	0.08482257	554	1.105e-11	1.793e-08	SLC26A5.55 POU2F3.105 KCNH5.117 PRDM14.134 DKKL1.161 NCMAP.166
REACTOME_GPCR_LIGAND_BINDING	0.09562772	397	7.231e-11	9.383e-08	NTS.75 TAS2R.917 P2RY1.138 AVP.182 HTR1B.191 ADRA2C.197
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	0.10826196	296	1.652e-10	1.786e-07	NTS.75 P2RY1.138 AVP.182 HTR1B.191 ADRA2C.197 GPER1.198
BLALOCK_ALZHEIMERS_DISEASE_DN	0.05599409	1127	3.559e-10	3.299e-07	GNAI4.5 RGS2.9 NNT.14 PPIA.17 KIFBP.45 KCNAB1.49
REACTOME_SIGNALING_BY_GPCR	0.07306176	624	5.846e-10	4.741e-07	GNAI4.5 RGS2.9 PDE1C.20 GPR83.38 NTS.75 GPR27.90
BENPORATH_EED_TARGETS	0.05586783	922	1.196e-08	7.869e-06	GNAI4.5 FOXJ1.25 TCEA3.47 KCNAB1.49 SLC8A3.80 CLIP4.107
REACTOME_G_ALPHA_1_SIGNALING_EVENTS	0.10191345	265	1.213e-08	7.869e-06	GNAI4.5 PDE1C.20 TAS2R41.97 RGS22.142 HTR1B.191 ADRA2C.197
REACTOME_NEURONAL_SYSTEM	0.08012928	379	9.413e-08	5.552e-05	KCNAB1.49 KCNH5.117 KCNJ4.118 CACNA1B.121 GLRB.162 PRKCG.215
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	0.23838999	41	1.286e-07	6.993e-05	HTR1B.191 ADRA2C.197 ADRB1.282 TAAR.442 HTR4.635 CHRM4.661
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR	0.11656563	168	1.935e-07	9.899e-05	NTS.75 AVP.182 GPER1.188 EDNR2.287 CCR4.501 OPRM1.517
REACTOME_CARDIAC_CONDUCTION	0.13863595	119	1.801e-07	8.969e-05	SLC8A3.80 KCNJ4.118 SCNSA.231 AHCYL1.257 KCNK1.269 KCNP3.320
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.07630705	395	2.142e-07	9.266e-05	ODF2.16 CFA69.19 FOXJ1.25 SNTN.35 CDC65.52 DNAH6.51
REACTOME_PEROXISOMAL_LIPID_METABOLISM	-0.27479402	29	3.034e-07	1.194e-04	DEC2R.5 ACOKX3.75 NUDT7.133 AMACR.232 ACOKX1.247 ACOT8.429
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.10357687	206	3.129e-07	1.194e-04	GP9R83.38 GPR27.90 P2RY1.138 HTR1B.191 ADRA2C.197 GPER1.198
REACTOME_POTASSIUM_CHANNELS	0.15539461	90	3.545e-07	1.278e-04	KCNAB1.49 KCNH5.117 KCNJ4.118 HCN1.255 KCNK1.269 KCNJ3.352
BENPORATH_PRC2_TARGETS	0.06175446	580	4.298e-07	1.432e-04	GNAI4.5 FOXJ1.25 TCEA3.47 KCNAB1.49 TAF4.109 CACNA1B.121
KEGG_PEROXISOME	-0.16548894	78	4.414e-07	1.432e-04	DEC2R.5 ACOKX3.75 PRDX5.110 PXMP4.152 AMACR.232 ACOKX1.247
REACTOME_MUSCLE_CONTRACTION	0.10783909	913	5.070e-07	1.566e-04	SLC8A3.80 KCNJ4.118 TCAP.124 SCNSA.231 AHCYL1.257 KCNK1.269
BENPORATH_SUZ12_TARGETS	0.04881593	917	6.762e-07	1.774e-04	GNAI4.5 TSC22D3.11 FOXJ1.25 GPR83.38 TCEA3.47 KCNAB1.49
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	0.07964653	331	6.834e-07	1.774e-04	CADPS2.58 GPR27.90 ADRA2C.197 SCNSA.231 TLX3.244 HCN1.255
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	0.19260982	56	6.231e-07	1.774e-04	GABRR2.521 MDMA.543 GABRR1.723 NIPK2.831 TUBGCP5.1004 FSHB.1097
WP_MONOAMINE_GPCRS	0.25438354	32	6.371e-07	1.774e-04	HTR1B.191 ADRA2C.197 ADRB1.282 HTR4.635 CHRM4.661 HTR4.729
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	0.07899812	331	8.411e-07	2.099e-04	GPR27.90 POU2F3.105 ADRA2C.197 SCNSA.231 TLX3.244 HCN1.255
SENGUPTA_NASOPHARYNGEAL_CARCINOMA_DN	0.08507649	280	1.024e-06	2.461e-04	FOXJ1.25 SNTN.35 HYDIN.46 TCEA3.47 CDC65.52 CDCD113.113
REACTOME_G_ALPHA_S_SIGNALING_EVENTS	0.12198281	134	1.114e-06	2.582e-04	GP9R83.38 GPR27.90 AVP.182 GPER1.198 ADRB1.282 FSHR.356
KIM_ALL_DISORDERS_CALB1_CORR_UP	0.06281892	510	1.343e-06	3.004e-04	NDUFV1.10 KIFBP.45 KCNAB1.49 CRMP1.110 UQCRCF5.158 GLRB.162
WP_RAC1PAK1P38MMP2_CORRWAY	0.16736108	66	2.604e-06	5.631e-04	STAT5B.26 CTNNB1.103 TEK.416 CRK.462 NOS1.623 DOK2.734
WP_NEUROINFLAMMATION_AND_GLUTAMATERGIC_S	0.11624503	136	2.933e-06	6.139e-04	PRKCG.215 GRIK1.396 IGF1.408 NOS1.623 GRIK2.668 SLC38A2.862
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNEL	0.20740768	42	3.321e-06	6.734e-04	KCNAB1.49 KCNH5.117 KCNF1.373 KCND1.460 KCND2.629 KCNA3.788
REACTOME_PEROXISOMAL_PROTEIN_IMPORT	-0.18059605	55	3.497e-06	6.876e-04	DEC2R.5 ACOKX3.75 NUDT7.133 AMACR.232 ACOKX1.247 ECH1.366
REACTOME_DISEASES_OF_METABOLISM	-0.08989779	223	3.894e-06	7.431e-04	NDOT01.65 CYP2A4.168 MCCO1.74 ABCA3.80 ALG1.205 SEMA5A.306
KEGG_LYSOSOME	-0.12036767	110	1.315e-05	2.437e-03	CTSB.95 LAMP3.194 ATP6VD01.372 LAMP2.394 HVAL.1437 ARSG.525
MATZUK_SPERMATOZOIA	0.12197484	102	2.107e-05	3.796e-03	AAD1.34 SPAG16.89 CREM.95 LDHC.106 FHLS.106 AGFG1.196
REACTOME_FATTY_ACID_METABOLISM	-0.09680250	158	2.746e-05	4.815e-03	DEC2R.5 HACD3.7 CYP1A1.44 ACOKX3.75 ACOT13.125 NUDT7.133
REACTOME_DNA_DOUBLE_STRAND_BREAK_REPAIR	-0.10518919	130	3.516e-05	6.003e-03	POLK.258 ERCC4.411 RAD51D.427 PIAS4.543 ELK2.462 BAP1.644
REACTOME_DNA_REPAIR	-0.07203303	276	3.981e-05	6.623e-03	MUTYH.38 NER08D.51 EPRD05.121 POLK.258 ALKBH2.273 ERCC4.411
WP_PEPTIDE_GPCRS	0.14186422	70	4.091e-05	6.636e-03	EDNR4.287 FSHR.356 CCR4.501 OPRM1.517 NPY1R.542 CCR1.593

GO_Biological_Process_2023 Top pathways by permutation

Geneset	stat	num_genes	pval	p.adj	gene.vals
Fatty Acid Catabolic Process (GO:0009062)	-0.19808537	58	1.853e-07	6.390e-04	NUDT7.133 ACADS.192 ACN5.217 ABHD3.262 ACOT8.429 CPT2.489
Metal Ion Transport (GO:0030001)	0.11981291	157	2.372e-07	6.390e-04	KCNAB1.49 CAV1.65 SCNSA.231 KCNK1.269 TUSC3.321 KCNJ3.352
Potassium Ion Transport (GO:0006813)	0.13157259	119	7.495e-07	1.346e-03	KCNAB1.49 KCNH5.117 HCN1.255 KCNK1.269 KCNJ3.352 KCNF1.373
RNA Ion Transmembrane Transport (G	0.12008044	132	1.998e-06	2.691e-03	KCNH5.117 KCNJ4.118 HCN1.255 KCNK1.269 SLC12A2.319 KCNJ3.352
G Protein-Coupled Receptor Signaling Pat	0.18990762	47	6.751e-06	5.196e-03	HTR1B.191 OPRM1.517 NPY1R.542 CCR1.593 HTR4.635 CHRM4.661
RNA Modification (GO:0009651)	-0.19114603	47	5.878e-06	5.196e-03	LCMT2.40 MRK1.86 DTWD1.97 RPLJ1.468 VDR4.481 TRMT1.490
Regulation Of Synaptic Transmission, Glu	0.17749290	54	6.567e-06	5.196e-03	HCN1.255 GRIK1.396 CACN27.616 SLC38A2.852 DRD2.954 PTK2B.961
Chemical Synaptic Transmission (GO:00072	0.07969122	254	1.333e-05	6.531e-03	CACNA1B.121 UNC119.145 GLRB.162 HTR1B.191 EYOC4.192 SNAPIN.228
Cilium Movement (GO:0003341)	0.18531102	47	1.121e-05	6.531e-03	HYDIN.46 TEKTS.145 NME5.222 SPEF2.485 CFAPT70.503 SPAG6.538
Fatty Acid Beta-Oxidation (GO:0006635)	-0.18407774	47	1.282e-05	6.531e-03	DEC2R.5 ACOKX3.75 ACADS.192 AMACR.232 ACOKX1.247 ACOT8.429
Recombinational Repair (GO:0000725)	-0.13416802	89	1.249e-05	6.531e-03	FBH1.240 SFR1.253 ERCC4.411 RAD51D.427 SLX4.462 HNSP.614
Anterograde Trans-Synaptic Signaling (GO	0.09385747	180	1.488e-05	6.682e-03	CACNA1B.121 UNC119.145 GLRB.162 HTR1B.191 EYOC4.192 GRIK1.396
Nuclear Membrane Organization (GO:007176	0.23828460	26	2.618e-05	1.007e-02	GPER1.198 CHMP3.699 VPS4A.855 CHMP7.1498 TARDBP.1055 NSFCL1.1207
Regulation Of Cation Channel Activity (G	0.17230707	50	2.531e-05	1.007e-02	KCNAB1.49 CAVP5.68 PIRT.180 HCN1.255 EDNR4.287 CACNB1.403
Nuclear Membrane Reassembly (GO:0031468)	0.26336210	21	2.953e-05	1.001e-02	RCC1.13 CHMP3.699 VPS4A.855 CHMP7.1048 NSFCL1C.1207 CHMP4C.1804
Double-Strand Break Repair Via Homologou	-0.11633290	105	3.925e-05	1.322e-02	HNRD622.197 FBH1.240 SFR1.253 ERCC4.411 RAD51D.427 SLX4.462
Adenylate Cyclase-Inhibiting G Protein-C	0.17260768	46	5.172e-05	1.431e-02	HTR1B.191 OPRM1.517 NPY1R.542 CHRM4.661 HTR1D.762 OPR1.1912
Double-Strand Break Repair (GO:0006302)	-0.09297876	158	5.752e-05	1.431e-02	FBH1.240 SFR1.253 ERCC4.411 RAD51D.427 PIAS4.543 SLX4.462
Inorganic Cation Import Across Plasma Me	0.12032186	96	4.742e-05	1.431e-02	SLC8A3.80 KCNJ4.118 CACNA1B.121 SCNSA.231 SLC12A2.319 KCNJ3.352
Monoanionic Cation Transmembrane Transp	0.07115212	273	5.634e-05	1.431e-02	NNT.14 SLC8A3.80 KCNH5.117 SCNSA.231 HCN1.255 KCNK1.269
Peptidyl-Tyrosine Phosphorylation (GO:00	0.14428612	65	5.844e-05	1.431e-02	FGFR.264 TEK.416 EPHB2.470 PRLR.617 PTK2B.961 AB13.1050
RNA Modification (GO:0006400)	0.14088633	66	5.252e-05	1.431e-02	LCMT2.40 DTWD1.97 THUMP2.136 TRMT4A.244 TRMT10A.369 THADA.425
Neuropeptide Signaling Pathway (GO:00072	0.14557495	63	6.541e-05	1.532e-02	GP9R83.38 NTS.75 GLRB.162 OPRM1.517 RXFP3.582 OPR1.1912
Regulation Of Neurotransmitter Receptor	0.18243516	39	8.136e-05	1.827e-02	SHISA8.305 PRRT1.337 OPRM1.517 CACNG7.616