Geneset	stat	num.genes	pval	p.adj	gene.vals
Fatty Acid Catabolic Process (GO:0009062	-0.19808537	58	1.853e-07		NUDT7:133 ACADS:192 ACOX1:247 ABHD3:262 ACOT8:429 CPT2:489
Metal Ion Transport (GO:0030001)	0.11981291	157	2.372e-07		KCNAB1:49 CAV1:65 SCN5A:231 KCNK1:269 TUSC3:321 KCNJ3:352
Potassium Ion Transport (GO:0006813)	0.13157259	119	7.495e-07		KCNAB1:49 KCNH5:117 HCN1:255 KCNK1:269 KCNJ3:352 KCNF1:373
Potassium Ion Transmembrane Transport (G	0.12008044	132	1.998e-06		KCNH5:117 KCNJ14:118 HCN1:255 KCNK1:269 SLC12A2:319 KCNJ3:352
G Protein–Coupled Receptor Signaling Pat	0.18990762	47	6.751e-06		HTR1B:191 OPRM1:517 NPY1R:542 CCR1:593 HTR4:635 CHRM4:661
RNA Modification (GO:0009451)	-0.19114603	47	5.878e-06		LCMT2:40 MRM1:86 DTWD1:97 PUS7L:468 WDR4:481 TRDMT1:490
Regulation Of Synaptic Transmission, Glu	0.17745290	54	6.567e-06		HCN1:255 GRIK1:396 CACNG7:616 SLC38A2:852 DRD2:954 PTK2B:961
Chemical Synaptic Transmission (GO:00072	0.07969122	254	1.333e-05		CACNA1B:121 UNC119:145 GLRB:162 HTR1B:191 EXOC4:192 SNAPIN:228
Cilium Movement (GO:0003341)	0.18531102	47	1.121e-05		HYDIN:46 TEKT5:146 NME5:222 SPEF2:485 CFAP70:503 SPAG6:538
Fatty Acid Beta-Oxidation (GO:0006635)	-0.18407774	47	1.282e-05	6.531e-03	DECR2:5 ACOX3:75 ACADS:192 AMACR:232 ACOX1:247 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 SWSAP1:614
Anterograde Trans-Synaptic Signaling (GO	0.09385747	180	1.488e-05	6.682e-03	CACNA1B:121 UNC119:145 GLRB:162 HTR1B:191 EXOC4:192 GRIK1:396
Nuclear Membrane Organization (GO:007176	0.23828460	26	2.618e-05	1.007e-02	GPER1:198 CHMP3:699 VPS4A:855 CHMP7:1048 TARDBP:1055 NSFL1C:1207
Regulation Of Cation Channel Activity (G	0.17230707	50	2.531e-05	1.007e-02	KCNAB1:49 CABP5:68 PIRT:180 HCN1:255 EDNRA:287 CACNB1:403
Nuclear Membrane Reassembly (GO:0031468)	0.26336210	21	2.953e-05	1.061e-02	RCC1:13 CHMP3:699 VPS4A:855 CHMP7:1048 NSFL1C:1207 CHMP4C:1804
Double-Strand Break Repair Via Homologou	-0.11633290	105	3.925e-05	1.322e-02	MCMDC2:197 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 OPRL1:912
Double-Strand Break Repair (GO:0006302)	-0.09297876	158	5.752e-05	1.431e-02	FBH1:240 SFR1:253 ERCC4:411 RAD51D:427 PIAS4:453 SLX4:462
Inorganic Cation Import Across Plasma Me	0.12032186	96	4.742e-05	1.431e-02	SLC8A3:80 KCNJ14:118 CACNA1B:121 SCN5A:231 SLC12A2:319 KCNJ3:352
Monoatomic Cation Transmembrane Transpor	0.07115212	273	5.634e-05	1.431e-02	NNT:14 SLC8A3:80 KCNH5:117 SCN5A:231 HCN1:255 KCNK1:269
Peptidyl-Tyrosine Phosphorylation (GO:00	0.14428612	65	5.844e-05	1.431e-02	FGR:264 TEK:416 EPHB2:470 PRLR:617 PTK2B:961 ABI3:1050
tRNA Modification (GO:0006400)	-0.14408863	66	5.252e-05	1.431e-02	LCMT2:40 DTWD1:97 THUMPD2:136 TRMT44:244 TRMT10A:369 THADA:425
Neuropeptide Signaling Pathway (GO:00072	0.14557495	63	6.541e-05	1.532e-02	GPR83:38 NTS:75 GLRB:162 OPRM1:517 RXFP3:582 OPRL1:912
Regulation Of Neurotransmitter Receptor	0.18243516	39	8.136e-05	1.827e-02	SHISA8:305 PRRT1:337 OPRM1:517 CACNG7:616 PTK2B:961 CNIH3:2063
Regulation Of Monoatomic Ion Transmembra	0.14515088	61	8.952e-05	1.929e-02	HCN1:255 SHISA8:305 PRRT1:337 WNK3:346 PHB2:347 OPRM1:517
DNA Repair (GO:0006281)	-0.06879692	274	9.569e-05	1.983e-02	MUTYH:38 FBH1:240 ALKBH2:273 MGME1:274 ERCC4:411 RAD51D:427
Regulation Of Potassium Ion Transport (G	0.21065273	28	1.149e-04	2.292e-02	KCNAB1:49 KCNIP3:320 NOS1:623 VIP:789 KCNAB2:815 DRD2:954
Cellular Response To Oxygen–Containing C	0.05926340	361	1.212e-04	2.332e-02	CIB2:27 IL37:74 LCP1:91 P2RY1:138 LAMTOR4:163 SELENOS:172
Protein Localization To Cell Periphery (0.09724065	129	1.413e-04	2.624e-02	EHD3:8 RDX:36 CAV1:65 P2RY1:138 PRPH2:148 KCNIP3:320
Apical Protein Localization (GO:0045176)	-0.36474397	9	1.512e-04	2.716e-02	INSC:362 SHROOM3:374 SHROOM2:656 CELSR1:1765 MAL:1864 VANGL2:2066
Cardiac Conduction (GO:0061337)	0.16647691	43	1.600e-04	2.781e-02	CAV1:65 BIN1:73 SCN5A:231 HCN1:255 KCNJ3:352 SLC9A1:400
Maturation Of SSU-rRNA (GO:0030490)	-0.18757746	33	1.933e-04		WDR46:265 NOB1:312 UTP6:622 NOL11:725 SPPL2B:962 NGDN:1076
Glycosphingolipid Catabolic Process (GO:	-0.35702471	9	2.082e-04		GLA:857 NEU1:1230 NEU3:1277 NEU4:1372 HEXB:1598 GM2A:1985
Monocarboxylic Acid Metabolic Process (G	-0.11787246	83	2.093e-04		DECR2:5 CYP1A1:44 MCCC1:74 AMACR:232 NAAA:410 ACSL4:428
Mitochondrial Translation (GO:0032543)	-0.10783731	96	2.665e-04		GADD45GIP1:3 GFM1:37 MRPL58:71 QRSL1:72 MTIF3:149 GFM2:280
Regulation Of Cardiac Muscle Contraction	0.18851776	31	2.819e-04		RGS2:9 SCN5A:231 SLC9A1:400 SLC8A1:535 NOS1:623 PRKACA:1406
Cardiac Muscle Cell Action Potential (GO	0.19713713	28	3.069e-04		SCN5A:231 SLC8A1:535 SCN3B:937 DMD:1629 KCNE2:2086 PKP2:2170
tRNA Methylation (GO:0030488)	-0.17415533	36	3.011e-04		LCMT2:40 THUMPD2:136 TRMT44:244 TRMT10A:369 THADA:425 WDR4:481
Fatty Acid Oxidation (GO:0019395)	-0.15139589	47	3.325e-04		ACADS:192 ACOX1:247 CPT2:489 PHYH:491 ABCD4:528 HACL1:554
Regulation Of Heart Rate By Cardiac Cond	0.16748158	38	3.558e-04		CAV1:65 BIN1:73 SCN5A:231 HCN1:255 KCNJ3:352 KCNJ5:618
. Togalation of Floar Flate by Cardido Oblid	3.13.10100	- 50	3.0000 04	000 02	5 1.00 Billing Collot incollot 110111.200 1101100.002 1101100.010

EnrichmentHsSymbolsFile2 Top pathways by permulation

NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	-0.30656540	99	6.110e-26	3.964e-22	DECR2:5 RPUSD1:15 WFIKKN1:28 PGAP6:45 MCRIP2:84 TRAF7:102
BENPORATH_ES_WITH_H3K27ME3	0.06650965	982	2.767e-12	8.976e-09	GNA14:5 FOXJ1:25 TCEA3:47 KCNAB1:49 SLC26A5:55 CLIP4:107
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	0.12319896	261	8.105e-12	1.753e-08	GPR83:38 P2RY1:138 GLRB:162 HTR1B:191 ADRA2C:197 GH1:270
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 TAS2R41:97 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	GNA14:5 RGS2:9 NNT:14 PPIA:17 KIFBP:45 KCNAB1:49
REACTOME_SIGNALING_BY_GPCR	0.07306176	624	5.846e-10	4.741e-07	GNA14:5 RGS2:9 PDE1C:20 GPR83:38 NTS:75 GPR27:90
BENPORATH_EED_TARGETS	0.05586783	922	1.196e-08	7.869e-06	GNA14:5 FOXJ1:25 TCEA3:47 KCNAB1:49 SLC8A3:80 CLIP4:107
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	0.10191345	265	1.213e-08	7.869e-06	GNA14:5 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 KCNJ14:118 CACNA1B:121 GLRB:162 PRKCG:215
REACTOME_AMINE_LIGAND_BINDING_RECEPTORS	0.23839890	41	1.286e-07	6.953e-05	HTR1B:191 ADRA2C:197 ADRB1:282 TAAR5:442 HTR4:635 CHRM4:661
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR	0.11656653	168	1.935e-07	8.969e-05	NTS:75 AVP:182 GPER1:198 EDNRA:287 CCR4:501 OPRM1:517
REACTOME_CARDIAC_CONDUCTION	0.13863595	119	1.801e-07	8.969e-05	SLC8A3:80 KCNJ14:118 SCN5A:231 AHCYL1:257 KCNK1:269 KCNIP3:320
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.07630705	395	2.142e-07	9.266e-05	ODF2:16 CFAP69:19 FOXJ1:25 SNTN:35 CCDC65:52 DNAH6:54
REACTOME_PEROXISOMAL_LIPID_METABOLISM	-0.27479402	29	3.034e-07	1.194e-04	DECR2:5 ACOX3:75 NUDT7:133 AMACR:232 ACOX1:247 ACOT8:429
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.10357687	206	3.129e-07	1.194e-04	GPR83:38 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 KCNJ14:118 HCN1:255 KCNK1:269 KCNJ3:352
BENPORATH_PRC2_TARGETS	0.06175446	580	4.298e-07	1.432e-04	GNA14:5 FOXJ1:25 TCEA3:47 KCNAB1:49 TAFA4:109 CACNA1B:121
KEGG_PEROXISOME	-0.16548894	78	4.414e-07	1.432e-04	DECR2:5 ACOX3:75 PRDX5:110 PXMP4:152 AMACR:232 ACOX1:247
REACTOME_MUSCLE_CONTRACTION	0.10783909	183	5.070e-07	1.566e-04	SLC8A3:80 KCNJ14:118 TCAP:124 SCN5A:231 AHCYL1:257 KCNK1:269
BENPORATH_SUZ12_TARGETS	0.04881593	917	6.762e-07	1.774e-04	GNA14:5 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 SCN5A:231 TLX3:244 HCN1:255
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME	0.19260982	56	6.231e-07	1.774e-04	GABRR2:521 MDM4:543 GABRR1:723 NIPA2:831 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 HTR2A:729
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	0.07899812	331	8.411e-07	2.099e-04	GPR27:90 POU2F3:105 ADRA2C:197 SCN5A: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 CCDC65:52 CCDC113:113
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS	0.12198281	134	1.114e-06	2.582e-04	GPR83:38 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 UQCRFS1:158 GLRB:162
WP_RAC1PAK1P38MMP2_PATHWAY	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 GRIK2:658 SLC38A2:852
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	-0.18090605	55	3.497e-06	6.876e-04	DECR2:5 ACOX3:75 NUDT7:133 AMACR:232 ACOX1:247 ECH1:366
REACTOME_DISEASES_OF_METABOLISM	-0.08989779	223	3.894e-06	7.431e-04	NOTCH1:65 CYP24A1:68 MCCC1:74 ABCA3:80 ALG1:205 SEMA5A:306
KEGG_LYSOSOME	-0.12036767	110	1.315e-05	2.437e-03	CTSB:95 LAMP3:194 ATP6V0D1:372 LAMP2:394 HYAL1:437 ARSG:525
MATZUK_SPERMATOZOA	0.12197484	102	2.107e-05	3.796e-03	ADAD1:34 SPAG16:89 CREM:95 LDHC:106 FHL5:108 AGFG1:196
REACTOME_FATTY_ACID_METABOLISM	-0.09680250	158	2.746e-05	4.815e-03	DECR2:5 HACD3:7 CYP1A1:44 ACOX3:75 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 PIAS4:453 SLX4:462 BAP1:644
REACTOME_DNA_REPAIR	-0.07203303	276	3.981e-05	6.623e-03	MUTYH:38 INO80D:51 EP300:131 POLK:258 ALKBH2:273 ERCC4:411
WP_PEPTIDE_GPCRS	0.14186422	70	4.091e-05	6.636e-03	EDNRA:287 FSHR:356 CCR4:501 OPRM1:517 NPY1R:542 CCR1:593

gene.vals

RGS2:9 NDUFV1:10 CLDN1:15 PPIA:17 CIB2:27 MAGI1:42 ARHGAP31:42 EP300:131 LRP5:153 CCDC22:210 EXT2:348 FBN2:352

EIF3A:12 SND1:30 HYDIN:46 CADPS2:58 NTS:75 FOXP1:81

NTS:75 AVP:182 HTR1B:191 HDAC2:212 MTHFR:266 GH1:270 TSC22D3:11 CIB2:27 LECT2:56 CAV1:65 FAIM2:67 IDE:99

STAT5B:26 CAV1:65 FAIM2:67 BIN1:73 NTS:75 FOXP1:81

num.genes pval p.adj

1.810e-06 1.767e-02

3.602e-06 1.767e-02

5.929e-06 1.939e-02

2.144e-05 3.113e-02

1.806e-05 3.113e-02

1.662e-05 3.113e-02

1612

212

606

336

1436

0.03671360

-0.09263182

0.05441537

0.06429785

0.06843016

0.03481667

Geneset

Schizophrenia

Ventricular Septal Defects

Autistic Disorder

Alcoholic Intoxication, Chronic

Hyperinsulinism

Neuroblastoma

DisGeNET Top pathways by permulation

Neurobiastoma	0.00+01001	1730			
Pain	0.06117556	414	2.221e-05	3.113e-02	NTS:75 P2RY1:138 RAB7B:140 AVP:182 ADRA2C:197 TBPL1:240
Renal salt wasting	-0.30085310	16	3.100e-05	3.802e-02	BSND:294 SLC12A1:403 CLCNKA:501 CYP11A1:770 CLCNKB:916 HSD3B2:95
Depressive disorder	0.04730531	642	5.201e-05	5.669e-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 SCN5A: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	SCN5A:231 TBPL1:240 HCN1:255 KCNJ3:352 KCNJ5:618 CNGA3:682
Decreased platelet count	-0.09650374	139	8.866e-05	5.759e-02	GP9:246 ERCC4:411 SLX4:462 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		NDUFV1:10 SND1:30 CADPS2:58 FOXP1:81 TTC25:164 AVP:182
Kartagener Syndrome	0.11497333	93	1.299e-04	6.813e-02	FOXJ1:25 HYDIN:46 CCDC65:52 DNAH6:54 CDR2:100 TTC25:164
Post–Traumatic Stress Disorder	0.11397734	95		6.813e-02	TSC22D3:11 STAT5B:26 OPRM1:517 NOS1:623 ENDOU:641 SGK1:885
Amino Acid Metabolism, Inherited Disorde	-0.31634197	12	1.481e-04	7.266e-02	ARG1:333 D2HGDH:969 PRODH:1361 GAMT:1846 MAT1A:1885 SECISBP2:201
Diabetes Mellitus, Insulin-Dependent	0.03961672	739	2.932e-04	1.027e-01	SKIV2L:7 RGS2:9 STAT5B:26 IL37:74 IDE:99 SELENOS:172
Epilepsy, Temporal Lobe	0.08367025	160	2.694e-04	1.027e-01	GNA14:5 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 GNAT2:1109 PDE6C:1325
Emotional Stress	0.35083785	9		1.027e-01	AVP:182 DRD2:954 MSH2:1160 OXT:1518 RCAN1:2569 HTR2C:2725
Hodgkin Disease	0.04822342	493	2.760e-04		STAT5B:26 SND1:30 FOXP1:81 EBF1:156 TIMP2:238 MTHFR:266
Hypernatriuria	-0.43261385	6	2.427e-04	1.027e-01	BSND:294 CLCNKA:501 CYP11A1:770 CLCNKB:916 HSD3B2:950 AVPR2:319
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 CHRM2:1096 APOA4:1536
Diabetes Mellitus, Non-Insulin-Dependent	0.03003733	1346	3.051e-04		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 TBX1:607 ADAMTS13:719 PHEX:739
Familial migraine	0.39144377	7	3.351e-04	1.060e-01	HTR1B:191 KCNA3:788 KCNK18:857 CSNK1D:1811 SLC4A4:2287 ATP1A2:249
AIDS Dementia Complex	0.16858839	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	0.11295157	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 ABCA4:915 CACNA2D4:1113 CTNS:1449 ELOVL4:153
Tracheoesophageal Fistula	-0.15647788	43	3.876e-04	1.061e-01	CYBB:325 ERCC4:411 SLX4:462 ITGA8:504 USB1:751 FANCG:898
Bilateral cataracts (disorder)	0.10053937	103		1.122e-01	CRYBA4:59 CRYBA1:297 CLPB:466 BFSP1:556 EPHA2:657 MIP:799
Hepatomegaly	-0.05647693	332	4.347e-04	1.122e-01	GFM1:37 CYP1A1:44 LRP5:153 ALG1:205 AMACR:232 ACOX1:247
Cataract, Central Saccular, With Sutural		6	5.008e-04		CRYBA1:297 MIP:799 CRYGS:820 GJA8:832 BFSP2:1310 CRYBB2:4533
Andersen Syndrome	0.21440978	22		1.198e-01	SCN5A:231 MTHFR:266 KCNJ5:618 KCNA3:788 KCNJ12:958 PRKAR1A:964

1.982e-05 9.437e-03

1.219e-04 2.128e-02

2.596e-04 2.128e-02

2.546e-04 2.128e-02

2.683e-04 2.128e-02 1.755e-04 2.128e-02

3.393e-04 2.221e-02

stat

0.06766867

0.08986104

-0.23056772

-0.16971030

-0.04911471

0.07921951

0.06246926

MP0002063 abnormal learning/memory/cond

MP0004085 abnormal heartbeat

MP0003172 abnormal lysosome physiology

MP0008058 abnormal DNA repair

MP0002925 abnormal cardiovascular devel

MP0002272 abnormal nervous system

MP0002572 abnormal emotion/affect behav

num.genes

355

39

194

290

p.adj

KCNAB1:49 CADPS2:58 CAV1:65 CREM:95 CRMP1:110 CACNA1B:121

FOXP1:81 CACNA1B:121 NDUFS4:152 HDAC2:212 SCN5A:231 ADRB1:282 HPS1:270 CTSD:626 NAGPA:833 IDS:986 NEU4:1372 MANBA:1807

POLK:258 ALKBH2:273 GADD45A:666 NHEJ1:692 BRCA2:963 PNP:1014

HEG1:48 NOTCH1:65 SEC24B:98 EP300:131 LRP5:153 NFATC3:208

RGS2:9 KCNAB1:49 SLC26A5:55 CACNA1B:121 CNTNAP1:310 GRIK1:396

RGS2:9 HYDIN:46 CADPS2:58 CAV1:65 CREM:95 KCNH5:117

MGI_Mammalian_Phenotype_Level_4 Top pathways by permulation

MP0003953 abnormal hormone level		290	3.3936-04	2.2210 02	KG32.9 111 DIN.40 CADF 32.30 CAV 1.03 CREW.93 KCN113.117
	0.04603030	556	3.732e-04	2.221e-02	STAT5B:26 CAV1:65 CACNA1B:121 AVP:182 DDX20:187 UCN2:249
MP0003252 abnormal bile duct	-0.21289931	22	5.570e-04	2.946e-02	NR1H4:544 JAG1:551 SCP2:766 PKD1:861 PKHD1:867 CYP8B1:1328
/IP0005645 abnormal hypothalamus physiol	0.24125094	16	8.452e-04	4.023e-02	CACNA1B:121 AVP:182 HMX3:293 NOS1:623 HMX2:947 PROKR2:1608
MP0000598 abnormal liver morphology	-0.04476288	471	1.313e-03	5.683e-02	CYP1A1:44 SIN3B:176 MTAP:221 AMACR:232 ACOX1:247 TGFBR3:296
MP0001970 abnormal pain threshold	0.07440851	151	1.796e-03	6.108e-02	CACNA1B:121 NDUFS4:152 PIRT:180 KCNIP3:320 GRIK1:396 STOML3:461
MP0003698 abnormal male reproductive	0.04276208	491	1.763e-03	6.108e-02	ODF2:16 SMC1B:28 ADAD1:34 HYDIN:46 SPAG16:89 MAEL:94
MP0003635 abnormal synaptic transmissio	0.04575783	422	1.781e-03	6.108e-02	KCNAB1:49 CADPS2:58 SLC8A3:80 CRMP1:110 CACNA1B:121 HDAC2:212
MP0009745 abnormal behavioral response	0.06198011	204	2.637e-03	8.368e-02	FAIM2:67 CTNNB1:103 CACNA1B:121 LGI1:369 PLCL1:456 UNC79:465
MP0002909 abnormal adrenal gland	0.18475779	21	3.424e-03	8.977e-02	SNAPIN:228 EGLN3:785 DRD2:954 PRKAR1A:964 SLC23A2:1577 DRD5:1742
MP0000465 gastrointestinal hemorrhage	0.17241406	24	3.510e-03	8.977e-02	CTNNB1:103 SLC12A2:319 AQP3:554 RUNX1T1:1531 FES:1857 IL18:2103
MP0000747 muscle weakness	-0.12068367	49	3.583e-03	8.977e-02	NFATC3:208 FBN2:352 PEX5:416 MTM1:577 CACNA1A:796 PMP22:998
MP0005085 abnormal gallbladder physiolo	-0.17056653	25	3.208e-03	8.977e-02	AMACR:232 ABCG8:237 GPBAR1:298 NR1H4:544 JAG1:551 SCP2:766
MP0002398 abnormal bone marrow	-0.03173536	792	4.306e-03	1.025e-01	EBI3:12 HSH2D:36 NOTCH1:65 IL2RB:66 TSPAN32:89 AFF1:126
MP0005551 abnormal eye electrophysiolog	0.06964054	139	5.006e-03	1.135e-01	UNC119:145 PRPH2:148 NDUFS4:152 RCVRN:207 CNTNAP1:310 PDE6B:340
MP0004811 abnormal neuron physiology	0.04873683	275	6.403e-03	1.385e-01	CADPS2:58 KIF2A:93 CRMP1:110 NDUFS4:152 PIRT:180 DBNL:281
MP0002429 abnormal blood cell	-0.02505848	1189	8.324e-03	1.723e-01	EBI3:12 HSH2D:36 CYP1A1:44 ITGB6:50 NOTCH1:65 IL2RB:66
MP0005365 abnormal bile salt	-0.14885021	26	8.727e-03	1.731e-01	GPBAR1:298 PEX5:416 NCOA6:590 HSD17B4:728 SCP2:766 EHHADH:1026
MP0002210 abnormal sex determination	0.04259286	328	9.639e-03	1.786e-01	SMC1B:28 SPAG16:89 MAEL:94 CREM:95 FHL5:108 HTR1B:191
MP0002277 abnormal respiratory mucosa	0.16714930	20	9.756e-03	1.786e-01	SIX1:406 CRK:462 CFTR:880 TACR1:2639 FGF10:2826 HOXA5:2960
MP0005334 abnormal fat pad	0.05892958	150	1.372e-02	1.935e-01	STAT5B:26 CAV1:65 ADRB1:282 FSHR:356 GPD2:427 NPY1R:542
MP0005332 abnormal amino acid	-0.06809883	116	1.198e-02	1.935e-01	ARG1:333 LAMP2:394 SLC12A1:403 TSTA3:407 UPK3A:415 NOS2:760
MP0005380 embryogenesis phenotype	-0.03654130	406	1.423e-02	1.935e-01	GADD45GIP1:3 NOTCH1:65 TGIF1:116 EP300:131 PTK7:164 NFATC3:208
MP0003959 abnormal lean body	0.09618600	58	1.162e-02	1.935e-01	STAT5B:26 OPRM1:517 GHR:726 RICTOR:748 NEUROG3:757 BSX:928
MP0003950 abnormal plasma membrane	0.22698949	10	1.299e-02	1.935e-01	CAV1:65 PIGA:1560 DMD:1629 UGCG:1850 GLRX:2194 MPP4:3013
MP0002064 seizures	0.04612380	253	1.313e-02	1.935e-01	FAIM2:67 CREM:95 CTNNB1:103 NDUFS4:152 SCN5A:231 DBNL:281
MP0001697 abnormal embryo size	-0.03705107	408	1.273e-02	1.935e-01	GADD45GIP1:3 ECSIT:11 NOTCH1:65 SEC24B:98 EP300:131 E4F1:135
1P0001672 abnormal embryogenesis/ devel	-0.03654130	406	1.423e-02	1.935e-01	GADD45GIP1:3 NOTCH1:65 TGIF1:116 EP300:131 PTK7:164 NFATC3:208
MP0003937 abnormal limbs/digits/tail de	-0.07247460	101	1.246e-02	1.935e-01	ADAMTS20:320 FBN2:352 AXIN1:448 DACT1:552 INTU:584 SOX9:599
1P0008875 abnormal xenobiotic pharmacok	-0.17548619	16	1.519e-02	2.009e-01	CYP1A1:44 SLC22A1:688 COMT:731 CYP1A2:1756 ADH7:2304 POR:4080
MP0002066 abnormal motor capabilities/c	0.02376862	1077	1.578e-02	2.030e-01	FOXJ1:25 HYDIN:46 CADPS2:58 CAV1:65 TMC1:69 SLC8A3:80
MP0003283 abnormal digestive organ	-0.26193156	7	1.645e-02	2.060e-01	PDX1:450 SHH:2352 NKX3-2:3692 IHH:3707 PKD2:5443 MEGF8:6182
MP0002102 abnormal ear morphology	0.19808487	12	1.759e-02	2.147e-01	TMC1:69 EXT1:384 TYRP1:1074 DLX6:1161 HOXA2:1235 CASP3:2117
MP0004272 abnormal basement membrane	-0.12462572	29	2.043e-02	2 210e-01	RECK:370 COL18A1:994 KDR:1304 ADM:1557 LAMA2:1583 LAMC2:1993

tissue_specific Top pathways by permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
testis	0.04735964	1372	4.796e-08	2.590e-06	HORMAD1:4 ODF2:16 ACRBP:22 CPA5:23 FOXJ1:25 SMC1B:28
Brodmann.area.9	0.08833173	180	5.063e-05	1.367e-03	KCNH5:117 GLRB:162 NECAB1:195 CLEC2L:233 HCN1:255 NEUROD6:303
EBV.lymphocyte	-0.04042401	670	5.618e-04	1.011e-02	EBI3:12 HSH2D:36 IL2RB:66 SERPINB10:83 SLC9A7:114 LAMP3:194
liver	-0.05384233	327	9.874e-04	1.333e-02	DECR2:5 TM6SF2:24 CREB3L3:26 HAAO:56 CLDN14:127 IDO2:132
blood	-0.05402381	275	2.345e-03	1.820e-02	DHX34:30 LY6G6F:46 STX11:55 TSPAN32:89 GP9:246 HBQ1:521
cortex.kidney	-0.08355652	114	2.174e-03	1.820e-02	ITGB6:50 CYP24A1:68 DMRT2:171 FMO1:219 BSND:294 SLC12A1:403
spleen	-0.05203831	297	2.359e-03	1.820e-02	GMFG:8 NIBAN3:62 CORO7:150 NAIP:206 VPREB3:207 GP9:246
pituitary.gland	0.06022316	213	2.713e-03	1.831e-02	NTS:75 ELAPOR1:170 CSH2:265 GH1:270 CFAP47:289 TUSC3:321
subcutaneous.adipose	-0.09939692	72	3.654e-03	2.192e-02	CYP1A1:44 ACACB:157 RDH5:243 GPD1:286 GPBAR1:298 LGALS12:307
cerebellar.hemisphere	0.03569561	508	7.244e-03	3.912e-02	GPR83:38 CADPS2:58 RNF112:83 CHN2:130 TMEM178A:147 TLX3:244
thyroid	-0.05963548	151	1.203e-02	5.906e-02	RHPN1:49 RGL3:54 CTSB:95 IDO2:132 SNX22:180 RASEF:292
aorta	-0.05513319	154	1.907e-02	8.583e-02	SYNPO:31.5 SCRG1:107 HMCN1:168 ERG:220 IGFBPL1:322 ITGA11:494
hypothalamus	0.08032841	66	2.445e-02	1.016e-01	NTS:75 PIRT:180 AVP:182 GRIK1:396 BRINP3:455 SYT6:772
C1.spinal.cord	0.04344371	182	4.507e-02	1.623e-01	PLEKHB1:62 SLC31A2:66 TAFA4:109 ARHGAP22:120 VXN:150 CLDND1:245
hippocampus.proper	0.18371831	10	4.433e-02	1.623e-01	NTS:75 NEUROD6:303 NEUROG3:757 CABP7:1767 OLIG2:1788 SLC17A7:2288
cerebellum	0.02930582	375	5.572e-02	1.881e-01	GPR83:38 SLC26A5:55 RNF112:83 CACNA1B:121 CHN2:130 TMEM178A:147
tibial.nerve	-0.03886751	192	6.575e-02	2.088e-01	DLEU7:91 IL17B:96 MMP28:225 SOX8:233 TMPRSS5:259 SEMA5A:306
coronary.artery	0.12897815	15	8.390e-02	2.517e-01	PCOLCE2:410 HEYL:935 ST6GALNAC5:1786 COL4A1:1931 CCL19:2120 CCDC190:2
transverse.colon	-0.03912761	147	1.039e-01	2.953e-01	WNK4:151 NR1I2:289 GLOD5:305 MYO1A:535 B3GNT7:579 FOXH1:791
left.ventricle	0.05563990	68	1.137e-01	3.071e-01	CKMT2:39 TCAP:124 SCN5A:231 ASB15:415 LMOD2:531 TNNT2:779
cerebral.cortex	0.04335458	107	1.232e-01	3.167e-01	FAIM2:67 RCVRN:207 CLEC2L:233 NEUROD6:303 ELFN2:318 FAM163B:348
esophagus.mucosa	0.03004880	218	1.303e-01	3.197e-01	TP53I3:24 LEXM:76 P2RY1:138 KRT24:143 SPINK7:284 SPINK5:335
nucleus.accumbens	0.03979965	99	1.732e-01	3.924e-01	PRKCG:215 CPNE5:338 ANKRD34B:496 KCTD4:651 CHRM4:661 HTR1D:762
suprapubic.skin	0.02854281	194	1.744e-01	3.924e-01	CLDN1:15 IL37:74 TNS4:102 POU2F3:105 RAB7B:140 UCN2:249
peyers.patch	-0.02896253	167	2.001e-01	4.157e-01	TM6SF2:24 CREB3L3:26 NR1I2:289 GLOD5:305 ACY3:406 SLC5A9:442
putamen	0.09968393	14	1.968e-01	4.157e-01	LRRC10B:246 PDE10A:738 GPR88:972 KCNH4:1123 FAM237A:1589 OPALIN:3406
endocervix	-0.03998729	72	2.423e-01	4.845e-01	LCN10:199 METTL27:252 LAMC3:293 COLEC12:367 SMPDL3A:383 MMP11:475
caudate.nucleus	0.06113452	26	2.811e-01	5.422e-01	LRRC10B:246 SLC35D3:291 VAX1:792 GPR88:972 FAM237A:1589 MAPK4:2834
adrenal.gland	-0.02648979	108	3.440e-01	5.992e-01	ADGRV1:159 SLC14A2:193 GALM:231 FNDC4:434 ZNF275:519 FADS2:573
ectocervix	-0.05555116	25	3.368e-01	5.992e-01	TSKU:34 KCNK6:846 PTHLH:1287 PAPPA2:1508 KRT34:1558 MMRN1:2966
lung	-0.02394555	139	3.329e-01	5.992e-01	ITGB6:50 ABCA3:80 LAMP3:194 GP9:246 LRRN4:676 COX4I2:705
amygdala	0.07181305	9	4.558e-01	7.239e-01	NEUROD6:303 TNR:1637 LHFPL3:1930 SLC17A7:2288 PTPRZ1:5501 PCDH15:830
leg.skin	0.01523986	217	4.439e-01	7.239e-01	IL37:74 POU2F3:105 UCN2:249 SLC46A2:272 LGALSL:313 SPINK5:335
vagina	0.02388102	91		7.239e-01	LEXM:76 SPINK7:284 SPINK5:335 DSC3:511 KRT5:557 ENDOU:641
sigmoid.colon	0.02816289	50	4.919e-01		TES:488 NKX2-3:559 VIP:789 GDNF:1026 TACR2:1057 LIMS2:1070
tibial.artery	-0.01897518	107		7.497e-01	TRABD2B:69 SYTL2:379 HEY2:417 JAG1:551 SLIT3:767 AOC3:771
breast	0.04634719	15	5.345e-01		KRT5:557 HCAR1:1216 LEP:3154 GSC:3492 THRSP:4849 LMX1B:5051
prostate	0.02836241	38		7.757e-01	ACP3:242 STEAP2:407 KRT5:557 NTF4:790 TRPM8:1239 NPY:1335
minor.salivary.gland	-0.01917650	69		7.921e-01	OXGR1:191 SOX9:599 BPIFB6:1132 JCHAIN:1197 PAX3:1695 MMP7:1879
stomach	-0.01684755	86		7.921e-01	TMPRSS2:21 VWA2:178 PIK3C2G:863 PSAPL1:1250 EPN3:1393 HNF1A:1808