





Top Positive genes by P-value non-permulated

Top Negative genes by P-value non-permulated

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

Gene Rho P p.adj qValueNoperm

WNK4 6.642342 1.852427e-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
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

P p.adj qValueNoperm

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 NDST3:22 CNTN4:26 ADCY1:43
Channelopathies	-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	5.618e-03	ATF6:4 CNTN3:12 CNTN4:26 RYR2:32 ZNF277:35 CHL1:76
HIV Infections	-0.05482550	639	2.863e-06	5.618e-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 RNF112:59
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 BFSP2:412 CRYAA:480 CRYBB1:865
Seizures, Focal	-0.10086998	123	1.150e-04	8.056e-02	SCN9A:44 KCNQ3:168 DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387
Complex partial seizures	-0.10682440	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 HCN4:375 SCN5A:698 TGFB1:704 CACNA1D:778
Cataract, Central Saccular, With Sutural	-0.44370818	6	1.672e-04	1.035e-01	GJA8:142 MIP:344 BFSP2:412 CRYBA1:692 CRYGS:1349 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 SCNN1A: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 CHRM1:420
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 JMJD1C:910 TRPM6:979 SLC12A1:1014
Alcoholic Intoxication, Chronic	-0.05312486	376	4.381e-04	1.249e-01	CNTN4:26 ADCY1:43 GRM2:63 DSCAML1:98 MTHFR:123 TAC1:132
Diabetes Mellitus, Non-Insulin-Dependent	-0.02903266	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	-0.07614966	164	7.893e-04	1.249e-01	GRM2:63 KCNQ3:168 ACOT7:240 BIN1:256 GLUL:266 SLC2A1:308
Seizures, Auditory	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRM1:420
Seizures, Clonic	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRM1:420
Seizures, Sensory	-0.09989773	95	7.784e-04		DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRM1:420
Seizures, Somatosensory	-0.09989773	95	7.784e-04	1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRM1:420
Ventricular tachycardia, polymorphic	-0.34365553	8	7.628e-04	1.249e-01	RYR2:32 HCN4:375 SCN5A:698 KCNQ1:892 KCNH2:958 CASQ2:1815
Atonic Absence Seizures	-0.09989773	95		1.249e-01	DRD2:296 SLC2A1:308 HCN1:381 CHRNA3:387 GABRA5:416 CHRM1:420
Aura	-0.13113566	59		1.249e-01	CHRM2:144 HCN1:381 CHRM1:420 SCN1A:450 SLC12A5:519 GABRB3:630

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

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: REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT -0.09903491 294 5.641e-09 1.068e-05 CXCR5:46 TAC1:132 CHRM2:144 PLPPR4:152 NTSR1:153 UTSZR:1 REACTOME_MUSCLE_CONTRACTION -0.12223484 190 6.586e-09 1.068e-05 RYR2:32 SCN9A:44 LMOD1:57 HIPK1:60 ITPR1:117 ITGA1:118 REACTOME_GFOR_LIGAND_BINDING -0.08525270 396 6.537e-09 1.068e-05 VIPR1:24 CXCR5:46 GRM2:63 TAC1:132 CHRM2:144 GRM6:14 KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC -0.10117404 259 2.223e-08 2.885e-05 VIPR1:24 GRM2:63 CHRM2:144 GRM6:14 REM2:65 APBA2:91 DSCAML1:5 MIKKELSEN_MEF_HCP_WITH_H3K27ME3 -0.08659299 555 3.837e-08 4.149e-05 CNTN4:26 RYR2:32 CSMD1:62 UGT8:65 APBA2:91 DSCAML1:5 REACTOME_NEURONAL_SYSTEM -0.08049448 385 6.522e-08 6.045e-05 ADCY1:43 KCNA10:79 APBA2:91 KCNJ12:139 KCNV2:151 KCNJ14:16 NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON 0.20371628 52 3.769e-07
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT
REACTOME_MUSCLE_CONTRACTION
REACTOME_GPCR_LIGAND_BINDING
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC -0.10117404 259 2.223e-08 2.885e-05 VIPR1:24 GRM2:63 CHRM2:144 GRM6:148 NTSR1:153 UTS2R:1 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:S REACTOME_NEURONAL_SYSTEM -0.08049448 385 6.522e-08 6.045e-05 ADCY1:43 KCNA10:79 APBA2:91 KCNJ12:139 KCNV2:151 KCNJ14:10 REACTOME_CARDIAC_CONDUCTION -0.14046100 121 9.739e-08 7.898e-05 RYR2:32 SCN9A:44 HIPK1:60 ITPR1:117 KCNJ12:139 KCNJ14:13 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:2 WP_GPCRS_CLASS_A_RHODOPSINLIKE -0.10093792 206 6.180e-07 4.010e-04 CXCR5:46 CHRM2:144 NTSR1:153 MAS1:228 DRD2:296 DRD5:4 REACTOME_POTASSIUM_CHANNELS -0.14998331 91 7.741e-07 4.566e-04 KCNA10:79 KCNJ12:139 KCNV2:151 KCNJ14:158 KCNQ3:168 KCNF REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR -0.10943447 166 1.184e-06 6.401e-04 CXCR5:46 TAC1:132 NTSR1:153 UTS2R:167 CSMD1:62 SYT6:71 REACTOME_G_ALPHA_I_SIGNALLING_EVENTS -0.08
MIKKELSEN_MEF_HCP_WITH_H3K27ME3
REACTOME_NEURONAL_SYSTEM
REACTOME_CARDIAC_CONDUCTION
NIKOLSKY_BREAST_CANCER_8P12_P11_AMPLICON
WP_GPCRS_CLASS_A_RHODOPSINLIKE -0.10093792 206 6.180e-07 4.010e-04 CXCR5:46 CHRM2:144 NTSR1:153 MAS1:228 DRD2:296 DRD5:4 REACTOME_POTASSIUM_CHANNELS -0.14998331 91 7.741e-07 4.566e-04 KCNA10:79 KCNJ12:139 KCNV2:151 KCNJ14:158 KCNQ3:168 KCNF REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR -0.10943447 166 1.184e-06 6.401e-04 CXCR5:46 TAC1:132 NTSR1:153 UTS2R:167 QRFPR:223 NPS:3 BENPORATH_ES_WITH_H3K27ME3 -0.04565189 983 1.579e-06 7.089e-04 HSF4:19 CSF1:51 PHLDB1:53 LMOD1:57 CSMD1:62 SYT6:71 REACTOME_G_ALPHA_I_SIGNALLING_EVENTS -0.08546827 269 1.478e-06 7.089e-04 ADCY1:43 CXCR5:46 GRM2:63 ITPR1:117 CHRM2:144 GRM6:14
REACTOME_POTASSIUM_CHANNELS
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR
BENPORATH_ES_WITH_H3K27ME3
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS -0.08546827 269 1.478e-06 7.089e-04 ADCY1:43 CXCR5:46 GRM2:63 ITPR1:117 CHRM2:144 GRM6:14
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
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON 0.12789472 100 1.005e-05 3.834e-03 PGAP6:283 ZNF213:465 SPSB3:474 EME2:495 RHBDL1:560 WDR9
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 KCNF1:320 KCNAB1:469 KCNV
WP_CALCIUM_REGULATION_IN_CARDIAC_CELLS
BENPORATH_SUZ12_TARGETS -0.04087393 918 3.140e-05 9.700e-03 HSF4:19 CSF1:51 PHLDB1:53 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 CEP170:111 ADAMTS4:135 CDH19:1
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 TYW
REACTOME_NERVOUS_SYSTEM_DEVELOPMENT
REACTOME_PHASE_0_RAPID_DEPOLARISATION
REACTOME_SIGNALING_BY_RECEPTOR_TYROSINE0.05087542 503 1.007e-04 2.513e-02 DNM3:81 BAIAP2:100 ITPR1:117 WWP1:125 PTK2B:136 ARC:14
STARK_HYPPOCAMPUS_22Q11_DELETION_UP
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3
BENPORATH_EED_TARGETS
LIU_OVARIAN_CANCER_TUMORS_AND_XENOGRAFTS
REACTOME_G_ALPHA_S_SIGNALLING_EVENTS
NIKOLSKY_BREAST_CANCER_15Q26_AMPLICON
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER
SERVITJA_ISLET_HNF1A_TARGETS_UP
DAZARD_RESPONSE_TO_UV_NHEK_DN 0.06356511 284 2.359e-04 4.240e-02 DST:57 BPTF:69 GSE1:145 TMEM131L:163 AKAP9:181 ASXL1:2
KEGG_PURINE_METABOLISM -0.08623413 149 2.845e-04 5.128e-02 ADCY1:43 PDE5A:220 PDE6B:258 PDE1C:306 ALLC:425 CANT1:
NIKALSKY RDENST CANICED 20142 (142 AMDLICA) - A 100589874 - 129 - 2 (1495 A4 E 2025 A2 - MAVT4:27 NITCD4:4E2 DTEL4:224 DEACTD3:20A 7DTD46:4AA TEAD3
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO

GO_Biological_Process_2023 Top pathways by non-permulation

NIKOLSKY_BREAST_CANCER_8Q12_Q22_AMPLICON -0.09404219
WP_PRADERWILLI_AND_ANGELMAN_SYNDROME -0.13833289

122 3.381e-04 5.584e-02 TMEM64:20 MMP16:95 RBM12B:138 ZFHX4:147 NECAB1:215 OSGIN2:242

56 3.442e-04 5.584e-02 HERC2:13 GABRR1:342 GABRA5:416 GABRB3:630 UBE3A:689 GABRG3:740

Geneset	stat	num.genes	pval	p.adj	gene.vals
Cardiac Conduction (GO:0061337)	-0.21969546	44	•	2.021e-03	ANK2:15 CAMK2D:163 BIN1:256 SCN3B:279 HCN4:375 HCN1:381
Chemical Synaptic Transmission (GO:00072	-0.08867750	256		2.021e-03	GRM2:63 APBA2:91 CHRM2:144 NTSR1:153 KCNQ3:168 CACNA1B:173
Metal Ion Transport (GO:0030001)	-0.11290351	156		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		2.021e-03	ANK2:15 CAMK2D:163 BIN1:256 SCN3B:279 HCN4:375 HCN1:381
Regulation Of Synaptic Transmission, Glu	-0.18765103	54		2.021e-03	TSHZ3:8 GRM2:63 PTK2B:136 GRM6:148 PLPPR4:152 DRD2:296
Regulation Of Monoatomic Ion Transmembra	-0.17125026	62		2.848e-03	ANK2:15 PTK2B:136 SCN3B:279 HCN4:375 HCN1:381 SCN2B:436
Anterograde Trans–Synaptic Signaling (GO	-0.09580404	182		5.270e-03	GRM2:63 APBA2:91 CHRM2:144 NTSR1:153 KCNQ3:168 CACNA1B:173
Calcium Ion Import Across Plasma Membran	-0.22438541	33		5.270e-03	TRPM1:3 SCN9A:44 CACNA1B:173 CACNA1S:355 SCN1A:450 SLC8A3:561
Potassium Ion Transmembrane Transport (G	-0.11337585	132		5.270e-03	KCNA10:79 KCNJ12:139 KCNV2:151 KCNJ14:158 KCNQ3:168 KCNT2:186
tRNA Modification (GO:0006400)	0.15599749	66		6.439e-03	THADA:106 TRMT10A:155 DTWD1:185 TRMO:256 TRMT1:376 TYW1B:421
Potassium Ion Transport (GO:0006813)	-0.11397943	120		8.200e-03	KCNA10:79 KCNJ12:139 KCNV2:151 KCNQ3:168 KCNF1:320 KCNK1:360
Monoatomic Cation Transmembrane Transpor	-0.07392258	273		1.281e-02	TRPM1:3 SCN9A:44 KCNA10:79 CNGB3:105 KCNV2:151 KCNQ3:168
Adenylate Cyclase–Inhibiting G Protein–C	-0.07552236	46		1.591e-02	CHRM2:144 DRD2:296 CHRM1:420 HTR1B:467 HTR1A:522 CHRM3:593
	0.11811212	100		1.770e-02	GFM2:227 GATB:336 GADD45GIP1:346 FASTKD1:517 POLRMT:584 PTCD3:767
Mitochondrial Gene Expression (GO:014005 Ventricular Cardiac Muscle Cell Action P	-0.28209781	16		3.367e-02	RYR2:32 SCN3B:279 KCNE4:550 SCN5A:698 KCNQ1:892 KCNH2:958
		-			RYR2:32 SCN3B:279 KCNE4:550 SCN5A:698 KCNE4:550 SCN5A:698
Cardiac Muscle Cell Action Potential Inv	-0.20967751	28		3.825e-02 3.825e-02	TRPM1:3 SCN9A:44 KCNJ12:139 KCNJ14:158 CACNA1B:173 CACNA1S:355
Inorganic Cation Import Across Plasma Me	-0.11300661	96			
Regulation Of Monoatomic Cation Transmem	-0.17981898	38		3.825e-02	DPP6:247 HCN4:375 HCN1:381 KCNAB1:469 SCN5A:698 CACNA1D:778
Somatic Recombination Of Immunoglobulin	0.38974552	8		3.825e-02	MSH3:291 TCF3:428 PRKDC:1130 NHEJ1:1232 LIG4:1556 MSH6:2026
Positive Regulation Of DNA Metabolic Pro	0.10824944	103		4.059e-02	SLX4:84 STON1:252 ATAD5:262 EGF:273 ERCC6:287 BABAM1:344
Mitochondrial Translation (GO:0032543)	0.11052885	96		4.463e-02	GFM2:227 GATB:336 GADD45GIP1:346 MTRF1:687 PTCD3:767 MRPS25:940
Regulation Of Neurotransmitter Receptor	-0.17225520	39		4.463e-02	PTK2B:136 NETO1:180 DLGAP2:257 NPTX1:474 CRH:791 SHISA9:919
Sister Chromatid Segregation (GO:0000819	0.18744238	33		4.463e-02	CHAMP1:126 ESPL1:162 SMC4:313 SGO1:476 SPAG5:731 WAPL:775
Visual Perception (GO:0007601)	-0.11231277	93		4.463e-02	TRPM1:3 ATF6:4 GRM6:148 GNAT2:169 NXNL2:199 PRPH2:339
tRNA Methylation (GO:0030488)	0.17853060	36		4.551e-02	THADA:106 TRMT10A:155 TRMO:256 TRMT10B:356 TRMT1:376 TRMT5:391
Cardiac Muscle Cell Action Potential (GO	-0.19693481	29		4.950e-02	SCN3B:279 HCN4:375 SCN2B:436 SCN1A:450 SCN5A:698 CACNA1D:778
Membrane Organization (GO:0061024)	-0.08549280	155		4.950e-02	ANK2:15 SYNJ1:34 ACE2:87 LPCAT2:198 BIN1:256 EGFR:321
Modulation Of Chemical Synaptic Transmis	-0.09685138	118		5.512e-02	GRM2:63 GRM6:148 PLPPR4:152 CACNA1B:173 DLGAP2:257 DRD2:296
Sensory Perception Of Light Stimulus (GO	-0.10804818	94	3.001e-04	5.576e-02	TRPM1:3 ATF6:4 GNAT2:169 USH2A:177 NXNL2:199 PRPH2:339
Cell-Cell Adhesion Via Plasma-Membrane A	-0.08632527	144	3.600e-04	6.061e-02	CNTN4:26 SELP:93 DSCAML1:98 IGSF9:184 NECTIN4:250 TENM3:316
Regulation Of DNA-templated Transcriptio	0.02722861	1647	3.579e-04	6.061e-02	ZNF292:6 SAFB2:16 JMY:25 ZEB1:33 ZSCAN29:44 MLLT10:45
Regulation Of Potassium Ion Transport (G	-0.19173898	29	3.535e-04	6.061e-02	ANK2:15 PTK2B:136 DPP6:247 DRD2:296 KCNAB1:469 CACNA1D:778
Mitochondrial RNA Metabolic Process (GO:	0.23553289	19	3.799e-04	6.203e-02	FASTKD1:517 POLRMT:584 FASTKD3:807 FASTKD5:876 TEFM:1226 MTERF2:1298
Cobalamin Transport (GO:0015889)	0.41645529	6	4.112e-04	6.517e-02	CBLIF:136 CUBN:201 ABCD4:655 ABCD1:1391 TCN1:2569 TCN2:3271
Positive Regulation Of Synaptic Transmis	-0.12093139	71	4.319e-04	6.649e-02	TSHZ3:8 PTK2B:136 SHANK2:364 NPS:388 PLK2:389 SLC8A3:561
Inorganic Cation Transmembrane Transport	-0.06142472	276	4.723e-04	7.069e-02	TRPM1:3 SCN9A:44 KCNA10:79 KCNV2:151 KCNQ3:168 SCN3B:279
Action Potential (GO:0001508)	-0.17359311	33	5.610e-04	8.169e-02	SCN3B:279 KCNE4:550 CHRNA4:639 SCN5A:698 KCNQ1:892 KCNH2:958
Monocarboxylic Acid Transport (GO:001571	0.12370879	63	6.918e-04	9.809e-02	ABCB4:98 SLC10A2:217 ARID4A:237 SLC10A1:245 SLC16A5:437 FABP1:692
Neuropeptide Signaling Pathway (GO:00072	-0.12448040	61	7.806e-04	1.051e-01	SORCS2:69 SORL1:89 NTSR1:153 UTS2R:167 RXFP3:834 OPRL1:876
Positive Regulation Of Calcium Ion Trans	-0.15776926	38	7.687e-04	1.051e-01	ANK2:15 GRM6:148 THY1:402 CEMIP:576 CAPN3:669 CALCR:715

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0002398 abnormal bone marrow	0.04455376	794	5.969e-05	1.421e-02	ANK1:5 ZEB1:33 DST:57 JAK3:73 HSH2D:77 PPARG:118
MP0005551 abnormal eye electrophysiolog	-0.10286973	138	3.602e-05	1.421e-02	TRPM1:3 CSF1:51 CNGB3:105 NR2E3:126 GJA8:142 GRM6:148
MP0002429 abnormal blood cell	0.03517702	1191	2.079e-04	3.299e-02	ANK1:5 ZEB1:33 PTPN13:35 MYO9B:61 NAGLU:65 JAK3:73
MP0004085 abnormal heartbeat	-0.08067707	158	5.392e-04	3.569e-02	ANK2:15 RYR2:32 ACE2:87 CHRM2:144 CACNA1B:173 FOXP1:210
MP0002085 abnormal embryonic tissue	0.04161889	653	5.555e-04	3.569e-02	ZEB1:33 BPTF:69 C2CD3:80 ECSIT:91 NSD1:137 ESPL1:162
MP0003252 abnormal bile duct	0.21720384	22	4.290e-04	3.569e-02	PKHD1:90 ABCB4:98 ABCB11:221 CYP8B1:348 NR1H4:587 PKD1:818
MP0002272 abnormal nervous system	-0.07227279	195	5.999e-04	3.569e-02	RYR2:32 SLC26A5:141 ARC:143 CHRM2:144 KCNQ3:168 CACNA1B:173
MP0003635 abnormal synaptic transmissio	-0.05203614	424	3.683e-04	3.569e-02	SYNJ1:34 ADCY1:43 SCN9A:44 GRM2:63 DSCAML1:98 BAIAP2:100
MP0002084 abnormal developmental patter	0.05321883	360	7.295e-04	3.858e-02	LAMA1:23 BPTF:69 C2CD3:80 ECSIT:91 NSD1:137 INVS:188
MP0000598 abnormal liver morphology	0.04651139	471	8.394e-04	3.996e-02	ANK1:5 ERCC5:31 NAGLU:65 PKHD1:90 ABCB4:98 PREX1:107
MP0003868 abnormal feces composition	0.18822913	25	1.145e-03	4.191e-02	ABCB4:98 SLC10A2:217 CYP8B1:348 APC:467 CYP7A1:537 VWF:612
MP0002572 abnormal emotion/affect behav	-0.05696753	290	1.082e-03	4.191e-02	NDST3:22 ADCY1:43 GRM2:63 CHL1:76 APBA2:91 TAC1:132
MP0002063 abnormal learning/memory/cond	-0.05158875	356	1.123e-03	4.191e-02	ADCY1:43 ACSM4:56 CHL1:76 APBA2:91 BAIAP2:100 ARC:143
MP0001666 abnormal nutrient absorption	0.14350101	42	1.334e-03	4.534e-02	ABCB4:98 SLC10A2:217 VDR:318 CYP8B1:348 CYP7A1:537 ITGB1:638
MP0002135 abnormal kidney morphology	0.04437587	449	1.822e-03	5.782e-02	ANK1:5 NAGLU:65 PKHD1:90 TET2:92 INVS:188 SERPINE1:195
MP0009745 abnormal behavioral response	-0.06169749	204	2.756e-03	8.198e-02	RYR2:32 GRM2:63 LYST:64 ADAMTS4:135 CHRM2:144 CACNA1B:173
MP0005365 abnormal bile salt	0.16236516	26	4.227e-03	1.006e-01	SLC10A2:217 ABCB11:221 POR:325 CYP8B1:348 CYP7A1:537 PNLIP:705
MP0008058 abnormal DNA repair	0.13428813	39	3.801e-03	1.006e-01	POLK:49 ERCC6:287 TEX15:436 APC:467 GADD45A:548 ALKBH2:864
MP0000678 abnormal parathyroid gland	0.18247733	21	3.843e-03	1.006e-01	VDR:318 GCM2:403 PTHLH:702 PHC1:1360 CASR:1933 PTH:2141
MP0002064 seizures	-0.05338869	254	4.019e-03	1.006e-01	RYR2:32 SYNJ1:34 SCN9A:44 ITPR1:117 ADAMTS4:135 KCNQ3:168
MP0000716 abnormal immune system	0.02892807	972	4.700e-03	1.065e-01	ANK1:5 ZEB1:33 PTPN13:35 MYO9B:61 NAGLU:65 JAK3:73
MP0004808 abnormal hematopoietic stem	0.10325459	61	5.479e-03	1.185e-01	MECOM:190 ARID4A:237 RAPGEF2:278 TCF3:428 MAN2A1:447 IL6:949
MP0004019 abnormal vitamin homeostasis	0.12445619	41	5.964e-03	1.189e-01	CLDN16:100 CYP27A1:197 CUBN:201 VDR:318 CYP7A1:537 CYP24A1:683
MP0002932 abnormal joint morphology	0.07680484	108	6.205e-03	1.189e-01	ZEB1:33 FBN2:46 FOXC2:323 CDX1:400 GDF5:658 DMRT2:676
MP0002019 abnormal tumor incidence	0.03991049	425	6.243e-03	1.189e-01	ZEB1:33 ABCB4:98 PPARG:118 FANCM:144 GTF2IRD1:176 MTBP:191
MP0002925 abnormal cardiovascular devel	0.03656011	509	6.564e-03	1.202e-01	C2CD3:80 GTF2IRD1:176 INVS:188 MECOM:190 SERPINE1:195 CUBN:201
MP0003935 abnormal craniofacial develop	0.05076111	244	7.290e-03	1.285e-01	ZEB1:33 GTF2IRD1:176 MECOM:190 ENAM:272 FOXC2:323 POR:325
MP0002113 abnormal skeleton development	0.03995094	384	8.978e-03	1.526e-01	ZEB1:33 FBN2:46 NBR1:128 ROR1:202 ERCC6:287 VDR:318
MP0001970 abnormal pain threshold	-0.06075639	149	1.131e-02	1.763e-01	TSHZ3:8 ADCY1:43 TAC1:132 CHRM2:144 NTSR1:153 CACNA1B:173
MP0005253 abnormal eye physiology	-0.07715427	91	1.148e-02	1.763e-01	TRPM1:3 CNGB3:105 NR2E3:126 GJA8:142 EGFLAM:235 SEMA4A:324
MP0010094 abnormal chromosome stability	0.09441523	61	1.110e-02	1.763e-01	CENPE:149 FANCG:321 SIRT6:698 REV3L:718 POLQ:811 USP1:854
MP0003195 calcinosis	0.24785408	8	1.525e-02	2.149e-01	SLC12A1:1014 ENPP1:1096 AGXT:1352 CASR:1933 ABCC6:3143 SPP1:3898
MP0005085 abnormal gallbladder physiolo	0.14041932	25	1.526e-02	2.149e-01	ABCB4:98 CYP27A1:197 SLC10A2:217 ABCB11:221 CYP8B1:348 CYP7A1:53
MP0003959 abnormal lean body	-0.09215321	58	1.562e-02	2.149e-01	DDR2:31 CBL:149 DLL1:239 RPTOR:337 VIPR2:427 FTO:457
MP0003937 abnormal limbs/digits/tail de	0.06999507	101	1.580e-02	2.149e-01	FBN2:46 MECOM:190 POR:325 DACT1:443 APC:467 ITGB1:638
MP0002722 abnormal immune system	0.02975961	604	1.701e-02	2.249e-01	ANK1:5 ERCC5:31 ZEB1:33 JAK3:73 HSH2D:77 PKHD1:90
MP0002822 catalepsy	-0.27824411	6	1.830e-02	2.355e-01	DRD2:296 CHRM4:1264 RXRG:1586 DBH:1884 CNR1:7511.5 FAAH:7511.5
MP0005220 abnormal exocrine pancreas	0.09917636	46	2.035e-02	2.549e-01	PKHD1:90 INVS:188 MAN2B1:713 PKD1:818 BICC1:829 STK11:961
MP0001529 abnormal vocalization	-0.14839162	20	2.177e-02	2.657e-01	CHRM2:144 DRD2:296 TACR1:411 LBR:800 CHRM4:1264 DHCR7:1898
MP0002066 abnormal motor capabilities/c	-0.02215226	1079	2.427e-02	2.763e-01	TSHZ3:8 HERC2:13 ANK2:15 IREB2:29 SYNJ1:34 CYLD:45

tissue_specific Top pathways by non-permulation

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Geneset	stat	num.genes	pval	p.adj	gene.vals
Brodmann.area.9	-0.10318586	181		1.115e-04	CSMD1:62 HS3ST2:118 PLPPR4:152 KCNQ3:168 B3GALT2:172 NETO1:180
cerebral.cortex	-0.08907973	107	1.537e-03	3.090e-02	CSMD1:62 HECW1:204 MAS1:228 ARNT2:272 KCNF1:320 RS1:350
minor.salivary.gland	0.10949978	69	1.717e-03	3.090e-02	ODAM:132 ENPP3:303 PRSS8:621 AMTN:679 SCNN1A:737 IRX1:793
blood	0.04473376	275	1.175e-02	1.427e-01	JAK3:73 PREX1:107 DHX34:141 NLRP12:174 BPI:184 TREML2:224
cerebellar.hemisphere	-0.03133630	507	1.850e-02	1.427e-01	NDST3:22 MYT1:37 ADCY1:43 RNF112:59 DNM3:81 PHTF1:82
peyers.patch	0.05441915	167	1.608e-02	1.427e-01	TINAG:87 CREB3L3:102 SLC10A2:217 CDHR2:372 DQX1:382 MALRD1:385
thyroid	0.05717091	151	1.606e-02	1.427e-01	PRTG:8 IDO2:9 WDR72:110 PLEKHG4B:248 MIOX:296 CLCNKA:301
pancreas	0.06902774	94	2.129e-02	1.437e-01	TMED6:212 EGF:273 KCNK16:285 CPA2:408 CELA3B:527 GNMT:634
EBV.lymphocyte	0.02545776	671	2.971e-02	1.605e-01	DLGAP5:37 HSH2D:77 RUFY4:86 PARPBP:99 IL23R:125 IL27RA:130
hypothalamus	-0.07825274	66	2.839e-02	1.605e-01	SCN9A:44 SYT6:71 BRINP3:94 QRFPR:223 GRIK1:571 CALCR:715
pituitary.gland	-0.04122713	212	4.055e-02	1.991e-01	ARC:143 PLPPR4:152 WDR17:164 IL5RA:174 RASD1:238 SCN3B:279
cerebellum	-0.03021284	373	4.913e-02	2.080e-01	NOS1AP:2 ANK2:15 MYT1:37 RNF112:59 PHTF1:82 TMEM266:90
ectocervix	0.11332393	25	5.008e-02	2.080e-01	COL27A1:94 RIPOR3:239 PTHLH:702 TRHDE:1901 KRT34:2291 MMRN1:2853
liver	0.02980417	323	6.986e-02	2.695e-01	IDO2:9 DMGDH:55 ABCB4:98 CREB3L3:102 ANGPTL3:142 PGLYRP2:180
cortex.kidney	0.04418903	113	1.065e-01	3.834e-01	TINAG:87 PKHD1:90 CLDN16:100 CUBN:201 ENAM:272 CLCNKB:282
C1.spinal.cord	-0.03352081	181	1.230e-01	4.153e-01	UGT8:65 DSCAML1:98 SLC5A11:103 ZNF536:112 ANLN:121 PDE6B:258
sigmoid.colon	-0.06000904	52	1.353e-01	4.299e-01	CHRM2:144 NTSR1:153 LIMS2:369 CHRNA3:387 DPT:765 GDNF:804
putamen	-0.09840398	15	1.873e-01	4.698e-01	GPR88:570 PDE10A:833 LRRC10B:1605 OPALIN:1624 KCNH4:2113 DIPK1C:2680
skeletal.muscle	-0.02607047	239	1.699e-01	4.698e-01	MYH8:124 MYOM2:133 LMOD2:154 BIN1:256 CACNA1S:355 CAVIN4:413
spleen	0.02309274	298	1.765e-01	4.698e-01	AKNA:70 STAB2:105 PATL2:160 NIBAN3:196 ICAM3:292 MPEG1:295
ransformed.skin.fibroblast	-0.02454724	258	1.800e-01	4.698e-01	CNTN3:12 ZNF281:16 DDR2:31 CSF1:51 ADAMTS6:108 ARSJ:127
transverse.colon	0.03133048	148	1.914e-01	4.698e-01	WNK4:2 TINAG:87 ATP2C2:228 SEMA4G:380 DQX1:382 CDX1:400
subcutaneous.adipose	0.04283590	72	2.103e-01	4.938e-01	CYP1A1:116 PPARG:118 ACACB:363 SIGLEC1:448 VWF:612 GPBAR1:1063
greater.omentum	-0.06083692	32	2.343e-01	5.061e-01	ADAMTS4:135 BNC1:192 ADAMTS9:565 GFPT2:1191 CH25H:1359 FFAR3:1490
substantia.nigra	0.10094078	12	2.262e-01	5.061e-01	DBX2:1613 RPE65:2259 CHRM5:3425 C10orf105:3579 FOXB1:8635.5 KCNE5:8635.
left.ventricle	-0.03995084	68	2.561e-01	5.319e-01	MYOM2:133 LMOD2:154 RD3L:544 SCN5A:698 TENM2:725 TNNT2:828
fallopian.tube	0.04301333	52	2.844e-01	5.485e-01	GREB1L:286 ADAMTS3:627 CCDC17:983 ADGRG4:1259 LDLRAD1:1260 GMNC:12
prostate	-0.05070939	38	2.802e-01	5.485e-01	NR2E3:126 HOXB13:521 ACP3:528 ALDH1A3:538 TRPM8:575 CDH26:1324
esophagus.mucosa	0.01980909	219	3.175e-01	5.714e-01	ADGRF1:7 ZNF185:22 RAB11FIP1:79 ESPL1:162 PPL:189 SULT2B1:327
hippocampus.proper	-0.08811336	11	3.118e-01	5.714e-01	NEUROD6:511 NTS:2037 NEUROD2:7511.5 SLC17A7:7511.5 HRK:7511.5 OLIG2:751
adrenal.gland	0.02417343	108	3.878e-01	6.377e-01	ADGRV1:3 SLC14A2:147 CYP11A1:170 WHRN:242 STAR:288 CYP17A1:304
nucleus.accumbens	-0.02526012	98	3.897e-01		JAKMIP1:349 GABRA5:416 INSYN2A:495 GPR88:570 PRKCG:611 KCTD4:633
stomach	0.02724371	86	3.844e-01	6.377e-01	PGC:4 B4GALNT3:122 CBLIF:136 MECOM:190 TMED6:212 TMPRSS2:229
tibial.artery	-0.02301793	110	4.067e-01	6.459e-01	LMOD1:57 OLFML2B:102 PPP1R12B:165 RNF180:302 SDK1:331 PRELP:351
uterus	0.02981376	61	4.219e-01	6.510e-01	CHRDL2:334 TEX15:436 WT1:478 MEIS3:937 CLEC4F:1005 ENPP1:1096

4.914e-01 6.792e-01

5.031e-01 6.792e-01

4.883e-01 6.792e-01

4.763e-01 6.792e-01

-0.07150227

0.04061501

0.01927937

0.01467518

0.02524228

102

191

67

bladder

ovary

tibial.nerve

eye.development

4.578e-01 6.792e-01 TNR:404 NEUROD6:511 PTPRZ1:1033 LHFPL3:7511.5 NEUROD2:7511.5 PCDH15:7511.5

CLEC3A:308 UPK1A:887 SNX31:1313 SEMA3E:2747 UPK1B:2857 ACER2:8635.5

FFAR1:59 BAMBI:199 MCC:209 STAR:288 TMEM221:311 ADAMTS16:653

PLXNB3:96 INSC:139 CUBN:201 KANK4:362 EHBP1:472 SECISBP2L:778

FOXC2:323 SP1:1520 SMAD5:1551 BMP4:1851 TBX5:1932 MAF:2016