





SRCAP	5.771540	4.713030e-08	4.918e-05	4.679e-02
SCARF1	5.282567	7.643190e-07	3.627e-04	1.487e-01
DAXX	5.269947	8.187774e-07	3.627e-04	1.487e-01
PLA2R1	5.206789	1.152816e-06	4.237e-04	1.511e-01
PTPRB	5.198360	1.206327e-06	4.298e-04	1.511e-01
CATSPERB	5.170543	1.400488e-06	4.622e-04	1.526e-01
ACIN1	5.104601	1.988958e-06	6.069e-04	1.681e-01
LRPPRC	5.089314	2.156170e-06	6.132e-04	1.681e-01
CATSPERE	5.082316	2.237161e-06	6.132e-04	1.681e-01

 Gene
 Rho
 P
 p.adj
 qValueNoperm

 ZFYVE9
 6.753935
 8.633311e-11
 2.793e-07
 9.033e-04

Top Positive genes by P-value non-permulated

Gene	Rho	Р	p.adj	qValueNoperm
PLEC	-7.520817	3.266093e-13	5.282e-09	8.543e-05
CAPN8	-7.183466	4.077956e-12	3.298e-08	2.667e-04
PKD1L1	-7.001313	1.521446e-11	8.202e-08	4.422e-04
TRANK1	-6.810289	5.844172e-11	2.363e-07	9.033e-04
PER2	-6.500839	4.792392e-10	1.292e-06	3.482e-03
CAMSAP1	-6.345555	1.329749e-09	3.072e-06	7.098e-03
DNAH9	-6.224521	2.898170e-09	5.859e-06	1.184e-02
C7orf57	-6.173059	4.018862e-09	7.222e-06	1.298e-02
OFD1	-6.092896	6.653163e-09	1.076e-05	1.740e-02
SLC17A4	-5.968967	1.432562e-08	2.106e-05	2.939e-02

Top Negative genes by P-value non-permulated

Geneset	stat	num.genes	pval	p.adj	gene.vals
Left ventricular noncompaction cardiomyo	-0.26601716	28	1.112e-06	6.826e-03	PLEC:1 DSP:13 MYH7B:153 MUL1:247 TNNT2:543 PLEKHM2:1049
Mitochondrial Diseases	0.07592552	346	1.391e-06	6.826e-03	LRPPRC:10 GGTLC3:11 TMEM126B:18 TMEM70:30 NDUFS5:33 NDUFB4:74
Adult Medulloblastoma	0.14795590	58	9.843e-05	1.032e-01	DNMT1:184 MDM2:284 BRD4:368 L3MBTL3:386 KDM4B:437 MELK:542
Fibrosarcoma	0.07386566	259	4.575e-05	1.032e-01	ANGPT4:25 CASP8:126 EGF:143 LRIF1:145 SLCO6A1:161 UCN:220
Increased CSF lactate	0.15442003	53	1.018e-04	1.032e-01	LRPPRC:10 TMEM126B:18 NDUFA12:202 AIFM1:282 TIMMDC1:328 NDUFAF1:410
Junctional split	-0.46371259	6	8.366e-05	1.032e-01	PLEC:1 ITGB4:37 LAMC2:340 LAMB3:424 ITGA6:1212 LAMA3:1413
Medullomyoblastoma	0.17622685	41	9.519e-05	1.032e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 PTCH2:956
Melanotic medulloblastoma	0.17622685	41	9.519e-05	1.032e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 PTCH2:956
Primary microcephaly	0.10937227	105	1.105e-04	1.032e-01	FANCM:116 ORC1:170 CKAP2L:179 CENPE:206 CEP135:223 TRMT10A:301
Substance-Related Disorders	-0.10816477	114	6.811e-05	1.032e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNP3:243 CFTR:374 SLC18A2:411
Substance Dependence	-0.09886097	128	1.157e-04	1.032e-01	NRCAM:48 CADPS2:99 PCDH15:110 HTR1B:174 ADH7:238 CSRNP3:243
Organic Mental Disorders, Substance-Indu	-0.10346026	107	2.227e-04	1.159e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNP3:243 CFTR:374 SLC45A2:422
Desmoplastic Medulloblastoma	0.15413075	48	2.224e-04	1.159e-01	DNMT1:184 BRD4:368 L3MBTL3:386 KDM4B:437 ERBB2:795 PTCH2:956
Epidermolysis bullosa inversa dystrophic	-0.43534572	6	2.216e-04	1.159e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMC1:903 LAMA3:1413 COL17A1:2995
NADH:Q(1) Oxidoreductase deficiency	0.21594760	25	1.866e-04	1.159e-01	TMEM126B:18 AIFM1:282 TIMMDC1:328 NDUFB10:401 NDUFAF1:410 NDUFB11:813
Parakeratosis	-0.27518653	15	2.245e-04	1.159e-01	DSP:13 CARD14:84 NLRP1:197 TNC:210 IL23A:663 RHBDF2:1112
Plantar hyperkeratosis	-0.44505934	6	1.597e-04	1.159e-01	PLEC:1 ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995
Prescription Drug Abuse	-0.10346026	107	2.227e-04	1.159e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNP3:243 CFTR:374 SLC45A2:422
Substance abuse problem	-0.09291603	138	1.694e-04	1.159e-01	NRCAM:48 CADPS2:99 PCDH15:110 IL16:122 HTR1B:174 CSRNP3:243
Epidermolysis Bullosa Simplex	-0.22500876	21	3.585e-04	1.675e-01	PLEC:1 ITGB4:37 KRT80:50 KRT17:344 MMP9:451 DES:464
Joint hyperflexibility	0.10052284	106	3.566e-04	1.675e-01	SRCAP:2 ORC1:170 CENPE:206 SOS1:276 LMX1B:303 RAF1:619
Drug Dependence	-0.08061129	161	4.300e-04	1.758e-01	PER2:5 NRCAM:48 CADPS2:99 PCDH15:110 GRM3:113 HTR1B:174
Herlitz Disease	-0.45638109	5	4.089e-04	1.758e-01	ITGB4:37 LAMC2:340 LAMB3:424 ITGA6:1212 LAMA3:1413 NA
Specific learning disability	0.10876446	88	4.279e-04	1.758e-01	NSD1:15 CKAP2L:179 LTBP4:292 TWNK:294 JMJD1C:348 DGCR6:603
Anemia, Macrocytic	0.17408436	33	5.408e-04	2.036e-01	TET2:81 RPL26:478 SFXN4:1068 RPL27:1139 GATA1:1161 TP53:1528
CONOTRUNCAL ANOMALY FACE SYNDROME	0.21690375	21	5.811e-04	2.036e-01	JMJD1C:348 GDF1:371 DGCR6:603 NKX2-6:714 SEC24C:1103 TBX1:1105
Drug habituation	-0.08856437	127	5.812e-04	2.036e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNP3:243 CFTR:374 SLC45A2:422
Persistant truncus arteriosus	0.21699969	21	5.778e-04	2.036e-01	JMJD1C:348 GDF1:371 NKX2-6:714 GJA5:818 SEC24C:1103 TBX1:1105
Congenital pyloric atresia	-0.44201687	5	6.192e-04	2.095e-01	PLEC:1 ITGB4:37 LAMC2:340 ITGA6:1212 COL17A1:2995 NA
EPIDERMOLYSIS BULLOSA, JUNCTIONAL, LOCAL	-0.43399892	5	7.767e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Adult junctional epidermolysis bullosa (-0.43399892	5	7.767e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Epidermolysis Bullosa Progressiva	-0.43399892	5	7.767e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Increased serum lactate	0.10080561	95	6.966e-04	2.117e-01	LRPPRC:10 TMEM70:30 NDUFA12:202 AIFM1:282 TWNK:294 POLG2:443
JEB-I	-0.43399892	5	7.767e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Oral mucosal blisters	-0.31105218	10	6.593e-04	2.117e-01	PLEC:1 DSP:13 ITGB4:37 LAMC2:340 LAMB3:424 ITGA6:1212
Palmar hyperhidrosis	-0.43399892	5	7.767e-04	2.117e-01	ITGB4:37 LAMC2:340 LAMB3:424 LAMA3:1413 COL17A1:2995 NA
Drug Use Disorders	-0.09243524	110	8.261e-04	2.191e-01	NRCAM:48 CADPS2:99 PCDH15:110 CSRNP3:243 CFTR:374 SLC45A2:422
MITOCHONDRIAL COMPLEX I DEFICIENCY	0.18452191	27	9.073e-04	2.343e-01	TMEM126B:18 TIMMDC1:328 NDUFAF1:410 NDUFB11:813 NDUFS8:852 GDAP1:905
Shprintzen syndrome	0.16601209	33	9.694e-04	2.439e-01	JMJD1C:348 PRODH:433 DGCR6:603 CLDN5:612 CHRD:814 DGCR6L:973
		0.4			

EnrichmentHsSymbolsFile2 Top pathways by non-permulation

1.031e-03 2.530e-01

MCPH1:215 ULK2:305 SACS:328 SLC18A2:411 GRIP1:423 SYNE1:456

NEB:26 CACNA1G:54 CAMK2B:64 MYBPC2:71 RYR3:205 TNNI2:207

PER2:5 EVPL:11 DSP:13 ITGB4:37 NRCAM:48 CLIC3:57

Abnormality of brain morphology

REACTOME_MUSCLE_CONTRACTION

JAEGER_METASTASIS_DN

Geneset	stat	num.genes	pval	p.adj	gene.vals
FISCHER_DREAM_TARGETS	0.07526136	882	5.347e-14	3.237e-10	CEP192:17 KIF18A:27 RBL1:42 SMCHD1:43 ZNF518A:46 EHBP1:80
JOHNSTONE_PARVB_TARGETS_3_DN	0.07841489	790	9.979e-14	3.237e-10	TFAM:13 QSER1:20 KIF18A:27 NDUFS5:33 RBL1:42 SMCHD1:43
DODD_NASOPHARYNGEAL_CARCINOMA_UP	-0.05739325	1463	4.375e-13	9.462e-10	PER2:5 CAMSAP1:6 DNAH9:7 C7orf57:8 EVPL:11 TGM1:12
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.06125876	1244	6.797e-13	1.102e-09	LRPPRC:10 TFAM:13 CEP192:17 QSER1:20 KIF18A:27 TMEM70:30
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.08228366	598	8.095e-12	1.050e-08	LRPPRC:10 TFAM:13 KIF18A:27 ZNF644:37 RBL1:42 ADAM9:51
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.07863949	595	7.111e-11	7.689e-08	CEP192:17 QSER1:20 ZNF302:22 BPTF:26 KIF18A:27 RLF:29
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.12548679	208	4.734e-10	4.388e-07	BDKRB1:58 SSTR4:76 FFAR2:85 GPR37L1:89 HTR1B:174 P2RY4:194
PUJANA_BRCA1_PCC_NETWORK	0.04749485	1501	1.332e-09	1.080e-06	DAXX:4 TMEM131L:9 TFAM:13 RBL1:42 NR2C1:57 TCL1A:71
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	-0.19249212	78	4.244e-09	3.060e-06	EVPL:11 TGM1:12 DSP:13 KRT80:50 KRT20:51 KRT15:83
REACTOME_KERATINIZATION	-0.18314672	85	5.435e-09	3.526e-06	EVPL:11 TGM1:12 DSP:13 KRT80:50 KRT20:51 KRT15:83
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	0.04928145	1201	1.296e-08	7.645e-06	KIF18A:27 TMEM70:30 LARP4:89 TPX2:98 TEAD2:106 TMPO:129
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.06972889	555	2.279e-08	1.232e-05	SLC47A1:41 JAG2:47 CAMK2B:64 PCNX2:158 DSG2:177 THBS4:214
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.15995050	101	2.849e-08	1.422e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
REACTOME_RNA_POLYMERASE_II_TRANSCRIPTION	0.05120458	1026	3.935e-08	1.824e-05	DAXX:4 LRPPRC:10 MGA:14 ZNF302:22 RBL1:42 NR2C1:57
NIKOLSKY_BREAST_CANCER_20Q12_Q13_AMPLICO	-0.13865741	128	6.233e-08	2.594e-05	HELZ2:96 FAM217B:170 ARFGAP1:260 COL20A1:270 TOMM34:324 NPBWR2:407
REACTOME_SIGNALING_BY_GPCR	-0.06342328	631	6.397e-08	2.594e-05	TACR2:17 GPR132:32 ARHGEF11:42 BDKRB1:58 CAMK2B:64 SSTR4:76
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.07418927	452	7.247e-08	2.766e-05	ZFYVE9:1 LRPPRC:10 BPTF:26 UBR2:36 SMCHD1:43 EIF4G3:52
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.06147432	661	8.368e-08	3.016e-05	ETAA1:39 RBL1:42 TPX2:98 HASPIN:105 FANCM:116 WDR76:130
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.17077547	81	1.094e-07	3.735e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
REACTOME_NEURONAL_SYSTEM	-0.07854928	386	1.292e-07	4.190e-05	KCNV2:62 CAMK2B:64 KCNN3:183 KCNF1:195 PANX1:216 CACNA1E:235
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	0.06100706	637	1.742e-07	5.381e-05	QSER1:20 KIF18A:27 RLF:29 TPTE:31 ZNF644:37 MFN1:73
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.08789174	295	2.217e-07	6.539e-05	TACR2:17 GPR132:32 BDKRB1:58 SSTR4:76 FFAR2:85 GPR37L1:89
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.12282450	149	2.355e-07	6.545e-05	LRPPRC:10 TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270
BENPORATH_CYCLING_GENES	0.06175136	606	2.421e-07	6.545e-05	ZNF414:72 CSH2:86 TPX2:98 TMPO:129 CCNB1:141 LRIF1:145
REACTOME_CELL_CYCLE	0.06057985	622	2.906e-07	7.251e-05	DAXX:4 CEP192:17 KIF18A:27 CENPT:41 RBL1:42 RNF168:66
REACTOME_COMPLEX_I_BIOGENESIS	0.21432722	48	2.808e-07	7.251e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 TIMMDC1:328
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	0.07191598	427	3.821e-07	9.183e-05	LRPPRC:10 QSER1:20 KIF18A:27 RBL1:42 AFP:79 TPX2:98
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.21264431	47	4.599e-07	1.066e-04	TMEM126B:18 TMEM70:30 NDUFS5:33 NDUFB4:74 DMAC1:112 NDUFA12:202
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.09087926	260	4.801e-07	1.074e-04	TACR2:17 BDKRB1:58 SSTR4:76 GRM3:113 TAAR6:129 HTR1B:174
ZHANG_BREAST_CANCER_PROGENITORS_UP	0.07155700	415	6.269e-07	1.356e-04	CEP192:17 RBL1:42 SMCHD1:43 SYDE2:53 ADAMTS20:78 TMPO:129
DACOSTA_UV_RESPONSE_VIA_ERCC3_DN	0.05036052	827	1.042e-06	2.181e-04	ZFYVE9:1 TMEM131L:9 LRPPRC:10 ATP2B4:21 BPTF:26 RLF:29
SHEN_SMARCA2_TARGETS_UP	0.07021190	408	1.242e-06	2.519e-04	TMEM126B:18 ZNF302:22 UBR2:36 MAP4K3:91 ANKHD1:99 AGGF1:123
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.16113155	75	1.419e-06	2.743e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
WONG_MITOCHONDRIA_GENE_MODULE	0.09950710	198	1.438e-06	2.743e-04	LRPPRC:10 TFAM:13 NDUFS5:33 NIPSNAP1:69 NDUFB4:74 NDUFA12:202
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	0.03932040	1338	1.875e-06	3.476e-04	ZNF302:22 NIPSNAP1:69 CASP8:126 RBBP7:134 PPP4R1:156 CTH:160
KIM_WT1_TARGETS_DN	0.06605558	432	2.728e-06	4.916e-04	ZNF302:22 KIF18A:27 TPTE:31 LARP4:89 MAP4K3:91 CENPC:127
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.21642022	38	3.917e-06	6.572e-04	IQCE:375 TMEM184A:376 BRAT1:512 MRM2:552 MAD1L1:601 FBXL18:658
REACTOME_RESOLUTION_OF_SISTER_CHROMATID_	0.12256632	119	3.950e-06	6.572e-04	KIF18A:27 CENPT:41 CENPC:127 CCNB1:141 SPDL1:149 CENPE:206

GO_Biological_Process_2023 Top pathways by non-permulation

4.038e-06 6.572e-04

4.052e-06 6.572e-04

-0.09712311

-0.09115185

190

216

Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO:	0.22989712	48	3.654e-08	6.956e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 DMAC1:112 NDUFC2:270 NDUFB5:358
Mitochondrial Respiratory Chain Complex	0.22989712	48	3.654e-08	6.956e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 DMAC1:112 NDUFC2:270 NDUFB5:358
Mitochondrial Respiratory Chain Complex	0.18138349	77	3.873e-08	6.956e-05	TMEM126B:18 NDUFS5:33 NDUFB4:74 DMAC1:112 NDUFC2:270 AIFM1:282
Intermediate Filament Organization (GO:0	-0.21587292	50	1.312e-07	1.768e-04	DSP:13 KRT80:50 KRT20:51 KRT15:83 KRT78:135 KRT13:150
Muscle Contraction (GO:0006936)	-0.16039684	88	2.059e-07	2.219e-04	TACR2:17 MYH13:27 ARHGEF11:42 MYOM2:91 MYOF:196 RYR3:205
Oxidative Phosphorylation (GO:0006119)	0.19867736	55	3.528e-07	3.168e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Proton Motive Force-Driven Mitochondrial	0.21079171	47	5.838e-07	3.945e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Regulation Of DNA-templated Transcriptio	0.03809730	1648	5.857e-07	3.945e-04	SRCAP:2 DAXX:4 TFAM:13 NSD1:15 ATP2B4:21 BPTF:26
Chemical Synaptic Transmission (GO:00072	-0.08904294	257	9.872e-07	5.910e-04	RIMBP2:53 GRM3:113 HTR1B:174 CACNA1E:235 GABRR1:255 GABRR3:322
Monoatomic Cation Transmembrane Transpor	-0.08538779	273	1.338e-06	7.209e-04	TRPM5:22 CACNA1G:54 KCNV2:62 TRPV6:134 KCNN3:183 KCNF1:195
Aerobic Respiration (GO:0009060)	0.18814482	54	1.762e-06	8.631e-04	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Aerobic Electron Transport Chain (GO:001	0.18656458	54	2.150e-06	9.652e-04	NDUFS5:33 NDUFB4:74 NDUFC2:270 NDUFB5:358 NDUFB10:401 NDUFAF1:410
Mitochondrial ATP Synthesis Coupled Elec	0.18391519	55	2.424e-06	1.005e-03	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Atrial Cardiac Muscle Cell Action Potent	-0.40435434	11	3.426e-06	1.319e-03	CACNB2:371 KCNQ1:549 KCNN2:643 SCN5A:1268 GJC1:1501 KCNE5:1549
Striated Muscle Contraction (GO:0006941)	-0.18412530	52	4.437e-06	1.594e-03	ARHGEF11:42 MYH7B:153 RYR3:205 TNNI2:207 MYH8:306 TNNT3:542
Proton Motive Force–Driven ATP Synthesis	0.18169535	51	7.270e-06	2.351e-03	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
tRNA Methylation (GO:0030488)	0.21592462	36	7.418e-06	2.351e-03	THADA:65 BCDIN3D:164 TRMT10A:301 TRMT10B:349 TRMT61B:373 TRMT1L:477
Anterograde Trans-Synaptic Signaling (GO	-0.09305256	183	1.500e-05	4.489e-03	GRM3:113 HTR1B:174 CACNA1E:235 GABRR1:255 GABRR3:322 GPR176:370
Regulation Of Transcription By RNA Polym	0.03230745	1714	1.650e-05	4.679e-03	SRCAP:2 NSD1:15 ATP2B4:21 BPTF:26 ZSCAN29:28 ZSCAN5B:35
Neuron Projection Morphogenesis (GO:0048	-0.10705733	135	1.821e-05	4.907e-03	NRCAM:48 DIP2A:250 DTNBP1:264 DBNL:330 TRIO:389 SLITRK1:488
Regulation Of Gene Expression (GO:001046	0.04120891	950	2.325e-05	5.965e-03	SRCAP:2 DAXX:4 NSD1:15 ATP2B4:21 BPTF:26 RBL1:42
Regulation Of DNA Methylation–Dependent	0.32512842	14	2.535e-05	6.209e-03	TET1:159 SETDB2:252 TASOR:370 L3MBTL3:386 ATF7IP2:749 SAMD1:812
Mitochondrial Electron Transport, NADH T	0.21728975	31	2.844e-05	6.662e-03	NDUFS5:33 NDUFB4:74 NDUFC2:270 NDUFB5:358 NDUFB10:401 NDUFAF1:410
Inorganic Cation Transmembrane Transport	-0.07272632	277	3.374e-05	7.575e-03	TRPM5:22 CACNA1G:54 KCNV2:62 TRPV6:134 KCNN3:183 KCNF1:195
Cellular Respiration (GO:0045333)	0.13616947	71	7.391e-05	1.593e-02	NDUFS5:33 NDUFB4:74 NDUFA12:202 NDUFC2:270 NDUFB5:358 NDUFB10:401
Translation (GO:0006412)	0.07789452	216	8.440e-05	1.749e-02	NARS1:94 RARS1:283 ZAR1:366 ZAR1L:425 MRPL3:445 RPL26:478
Supramolecular Fiber Organization (GO:00	-0.06742834	283	1.023e-04	2.042e-02	DSP:13 POF1B:44 KRT80:50 KRT20:51 KRT15:83 HIP1R:98
Metal Ion Transport (GO:0030001)	-0.08820829	158	1.353e-04	2.603e-02	SLC17A4:10 TRPV6:134 SLC17A3:164 KCNF1:195 RYR3:205 PANX1:216
Myofibril Assembly (GO:0030239)	-0.16370606	45	1.463e-04	2.681e-02	MYOM2:91 CASQ1:259 LMOD2:286 OBSCN:440 TNNT3:542 TNNT2:543
Synapse Organization (GO:0050808)	-0.10168435	117	1.493e-04	2.681e-02	NRCAM:48 ELFN1:70 ARHGAP39:179 TNC:210 SLC8A3:296 SDK2:323
Regulation Of Heart Rate By Cardiac Cond	-0.17343048	39	1.797e-04	3.124e-02	DSP:13 CACNA1G:54 DSG2:177 CACNB2:371 KCNQ1:549 DSC2:749
Neuropeptide Signaling Pathway (GO:00072	-0.13588049	62	2.181e-04	3.672e-02	SSTR4:76 SORL1:125 NPBWR2:407 GPR84:420 RXFP3:509 PENK:520
Cardiac Muscle Contraction (GO:0060048)	-0.19367830	30	2.423e-04	3.754e-02	TNNT2:543 KCNQ1:549 GSN:692 TCAP:763 RYR2:1147 SCN5A:1268
Chromatin Remodeling (GO:0006338)	0.07443103	207	2.342e-04	3.754e-02	DAXX:4 BPTF:26 RNF168:66 CHD8:82 RBBP7:134 HCFC2:152
Modulation Of Chemical Synaptic Transmis	-0.09795472	118	2.439e-04	3.754e-02	GRM3:113 MCTP2:118 OTOF:169 MYOF:196 CLSTN1:217 DYSF:280
Chromatin Organization (GO:0006325)	0.06983130	233	2.540e-04	3.802e-02	DAXX:4 BPTF:26 CHD8:82 RBBP7:134 HCFC2:152 SUV39H2:154
Potassium Ion Transmembrane Transport (G	-0.09204745	132	2.683e-04	3.907e-02	KCNV2:62 KCNN3:183 KCNF1:195 SLC24A4:284 KCNH3:295 KCNA10:321
Positive Regulation Of Tyrosine Phosphor	0.15002375	49	2.827e-04	4.008e-02	CSH2:86 TSLP:175 LYN:213 CSH1:266 GH2:344 GH1:374
Regulation Of Tyrosine Phosphorylation O	0.13643522	59	2.927e-04	4.044e-02	CSH2:86 TSLP:175 LYN:213 CSH1:266 GH2:344 GH1:374
Mitochondrial Gene Expression (GO:014005	0.10470016	100	3.034e-04	4.086e-02	TFAM:13 TFB2M:148 POLRMT:249 TWNK:294 MRPL3:445 PTCD3:663

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0002086 abnormal extraembryonic tissu	0.06853107	476	7.645e-07	3.639e-04	DAXX:4 PTPRB:6 NSD1:15 BPTF:26 SMCHD1:43 HAS2:62
MP0001970 abnormal pain threshold	-0.10565575	150	9.908e-06	1.337e-03	BDKRB1:58 SSTR4:76 GABRR1:255 ADCY1:287 PTPRZ1:341 P2RX7:405
MP0002084 abnormal developmental patter	0.06912749	360	1.143e-05	1.337e-03	DAXX:4 PTPRB:6 NSD1:15 BPTF:26 HAS2:62 CHD8:82
MP0002080 prenatal lethality	0.03991168	1339	1.169e-05	1.337e-03	DAXX:4 PTPRB:6 TFAM:13 NSD1:15 BPTF:26 UBR2:36
MP0001697 abnormal embryo size	0.06421591	413	1.405e-05	1.337e-03	DAXX:4 PTPRB:6 BPTF:26 MFN1:73 CASP8:126 MED1:189
MP0002085 abnormal embryonic tissue	0.05007365	653	3.265e-05	2.591e-03	DAXX:4 TFAM:13 NSD1:15 BPTF:26 HAS2:62 ADAMTS20:78
MP0003635 abnormal synaptic transmissio	-0.05687669	425	9.719e-05	6.609e-03	NRCAM:48 CAMK2B:64 CADPS2:99 ADD2:193 RYR3:205 TNC:210
MP0000598 abnormal liver morphology	0.04854552	472	4.848e-04	2.706e-02	CASP8:126 CTH:160 MED1:189 SENP1:203 DNMT3B:219 GRB14:269
MP0002572 abnormal emotion/affect behav	-0.06046406	291	5.116e-04	2.706e-02	CADPS2:99 GRM3:113 WFS1:133 HTR1B:174 RYR3:205 TNC:210
MP0002148 abnormal hypersensitivity rea	-0.09414443	102	1.106e-03	5.266e-02	SSTR4:76 PTAFR:203 FCER1A:289 MME:302 EPHB6:414 SEMA4A:446
MP0002135 abnormal kidney morphology	0.04539508	450	1.409e-03	6.097e-02	TET2:81 TRPV1:85 CASP8:126 LRRK2:204 CASP1:205 LYN:213
MP0002088 abnormal embryonic growth/wei	0.05028622	336	1.993e-03	7.904e-02	DAXX:4 PTPRB:6 BPTF:26 HAS2:62 MFN1:73 MED1:189
MP0005380 embryogenesis phenotype	0.04455853	407	2.758e-03	9.378e-02	DAXX:4 PTPRB:6 BPTF:26 HAS2:62 MFN1:73 NLRP5:178
MP0001672 abnormal embryogenesis/ devel	0.04455853	407	2.758e-03	9.378e-02	DAXX:4 PTPRB:6 BPTF:26 HAS2:62 MFN1:73 NLRP5:178
MP0003984 embryonic growth retardation	0.04884092	328	2.989e-03	9.485e-02	DAXX:4 PTPRB:6 BPTF:26 HAS2:62 MFN1:73 MED1:189
MP0002069 abnormal eating/drinking beha	-0.04385105	401	3.435e-03	9.684e-02	PLEC:1 PER2:5 TGM1:12 NEB:26 ITGB4:37 DGAT2:112
MP0004197 abnormal fetal growth/weight/	0.06505230	174	3.459e-03	9.684e-02	RBL1:42 SENP1:203 HSD17B2:256 MDM2:284 GAB1:318 FBXW8:369
MP0000313 abnormal cell death	0.04076316	457	3.887e-03	1.028e-01	DAXX:4 TFAM:13 CASP8:126 CTH:160 DNMT1:184 SENP1:203
MP0004947 skin inflammation	-0.09616928	70	5.627e-03	1.410e-01	RAG1:105 TRPV6:134 PKP3:242 MME:302 CARD11:309 CBL:332
MP0003121 genomic imprinting	0.16247054	23	7.078e-03	1.685e-01	SMCHD1:43 DNMT1:184 ARID4A:440 HELLS:494 ATRX:691 UBE3A:1440
	-0.04220612	357	7.610e-03	1.725e-01	PER2:5 NRCAM:48 CADPS2:99 WFS1:133 HTR1B:174 ADD2:193
MP0002116 abnormal craniofacial bone	0.04223023	348	8.318e-03	1.800e-01	RBL1:42 DNMT3B:219 ARSB:221 LMX1B:303 SIRT6:341 BRD4:368
MP0000749 muscle degeneration	-0.12427876	35	1.114e-02	2.305e-01	PLEC:1 MYOF:196 DYSF:280 IGHMBP2:441 DES:464 BAG3:595
MP0004215 abnormal myocardial fiber	-0.09906370	53	1.293e-02	2.564e-01	CACNB2:371 MMP9:451 DES:464 TNNT2:543 RYR2:1147 SCN5A:1268
MP0002837 dystrophic cardiac calcinosis	-0.22837435	9	1.773e-02	2.595e-01	SLC2A4:412 MMP9:451 DES:464 MYH6:1577 MYBPC3:1707 GSTZ1:8437
MP0002733 abnormal thermal nociception	-0.07342359	92	1.559e-02	2.595e-01	BDKRB1:58 PTPRZ1:341 PROKR1:710 KCND2:741 KCNA6:1015 PRKAR1B:106
MP0002169 no abnormal phenotype	0.02236002	1166	1.927e-02	2.595e-01	SCARF1:3 DAXX:4 TFAM:13 RBL1:42 ADAM9:51 NR2C1:57
MP0000266 abnormal heart morphology	0.02726861	699	1.985e-02	2.595e-01	PTPRB:6 TFAM:13 HAS2:62 CASP8:126 HIF3A:135 MED1:189
MP0001502 abnormal circadian rhythm	-0.10145608	46	1.763e-02	2.595e-01	PER2:5 CADPS2:99 TNC:210 PER1:492 PROKR2:537 PER3:547
MP0008874 decreased physiological sensi	-0.06217592	119	2.017e-02	2.595e-01	BDKRB1:58 NR1I3:173 KIF26A:198 CACNA1E:235 MAP3K6:387 PARP1:404
MP0002925 abnormal cardiovascular devel	0.03178801	509	1.810e-02	2.595e-01	PTPRB:6 TFAM:13 HAS2:62 ANGPTL6:96 CASP8:126 MED1:189
MP0000343 altered response to	-0.09859700	52	1.425e-02	2.595e-01	TGM2:38 SLC2A4:412 MMP9:451 CCR5:559 NT5E:868 F13A1:1074
MP0002067 abnormal sensory capabilities	-0.04291757	261	1.915e-02	2.595e-01	CADPS2:99 PCDH15:110 CACNA1E:235 DYSF:280 DBNL:330 PTPRZ1:341
MP0003935 abnormal craniofacial develop	0.04442834	244	1.884e-02	2.595e-01	RBL1:42 GAB1:318 GDF1:371 FUZ:375 SP3:399 TRPM6:420
MP0000432 abnormal head morphology	0.03940209	311	1.948e-02	2.595e-01	RBL1:42 MED1:189 DNMT3B:219 ARSB:221 HSD17B2:256 GDF1:371
MP0002873 normal phenotype	0.02288569	1171	1.644e-02	2.595e-01	SCARF1:3 DAXX:4 TFAM:13 RBL1:42 ADAM9:51 NR2C1:57
	-0.05017658	204	1.490e-02		PER2:5 CACNA1G:54 WFS1:133 KCNH3:295 SLC18A2:411 CCR5:559
MP0003119 abnormal digestive system	0.08763746	58	2.149e-02		GDF1:371 FOXL1:418 CHRD:814 GADD45GIP1:1061 ERCC5:1165 IGF2BP1:18
MP0004859 abnormal synaptic plasticity	-0.11894784	31	2.218e-02		CAMK2B:64 ADD2:193 TNC:210 ADCY1:287 BDNF:851 CPLX1:1269
	0.14625444	20		2.825e-01	CXCR2:390 HESX1:521 RELB:1541 SOX2:1563 C3AR1:1605 RORA:2023

tissue_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
EBV.lymphocyte	0.07600562	671	8.522e-11	4.602e-09	TMEM131L:9 KIF18A:27 RBL1:42 TCL1A:71 SLAMF7:93 ANGPTL6:96
esophagus.mucosa	-0.09576288	220	1.275e-06	2.295e-05	EVPL:11 TGM1:12 IQANK1:23 BNC1:35 ENDOU:52 RNF222:56
skeletal.muscle	-0.09287398	239	1.012e-06	2.295e-05	PYGM:15 NEB:26 MYBPC2:71 MYOM2:91 IGFN1:166 TNNI2:207
leg.skin	-0.09257196	217	3.301e-06	4.456e-05	EVPL:11 DSP:13 BNC1:35 POF1B:44 KRT80:50 ENDOU:52
vagina	-0.12589930	91	3.573e-05	3.859e-04	EVPL:11 BNC1:35 ENDOU:52 RNF222:56 MAB21L4:82 KRT78:135
suprapubic.skin	-0.07135684	194	6.849e-04	6.164e-03	EVPL:11 BNC1:35 KRT80:50 ENDOU:52 RNF222:56 MAB21L4:82
liver	0.04412041	328	6.863e-03	5.294e-02	MOGAT1:58 AFP:79 PRODH2:101 SLCO1B1:128 CTH:160 HSD17B2:256
nucleus.accumbens	-0.07540811	98	1.023e-02	6.905e-02	SV2C:156 OTOF:169 CACNA1E:235 DACH2:380 HTR1D:391 PTPN5:415
Brodmann.area.9	-0.05383857	182	1.301e-02	7.778e-02	NRCAM:48 CALHM1:163 CSRNP3:243 NECAB1:251 GPR26:357 HECW1:372
left.ventricle	-0.08608123	68	1.440e-02	7.778e-02	MYOM2:91 MYH7B:153 MYZAP:262 LMOD2:286 CKMT2:290 TNNT2:543
pancreas	0.06654376	94	2.642e-02	1.297e-01	CATSPERB:7 CELA3A:47 PRODH2:101 G6PC2:109 FBXW12:114 EGF:143
sigmoid.colon	-0.08685074	52	3.066e-02	1.380e-01	TACR2:17 DES:464 HDAC4:1224 PLEKHO1:1342 ROR2:1435 GJC1:1501
atrium.auricle	-0.06011736	90	4.964e-02	1.927e-01	MYOM2:91 LMOD2:286 CKMT2:290 TNNT2:543 FSD2:659 ADPRHL1:660
cerebral.cortex	-0.05512582	107	4.996e-02	1.927e-01	ADGRA1:39 CALHM1:163 KCNF1:195 KCNH3:295 FAM163B:350 HECW1:372
putamen	-0.13942501	15	6.169e-02	2.221e-01	RGS9:87 GRM3:113 GPR88:1847 DIPK1C:2147 SLC18A3:2240 LRRC10B:2740
cerebellum	-0.02766304	376	7.054e-02	2.381e-01	TRANK1:4 CACNA1G:54 SSTR4:76 ESYT3:132 PCNX2:158 APC2:182
peyers.patch	-0.03944902	167	8.097e-02	2.572e-01	SLC17A4:10 TRPM5:22 KRT20:51 EPS8L3:59 VIL1:130 RNF186:162
coronary.artery	0.11900080	15	1.108e-01	3.323e-01	GJA5:818 SPINK13:1942 PCOLCE2:2329 CCN3:2544 MYO18B:7737 SOST:7737
testis	0.01355181	1377	1.176e-01	3.343e-01	CATSPERE:12 CATSPERG:24 TPTE:31 ZSCAN5B:35 HOMEZ:40 OVCH1:45
thyroid	0.03541287	151	1.359e-01	3.669e-01	PLA2R1:5 CLCNKA:16 ISM1:192 GGTLC1:194 CLUL1:1137 RASSF4:1176
ectocervix	0.07935575	25	1.701e-01	3.858e-01	PTHLH:1278 PAPPA2:1774 EDNRA:2370 GDF7:7737 TRHDE:7737 ADAMTSL5:773
endocervix	-0.04676241	72	1.715e-01	3.858e-01	TGM2:38 ZNF516:55 BDKRB1:58 ELFN1:70 PWP2:111 NXNL2:192
greater.omentum	0.07026966	33	1.630e-01	3.858e-01	MTARC1:651 BTNL9:690 SLC7A10:1667 GFPT2:1966 TCF15:2026 FFAR3:7737
transformed.skin.fibroblast	0.02523438	258	1.681e-01	3.858e-01	ADAM9:51 HAS2:62 IGF2BP2:150 ADAMTS6:321 PTPRQ:336 P4HA3:476
uterus	0.04983277	61	1.795e-01	3.877e-01	ATP2B4:21 MEIS3:267 HOXA10:455 PTK7:629 DENND2B:1234 HOXD8:1463
fallopian.tube	0.05212836	52	1.945e-01	4.040e-01	RARRES1:121 TUBA4B:997 BCHE:1039 HOXA3:1146 LDLRAD1:1721 PI15:1881
breast	-0.08957719	15	2.300e-01	4.502e-01	THRSP:587 NPY2R:665 TNN:1320 KRT5:1705 TFAP2B:1997 HCAR1:2990
caudate.nucleus	-0.06758365	26	2.335e-01	4.502e-01	GPR37L1:89 GRM3:113 TAC1:739 MLC1:1213 PDE1B:1425 GPR88:1847
amygdala	-0.10403899	9	2.799e-01	5.039e-01	PCDH15:110 PTPRZ1:341 TNR:2453 BCAN:8437 LHFPL3:8437 NEUROD2:8437
cerebellar.hemisphere	-0.01461145	510	2.707e-01	5.039e-01	CAMK2B:64 ANKRD34C:65 MINAR1:68 SSTR4:76 CADPS2:99 PAXIP1:121
spleen	0.01809950	298	2.894e-01	5.041e-01	SCARF1:3 TCL1A:71 CASP8:126 CASP1:205 NTN4:234 CD244:353
minor.salivary.gland	-0.03528827	69	3.123e-01	5.270e-01	CRACR2A:394 ITPRID1:469 SLC6A14:528 VTCN1:790 MMP10:882 PIGR:1080
esophagogastric.junction	0.09861774	8	3.342e-01	5.469e-01	ADCY5:1877 BARX1:7737 CHRM3:7737 COL4A5:7737 F2RL2:7737 GADL1:7737
blood	0.01290513	274	4.681e-01	7.325e-01	TCL1A:71 VNN2:132 MEFV:165 CSF2RA:265 NLRC4:277 CASP5:382
hippocampus.proper	0.06061670	11	4.865e-01	7.325e-01	CNIH2:1740 NEUROD2:7737 NEUROD6:7737 SLC17A7:7737 HRK:7737 OLIG2:773

5.357e-01 7.819e-01

6.155e-01 8.523e-01

6.128e-01 8.523e-01

6.694e-01 9.037e-01

-0.01939689

0.01405757

-0.01806692

-0.01223362

66

103

stomach adrenal.gland

hypothalamus

ovary

0.03253872 38 4.884e-01 7.325e-01 TTC6:140 CPAMD8:200 SHROOM1:768 TNFSF15:775 SCUBE2:1549 MKX:1750

CAPN8:2 MYH13:27 EPS8L3:59 CAPN9:588 CYP2S1:679 MUC1:705

KLF14:230 ADGRV1:285 CYP17A1:385 MGST1:481 SCARB1:798 KCNK3:857

PCDH15:110 SYT6:228 DLX2:382 NPY2R:665 LY6H:1001 GABRG3:1098

SUSD4:74 GREB1:312 CLSTN2:413 MMP21:426 OLFML1:624 GLI2:667