





 Gene
 Rho
 P
 p.adj
 qValueNoperm

 THADA
 7.364298
 1.068487e-12
 8.626e-09
 5.097e-05

 KIAA0825
 6.584929
 2.730625e-10
 4.008e-07
 5.883e-04

 MUC20
 6.380131
 1.061617e-09
 1.224e-06
 9.849e-04

 ZSCAN29
 6.365717
 1.166281e-09
 1.230e-06
 9.849e-04

 BPTF
 6.324699
 1.522362e-09
 1.294e-06
 9.849e-04

 PTPN13
 6.316415
 1.606200e-09
 1.297e-06
 9.849e-04

 CEP192
 6.295732
 1.835719e-09
 1.349e-06
 9.849e-04

9.849e-04

9.849e-04

9.849e-04

PTCD3 6.248656 2.483998e-09 1.671e-06

AKAP9 6.239050 2.641410e-09 1.706e-06

MBD4 6.221432 2.955821e-09 1.708e-06

Top Positive genes by P-value non-permulated

BCLAF3	-7.533746	2.958306e-13	4.776e-09	5.097e-05
NAV1	-7.297458	1.759527e-12	9.470e-09	5.097e-05
ZBTB41	-7.008288	1.447507e-11	5.843e-08	2.098e-04
MMP16	-6.962093	2.011525e-11	6.496e-08	2.098e-04
DDX59	-6.817231	5.568727e-11	1.284e-07	2.963e-04
SCN9A	-6.824117	5.308058e-11	1.284e-07	2.963e-04
PPP1R12B	-6.753589	8.653910e-11	1.747e-07	3.525e-04
KDM5B	-6.640724	1.872871e-10	3.360e-07	5.883e-04
LOXHD1	-6.607795	2.340518e-10	3.779e-07	5.883e-04
DPY19L3	-6.424309	7.948193e-10	1.069e-06	9.849e-04

P p.adj qValueNoperm

Top Negative genes by P-value non-permulated

Geneset	stat	num.genes	pval	p.adj	gene.vals
Schizophrenia	-0.05642985	1625	1.744e-13	1.711e-09	NAV1:2 MMP16:4 NDST3:19 CSMD1:23 NOS1AP:25 HERC2:34
Autism Spectrum Disorders	-0.08636153	483	1.116e-10	4.921e-07	MMP16:4 CSMD1:23 RYR2:32 HERC2:34 LRRN3:41 EHMT1:44
Autistic Disorder	-0.07640121	615	1.505e-10	4.921e-07	ATF6:26 RYR2:32 DOCK4:35 EHMT1:44 CNTN3:51 CHL1:57
Epilepsy, Temporal Lobe	-0.11544030	164	3.612e-07	7.821e-04	KCNQ3:69 GRM2:88 GABRB3:124 PAG1:141 SLC2A1:290 GRIK1:297
Alzheimer's Disease	-0.03842108	1666	3.986e-07	7.821e-04	BLMH:18 CSMD1:23 RYR2:32 F13B:39 EHMT1:44 SORL1:47
Alcoholic Intoxication, Chronic	-0.07554291	376	5.742e-07	9.390e-04	ADCY1:53 GRM2:88 CNTN4:91 HTR1B:114 GABRR1:123 GABRB3:124
Channelopathies	-0.20441645	48	9.747e-07	1.366e-03	SCN9A:5 RYR2:32 ANK2:42 CACNA1S:100 CNGB3:159 SHANK3:171
Generalized seizures	-0.12186189	120	4.172e-06	4.539e-03	HTR1B:114 GABRB3:124 SYNJ1:179 CHRM1:287 SLC2A1:290 GRIK1:297
Mood Disorders	-0.07745801	303	3.925e-06	4.539e-03	ADCY1:53 CHL1:57 VIPR2:58 GRM2:88 HTR1B:114 TAC1:150
nervous system disorder	-0.06868849	382	4.626e-06	4.539e-03	EHMT1:44 SETX:190 SHANK2:201 SLC2A1:290 GRIK1:297 PON1:314
Diabetes Mellitus, Non-Insulin-Dependent	-0.03786013	1350	5.123e-06	4.569e-03	NOS1AP:25 ATF6:26 RYR2:32 PCNX2:40 ANK2:42 EHMT1:44
Mental Depression	-0.05859671	509	7.183e-06	5.873e-03	NOS1AP:25 ADCY1:53 CHL1:57 VIPR2:58 HTR1B:114 GABRB3:124
Neuralgia	-0.14089322	83	9.335e-06	7.045e-03	SCN9A:5 GRM2:88 TAC1:150 TRPM8:167 DRD2:333 TACR1:365
Aura	-0.16446877	59	1.265e-05	8.275e-03	GABRB3:124 CHRM1:287 SCN2A:306 HCN1:405 TSC1:478 SLC12A5:555
Awakening Epilepsy	-0.16446877	59	1.265e-05	8.275e-03	GABRB3:124 CHRM1:287 SCN2A:306 HCN1:405 TSC1:478 SLC12A5:555
Bipolar Disorder	-0.04804998	724	1.354e-05	8.305e-03	DPY19L3:10 NDST3:19 CSMD1:23 NOS1AP:25 SORL1:47 ADCY1:53
Seizures, Focal	-0.11275480	123	1.625e-05	8.390e-03	SCN9A:5 KCNQ3:69 HTR1B:114 CHRM1:287 SLC2A1:290 GRIK1:297
HIV Infections	-0.05060780	639	1.558e-05	8.390e-03	VIPR1:62 IL16:103 TMEM132D:126 GEM:134 CYLD:137 TAC1:150
Mental disorders	-0.07524544	282	1.498e-05	8.390e-03	CSMD1:23 NOS1AP:25 MYT1:86 HTR1B:114 PLPPR4:128 SHANK3:171
Depressive disorder	-0.04937112	646	2.270e-05	1.113e-02	NOS1AP:25 ADCY1:53 CHL1:57 VIPR2:58 HTR1B:114 WDR11:120
Major Depressive Disorder	-0.05774971	460	2.517e-05	1.176e-02	VIPR2:58 GRM2:88 HTR1B:114 TAC1:150 MCTP2:158 DDC:200
Epilepsy, Cryptogenic	-0.15397051	61	3.242e-05	1.210e-02	GABRB3:124 CHRM1:287 SCN2A:306 HCN1:405 TSC1:478 SLC12A5:555
Increased CSF lactate	0.16456012	53	3.453e-05	1.210e-02	LRPPRC:39 TIMMDC1:438 NDUFA9:570 TMEM126B:644 NDUFAF1:891 GFM1:1036
Mitochondrial Diseases	0.06506242	347	3.451e-05	1.210e-02	LRPPRC:39 ECSIT:52 GFM2:86 MTPAP:121 POLG2:122 COA1:124
Obesity	-0.03166200	1647	3.219e-05	1.210e-02	ATF6:26 HERC2:34 EHMT1:44 SORL1:47 LGR6:68 CNTN4:91
Psychotic Disorders	-0.07299263	276	3.247e-05	1.210e-02	LMOD2:56 GRM2:88 HTR1B:114 DDC:200 GABRG3:240 KIDINS220:281
Tonic Seizures	-0.12221321	98	2.981e-05	1.210e-02	HTR1B:114 CHRM1:287 SLC2A1:290 GRIK1:297 SCN2A:306 DRD2:333
Unipolar Depression	-0.05712210	463	2.908e-05	1.210e-02	CSMD1:23 HTR1B:114 MCTP2:158 DDC:200 SELP:203 EGFR:230
Neuroblastoma	-0.03299064	1453	4.067e-05	1.376e-02	KDM5B:8 HERC2:34 DOCK4:35 URGCP:37 LRRN3:41 ANK2:42
Abnormal behavior	-0.06536157	331	4.782e-05	1.564e-02	CSMD1:23 NOS1AP:25 GRM2:88 HTR1B:114 PLPPR4:128 TAC1:150
Absence Seizures	-0.10966078	115	5.005e-05	1.584e-02	SCN9A:5 EHMT1:44 HTR1B:114 CHRM1:287 SLC2A1:290 GRIK1:297
Complex partial seizures	-0.11173103	110	5.302e-05	1.626e-02	HTR1B:114 CHRM1:287 SLC2A1:290 GRIK1:297 DRD2:333 HCN1:405
Andersen Syndrome	-0.24630530	22	6.377e-05	1.896e-02	RYR2:32 ANK2:42 KCNJ12:195 PON1:314 KCNJ5:546 MTHFR:655
NADH:Q(1) Oxidoreductase deficiency	0.22933561	25	7.242e-05	2.090e-02	TIMMDC1:438 TMEM126B:644 NDUFAF1:891 NDUFAF6:1067 NDUFS3:1122 NDUFB10:1293
Alzheimer's Disease, Focal Onset	-0.13234083	74		2.204e-02	BLMH:18 SORL1:47 ARC:202 BAX:309 IGF1R:363 BIN1:382
Acute Confusional Senile Dementia	-0.13234083	74		2.204e-02	BLMH:18 SORL1:47 ARC:202 BAX:309 IGF1R:363 BIN1:382
Asthma	-0.03626775	1061		2.204e-02	PPP1R12B:7 DENND1B:11 CSMD1:23 ATF6:26 RYR2:32 HERC2:34
Central neuroblastoma	-0.03189942	1414		2.204e-02	KDM5B:8 HERC2:34 DOCK4:35 URGCP:37 LRRN3:41 ANK2:42
Hypertensive disease	-0.03567892	1108		2.204e-02	CSMD1:23 MOV10:31 RYR2:32 SORL1:47 SLC22A6:59 CNTN4:91
Tonic – clonic seizures	-0.09410443	146	8.987e-05		SCN9A:5 KCNQ3:69 HTR1B:114 GABRB3:124 SYNJ1:179 CHRM1:287

## EnrichmentHsSymbolsFile2 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	-0.09301802	555	8.918e-14	2.893e-10	CSMD1:23 RYR2:32 UGT8:36 PCNX2:40 KCNQ3:69 IKZF1:76
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	-0.13514559	259	7.904e-14	2.893e-10	VIPR2:58 VIPR1:62 GRM2:88 HTR1B:114 HRH2:118 GABRR1:123
REACTOME_NEURONAL_SYSTEM	-0.10806347	385	4.027e-13	8.709e-10	PPFIA4:15 ADCY1:53 KCNQ3:69 APBA2:85 KCNV1:90 KCNF1:98
BENPORATH_ES_WITH_H3K27ME3	-0.06539734	983	6.091e-12	9.879e-09	LMOD1:20 CSMD1:23 SYT6:45 BRINP3:66 KCNQ3:69 HSF4:70
REACTOME_SIGNALING_BY_GPCR	-0.07888953	629	1.874e-11	2.432e-08	ADCY1:53 GPR37L1:54 VIPR2:58 VIPR1:62 GRM2:88 HTR1B:114
NIKOLSKY_BREAST_CANCER_16P13_AMPLICON	0.19077763	100	4.472e-11	4.836e-08	PGAP6:197 SPSB3:489 ZNF213:564 PRSS27:587 DECR2:649 WDR24:837
REACTOME_GPCR_LIGAND_BINDING	-0.08938534	396	1.175e-09	1.089e-06	GPR37L1:54 VIPR2:58 VIPR1:62 GRM2:88 HTR1B:114 HRH2:118
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	-0.09588533	331	2.244e-09	1.820e-06	RYR2:32 VIPR1:62 ZNF536:136 PTGFRN:140 BNC1:181 KCNK1:187
BENPORATH_SUZ12_TARGETS	-0.05813332	918	3.200e-09	2.307e-06	CYP4X1:12 CSMD1:23 SYT6:45 VIPR2:58 BRINP3:66 KCNQ3:69
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.27105765	38	7.424e-09	4.491e-06	CHST12:160 ADAP1:380 INTS1:436 SUN1:487 TMEM184A:758 TTYH3:850
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.09818012	294	7.614e-09	4.491e-06	GPR37L1:54 HTR1B:114 HRH2:118 PLPPR4:128 TAC1:150 S1PR1:222
REACTOME_POTASSIUM_CHANNELS	-0.17178428	91	1.513e-08	7.550e-06	KCNQ3:69 KCNV1:90 KCNF1:98 KCNJ14:149 KCNA10:185 KCNK1:187
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.23914035	47	1.423e-08	7.550e-06	ECSIT:52 COA1:124 TIMMDC1:438 DMAC2:510 TMEM126B:644 TMEM186:753
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.11406410	206	1.763e-08	8.168e-06	GPR37L1:54 HTR1B:114 HRH2:118 OPN3:250 GPR17:279 CHRM1:287
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	-0.07791280	419	5.021e-08	2.172e-05	PCNX2:40 SYT6:45 KCNQ3:69 HS3ST2:133 SLC35F3:144 CLMP:208
REACTOME_COMPLEX_I_BIOGENESIS	0.22501657	48	6.968e-08	2.825e-05	ECSIT:52 COA1:124 TIMMDC1:438 NDUFA9:570 TMEM126B:644 TMEM186:753
REACTOME_VOLTAGE_GATED_POTASSIUM_CHANNEL	-0.23936212	42	8.035e-08	3.067e-05	KCNQ3:69 KCNV1:90 KCNF1:98 KCNA10:185 KCNA4:216 KCNAB1:236
REACTOME_G_ALPHA_I_SIGNALLING_EVENTS	-0.09487304	269	9.097e-08	3.279e-05	ADCY1:53 GPR37L1:54 GRM2:88 HTR1B:114 ITPR1:186 OPN3:250
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.06759978	528	1.224e-07	4.181e-05	CAMSAP2:21 RYR2:32 DOCK4:35 SORL1:47 CHL1:57 VIPR1:62
REACTOME_MUSCLE_CONTRACTION	-0.11095553	190	1.395e-07	4.526e-05	SCN9A:5 LMOD1:20 RYR2:32 KCNJ14:149 NEB:157 ITPR1:186
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.14868490	101	2.476e-07	7.650e-05	LRPPRC:39 ECSIT:52 COA1:124 TIMMDC1:438 NDUFA9:570 TMEM126B:644
WP_CALCIUM_REGULATION_IN_CARDIAC_CELLS	-0.12656194	137	3.237e-07	9.546e-05	RYR2:32 ADCY1:53 CACNA1S:100 CACNA1B:152 ITPR1:186 GJC2:258
BENPORATH_EED_TARGETS	-0.04937037	928	4.325e-07	1.220e-04	CSMD1:23 VIPR2:58 BRINP3:66 KCNQ3:69 HSF4:70 GPR88:72
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.05786627	661	4.552e-07	1.231e-04	KIAA0825:2 DLGAP5:12 KIF24:18 UBAP2:22 TBCCD1:35 PARPBP:47
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	-0.07963433	331	6.844e-07	1.708e-04	RYR2:32 VIPR1:62 HECW1:67 IKZF1:76 ZNF536:136 BNC1:181
REACTOME_TRANSMISSION_ACROSS_CHEMICAL_SY	-0.09225929	246	6.584e-07	1.708e-04	PPFIA4:15 ADCY1:53 GABRR1:123 GABRB3:124 CACNA1B:152 KCNJ12:195
REACTOME_MITOCHONDRIAL_TRANSLATION	0.14944352	92	7.390e-07	1.776e-04	PTCD3:8 GFM2:86 GADD45GIP1:199 MRPS31:244 MRPS35:413 MTIF2:429
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.15771680	81	9.375e-07	2.172e-04	LRPPRC:39 ECSIT:52 COA1:124 TIMMDC1:438 NDUFA9:570 TMEM126B:644
WP_OXIDATIVE_PHOSPHORYLATION	0.20731567	46	1.153e-06	2.580e-04	ATP6AP2:408 NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PO:1120 NDUFS3:1122
REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-0.05489583	665	1.593e-06	3.445e-04	WWP1:16 RYR2:32 TRPM1:49 ADCY1:53 SLC22A6:59 ATP11C:63
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.05693541	594	2.413e-06	5.051e-04	BPTF:5 PTPN13:6 CEP192:7 MBD4:10 DLGAP5:12 BDP1:16
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04088708	1165	3.285e-06	6.660e-04	NETO2:24 NOS1AP:25 HERC2:34 LRRN3:41 CHL1:57 UAP1:65
FISCHER_DREAM_TARGETS	0.04627947	882	3.730e-06	7.333e-04	CEP192:7 DLGAP5:12 LCORL:14 KIF24:18 PARPBP:47 ATAD5:61
MIKKELSEN_NPC_HCP_WITH_H3K4ME3_AND_H3K27	-0.09508381	199	3.895e-06	7.433e-04	CSMD1:23 ELFN1:46 GPR88:72 PTGFRN:140 KCNK1:187 CDHR1:234
YOSHIMURA_MAPK8_TARGETS_UP	-0.04133177	1108	4.323e-06	8.014e-04	SCN9A:5 KCNQ3:69 AQP6:73 APBA2:85 RNF112:93 CACNA1S:100
DACOSTA_UV_RESPONSE_VIA_ERCC3_COMMON_DN	0.06252872	452	5.667e-06	1.021e-03	BPTF:5 AKAP9:9 ZNF292:19 C2CD3:30 LRPPRC:39 MDN1:62
REACTOME_PEPTIDE_LIGAND_BINDING_RECEPTOR	-0.10141779	166	6.718e-06	1.178e-03	GPR37L1:54 TAC1:150 MC4R:361 TACR1:365 CCR1:517 UTS2R:538
LEE_TARGETS_OF_PTCH1_AND_SUFU_DN	-0.14131846	83	8.666e-06	1.480e-03	ITPR1:186 KCNK1:187 CALB1:271 CAMK2D:334 PRKCG:375 SEZ6L2:396

## GO\_Biological\_Process\_2023 Top pathways by non-permulation

9.052e-06 1.506e-03

9.448e-06 1.532e-03

MMP16:4 SCN9A:5 KCNT2:17 LMOD1:20 CSMD1:23 DOCK4:35

SCN9A:5 RYR2:32 KCNJ14:149 ITPR1:186 KCNK1:187 KCNJ12:195

1337

-0.11669499

LIU\_OVARIAN\_CANCER\_TUMORS\_AND\_XENOGRAFTS -0.03663151

REACTOME\_CARDIAC\_CONDUCTION

Chamical Syrappic Transmission (GO-00072   -0.12125643   256   2.8926-01   1.5586-07   KND3-26 RAPBA-255 GRM288 HTRB:114 HRRI-2116 GABRRI-1123	Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO: 0.25216054 48 1.540e-09 1.801e-06 ECSITS2 COA1:124 TMEMBAG-202 DMACC2510 NDUFA9570 TMEM128:8644 Monastornic Cation Transmertrane Transpor - 0.1064981 273 1.672e-09 1.801e-06 SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:90 CACNAIS:100 Metal Ion Transport (GO:0000001) -0.13800038 196 2.274e-09 2.424e-06 SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:90 CACNAIS:100 Modulation Of Comercia Syrupide Transmis - 1.6560987 18 5.613e-09 4.320e-06 SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:90 CACNAIS:100 Modulation Of Comercia Syrupide Transmis - 1.0560987 19 5.503e-09 5.052e-06 SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:90 CACNAIS:100 GRAVE-28 PLEPRR-128 CACNAIS-1125 MCTP2-136 CDLP-128 DLGAP2-248 Minochondrial Gene Expression (GO:014005 0.16750599 100 7.500e-09 5.052e-06 FCD3:3 POLRMT-53: FASTKD1:72 FASTKD5:74 GFM2:65 CADD45GIP1-1199 CPACNAIS-100 Perassium Ion Transport (GO:00008813) -0.14994468 120 1.450e-09 8.052e-06 KCNQ3:69 KCNV1:90 KCNF1:98 KCNAI-1168 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1188 KCNAI-1189 KC	Chemical Synaptic Transmission (GO:00072	-0.12125643	256	2.892e-11	1.558e-07	KCNQ3:69 APBA2:85 GRM2:88 HTR1B:114 HRH2:118 GABRR1:123
Milochondrial Respiratory Chain Complex   0.25216054   48   1.5400-09   1.0010-06   ECSIT.52 COA1.124 THEMIZBA.202 DMAC2.510 NDUFAG.570 TMEMIZBS.844	Potassium Ion Transmembrane Transport (G	-0.15637176	132	5.992e-10	1.614e-06	KCNT2:17 KCNQ3:69 KCNV1:90 KCNF1:98 KCNJ14:149 KCNA10:185
Monatomic Cation Transpert (GO:0003001)	NADH Dehydrogenase Complex Assembly (GO:	0.25216054	48	1.540e-09	1.801e-06	ECSIT:52 COA1:124 TMEM126A:202 DMAC2:510 NDUFA9:570 TMEM126B:644
Metal Ion Transport (GO:030001)	Mitochondrial Respiratory Chain Complex	0.25216054	48	1.540e-09	1.801e-06	ECSIT:52 COA1:124 TMEM126A:202 DMAC2:510 NDUFA9:570 TMEM126B:644
Modulation Of Chemical Synaptic Transmis   -0.1596987   118   5.61309   4.20906   CRMZ-88 PLPPR4-128 CACNA15-132 MCTP2-158 DLGAP2-248   Mitochnoridal Gene Expression (GO.014005   0.16750599   100   7.5000-09   5.052006   PTCD3.8 PCINT.53 FASTKD17-72 FASTKD5.74 GFMZ-86 GADD45GIP1.199   Anterograde Trans-Synaptic Signaling (GO   -0.12313147   182   1.1300-08   8.0300-06   KCN03.69 ARXIV-190 KCNF1-98 KCNA10-186 KCNK1-187 KCN112-195   Inorganic Calion Transmembrane Transport (GO.0006813)   -0.14994468   120   1.4900-08   8.0300-06   KCN03.69 ARXIV-190 KCNF1-98 KCNA10-186 KCNK1-187 KCN112-195   Regulation Of Synaptic Transmission, Glu   -0.21829470   54   2.9440-08   1.3220-05   TSNZ-355 GRMZ-88 PLPPR4-128 SHANK3-171 CDH2-188 PTKZ6-192   Mitochnoridal Translation (GO.0032543)   0.15922756   96   7.3030-08   3.0276-05   PTCD3.8 GFMZ-86 GADD45GIP1-199 MRPS31-244 MTIF2-429 MTRF1-155   Mitochnoridal Respiratory Chain Complex   0.17184681   77   1.9140-07   7.3560-05   PCD3.8 GFMZ-86 GADD45GIP1-199 MRPS31-244 MTIF2-429 MTRF1-155   Calcium lon Import Across Plasma Membran   0.25595906   33   3.6470-07   1.3100-04   SCN8A-5 TRPM1-49 CACNA15-100	Monoatomic Cation Transmembrane Transpor	-0.10645981	273	1.672e-09	1.801e-06	SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:98 CACNA1S:100
Mitochondrial Gene Expression (GO:01005   0.16756999   100   7.500e-09   5.502e-06   PTCD38 POLRMT-53 FASTKD1:72 FASTKD5:74 GFR286 GADD450P1:199	Metal Ion Transport (GO:0030001)	-0.13900836	156	2.274e-09	2.042e-06	SCN9A:5 RYR2:32 SLC17A4:43 KCNV1:90 KCNF1:98 CACNA1S:100
Antergrande Trans-Synaptic Signaling (OC	Modulation Of Chemical Synaptic Transmis	-0.15560987	118	5.613e-09	4.320e-06	GRM2:88 PLPPR4:128 CACNA1B:152 MCTP2:158 CDH2:188 DLGAP2:248
Potassium Ion Transport (GO:0006813)	Mitochondrial Gene Expression (GO:014005	0.16750599	100	7.500e-09	5.052e-06	PTCD3:8 POLRMT:53 FASTKD1:72 FASTKD5:74 GFM2:86 GADD45GIP1:199
Inorganic Cation Transmembrane Transport	Anterograde Trans-Synaptic Signaling (GO	-0.12313147	182	1.113e-08	6.666e-06	KCNQ3:69 APBA2:85 GRM2:88 HTR1B:114 HRH2:118 GABRR1:123
Regulation Of Synaptic Transmission, Glu   -0.21829470   54   2.9446-08   3.2226-05   TSH2'355 GRM2'88 PLPPR4'128 SHANK3'17 CDH2'188 PTK2B'192   Mitochondrial Translation (GC.0032543)   0.15982756   96   7.3036-08   3.0276-05   PTCD3:8 GFM2'86 GADD45GPI1'199 MRPS31:244 MTIF2'429 MTRF1:545   Mitochondrial Respiratory Chain Complex   0.17184861   77   1.9146-07   7.3656-05   ECSIT-52 COA1:124 TMEM/26A:202 FASTKD3:330 DMAC2:510 NDUFA9:570   Calcium Ion Import Across Plasma Membran   -0.25595096   33   3.6476-07   1.3106-04   SCN9A'S TRPM1'49 CACNA15:100 CACNA1B:152 SCN2A'306 CLU-446   Mitochondrial RNA Metabolic Process (GO:   0.31571013   19   1.9046-06   6.4126-04   POLRMT:53 FASTKD1'72 FASTKD5'74 FASTKD3:330 TFB2M:68 TFAM:708   Inorganic Cation Import Across Plasma Me   -0.15888113   96   2.2516-06   7.1356-04   SCN9A'S TRPM1'49 CACNA15:100 KCNJ14:149 CACNA1B:152 KCNJ12:195   Proton Motive Force-Driven Mitochondrial   0.19599848   47   3.3876-06   1.0296-03   TRAD3-570 ATPSPD:747 NDUFV3:952 ATPSPD:1120 NDUFS3:1122 NDUFB10:1293   TRNA Modification (GC:0006400)   0.16488193   66   3.6956-06   1.0296-03   THADA:1 TRM1'10A:1 DTWD1:103 TRDM1':302 KTI12:333 CTU2:448   TRNA Methylation (GC:0006816)   -0.12854594   105   5.5276-06   1.3546-03   TRAD3-1570 ATPSPD:747 NDUFV3:952 ATPSPD:1120 NDUFS3:1122 NDUFB10:1293   TRNA Methylation (GC:0030488)   0.21744950   36   6.3926-06   1.4986-03   THADA:1 TRM1'10A:4   TRM1'10A:4   TRM1'10B:378 TRM1'10B:	Potassium Ion Transport (GO:0006813)	-0.14994468	120	1.490e-08	8.030e-06	KCNQ3:69 KCNV1:90 KCNF1:98 KCNA10:185 KCNK1:187 KCNJ12:195
Mitochondrial Translation (GO:0032543)   0.15922756   96   7.303e-08   3.027e-05   PTCD3:8 GFM2:86 GADD45GIP1:199 MRPS31:244 MTIF2:429 MTRF1:545	Inorganic Cation Transmembrane Transport	-0.09821523	276	2.272e-08	1.113e-05	SCN9A:5 TRPM1:49 KCNQ3:69 KCNV1:90 KCNF1:98 CACNA1S:100
Mitochondrial Respiratory Chain Complex   0.17184681   77   1.914e-07   7.365e-05   ECSIT:52 COA1:124 TMEM126A:202 FASTKD3:330 DMAC2:510 NDUFA9:570   1.310e-04   SCN9A:5 TRPM1:49 CACNA15:100 CACNA18:162 SCN2A:306 CLU-446   SCN9A:5 TRPM1:49 CACNA15:100 CACNA18:162 SCN2A:306 CLU-446   Mitochondrial RNA Metabolic Process (GO: 0.31571013   9   1.904e-06   6.412e-04   SCN9A:5 TRPM1:49 CACNA15:100 CACNA18:162 SCN2A:306 CLU-446   SCN9A:5 TRPM1:49 CACNA15:100 KCN.14:149 CACNA18:152 KCNJ12:195   Protor Motive Force-Driven Mitochondrial   0.1959948   47   3.387e-06   1.014e-03   NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PC:1120 NDUFS3:1122 NDUFB10:1293   TRADA-11 TRMT10A:41 DTWD1:103 TRDMT1:302 KTI12:333 CTU2-448   Protor Motive Force-Driven ATP Synthesis   0.1688193   66   3.695e-06   1.029e-03   THADA-1 TRMT10A:41 DTWD1:103 TRDMT1:302 KTI12:333 CTU2-448   TRADA-12 TRMT10A-14 DTWD1:103 TRDMT1:302 KTI12:333 CTU2-448   TRADA-12 TRMT10A-14 DTWD1:103 TRDMT1:302 KTI12:333 CTU2-448   NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PC:1120 NDUFS3:1122 NDUFB10:1293   TRADA-12 TRMT10A-14 DTWD1:103 TRDMT1:302 KTI12:333 CTU2-448   NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PC:1120 NDUFS3:1122 NDUFB10:1293   TRADA-12 TRMT10A-14 DTWD1:103 TRMT1:302 KTI12:333 CTU2-448   NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PC:1120 NDUFS3:1122 NDUFB10:1293   TRADA-12 TRMT10A-14 DTWD1:103 TRMT1:302 KTI12:333 CTU2-448   NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PC:1120 NDUFS3:1122 NDUFB10:1293   NDUFA9:570 ATP5PD:747 TRDMT1:302 TRMT10B:378 TRMT61B:471   Cardiac Conduction (GO:0006816)   0.17303310   55 8.898e-06   1.782e-03   ANX2:42 CAMX2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546   NDUFA9:570 ATP5PD:747 TEPM:749 NDUFV3:952 ATP5PC:1120 NDUFS3:1122 NDUFS3:1122 NDUFS3:1122 NDUFS3:1122 NDUFS3:1122 NDUFS3:1122 NDUFS3:1122 NDUFS3:1122 NDUFS3:1123 NDUFS3:1436 NDUFS3:1123 NDUFS3:1436 NDUFS3:1436 NDUFS3:1436 NDUFS3:1436	Regulation Of Synaptic Transmission, Glu	-0.21829470	54	2.944e-08	1.322e-05	TSHZ3:55 GRM2:88 PLPPR4:128 SHANK3:171 CDH2:188 PTK2B:192
Calcium Ion Import Across Plasma Membran   -0.25595096   33   3.647e-07   1.310e-04   SCN9A:5 TRPM1:49 CACNA1S:100 CACNA1B:152 SCN2A:306 CLU:446   Mitochondrial RNA Metabolic Process (GC)   0.3157103   19   1.904e-06   6.412e-04   POLRMT:53 FASTRD1:72 FASTRD5:330 TFBZM:636 TFAM:708   Postive Regulation Of Lord Robust Process (GC)   0.3157103   19   1.904e-06   6.412e-04   POLRMT:53 FASTRD1:72 FASTRD5:74 FASTRD3:330 TFBZM:636 TFAM:708   Postive Regulation Of Synaptic Transmis   -0.15876183   71   3.821e-06   1.029e-03   TSPAD:70 ATPSPD:747 NDUFV3:952 ATPSPD:1120 NDUFS3:1122 NDUFBI0:1293   TSPAD:70 ATPSPD:70	Mitochondrial Translation (GO:0032543)	0.15922756	96	7.303e-08	3.027e-05	PTCD3:8 GFM2:86 GADD45GIP1:199 MRPS31:244 MTIF2:429 MTRF1:545
Mitochondrial RNA Metabolic Process (GO: 0.31571013	Mitochondrial Respiratory Chain Complex	0.17184681	77	1.914e-07	7.365e-05	ECSIT:52 COA1:124 TMEM126A:202 FASTKD3:330 DMAC2:510 NDUFA9:570
Inorganic Cation Import Across Plasma Me	Calcium Ion Import Across Plasma Membran	-0.25595096	33	3.647e-07	1.310e-04	SCN9A:5 TRPM1:49 CACNA1S:100 CACNA1B:152 SCN2A:306 CLU:446
Proton Motive Force-Driven Mitochondrial   0.19599848   47   3.387e-06   1.014e-03   NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PO:1120 NDUFS3:1122 NDUFB10:1293	Mitochondrial RNA Metabolic Process (GO:	0.31571013	19	1.904e-06	6.412e-04	POLRMT:53 FASTKD1:72 FASTKD5:74 FASTKD3:330 TFB2M:636 TFAM:708
Positive Regulation Of Synaptic Transmis tRNA Modification (GO:0006400) 0.16488193 66 3.695e-06 1.029e-03 THADA:1 TRMT10A:41 DTWD1:103 TRDMT1:302 KTI12:333 CTU2:448 Proton Motive Force-Driven ATP Synthesis 0.18590640 51 4.441e-06 1.395e-03 NDLFA9:570 ATP5PD:747 NDLFV3:952 ATP5PO:1120 NDLFS3:1122 NDLFB10:1293 NDLFA9:570 ATP5PD:747 NDLFV3:952 ATP5PO:1120 NDLFS3:1122 NDLFB10:1293 NDLFA9:570 ATP5PD:747 NDLFV3:952 ATP5PO:1120 NDLFS3:1122 NDLFB10:1293 RPXR:32 TRPM1:49 CACNA1S:100 TRPM8:167 TRPC4:169 ITPR1:186 1.395e-03 RPXR:32 TRPM1:49 CACNA1S:100 TRPM8:167 TRPC4:169 ITPR1:186 RPXR:32 TRPM1:49 CACNA1S:100 TRPM8:167 ADIPORI:301 TRPM8:167 TRPM8:167 ADIPORI:301 TRPM8:167 TRPM8:167 ADIPORI:301 TRPM8:167 TRPM8:167 ADIPORI:301 TRPM8:1	Inorganic Cation Import Across Plasma Me	-0.13988113	96	2.251e-06	7.135e-04	SCN9A:5 TRPM1:49 CACNA1S:100 KCNJ14:149 CACNA1B:152 KCNJ12:195
RNA Modification (GC:0006400)   0.16488193   66   3.695e-06   1.029e-03   THADA:1 TRMT10A:41 DTWD1:103 TRDMT1:302 KT112:333 CTU2:448	Proton Motive Force-Driven Mitochondrial	0.19599848	47	3.387e-06	1.014e-03	NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PO:1120 NDUFS3:1122 NDUFB10:1293
Proton Motive Force—Driven ATP Synthesis Calcium Ion Transport (GC:0006816)	Positive Regulation Of Synaptic Transmis	-0.15876183	71	3.821e-06	1.029e-03	TSHZ3:55 SHANK3:171 PTK2B:192 SHANK2:201 PLK2:204 RIMS1:559
Calcium Ion Transport (GO:0006816)	tRNA Modification (GO:0006400)	0.16488193	66	3.695e-06	1.029e-03	THADA:1 TRMT10A:41 DTWD1:103 TRDMT1:302 KTI12:333 CTU2:448
tRNA Methylation (GO:0030488) 0.21744950 36 6.392e-06 1.498e-03 THADA:1 TRMT10A:41 TRMT5:217 TRDMT1:302 TRMT10B:378 TRMT61B:471 Cardiac Conduction (GO:0061337) -0.19474479 44 7.936e-06 1.782e-03 ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546 Oxidative Phosphorylation (GO:0006119) 0.17330310 55 8.898e-06 1.918e-03 NDUFA9:570 ATP5PD:747 TEFM:789 NDUFV3:952 ATP5PO:1120 NDUFS3:1122 Learning (GO:0007612) -0.19949653 41 9.977e-06 2.067e-03 GPR88:72 SHANK3:171 SYNJ1:179 SHANK2:201 DRD2:333 MAPK8IP2:400 Adenylate Cyclase-Inhibiting G Protein-C -0.18493473 46 1.445e-05 2.884e-03 GPR37L1:54 HTR18:114 CHRM1:287 DRD2:333 GRM8:688 HTR1A:675 Regulation Of Heart Rate By Cardiac Cond -0.19735113 39 2.021e-05 3.888e-03 ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546 Mitochondrial Electron Transport, NADH T 0.21927465 31 2.402e-05 4.314e-03 NDUFA9:570 NDUFA9:570 NDUFA9:570 NDUFA9:570 NDUFS3:1122 NDUFB10:1293 NDUFB9:1483 Regulation Of Cold-Induced Thermogenesis -0.10437128 138 2.402e-05 4.314e-03 EHMT1:44 TRPM8:167 ZNF423:238 ADIPORT:301 ZNF516:332 IGF18:363 Regulation Of Monoatomic Cation Transmem -0.19560449 38 3.039e-05 5.282e-03 KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671 Membrane Organization (GO:0061024) -0.09530425 155 4.412e-05 7.087e-03 ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496 Positive Regulation Of Metabolic Process -0.11741028 101 4.682e-05 7.087e-03 EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF18:363 CD36:408 Regulation Of Nonoatomic lon Transmembra -0.14952550 62 4.735e-05 7.087e-03 ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NPED4L:606 Regulation Of Neurotransmitter Receptor -0.18857046 39 4.642e-05 7.087e-03 ANK2:42 PTK2B:192 MAPK8IP2:400 CRH:576 NPED4L:606 Regulation Of Neurotransmitter Receptor -0.18857046 39 4.642e-05 7.087e-03 ANK2:42 PTK2B:192 MAPK8IP2:400 CRH:576 NPED4L:606 Regulation Of Neurotransmitter Receptor -0.18857046 39 4.642e-05 7.087e-03 ANK2:42 PTK2B:192 LGAB:2:426 DPP6:265 DRD2:333 CACNA1D:688 Positive Regulation Of Cold-Induced Ther -0.11965058	Proton Motive Force–Driven ATP Synthesis	0.18590640	51	4.441e-06	1.139e-03	NDUFA9:570 ATP5PD:747 NDUFV3:952 ATP5PO:1120 NDUFS3:1122 NDUFB10:1293
Cardiac Conduction (GO:0061337)	Calcium Ion Transport (GO:0006816)	-0.12854594	105	5.527e-06	1.354e-03	RYR2:32 TRPM1:49 CACNA1S:100 TRPM8:167 TRPC4:169 ITPR1:186
Oxidative Phosphorylation (GO:0006119)         0.17330310         55         8.898e-06         1.918e-03         NDUFA9:570 ATP5PD:747 TEFM:789 NDUFV3:952 ATP5PO:1120 NDUFS3:1122           Learning (GO:0007612)         -0.19949653         41         9.977e-06         2.067e-03         GPR88:72 SHANK3:171 SYNJ1:179 SHANK2:201 DRD2:333 MAPK8IP2:400           Adenylate Cyclase-Inhibiting G Protein-C         -0.18493473         46         1.445e-05         2.884e-03         GPR37L1:54 HTR1B:114 CHRM1:287 DRD2:333 GRM8:588 HTR1A:675           Regulation Of Heart Rate By Cardiac Cond         -0.19735113         39         2.021e-05         3.888e-03         ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546           Mitochondrial Electron Transport, NADH T         0.21927465         31         2.402e-05         4.314e-03         NDUFA9:570 NDUFAF1:891 NDUFV3:952 NDUFS3:1122 NDUFB10:1293 NDUFB9:1483           Regulation Of Cold-Induced Thermogenesis         -0.10437128         138         2.402e-05         4.314e-03         EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGF1R:363           Regulation Of Monoatomic Cation Transmem         -0.19560449         38         3.039e-05         5.282e-03         KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671           Membrane Organization (GO:00061024)         -0.09530425         155         4.412e-05         7.087e-03         ANK2:42 SYNJI:179 EGFR:330 BIN1:382 LMNB1:415 ACE2:496	tRNA Methylation (GO:0030488)	0.21744950	36	6.392e-06	1.498e-03	THADA:1 TRMT10A:41 TRMT5:217 TRDMT1:302 TRMT10B:378 TRMT61B:471
Learning (GO:0007612)	Cardiac Conduction (GO:0061337)	-0.19474479	44	7.936e-06	1.782e-03	ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546
Adenylate Cyclase—Inhibiting G Protein—C  Regulation Of Heart Rate By Cardiac Cond  O.19735113  O.2021e—05  Regulation Of Heart Rate By Cardiac Cond  O.19735113  O.21927465  Regulation Of Cold—Induced Thermogenesis  Regulation Of Monoatomic Cation Transmem  O.19560449  O.19530425  Regulation Of Metabolic Process  Regulation Of Metabolic Process  Regulation Of Metabolic Process  Regulation Of Monoatomic In Transmembra  Regulation Of Monoatomic In Transmembra  Regulation Of Monoatomic In Transmembra  Regulation Of Neurotransmitter Receptor  Regulation Of Neurotransmitter Receptor  Regulation Of Potassium Ion Transport (G  O.201978480  O.19978480  O	Oxidative Phosphorylation (GO:0006119)	0.17330310	55	8.898e-06	1.918e-03	NDUFA9:570 ATP5PD:747 TEFM:789 NDUFV3:952 ATP5PO:1120 NDUFS3:1122
Regulation Of Heart Rate By Cardiac Cond  -0.19735113  39  2.021e-05  3.888e-03  ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546  Mitochondrial Electron Transport, NADH T  0.21927465  31  2.402e-05  4.314e-03  NDUFA9:570 NDUFA1:891 NDUFV3:952 NDUFS3:1122 NDUFB10:1293 NDUFB9:1483  Regulation Of Cold-Induced Thermogenesis  -0.10437128  138  2.402e-05  4.314e-03  EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGF1R:363  Regulation Of Monoatomic Cation Transmem  -0.19560449  38  3.039e-05  5.282e-03  KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671  Membrane Organization (GO:0061024)  -0.09530425  Positive Regulation Of Metabolic Process  -0.11741028  101  4.682e-05  7.087e-03  ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496  Positive Regulation Of DNA-templated Transcriptio  0.03124259  1647  4.213e-05  7.087e-03  ANK2:42 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65  Regulation Of Monoatomic Ion Transmembra  -0.14952550  62  4.735e-05  7.087e-03  ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606  Regulation Of Potassium Ion Transport (G  -0.21519344  29  6.082e-05  8.857e-03  ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688  Positive Regulation Of Cold-Induced Ther  -0.11965058  93  6.828e-05  9.917e-03  SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Learning (GO:0007612)	-0.19949653	41	9.977e-06	2.067e-03	GPR88:72 SHANK3:171 SYNJ1:179 SHANK2:201 DRD2:333 MAPK8IP2:400
Mitochondrial Electron Transport, NADH T         0.21927465         31         2.402e-05         4.314e-03         NDUFA9:570 NDUFAF1:891 NDUFV3:952 NDUFS3:1122 NDUFB10:1293 NDUFB9:1483           Regulation Of Cold-Induced Thermogenesis         -0.10437128         138         2.402e-05         4.314e-03         EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGF1R:363           Regulation Of Monoatomic Cation Transmem         -0.19560449         38         3.039e-05         5.282e-03         KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671           Membrane Organization (GO:0061024)         -0.09530425         155         4.412e-05         7.087e-03         ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496           Positive Regulation Of Metabolic Process         -0.11741028         101         4.682e-05         7.087e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408           Regulation Of DNA-templated Transcriptio         0.03124259         1647         4.213e-05         7.087e-03         ZSCAN29:4 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65           Regulation Of Monoatomic Ion Transmembra         -0.14952550         62         4.735e-05         7.087e-03         ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606           Regulation Of Potassium Ion Transport (G         -0.21519344         29         6.082e-05         8.857e-03         ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688	Adenylate Cyclase–Inhibiting G Protein–C	-0.18493473	46	1.445e-05	2.884e-03	GPR37L1:54 HTR1B:114 CHRM1:287 DRD2:333 GRM8:588 HTR1A:675
Regulation Of Cold-Induced Thermogenesis         -0.10437128         138         2.402e-05         4.314e-03         EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGF1R:363           Regulation Of Monoatomic Cation Transmem         -0.19560449         38         3.039e-05         5.282e-03         KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671           Membrane Organization (G0:0061024)         -0.09530425         155         4.412e-05         7.087e-03         ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496           Positive Regulation Of Metabolic Process         -0.11741028         101         4.682e-05         7.087e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408           Regulation Of DNA-templated Transcriptio         0.03124259         1647         4.213e-05         7.087e-03         ZSCAN29:4 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65           Regulation Of Monoatomic Ion Transmembra         -0.14952550         62         4.735e-05         7.087e-03         ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606           Regulation Of Neurotransmitter Receptor         -0.18857046         39         4.642e-05         7.087e-03         NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647           Regulation Of Potassium Ion Transport (G         -0.21519344         29         6.082e-05         8.857e-03         ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688	Regulation Of Heart Rate By Cardiac Cond	-0.19735113	39	2.021e-05	3.888e-03	ANK2:42 CAMK2D:334 BIN1:382 HCN1:405 KCNJ3:467 KCNJ5:546
Regulation Of Monoatomic Cation Transmem         -0.19560449         38         3.039e-05         5.282e-03         KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671           Membrane Organization (GO:0061024)         -0.09530425         155         4.412e-05         7.087e-03         ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496           Positive Regulation Of Metabolic Process         -0.11741028         101         4.682e-05         7.087e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408           Regulation Of DNA-templated Transcriptio         0.03124259         1647         4.213e-05         7.087e-03         ZSCAN29:4 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65           Regulation Of Monoatomic Ion Transmembra         -0.14952550         62         4.735e-05         7.087e-03         ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606           Regulation Of Neurotransmitter Receptor         -0.18857046         39         4.642e-05         7.087e-03         NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647           Regulation Of Potassium Ion Transport (G         -0.21519344         29         6.082e-05         8.857e-03         ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688           Positive Regulation Of Cold-Induced Ther         -0.11965058         93         6.828e-05         9.681e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408	Mitochondrial Electron Transport, NADH T	0.21927465	31	2.402e-05	4.314e-03	NDUFA9:570 NDUFAF1:891 NDUFV3:952 NDUFS3:1122 NDUFB10:1293 NDUFB9:1483
Membrane Organization (GO:0061024)         -0.09530425         155         4.412e-05         7.087e-03         ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496           Positive Regulation Of Metabolic Process         -0.11741028         101         4.682e-05         7.087e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408           Regulation Of DNA-templated Transcriptio         0.03124259         1647         4.213e-05         7.087e-03         ZSCAN29:4 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65           Regulation Of Monoatomic Ion Transmembra         -0.14952550         62         4.735e-05         7.087e-03         ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606           Regulation Of Neurotransmitter Receptor         -0.18857046         39         4.642e-05         7.087e-03         NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647           Regulation Of Potassium Ion Transport (G         -0.21519344         29         6.082e-05         8.857e-03         ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688           Positive Regulation Of Cold-Induced Ther         -0.11965058         93         6.828e-05         9.681e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408           Sister Chromatid Segregation (GO:0000819         0.19978480         33         7.178e-05         9.917e-03         SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681 <td>Regulation Of Cold-Induced Thermogenesis</td> <td>-0.10437128</td> <td>138</td> <td>2.402e-05</td> <td>4.314e-03</td> <td>EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGF1R:363</td>	Regulation Of Cold-Induced Thermogenesis	-0.10437128	138	2.402e-05	4.314e-03	EHMT1:44 TRPM8:167 ZNF423:238 ADIPOR1:301 ZNF516:332 IGF1R:363
Positive Regulation Of Metabolic Process	Regulation Of Monoatomic Cation Transmem	-0.19560449	38	3.039e-05	5.282e-03	KCNAB1:236 DPP6:265 HCN1:405 NEDD4L:606 BPIFA1:626 HCN4:671
Regulation Of DNA-templated Transcriptio         0.03124259         1647         4.213e-05         7.087e-03         ZSCAN29:4 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65           Regulation Of Monoatomic Ion Transmembra         -0.14952550         62         4.735e-05         7.087e-03         ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606           Regulation Of Neurotransmitter Receptor         -0.18857046         39         4.642e-05         7.087e-03         NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647           Regulation Of Potassium Ion Transport (G         -0.21519344         29         6.082e-05         8.857e-03         ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688           Positive Regulation Of Cold-Induced Ther         -0.11965058         93         6.828e-05         9.681e-03         EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408           Sister Chromatid Segregation (GO:0000819         0.19978480         33         7.178e-05         9.917e-03         SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Membrane Organization (GO:0061024)	-0.09530425	155	4.412e-05	7.087e-03	ANK2:42 SYNJ1:179 EGFR:230 BIN1:382 LMNB1:415 ACE2:496
Regulation Of Monoatomic Ion Transmembra       -0.14952550       62       4.735e-05       7.087e-03       ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606         Regulation Of Neurotransmitter Receptor       -0.18857046       39       4.642e-05       7.087e-03       NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647         Regulation Of Potassium Ion Transport (G       -0.21519344       29       6.082e-05       8.857e-03       ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688         Positive Regulation Of Cold-Induced Ther       -0.11965058       93       6.828e-05       9.681e-03       EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408         Sister Chromatid Segregation (GO:0000819       0.19978480       33       7.178e-05       9.917e-03       SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Positive Regulation Of Metabolic Process	-0.11741028	101	4.682e-05	7.087e-03	EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408
Regulation Of Neurotransmitter Receptor       -0.18857046       39       4.642e-05       7.087e-03       NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647         Regulation Of Potassium Ion Transport (G       -0.21519344       29       6.082e-05       8.857e-03       ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688         Positive Regulation Of Cold-Induced Ther       -0.11965058       93       6.828e-05       9.681e-03       EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408         Sister Chromatid Segregation (GO:0000819       0.19978480       33       7.178e-05       9.917e-03       SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Regulation Of DNA-templated Transcriptio	0.03124259	1647	4.213e-05	7.087e-03	ZSCAN29:4 BPTF:5 LCORL:14 ZNF292:19 ZFP90:32 NSD1:65
Regulation Of Potassium Ion Transport (G       -0.21519344       29       6.082e-05       8.857e-03       ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688         Positive Regulation Of Cold-Induced Ther       -0.11965058       93       6.828e-05       9.681e-03       EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408         Sister Chromatid Segregation (GO:0000819       0.19978480       33       7.178e-05       9.917e-03       SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Regulation Of Monoatomic Ion Transmembra	-0.14952550	62	4.735e-05	7.087e-03	ANK2:42 PTK2B:192 MAPK8IP2:400 HCN1:405 CRH:576 NEDD4L:606
Positive Regulation Of Cold-Induced Ther -0.11965058 93 6.828e-05 9.681e-03 EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408 Sister Chromatid Segregation (GO:0000819 0.19978480 33 7.178e-05 9.917e-03 SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Regulation Of Neurotransmitter Receptor	-0.18857046	39	4.642e-05	7.087e-03	NETO1:87 PTK2B:192 DLGAP2:248 MAPK8IP2:400 CRH:576 NPTX1:647
Sister Chromatid Segregation (GO:0000819 0.19978480 33 7.178e-05 9.917e-03 SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681	Regulation Of Potassium Ion Transport (G	-0.21519344	29	6.082e-05	8.857e-03	ANK2:42 PTK2B:192 KCNAB1:236 DPP6:265 DRD2:333 CACNA1D:688
	Positive Regulation Of Cold-Induced Ther	-0.11965058	93	6.828e-05	9.681e-03	EHMT1:44 TRPM8:167 ADIPOR1:301 ZNF516:332 IGF1R:363 CD36:408
Aerobic Respiration (GO:0009060) 0.15425124 54 8.927e_05 1.203e_02 MTFR2:407 NDI IFΔ9:570 TFFM:789 NDI IF\/3:952 NDI IFS3:4122 NDI IFR10:1293	Sister Chromatid Segregation (GO:0000819	0.19978480	33	7.178e-05	9.917e-03	SPAG5:63 SGO1:106 SMC4:237 ESPL1:243 CHAMP1:334 KIFC1:681
7.6.000 1.00piidiidii (00.000000) 0.10420124 04 0.0210 00 1.2006-02 1011 112.401 1001 1001 10.01 1001 00.012 10001 00.1122 10001 010.1233	Aerobic Respiration (GO:0009060)	0.15425124	54	8.927e-05	1.203e-02	MTFR2:407 NDUFA9:570 TEFM:789 NDUFV3:952 NDUFS3:1122 NDUFB10:1293

## MGI\_Mammalian\_Phenotype\_Level\_4 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003635 abnormal synaptic transmissio	-0.08075170	424	3.252e-08	1.548e-05	SCN9A:5 ADCY1:53 NETO1:87 GRM2:88 GABRB3:124 CACNA1B:152
MP0002572 abnormal emotion/affect behav	-0.08639334	290	7.181e-07	1.709e-04	NDST3:19 EHMT1:44 ADCY1:53 CHL1:57 APBA2:85 GRM2:88
MP0002063 abnormal learning/memory/cond	-0.07444661	356	2.585e-06	4.102e-04	EHMT1:44 ADCY1:53 CHL1:57 APBA2:85 NETO1:87 HTR1B:114
MP0002066 abnormal motor capabilities/c	-0.04473052	1079	5.387e-06	6.411e-04	HERC2:34 ANK2:42 EHMT1:44 TSHZ3:55 VIPR2:58 APBA2:85
MP0002272 abnormal nervous system	-0.09406270	195	7.958e-06	7.576e-04	RYR2:32 KCNQ3:69 GABRR1:123 GABRB3:124 CACNA1B:152 ARC:202
MP0002085 abnormal embryonic tissue	0.05213706	653	1.526e-05	9.663e-04	BPTF:5 C2CD3:30 CUBN:34 ECSIT:52 NSD1:65 MACF1:68
MP0002429 abnormal blood cell	0.04088595	1191	1.624e-05	9.663e-04	PTPN13:6 JAK3:44 MECOM:69 ARHGEF6:81 NPHP3:90 PTPN2:96
MP0009745 abnormal behavioral response	-0.09002974	204	1.251e-05	9.663e-04	RYR2:32 EHMT1:44 GRM2:88 GABRB3:124 CACNA1B:152 LYST:218
MP0002084 abnormal developmental patter	0.06648747	360	2.438e-05	1.289e-03	BPTF:5 C2CD3:30 CUBN:34 ECSIT:52 NSD1:65 MACF1:68
MP0001970 abnormal pain threshold	-0.09816562	149	4.267e-05	2.031e-03	ADCY1:53 TSHZ3:55 GABRR1:123 TAC1:150 CACNA1B:152 TRPM8:167
MP0002398 abnormal bone marrow	0.04422464	794	6.766e-05	2.928e-03	JAK3:44 MECOM:69 ARHGEF6:81 PTPN2:96 IL27RA:159 NFATC3:162
MP0002080 prenatal lethality	0.03561181	1339	9.217e-05	3.656e-03	BPTF:5 C2CD3:30 CUBN:34 ECSIT:52 NSD1:65 MACF1:68
MP0005380 embryogenesis phenotype	0.05736382	407	1.164e-04	3.958e-03	BPTF:5 NACA:110 LAMA1:115 NFATC3:162 GADD45GIP1:199 HTR2B:211
MP0001672 abnormal embryogenesis/ devel	0.05736382	407	1.164e-04	3.958e-03	BPTF:5 NACA:110 LAMA1:115 NFATC3:162 GADD45GIP1:199 HTR2B:211
MP0002067 abnormal sensory capabilities	-0.07028580	261	1.249e-04	3.964e-03	CACNA1S:100 GABRB3:124 CACNA1B:152 TRPM8:167 ITPR1:186 SELP:203
MP0002882 abnormal neuron morphology	-0.04020239	881	1.576e-04	4.688e-03	LOXHD1:9 ANK2:42 OFD1:106 GABRB3:124 PLXNC1:132 CNGB3:159
MP0004085 abnormal heartbeat	-0.08580998	158	2.326e-04	6.513e-03	RYR2:32 ANK2:42 CACNA1B:152 CDH2:188 EGFR:230 VAV3:320
MP0005551 abnormal eye electrophysiolog	-0.09066355	138	2.712e-04	7.171e-03	TRPM1:49 GABRR1:123 CNGB3:159 SEMA4A:217 PDE6B:228 CDHR1:234
MP0002064 seizures	-0.06641747	254	3.453e-04	8.652e-03	SCN9A:5 RYR2:32 KCNQ3:69 NETO1:87 HRH2:118 GABRB3:124
MP0002086 abnormal extraembryonic tissu	0.04870333	476	4.422e-04	1.052e-02	BPTF:5 DLGAP5:12 CUBN:34 NSD1:65 MECOM:69 LAMA1:115
MP0001697 abnormal embryo size	0.05124286	413	5.292e-04	1.199e-02	BPTF:5 CUBN:34 ECSIT:52 MECOM:69 LAMA1:115 NFATC3:162
MP0003935 abnormal craniofacial develop	0.06509858	244	5.791e-04	1.253e-02	MECOM:69 GCM2:187 ZEB1:229 ENAM:274 FOXC2:299 UHRF1:307
MP0002925 abnormal cardiovascular devel	0.04443362	509	9.546e-04	1.976e-02	C2CD3:30 CUBN:34 MECOM:69 NFATC3:162 TGFBR3:164 HTR2B:211
MP0003252 abnormal bile duct	0.20286589	22	1.005e-03	1.993e-02	PKHD1:95 ABCB11:144 NR1H4:304 CYP8B1:356 BICC1:1168 PKD2:1190
MP0003984 embryonic growth retardation	0.05216446	328	1.520e-03	2.895e-02	BPTF:5 NACA:110 LAMA1:115 NFATC3:162 GADD45GIP1:199 HTR2B:211
MP0002088 abnormal embryonic growth/wei	0.05042220	336	1.938e-03	3.417e-02	BPTF:5 NACA:110 LAMA1:115 NFATC3:162 GADD45GIP1:199 HTR2B:211
MP0010094 abnormal chromosome stability	0.11543999	61	1.902e-03	3.417e-02	CENPE:100 FANCG:289 POLQ:410 LIG4:475 REV3L:493 SIRT6:529
MP0003868 abnormal feces composition	0.17836391	25	2.057e-03	3.497e-02	CYP8B1:356 APC:490 CYP7A1:733 SLC10A2:904 ITGB1:975 NCOA6:1224
MP0004808 abnormal hematopoietic stem	0.11255430	61	2.465e-03	4.046e-02	MECOM:69 ARID4A:367 TCF3:455 LIG4:475 ATR:1145 RAPGEF2:1267
MP0000716 abnormal immune system	0.03033493	972	3.033e-03	4.812e-02	PTPN13:6 JAK3:44 MECOM:69 ARHGEF6:81 PTPN2:96 IL27RA:159
MP0000598 abnormal liver morphology	0.03963394	471	4.432e-03	6.805e-02	ERCC5:49 MECOM:69 PKHD1:95 ABCB11:144 TGFBR3:164 ESPL1:243
MP0000703 abnormal thymus morphology	0.04580104	339	4.696e-03	6.985e-02	JAK3:44 NFATC3:162 ZEB1:229 ASXL1:269 AIRE:305 PHC1:312
MP0001968 abnormal touch/ nociception	-0.14068412	33	5.259e-03	7.586e-02	TRPM8:167 TACR1:365 SLC12A5:555 PRKAR1B:795 PTPRZ1:810 OPRL1:1060
MP0002396 abnormal hematopoietic system	0.17320026	21	6.073e-03	7.971e-02	JAK3:44 TCF3:455 APC:490 BRCA2:1129 CSF3R:1437 TNFRSF11A:1825
MP0002095 abnormal skin pigmentation	0.11701789	46	6.196e-03	7.971e-02	DST:183 ADAMTS20:337 ACD:353 APC:490 HPS5:514 ANK1:672
MP0001501 abnormal sleep pattern	-0.13480870	35	5.897e-03	7.971e-02	CACNA1B:152 KCNC2:547 NPAS2:567 CADPS2:678 FOS:1518 UBE3A:1558
MP0002932 abnormal joint morphology	0.07713849	108	5.984e-03	7.971e-02	FBN2:56 ZEB1:229 FOXC2:299 PHC1:312 DMRT2:481 SHARPIN:765
MP0003119 abnormal digestive system	0.10292866	58	6.924e-03	8.673e-02	ERCC5:49 GADD45GIP1:199 APC:490 RAPGEF2:1267 FOXL1:1307 SALL4:1360
MP0002069 abnormal eating/drinking beha	-0.04007350	401	7.501e-03	9.155e-02	EHMT1:44 VIPR2:58 APBA2:85 HTR1B:114 GABRB3:124 CACNA1B:152
MP0001529 abnormal vocalization	-0.17139985	20	8.046e_03	9.575e-02	DRD2:333 TACR1:365 WFS1:585 CHRM2:770 LBR:808 CHRM4:931

tissue\_specific Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Brodmann.area.9	-0.132345736	181	1.139e-09	6.152e-08	CSMD1:23 HECW1:67 KCNQ3:69 NETO1:87 KCNV1:90 NECAB1:95
cerebellar.hemisphere	-0.049242367	507	2.145e-04	4.647e-03	PPFIA4:15 NDST3:19 ADCY1:53 FAM135B:61 APBA2:85 MYT1:86
EBV.lymphocyte	0.042791290	671	2.582e-04	4.647e-03	DLGAP5:12 PARPBP:47 ATAD5:61 SFMBT2:91 CENPE:100 SGO1:106
hypothalamus	-0.104593810	66	3.394e-03	3.728e-02	SCN9A:5 SYT6:45 BRINP3:66 GABRG3:240 GRIK1:297 MC4R:361
putamen	-0.218213397	15	3.452e-03	3.728e-02	GPR88:72 KCNH4:302 LRRC10B:524 PDE10A:744 RGS9:1119 OPALIN:1546
cerebellum	-0.043540337	373	4.577e-03	4.119e-02	PPFIA4:15 NOS1AP:25 PCNX2:40 ANK2:42 FAM135B:61 MYT1:86
nucleus.accumbens	-0.081474168	98	5.529e-03	4.265e-02	GPR88:72 KCNA4:216 LRRC7:312 INSYN2A:368 PRKCG:375 GPR6:556
cerebral.cortex	-0.072932265	107	9.501e-03	6.413e-02	CSMD1:23 HECW1:67 KCNF1:98 FAM163B:220 RS1:254 CHRM1:287
C1.spinal.cord	-0.055378077	181	1.084e-02	6.507e-02	UGT8:36 ZNF536:136 PDE6B:228 GJC2:258 ACSBG1:323 ANLN:337
pancreas	0.072194834	94	1.602e-02	8.650e-02	TMED6:196 CELA3B:247 G6PC2:267 EGF:360 CATSPERB:740 PLA2G1B:828
pituitary.gland	-0.044824644	212	2.596e-02	1.274e-01	PLPPR4:128 RASD1:151 WDR17:163 ARC:202 DRD2:333 SEZ6L2:396
transverse.colon	0.052569468	148	2.837e-02	1.277e-01	WNK4:83 ATP2C2:242 SMPDL3B:697 DQX1:772 SLC26A2:907 MTMR11:981
uterus	0.076942292	61	3.821e-02	1.587e-01	CHRDL2:139 TEX15:582 ATP2B4:676 PTK7:687 CLEC4F:775 MEIS3:896
testis	0.017611364	1374	4.223e-02	1.629e-01	KIF24:18 ANKRD31:33 NLRP14:48 MYO3A:51 SPAG5:63 PIGV:78
fallopian.tube	0.079578742	52	4.765e-02	1.715e-01	ADGRG4:736 CCDC17:787 LDLRAD1:834 RARRES1:846 GREB1L:868 ADAMTS3:90
subcutaneous.adipose	0.063387280	72	6.379e-02	2.153e-01	SIGLEC1:331 PPARG:434 CYP1A1:689 GPBAR1:985 PLIN2:1319 ITIH5:1357
blood	0.030889689	275	8.191e-02	2.317e-01	MEFV:24 JAK3:44 BIN2:54 BPI:136 PRSS57:182 NLRC4:189
minor.salivary.gland	0.059998807	69	8.581e-02	2.317e-01	PIP:55 ODAM:314 CHST9:724 PRSS8:918 MMP27:1263 BPIFB6:1362
peyers.patch	0.040345701	167	7.431e-02	2.317e-01	MALRD1:174 CREB3L3:192 CDHR2:382 MEP1A:385 SLC51A:696 DQX1:772
spleen	0.029791108	298	8.122e-02	2.317e-01	STAB2:60 ARHGAP4:98 AKNA:209 DENND1C:212 PATL2:315 ADGRE1:497
sigmoid.colon	-0.062034476	52	1.226e-01	3.153e-01	LIMS2:448 DES:474 CHRM2:770 NTSR1:806 CHRNA3:863 HDAC4:1009
caudate.nucleus	-0.078539655	26	1.662e-01	3.589e-01	GPR37L1:54 GPR88:72 TAC1:150 MLC1:296 LRRC10B:524 RLBP1:792
ectocervix	0.083060217	25	1.510e-01	3.589e-01	COL27A1:82 PTHLH:322 RIPOR3:737 MATN2:2906 ADAMTSL5:3225 TSKU:3554
hippocampus.proper	-0.120721643	11	1.658e-01	3.589e-01	NEUROD6:402 FEZF2:2335 OLIG2:2757 NTS:2960 NEUROD2:7776 SLC17A7:7776
liver	0.023296838	323	1.565e-01	3.589e-01	CA5A:66 ADH6:140 ABCB11:144 SERPINA7:188 CREB3L3:192 IDO2:240
atrium.auricle	0.040275010	90	1.885e-01	3.915e-01	TNNI3K:295 XIRP1:401 CCDC141:744 MYO18B:921 SMCO1:1104 TBX5:1363
aorta	0.027056433	154	2.500e-01	5.000e-01	FILIP1L:181 KCNK15:198 KCNK17:230 SCUBE3:236 ITGA9:287 HMCN1:325
cortex.kidney	0.030237357	113	2.694e-01	5.195e-01	CUBN:34 PKHD1:95 ENAM:274 KIF12:428 DMRT2:481 CYP24A1:632
amygdala	-0.102262245	9	2.882e-01	5.367e-01	TNR:376 NEUROD6:402 PTPRZ1:810 LHFPL3:2813 NEUROD2:7776 PCDH15:7776
ansformed.skin.fibroblast	-0.016521756	258	3.668e-01	6.603e-01	ZNF281:29 CNTN3:51 DDR2:97 COL3A1:117 FST:173 BNC1:181
coronary.artery	0.060798949	15	4.152e-01	7.006e-01	SUSD5:813 MYO18B:921 MTHFD1L:1262 SOST:2116 GJA5:3131 CCN3:8371
stomach	0.026006484	86	4.064e-01	7.006e-01	MECOM:69 B4GALNT3:148 PGC:156 TMED6:196 TMPRSS2:284 COL2A1:512
esophagogastric.junction	-0.077096230	8	4.503e-01	7.369e-01	COL4A5:1873 CHRM3:2727 ADCY5:7776 BARX1:7776 F2RL2:7776 GADL1:7776

skeletal.muscle -0.013639243 239 4.728e-01 7.508e-01 LMOD2:56 MYOM2:77 CACNA1S:100 CAVIN4:111 NEB:157 MYBPH:178

5.532e-01 8.298e-01

5.870e-01 8.566e-01

6.104e-01 8.674e-01

6.310e-01 8.737e-01

6.672e-01 9.007e-01

5.380e-01 8.298e-01 PRUNE2:36 CCDC69:258 CYSLTR1:2174 SMTN:2349 RGMB:2816 PALLD:3340

PLEKHG4B:126 PLA2R1:128 PRTG:165 SCUBE3:236 IDO2:240 TLE6:317

CUBN:34 INSC:94 GJC3:118 EHBP1:210 PLXNB3:466 GLI1:540

PPP1R12B:7 LMOD1:20 HTR1B:114 OLFML2B:175 KCNAB1:236 SDK1:280

BLMH:18 INAVA:33 TRIM29:48 TRPM1:49 PKP1:119 DSG3:180

KRT5:1764 NPY2R:2331 THRSP:2598 ADIPOQ:7776 ALX4:7776 CIDEC:7776

esophagus.muscularis.mucosa 0.034935445 26

tibial.nerve

tibial.artery

leg.skin

breast

0.014081286 0.011503582

-0.014133989

-0.009581991

-0.032089377

191

110

216

15