GO_Biological_Process_2023 Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NADH Dehydrogenase Complex Assembly (GO:	−0.34082393	49	1.587e−16	4.290e−13	TMEM126B:3 NDUFA11:49 ECSIT:63 NDUFAF1:73 NDUFB8:148 NDUFB5:190
Mitochondrial Respiratory Chain Complex	−0.34082393	49	1.587e−16	4.290e−13	TMEM126B:3 NDUFA11:49 ECSIT:63 NDUFAF1:73 NDUFB8:148 NDUFB5:190
Mitochondrial Gene Expression (GO:014005	−0.23505441	102	2.542e−16	4.582e−13	TFAM:14 TEFM:93 POLRMT:101 TFB2M:112 TWNK:217 MRPS14:376
Mitochondrial Translation (GO:0032543)	−0.22711501	97	1.150e−14	1.555e−11	MRPS14:376 GADD45GIP1:477 FASTKD2:485 MRPS9:488 MRPS5:509 MRPL22:559
Mitochondrial ATP Synthesis Coupled Elec	−0.27220331	65	3.343e−14	3.615e−11	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Aerobic Electron Transport Chain (GO:001	−0.27107537	64	6.639e−14	5.983e−11	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Mitochondrial Respiratory Chain Complex	−0.23698959	82	1.244e−13	9.608e−11	TMEM126B:3 NDUFA11:49 ECSIT:63 NDUFAF1:73 NDUFB8:148 NDUFB5:190
Intermediate Filament Organization (GO:0	0.25637844	65	9.107e−13	6.155e−10	PKP1:8 DSP:30 KRT17:105 KRT80:119 KRT20:129 DES:220
Monoatomic Cation Transmembrane Transpor	0.12346999	277	1.821e−12	1.094e−09	TRPM5:13 TRPV6:31 SLC24A3:125 KCNQ3:126 CACNA1S:152 SLC24A4:169
Oxidative Phosphorylation (GO:0006119)	−0.26105936	59	4.166e−12	2.252e−09	NDUFA11:49 TEFM:93 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422
Proton Motive Force−Driven Mitochondrial	−0.27879639	50	9.319e−12	4.581e−09	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Translation (GO:0006412)	−0.13473174	208	2.376e−11	1.071e−08	MRPS14:376 ZAR1:424 HBS1L:440 GADD45GIP1:477 FASTKD2:485 MRPS9:488
Mitochondrial Electron Transport, NADH T	−0.32843823	33	6.670e−11	2.774e−08	NDUFAF1:73 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Proton Motive Force−Driven ATP Synthesis	−0.25205853	55	1.030e−10	3.976e−08	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Chemical Synaptic Transmission (GO:00072	0.11476942	263	1.697e−10	6.118e−08	KCNQ3:126 HRH2:130 CACNA1E:166 GRIK4:236 HTR5A:246 SLC18A3:251
Inorganic Cation Transmembrane Transport	0.11013440	280	2.622e−10	8.860e−08	TRPM5:13 TRPV6:31 SLC24A3:125 KCNQ3:126 CACNA1S:152 SLC24A4:169
Cilium Organization (GO:0044782)	−0.12170787	221	5.042e−10	1.604e−07	KIAA0586:44 KIF27:46 ARL13B:87 GBF1:126 CENPJ:149 IQCG:231
tRNA Modification (GO:0006400)	−0.21526005	67	1.137e−09	3.416e−07	MTO1:174 TYW5:244 PUS10:301 TRMT10A:361 METTL8:364 DTWD1:394
Cilium Assembly (GO:0060271)	−0.11396835	232	2.474e−09	7.040e−07	TBC1D32:31 KIAA0586:44 KIF27:46 ARL13B:87 GBF1:126 CENPJ:149
Muscle Contraction (GO:0006936)	0.17646929	91	6.161e−09	1.666e−06	MYH2:11 MYH13:54 MYOF:127 CACNA1S:152 DES:220 MYH1:239
Cellular Respiration (GO:0045333)	−0.18370358	82	9.167e−09	2.360e−06	NDUFA11:49 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451
Aerobic Respiration (GO:0009060)	−0.21956862	57	1.001e−08	2.460e−06	NDUFA11:49 TEFM:93 NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422
Calcium Ion Transmembrane Import Into Cy	0.18574261	79	1.180e−08	2.774e−06	TRPV6:31 CACNA1I:148 CACNA1S:152 CACNA1E:166 SLC24A4:169 CACNA1G:287
Calcium Ion Transport (GO:0006816)	0.15520251	110	1.950e−08	4.393e−06	TRPM5:13 TRPV6:31 SLC24A3:125 CACNA1S:152 SLC24A4:169 CACNA1G:287
Sensory Perception Of Smell (GO:0007608)	0.11040761	208	4.383e−08	9.481e−06	SLC24A4:169 OR10A2:211 OR2H2:369 OR10D3:475 DRD2:522 OR10C1:636
Potassium Ion Transmembrane Transport (G	0.13547872	135	5.751e−08	1.196e−05	SLC24A3:125 KCNQ3:126 SLC24A4:169 KCNK10:225 KCNJ12:259 KCNH2:365
Potassium Ion Transport (GO:0006813)	0.13631751	121	2.319e−07	4.645e−05	SLC24A3:125 KCNQ3:126 SLC24A4:169 KCNK10:225 KCNJ12:259 KCNH2:365
Positive Regulation Of DNA Metabolic Pro	−0.14608275	104	2.729e−07	5.269e−05	RNF168:52 STON1:61 SMCHD1:136 ABRAXAS1:141 DNA2:193 UIMC1:291
Response To Calcium Ion (GO:0051592)	0.14622412	100	4.487e−07	8.365e−05	SYT2:18 TRPV6:31 ADCY1:32 SYT8:179 RASGRP2:240 SYT6:275
Neuron Projection Morphogenesis (GO:0048	0.12392007	139	4.761e−07	8.582e−05	ADGRB1:39 NRCAM:96 CTTN:149 TRIO:200 FLRT1:218 TNN:252
DNA Repair (GO:0006281)	−0.08740794	281	5.052e−07	8.811e−05	RNF168:52 STON1:61 USP44:64 TOPBP1:123 ABRAXAS1:141 DNA2:193
Cardiac Conduction (GO:0061337)	0.21419307	45	6.722e−07	1.136e−04	DSP:30 DSG2:104 CACNA1G:287 KCNH2:365 DSC2:569 CACNB2:890
Regulation Of Heart Rate By Cardiac Cond	0.22627703	40	7.413e−07	1.215e−04	DSP:30 DSG2:104 CACNA1G:287 KCNH2:365 DSC2:569 CACNB2:890
tRNA Methylation (GO:0030488)	−0.23693916	36	8.735e−07	1.389e−04	MTO1:174 TRMT61B:285 TRMT10C:293 TRMT10A:361 METTL8:364 FTSJ1:505
Anterograde Trans−Synaptic Signaling (GO	0.10311036	190	1.010e−06	1.560e−04	KCNQ3:126 HRH2:130 CACNA1E:166 GRIK4:236 HTR5A:246 SLC18A3:251
Modulation Of Chemical Synaptic Transmis	0.12903473	118	1.332e−06	2.001e−04	MYOF:127 TRIO:200 GRIK4:236 OTOF:272 GRM2:438 DRD2:522
Calcium Ion Transmembrane Transport (GO:	0.15800063	78	1.434e−06	2.095e−04	TRPM5:13 TRPV6:31 SLC24A3:125 CACNA1S:152 SLC24A4:169 CACNA1G:287
Cellular Response To Calcium Ion (GO:007	0.16811948	67	1.980e−06	2.818e−04	SYT2:18 ADCY1:32 SYT8:179 RASGRP2:240 SYT6:275 CAPN3:448
Metal Ion Transport (GO:0030001)	0.10488688	169	2.671e−06	3.702e−04	SLC17A4:9 TRPV6:31 CACNA1S:152 KCNJ12:259 CHRNA4:393 ITPR1:416
Mitochondrial RNA Metabolic Process (GO:	−0.29839148	20	3.852e−06	5.207e−04	TFAM:14 TEFM:93 POLRMT:101 TFB2M:112 TWNK:217 FASTKD1:431

EnrichmentHsSymbolsFile2 Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_KERATINIZATION	0.22485940	214	9.785e−30	6.355e−26	PKP1:8 DSP:30 KRTAP6−1:34 KRTAP10−1:83 KRTAP10−3:84 DSG2:104
FISCHER_DREAM_TARGETS	−0.10069796	924	5.494e−25	1.784e−21	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 CEP192:39 SGO2:62
JOHNSTONE_PARVB_TARGETS_3_DN	−0.09707511	794	2.019e−20	4.369e−17	CCPG1:1 UBAP2:5 FAM13B:6 SRFBP1:8 DLGAP5:10 TFAM:14
MARSON_BOUND_BY_E2F4_UNSTIMULATED	−0.10201173	664	4.108e−19	6.670e−16	UBAP2:5 DLGAP5:10 PARPBP:29 LRRC40:33 SGO2:62 DNMT1:74
REACTOME_NEURONAL_SYSTEM	0.13056085	394	6.861e−19	8.911e−16	SHANK2:3 SYT2:18 PPFIA1:23 ADCY1:32 GJA10:91 PPFIA4:107
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	0.22527613	128	1.407e−18	1.522e−15	PKP1:8 DSP:30 DSG2:104 KRT17:105 KRT80:119 KRT20:129
REACTOME_SENSORY_PERCEPTION	0.10279761	603	8.354e−18	7.750e−15	TRPM5:13 RGS9:52 MYO15A:68 OR10A2:211 OR51E2:230 OTOF:272
HAMAI_APOPTOSIS_VIA_TRAIL_UP	−0.09519660	625	5.595e−16	4.542e−13	FAM13B:6 DLGAP5:10 CEP350:22 ATAD2:27 PARPBP:29 KIF18A:30
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	−0.09655581	601	7.640e−16	5.513e−13	CCPG1:1 DLGAP5:10 LRPPRC:13 TFAM:14 ATAD2:27 PARPBP:29
MARTENS_TRETINOIN_RESPONSE_UP	0.08438836	788	1.041e−15	5.647e−13	SHANK2:3 CEP170B:19 TRIM29:35 AXIN2:98 JAG2:138 RNF186:139
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	−0.24471771	90	1.043e−15	5.647e−13	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 ECSIT:63 NDUFAF1:73
DODD_NASOPHARYNGEAL_CARCINOMA_DN	−0.06723991	1278	1.042e−15	5.647e−13	TET1:2 DLGAP5:10 LRPPRC:13 TFAM:14 MTPAP:25 ATAD2:27
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	−0.33691063	47	1.345e−15	6.720e−13	TMEM126B:3 TIMMDC1:56 ECSIT:63 NDUFAF1:73 TMEM70:95 NDUFB8:148
REACTOME_DEVELOPMENTAL_BIOLOGY	0.07004333	1097	7.012e−15	3.253e−12	PKP1:8 DSP:30 KRTAP6−1:34 SEMA7A:58 KRTAP10−1:83 KRTAP10−3:84
REACTOME_MITOCHONDRIAL_TRANSLATION	−0.23115179	93	1.344e−14	5.820e−12	MRPS35:322 MRPS14:376 GADD45GIP1:477 MRPS9:488 MRPS5:509 MRPL22:559
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	−0.20979641	112	1.764e−14	6.737e−12	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 ECSIT:63 NDUFAF1:73
REACTOME_COMPLEX_I_BIOGENESIS	−0.31996423	48	1.739e−14	6.737e−12	TMEM126B:3 NDUFA11:49 TIMMDC1:56 ECSIT:63 NDUFAF1:73 NDUFB8:148
REACTOME_SIGNALING_BY_GPCR	0.08400692	687	7.518e−14	2.712e−11	GPR37L1:12 TAAR6:28 ADCY1:32 RGS9:52 CALCA:63 TIAM1:111
WP_GPCRS_CLASS_A_RHODOPSINLIKE	0.13432814	253	2.006e−13	6.856e−11	GPR37L1:12 HRH2:130 FFAR2:150 GPR68:174 GPER1:188 GPR35:205
MEISSNER_NPC_HCP_WITH_H3K4ME2_AND_H3K27M	0.11476644	340	3.870e−13	1.256e−10	SYT2:18 BNC1:26 ADGRB1:39 LAD1:42 SEMA7A:58 JAG2:138
MIKKELSEN_MEF_HCP_WITH_H3K27ME3	0.08850454	577	4.363e−13	1.349e−10	ADGRB1:39 LAD1:42 DSG2:104 KCNQ3:126 HRH2:130 JAG2:138
REACTOME_CELL_CYCLE	−0.08305517	652	5.582e−13	1.648e−10	DAXX:12 KIF18A:30 CEP192:39 SYNE2:43 RNF168:52 SGO2:62
KEGG_CALCIUM_SIGNALING_PATHWAY	0.15946070	168	1.036e−12	2.925e−10	ADCY1:32 HRH2:130 CACNA1I:148 CACNA1S:152 CACNA1E:166 HTR5A:246
MIKKELSEN_MCV6_HCP_WITH_H3K27ME3	0.10049285	426	1.263e−12	3.419e−10	SYT2:18 ADGRB1:39 SEMA7A:58 ZBTB16:76 KCNQ3:126 CLMP:143
BENPORATH_ES_WITH_H3K27ME3	0.06463374	1063	1.462e−12	3.797e−10	PKP1:8 PLEC:15 BNC1:26 PHLDB1:45 RGS9:52 CALCA:63
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	−0.06071051	1204	1.845e−12	4.608e−10	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 LARP4:38 SGO2:62
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	0.33247509	37	2.593e−12	6.233e−10	INTS1:109 GPER1:188 ZFAND2A:199 SNX8:387 MAD1L1:459 AP5Z1:508
REACTOME_MUSCLE_CONTRACTION	0.14500232	196	2.687e−12	6.233e−10	MYBPC2:144 MME:145 CASQ1:147 CACNA1I:148 DES:220 KCNK10:225
REACTOME_OLFACTORY_SIGNALING_PATHWAY	0.10246751	390	4.139e−12	9.269e−10	OR10A2:211 OR51E2:230 OR4K15:315 OR2H2:369 OR9K2:400 OR10D3:475
GOBERT_OLIGODENDROCYTE_DIFFERENTIATION_U	−0.08599122	558	4.358e−12	9.433e−10	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 CEP192:39 KIAA0586:44
YOSHIMURA_MAPK8_TARGETS_UP	0.05905172	1226	4.813e−12	1.008e−09	AFDN:4 SYT2:18 ADH7:37 ARC:49 RGS9:52 CALCA:63
KEGG_OLFACTORY_TRANSDUCTION	0.10253300	377	8.933e−12	1.813e−09	OR10A2:211 OR51E2:230 OR4K15:315 OR2H2:369 OR9K2:400 OR6B3:501
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	−0.14435381	186	1.170e−11	2.302e−09	DLGAP5:10 PARPBP:29 KIF18A:30 SGO2:62 KIF22:90 KIF2C:108
WP_2Q37_COPY_NUMBER_VARIATION_SYNDROME	0.17186962	129	1.613e−11	3.080e−09	PER2:2 CALCA:63 PASK:65 KIF1A:161 GPR35:205 PPP1R7:244
BLANCO_MELO_BRONCHIAL_EPITHELIAL_CELLS_I	−0.14567517	175	3.083e−11	5.720e−09	KIF2C:108 SPAG5:163 NEXN:164 GCNT3:201 FANCG:202 KIF20A:251
MIKKELSEN_NPC_HCP_WITH_H3K27ME3	0.10550387	335	3.454e−11	6.230e−09	SYT2:18 BNC1:26 ADGRB1:39 LAD1:42 JAG2:138 LMX1A:306
REACTOME_CELL_CYCLE_CHECKPOINTS	−0.11719376	270	3.598e−11	6.315e−09	KIF18A:30 RNF168:52 SGO2:62 CENPC:70 CENPT:71 KIF2C:108
KEGG_NEUROACTIVE_LIGAND_RECEPTOR_INTERAC	0.11650318	265	7.010e−11	1.198e−08	TAAR6:28 HRH2:130 GPR35:205 GRIK4:236 HTR5A:246 ADORA2A:269
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	−0.19876994	89	9.209e−11	1.533e−08	NDUFB8:148 NDUFB5:190 NDUFB10:418 NDUFS5:422 NDUFB3:451 NDUFB4:502
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	−0.08756792	438	3.619e−10	5.875e−08	DLGAP5:10 LRPPRC:13 MTPAP:25 ATAD2:27 PARPBP:29 KIF18A:30

DisGeNET Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Schizophrenia	0.05648410	1731	2.403e−14	2.359e−10	SHANK2:3 SORL1:5 TRANK1:7 PLEC:15 NAV1:17 TAAR6:28
Arthrogryposis	0.09909345	298	4.549e−09	2.233e−05	MYH2:11 PLEC:15 SYT2:18 OFD1:121 COL6A1:158 IGHMBP2:176
Bipolar Disorder	0.06247038	755	7.235e−09	2.368e−05	PER2:2 SORL1:5 TRANK1:7 TAAR6:28 TRPV6:31 ADCY1:32
Increased CSF lactate	−0.21571940	56	2.394e−08	5.876e−05	TMEM126B:3 LRPPRC:13 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 TRMT10C:293
Charcot−Marie−Tooth Disease	0.09819164	268	3.482e−08	6.837e−05	SYT2:18 DSP:30 SBF1:33 PRKN:57 MYO15A:68 DSG2:104
NADH:Q(1) Oxidoreductase deficiency	−0.30491833	25	1.317e−07	1.847e−04	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451
Primary microcephaly	−0.14646853	110	1.154e−07	1.847e−04	CENPJ:149 DNA2:193 FANCG:202 STIL:219 XRCC4:255 KNL1:350
Autism Spectrum Disorders	0.06649237	516	2.808e−07	2.757e−04	SHANK2:3 MKI67:10 PRKN:57 KMT5B:61 PPP1R13B:64 ZNF423:80
Autistic Disorder	0.06024552	637	2.642e−07	2.757e−04	SHANK2:3 SDK1:20 HTT:46 PRKN:57 ZNF407:60 CALCA:63
Mitochondrial Diseases	−0.07909509	363	2.566e−07	2.757e−04	TMEM126B:3 LRPPRC:13 MTPAP:25 NDUFA11:49 ECSIT:63 NDUFAF1:73
Reflex, Deep Tendon, Absent	0.12974571	129	3.748e−07	3.067e−04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Absent reflex	0.12974571	129	3.748e−07	3.067e−04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Congenital myopathy (disorder)	0.14018054	109	4.416e−07	3.335e−04	MYH2:11 CASQ1:147 CACNA1S:152 COL6A1:158 IGHMBP2:176 DES:220
Absent tendon reflex	0.12988190	126	4.964e−07	3.482e−04	SYT2:18 SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 BICD2:295
Mood Disorders	0.07987856	319	1.029e−06	6.735e−04	ZHX3:24 TAAR6:28 ADCY1:32 HTT:46 PPP1R13B:64 ADARB1:157
MITOCHONDRIAL COMPLEX I DEFICIENCY	−0.27270922	26	1.491e−06	9.151e−04	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB3:451 FOXRED1:619
Congenital pes cavus	0.12653047	120	1.745e−06	9.517e−04	SYT2:18 ANOS1:77 MME:145 HSD17B4:320 L1CAM:326 INF2:410
Unipolar Depression	0.06365788	487	1.737e−06	9.517e−04	ZHX3:24 HTT:46 ZBTB16:76 ACSL4:92 ADARB1:157 TRIO:200
Ciliopathies	−0.10474399	174	1.969e−06	1.018e−03	TBC1D32:31 KIAA0586:44 ARL13B:87 NME8:273 NPHP3:306 BUB1B:318
Gait, Drop Foot	0.25007073	30	2.142e−06	1.052e−03	IGHMBP2:176 L1CAM:326 INF2:410 MPZ:602 GNE:649 TTN:825
Abnormal mitochondria in muscle tissue	−0.27011667	25	2.950e−06	1.379e−03	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB10:418 NDUFB3:451
Acute necrotizing encephalopathy	−0.30034987	20	3.327e−06	1.485e−03	TMEM126B:3 NDUFA11:49 TIMMDC1:56 NDUFAF1:73 NDUFB3:451 FOXRED1:619
Myopathy	0.07025291	358	5.469e−06	2.335e−03	MYH2:11 PLEC:15 CASQ1:147 COL6A1:158 IGHMBP2:176 DES:220
Abnormal behavior	0.07148187	341	6.270e−06	2.565e−03	SHANK2:3 HTT:46 NRCAM:96 ADARB1:157 HTR5A:246 HDAC4:291
Myocardial Infarction	0.04480251	896	6.918e−06	2.717e−03	SBF1:33 ARC:49 ALMS1:103 PC:185 GPER1:188 NDST1:204
Congestive heart failure	0.04714750	791	8.074e−06	2.936e−03	DSP:30 TRPV6:31 HTT:46 ARC:49 AIMP2:74 ALMS1:103
Spasmodic torticollis	0.26362179	24	7.827e−06	2.936e−03	COL6A1:158 KCTD17:368 DRD2:522 PNKD:561 CACNA1B:716 SCP2:1254
Mental Depression	0.05666113	534	8.616e−06	3.022e−03	PER2:2 ADCY1:32 HTT:46 ACSL4:92 KRT20:129 GRIK4:236
Foot−drop	0.20237383	40	9.539e−06	3.122e−03	MME:145 IGHMBP2:176 DES:220 INF2:410 MPZ:602 GNE:649
Heart failure	0.04858939	732	9.225e−06	3.122e−03	DSP:30 HTT:46 ARC:49 AIMP2:74 ALMS1:103 MME:145
Chromosome Breakage	−0.20190579	40	1.000e−05	3.168e−03	FANCG:202 XRCC4:255 BRCA1:300 FANCM:414 DNMT3B:780 IL4:927
Alzheimer's Disease	0.03187802	1795	1.231e−05	3.777e−03	PER2:2 SHANK2:3 SORL1:5 HTT:46 ARC:49 LGR6:51
nervous system disorder	0.06332214	407	1.294e−05	3.850e−03	SHANK2:3 HTT:46 CALCA:63 ACKR3:254 NOTCH1:258 ATP7B:273
Distal muscle weakness	0.14617587	74	1.397e−05	4.023e−03	SYT2:18 COL6A1:158 IGHMBP2:176 DES:220 INF2:410 MPZ:602
Torticollis	0.24585795	26	1.434e−05	4.023e−03	COL6A1:158 KCTD17:368 DRD2:522 PNKD:561 CACNA1B:716 DNM2:1182
Depressive disorder	0.04914697	678	1.522e−05	4.150e−03	PER2:2 TAAR6:28 ADCY1:32 HTT:46 AIMP2:74 ANOS1:77
Distal sensory impairment	0.15060127	68	1.774e−05	4.709e−03	SBF1:33 MME:145 KIF1A:161 IGHMBP2:176 PIK3R5:363 INF2:410
Major Depressive Disorder	0.05651225	486	2.226e−05	5.670e−03	TAAR6:28 HTT:46 ZBTB16:76 ADARB1:157 GRIK4:236 ACKR3:254
Pervasive Development Disorder	0.11216959	120	2.252e−05	5.670e−03	SHANK2:3 HTT:46 PRKN:57 KMT5B:61 TRIO:200 KMT2C:227
Distal limb muscle weakness due to perip	0.14125547	75	2.376e−05	5.832e−03	SYT2:18 COL6A1:158 IGHMBP2:176 DES:220 INF2:410 MPZ:602

MGI_Mammalian_Phenotype_Level_4 Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
MP0003635 abnormal synaptic transmissio	0.09019531	425	6.037e−10	2.874e−07	SYT2:18 ADCY1:32 ARC:49 NRCAM:96 ADARB1:157 CACNA1E:166
MP0001929 abnormal gametogenesis	−0.08306070	470	2.406e−09	5.727e−07	ARID4A:86 FGD2:145 ADCY10:173 FANCG:202 SYCP1:216 EIF4G3:234
MP0003698 abnormal male reproductive	−0.06637641	521	5.859e−07	9.296e−05	CATSPER2:41 CLGN:84 ADCY10:173 FANCG:202 SYCP1:216 EIF4G3:234
MP0002066 abnormal motor capabilities/c	0.04659325	1087	1.822e−06	1.497e−04	PER2:2 SYT2:18 HTT:46 NRCAM:96 HRH2:130 CACNA1S:152
MP0002063 abnormal learning/memory/cond	0.07591129	356	1.590e−06	1.497e−04	PER2:2 ADCY1:32 HTT:46 ARC:49 NRCAM:96 HTR5A:246
MP0009745 abnormal behavioral response	0.09790641	205	1.887e−06	1.497e−04	PER2:2 CALCA:63 SLC18A3:251 ADORA2A:269 CACNA1G:287 UPP1:377
MP0010094 abnormal chromosome stability	−0.16744916	65	3.340e−06	2.271e−04	FANCG:202 XRCC4:255 BRCA1:300 MBD1:313 BUB1B:318 CENPE:392
MP0002085 abnormal embryonic tissue	−0.05180204	655	1.610e−05	9.580e−04	ADAMTS20:9 CUBN:11 DAXX:12 TFAM:14 NSD1:24 ECSIT:63
MP0002067 abnormal sensory capabilities	0.07410385	267	4.273e−05	2.034e−03	HTT:46 CACNA1S:152 CACNA1E:166 IGHMBP2:176 GRIK4:236 HDAC4:291
MP0002064 seizures	0.07614848	255	3.886e−05	2.034e−03	HTT:46 KCNQ3:126 HRH2:130 ADARB1:157 GRIK4:236 SLC18A3:251
MP0003077 abnormal cell cycle	−0.09570616	153	5.262e−05	2.129e−03	ITGB1:152 RIF1:179 MED1:208 BRCA1:300 BUB1B:318 CENPE:392
MP0002572 abnormal emotion/affect behav	0.07068146	287	5.366e−05	2.129e−03	ADCY1:32 HTT:46 ARC:49 ULK2:155 CACNA1E:166 HTR5A:246
MP0002210 abnormal sex determination	−0.06338802	350	7.003e−05	2.564e−03	FANCG:202 SYCP1:216 EIF4G3:234 BRCA1:300 MAGEL2:373 RNF17:386
MP0005620 abnormal muscle contractility	0.08102015	206	7.733e−05	2.579e−03	CASQ1:147 CACNA1S:152 COL6A1:158 DES:220 TNNT2:380 APOE:461
MP0000653 abnormal sex gland	−0.05226620	523	8.129e−05	2.579e−03	AFP:53 ARID4A:86 FANCG:202 SYCP1:216 EIF4G3:234 BRCA1:300
MP0002429 abnormal blood cell	−0.03635617	1240	9.287e−05	2.763e−03	SPIC:40 ARID4A:86 NR2C1:99 IL23R:113 PTPN12:131 ITGB1:152
MP0002272 abnormal nervous system	0.08022435	197	1.279e−04	3.581e−03	PLEC:15 ARC:49 NRCAM:96 KCNQ3:126 GRIK4:236 CACNA1G:287
MP0002086 abnormal extraembryonic tissu	−0.05156409	486	1.690e−04	4.469e−03	DLGAP5:10 CUBN:11 DAXX:12 NSD1:24 NANOG:65 BPTF:66
MP0000689 abnormal spleen morphology	−0.04830224	552	1.911e−04	4.548e−03	SPIC:40 DNMT1:74 ARID4A:86 GRB14:153 IKZF3:256 SERPINI2:302
MP0000313 abnormal cell death	−0.05242775	463	1.831e−04	4.548e−03	DAXX:12 TFAM:14 DNMT1:74 CTH:116 UBR5:127 ITGB1:152
MP0000749 muscle degeneration	0.17594437	36	2.677e−04	6.067e−03	PLEC:15 MYOF:127 CACNA1S:152 IGHMBP2:176 DES:220 PFKM:388
MP0000598 abnormal liver morphology	−0.04992233	482	2.856e−04	6.180e−03	XIRP2:26 ARID4A:86 CTH:116 PTPN12:131 ITGB1:152 GRB14:153
MP0001119 abnormal female reproductive	−0.06010604	295	5.021e−04	1.039e−02	AFP:53 ARID4A:86 SMCHD1:136 FANCG:202 SYCP1:216 BRCA1:300
MP0000716 abnormal immune system	−0.03467999	1013	5.457e−04	1.082e−02	SPIC:40 ARID4A:86 IL23R:113 PTPN12:131 NFATC3:156 CRLF2:158
MP0001145 abnormal male reproductive	−0.04806045	457	6.514e−04	1.240e−02	FANCG:202 SYCP1:216 EIF4G3:234 BRCA1:300 AGTPBP1:324 RNF17:386
MP0001970 abnormal pain threshold	0.07835581	152	9.666e−04	1.770e−02	ADCY1:32 CALCA:63 HOXB13:88 KIF1A:161 ADORA2A:269 HDAC4:291
MP0002723 abnormal immune serum	−0.03886331	649	1.269e−03	2.237e−02	IL23R:113 PTPN12:131 CRLF2:158 IL27RA:197 GCNT3:201 IKZF3:256
MP0002135 abnormal kidney morphology	−0.04537609	455	1.316e−03	2.237e−02	TET2:4 CUBN:11 ARID4A:86 IKZF3:256 BRCA1:300 NPHP3:306
MP0001800 abnormal humoral immune	−0.05077512	333	1.860e−03	3.053e−02	CRLF2:158 GCNT3:201 IKZF3:256 GABPB2:346 SH2D3C:405 REV3L:416
MP0004957 abnormal blastocyst morpholog	−0.09936407	82	1.978e−03	3.138e−02	NANOG:65 ITGB1:152 CHD8:367 AHCTF1:402 NUSAP1:429 LAMA1:434
MP0002084 abnormal developmental patter	−0.04782237	366	2.192e−03	3.366e−02	CUBN:11 DAXX:12 NSD1:24 ECSIT:63 NANOG:65 BPTF:66
MP0001486 abnormal startle reflex	0.08896226	96	2.762e−03	4.042e−02	LOXHD1:128 OTOF:272 APOE:461 NTSR1:518 DRD2:522 CACNA1B:716
MP0002876 abnormal thyroid physiology	−0.19828553	19	2.802e−03	4.042e−02	MED1:208 GHR:499 CGA:1054 AIRE:1447 GLIS3:1571 GFRA4:2849
MP0002080 prenatal lethality	−0.02699920	1335	2.898e−03	4.057e−02	CUBN:11 DAXX:12 TFAM:14 NSD1:24 SPIC:40 ECSIT:63
MP0004085 abnormal heartbeat	0.06806791	160	3.292e−03	4.353e−02	CALCA:63 IGHMBP2:176 HIRA:237 ADORA2A:269 CACNA1G:287 KCNH2:365
MP0003693 abnormal embryo hatching	−0.17361362	24	3.285e−03	4.353e−02	VEZT:103 KIF11:475 RBBP8:507 CDC25A:1235 CDCA8:1236 PARG:2207
MP0000579 abnormal nail morphology	0.18433457	21	3.496e−03	4.497e−02	KRT17:105 ITGB4:223 L1CAM:326 EGFR:686 KRT75:977 KRT6A:1248
MP0003121 genomic imprinting	−0.15587105	29	3.733e−03	4.556e−02	DNMT1:74 ARID4A:86 SMCHD1:136 MAGEL2:373 PLAGL1:420 PEG10:836
MP0002971 abnormal brown adipose	0.09686093	76	3.675e−03	4.556e−02	CACNA1S:152 GPR68:174 APOE:461 MOGAT2:737 RPTOR:1013 C3:1147
MP0002161 abnormal fertility/fecundity	−0.03068056	865	4.079e−03	4.854e−02	DLGAP5:10 CATSPER2:41 AFP:53 DNMT1:74 CLGN:84 ARID4A:86

tissue_specific Top pathways by non−permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
testis	−0.13832981	1678	1.777e−68	9.598e−67	CCDC148:15 MTPAP:25 ZBBX:28 ZYG11A:34 KIF27:46 CT55:48
leg.skin	0.13887164	288	1.077e−15	2.909e−14	PKP1:8 INAVA:22 BNC1:26 DSP:30 TRIM29:35 PSAPL1:67
EBV.lymphocyte	−0.08265165	753	7.214e−14	1.298e−12	DLGAP5:10 ATAD2:27 PARPBP:29 KIF18A:30 KIF2C:108 IL23R:113
suprapubic.skin	0.12212317	259	2.103e−11	2.839e−10	PKP1:8 BNC1:26 PSAPL1:67 AADACL2:89 NKPD1:99 KRT17:105
cerebellar.hemisphere	0.07787661	542	1.300e−09	1.404e−08	SYT2:18 ADCY1:32 ARHGAP44:90 MYT1:100 PPFIA4:107 TIAM1:111
cerebral.cortex	0.14936925	110	7.057e−08	6.351e−07	ADGRB1:39 KIF1A:161 DPYSL4:262 POU6F2:425 HECW1:551 MCHR1:581
cerebellum	0.07260181	409	7.177e−07	5.234e−06	TRANK1:7 SYT2:18 GLRA4:73 MYT1:100 PPFIA4:107 TIAM1:111
skeletal.muscle	0.09025646	258	7.753e−07	5.234e−06	MYH2:11 MYBPC2:144 CASQ1:147 CACNA1S:152 MYH1:239 PYGM:292
Brodmann.area.9	0.09778598	185	5.253e−06	3.152e−05	NRCAM:96 KCNQ3:126 NECAB1:198 OLFM1:356 POU6F2:425 GPR26:479
esophagus.mucosa	0.07743980	263	1.875e−05	1.012e−04	PKP1:8 BNC1:26 ADH7:37 LAD1:42 FAM83H:124 RNF222:194
pancreas	−0.09460248	118	4.097e−04	2.011e−03	TMED6:188 CATSPERB:246 SERPINI2:302 ERP27:332 FBXW12:345 G6PC2:555
nucleus.accumbens	0.09733599	105	5.980e−04	2.484e−03	INSYN2A:113 CACNA1E:166 OTOF:272 JAKMIP1:276 SV2C:414 ARPP21:654
vagina	0.09205920	119	5.542e−04	2.484e−03	PKP1:8 BNC1:26 RNF222:194 SLURP1:253 LCE3D:304 NOD2:312
putamen	0.17511245	17	1.248e−02	4.813e−02	RGS9:52 SLC18A3:251 DIPK1C:623 OPALIN:1651 CORT:2933 LRRC10B:3207
endocervix	0.07506821	79	2.145e−02	7.723e−02	MRGPRE:1 ELFN1:41 KIF26A:66 ZNF516:93 SPON2:286 MLPH:417
greater.omentum	0.10652372	38	2.325e−02	7.848e−02	BNC1:26 AADACL4:383 ITLN1:422 THRSP:630 ADAMTS4:779 FAM89A:952
hypothalamus	0.07156423	78	2.935e−02	9.322e−02	SYT6:275 PNMA6F:477 PNMA5:688 RTL1:782 KISS1R:879 DNER:975
tibial.artery	0.05582169	113	4.124e−02	1.237e−01	SDK1:20 PPP1R12B:142 ADARB1:157 OR51E2:230 TNC:303 INHBA:349
amygdala	0.18028731	9	6.114e−02	1.572e−01	TNR:440 PTPRZ1:493 PCDH15:3256 NEUROD6:6152 SLC17A7:6846 SLC38A8:7145
C1.spinal.cord	0.03971908	194	5.831e−02	1.572e−01	ACSBG1:114 CDH20:208 MAGEC3:436 CHADL:562 TTYH2:589 PLAAT3:591
sigmoid.colon	0.07755972	51	5.580e−02	1.572e−01	DES:220 HDAC4:291 TACR2:335 MRGPRD:367 NTSR1:518 GREM2:812
left.ventricle	0.06413733	68	6.810e−02	1.672e−01	MYL3:256 LMOD2:328 TNNT2:380 MYOM2:769 TENM2:1212 CKMT2:1281
peyers.patch	0.03553920	199	8.630e−02	1.970e−01	SLC17A4:9 TRPM5:13 MGAM2:118 KRT20:129 TREH:131 EPS8L3:133
transverse.colon	0.03834125	169	8.754e−02	1.970e−01	SLC17A4:9 DSG2:104 KRT20:129 EPS8L3:133 RNF186:139 MUC2:192
fallopian.tube	−0.06111042	60	1.023e−01	2.126e−01	BCHE:150 ATP8B4:268 ADAMTS3:295 CCDC17:460 TUBA4B:463 CCDC198:863
prostate	−0.06637422	52	9.841e−02	2.126e−01	CPAMD8:58 TTC6:330 SHROOM1:445 MSMB:568 TNFSF15:946 MKX:970
blood	0.02271908	347	1.515e−01	3.029e−01	HRH2:130 FFAR2:150 STX11:214 FUT7:224 TUBB1:332 PIK3R5:363
esophagogastric.junction	−0.12399366	9	1.978e−01	3.815e−01	F2RL2:1282 RTL3:2797 NKX6−1:4194 GADL1:5652 ADCY5:6799 COL4A5:7006
stomach	0.03546474	99	2.244e−01	4.040e−01	MYH13:54 PSAPL1:67 EPS8L3:133 CAPN8:171 VWA2:372 TM4SF5:379
eye.development	0.04254519	69	2.229e−01	4.040e−01	NOTCH1:258 TKT:523 BMP7:1078 TBX5:1425 CRX:1446 FGFR2:1635
hippocampus.proper	0.09538935	13	2.339e−01	4.074e−01	GRP:928 LCN1:1666 CTXND1:1693 NEUROD6:6152 OLIG2:6296 CABP7:6700
caudate.nucleus	0.06345781	28	2.456e−01	4.144e−01	GPR37L1:12 MLC1:40 TAC1:1761 PDE1B:2622 LRRC10B:3207 VAX1:3381
subcutaneous.adipose	0.03595714	82	2.618e−01	4.284e−01	GPD1:282 FASN:514 THRSP:630 F13A1:684 ACACB:896 PRG2:1036
Brodmann.area.24	0.05357897	33	2.873e−01	4.564e−01	DOK6:1564 UPP2:2270 MT3:2809 FAM189A1:2974 SHANK1:3151 GRIN3A:3627
bladder	0.05376583	30	3.086e−01	4.761e−01	UGT1A6:1295 PSCA:1571 PADI3:1835 KRT13:2204 ACSM6:2275 ABCC4:2898
transformed.skin.fibroblast	0.01656334	276	3.488e−01	5.232e−01	BNC1:26 ZNF281:81 MYOF:127 CLMP:143 MME:145 COL6A1:158
esophagus.muscularis.mucosa	−0.04764841	28	3.833e−01	5.594e−01	CCDC69:740 F2RL2:1282 PRUNE2:1425 COL4A6:2457 CST5:3622 CNTNAP3:4029
aorta	0.01798357	156	4.410e−01	6.266e−01	NAV1:17 LGR6:51 MTUS2:243 CYP4X1:330 PDGFA:635 GABRR1:637
tibial.nerve	0.01462615	205	4.739e−01	6.561e−01	SLC24A4:169 ITGB4:223 ENTPD2:298 MYOC:389 INF2:410 OR6B3:501
breast	0.04166667	20	5.191e−01	6.663e−01	TNN:252 THRSP:630 KRT5:1910 NPY2R:2176 PLIN1:3226 ADIPOQ:3410