Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_KERATINIZATION	-0.20873189	202	1.659e-24	1.077e-20	EVPL:5 KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	-0.25072635	126	2.625e-22	8.523e-19	EVPL:5 KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86
DODD_NASOPHARYNGEAL_CARCINOMA_DN	0.07281056	1273	4.423e-18	9.574e-15	KIF18A:2 FGD6:14 TFAM:29 LRPPRC:41 ZNF557:45 TPX2:52
FISCHER_DREAM_TARGETS	0.08327049	920	1.632e-17	2.649e-14	KIF18A:2 OBI1:11 TRIM59:33 CENPC:51 TPX2:52 WDR76:54
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	0.10155905	602	2.198e-17	2.855e-14	KIF18A:2 ZNF644:25 TFAM:29 LRPPRC:41 WDR76:54 NIFK:58
JOHNSTONE_PARVB_TARGETS_3_DN	0.08421993	793	9.888e-16	1.070e-12	KIF18A:2 SENP7:7 OBI1:11 CEP350:20 TFAM:29 UBAP2:47
REACTOME_CELL_CYCLE	0.08768495	647	3.384e-14	3.140e-11	DAXX:1 KIF18A:2 CENPT:8 UIMC1:10 ESCO1:32 CENPC:51
ZHANG_BREAST_CANCER_PROGENITORS_UP	0.09460831	414	4.419e-11	3.188e-08	SYDE2:3 TRIM59:33 SLF1:60 CTH:62 KIF2C:64 SMCHD1:74
REACTOME_CELL_CYCLE_CHECKPOINTS	0.11733024	268	4.036e-11	3.188e-08	KIF18A:2 CENPT:8 UIMC1:10 CENPC:51 KIF2C:64 PHF20:65
WP_GPCRS_CLASS_A_RHODOPSINLIKE	-0.11865440	249	1.197e-10	6.793e-08	P2RY4:11 SSTR4:67 PTAFR:70 BDKRB1:238 SSTR3:294 ACKR3:299
HAMAI_APOPTOSIS_VIA_TRAIL_UP	0.07569126	624	1.255e-10	6.793e-08	KIF18A:2 OBI1:11 CEP350:20 TASOR:23 ZNF644:25 CENPC:51
SHEDDEN_LUNG_CANCER_POOR_SURVIVAL_A6	0.08967520	440	1.243e-10	6.793e-08	KIF18A:2 LRPPRC:41 GLMN:48 TPX2:52 WDR76:54 KIF2C:64
KINSEY_TARGETS_OF_EWSR1_FLII_FUSION_UP	0.05499208	1210	1.611e-10	8.046e-08	KIF18A:2 OBI1:11 TPX2:52 WDR76:54 NIFK:58 SLF1:60
MARTENS_TRETINOIN_RESPONSE_UP	-0.06711415	782	2.082e-10	9.656e-08	PIK3R5:23 CEP170B:26 MUC2:32 RNF186:36 CARD14:38 TRIM29:53
RODRIGUES_THYROID_CARCINOMA_ANAPLASTIC_U	0.07194496	673	2.291e-10	9.917e-08	KIF18A:2 ZNF644:25 ATP13A3:35 TPX2:52 NIFK:58 RESF1:76
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.07182736	664	3.189e-10	1.294e-07	UBAP2:47 TPX2:52 WDR76:54 KIF2C:64 TTK:84 DZIP3:85
REACTOME_CELL_CYCLE_MITOTIC	0.08034050	520	4.058e-10	1.550e-07	KIF18A:2 CENPT:8 ESCO1:32 CENPC:51 TPX2:52 KIF2C:64
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.25677589	47	1.131e-09	4.079e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUFS5:59 TMEM70:
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.16613187	112	1.272e-09	4.284e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUFS5:
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.18503144	90	1.319e-09	4.284e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUFS5:
PUJANA_BRCA1_PCC_NETWORK	0.04611602	1515	2.778e-09	8.590e-07	DAXX:1 TFAM:29 ATP13A3:35 GLMN:48 CENPC:51 TPX2:52
WONG_MITOCHONDRIA_GENE_MODULE	0.11518508	214	6.580e-09	1.942e-06	NDUFB5:6 NDUFB10:12 TFAM:29 NDUFB8:31 ATP13A3:35 LRPPRC:41
GRAESSMANN_APOPTOSIS_BY_DOXORUBICIN_DN	0.04251398	1698	8.005e-09	2.260e-06	MGA:17 CRLF2:21 ZNF644:25 PLA2R1:44 PHF20:65 PHF3:72
KEGG_OXIDATIVE_PHOSPHORYLATION	0.15484821	114	1.139e-08	3.083e-06	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 ATP5PB:1
REACTOME_MITOTIC_PROMETAPHASE	0.11708675	195	1.778e-08	4.620e-06	KIF18A:2 CENPT:8 CENPC:51 KIF2C:64 NDC80:142 AKAP9:149
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.17225577	89	1.966e-08	4.911e-06	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 ATP5PB:155 NDUFS3:22
KIM_WT1_TARGETS_DN	0.07765376	445	2.116e-08	4.989e-06	KIF18A:2 FGD6:14 CEP350:20 CENPC:51 KIF2C:64 PHF3:72
MOOTHA_VOXPHOS	0.17473325	86	2.151e-08	4.989e-06	NDUFB5:6 NDUFB8:31 NDUFS5:59 ATP5PB:155 NDUFS3:224 ATP5PD:22
REACTOME_COMPLEX_I_BIOGENESIS	0.23307818	48	2.322e-08	5.201e-06	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUFS5:59 NDUFA11:
REACTOME_CLASS_A_1_RHODOPSIN_LIKE_RECEPT	-0.08958244	324	3.130e-08	6.775e-06	RXFP4:3 P2RY4:11 SSTR4:67 PTAFR:70 TACR2:184 GPR132:188
REACTOME_SENSORY_PERCEPTION	-0.06642596	596	3.361e-08	7.040e-06	CALHM1:46 PCDH15:57 OTOF:159 OR10S1:217 OR10R2:225 OR5M10:26
REACTOME_M_PHASE	0.08204169	384	3.631e-08	7.368e-06	KIF18A:2 CENPT:8 CENPC:51 KIF2C:64 NUP205:87 TPR:97
SHEN_SMARCA2_TARGETS_UP	0.07906757	409	4.391e-08	8.641e-06	CEP350:20 TMEM126B:43 CENPC:51 PHF3:72 AGGF1:96 TRMT1L:106
REACTOME_SIGNALING_BY_GPCR	-0.06074576	682	7.135e-08	1.363e-05	RXFP4:3 P2RY4:11 ARHGEF11:21 PIK3R5:23 SSTR4:67 PTAFR:70
WONG_EMBRYONIC_STEM_CELL_CORE	0.08772903	318		1.461e-05	NDUFB10:12 NDUFB8:31 NIFK:58 TTK:84 NDUFA11:108 NDC80:142
WP_OXIDATIVE_PHOSPHORYLATION	0.21587730	51		1.746e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 ATP5PB:1
ROSTY_CERVICAL_CANCER_PROLIFERATION_CLUS	0.13120776	138		1.839e-05	TPX2:52 KIF2C:64 TTK:84 NDC80:142 KIF4A:220 DLGAP5:274
NUYTTEN_EZH2_TARGETS_DN	0.05082026	959		1.917e-05	NDUFB10:12 ZNF644:25 TFAM:29 TPX2:52 WDR76:54 SLF1:60
FEVR_CTNNB1_TARGETS_DN	0.06758516	529		1.917e-05	KIF18A:2 TFAM:29 TTK:84 LARP4:118 CD2AP:119 GRSF1:123
DEACTOME THE OUTDIO ACID TOA OVOLE AND D	0.40005504	400	4.070 07	0.000	NOUTEDS O NOUTED 40 40 NOUTED 04 L DDDDD 44 TNEW 400D 40 NOUTED 5

DisGeNET Top pathways by non-permulation

1.373e-07 2.229e-05 NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUFS5:59

DSP:49 DSG2:364 MPO:431 FLNC:441 DES:451 TTN:480

PRTN3:229 NOD2:289 CYBB:811 NCF2:945 NCF1:1055 PTPN22:1299

REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R 0.12005591

Conduction disorder of the heart

Granulomatosis

-0.10081556

-0.29561828

Geneset	stat	num.genes	pval	p.adj	gene.vals
Mitochondrial Diseases	0.07876704	363	2.883e-07	2.831e-03	NDUFB5:6 NDUFB10:12 NDUFB8:31 LRPPRC:41 TMEM126B:43 NDUFS5:59
Increased CSF lactate	0.16384078	56	2.249e-05	4.417e-02	LRPPRC:41 TMEM126B:43 NDUFA11:108 FASTKD2:143 TIMMDC1:211 NDUFS3:224
Left ventricular noncompaction cardiomyo	-0.22031450	31	2.191e-05	4.417e-02	PLEC:9 DSP:49 MUL1:331 TTN:480 PRKN:605 MYH7B:1066
Palmoplantar Keratosis	-0.12860891	95	1.508e-05	4.417e-02	PLEC:9 CARD14:38 DSP:49 KRT17:80 PKP1:120 ALOX12B:122
Primary microcephaly	0.12050223	110	1.296e-05	4.417e-02	NIPBL:124 TRMT10A:194 CEP152:206 XRCC4:272 SASS6:355 KNL1:439
Erythrokeratoderma	-0.18748458	41	3.290e-05	5.385e-02	CARD14:38 DSP:49 KRT17:80 ALOX12B:122 FAM83G:285 RHBDF2:302
Increased serum lactate	0.11595816	99	6.818e-05	8.369e-02	LRPPRC:41 TMEM70:101 FASTKD2:143 TWNK:178 NDUFS3:224 MRPL3:243
Parakeratosis	-0.28835621	16	6.520e-05	8.369e-02	CARD14:38 DSP:49 TNC:60 NLRP1:300 RHBDF2:302 TRPV3:1493
Epidermolysis Bullosa Simplex	-0.23341254	23	1.069e-04	1.166e-01	PLEC:9 ITGB4:13 KRT80:78 KRT17:80 TGM5:249 KRT9:413
Hypotrichosis	-0.14484698	57	1.566e-04	1.398e-01	PKP1:120 ALOX12B:122 TGM1:190 ABCA12:368 KRT71:502 DSG4:671
Seckel syndrome	0.18787626	34	1.505e-04	1.398e-01	CEP152:206 DNA2:473 CENPJ:475 DNMT1:654 CENPE:781 ATR:783
Pachyonychia Congenita	-0.30902012	12	2.101e-04	1.719e-01	KRT80:78 KRT17:80 KRT6B:372 KRT9:413 SLURP1:1017 KRT6A:1244
Anemia, Macrocytic	0.18542640	33	2.283e-04	1.724e-01	SFXN4:263 TET2:348 SF3B1:702 ADH1B:776 RPL26:920 RPS26:1416
Psychomotor retardation, mild	0.23860386	19	3.179e-04	1.856e-01	RNF168:66 CEP152:206 CENPJ:475 CDC6:633 CENPE:781 ATR:783
Acanthosis	-0.18134126	33	3.130e-04	1.856e-01	CARD14:38 KRT13:86 ALOX12B:122 TGM1:190 NLRP1:300 GJB4:433
Amphetamine-Related Disorders	-0.12343500	70	3.591e-04	1.856e-01	MYO5B:353 ZNF423:402 HTR6:440 SLC6A3:558 PRDM2:610 HTR1B:806
Amphetamine Abuse	-0.12343500	70	3.591e-04	1.856e-01	MYO5B:353 ZNF423:402 HTR6:440 SLC6A3:558 PRDM2:610 HTR1B:806
Amphetamine Addiction	-0.12343500	70	3.591e-04	1.856e-01	MYO5B:353 ZNF423:402 HTR6:440 SLC6A3:558 PRDM2:610 HTR1B:806
Mild global developmental delay	0.23860386	19	3.179e-04	1.856e-01	RNF168:66 CEP152:206 CENPJ:475 CDC6:633 CENPE:781 ATR:783
Glycogen Storage Disease Type V	-0.27163278	14	4.334e-04	2.128e-01	SLC2A4:178 PYGM:309 ATP2A1:774 MADD:867 AMPD1:878 PYGL:944
Absent earlobe	0.28887269	12	5.305e-04	2.429e-01	CEP152:206 CENPJ:475 CENPE:781 ATR:783 RBBP8:899 PLK4:1051
Cornelia De Lange Syndrome	0.18884307	28	5.442e-04	2.429e-01	NIPBL:124 AFF4:380 CENPJ:475 ATR:783 ESCO2:1248 NAALADL2:1294
Arthrogryposis	-0.05783313	297	6.358e-04	2.715e-01	PLEC:9 ITGB4:13 OFD1:59 TSC1:79 CHRNA4:183 COL6A1:192
NADH:Q(1) Oxidoreductase deficiency	0.19555160	25	7.146e-04	2.825e-01	NDUFB10:12 TMEM126B:43 NDUFA11:108 TIMMDC1:211 NDUFS3:224 NDUFAF1:32
Poor school performance	0.03286879	946	7.191e-04	2.825e-01	NSD1:5 MAGEL2:36 CLCNKA:75 CLCNKB:90 SRCAP:93 TPR:97
Coughing	-0.10457802	86	8.106e-04	3.062e-01	PER2:4 DSP:49 TSC1:79 RTEL1:170 TACR2:184 PRTN3:229
Hyperkeratosis, Epidermolytic	-0.24087328	16	8.511e-04	3.095e-01	DSP:49 KRT80:78 ALOX12B:122 TGM1:190 KRT9:413 GJB4:433
Monilethrix	-0.42754797	5	9.294e-04	3.260e-01	KRT80:78 DSG4:671 KRT81:921 KRT86:2405 KRT83:2689 NA
Periodic syndrome	0.41850746	5	1.191e-03	4.033e-01	TNF:515 XBP1:1018 NLRP3:1456 MEFV:1800 TNFRSF1A:2961 NA
Hypertrichosis	0.13333547	49	1.249e-03	4.088e-01	NDUFS3:224 NDUFA12:310 BMS1:929 NDUFA10:1004 SRD5A3:1049 INSR:1200
Junctional split	-0.37872272	6	1.315e-03	4.164e-01	PLEC:9 ITGB4:13 LAMC2:745 ITGA6:1729 LAMB3:2165 LAMA3:8811.5
Bulbous nasal tip	0.10253796	80	1.536e-03	4.308e-01	AP4E1:15 SRCAP:93 JMJD1C:126 SEC24C:413 DOCK6:448 DYRK1A:565
Bulbous nose	0.10253796	80	1.536e-03	4.308e-01	AP4E1:15 SRCAP:93 JMJD1C:126 SEC24C:413 DOCK6:448 DYRK1A:565
Potato nose	0.10253796	80	1.536e-03	4.308e-01	AP4E1:15 SRCAP:93 JMJD1C:126 SEC24C:413 DOCK6:448 DYRK1A:565
T-lymphocyte immunodeficiency	-0.37444618	6	1.491e-03	4.308e-01	CD3E:214 SIPA1:545 LBR:911 RAG1:1117 SFTPA1:2368 SMARCAL1:8811.5
Dull intelligence	0.03111849	911	1.653e-03	4.386e-01	NSD1:5 MAGEL2:36 CLCNKA:75 CLCNKB:90 SRCAP:93 NIPBL:124
Low intelligence	0.03111849	911	1.653e-03	4.386e-01	NSD1:5 MAGEL2:36 CLCNKA:75 CLCNKB:90 SRCAP:93 NIPBL:124
Acidosis, Lactic	0.07253296	153	1.996e-03	5.100e-01	TFAM:29 LRPPRC:41 TMEM126B:43 TMEM70:101 NDUFA11:108 FASTKD2:143

customGeneSet Top pathways by non-permulation

2.100e-03 5.100e-01

2.133e-03 5.100e-01

Geneset	stat	num.genes	pval	p.adj	gene.vals
HumanLocalAdaptionDietAll	-0.06950067	13	4.367e-01	8.580e-01	SLC22A5:2454 AS3MT:8811.5 GPX1:8811.5 GPX3:8811.5 CELF1:8811.5 SEPSECS:8811.5
NAFLDGWAS	0.01515152	15	8.580e-01	8.580e-01	ADH1B:776 MTARC1:1149 INSR:1200 TOR1B:2862 TM6SF2:9694.5 APOE:9694.5
expressionDirectionalSelection	0.03316327	42	6.401e-01	8.580e-01	HLA-DQA1:379 TLR10:521 SCAPER:609 UBE2U:1672 HLA-DQA2:2216 ZBTB12:2383
NA	NA	NA	NA	NA	NA NA NA NA NA
NA.1	NA	NA	NA	NA	NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA
NA.14	NA	NA	NA	NA	NA NA NA NA NA
NA.15	NA	NA	NA	NA	NA NA NA NA NA
NA.16	NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA
NA.18	NA	NA	NA	NA	NA NA NA NA NA
NA.19	NA	NA	NA	NA	NA NA NA NA NA
NA.20	NA	NA	NA	NA	NA NA NA NA NA
NA.21	NA	NA	NA	NA	NA NA NA NA NA
NA.22	NA	NA	NA	NA	NA NA NA NA NA
NA.23	NA	NA	NA	NA	NA NA NA NA NA
NA.24	NA	NA	NA	NA	NA NA NA NA NA
NA.25	NA	NA	NA	NA	NA NA NA NA NA
NA.26	NA	NA	NA	NA	NA NA NA NA NA
NA.27	NA	NA	NA	NA	NA NA NA NA NA
NA.28	NA	NA	NA	NA	NA NA NA NA NA
NA.29	NA	NA	NA	NA	NA NA NA NA NA
NA.30	NA	NA	NA	NA	NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA
NA.35	NA	NA	NA	NA	NA NA NA NA NA NA

GO_Biological_Process_2023 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Intermediate Filament Organization (GO:0	-0.30511671	65	1.877e-17	1.015e-13	KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86 PKP1:120
IADH Dehydrogenase Complex Assembly (GO:	0.26962338	49	6.744e-11	1.215e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUFS5:59 NDUFA11:108
Mitochondrial Respiratory Chain Complex	0.26962338	49	6.744e-11	1.215e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUFS5:59 NDUFA11:108
Mitochondrial Respiratory Chain Complex	0.20256638	82	2.370e-10	3.203e-07	NDUFB5:6 NDUFB10:12 NDUFB8:31 TMEM126B:43 NDUFS5:59 NDUFA11:108
Aerobic Electron Transport Chain (GO:001	0.19732128	64	4.883e-08	4.077e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFS3:224 NDUFAF1:321
Mitochondrial ATP Synthesis Coupled Elec	0.19621477	65	4.579e-08	4.077e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFS3:224 NDUFA12:310
Oxidative Phosphorylation (GO:0006119)	0.20495350	59	5.278e-08	4.077e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 TEFM:129
Proton Motive Force-Driven Mitochondrial	0.22111199	50	6.439e-08	4.352e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 ATP5PB:155
Cellular Respiration (GO:0045333)	0.17000705	82	1.055e-07	6.339e-05	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 NDUFS3:224
Proton Motive Force–Driven ATP Synthesis	0.20299367	54	2.508e-07	1.356e-04	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 ATP5PB:155
Supramolecular Fiber Organization (GO:00	-0.08529381	305	3.344e-07	1.644e-04	KRT20:47 DSP:49 KRT80:78 KRT17:80 KRT13:86 HIP1R:194
Mitochondrial Electron Transport, NADH T	0.25140340	33	5.831e-07	2.627e-04	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFS3:224 NDUFAF1:321
Translation (GO:0006412)	0.09297589	208	4.027e-06	1.675e-03	MARS1:91 FASTKD2:143 SRBD1:239 MRPL3:243 ZAR1:282 RARS1:317
Aerobic Respiration (GO:0009060)	0.16778083	57	1.193e-05	4.607e-03	NDUFB5:6 NDUFB10:12 NDUFB8:31 NDUFS5:59 NDUFA11:108 TEFM:129
Regulation Of DNA Metabolic Process (GO:	0.11312362	121	1.774e-05	6.394e-03	UIMC1:10 OBI1:11 ESCO1:32 SLF1:60 SLF2:189 SMG6:347
Muscle Contraction (GO:0006936)	-0.12610523	92	2.967e-05	1.003e-02	ARHGEF11:21 CHRNB2:39 TACR2:184 MYOF:371 LMOD2:382 MYH2:420
Epidermis Development (GO:0008544)	-0.13092134	84	3.415e-05	1.086e-02	EVPL:5 DSP:49 KRT15:204 HOXB13:221 OVOL3:223 ALDH3A2:227
Mitochondrial Gene Expression (GO:014005	0.11717528	102	4.422e-05	1.328e-02	TFAM:29 TEFM:129 FASTKD2:143 TWNK:178 TFB2M:231 MRPL3:243
tRNA Methylation (GO:0030488)	0.18435309	36	1.299e-04	3.697e-02	TRMT1L:106 TRMT61B:111 TRMT10A:194 THADA:297 MTO1:394 TRMT10B:494
Monoatomic Cation Transmembrane Transpor	-0.06661224	277	1.436e-04	3.698e-02	KCNN3:45 CACNA1G:96 P2RX7:134 SLC6A18:175 KCNH3:181 SLC24A4:269
Peptide Cross-Linking (GO:0018149)	-0.22441734	24	1.418e-04	3.698e-02	EVPL:5 DSP:49 TGM1:190 TGM5:249 TGM2:254 COL3A1:649
Regulation Of DNA Replication (GO:000627	0.12776350	73	1.624e-04	3.817e-02	OBI1:11 ESCO1:32 BRPF3:163 STON1:452 DNA2:473 USP37:501
Regulation Of Heart Rate By Cardiac Cond	-0.17263087	40	1.590e-04	3.817e-02	DSP:49 CACNA1G:96 DSG2:364 KCNH2:685 CACNB2:797 KCNE5:1294
Cytoplasmic Translation (GO:0002181)	0.12602212	74	1.802e-04	4.061e-02	RPL30:617 RPL23A:722 FTSJ1:764 RPL26L1:890 RPL26:920 RPS9:1135
Regulation Of Transcription By RNA Polym	0.02635899	1924	2.013e-04	4.355e-02	NSD1:5 ZNF644:25 MAGEL2:36 ZSCAN29:42 ZNF557:45 HCFC2:61
Peptide Biosynthetic Process (GO:0043043	0.09097471	137	2.423e-04	5.038e-02	SRBD1:239 MRPL3:243 ZAR1:282 ZAR1L:350 MRPL42:582 RPL30:617
Chemical Synaptic Transmission (GO:00072	-0.06486298	263	3.073e-04	5.684e-02	CHRNB2:39 GABRR3:161 RIMBP2:171 CHRNA4:183 GRIN3B:208 CORT:240
Long-Chain Fatty Acid Biosynthetic Proce	-0.21261088	24	3.123e-04	5.684e-02	ALOX12B:122 ACSBG1:165 GSTM4:544 ALOXE3:800 GSTM2:1329 ALOX5:1436
Mitochondrial RNA Metabolic Process (GO:	0.23270548	20	3.154e-04	5.684e-02	TFAM:29 TEFM:129 FASTKD2:143 TWNK:178 TFB2M:231 POLRMT:797
Potassium Ion Transmembrane Transport (G	-0.09051281	135	2.887e-04	5.684e-02	KCNN3:45 KCNH3:181 SLC24A4:269 KCNG2:471 KCNV2:572 KCNB2:580
Adenylate Cyclase–Modulating G Protein–C	-0.08262808	158	3.473e-04	6.057e-02	PSAPL1:2 CALCA:84 ADGRG4:140 GPR78:200 CORT:240 GRM8:263
Positive Regulation Of Cell Cycle Proces	0.09645366	114	3.813e-04	6.443e-02	TPR:97 NCAPD3:128 NDC80:142 ZNF16:186 USP19:284 SPAG5:351
Gene Expression (GO:0010467)	0.06299172	266	4.242e-04	6.951e-02	NOL9:83 TPR:97 FASTKD2:143 CASC3:180 RBM6:187 SRBD1:239
Mitochondrial Translation (GO:0032543)	0.10323442	97	4.487e-04	7.136e-02	FASTKD2:143 MRPL3:243 MRPL1:370 MRPL42:582 MRPS28:600 MTG1:731
Positive Regulation Of DNA Metabolic Pro	0.09934479	104	4.718e-04	7.289e-02	UIMC1:10 RNF168:66 SMCHD1:74 BRPF3:163 RNF8:374 STON1:452
Long-Chain Fatty Acid Metabolic Process	-0.11637930	75	4.980e-04	7.480e-02	ALOX12B:122 ACSBG1:165 SLC27A2:472 GSTM4:544 ALOXE3:800 ELOVL2:1077
tRNA Modification (GO:0006400)	0.12277072	67	5.154e-04	7.532e-02	TRMT10A:194 THADA:297 MTO1:394 TYW5:593 DTWD1:743 FTSJ1:764
Hepoxilin Biosynthetic Process (GO:00511	-0.37628755	7	5.653e-04	7.837e-02	ALOX12B:122 ALOXE3:800 GSTM2:1329 ALOX15:1514 GSTM1:1776 ALOX15B:1836
Hepoxilin Metabolic Process (GO:0051121)	-0.37628755	7	5.653e-04	7.837e-02	ALOX12B:122 ALOXE3:800 GSTM2:1329 ALOX15:1514 GSTM1:1776 ALOX15B:1836
Mitotic Sister Chromatid Segregation (GO	0.09424676	111	6.130e-04	8.286e-02	KIF18A:2 TPX2:52 KIF2C:64 NCAPD3:128 NDC80:142 KIF22:168

DAXX:1 NSD1:5 TFAM:29 LTN1:50 PTPRB:56 SMCHD1:74

7.516e-07 3.578e-04

MP0002080 prenatal lethality

0.04485843

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

Wir 0002000 promatar formatity	0.01100010	1000	7.0100 07	0.0700 01	D/V/X.1 140D 1.0 1174W.20 E1141.00 1 11 14D.00 GMG11D 1.7 1
MP0001970 abnormal pain threshold	-0.08582857	152	3.007e-04	3.578e-02	CHRNB2:39 SSTR4:67 MRGPRD:83 CALCA:84 PTPRZ1:110 P2RX7:134
MP0002085 abnormal embryonic tissue	0.04545307	654	1.558e-04	3.578e-02	DAXX:1 NSD1:5 TFAM:29 CHD8:81 ADAMTS20:113 ARL13B:179
MP0002086 abnormal extraembryonic tissu	0.04970310	486	2.885e-04	3.578e-02	DAXX:1 NSD1:5 PTPRB:56 SMCHD1:74 NFATC3:125 SETD2:261
MP0002088 abnormal embryonic growth/wei	0.05716094	343	3.826e-04	3.643e-02	DAXX:1 PTPRB:56 NFATC3:125 SETD2:261 CDC25A:286 AFF4:380
MP0003121 genomic imprinting	0.18590573	28	6.768e-04	5.370e-02	MAGEL2:36 SMCHD1:74 ATRX:620 DNMT1:654 CITED1:761 PEG3:856
MP0003984 embryonic growth retardation	0.05325063	336	1.049e-03	6.241e-02	DAXX:1 PTPRB:56 NFATC3:125 SETD2:261 CDC25A:286 AFF4:380
MP0001697 abnormal embryo size	0.04885170	405	1.043e-03	6.241e-02	DAXX:1 PTPRB:56 NFATC3:125 PXN:275 VCAM1:290 ITGB8:298
MP0005380 embryogenesis phenotype	0.04664860	417	1.508e-03	7.177e-02	DAXX:1 NLRP5:55 PTPRB:56 NFATC3:125 KIF22:168 SETD2:261
MP0001672 abnormal embryogenesis/ devel	0.04664860	417	1.508e-03	7.177e-02	DAXX:1 NLRP5:55 PTPRB:56 NFATC3:125 KIF22:168 SETD2:261
MP0003077 abnormal cell cycle	0.07294734	152	2.125e-03	9.194e-02	CDC25A:286 GIGYF2:349 NUMA1:420 MED1:435 NUSAP1:469 ITGB1:549
MP0000579 abnormal nail morphology	-0.19055801	21	2.536e-03	1.006e-01	ITGB4:13 KRT17:80 KRT6B:372 GLI3:651 DSG4:671 ATP2A2:1106
MP0000313 abnormal cell death	0.03890703	463	5.499e-03	2.014e-01	DAXX:1 TFAM:29 CTH:62 XRCC4:272 CDC25A:286 RNF8:374
MP0001929 abnormal gametogenesis	0.03820573	470	6.054e-03	2.058e-01	ADCY10:19 UBR2:164 KL:172 EIF4G3:218 NAT2:222 GHR:325
MP0000598 abnormal liver morphology	0.03679093	482	7.505e-03	2.382e-01	CTH:62 APOA1:88 GRB14:196 PECAM1:280 ASAH1:304 GHR:325
MP0003635 abnormal synaptic transmissio	-0.03804763	425	9.033e-03	2.687e-01	CHRNB2:39 TNC:60 ARC:75 PTPRZ1:110 KCNH3:181 NCDN:182
MP0002429 abnormal blood cell	0.02372926	1241	1.073e-02	3.005e-01	CRLF2:21 LRRK2:49 APOA1:88 CD2AP:119 NFATC3:125 SIRPA:167
MP0002572 abnormal emotion/affect behav	-0.04312037	287	1.374e-02	3.270e-01	CHRNB2:39 TNC:60 ARC:75 P2RX7:134 CHRNA4:183 GRIN3B:208
MP0003943 abnormal hepatobiliary system	0.09661510	55	1.353e-02	3.270e-01	MED1:435 CBFB:651 SLC20A1:660 GATA6:936 XBP1:1018 FOXM1:1516
MP0004197 abnormal fetal growth/weight/	0.05498354	177	1.266e-02	3.270e-01	NIPBL:124 BAZ1B:197 XRCC4:272 TRPM6:305 GHR:325 SENP1:537
MP0001529 abnormal vocalization	-0.15769015	19	1.746e-02	3.291e-01	DHCR7:621 LBR:911 E2F4:923 DRD2:1224 WFS1:2041 CHRM4:2361
MP0002161 abnormal fertility/fecundity	0.02516570	862	1.867e-02	3.291e-01	ADCY10:19 CATSPER2:26 MAGEL2:36 NLRP5:55 NFATC3:125 ATXN2:162
MP0002084 abnormal developmental patter	0.03711546	364	1.774e-02	3.291e-01	DAXX:1 NSD1:5 PTPRB:56 CHD8:81 ARL13B:179 SETD2:261
MP0003122 maternal imprinting	0.17446693	16	1.579e-02	3.291e-01	MAGEL2:36 PEG3:856 PLAGL1:883 SGCE:2422 IGF2:3241 ARID4A:3336
MP0000653 abnormal sex gland	0.03197622	520	1.620e-02	3.291e-01	MAGEL2:36 ATXN2:162 UBR2:164 KL:172 AFP:208 EIF4G3:218
MP0010094 abnormal chromosome stability	0.08490709	65	1.841e-02	3.291e-01	XRCC4:272 RNF8:374 FANCG:456 MBD1:558 AICDA:665 CENPE:781
MP0009745 abnormal behavioral response	-0.04922266	205	1.659e-02	3.291e-01	PER2:4 CALCA:84 CACNA1G:96 KCNH3:181 NCDN:182 CHRNA4:183
MP0003699 abnormal female reproductive	0.03397296	426	1.961e-02	3.334e-01	MAGEL2:36 NLRP5:55 UBR2:164 AFP:208 DLGAP5:274 ZAR1:282
MP0000266 abnormal heart morphology	0.02603671	712	2.465e-02	3.666e-01	TFAM:29 PTPRB:56 CD2AP:119 NIPBL:124 NFATC3:125 HIF3A:146
MP0000689 abnormal spleen morphology	0.02874985	551	2.652e-02	3.666e-01	CD2AP:119 GRB14:196 PECAM1:280 TNFSF11:311 GHR:325 RNF8:374
MP0003221 abnormal cardiomyocyte apopto	0.10428766	40	2.282e-02	3.666e-01	TFAM:29 CASP8:493 MDM2:740 MAPK9:1475 BACH1:1527 YWHAQ:1803
MP0001666 abnormal nutrient absorption	-0.09488356	46	2.643e-02	3.666e-01	TREH:28 MUC2:32 NPC1L1:51 SLC2A4:178 ABCB4:313 TRPV6:479
MP0003698 abnormal male reproductive	0.02994877	520	2.432e-02	3.666e-01	ADCY10:19 CATSPER2:26 MAGEL2:36 UBR2:164 EIF4G3:218 KHDRBS1:31
MP0003935 abnormal craniofacial develop	0.04175557	246	2.658e-02	3.666e-01	BAZ1B:197 HESX1:238 SETD2:261 ITGB8:298 TRPM6:305 ITGB1:549
MP0002272 abnormal nervous system	-0.04644439	196	2.696e-02	3.666e-01	PLEC:9 CHRNB2:39 ARC:75 MRGPRD:83 CACNA1G:96 PER3:157
MP0002210 abnormal sex determination	0.03321904	349	3.744e-02	3.742e-01	MAGEL2:36 EIF4G3:218 GHR:325 SPAG16:361 RNF8:374 AFF4:380
MP0002837 dystrophic cardiac calcinosis	-0.20039503	9	3.746e-02	3.742e-01	SLC2A4:178 DES:451 MMP9:1717 MYBPC3:1733 GSTZ1:8811.5 SCG5:8811
MP0002398 abnormal bone marrow	0.02287701	813	3.685e-02	3.742e-01	CRLF2:21 CD2AP:119 NFATC3:125 SIRPA:167 G6PC2:271 TNFSF11:311
MP0002733 abnormal thermal nociception	-0.06422365	94	3.248e-02	3.742e-01	MRGPRD:83 PTPRZ1:110 BDKRB1:238 NTSR1:891 CDK5R1:967 NAV2:101
MP0000427 abnormal hair cycle	-0.09715517	40	3.395e-02	3.742e-01	KRT17:80 KSR1:596 DSG4:671 CTSL:971 MPZL3:1284 DSG3:1323

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testis	0.05511403	1637	5.418e-12	2.925e-10	RANBP17:16 CATSPERE:18 ADCY10:19 CATSPERD:24 FAM169A:53 ZIM2:57
leg.skin	-0.11776606	286	1.244e-11	3.358e-10	PSAPL1:2 EVPL:5 BNC1:10 ARHGAP40:34 CARD14:38 DSP:49
EBV.lymphocyte	0.06413144	749	7.044e-09	9.510e-08	KIF18A:2 TRIM59:33 TPX2:52 WDR76:54 KIF2C:64 TTK:84
suprapubic.skin	-0.10669183	257	5.566e-09	9.510e-08	PSAPL1:2 EVPL:5 BNC1:10 CARD14:38 RNF222:76 KRT80:78
esophagus.mucosa	-0.07768668	261	1.900e-05	2.052e-04	EVPL:5 BNC1:10 ADH7:43 FAM83H:65 RNF222:76 PTK6:81
vagina	-0.09500137	118	3.876e-04	3.489e-03	EVPL:5 BNC1:10 RNF222:76 KRT13:86 ENDOU:111 PKP1:120
peyers.patch	-0.06222554	196	2.877e-03	2.219e-02	SLC17A4:14 MOGAT3:20 EPS8L3:22 TREH:28 MUC2:32 RNF186:36
cerebral.cortex	-0.06825741	109	1.422e-02	8.531e-02	PNMA8B:7 CHRNB2:39 CALHM1:46 KCNH3:181 FAM163B:187 KCNB2:580
putamen	-0.17196344	17	1.415e-02	8.531e-02	CORT:240 GRM3:256 RGS9:281 SLC18A3:1341 DIPK1C:1502 OPALIN:1956
endocervix	-0.07150707	76	3.163e-02	1.708e-01	ELFN1:77 XKR5:177 PWP2:197 BDKRB1:238 TGM2:254 PLPP3:343
skeletal.muscle	-0.03825331	258	3.626e-02	1.780e-01	STYXL2:52 CASQ1:54 SLC2A4:178 PYGM:309 FSD2:312 ANKRD23:329
minor.salivary.gland	-0.06104155	91	4.490e-02	2.021e-01	MMP7:248 SERINC2:325 KRT6B:372 MUC16:406 ATP6V1B1:550 MMP10:626
blood	-0.02499530	342	1.172e-01	3.330e-01	PIK3R5:23 PTAFR:70 TUBB1:73 TYMP:114 PRTN3:229 CD300LB:235
breast	-0.10167497	20	1.157e-01	3.330e-01	TNN:109 MUCL1:770 THRSP:864 NPY2R:1703 MAP1LC3C:1746 SCGB2A2:2482
nucleus.accumbens	-0.04548854	104	1.104e-01	3.330e-01	SV2C:106 OTOF:159 NCDN:182 HTR6:440 TMEM272:461 CPNE5:493
spleen	-0.02440447	362	1.160e-01	3.330e-01	CD1D:35 UNC13D:133 CD3E:214 PRR5L:233 PITPNM3:262 GIMAP4:292
stomach	-0.04601734	99	1.150e-01	3.330e-01	CAPN8:1 PSAPL1:2 EPS8L3:22 MUCL3:127 VWA2:139 CBLIF:153
transverse.colon	-0.03765512	168	9.435e-02	3.330e-01	RXFP4:3 SLC17A4:14 MOGAT3:20 EPS8L3:22 MUC2:32 RNF186:36
uterus	0.06266860	62	8.863e-02	3.330e-01	ADAMTS19:342 ATP2B4:362 RSPO3:441 EMX2:832 DENND2B:979 HOXD8:1131
greater.omentum	-0.05875069	38	2.107e-01	5.084e-01	BNC1:10 MUC16:406 ITLN1:629 THRSP:864 BARX1:1064 ALOX15:1514
left.ventricle	-0.04360628	69	2.116e-01	5.084e-01	MYZAP:71 FSD2:312 LMOD2:382 MYL3:514 CKMT2:603 MYOM2:665
pituitary.gland	0.02376644	232	2.166e-01	5.084e-01	CSH1:109 HFM1:139 CSHL1:140 VWDE:165 GH2:214 SAMD11:221
sigmoid.colon	-0.05239258	51	1.964e-01	5.084e-01	MRGPRD:83 TACR2:184 DES:451 NT5DC3:704 NTSR1:891 HDAC4:1903
thyroid	0.02484426	175	2.602e-01	5.854e-01	PLA2R1:44 CLCNKA:75 SMPDL3B:400 CLUL1:566 TLE6:766 SCUBE3:839
amygdala	-0.10279954	9	2.857e-01	6.171e-01	PCDH15:57 PTPRZ1:110 TNR:2455 BCAN:8811.5 NEUROD2:8811.5 NEUROD6:8811.5
fallopian.tube	0.03892991	60	2.980e-01	6.190e-01	BCHE:586 SERTM1:879 CDHR4:880 CCDC17:884 TUBA4B:1206 CFAP157:1666
pancreas	0.02659399	117	3.226e-01	6.452e-01	CATSPERB:9 FBXW12:153 TMED6:173 G6PC2:271 TRIM50:288 NPHS1:388
adrenal.gland	0.02462234	115	3.638e-01	6.837e-01	RMDN2:648 MGST1:670 ADGRV1:734 KCNK3:752 GALM:1012 HSD3B2:1155
caudate.nucleus	-0.05018673	27	3.672e-01	6.837e-01	GRM3:256 GPR37L1:333 MLC1:680 PDE1B:1058 HS3ST5:8811.5 ACBD7:8811.5
tibial.nerve	-0.01548488	203	4.505e-01	8.110e-01	ITGB4:13 SPTBN5:19 XAGE2:90 SLC24A4:269 INF2:392 TMEM215:393
subcutaneous.adipose	-0.02271224	81	4.811e-01	8.381e-01	SYNE3:396 LGALS12:749 INHBB:835 GPD1:859 THRSP:864 G0S2:972
aorta	-0.01128251	156	6.288e-01	8.434e-01	C1QTNF8:266 MTUS2:326 MYH9:477 MEGF6:553 MYH10:556 MYO1D:721
atrium.auricle	-0.01712991	95	5.653e-01	8.434e-01	ALPK2:126 FSD2:312 LMOD2:382 MYBPHL:517 CKMT2:603 MYOM2:665
bladder	-0.02545688	29	6.355e-01	8.434e-01	KRT13:86 PADI3:1016 ABCC4:1181 ACSM6:2087 UPK1B:2360 ACER2:8811.5
Brodmann.area.24	-0.03040698	33	5.460e-01	8.434e-01	UPP2:883 KCNS1:1685 SLC25A18:1696 SLC39A12:2522 SMIM10L2A:8811.5 NEUROD2:8811.5

SFTPB:55 XAGE2:90 LTK:104 NKD2:198 FCN3:383 EPAS1:415

CPAMD8:1290 H2BC5:1808 MSMB:1956 SHROOM1:1977 TTC6:2007 MKX:2462

SLC6A3:558 KCNE5:1294 CHRM5:8811.5 FOXB1:8811.5 KLHL1:8811.5 RET:8811.5

TNC:60 GPR20:652 HRCT1:716 HTR1B:806 FHL5:1062 TAGLN:1086

-0.01092518

0.02190000

-0.04069366

-0.01278982

lung

prostate

substantia.nigra

tibial.artery

158

11

6.376e-01 8.434e-01

5.928e-01 8.434e-01

6.404e-01 8.434e-01

6.386e-01 8.434e-01