Geneset	stat	num.genes	pval	p.adj	gene.vals
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT_	0.17291287	112	2.636e-10	1.712e-06	NDUFB10:6 TMEM126B:7 LRPPRC:11 TIMMDC1:23 ATP5PB:39 ATP5PO:100
REACTOME_RESPIRATORY_ELECTRON_TRANSPORT	0.17187672	90	1.762e-08	3.814e-05	NDUFB10:6 TMEM126B:7 LRPPRC:11 TIMMDC1:23 COX11:124 UQCRFS1:191
WP_MITOCHONDRIAL_COMPLEX_I_ASSEMBLY_MODE	0.23879160	47	1.485e-08	3.814e-05	NDUFB10:6 TMEM126B:7 TIMMDC1:23 NDUFB5:240 TMEM186:268 NDUFB7:291
REACTOME_MITOCHONDRIAL_TRANSLATION	0.16155290	93	7.343e-08	1.192e-04	PTCD3:58 MRPL42:73 MRPS35:98 MRPL3:120 MRPS28:128 MRPS31:236
NIKOLSKY_BREAST_CANCER_7P22_AMPLICON	-0.24929614	37	1.543e-07	1.670e-04	SNX8:7 GPER1:14 EIF3B:28 INTS1:34 BRAT1:82 ADAP1:120
REACTOME_THE_CITRIC_ACID_TCA_CYCLE_AND_R	0.11997415	162	1.399e-07	1.670e-04	NDUFB10:6 TMEM126B:7 LRPPRC:11 TIMMDC1:23 ATP5PB:39 ATP5PO:100
FISCHER_DREAM_TARGETS	0.05069115	921	2.122e-07	1.969e-04	KNL1:10 SPAG5:17 SASS6:64 CDC25C:68 NEIL3:91 TRIM59:93
REACTOME_COMPLEX_I_BIOGENESIS	0.21147316	48	4.013e-07	2.172e-04	NDUFB10:6 TMEM126B:7 TIMMDC1:23 NDUFB5:240 TMEM186:268 NDUFB7:291
REACTOME_KERATINIZATION	-0.10340792	206	3.202e-07	2.172e-04	KRT38:42 KRT77:149 KRTAP4-8:225 TGM1:245 DSG3:274 KRTAP12-4:426
WP_ELECTRON_TRANSPORT_CHAIN_OXPHOS_SYSTE	0.15771373	89	2.733e-07	2.172e-04	NDUFB10:6 ATP5PB:39 ATP5PO:100 COX11:124 UQCRFS1:191 NDUFB5:240
WONG_MITOCHONDRIA_GENE_MODULE	0.10080692	214	3.829e-07	2.172e-04	NDUFB10:6 LRPPRC:11 ATP5PB:39 MRPL42:73 ATP5PO:100 MRPL3:120
KEGG_OXIDATIVE_PHOSPHORYLATION	0.13808337	114	3.570e-07	2.172e-04	NDUFB10:6 ATP5PB:39 ATP5PO:100 COX11:124 UQCRFS1:191 NDUFB5:240
WP_OXIDATIVE_PHOSPHORYLATION	0.18252922	51	6.517e-06	3.256e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 NDUFB5:240 NDUFB7:291 NDUFB2:311
CREIGHTON_ENDOCRINE_THERAPY_RESISTANCE_2	0.06498411	405	7.536e-06	3.262e-03	TTC12:20 CEP350:29 NGRN:38 FAM149A:55 LRRC23:60 IQCH:72
KEGG_PARKINSONS_DISEASE	0.12372090	110	7.434e-06	3.262e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 UQCRFS1:191 NDUFB5:240 UQCRH:272
REACTOME_TRANSLATION	0.07847908	269	9.660e-06	3.921e-03	PTCD3:58 MRPL42:73 MRPS35:98 NARS2:110 MRPL3:120 MRPS28:128
REACTOME_FORMATION_OF_THE_CORNIFIED_ENVE	-0.11344731	126	1.105e-05	4.222e-03	KRT38:42 KRT77:149 TGM1:245 DSG3:274 KRT37:451 PKP1:497
MOOTHA_VOXPHOS	0.13548246	86	1.414e-05	5.103e-03	ATP5PB:39 ATP5PO:100 COX11:124 UQCRFS1:191 NDUFB5:240 UQCRH:272
LEE_BMP2_TARGETS_UP	-0.04488805	730	3.897e-05	1.332e-02	BPHL:8 ENPP3:18 TRPV6:19 CLU:30 ENTPD1:33 PROM1:92
FEVR_CTNNB1_TARGETS_UP	-0.04500288	662	8.314e-05	2.700e-02	CLU:30 CTRL:37 SLCO2A1:53 PNLIPRP1:86 SLC1A1:90 SLC6A3:135
MARSON_BOUND_BY_E2F4_UNSTIMULATED	0.04390016	664	1.209e-04	3.739e-02	KNL1:10 SPAG5:17 SASS6:64 CDC25C:68 TTLL5:69 NEIL3:91
REACTOME_RRNA_PROCESSING_IN_THE_MITOCHON	0.34823450	9	2.970e-04	8.424e-02	TRMT10C:117 MRM3:292 NSUN4:398 PRORP:484 MTERF4:900 HSD17B10:1741
KEGG_HUNTINGTONS_DISEASE	0.08317666	159	2.983e-04	8.424e-02	NDUFB10:6 ATP5PB:39 ATP5PO:100 DNAH2:103 UQCRFS1:191 NDUFB5:240
REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-0.04001603	701	3.225e-04	8.725e-02	TRPV6:19 DMTN:29 SLCO2A1:53 ATP1A1:70 NPC1:74 SLC1A1:90
REACTOME_METABOLISM_OF_LIPIDS	-0.03874384	722	4.127e-04	1.072e-01	MOGAT3:2 LRP2:23 ACSL6:39 OSBP:65 PLPP3:73 HEXB:78
REACTOME_CRISTAE_FORMATION	0.18702677	29	4.903e-04	1.225e-01	ATP5PB:39 ATP5PO:100 MTX1:256 IMMT:868 ATP5PD:1230 APOOL:1232
REACTOME_ANCHORING_OF_THE_BASAL_BODY_TO_	0.10006256	97	6.631e-04	1.538e-01	TCTN3:157 AKAP9:205 CEP162:313 RPGRIP1L:395 CENPJ:432 CEP83:536
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.03708408	734	6.562e-04	1.538e-01	ST6GAL2:16 RALGAPA2:20 CLU:30 FHDC1:50 OPN3:68 ATP1A1:70
REACTOME_SPERM_MOTILITY_AND_TAXES	0.32204114	9	8.204e-04	1.665e-01	CATSPERB:18 CATSPER3:967 HVCN1:1154 CATSPER2:1603 CATSPER1:1853 CATSPERD:209
REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTE	0.05823177	284	7.464e-04	1.665e-01	ATP5PB:39 TWNK:90 ATP5PO:100 TCTN3:157 POLRMT:174 AKAP9:205
REACTOME_SLC_MEDIATED_TRANSMEMBRANE_TRAN	-0.06249935	244	7.840e-04	1.665e-01	SLCO2A1:53 SLC1A1:90 LCN1:100 RHCG:102 SLC39A3:105 SLC6A3:135
WP_GENES_RELATED_TO_PRIMARY_CILIUM_DEVEL	0.09702605	100	8.038e-04	1.665e-01	SASS6:64 TCTN3:157 CPLANE1:162 TMEM231:168 CEP162:313 ARL13B:344
FISCHER_G2_M_CELL_CYCLE	0.06278903	233	9.735e-04	1.916e-01	SPAG5:17 CEP350:29 CDC25C:68 NEIL3:91 TRIM59:93 HMGB2:115
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	-0.18736067	25	1.184e-03	2.261e-01	SLC6A3:135 EXOC3:263 LPCAT1:276 SLC6A18:374 SLC9A3:384 TPPP:411
REACTOME_METABOLISM_OF_STEROIDS	-0.07582706	151	1.310e-03	2.430e-01	LRP2:23 OSBP:65 HSD17B4:187 VDR:200 INSIG1:298 LGMN:340
NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON	0.20303494	20	1.669e-03	2.630e-01	ZNF793:141 ZNF875:273 ZNF527:346 ZNF568:783 ZNF529:953 ZNF585B:1104
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.06661473	186	1.745e-03	2.630e-01	SPAG5:17 APOD:25 TRIM59:93 HMGB2:115 PDGFD:244 MELK:334
AFFAR_YY1_TARGETS_UP	-0.06567701	193	1.670e-03	2.630e-01	LRP2:23 CLU:30 LGALS9:49 MS4A1:196 FLT1:358 PBX4:440

DisGeNET Top pathways by non-permulation

RHCG:102 SLC39A3:105 SLC6A3:135 SLC6A6:176 SLC22A8:281 SLC30A10:296

ATP1A1:70 SLC1A1:90 SLC22A8:281 SLC6A18:374 SLC9A3:384 SLC22A6:409

STK11:4 PER2:40 XRCC3:59 SUGP1:114 VDR:200 LOXL2:255

STK11:4 LGALS9:49 NPC1:74 PRKDC:79 IFNA2:80 PROM1:92 STK11:4 ST6GAL2:16 CLU:30 PER2:40 LGALS9:49 XRCC3:59

NA NA NA NA NA

NA NA NA NA NA

1.506e-03 2.630e-01

1.513e-03 2.630e-01

REACTOME_TRANSPORT_OF_BILE_SALTS_AND_ORG -0.10019836

Esophageal carcinoma

Multiple Myeloma

Squamous cell carcinoma

NA.36

-0.03882019

-0.02840299

-0.02393549

1149

1690

-0.12256434

WP_PROXIMAL_TUBULE_TRANSPORT

Geneset	stat	num.genes	pval	p.adj	gene.vals
Mitochondrial Diseases	0.08851375	363	8.108e-09	7.962e-05	NDUFB10:6 TMEM126B:7 LRPPRC:11 CLPB:13 TWNK:90 NARS2:110
Increased serum lactate	0.15578550	99	8.772e-08	4.307e-04	LRPPRC:11 TWNK:90 NARS2:110 TRMT10C:117 MRPL3:120 AIFM1:225
Increased CSF lactate	0.19266764	56	6.214e-07	2.034e-03	TMEM126B:7 LRPPRC:11 TIMMDC1:23 TRMT10C:117 AIFM1:225 HTRA2:294
Lactic acidemia	0.12631452	123	1.355e-06	3.327e-03	TMEM126B:7 LRPPRC:11 TIMMDC1:23 TRMT10C:117 NDUFAF4:364 BCS1L:379
Autoimmune Diseases	-0.04604066	942	2.257e-06	4.432e-03	RTL1:9 GYPA:11 LRP2:23 ENTPD1:33 LGALS9:49 GRM3:52
Liver neoplasms	-0.03803269	1186	1.408e-05	2.305e-02	STK11:4 ENPP3:18 CLU:30 PROM1:92 ACOT12:112 SUGP1:114
Acidosis, Lactic	0.09502953	153	5.130e-05	7.196e-02	TMEM126B:7 LRPPRC:11 TIMMDC1:23 TRMT10C:117 NDUFAF4:364 BCS1L:379
Colorectal Cancer	-0.02324786	2875	1.163e-04	1.388e-01	SHROOM2:3 STK11:4 LONRF2:5 SNX8:7 GYPA:11 ERCC6:13
Lung diseases	-0.05889803	362	1.272e-04	1.388e-01	PRKDC:79 IFNB1:94 MUL1:126 IL13:183 VDR:200 ADORA1:253
Central neuroblastoma	-0.02991724	1508	1.426e-04	1.400e-01	STK11:4 LCMT1:6 RTL1:9 LRP2:23 CLU:30 PER2:40
Impaired exercise tolerance	0.12960479	69	1.991e-04	1.778e-01	TMEM126B:7 TIMMDC1:23 TWNK:90 DMD:185 NDUFAF4:364 BCS1L:379
Malignant neoplasm of esophagus	-0.04481493	580	2.511e-04	2.055e-01	STK11:4 PER2:40 XRCC3:59 SUGP1:114 ADH7:191 VDR:200
Fibrosis, Liver	-0.04900958	471	2.918e-04	2.204e-01	CLU:30 ZNF267:72 NPC1:74 IFNB1:94 SUGP1:114 MUL1:126
Adenocarcinoma	-0.02786238	1564	3.188e-04	2.236e-01	STK11:4 TRPV6:19 CLU:30 XRCC3:59 NPC1:74 PROM1:92
Hypertensive disease	-0.03105089	1201	3.630e-04	2.376e-01	STK11:4 GYPA:11 ERCC6:13 GPER1:14 LRP2:23 CLU:30
Lung Neoplasms	-0.03231170	1081	4.055e-04	2.489e-01	STK11:4 ERCC6:13 CLU:30 CT47A11:76 PRKDC:79 IFNA2:80
Ciliopathies	0.07693066	173	4.948e-04	2.858e-01	CCDC39:113 TCTN3:157 CPLANE1:162 TMEM231:168 CRB2:321 KIAA0586:340
Ichthyosiform Erythroderma, Congenital	-0.22121475	20	6.159e-04	2.880e-01	ALOX12B:104 ABCA12:232 TGM1:245 STS:315 LOX:339 SLC27A4:950
Eczema	-0.04886775	422	6.146e-04	2.880e-01	CABIN1:125 IL13:183 MS4A1:196 VDR:200 CLDN7:208 IL31:238
NADH:Q(1) Oxidoreductase deficiency	0.19851442	25	5.921e-04	2.880e-01	NDUFB10:6 TMEM126B:7 TIMMDC1:23 AIFM1:225 NDUFAF4:364 NDUFAF1:1009
Patchy palmoplantar keratoderma	-0.44275603	5	6.062e-04	2.880e-01	GJB3:270 GJB4:283 GJA1:1323 KDSR:1593 DSP:1743 NA
Hepatitis C, Chronic	-0.05204772	338	1.058e-03	2.955e-01	LGALS9:49 IFNA2:80 IFNB1:94 VDR:200 ABCB4:209 IL6:272
Acanthosis	-0.16559647	33	9.970e-04	2.955e-01	ALOX12B:104 TGM1:245 GJB3:270 GJB4:283 ATP2A2:631 KRT1:811
Cystic Fibrosis	-0.04248132	522	9.689e-04	2.955e-01	GYPA:11 TRPV6:19 ENTPD1:33 INTS1:34 NPC1:74 IFNB1:94
Cytochrome-c Oxidase Deficiency	0.15414893	40	7.453e-04	2.955e-01	LRPPRC:11 COX7A1:534 COX20:657 MRPL44:882 FASTKD2:886 SCO1:1098
Esophageal Neoplasms	-0.04169917	553	8.696e-04	2.955e-01	STK11:4 PER2:40 XRCC3:59 CT47A11:76 SUGP1:114 ADH7:191
Experimental Organism Basal Cell Carcino	-0.06037483	259	8.537e-04	2.955e-01	STK11:4 ERCC6:13 EXOC2:21 XRCC3:59 S1PR3:87 MUL1:126
Infection	-0.04567803	466	7.826e-04	2.955e-01	PRKDC:79 IFNB1:94 CD63:124 BCL2L11:168 IL13:183 VDR:200
MITOCHONDRIAL COMPLEX I DEFICIENCY	0.18726146	26	9.513e-04	2.955e-01	TMEM126B:7 TIMMDC1:23 NDUFAF4:364 NDUFA10:778 GDAP1:805 NDUFAF1:1009
Neuroblastoma	-0.02541718	1547	1.083e-03	2.955e-01	STK11:4 LCMT1:6 RTL1:9 LRP2:23 CLU:30 PER2:40
Obesity	-0.02388536	1789	1.073e-03	2.955e-01	MOGAT3:2 STK11:4 GPER1:14 LRP2:23 EHMT1:36 PER2:40
Palmoplantar Keratosis	-0.09866800	95	8.999e-04	2.955e-01	ALOX12B:104 ABCA12:232 TGM1:245 GJB3:270 GJB4:283 COL14A1:338
Primary microcephaly	0.09257442	110	8.076e-04	2.955e-01	KNL1:10 SASS6:64 XRCC4:324 NIN:356 CENPJ:432 ATRX:456
Solid Neoplasm	-0.03534626	773	9.338e-04	2.955e-01	STK11:4 GYPA:11 TRPV6:19 OPRPN:22 OSBP:65 PROM1:92
Steroid-resistant nephrotic syndrome	0.19063860	25	9.706e-04	2.955e-01	FAT1:53 CRB2:321 NPHS1:482 NPHS2:604 COQ8B:1460 MYO1E:1508
Steroid resistant nephrotic syndrome of	0.19966041	24	7.109e-04	2.955e-01	FAT1:53 CRB2:321 NPHS1:482 NPHS2:604 COQ8B:1460 MYO1E:1508
Colorectal Carcinoma	-0.02031880	2531	1.335e-03	3.414e-01	SHROOM2:3 STK11:4 ERCC6:13 ENPP3:18 TRPV6:19 CLU:30

customGeneSet Top pathways by non-permulation

1.326e-03 3.414e-01

1.391e-03 3.414e-01

1.383e-03 3.414e-01

Geneset	stat	num.genes	pval	p.adj	gene.vals
NAFLDGWAS	-0.0709090909	15	-	7.191e-01	GPAM:1239 PNPLA3:1473 MTTP:1852 TM6SF2:8718 APOE:8718 TRIB1:8718
expressionDirectionalSelection	0.0501700680	42			ZBTB12:864 SCAPER:1326 ZNF19:1344 GSDMD:1681 TLR10:2061 SPG7:3170
HumanLocalAdaptionDietAll	-0.0006747638	13		9.940e-01	SLC22A5:701 LCT:8718 AS3MT:8718 GPX1:8718 GPX3:8718 CELF1:8718
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.12	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
NA.16	NA NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA	NA	NA	NA	NA NA NA NA NA
NA.17	NA 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
NA.21	NA	NA	NA	NA	NA NA NA NA NA
NA.22	NA NA	NA	NA	NA NA	NA NA NA NA NA
NA.23	NA NA	NA	NA	NA	NA NA NA NA NA
NA.24	NA NA	NA	NA	NA	NA NA NA NA NA
NA.25	NA NA	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.28	NA	NA NA	NA	NA	NA NA NA NA NA
NA.29	NA NA	NA NA	NA	NA	NA NA NA NA NA NA
NA.30	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA NA
NA.31	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA NA
NA.31 NA.32	NA NA	NA NA	NA NA	NA NA	NA NA NA NA NA NA
NA.32 NA.33		NA NA		NA NA	NA NA NA NA NA
	NA NA		NA NA		NA NA NA NA NA NA NA NA NA NA NA
NA.34	NA	NA	NA	NA	INA INA INA INA INA

GO_Biological_Process_2023 Top pathways by non-permulation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Mitochondrial Respiratory Chain Complex	0.21232146	82	3.128e-11	1.691e-07	NDUFB10:6 TMEM126B:7 UQCRFS1:191 AIFM1:225 NDUFB5:240 TMEM186:268
NADH Dehydrogenase Complex Assembly (GO:	0.24260142	49	4.300e-09	7.750e-06	NDUFB10:6 TMEM126B:7 NDUFB5:240 TMEM186:268 NDUFB7:291 NDUFB2:311
Mitochondrial Respiratory Chain Complex	0.24260142	49	4.300e-09	7.750e-06	NDUFB10:6 TMEM126B:7 NDUFB5:240 TMEM186:268 NDUFB7:291 NDUFB2:311
Cilium Assembly (GO:0060271)	0.10584537	234	2.677e-08	2.895e-05	SPAG17:71 CCDC39:113 TCTN3:157 CPLANE1:162 TMEM231:168 FAM149B1:187
Mitochondrial Gene Expression (GO:014005	0.15963371	102	2.633e-08	2.895e-05	PTCD3:58 MRPL42:73 TWNK:90 MRPL3:120 MRPS28:128 POLRMT:174
Mitochondrial Translation (GO:0032543)	0.15587776	97	1.162e-07	1.047e-04	PTCD3:58 MRPL42:73 MRPL3:120 MRPS28:128 MRPS31:236 MTRF1:353
Cilium Organization (GO:0044782)	0.09278094	222	2.031e-06	1.569e-03	TCTN3:157 CPLANE1:162 TMEM231:168 FAM149B1:187 FBXW8:265 CEP162:313
Proton Motive Force-Driven Mitochondrial	0.19231843	50	2.574e-06	1.740e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 NDUFB5:240 NDUFB7:291 NDUFB2:311
Oxidative Phosphorylation (GO:0006119)	0.17600250	59	2.968e-06	1.783e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 NDUFB5:240 UQCRH:272 NDUFB7:291
Mitochondrial ATP Synthesis Coupled Elec	0.16574656	65	3.873e-06	2.094e-03	NDUFB10:6 UQCRFS1:191 NDUFB5:240 UQCRH:272 NDUFB7:291 NDUFB2:311
Aerobic Electron Transport Chain (GO:001	0.16217735	64	7.329e-06	3.467e-03	NDUFB10:6 UQCRFS1:191 NDUFB5:240 UQCRH:272 NDUFB7:291 NDUFB2:311
Proton Motive Force–Driven ATP Synthesis	0.17608392	54	7.694e-06	3.467e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 NDUFB5:240 NDUFB7:291 NDUFB2:311
Mitochondrial RNA Metabolic Process (GO:	0.27637004	20	1.883e-05	7.619e-03	TWNK:90 POLRMT:174 FASTKD5:207 FASTKD1:388 TFAM:423 TFB2M:520
Translation (GO:0006412)	0.08607519	208	1.973e-05	7.619e-03	PTCD3:58 MRPL42:73 MRPL3:120 RPS6KB2:125 MRPS28:128 SRBD1:151
Mitochondrial Electron Transport, NADH T	0.19765702	33	8.547e-05	3.081e-02	NDUFB10:6 NDUFB5:240 NDUFB7:291 NDUFB2:311 NDUFA8:393 NDUFA10:778
Plasma Membrane Bounded Cell Projection	0.06975420	266	9.499e-05	3.210e-02	TCTN3:157 CPLANE1:162 TMEM231:168 FAM149B1:187 FBXW8:265 CEP162:313
Organic Substance Transport (GO:0071702)	-0.08091359	195	1.017e-04	3.235e-02	TRPV6:19 LRP2:23 CLU:30 SLCO2A1:53 RHCG:102 SLC6A4:123
Cellular Respiration (GO:0045333)	0.11901088	82	1.976e-04	5.638e-02	NDUFB10:6 UQCRFS1:191 NDUFB5:240 UQCRH:272 NDUFB7:291 NDUFB2:311
Mitochondrial RNA Processing (GO:0000963	0.35822050	9	1.981e-04	5.638e-02	TRMT10C:117 FASTKD5:207 FASTKD1:388 SUPV3L1:581 PNPT1:590 FASTKD2:886
Intermediate Filament Organization (GO:0	-0.13271753	65	2.175e-04	5.688e-02	KRT38:42 KRT77:149 KRT37:451 PKP1:497 KRT25:739 KRT17:779
Positive Regulation Of Mitochondrial Tra	0.28513738	14	2.209e-04	5.688e-02	NGRN:38 TRMT10C:117 MRPS27:634 TRUB2:789 FASTKD2:886 RPUSD3:1226
Axonemal Dynein Complex Assembly (GO:007	0.19604789	29	2.589e-04	6.363e-02	TTC12:20 DNAH2:103 CCDC39:113 CCDC65:414 DNAI1:715 CFAP73:719
Cilium Movement (GO:0003341)	0.14770532	50	3.045e-04	7.159e-02	SPAG17:71 CCDC39:113 CFAP206:221 TEKT1:578 DNAI1:715 CFAP73:719
Mitochondrial DNA Replication (GO:000626	0.33709711	9	4.618e-04	1.041e-01	TWNK:90 SSBP1:424 TEFM:709 POLG2:1037 PRIMPOL:1762 POLG:1983
Inorganic Cation Transmembrane Transport	-0.05950834	280	6.390e-04	1.382e-01	TRPV6:19 CLU:30 ATP1A1:70 RHCG:102 SLC39A3:105 SLC6A4:123
Peptide Biosynthetic Process (GO:0043043	0.08346762	137	7.585e-04	1.577e-01	MRPL42:73 MRPL3:120 RPS6KB2:125 SRBD1:151 DMD:185 MRPS15:411
tRNA Methylation (GO:0030488)	0.16161026	36	7.950e-04	1.592e-01	TRMT61B:41 THADA:46 TRMT10C:117 TRMT5:839 TRMT10A:1113 FTSJ1:1178
Intrinsic Apoptotic Signaling Pathway (G	-0.09359037	104	9.884e-04	1.798e-01	STK11:4 PRKDC:79 BCL2L11:168 MAP3K5:302 TRAF2:324 BAD:369
Mitochondrial Transcription (GO:0006390)	0.27439105	12	9.978e-04	1.798e-01	TWNK:90 POLRMT:174 TFAM:423 TFB2M:520 MTERF1:601 TEFM:709
Sensory Perception Of Pain (GO:0019233)	-0.21336099	20	9.570e-04	1.798e-01	P2RX7:627 RETREG1:766 CCR2:781 CCL2:867 CHRNB2:942 CHRNA4:1418
Non-Motile Cilium Assembly (GO:1905515)	0.17015248	31	1.045e-03	1.823e-01	ARL13B:344 CC2D2B:355 RPGRIP1L:395 RPGRIP1:473 C2CD3:576 TOGARAM1:629
Regulation Of Cold-Induced Thermogenesis	-0.07981216	141	1.090e-03	1.842e-01	STK11:4 EHMT1:36 PER2:40 IL13:183 GRB10:229 NOTCH1:343
Apoptotic Mitochondrial Changes (GO:0008	-0.16047904	34	1.206e-03	1.863e-01	CLU:30 ERBB4:354 BIK:367 BAD:369 HK2:600 GGCT:802
Monoatomic Cation Transmembrane Transpor	-0.05680201	277	1.187e-03	1.863e-01	TRPV6:19 CLU:30 ATP1A1:70 SLC39A3:105 SLC6A4:123 SLC6A3:135
Positive Regulation Of Chemotaxis (GO:00	-0.14334867	43	1.150e-03	1.863e-01	CNTN1:261 IL6:272 LGMN:340 F7:425 PDGFRB:570 VEGFA:656
Regulation Of Mitochondrial mRNA Stabili	0.37954725	6	1.283e-03	1.927e-01	FASTKD5:207 FASTKD1:388 PDE12:756 FASTKD2:886 FASTKD3:1630 TBRG4:9895
Regulation Of Mitochondrial Translation	0.19555479	22	1.500e-03	2.191e-01	LRPPRC:11 NGRN:38 TRMT10C:117 MRPS27:634 TRUB2:789 FASTKD2:886
Intrinsic Apoptotic Signaling Pathway In	-0.16928745	29	1.607e-03	2.287e-01	MAP3K5:302 TRAF2:324 BAG6:859 BAK1:999 RNF186:1071 DNAJC10:1165
Nitrogen Compound Transport (GO:0071705)	-0.07192611	161	1.672e-03	2.318e-01	LRP2:23 RHCG:102 SCARB2:113 SLC6A4:123 SLC6A3:135 SLC6A6:176
Aerobic Respiration (GO:0009060)	0.11981082	57	1.766e-03	2.361e-01	NDUFB10:6 NDUFB5:240 UQCRH:272 NDUFB7:291 NDUFB2:311 NDUFA8:393

MGI_Mammalian_Phenotype_Level_4 Top pathways by non-permulation

MP0008438 abnormal cutaneous collagen	stat	num.genes	pvai	p.aaj	gene.vais
wii 0000 1 30 abrioriliai cutariecus collageri	-0.005400036	15	9.423e-01	9.847e-01	THBS2:256 COL3A1:312 LOX:339 COL5A1:1137 TNXB:8718 PLOD3:8718
MP0002909 abnormal adrenal gland	0.065217391	23	2.796e-01	9.847e-01	LRRK2:665 CHGB:1048 PRKAR1A:1694 SNAPIN:2035 DRD5:2878 KCNK3:315
MP0000609 abnormal liver physiology	-0.022102535	379	1.502e-01	9.847e-01	ERCC6:13 NPC1:74 PRKDC:79 NPC1L1:84 GCK:143 ABCB4:209
MP0001730 embryonic growth arrest	0.001812061	182	9.336e-01	9.847e-01	NASP:195 HOPX:262 SKIL:301 TLN1:494 NODAL:509 UBR1:723
MP0001731 abnormal postnatal growth	-0.001797608	591	8.862e-01	9.847e-01	ERCC6:13 TRPV6:19 SLC6A3:135 GCK:143 TNS3:146 ITPKB:162
MP0002210 abnormal sex determination	0.006537595	350	6.818e-01	9.847e-01	MLH3:50 GHR:52 MEI1:83 CIB1:223 PROP1:247 FOXN1:331
MP0000604 amyloidosis	-0.033345415	34	5.020e-01	9.847e-01	CLU:30 CCR2:781 LRPAP1:916 PSEN1:943 ZDHHC13:1681 APOE:8718
MP0000598 abnormal liver morphology	-0.009122902	482	5.074e-01	9.847e-01	STK11:4 NPC1:74 HEXB:78 ABCB4:209 GRB10:229 IL6:272
MP0005334 abnormal fat pad	0.016748294	152	4.806e-01	9.847e-01	GHR:52 ATXN2:242 RICTOR:612 MOB4:1011 PNRC2:1143 STAT5A:1261
MP0005332 abnormal amino acid	0.005459586	113	8.423e-01	9.847e-01	CD2AP:384 NPHS2:604 SLC7A10:1076 MPV17:1179 SRR:1223 DAO:1241
MP0005330 cardiomyopathy	-0.009863449	70	7.764e-01	9.847e-01	SLC6A4:123 SLC6A6:176 PLRG1:284 ERBB4:354 POLD1:463 LDB3:713
MP0002269 muscular atrophy	0.003837677	86	9.026e-01	9.847e-01	DMD:185 AIFM1:225 HTRA2:294 PARL:438 SUPV3L1:581 BRCA1:605
MP0001765 abnormal ion homeostasis	-0.058613144	110	3.502e-02	9.847e-01	TRPV6:19 LRP2:23 RHCG:102 VDR:200 SCNN1G:325 SCGB1A1:562
MP0004043 abnormal pH regulation	-0.112870971	13	1.591e-01	9.847e-01	RHCG:102 SLC9A3:384 SLC12A1:1556 SLC26A7:1802 HIF1AN:8718 SOD2:87
MP0008961 abnormal basal metabolism	-0.040226077	18	5.551e-01	9.847e-01	PER2:40 HTR6:485 MARK2:1935 HIF1AN:8718 DECR1:8718 FOXA2:8718
MP0002837 dystrophic cardiac calcinosis	0.037454648	9	6.974e-01	9.847e-01	SGCD:2087 GSTZ1:9895 SCG5:9895 SLC2A4:9895 DNM1L:9895 MYBPC3:98
MP0005369 muscle phenotype	0.010838396	213	5.911e-01	9.847e-01	KL:61 DMD:185 HOPX:262 NCOA6:419 DCN:472 NF1:584
MP0009250 abnormal appendicular skeleto	-0.008554456	73	8.014e-01	9.847e-01	COMP:525 RLN1:823 TGFB2:837 CACNA1S:1869 ATF4:1878 FBN1:8718
MP0002998 abnormal bone remodeling	-0.011109867	115	6.830e-01		LRP2:23 IL6:272 CCR2:781 SH3BP2:894 ACP5:1093 HTR1B:1125
MP0002066 abnormal motor capabilities/c	-0.007291226	1086	4.554e-01		ERCC6:13 LRP2:23 EHMT1:36 PER2:40 ATP1A1:70 NPC1:74
MP0005248 abnormal Harderian gland	-0.061291998	16	3.964e-01		RARB:928 VSX2:1658 RARA:8718 CDKN1A:8718 CTNNB1:8718 RXRA:8718
MP0002419 abnormal innate immunity	-0.020057888	361		9.847e-01	ENTPD1:33 NPC1:74 PRKDC:79 IFNB1:94 VDR:200 TNIP2:211
MP0004133 heterotaxia	0.076885190	32	1.331e-01		RPGRIP1L:395 NODAL:509 MKS1:998 LEFTY1:1119 HHIP:2051 CFC1:2401
P0002396 abnormal hematopoietic system	0.010685517	22		9.847e-01	SNAI2:781 JAK3:1860 NFE2L1:9895 RAD50:9895 MEOX2:9895 DKC1:9895
MP0001529 abnormal vocalization	-0.004370904	19	9.475e-01	9.847e-01	WFS1:1380 DRD2:8718 DHCR7:8718 ACHE:8718 CHRM2:8718 NLGN3:8718
MP0004134 abnormal chest morphology	0.009840178	28	8.572e-01		NF1:584 CBFB:2420 PTCH1:2515 FBN1:9895 COL1A1:9895 NCKAP1L:9895
IP0001845 abnormal inflammatory respons	-0.031684562	508	1.839e-02	9.847e-01	STK11:4 PRKDC:79 S1PR3:87 TOP3B:95 CCL25:101 MGAT5:138
MP0004036 abnormal muscle relaxation	-0.039599294	41	3.816e-01		CASQ1:522 ATP2A2:631 VEGFA:656 ATP2A1:1404 MYL2:1799 NOS3:1816
MP0002398 abnormal bone marrow	0.002473651	813	8.214e-01		CHUK:59 AIRE:119 NFATC3:198 SAMSN1:229 HTRA2:294 SKIL:301
MP0000733 abnormal muscle development	0.014963316	68	6.710e-01		DMD:185 NF1:584 GAB1:1339 RELA:1491 DLL3:1900 MYF6:1965
MP0005423 abnormal somatic nervous	-0.084108546	11		9.847e-01	L1CAM:1276 TAS1R1:1427 SLC12A5:8718 EGR3:8718 ATP1A2:8718 DSCAM:8
MP0000230 abnormal systemic arterial	-0.035179284	151	1.397e-01		CACNA1B:127 VDR:200 NPAS2:242 APLNR:328 SLC6A18:374 SLC9A3:384
MP0003984 embryonic growth retardation	0.005131304	336		9.847e-01	CHM:88 ARNT:147 NFATC3:198 AIFM1:225 FBXW8:265 NCOA6:419
MP0002733 abnormal thermal nociception	-0.058212423	94	5.259e-02		SLC6A4:123 CACNA1B:127 ADORA1:253 TRPM8:364 SLC40A1:505 GPR3:55
MP0005387 immune system phenotype	-0.004340570	98		9.847e-01	IL13:183 IL6:272 MAN2A1:379 FGF7:519 STIM1:594 AHR:1022
MP0005386 behavior/neurological phenoty	0.005710676	95		9.847e-01	CHRM5:178 CCKBR:197 HTRA2:294 ATRX:456 NF1:584 GAB1:1339
MP0005385 cardiovascular system phenoty	-0.017140856	181		9.847e-01	SLC6A6:176 IL6:272 F2R:467 ATP2A2:631 TNNT2:635 VEGFA:656
MP0005384 cellular phenotype	0.007598710	431		9.847e-01	CHUK:59 MBD4:173 NFATC3:198 AIFM1:225 PTPN13:263 CYSLTR1:288
IP0001545 abnormal hematopoietic system	-0.053354566	35		9.847e-01	STK11:4 MATK:301 EP400:375 RAPGEF2:853 IFNGR1:1262 NR1H2:8718
iPuuu 1545 annonnai nemaionoleiic system	-0.017140856	181		9.847e-01	SLC6A6:176 IL6:272 F2R:467 ATP2A2:631 TNNT2:635 VEGFA:656

Geneset	stat	num.genes	pval	p.adj	gene.vals
testis	0.063524497	1655	1.422e-15	7.677e-14	SAXO1:1 CCDC110:8 KNL1:10 CLEC18C:12 CLPB:13 SPAG5:17
esophagus.mucosa	-0.045936877	261	1.144e-02	1.145e-01	RHCG:102 ADH7:191 TGM1:245 GJB3:270 DSG3:274 SERPINB1:335
fallopian.tube	0.103811184	60	5.520e-03	1.145e-01	CCDC198:37 BCHE:62 DTHD1:208 TUBA4B:282 CDHR4:339 LDLRAD1:370
minor.salivary.gland	-0.075910461	91	1.262e-02	1.145e-01	ENPP3:18 OPRPN:22 PROM1:92 TFCP2L1:311 OVOL2:317 BIK:367
peyers.patch	-0.053921700	199	9.262e-03	1.145e-01	MOGAT3:2 CCL25:101 SLC17A4:106 BTNL8:235 OLFM4:288 NR1I2:326
suprapubic.skin	-0.045594647	257	1.273e-02	1.145e-01	ALOX12B:104 KRT77:149 ABCA12:232 GJB3:270 DSG3:274 GJB4:283
stomach	-0.061647767	99	3.472e-02	2.678e-01	SLC9A3:384 CBLIF:413 PALM3:489 PSAPL1:560 CTSE:727 PHGR1:833
leg.skin	-0.035075267	286	4.359e-02	2.942e-01	ALOX12B:104 KRT77:149 ABCA12:232 GJB3:270 DSG3:274 GJB4:283
Brodmann.area.9	-0.040018717	183	6.376e-02	3.443e-01	RXFP1:108 KCNV1:140 HECW1:154 KCNQ5:182 MATK:301 DRGX:309
EBV.lymphocyte	0.020979607	750	5.800e-02	3.443e-01	KNL1:10 CCDC198:37 ZNF215:45 SASS6:64 CDC25C:68 NEIL3:91
nucleus.accumbens	-0.049902185	105	7.846e-02	3.572e-01	PRB2:117 RGS20:249 HTR6:485 KCNA4:575 NCDN:581 INSYN2A:624
putamen	-0.122959541	17	7.939e-02	3.572e-01	GRM3:52 RGS9:64 ANO3:683 DIPK1C:1030 SLC18A3:1384 CORT:1602
cortex.kidney	-0.038334846	131	1.317e-01	4.445e-01	TMEM72:25 SLC22A8:281 SLC22A12:391 CA12:405 SLC22A6:409 PLCXD2:430
ectocervix	-0.087961152	26	1.209e-01	4.445e-01	LRFN5:58 FGF7:519 COL5A1:1137 ESR1:1320 F10:1751 GDF7:8718
liver	-0.022606496	397	1.281e-01	4.445e-01	MOGAT3:2 NPC1L1:84 SLC17A4:106 ACOT12:112 ABCB4:209 SLC38A3:294
uterus	0.057290515	62	1.196e-01	4.445e-01	DENND2B:14 FRMD7:150 DCHS1:400 PTK7:513 TCF23:563 MEIS3:974
bladder	-0.077834346	29	1.473e-01	4.678e-01	ABCC4:980 KRT13:1124 PADI3:1245 UGT1A6:1290 RD3:1322 UPK1B:1926
caudate.nucleus	-0.074707144	28	1.716e-01	5.149e-01	GRM3:52 PRB2:117 MLC1:304 ANO3:683 GPR37L1:776 RLBP1:855
adrenal.gland	-0.034270836	116	2.043e-01	5.254e-01	MAP3K5:302 SLC40A1:505 MAP3K15:797 CYP11A1:1040 AKR1B1:1063 AOX1:1066
left.ventricle	-0.044611298	69	2.012e-01	5.254e-01	GJA3:438 HSPB7:506 TNNT2:635 MYL3:642 ADPRHL1:676 LDB3:713
vagina	-0.035385688	118	1.863e-01	5.254e-01	RHCG:102 GJB3:270 DSG3:274 SCNN1G:325 PKP1:497 NCCRP1:501
C1.spinal.cord	-0.024976006	194	2.339e-01	5.725e-01	GJC2:91 SEC14L5:148 CDH20:180 PIEZO2:607 TRPV5:757 ADARB2:767
sigmoid.colon	0.047263245	51	2.438e-01	5.725e-01	PLA2G2C:237 BMP3:245 HAND1:838 PLEKHO1:1330 GDNF:1501 TACR2:2046
cerebral.cortex	-0.031476627	109	2.582e-01	5.738e-01	DMTN:29 HECW1:154 DRGX:309 TPPP:411 LZTS1:641 PRKAR1B:715
transverse.colon	-0.025053955	168	2.657e-01	5.738e-01	MOGAT3:2 SLC17A4:106 CLDN7:208 TMEM171:269 NR1I2:326 BEST2:466
hippocampus.proper	-0.086476550	13	2.805e-01	5.826e-01	LCN1:100 FEZF2:1222 NTS:1567 NEUROD2:8718 NEUROD6:8718 SLC17A7:8718
hypothalamus	-0.033646044	78	3.057e-01	6.114e-01	RTL1:9 PCDH15:400 LUZP2:569 RTP5:677 GABRQ:869 RAB3C:1052
endocervix	-0.026457007	76	4.265e-01	6.979e-01	PLPP3:73 SPON2:195 XKR5:251 ELFN1:307 PRSS12:552 GABRE:997
esophagus.muscularis.mucosa	0.044522126	28	4.153e-01	6.979e-01	KCNMB1:54 CYSLTR1:288 PRUNE2:961 NTN1:1314 DPYSL3:1898 CHRM3:2230
lung	-0.019154534	161	4.046e-01	6.979e-01	SLCO2A1:53 SLC6A4:123 LPCAT1:276 ADAMTS8:290 PPBP:341 XAGE2:427
pituitary.gland	0.016087592	233	4.019e-01	6.979e-01	CSH1:15 VWA5B1:22 CSHL1:104 ZSWIM2:121 FAM183A:153 KCNH6:165
skeletal.muscle	-0.015682059	258	3.906e-01	6.979e-01	SMTNL1:507 GLRX:510 CASQ1:522 OBSCN:533 ATP2A2:631 PDE4D:651
spleen	-0.012485946	366	4.188e-01	6.979e-01	LGALS9:49 MS4A1:196 ICAM2:277 APLNR:328 PPBP:341 CD300A:356
amygdala	-0.074009901	9	4.421e-01	7.022e-01	PCDH15:400 BCAN:8718 LHFPL3:8718 NEUROD2:8718 NEUROD6:8718 PTPRZ1:8718
greater.omentum	-0.031084730	38	5.079e-01	7.618e-01	IL6:272 FAM89A:578 GPR4:725 BARX1:1345 BNC1:1372 RBP7:1901
thyroid	-0.014807337	176	5.009e-01	7.618e-01	LRP2:23 ZNF486:47 FHDC1:50 MGAT4C:103 TMEM171:269 PDE8B:303
Brodmann.area.24	0.032123620	33		7.641e-01	TAC3:460 DOK6:1624 IDS:1678 NCS1:1755 FAM107A:2591 DRD5:2878
	0.00770000	407	5.054 04	0.400 04	TRANKA 45 A001 0 00 MT01 4 04 ORTO4 400 MONTA 444 OA0NAAR 407

5.954e-01 8.460e-01

7.191e-01 9.235e-01

7.099e-01 9.235e-01

cerebellum

breast

cerebellar.hemisphere

-0.007798632

-0.023243277

-0.004796786

537

TRANK1:15 ACSL6:39 MTCL1:81 CRTC1:109 KCNT1:111 CACNA1B:127

TNN:1269 ADIPOQ:8718 ALX4:8718 ANKRD30A:8718 CIDEC:8718 FABP4:8718

ACSL6:39 TCEAL5:54 PDZD4:55 MTCL1:81 ADCY1:163 NKX6-3:184