

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

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 UQCRCF: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 UQCRCF:1:191 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 UQCRCF:1:191 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 LRRCC2:60 IQCH:72
KEGG_PARKINSONS_DISEASE	0.12372090	110	7.434e-06	3.262e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 UQCRCF:1:191 NDUFB5:240 UQCRCR:272
REACTOME_TRANSLATION	0.07847908	269	9.606e-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
MOOHTA_VOXPHOS	0.13548246	86	1.414e-05	5.103e-03	ATP5PB:39 ATP5PO:100 COX11:124 UQCRCF:1:191 NDUFB5:240 UQCRCR:272
LEE_BMP2_TARGETS_UP	-0.04488805	730	3.897e-05	1.332e-02	BPHL:8 ENPP3:18 TRPV6:19 CLU:30 ENTDP1:33 PROM1:92
FEVR_CTNNB1_TARGETS_UP	-0.04500288	662	8.314e-05	2.700e-02	CLU:30 CTR13:7 SLC02A1:53 PNLP1RP1:86 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 NEIL3:91 TLL5:69 NEIL3:91
REACTOME_RRNA_PROCESSING_IN_THE_MITOCHON	0.34824500	9	2.970e-04	8.424e-02	TRMT10C:117 MRMS:292 NSUN4:398 PROKRP:484 MTRF5A:190 HSD17B10:1741
KEGG_HUNTINGTONS_DISEASE	0.08317666	159	2.983e-04	8.424e-02	NDUFB10:6 ATP5PB:39 ATP5PO:100 DNAH2:73 UQCRCF:1:191 NDUFB5:240
REACTOME_TRANSPORT_OF_SMALL_MOLECULES	-0.04001603	701	3.225e-04	8.725e-02	TRPV6:19 DMTN1:29 SLC02A1:53 ATP1A1:70 NPC1:74 SLC1A1:90
REACTOME_METABOLISM_OF_LIPIDS	-0.03874384	722	4.127e-04	1.072e-01	MOGAT3:2 LRPP2:23 ACSL3:39 OSBP:65 PLPP3:73 HEXB:78
REACTOME_CRISTAE_FORMATION	0.18076277	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_	0.02649935	97	6.631e-04	1.538e-01	TCTN3:157 AKAP9:205 CEP162:313 RPRGR1P1:395 CENPJ:432 CEP83:536
RODRIGUES_THYROID_CARCINOMA_POORLY_DIFFE	-0.03708408	734	6.562e-04	1.538e-01	ST6GAL2:16 RALGAP2:20 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 HVCAN1:2114 CATSPER2:1603 CATSPER1:1853 CATSPERD:2094
REACTOME_ORGANELLE_BIOGENESIS_AND_MAINTA	0.05823177	284	7.464e-04	1.665e-01	ATP5PB:39 TWNK:90 ATP5PO:100 TCTN3:157 POLRMT:174 AKAP9:205
REACTOME_SLC_MEDIANATED_TRANSMEMBRANE_TRAN	-0.05823177	284	7.464e-04	1.665e-01	SLC02A1:53 SLC1A1:90 LCN1:100 RHC0:120 DNTA2:631 APL:132
WP_GENES_RELATED_TO_PRIMARY_CILIUM_DEVEL	0.09702605	100	8.038e-04	1.665e-01	SASS6:64 TCTN3:157 CLPANE1:162 TMEM231:168 NDUFB5:240 SLC39A3:105
FISCHER_G2_M_CELL_CYCLE	0.06278903	233	9.735e-04	1.916e-01	SPAG5:17 GPER1:14 CEP350:29 CDC25C:68 NEIL3:91 TRIM59:93 HMG2:115
NIKOLSKY_BREAST_CANCER_5P15_AMPLICON	-0.18736067	25	1.184e-03	2.261e-01	SLC6A3:135 EXOC3:263 LPCAT1:724 LRTP:174 SLC39A3:105 SLC6A3:135
REACTOME_METABOLISM_OF_STEROIDS	-0.07582706	151	3.104e-03	2.430e-01	LRP2:23 DSG3:275 HSD17B4:187 VDR:200 INSG1:298 LGMN:340
NIKOLSKY_BREAST_CANCER_19Q13.1_AMPLICON	0.20303494	20	1.669e-03	2.630e-01	ZNF793:141 ZNF875:123 ZNF527:346 ZNF568:783 ZNF529:545 ZNF585B:1104
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.06661473	186	1.745e-03	2.630e-01	SPAG5:17 APOD:25 TRIM59:93 HMG2:115 PDGF2:244 MELK:334
FFAR_Y11_TARGETS_UP	-0.06567701	193	1.670e-03	2.630e-01	LRP2:23 CLU:30 LGALS9:49 MS4A1:198 FLT1:358 PBX4:440
REACTOME_TRANSPORT_OF_BILE_SALTS_AND_ORG	-0.10019836	84	1.506e-03	2.630e-01	RHCG:102 SLC39A3:105 SLC6A3:135 SLC6A6:176 SLC22A8:281 SLC30A10:296
WP_PROXIMAL_TUBULE_TRANSPORT	-0.12256434	56	1.513e-03	2.630e-01	ATP1A1:70 SLC1A1:90 SLC22A8:281 SLC6A18:374 SLC9A3:384 SLC22A6:409

DisGeNET Top pathways by non-permutation

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 BC5L1:379
Autoimmune Diseases	-0.04604066	942	2.257e-06	4.432e-03	RTL1:9 GYPA11:1 TRPV2:23 ENTDP1:33 LGAL5:949 GRM3:52
Liver neoplasms	-0.03803269	1166	1.408e-05	2.305e-02	STK11:4 ENPP3:18 CLU:30 PROM1:92 ACOT12:112 SUGP1:114
Akosis, Lactic	0.09502953	153	5.130e-05	7.196e-02	TMEM126B:7 LRPPRC:11 TIMMDC1:23 TRMT10C:117 NDUFAF4:364 BC5L1:379
Colorectal Cancer	-0.02324786	2875	1.163e-04	1.388e-01	SHROOM2:3 STK11:4 LONRF2:55 SNX8:7 GYPA1:11 ERCC6:13
Lung diseases	-0.05898903	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 LCM1T1:6 RTL1:9 LRPP2:23 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 BC5L1:379
Malignant neoplasm of esophagus	-0.04481493	580	2.511e-04	2.055e-01	STK11:4 PER2:40 XRC3:59 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 XRC3:59 NPC1:74 PROM1:92
Hypertensive disease	-0.03105089	1201	3.630e-04	2.376e-01	STK11:4 GYPA1:11 ERCC6:13 GPER1:14 LRPP2:23 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	CDC39:113 TCTN3:157 CLPANE1:162 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	-0.0486775	422	6.146e-04	2.880e-01	CABIN1:125 IL13:183 MS4A1:196 VDR:200 CLDN7:208 IL21:238
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 palmo-plantar keratoderma	-0.44275603	5	6.062e-04	2.880e-01	GJB3:270 GJB4:283 GJA1:1323 KDSR:1535 PLP2:236 SIRT1:743 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	GYPA11:1 TRPV6:19 ENTDP1:33 INTS1:34 NPC1:74 IFNB1:94
Cytochrome-c Oxidase Deficiency	0.15414893	40	7.453e-04	2.955e-01	LRPPRC:11 COX1A1:534 COX20:657 MRPL4:882 FASTKD2:886 SCO1:1098
Esophageal Neoplasms	-0.04169373	553	8.696e-04	2.955e-01	STK11:4 PER2:40 XRC3:59 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 XRC3:59 SPPR3:87 MUL1:126
Infection	-0.04567803	466	7.826e-04	2.955e-01	PRKDC:79 IFNB1:94 CDB3:124 CLBL211:168 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 GDAPI:805 NDUFAF1:1009
Neuroblastoma	-0.02547178	1547	1.083e-03	2.955e-01	STK11:4 LCM1T1:6 RTL1:9 LRPP2:23 CLU:30 PER2:40
Obesity	-0.02388536	1789	1.073e-03	2.955e-01	MOGAT3:2 STK11:4 GPER1:14 LRPP2:23 EHMT1:36 PER2:40
Palmo-plantar 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 XRC3A:324 NIN:356 CENPJ:432 ATRX:456
Solid Neoplasm	-0.03534626	773	9.338e-04	2.955e-01	STK11:4 GYPA11:1 TRPV6:19 OPRN1:22 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 COOB8:1460 MYO1E:1508
Steroid resistant nephrotic syndrome of	0.19960441	24	7.109e-04	2.955e-01	FAT1:53 CRB2:321 NPHS1:482 NPHS2:604 COOB8:1460 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
Esophageal carcinoma	-0.03882019	595	1.326e-03	3.414e-01	STK11:4 PER2:40 XRC3:59 SUGP1:114 VDR:200 LXL2:255
Multiple Myeloma	-0.02840299	1149	1.391e-03	3.414e-01	STK11:4 LGALS9:49 NPC1:74 PRKDC:79 IFNA2:80 PROM1:92
Squamous cell carcinoma	-0.02393549	1690	1.383e-03	3.414e-01	STK11:4 STFGAL2:16 CLU:30 PER2:40 LGALS9:49 XRC3:59

customGeneSet Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NAFLDGWAS	-0.070909099	15	4.024e-01	7.191e-01	GPAM:1239 PNPLA3:1473 MTP1:1852 TM6SF2:8718 APOE:8718 TRIB1:8718
expressionDirectionalSelection	0.0501700680	42	4.794e-01	7.191e-01	ZBTB12:864 SCAPER:1326 ZNF19:1344 GSDMD:1681 TLR10:2061 SPG7:3170
HumanLocalAdaptionDietAll	-0.0006747638	13	9.940e-01	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
NA.1	NA	NA	NA	NA	NA NA NA NA NA NA
NA.2	NA	NA	NA	NA	NA NA NA NA NA NA
NA.3	NA	NA	NA	NA	NA NA NA NA NA NA
NA.4	NA	NA	NA	NA	NA NA NA NA NA NA
NA.5	NA	NA	NA	NA	NA NA NA NA NA NA
NA.6	NA	NA	NA	NA	NA NA NA NA NA NA
NA.7	NA	NA	NA	NA	NA NA NA NA NA NA
NA.8	NA	NA	NA	NA	NA NA NA NA NA NA
NA.9	NA	NA	NA	NA	NA NA NA NA NA NA
NA.10	NA	NA	NA	NA	NA NA NA NA NA NA
NA.11	NA	NA	NA	NA	NA NA NA NA NA NA
NA.12	NA	NA	NA	NA	NA NA NA NA NA NA
NA.13	NA	NA	NA	NA	NA NA NA NA NA NA
NA.14	NA	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
NA.18	NA	NA	NA	NA	NA NA NA NA NA NA
NA.19	NA	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
NA.22	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.26	NA	NA	NA	NA	NA NA NA NA NA NA
NA.27	NA	NA	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.30	NA	NA	NA	NA	NA NA NA NA NA NA
NA.31	NA	NA	NA	NA	NA NA NA NA NA NA
NA.32	NA	NA	NA	NA	NA NA NA NA NA NA
NA.33	NA	NA	NA	NA	NA NA NA NA NA NA
NA.34	NA	NA	NA	NA	NA NA NA NA NA NA
NA.35	NA	NA	NA	NA	NA NA NA NA NA NA
NA.36	NA	NA	NA	NA	NA NA NA NA NA NA

GO_Biological_Process_2023 Top pathways by non-permutation

NADH Dehydrogenase Complex Assembly (GO:0024061)	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 CDC39:113 TCTN3:157 CLPANE1:162 TMEM231:168 FAM149B:187
Mitochondrial Gene Expression (GO:014005)	0.15963371	1	2.633e-08	2.895e-05	PTCD3:58 MRPL42:73 TWNK:30 MRPL3:120 MRPS28:126 POLMT:74
Mitochondrial Translation (GO:0032543)	0.15827776	97	1.162e-07	1.047e-04	PTCD3:58 MRPL42:73 MRPL3:120 MRPS28:126 MRPS3:236 MTRF1:353
Cilium Organization (GO:0044782)	0.09978604	222	2.031e-06	1.569e-03	TCTN3:157 CLPANE1:162 TMEM231:168 FAM149B:187 FBXW8:265 CEP162:163
Proton Motive Force–Driven Mitochondrial Oxidative Phosphorylation (GO:0006119)	0.19231843	50	2.574e-06	1.740e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 NDUFB5:240 NDUFB7:291 NDUFB2:311
Mitochondrial ATP Synthesis Coupled Electron Transport	0.17600250	59	2.968e-06	1.783e-03	NDUFB10:6 ATP5PB:39 ATP5PO:100 NDUFB5:240 UQCRRH:272 NDUFB7:291
Mitochondrial ATP Synthesis Coupled Electron Transport	0.16574656	65	3.873e-06	2.094e-03	NDUFB10:6 UQCRCF:1:191 NDUFB5:240 UQCRRH:272 NDUFB7:291 NDUFB2:311
Aerobic Electron Transport Chain (GO:0006032)	0.16217735	64	3.299e-06	3.467e-03	NDUFB10:6 UQCRCF:1:191 NDUFB5:240 UQCRRH: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:0006974)	0.27637004	20	1.883e-05	7.619e-03	TWINK:90 POLMT:74 FASTKDS:207 FASTKD1:388 TFAM:423 TFB2M:520
Translation (GO:0006014)	0.08603519	208	1.973e-05	7.619e-03	PTCD3:58 MRPL42:73 MRPL3:120 RPS6KB2:125 MRPS28:126 SRBD1:151
Mitochondrial Electron Transport, NADH Dehydrogenase Complex	0.19765702	33	8.437e-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 CLPANE1:162 TMEM231:168 FAM149B:187 FBXW8:265 CEP162:163
Organic Substance Transport (GO:0071072)	-0.08091359	195	1.017e-04	3.235e-02	TRPV6:19 TRP2:230 CLCA2:153 RHCG:102 CLCA6:123
Cellular Respiration (GO:0045333)	0.11901088	82	1.976e-04	6.539e-02	NDUFB10:6 UQCRCF:1:191 NDUFB5:240 UQCRRH:272 NDUFB7:291 NDUFB2:311
Mitochondrial RNA Processing (GO:0000963)	0.33220505	9	1.981e-04	6.539e-02	TRMT10C:117 FASTKDS:207 FASTKD1:388 SUPVL31:581 PNPT1:590 FASTK2D:886
Intermediate Filament Organization (GO:0005574)	-0.13271753	65	2.175e-04	6.689e-02	KRT38:42 KRT71:49 KRT37:451 PKP1:497 KRT25:739 KRT17:779
Positive Regulation Of Mitochondrial Transcription	0.28513738	14	2.290e-04	6.689e-02	NGRN:38 TRMT10C:117 MRPS27:364 TRUB2:789 TRMT42:886 RPS28A:1226
Axonemal Dynein Complex Assembly (GO:0007037)	0.19604789	29	2.589e-04	6.636e-02	TTC12:20 DNAH2:30 CDC39:113 CDC6K5:414 DNA1:715 CAFAP7:719
Cilium Movement (GO:0003341)	0.14770532	50	2.456e-04	7.159e-02	SPAG17:71 CDC39:113 CAFAP26:221 TCT1:578 DNA1:715 CAFM:709
Mitochondrial DNA Replication (GO:000626)	-0.33509711	9	6.419e-04	1.041e-01	TWINK:90 SSBP1:424 TFAM1:709 POLG2:1037 PRIMPOL:1762 POLG:1983
Inorganic Cation Transmembrane Transport	-0.09305834	280	6.390e-04	1.382e-01	TRPV6:19 CLUJ3:30 ATPA1:70 RHCG:102 CLCA6:123 SLC6A4:123
Peptide Biosynthetic Process (GO:0043043)	0.08346762	137	7.955e-04	1.577e-01	MRML42:73 MRPL3:120 RPS6KB2:125 SRBD1:151 DMD:185 RPS15:411
RNA Methylation (GO:0030488)	0.16161026	36	7.580e-04	1.592e-01	TRMT61B:41 THADA:46 TRMT10C:117 TRMT5:839 TRMT10A:113 TTF3:1178
Intrinsic Apoptotic Signaling Pathway (GO:0006959)	-0.09359037	104	9.884e-04	1.798e-01	STK11:4 PRKDC:79 BCL2L1:168 MAP3K5:302 TRAF2:324 BAD:369
Mitochondrial Transcription (GO:0006930)	0.27439105	12	9.978e-04	1.798e-01	TWINK:90 POLMT:74 TFAM:423 TFB2M:520 MTERF1:611 CFAM:709
Sensory Perception Of Pain (GO:0191233)	-0.21336099	20	9.570e-04	1.798e-01	PRXK7:62 RETREG1:76 CCR2:781 CGL2:867 CHNRN2:634 CHRNA4:1418
Non-Motile Cilium Assembly (GO:1905515)	0.17015248	31	1.045e-03	1.823e-01	ARL13B:344 C202B:355 RGPRI3:195 RGPRI4:1473 C2C3:570 TGAAGAM1:629
Regulation Of Cold-Induced Thermogenesis	-0.0981216	141	1.090e-03	1.842e-01	STK11:4 CHMT1:36 PER2:40 IL13:183 GRB10:229 NOTCH1:343
Apoptotic Mitochondrial Changes (GO:0008000)	-0.17649704	34	1.269e-03	1.863e-01	CLUJ3:30 ERBB4:354 BIK:367 BAD:369 HK2:600 GCTG:802
Monocytic Cation Transmembrane Transport	-0.05680201	277	1.178e-03	1.863e-01	TRPV6:19 CLUJ3:30 ATPA1:70 SLC39A3:105 SLC6A4:123 SLC6A3:135
Positive Regulation Of Chemotaxis (GO:0000000)	-0.14334867	43	1.590e-03	1.863e-01	CNTN1:261 IL6:272 LGMN:340 F7:425 PDGFRB:590 VEGFA:656
Regulation Of Mitochondrial mRNA Stability	0.37964251	6	1.283e-03	1.927e-01	FASTKDS:207 FASTKD1:388 PDE12:756 FASTK2D:886 FASTK2D:886 FASTK2D:886
Regulation Of Mitochondrial Translation	0.19555479	22	1.509e-03	2.191e-01	LRPPRC:211 NGRN:38 TRMT10C:117 MRPS27:364 TRUB2:789 FASTK2D:886
Intrinsic Apoptotic Signaling Pathway In Mitochondria	-0.16928745	29	1.607e-03	2.287e-01	MAP3K5:302 TRAF2:324 BAG6:859 BAK1:999 RNF16:1071 DNACJ10:1165
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 UQCRRH:272 NDUFB7:291 NDUFB2:311 NDUFA8:393