

EnrichmentHsSymbolsFile2 Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
HOUNKPE_HOUSEKEEPING_GENES	-0.09130440	1073	1.004e-23	6.519e-20	USB1:9 PTEN:21 PA2G4:48 PPP1R11:51 EDC3:59 SNX27:73
DIAZ_CHRONIC_MYELOGENOUS_LEUKEMIA_UP	-0.04740120	1336	7.896e-09	2.564e-05	MAN2A2:25 PTPN6:38 ASAP2A:41 BCL2L1:57 TAF7:64 NQO2:65
KIM_ALL_DISORDERS_OLIGODENDROCYTE_NUMBER	-0.06201641	711	2.000e-08	3.862e-05	RPLP1:2 SL2C5A4:20 MAN2A2:25 PPP1R11:51 PSMD7:114 TUBA1A:125
KIM_BIPOLAR_DISORDER_OLIGODENDROCYTE_DEN	-0.06484147	643	2.256e-08	3.862e-05	RPLP1:2 SL2C5A4:20 MAN2A2:25 PPP1R11:51 RPL12:69 CDK16:77
REACTOME_METABOLISM_OF_RNA	-0.06372328	654	3.029e-08	3.935e-05	RPLP1:2 A1CF:33 EDC3:59 RPL12:69 PSMC3:89 TRMT9B:94
REACTOME_MRNA_SPLICING	-0.11753720	183	4.271e-08	4.623e-05	RNPS1:284 POLR2D:334 LENC1:355 HNRNP:374 SF3A1:431 DDX46:467
REACTOME_PROCESSING_OF_CAPPED_INTRON_CON	-0.09528719	254	1.764e-07	1.636e-04	ZC3H11A:171 RNPS1:284 THOC6:310 POLR2D:334 LENG1:355 HNRNPF:374
SPIELMAN_LYMPHOBLAST_EUROPEAN_VS_ASIAN_D	-0.06208345	573	4.108e-07	3.335e-04	PTEN:21 ERGIC3:111 MRPL49:157 DCTN4:170 COX7A2L:173 RPLA3:178
REACTOME_INFECTIOUS_DISEASE	-0.05000121	878	5.636e-07	4.067e-04	RPLP1:2 SL2C5A4:20 PTPN6:38 BCL2L1:57 TAF7:64 RPL12:69
BLALOCK_ALZHEIMERS_DISEASE_DN	-0.04262467	1189	8.774e-07	5.698e-04	PTEN:21 SYT5:35 PPP1R11:51 CDK16:77 MAP2K4:127 DIO2:160
REACTOME_HIV_INFECTION	-0.09460231	216	1.695e-06	1.001e-03	RPLP1:2 SL2C5A4:20 PTPN6:38 PSMC3:113 PSMD7:114 GTF2E1:121
KIM_ALL_DISORDERS_CALB1_CORR_UP	-0.06078117	517	2.395e-06	1.296e-03	SLC25A4:20 MAN2A2:25 PSMD7:114 MAP2K4:127 PRKAR2B:164 COX7A2L:173
KARLSSON_TGFB1_TARGETS_UP	-0.12579219	115	3.199e-06	1.598e-03	SRM:108 GEMIN3:122 TCPA:233 EIF5:300 SHMT2:311 GADD45G:332
REACTOME_ADAPTIVE_IMMUNE_SYSTEM	-0.05059337	727	3.704e-06	1.718e-03	RNF25:10 PTEN:21 PTPN6:38 PSMC3:89 DET1:110 PSMD3:113
REACTOME_METABOLISM_OF_AMINO_ACIDS_AND_D	-0.05759337	348	4.657e-06	2.016e-03	RPLP1:2 SL2C6A8:19 RPL12:69 PSMC3:89 SRM:108 PSMD3:113
FLORIO_NEOCORTEX_BASAL_RADIAL_GLIA_DN	0.06969056	186	5.200e-06	2.111e-03	KIF18A:64 SPAG5:87 APOD:139 DLGAP5:145 NCAPD2:219 TRIM59:321
REACTOME_DISEASES_OF_SIGNAL_TRANSDUCTION	-0.06509099	414	5.779e-06	2.207e-03	FZD8:7 PTEN:21 FGF18:29 DLL4:46 BCL2L1:57 PSMC3:89
CHAUHAN_RESPONSE_TO_METHOXYESTRADIOL_DN	-0.13359256	93	8.547e-06	2.828e-03	PTPN6:38 HERPUD1:49 RPL12:69 EIF3M:809 NME4:843 MARCKS:193
BLANGES_RAPAMYCIN_SENSITIVE_VIA_TSC1_AN	-0.06176213	67	9.146e-06	2.828e-03	NAA10:79 TCP1:223 PRDX3:283 PAIC3:1026 TUBB4A:1047 ACOT1:1384
LOPEZ_MBD_TARGETS	-0.04395223	895	9.061e-06	2.828e-03	NKIRAS2:1 COQ4:18 PA2G4:48 IRX4:63 NQO2:65 CDK16:77
DACOSTA_UV_RESPONSE_VIA_ERCC3_UP	-0.07490212	299	8.650e-06	2.828e-03	SLC6A8:19 PTPN6:38 PSMC3:89 PSMC3:113 PSMD7:114 GTF2E1:121
CAIRORELLI_UVC_RESPONSE_VIA_TP53_GROUP_B	-0.05515801	625	1.614e-05	4.765e-03	TSNAP1:67 PGLYRP1:71 EDEM1:124 HYL3:133 MSX2:1362 FANCM:391
BSOURELIL_ACUTE_PROMYELOCYTIC_LEUKEMIA_D	-0.04989694	543	1.689e-05	4.768e-03	SLC25A4:20 EDC3:59 PSMC3:89 PSMC3:113 TUBB2B:119 TJP2:137
DANG_MOOD_BY_MYC	-0.03971914	1010	2.102e-05	5.689e-03	MAN2A2:25 PTPN6:38 PA2G4:48 HERPUD1:49 CDK16:77 MNKN1:476
MOOTHA_PGC	-0.06178211	403	2.277e-05	5.915e-03	SLC25A4:20 RPA3:178 PSMC3:89 RPL12:69 KILG:138 KILG:261 TIMM10B:278
REACTOME_ANTIGEN_PROCESSING_UBIQUITINATI	-0.07173766	293	2.462e-05	5.921e-03	RNF25:10 PSMC3:89 DET1:110 PSMD3:113 PSMD7:114 KHLH:200
UV_MRNA_PROCESSING	-0.07173766	198	2.371e-05	5.921e-03	CELF2:37 RNPS1:284 SF3A1:431 CLASP:91 SRSF2:616 SRSF7:722
REACTOME_MRNA_SPLICING_MINOR_PATHWAY	-0.19246747	39	3.196e-05	7.353e-03	POLR2D:334 SRSF2:616 SRSF7:722 SNRNP40:867 DSDM2:392 RNPC3:1023
HSIAO_HOUSEKEEPING_GENES	-0.06427675	355	3.284e-05	7.530e-03	RPLP1:2 SL2C6A8:19 PTPN6:38 PTPN6:38 PSMD3:114 CLIC1:251
REACTOME_SIGNALING_BY_WNT	-0.06950061	300	3.553e-05	7.483e-03	FZD8:7 PSMC3:89 AXIN1:97 PSMD3:113 MAP2K4:114 AP2A1:188
BENPORATH_MYC_MAX_TARGETS	-0.04489804	736	3.617e-05	7.483e-03	RPLP1:2 TUBB2B:119 PSME1:324 KILG:348 SLC25A10:397 CASK:488
ENK_UV_RESPONSE_KERATINOCTE_UP	-0.05372796	506	3.687e-05	7.483e-03	SLC6A8:19 INSL4:50 PPP1R11:51 TAF7:64 RPL12:69 CDK16:77
GRAESSMANN_APOPTOSIS_BY_DOKRUBICIN_UP	-0.03702533	1096	3.915e-05	7.704e-03	SLC6A8:19 PTPN6:38 PA2G4:48 CDK16:77 MNKN1:476 PDHB:181
MARTENS_TRETINOLIN_RESPONSE_DN	-0.04469529	731	4.156e-05	7.938e-03	PA2G4:48 TAF7:64 CDK16:77 SRM:108 PSMD7:114 PDHB:181
REACTOME_SIGNALING_BY_NOTCH	-0.08061823	214	4.692e-05	8.730e-03	DLL4:46 PSMC3:89 PSMC3:113 PSMD7:114 STG3A1:145 TNRC6B:219
WAKABAYASHI_HAPOGENESIS_PPARG_RXRA_BOUN	-0.04185924	822	4.917e-05	8.869e-03	RASSF6:38 PTPN6:38 PML1:51 G56 EDC3:59 CLN3:211 MNKN1:476
REACTOME_CELLULAR_RESPONSES_TO_STIMULI	-0.06178213	752	5.961e-05	1.047e-02	RPLP1:2 HERPUD1:49 RPL12:69 PSMC3:89 MAP2K7:107 PSMD3:113
GRADE_COLON_AND_RECTAL_CANCER_UP	-0.07000982	174	6.801e-05	1.162e-02	PA2G4:48 NQO2:65 NAA10:79 ZDHHC9:117 GEMIN6:122 MDC1:132
PAL_PRMTs_TARGETS_UP	-0.08350840	190	7.312e-05	1.216e-02	FTSL1:54 PSMD3:113 PCDP61P:190 MCM2:195 KIF23:45
TIEN_INTESTINE_PROBIOTICS_2HR_UP	-0.22017858	27	7.493e-05	1.216e-02	SEL1L3:209 ANP3A:319 ST6GALNAC4:385 GAPDH:805 KDELR1:1533 HSPA8:1612

DisGeNET Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
Nephrosis, congenital	0.28936355	14	1.778e-04	3.678e-01	TREH:159 AFP:226 CD2AP:960 CRB2:1311 SIRPA:1364 NPHS1:1607
Acanthosis	0.18562834	33	2.247e-04	3.678e-01	CARD14:107 ALOX12B:478 TGM1:625 KRT13:772 ALOXES:1086 ENPP1:1596
Epileptic encephalopathy	-0.05064618	47	2.622e-04	3.678e-01	ALG2:24 ALG2:18 COQ4:18 SLC6A8:19 PTEN:21 SRPX2:90
Erythrokeratoderma	0.16551733	41	2.465e-04	3.678e-01	CARD14:107 DSP:407 ALOX12B:478 KRT17:706 ALOXES:1086 DES:1567
Non-Small Cell Lung Carcinoma	-0.02628227	1886	2.325e-04	3.678e-01	SLC6A8:19 PTEN:21 PTPN6:38 AQP1:42 DLL4:46 LINC28:47
Palmoaplanter Keratosis	0.11505943	95	1.081e-04	3.678e-01	PLEC:20 CARD14:107 DSP:407 ALOX12B:478 PKP1:508 TGM1:625
Primary microcephaly	0.10242299	110	2.101e-04	3.678e-01	KNL1:195 FANCD2:344 CDK5RAP2:290 ERCO8:309 SMRT1:582 FANCM:391
Pruritus	0.09112783	131	3.229e-04	3.964e-01	SSTR4:22 SCN9A:90 COL7A1:91 CARD14:107 GPBAR1:135 TRPV1:209
Absent earlobe	0.29611221	12	3.827e-04	4.176e-01	COL3A1:917 CENPJ:941 RBBP8:1429 ESCO2:1637 TRAF1:1745 CEP152:1805
Epilepsy	-0.03171990	1108	4.460e-04	4.379e-01	ALG2:4 ALG9:16 SLC6A8:19 PTEN:21 AQP1:42 NAA10:79
Angina, Unstable	-0.12626774	62	5.894e-04	5.117e-01	BDNF:470 TNFRSF11A:510 ITGA2B:517 GP1BA:529 F2:562 FSD1L:587
DEAFNESS, AUTOSOMAL RECESSIVE (disorder)	0.15485892	35	1.526e-03	5.117e-01	OTOF:487 PTPRQ:526 RIPOR2:681 CDH23:878 BDP1:1379 TFF1:1827
Hyalinosis, Segmental Glomerular	0.16869416	26	2.912e-03	5.117e-01	HAVCR1:110 MYH10:369 CD2AP:960 TGFBI:1272 CRB2:1311 NPHS1:1607
Hyperkeratosis, Epidermolytic	0.22927282	16	3.498e-03	5.117e-01	COL7A1:91 KRT80:276 DSP:407 ALOX12B:478 TGM1:625 ALOXES:1086
Mammary Carcinoma, Animal	-0.07417974	128	3.804e-03	5.117e-01	AQP1:42 TUBB2B:119 PSME1:324 KILG:348 SLC25A10:397 CASK:488
Mammary Neoplasms, Experimental	-0.07377260	148	1.984e-03	5.117e-01	AQP1:42 MAP2K7:107 TUBB2B:119 PSME1:324 KILG:348 SLC25A10:397
Other specified forms of pleural effusio	0.22778053	15	2.256e-03	5.117e-01	PTAFR:165 BDKRB1:529 PLAG2G:1083 TNF:2479 ELANE:3043 BDKRB2:3147
Abnormality of the hypothalamus-pituitar	0.25050544	14	1.174e-03	5.117e-01	PRTN3:423 RNF126:435 PTPN22:514 HESX1:548 LHX4:582 PROP1:1051
Adult Rickets	0.18842560	20	3.535e-03	5.117e-01	LRP2:112 DMP1:786 TGFBI:1272 ENPP1:1596 TNFSF11:2704 FGF23:2718
alpha 1-Antitrypsin Deficiency	0.15163550	35	1.912e-03	5.117e-01	ATF6:187 AQP1:42 CRP:549 BPI:809 A2M:1031 TGFBI:1272
Anaplastic carcinoma	-0.06230899	190	3.126e-03	5.117e-01	PTEN:21 PTPN1:42 BCL2L1:57 TUBB2B:119 LY96:130 PSME1:324
Animal Mammary Neoplasms	-0.07417974	128	3.804e-03	5.117e-01	AQP1:42 TUBB2B:119 PSME1:324 KILG:348 SLC25A10:397 CASK:488
Arthralgia	0.08199840	120	1.949e-03	5.117e-01	CALCA:324 CYP17A1:332 PRTN3:423 PTPN22:514 CRP:549 PTH1R:579
Arthropathy	0.08202515	117	2.029e-03	5.117e-01	LRPPRC:48 CPB1:259 CH3L1:448 CRP:549 HCR:693 NOD2:892
Autosomal Recessive Primary Microcephaly	0.21733440	25	2.029e-03	5.117e-01	KNL1:195 CDK5RAP2:290 SAS56:913 STL1:926 CENPJ:941 CEP135:1561
Carcinoma	-0.06818457	191	1.187e-03	5.117e-01	PTEN:21 AQP1:42 BCL2L1:57 TUBB2B:119 LY96:130 PSME1:324
Cellulitis of periorbital region	0.21026633	17	6.886e-03	5.117e-01	PIEZO1:320 PRTN3:423 PTPN22:514 BAZ1B:1184 GTF2I:1540 SUMF1:1559
Cerebral Infarction	-0.05643233	255	1.975e-03	5.117e-01	MAP2K7:107 TLK2:212 JUND:392 EPHX2:393 CXCL12:405 BDNF:470
Cholestasis in newborn	0.09453796	87	3.226e-03	5.117e-01	GPBAR1:135 ABCB1:139 PKHD1:799 MPI:971 PEX1:1141 ABCB4:1168
Chondroma	-0.28503820	10	1.801e-03	5.117e-01	BCL2L1:57 IDH1:813 RUNX2:1331 CD6:2076 IDH2:2673 SOX4:5187
Clubbed Fingers	0.21130522	21	8.030e-04	5.117e-01	DSP:407 STK11:412 PTH1R:579 SLC02A1:1039 RTKL:11388 SFTPA1:2733
Communication delay	0.37358949	5	3.649e-03	5.117e-01	NSD1:11 SRCAP:1002 GENE:1989 RAI1:3791 FLMN:4925 NA
Congenital ichthyosis	0.13364234	47	1.533e-03	5.117e-01	ALOX12B:478 TGM1:625 CYP4F2:758 ALOXES:1086 DMO:1273 TGM5:1320
Craniofacial Abnormalities	-0.06678024	177	2.226e-03	5.117e-01	PTEN:21 MSX2:146 MED13L:169 B3GAT3:180 RAX:233 FOXC2:383
Deficit in expressive language	0.30215825	9	1.695e-03	5.117e-01	NSD1:11 BPTF:475 SRCAP:1002 GENE:1989 UBE3A:3097 RAI1:3791
Disease of capillaries	-0.15886255	28	3.626e-03	5.117e-01	WDR1:181 PLG:672 AGT:703 SMDP1:193 SLC9C1:1375 PEMT:1849
Exaggerated acoustic startle response	-0.27161856	10	2.937e-03	5.117e-01	ARHGEF9:835 GPHN:842 ASNS:1233 HEXA:1997 KLC2:2696 SLC6A9:3520
Exaggerated startle response	-0.25292150	11	3.677e-03	5.117e-01	ARHGEF9:835 GPHN:842 ASNS:1233 HEXA:1997 KLC2:2696 SLC6A9:3520
Familial benign neonatal epilepsy	0.23970903	13	2.767e-03	5.117e-01	SCN2A:211 CHRNA4:736 LGI4:1646 KCNQ3:1910 SLC2A1:2871 CSTB:4068
Finnish congenital nephrotic syndrome	0.35661245	6	2.485e-03	5.117e-01	TREH:159 AFP:226 ALG1:1476 NPHS1:1607 NPHS2:2089 APLP1:10561

customGeneSet Top pathways by non-permutation

Geneset	stat	num.genes	pval	p.adj	gene.vals
NAFLDQWAS	0.12060606	15	1.544e-01	4.632e-01	INSR:2306 PNPLA3:3707 ADH1B:4161 MTARC1:4655 GPAM:7099 FTO:7303
HumanLactAdaptionDietAll	-0.06275304	13	4.825e-01	5.252e-01	SEPS2CS:814 CREBRF:1304 CELF1:2701 AS3MT:4174 GPX3:5444 SLC22A4:5680
expressionDirectionalSelection	-0.04506803	42	5.252e-01	5.252e-01	AXIN1:97 FADS1:669 COMM06:784 ITGAM:1062 LGSAL2:1284 MAPT:1771
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

Ubiquitin-Dependent Protein Catabolic Pr	-0.05887771	349	1.684e-04	1.055e-01	RNF25:10 HERPUD1:49 PPP1R1:51 PSMC3:89 AXIN1:97 PSMD3:113
RNA Processing (GO:0006396)	-0.02894775	170	1.965e-04	1.063e-01	USB1:9 CELF2:37 LIN28A:47 RNF1:54 PSMC28:418 KIN:288 HNRNPF:374
Protein Localization To Centrosome (GO:0	0.25798753	17	2.310e-04	1.136e-01	KIA0753:17 SPAG5:87 CEP250:116 MBMD1:204 CEP192:207 C2CD3:368
Establishment Of Mitotic Spindle Localiz	0.17989527	33	3.495e-04	1.575e-01	CDK5RAP2:290 NUMA1:551 NDC80:657 PKH1:799 ITGB1:895 HTT:974
Centromere Complex Assembly (GO:0034508)	0.27255774	14	1.412e-04	1.600e-01	CENPT:129 DLGAPs:145 CENPC:480 HJURP:698 NASP:1263 CENPF:1316
Monooctatic Carbon Transport (GO:0006812)	0.15826985	42	3.887e-04	1.600e-01	TRPM6:56 LRP2:112 CALHM1:132 PKD1L3:251 CNGB3:262 CLDN16:289
Inorganic Cation Transmembrane Transport	0.06067629	280	4.985e-04	1.1797e-01	SLC6A6:47 TRPM6:56 SCN9A:90 CLU:148 KCNN3:167 KCNA10:186
Mitochondrial RNA Metabolic Process (GO:	0.22271096	20	5.655e-04	1.911e-01	POLRMT:224 TRPM:211 TEFM:352 TFB2M:430 FASTKD1:434 TWNK:452
Mitochondrial RNA Processing (GO:0000963)	0.32799965	9	6.557e-04	1.970e-01	TRMT10C:415 FASTKD1:443 FASTKD7:509 FASTKD7:717 SUPV3L1:2491 FASTKD3:2767
Mitochondrion Disassembly (GO:0061726)	-0.16960460	34	6.227e-04	1.970e-01	WIPI2:250 FISI:398 MAP2K1LCB8:420 ATGB28:558 ATG3:613 CSD2:1031
Kinetochoe Assembly (GO:0051382)	0.32329135	9	7.836e-04	2.118e-01	CENPT:129 DLGAPs:145 CENPC:480 CENPF:1316 NPC1:1727 M51:32033
Protein Localization To Microtubule Orga	0.25111302	15	7.596e-04	2.118e-01	KIA0753:17 SPAG5:87 CEP250:116 MBMD1:204 CEP192:207 C2CD3:368
Attachment Of Mitotic Spindle Microtubul	0.27749092	12	8.737e-04	2.147e-01	CENPC:480 NDC80:657 KIF2C:863 DCT1:2906 M51:32033 CENPE:3178
Folic Acid Metabolic Process (GO:0046655)	-0.27234533	12	1.088e-03	2.147e-01	SHMT2:311 SLC19A1:567 DHFR2:583 MTHFD3:1329 SLCA461:2001 SHMT1:3448
Kinetochoe Organization (GO:0051383)	0.29776997	10	1.112e-03	2.147e-01	CENPT:129 DLGAPs:145 CENPC:480 CENPF:1316 NPC1:1727 M51:32033
Macroautophagy (GO:0016236)	-0.09603176	99	9.735e-04	2.147e-01	TBC1D5:80 VPS37B:155 CLN3:211 WIPI2:250 CHMP2A:280 MAP1LC3B:420
Monooctatic Carbon Transmembrane Transport	0.05761394	277	1.007e-03	2.147e-01	SLC6A6:47 TRPM6:56 SCN9A:90 CLU:148 KCNN3:167 KCNA10:186
Positive Regulation Of Telomere Capping	-0.24429859	15	1.054e-03	2.147e-01	MAP2K7:107 TNKS2:1128 NEK7:1291 MAPK1:1072 NASP:5:2112 MAP3K4:2309
Regulation Of Mitochondrial mRNA Stabili	0.39053763	6	9.230e-04	2.147e-01	FASTKD1:443 FASTKD7:509 FASTKD7:717 PDE12:1124 FASTKD3:2767 TBRG4:5555
Resolution Of Meiotic Recombination Inte	0.25690616	14	8.744e-04	2.147e-01	HFM1:234 SHOCH1:313 FANCM:391 RRM1:828 EME1:1019 EME2:1417
Autophagosome Maturation (GO:0097352)	-0.14253202	42	1.399e-03	2.161e-01	CLN3:211 WIPI2:250 CHMP2A:280 MAP1LC3B:420 UBQLN1:805 CHMP1A:1134
Autophagy Of Mitochondrion (GO:0000422)	-0.19386954	44	1.387e-03	2.161e-01	WIPI2:250 FISI:398 MAP2K1LCB8:420 ATGB28:558 ATG3:613 CSD2:1031
Positive Regulation Of DNA Biosynthetic	0.11572693	63	1.264e-03	2.161e-01	MAP2K7:107 TCP1:223 SMOCC7:717 AURKB:821 HMBXO1:900 KLF4:1018
Positive Regulation Of DNA-templated Tra	-0.02794451	1204	1.324e-03	2.161e-01	TAZF64: HAS3:75 DYRK1B:687 PSMC3:89 AXIN1:97 MAP2K7:107
Positive Regulation Of Telomerase Activ	-0.16352386	32	1.371e-03	2.161e-01	MAP2K7:107 TCP1:223 AURKB:821 HMBXO1:900 KLF4:1018 HSP90A1:1056
Positive Regulation Of Telomerase Maintena	-0.11659984	33	3.199e-03	2.161e-01	MAP2K7:107 TCP1:223 AURKB:821 HMBXO1:900 TNKS2:1128 ATN:1281
Purine-Containing Compound Metabolic Pro	-0.35173540	7	1.270e-03	2.161e-01	GUK1:187 HFI:1969 MACROD2:2089 TTR:2280 MACROD1:2900 PRPS1:3130
Sister Chromatid Segregation (GO:0000819	0.15766624	34	1.469e-03	2.207e-01	KIF18A:614 SPAG5:87 SMC4:565 NDC80:657 NUSAP1:983 SGO1:1603
Endonucleolytic Cleavage Of Tricostic	-0.28179719	12	1.689e-03	2.440e-01	NOL9:390 SDE2:1201 UTP20:1304 TRT:1976 NP14:1996 KRI1:4013
Vesicle Budding From Membrane (GO:000690	-0.16827027	29	1.715e-04	2.440e-01	TRAPPCC1:304 TRAPPCC5:504 GOLPH3L:1055 TMEED1:1016 TRAPPCC5:2164 CHMP4A:2215
Regulation Of Telomere Capping (GO:19043	-0.10795948	21	1.773e-03	2.459e-01	MAP2K7:107 USP7:543 AURKB:821 TNKS2:1128 NEK7:1291 MAPK1:1702
Homophilic Cell Adhesion Via Plasma Memb	0.11623849	60	1.857e-03	2.510e-01	HMCN1:247 CADM3:404 ROBO1:633 TENN3:832 ITGB1:895 PECAM1:1085

MGI_Mammalian_Phentotype_Level_4 Top pathways by non-permutation