

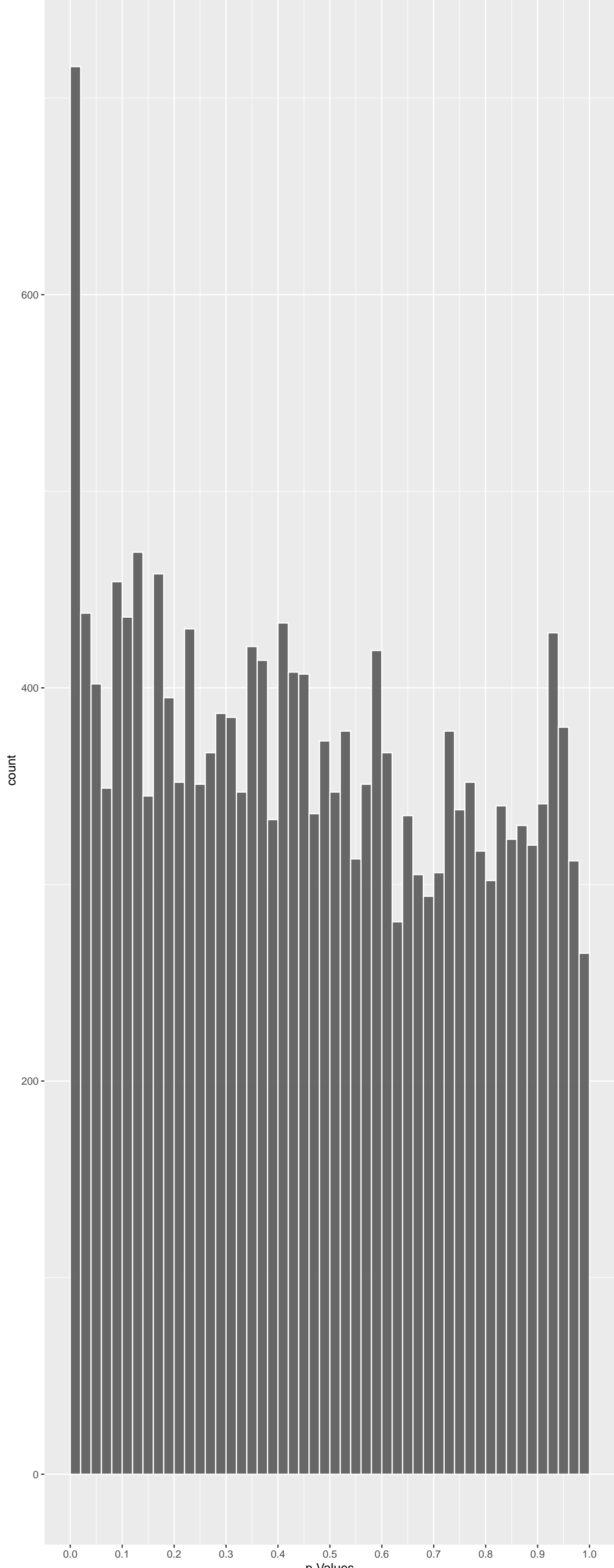
Top genes by P-value non-permulated

| Gene | Rho | N | P | p.adj | qValueNoperm |
|----------|-----------|-----|-----------|-----------|--------------|
| CAPN8 | 0.2881746 | 204 | 1.230e-12 | 2.291e-08 | 3.725e-04 |
| ANKRD35 | 0.2744398 | 203 | 5.540e-12 | 5.160e-08 | 4.196e-04 |
| RXFP4 | 0.2552635 | 161 | 7.063e-09 | 4.386e-05 | 1.433e-01 |
| DNAH2 | 0.1866714 | 213 | 1.312e-08 | 6.108e-05 | 1.433e-01 |
| BNC1 | 0.2002449 | 196 | 1.696e-08 | 6.318e-05 | 1.433e-01 |
| ADGRG4 | 0.2235319 | 172 | 2.534e-08 | 7.446e-05 | 1.433e-01 |
| USP43 | 0.1854671 | 206 | 2.798e-08 | 7.446e-05 | 1.433e-01 |
| PPP4R1 | 0.1968052 | 192 | 3.452e-08 | 8.038e-05 | 1.433e-01 |
| AGGF1 | 0.1996389 | 188 | 3.913e-08 | 8.100e-05 | 1.433e-01 |
| ITGB4 | 0.1791397 | 201 | 8.143e-08 | 1.264e-04 | 1.433e-01 |
| NSD1 | 0.1748890 | 206 | 8.047e-08 | 1.264e-04 | 1.433e-01 |
| TMEM131L | 0.1692543 | 213 | 7.931e-08 | 1.264e-04 | 1.433e-01 |
| ZNF292 | 0.1706157 | 209 | 9.607e-08 | 1.377e-04 | 1.433e-01 |
| POLM | 0.1706697 | 202 | 1.708e-07 | 1.989e-04 | 1.433e-01 |
| PRUNE2 | 0.1554104 | 222 | 1.675e-07 | 1.989e-04 | 1.433e-01 |
| ZZEF1 | 0.1631185 | 212 | 1.617e-07 | 1.989e-04 | 1.433e-01 |
| KIAA0753 | 0.1649811 | 208 | 1.841e-07 | 2.017e-04 | 1.433e-01 |
| ACAD10 | 0.1665332 | 204 | 2.177e-07 | 2.027e-04 | 1.433e-01 |
| CCPG1 | 0.1751602 | 194 | 2.177e-07 | 2.027e-04 | 1.433e-01 |
| MR1 | 0.1883105 | 179 | 2.503e-07 | 2.027e-04 | 1.433e-01 |
| PLEC | 0.1674169 | 202 | 2.348e-07 | 2.027e-04 | 1.433e-01 |
| SSTR4 | 0.2520543 | 134 | 2.498e-07 | 2.027e-04 | 1.433e-01 |
| STYXL2 | 0.1608269 | 210 | 2.391e-07 | 2.027e-04 | 1.433e-01 |
| DAXX | 0.1791397 | 184 | 3.579e-07 | 2.626e-04 | 1.482e-01 |
| HERC2 | 0.1636672 | 201 | 3.666e-07 | 2.626e-04 | 1.482e-01 |

Top genes by Q-Value non-permulated

| Gene | Rho | N | P | p.adj | qValueNoperm |
|----------|-----------|-----|-----------|-----------|--------------|
| CAPN8 | 0.2881746 | 204 | 1.230e-12 | 2.291e-08 | 3.725e-04 |
| ANKRD35 | 0.2744398 | 203 | 5.540e-12 | 5.160e-08 | 4.196e-04 |
| ACAD10 | 0.1665332 | 204 | 2.177e-07 | 2.027e-04 | 1.433e-01 |
| ADGRG4 | 0.2235319 | 172 | 2.534e-08 | 7.446e-05 | 1.433e-01 |
| AGGF1 | 0.1996389 | 188 | 3.913e-08 | 8.100e-05 | 1.433e-01 |
| BNC1 | 0.2002449 | 196 | 1.696e-08 | 6.318e-05 | 1.433e-01 |
| CCPG1 | 0.1751602 | 194 | 2.177e-07 | 2.027e-04 | 1.433e-01 |
| DNAH2 | 0.1866714 | 213 | 1.312e-08 | 6.108e-05 | 1.433e-01 |
| ITGB4 | 0.1791397 | 201 | 8.143e-08 | 1.264e-04 | 1.433e-01 |
| KIAA0753 | 0.1649811 | 208 | 1.841e-07 | 2.017e-04 | 1.433e-01 |
| MR1 | 0.1883105 | 179 | 2.503e-07 | 2.027e-04 | 1.433e-01 |
| NSD1 | 0.1748890 | 206 | 8.047e-08 | 1.264e-04 | 1.433e-01 |
| PLEC | 0.1674169 | 202 | 2.348e-07 | 2.027e-04 | 1.433e-01 |
| POLM | 0.1706697 | 202 | 1.708e-07 | 1.989e-04 | 1.433e-01 |
| PPP4R1 | 0.1968052 | 192 | 3.452e-08 | 8.038e-05 | 1.433e-01 |
| PRUNE2 | 0.1554104 | 222 | 1.675e-07 | 1.989e-04 | 1.433e-01 |
| RXFP4 | 0.2552635 | 161 | 7.063e-09 | 4.386e-05 | 1.433e-01 |
| SSTR4 | 0.2520543 | 134 | 2.498e-07 | 2.027e-04 | 1.433e-01 |
| STYXL2 | 0.1608269 | 210 | 2.391e-07 | 2.027e-04 | 1.433e-01 |
| CAMSAP1 | 0.1558413 | 201 | 7.835e-07 | 4.009e-04 | 1.482e-01 |
| DAXX | 0.1791397 | 184 | 3.579e-07 | 2.626e-04 | 1.482e-01 |

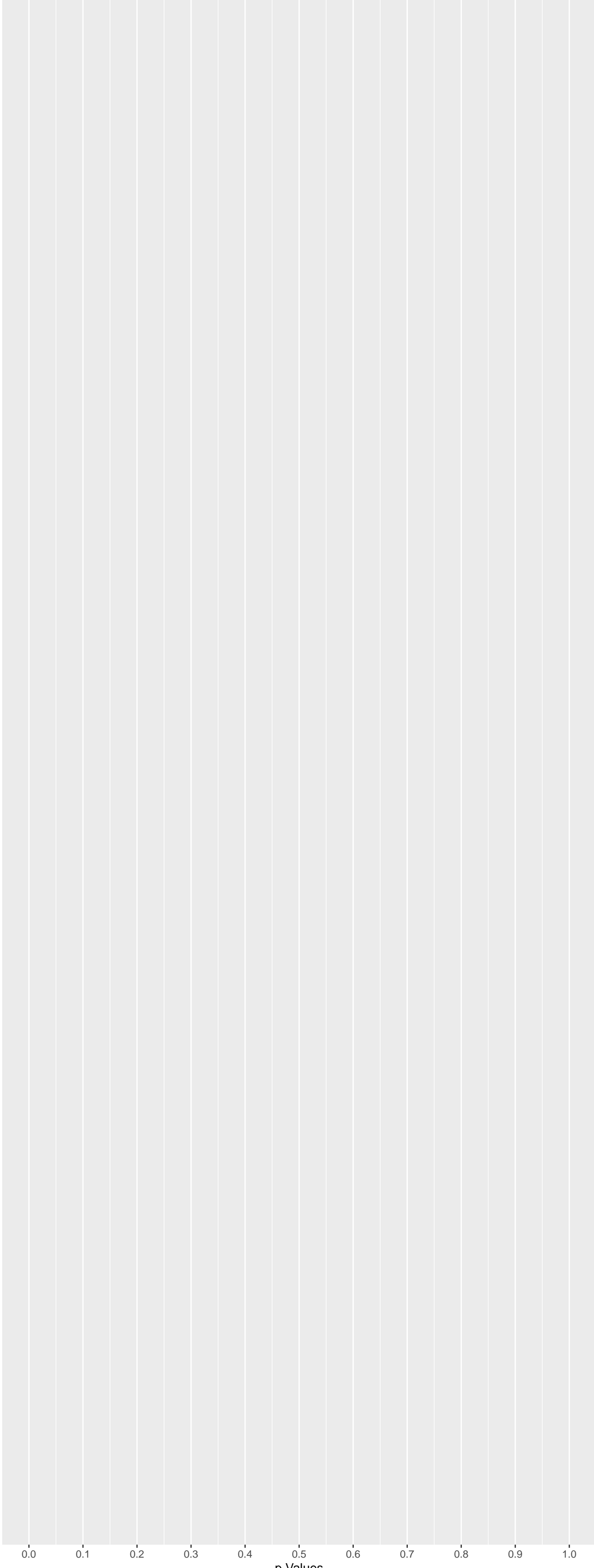
Positive Rho Non-permulated



Top Positive genes by P-value non-permulated

| Gene | Rho | N | P | p.adj | qValueNoperm |
|---------|-----------|-----|-----------|-----------|--------------|
| CAPN8 | 0.2881746 | 204 | 1.230e-12 | 2.291e-08 | 3.725e-04 |
| ANKRD35 | 0.2744398 | 203 | 5.540e-12 | 5.160e-08 | 4.196e-04 |
| RXFP4 | 0.2552635 | 161 | 7.063e-09 | 4.386e-05 | 1.433e-01 |
| DNAH2 | 0.1866714 | 213 | 1.312e-08 | 6.108e-05 | 1.433e-01 |
| BNC1 | 0.2002449 | 196 | 1.696e-08 | 6.318e-05 | 1.433e-01 |
| ADGRG4 | 0.2235319 | 172 | 2.534e-08 | 7.446e-05 | 1.433e-01 |
| USP43 | 0.1854671 | 206 | 2.798e-08 | 7.446e-05 | 1.433e-01 |
| PPP4R1 | 0.1968052 | 192 | 3.452e-08 | 8.038e-05 | 1.433e-01 |
| AGGF1 | 0.1996389 | 188 | 3.913e-08 | 8.100e-05 | 1.433e-01 |
| ITGB4 | 0.1791397 | 201 | 8.143e-08 | 1.264e-04 | 1.433e-01 |

Negative Rho Non-permulated



Top Negative genes by P-value non-permulated

| Gene | Rho | N | P | p.adj | qValueNoperm |
|------|-----|----|----|-------|--------------|
| NA | NA | NA | NA | NA | NA |
| NA.1 | NA | NA | NA | NA | NA |
| NA.2 | NA | NA | NA | NA | NA |
| NA.3 | NA | NA | NA | NA | NA |
| NA.4 | NA | NA | NA | NA | NA |
| NA.5 | NA | NA | NA | NA | NA |
| NA.6 | NA | NA | NA | NA | NA |
| NA.7 | NA | NA | NA | NA | NA |
| NA.8 | NA | NA | NA | NA | NA |
| NA.9 | NA | NA | NA | NA | NA |

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 MAN2A2:25 PTPN6:38 AQP1:42 DLL4:46 LINC24:47 |
| REACTOME_MRNA_SPLICING | -0.11753720 | 183 | 4.271e-08 | 4.623e-05 | RNPS1:284 POLR2D:334 LENC1:355 HNRNPF: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 RPL3A: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 PSMD3:113 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 TCP1:23 E1F5:300 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 | -0.05759336 | 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 |
| BILANGES_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 | -0.04395232 | 895 | 9.061e-06 | 2.828e-03 | NKIRAS2:1 COQ4:18 PA2G4:48 IRIX:63 NQO2:65 CDK16:77 |
| DACOSTA_UV_RESPONSE_VIA_ERCC3_UP | -0.07490212 | 299 | 8.650e-06 | 2.828e-03 | SLC6A8:19 PTPN6:38 LIN37:24 CDK16:77 PSMD3:113 PSMD3:89 |
| CAUSELLI_UVC_RESPONSE_VIA_TP53_GROUP_B | -0.05515801 | 625 | 1.614e-05 | 4.765e-03 | TSNAP1:67 PGLYRP1:71 EDEM1:124 HYL3:133 MSX2:136 WIP1:250 |
| SORELLI_ACUTE_PROMYELOCYTIC_LEUKEMIA_D | -0.04989694 | 643 | 1.689e-05 | 4.768e-03 | SLC25A4:20 EDC3:59 PSMC3:89 P1 PSMD3:89 TUBB2B:119 TJP2:137 |
| DANG_MOOD_BY_MYC | -0.03979154 | 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 KILG:183 GUK1:187 CDKN2D: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 | -0.07123329 | 198 | 2.371e-05 | 5.921e-03 | CELF2:37 RNPS1:284 SF3A1:431 CLASP1:931 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 RNP3C3:1023 |
| HSIAO_HOUSEKEEPING_GENES | -0.06427675 | 355 | 3.284e-05 | 7.353e-03 | RPLP1:2 SL2C6A8:19 PTPN6:38 PTPN6:38 PSMD3:113 CLIC1:251 |
| REACTOME_SIGNALING_BY_WNT | -0.06950060 | 300 | 3.535e-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 PTPN6:38 PA2G4:48 CDK16:77 MNKN1:78 MAP2K7:107 |
| 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 | -0.03702530 | 1096 | 3.915e-05 | 7.704e-03 | SLC6A8:19 PTPN6:38 AQP1:42 PA2G4:48 PSMC3:89 SCIN:95 |
| MARTENS_TRETINOLIN_RESPONSE_DN | -0.04469529 | 731 | 4.156e-05 | 7.938e-03 | PA2G4:48 TAF7:64 CDK16:77 SRM:108 PSMD7:114 PDHB:186 |
| REACTOME_SIGNALING_BY_NOTCH | -0.08061823 | 214 | 4.692e-05 | 8.705e-03 | DLL4:46 PSMC3:89 PSMC3:113 PSMD7:114 ST3GAL1:145 TNRC6B:219 |
| WAKABAYASHI_HYPOPHOSPHENIS_PPARG_RXRA_BOUN | -0.04185924 | 822 | 4.917e-05 | 8.869e-03 | RASSF6:38 PTPN6:38 PEXL1:656 EDC3:59 CLN3:211 MNKN1:476 |
| REACTOME_CELLULAR_RESPONSES_TO_STIMULI | -0.06178626 | 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 PSMD3:89 PDCD6IP:190 MCM2:195 KIF23:45 CCL12:405 |
| TIEN_INTESTINE_PROBIOTICS_2HR_UP | -0.22017858 | 27 | 7.493e-05 | 1.216e-02 | SEL1L3:209 ANP3A2:319 ST6GALNAC4:385 GAPDH:805 KDELR1:1533 HSPA8A: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 LINC24:47 |
| Palmoplantar 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 KITLG:384 SLC25A10:397 CASK:488 |
| Mammary Neoplasms, Experimental | -0.07377260 | 148 | 1.984e-03 | 5.117e-01 | AQP1:42 MAP2K7:107 TUBB2B:119 PSME1:324 KITLG:384 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 KITLG:384 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 MPI1:971 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 SMDP1:195 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:8161 MTARC1:4655 GPAM:7099 FTO:7303 |
| HumanLactAdaptionDietAll | -0.06275304 | 13 | 4.825e-01 | 5.252e-01 | SEPS2CS:814 CREBFR: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 LGALS2:1284 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

| | | | | | |
|---|-------------|------|-----------|------------|--|
| Positive Regulation Of Telomere Maintenance | -0.20109921 | 31 | 1.070e-04 | 8.263e-02 | MAPK2K7:107 TCP1:223 AURKB:821 HMBX01:900 TKNS2:1128 ATM:1281 |
| Cellular Response To Starvation (GO:00009 | -0.09299833 | 120 | 1.756e-04 | 1.055e-01 | PICK1:15 NUPR2:165 WIP2:250 MAP1LC3B:420 PKNKS1:424 TTCS447 |
| Ubiquitin-Dependent Protein Catabolic Pr | -0.05887771 | 349 | 1.684e-04 | 1.055e-01 | RNF25:10 HERPUD1:49 PPP1R11:51 PSMC3:89 AXIN1:97 PSMC2:113 |
| RNA Processing (GO:0006396) | -0.08247745 | 170 | 1.956e-04 | 1.063e-01 | USB1:9 CEF2:37 LIN28A:47 RNP51:284 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 MBD1:204 KPF1:92:207 C2CD3:368 |
| Establishment Of Mitotic Spindle Localiz | 0.17988527 | 33 | 3.495e-04 | 1.575e-01 | CDK5RAP2:290 NUMA1:551 NDC80:657 PHD1:799 ITGB1:895 HTT:794 |
| Centromere Complex Assembly (GO:0034508) | 0.27255774 | 14 | 1.424e-04 | 1.600e-01 | CENPT:129 DLGAPs:145 CENPC:480 HUJRP:698 NASP:1263 CENPF:1316 |
| Monostatic Cation Transport (GO:0006812) | 0.15826985 | 42 | 3.887e-04 | 1.600e-01 | TRPM6:56 LRPE:112 CALHM1:132 PKD1:33:251 CNGB3:262 CLDN16:289 |
| Inorganic Cation Transmembrane Transport | 0.00606729 | 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:242 TAFM:251 TEFM:352 TFB2M:430 FASTKD1:443 TWNK:452 |
| Mitochondrial RNA Processing (GO:0000963 | 0.32799965 | 9 | 6.557e-04 | 1.970e-01 | TRMT10C:415 FASTKD1:443 FASTKD7:509 FASTKD7:771 SUPV3L1:2491 FASTKD3:2767 |
| Mitochondrion Disassembly (GO:0061726) | -0.16960460 | 34 | 6.227e-04 | 1.970e-01 | WIP2:250 FISI:398 MAP1LC3B:420 ATGB2:558 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 MS12:3033 |
| Protein Localization To Microtubule Orga | 0.25111312 | 15 | 7.596e-04 | 2.118e-01 | KIA0753:17 SPAG5:87 CEP250:116 MBD1:204 KPF1:92:207 C2CD3:368 |
| Attachment Of Mitotic Spindle Microtubul | 0.27749092 | 12 | 8.737e-04 | 2.147e-01 | CENPC:480 NDC80:657 KIF2C:863 ODT1:2906 MS12:3033 CENPE:3178 |
| Folic Acid Metabolic Process (GO:0046655 | -0.27234533 | 12 | 1.088e-03 | 2.147e-01 | SHMT2:311 SLC19A1:567 DHFR2:583 MTHFD2:1329 SLC46A1:201 SHMT1:3448 |
| Kinetochoe Organization (GO:0051383) | 0.27769979 | 10 | 1.112e-03 | 2.147e-01 | CENPT:129 DLGAPs:145 CENPC:480 CENPF:1316 NPC1:1727 MS12:3033 |
| Macroautophagy (GO:0016236) | -0.09603176 | 99 | 9.735e-04 | 2.147e-01 | TBC1D5:80 VPS37B:155 CLN3:211 WIP2:250 CHMP2A:280 MAP1LC3B:420 |
| Monostatic Cation 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 | MAPK2K7:107 TKNS2:1128 NEK7:1291 MAPK1:1702 MAPK15:2112 MAPK3A:2309 |
| Regulation Of Mitochondrial mRNA Stabili | 0.39053763 | 6 | 9.230e-04 | 2.147e-01 | FASTKD1:443 FASTKD7:509 FASTKD7:771 PDE12:2114 FASTKD3:2767 TBRGA:5555 |
| Resolution Of Meiotic Recombination Inie | 0.25690166 | 14 | 8.744e-04 | 2.147e-01 | HFM1:234 SHOCl:313 FANCM:391 RMI1:828 EME1:1019 EME2:1417 |
| Autophagosome Maturation (GO:0097352) | -0.14253020 | 42 | 1.399e-03 | 2.161e-01 | CLN3:211 WIP2:250 CHMP2A:280 MAP1LC3B:420 UBQLN1:605 CHMP1A:1134 |
| Autophagy Of Mitochondrion (GO:0000422) | -0.19386954 | 44 | 1.387e-03 | 2.161e-01 | WIP2:250 FISI:398 MAP1LC3B:420 ATGB2:558 ATG3:613 CSD2:1031 |
| Positive Regulation Of DNA Biosynthetic | 0.11572693 | 63 | 1.264e-03 | 2.161e-01 | MAPK2K7:107 TCP1:223 SMOCC:777 AURKB:821 HMBX01:900 KLF4:1018 |
| Positive Regulation Of DNA-templated Tra | -0.02794451 | 1204 | 1.324e-03 | 2.161e-01 | TF7F:64 HAS3:75 DYRK1B:67 PSMC3:89 AXIN1:97 MAPK2K7:107 |
| Positive Regulation Of Telomerase Activi | -0.16352386 | 32 | 1.371e-03 | 2.161e-01 | MAPK2K7:107 TCP1:223 AURKB:821 HMBX01:900 KLF4:1018 HSP90AB1:1056 |
| Positive Regulation Of Telomere Maintena | -0.11559984 | 33 | 3.191e-03 | 2.161e-01 | MAPK2K7:107 TCP1:223 AURKB:821 HMBX01:900 TKNS2:1128 ATM:1281 |
| Purine-Containing Compound Metabolic Pro | -0.35173540 | 7 | 1.270e-03 | 2.161e-01 | GUK1:187 HIF1:1969 MACROD2:2089 TTR:2280 MACROD1:2990 PRPS1:3130 |
| Sister Chromatid Segregation (GO:0000819 | 0.17566624 | 34 | 1.469e-03 | 2.207e-01 | KIF18A:64 SPAG5:87 SMC4:565 NDC80:657 NUSAP1:983 SGO1:603 |
| Endonucleolytic Cleavage Of Tricostic | 0.26179719 | 12 | 1.689e-03 | 2.440e-01 | NOL9:390 SDE2:1201 UTP20:1304 TRT:1176 N916:19196 KRI1:4013 |
| Vesicle Budding From Membrane (GO:000690 | -0.16827027 | 29 | 1.715e-03 | 2.440e-01 | TRAPPCC1:304 TRAPPCC5:504 GOLPH3L:1055 TMED10:1196 TRAPPCC5:2164 CHMP4A:2215 |
| Regulation Of Telomere Capping (GO:19043 | -0.19705948 | 21 | 1.773e-03 | 2.459e-01 | MAPK2K7:107 USP7:543 AURKB:821 TKNS2:1128 NEK7:1291 MAPK1:1702 |
| Homophilic Cell Adhesion Via Plasma Memb | 0.11623849 | 60 | 1.857e-03 | 2.510e-01 | HMCN1:247 CADM3:504 ROBO1:633 TENN3:832 ITGB1:895 PECAM1:1085 |

MGI_Mammalian_Phenotype_Level_4 Top pathways by