

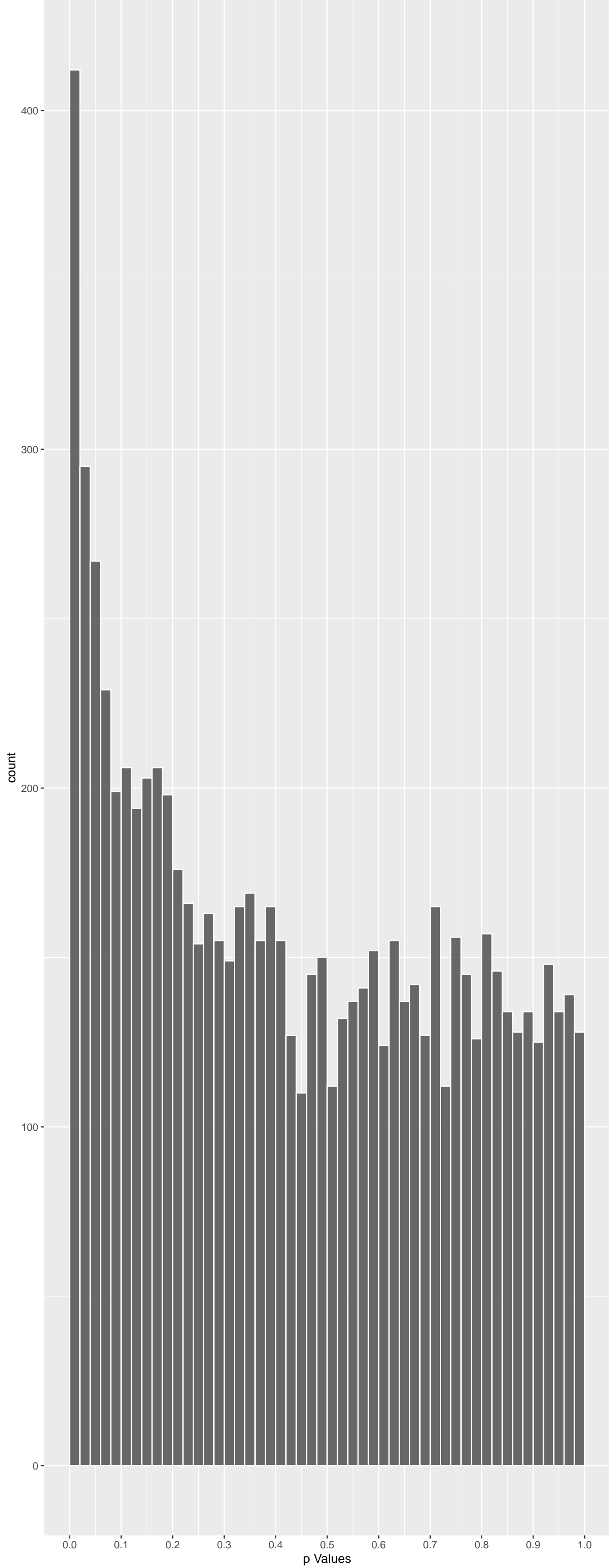
Top genes by P-value Permulated

| Gene | Rho | P | p.adj | permP | permPValue | qValueNoperm | qValuePerm |
|----------|-----------|--------------|-----------|-----------|------------|--------------|------------|
| PANK3 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| RPL8 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| YPEL5 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| H3C1 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| ZFYVE9 | 6.488004 | 2.609429e-10 | 8.456e-07 | 6.886e-06 | 6.886e-06 | 2.740e-03 | 1.831e-02 |
| CAPN8 | -7.341996 | 6.312949e-13 | 5.114e-09 | 3.932e-05 | 3.932e-05 | 4.143e-05 | 8.391e-02 |
| NLRP9 | 4.835339 | 3.987575e-06 | 6.999e-04 | 4.537e-05 | 4.537e-05 | 1.219e-01 | 8.391e-02 |
| CADPS2 | -4.440172 | 2.696612e-05 | 2.253e-03 | 5.049e-05 | 5.049e-05 | 1.872e-01 | 8.391e-02 |
| GGTLC3 | 4.899174 | 2.887218e-06 | 5.921e-04 | 6.558e-05 | 6.558e-05 | 1.176e-01 | 9.688e-02 |
| PTPRB | 5.553124 | 8.418288e-08 | 6.820e-05 | 8.774e-05 | 8.774e-05 | 5.525e-02 | 1.167e-01 |
| C7orf57 | -5.906952 | 1.045484e-08 | 1.412e-05 | 1.052e-04 | 1.052e-04 | 1.906e-02 | 1.272e-01 |
| NIPSNAP1 | 4.126133 | 1.106740e-04 | 6.336e-03 | 1.288e-04 | 1.288e-04 | 3.628e-01 | 1.296e-01 |
| OFD1 | -6.149700 | 2.328884e-09 | 4.193e-06 | 1.389e-04 | 1.389e-04 | 7.547e-03 | 1.296e-01 |
| PYGM | -5.631110 | 5.371611e-08 | 5.213e-05 | 1.494e-04 | 1.494e-04 | 4.968e-02 | 1.296e-01 |
| ACIN1 | 5.435539 | 1.638927e-07 | 1.155e-04 | 1.872e-04 | 1.872e-04 | 7.473e-02 | 1.296e-01 |
| GTSF1 | -3.176876 | 4.466126e-03 | 7.378e-02 | 1.873e-04 | 1.873e-04 | 1.000e+00 | 1.296e-01 |
| EVPL | -6.330639 | 7.324434e-10 | 1.695e-06 | 1.922e-04 | 1.922e-04 | 3.924e-03 | 1.296e-01 |
| CLIC3 | -4.761165 | 5.774365e-06 | 8.664e-04 | 2.036e-04 | 2.036e-04 | 1.249e-01 | 1.296e-01 |
| CALHM2 | -4.843225 | 3.832456e-06 | 6.943e-04 | 2.124e-04 | 2.124e-04 | 1.219e-01 | 1.296e-01 |
| TPX2 | 4.311389 | 4.866975e-05 | 3.568e-03 | 2.248e-04 | 2.248e-04 | 2.616e-01 | 1.296e-01 |
| CAB39L | -3.639186 | 8.205050e-04 | 2.417e-02 | 2.337e-04 | 2.337e-04 | 7.121e-01 | 1.296e-01 |
| POF1B | -5.112881 | 9.518477e-07 | 3.084e-04 | 2.415e-04 | 2.415e-04 | 9.995e-02 | 1.296e-01 |
| MAP4K3 | 3.900434 | 2.880617e-04 | 1.197e-02 | 2.424e-04 | 2.424e-04 | 4.914e-01 | 1.296e-01 |
| SGMS1 | -4.549464 | 1.613482e-05 | 1.623e-03 | 2.445e-04 | 2.445e-04 | 1.610e-01 | 1.296e-01 |
| EIF4E1B | 4.714582 | 7.266219e-06 | 9.571e-04 | 2.617e-04 | 2.617e-04 | 1.249e-01 | 1.296e-01 |

Top genes by Q-Value Permulated

| Gene | Rho | P | p.adj | permP | permPValue | qValueNoperm | qValuePerm |
|----------|-----------|--------------|-----------|-----------|------------|--------------|------------|
| PANK3 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| RPL8 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| YPEL5 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| H3C1 | 0.000000 | 1.000000e+00 | 1.000e+00 | 0.000e+00 | 0.000e+00 | 1.000e+00 | 0.000e+00 |
| ZFYVE9 | 6.488004 | 2.609429e-10 | 8.456e-07 | 6.886e-06 | 6.886e-06 | 2.740e-03 | 1.831e-02 |
| NLRP9 | 4.835339 | 3.987575e-06 | 6.999e-04 | 4.537e-05 | 4.537e-05 | 1.219e-01 | 8.391e-02 |
| CAPN8 | -7.341996 | 6.312949e-13 | 5.114e-09 | 3.932e-05 | 3.932e-05 | 4.143e-05 | 8.391e-02 |
| CADPS2 | -4.440172 | 2.696612e-05 | 2.253e-03 | 5.049e-05 | 5.049e-05 | 1.872e-01 | 8.391e-02 |
| GGTLC3 | 4.899174 | 2.887218e-06 | 5.921e-04 | 6.558e-05 | 6.558e-05 | 1.176e-01 | 9.688e-02 |
| PTPRB | 5.553124 | 8.418288e-08 | 6.820e-05 | 8.774e-05 | 8.774e-05 | 5.525e-02 | 1.167e-01 |
| C7orf57 | -5.906952 | 1.045484e-08 | 1.412e-05 | 1.052e-04 | 1.052e-04 | 1.906e-02 | 1.272e-01 |
| NIPSNAP1 | 4.126133 | 1.106740e-04 | 6.336e-03 | 1.288e-04 | 1.288e-04 | 3.628e-01 | 1.296e-01 |
| PYGM | -5.631110 | 5.371611e-08 | 5.213e-05 | 1.494e-04 | 1.494e-04 | 4.968e-02 | 1.296e-01 |
| ACIN1 | 5.435539 | 1.638927e-07 | 1.155e-04 | 1.872e-04 | 1.872e-04 | 7.473e-02 | 1.296e-01 |
| MAP4K3 | 3.900434 | 2.880617e-04 | 1.197e-02 | 2.424e-04 | 2.424e-04 | 4.914e-01 | 1.296e-01 |
| RAG1 | -4.341945 | 4.236811e-05 | 3.269e-03 | 3.112e-04 | 3.112e-04 | 2.496e-01 | 1.296e-01 |
| TPX2 | 4.311389 | 4.866975e-05 | 3.568e-03 | 2.248e-04 | 2.248e-04 | 2.616e-01 | 1.296e-01 |
| GTSF1 | -3.176876 | 4.466126e-03 | 7.378e-02 | 1.873e-04 | 1.873e-04 | 1.000e+00 | 1.296e-01 |
| CATSPER2 | 4.886353 | 2.928949e-06 | 5.832e-04 | 3.073e-04 | 3.073e-04 | 1.176e-01 | 1.296e-01 |
| PLEC | -7.485207 | 2.143042e-13 | 3.472e-09 | 3.119e-04 | 3.119e-04 | 4.143e-05 | 1.296e-01 |
| TMEM215 | -3.865207 | 3.322555e-04 | 1.310e-02 | 3.017e-04 | 3.017e-04 | 5.128e-01 | 1.296e-01 |
| SGMS1 | -4.549464 | 1.613482e-05 | 1.623e-03 | 2.445e-04 | 2.445e-04 | 1.610e-01 | 1.296e-01 |
| CALHM2 | -4.843225 | 3.832456e-06 | 6.943e-04 | 2.124e-04 | 2.124e-04 | 1.219e-01 | 1.296e-01 |
| NDUF55 | 4.794696 | 4.887657e-06 | 8.024e-04 | 2.836e-04 | 2.836e-04 | 1.249e-01 | 1.296e-01 |
| POF1B | -5.112881 | 9.518477e-07 | 3.084e-04 | 2.415e-04 | 2.415e-04 | 9.995e-02 | 1.296e-01 |

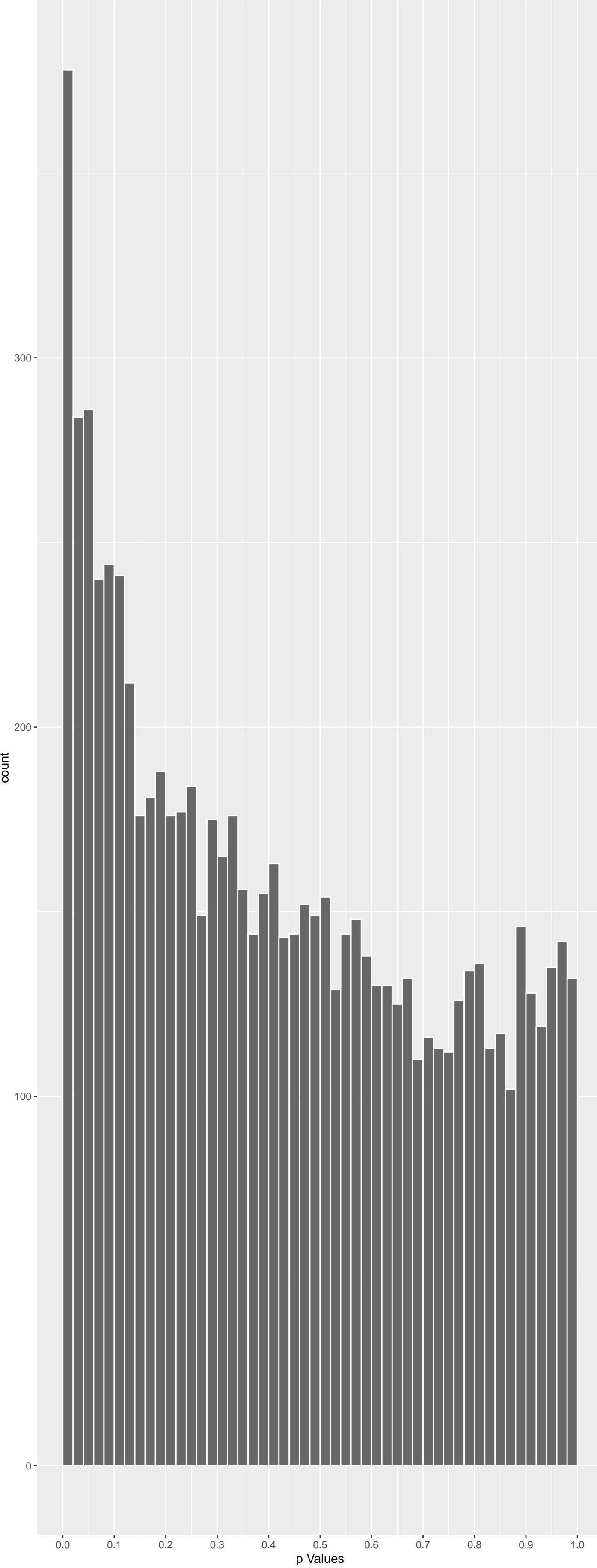
Positive Rho Permulated



Top Positive genes by P-value Permulated

| Gene | Rho | P | p.adj | permP | permPValue | qValueNoperm | qValuePerm |
|----------|----------|--------------|-----------|-----------|------------|--------------|------------|
| ZFYVE9 | 6.488004 | 2.609429e-10 | 8.456e-07 | 6.886e-06 | 6.886e-06 | 2.740e-03 | 1.831e-02 |
| NLRP9 | 4.835339 | 3.987575e-06 | 6.999e-04 | 4.537e-05 | 4.537e-05 | 1.219e-01 | 8.391e-02 |
| GGTLC3 | 4.899174 | 2.887218e-06 | 5.921e-04 | 6.558e-05 | 6.558e-05 | 1.176e-01 | 9.688e-02 |
| PTPRB | 5.553124 | 8.418288e-08 | 6.820e-05 | 8.774e-05 | 8.774e-05 | 5.525e-02 | 1.167e-01 |
| NIPSNAP1 | 4.126133 | 1.106740e-04 | 6.336e-03 | 1.288e-04 | 1.288e-04 | 3.628e-01 | 1.296e-01 |
| ACIN1 | 5.435539 | 1.638927e-07 | 1.155e-04 | 1.872e-04 | 1.872e-04 | 7.473e-02 | 1.296e-01 |
| TPX2 | 4.311389 | 4.866975e-05 | 3.568e-03 | 2.248e-04 | 2.248e-04 | 2.616e-01 | 1.296e-01 |
| MAP4K3 | 3.900434 | 2.880617e-04 | 1.197e-02 | 2.424e-04 | 2.424e-04 | 4.914e-01 | 1.296e-01 |
| EIF4E1B | 4.714582 | 7.266219e-06 | 9.571e-04 | 2.617e-04 | 2.617e-04 | 1.249e-01 | 1.296e-01 |
| NDUF55 | 4.794696 | 4.887657e-06 | 8.024e-04 | 2.836e-04 | 2.836e-04 | 1.249e-01 | 1.296e-01 |

Negative Rho Permulated



Top Negative genes by P-value Permulated

| Gene | Rho | P | p.adj | permP | permPValue | qValueNoperm | qValuePerm |
|---------|-----------|--------------|-----------|-----------|------------|--------------|------------|
| CAPN8 | -7.341996 | 6.312949e-13 | 5.114e-09 | 3.932e-05 | 3.932e-05 | 4.143e-05 | 8.391e-02 |
| CADPS2 | -4.440172 | 2.696612e-05 | 2.253e-03 | 5.049e-05 | 5.049e-05 | 1.872e-01 | 8.391e-02 |
| C7orf57 | -5.906952 | 1.045484e-08 | 1.412e-05 | 1.052e-04 | 1.052e-04 | 1.906e-02 | 1.272e-01 |
| OFD1 | -6.149700 | 2.328884e-09 | 4.193e-06 | 1.389e-04 | 1.389e-04 | 7.547e-03 | 1.296e-01 |
| PYGM | -5.631110 | 5.371611e-08 | 5.213e-05 | 1.494e-04 | 1.494e-04 | 4.968e-02 | 1.296e-01 |
| GTSF1 | -3.176876 | 4.466126e-03 | 7.378e-02 | 1.873e-04 | 1.873e-04 | 1.000e+00 | 1.296e-01 |
| EVPL | -6.330639 | 7.324434e-10 | 1.695e-06 | 1.922e-04 | 1.922e-04 | 3.924e-03 | 1.296e-01 |
| CLIC3 | -4.761165 | 5.774365e-06 | 8.664e-04 | 2.036e-04 | 2.036e-04 | 1.249e-01 | 1.296e-01 |
| CALHM2 | -4.843225 | 3.832456e-06 | 6.943e-04 | 2.124e-04 | 2.124e-04 | 1.219e-01 | 1.296e-01 |
| CAB39L | -3.639186 | 8.205050e-04 | 2.417e-02 | 2.337e-04 | 2.337e-04 | 7.121e-01 | 1.296e-01 |

GO_Biological_Process_2023 Top pathways by permulation

| Geneset | stat | num_genes | pval | p.adj | gene.vals |
|--|------------|-----------|-----------|-----------|---|
| Negative Regulation Of Gene Expression V | 0.4443979 | 5 | 5.786e-04 | 2.555e-02 | USP7:105 HELLS:341 UHRF1:431 UHRF2:738 ZNF45:2794 NA |
| Transmembrane Receptor Protein Tyrosine | -0.4113276 | 4 | 8.839e-03 | 9.078e-02 | TRIO:437 PTN:1193 PTPRD:1777 PTPRF:2041 NA NA |
| Striated Muscle Hypertrophy (GO:0014897) | -0.4146901 | 4 | 4.073e-03 | 9.377e-02 | TCAP:388 MYOC:1391 RYR2:1609 HTR2B:2232 NA NA |
| snRNA Transcription By RNA Polymerase II | -0.4082423 | 4 | 4.295e-03 | 9.766e-02 | SNAPC5:84 ICE2:1182 SNAPC1:1866 ZC3H8:2427 NA NA |
| Atrial Cardiac Muscle Cell To AV Node Ce | -0.4093389 | 6 | 5.158e-04 | 2.417e-02 | GJA1:638 SCN3B:822 KCNQ1:1341 SCN5A:1561 GJC1:1769 KCNE5:2838 |
| Atrial Cardiac Muscle Cell Action Potent | -0.4082423 | 11 | 2.757e-06 | 4.792e-04 | KCNQ2:933 KCANB2:377 GJA1:638 SCN3B:822 KCNQ3:1219 KCNQ1:1341 |
| Positive Regulation Of Peptidyl--Serine P | 0.3911883 | 4 | 6.734e-03 | 1.295e-01 | IFNG:257 LIF:403 IFNK:669 IFNE:5676 NA NA |
| Regulation Of Peptidyl--Serine Phosphoryl | 0.3911883 | 4 | 6.734e-03 | 1.295e-01 | IFNG:257 LIF:403 IFNK:669 IFNE:5676 NA NA |
| SA Node Cell Action Potentials (GO:008601 | -0.3804143 | 5 | 3.219e-03 | 8.299e-02 | CACNA1G:66 CACNA1D:583 SCN3B:822 SCN5A:1561 HCN4:6779 NA |
| Positive Regulation Of Opsinization (GO: | -0.3784966 | 4 | 8.747e-03 | 1.515e-01 | COLEC11:302 COLEC10:997 PLA2G5:3134 MYO18A:3607 NA NA |
| Regulation Of Glycogen (Starch) Synthase | 0.3685854 | 5 | 4.312e-03 | 9.766e-02 | INPP5K:699 PPP1R3F:924 IGFB2:2372 GSK3B:2946 GSK3A:3527 NA |
| RIG-I Signaling Pathway (GO:0039529) | -0.3677064 | 4 | 1.086e-02 | 1.753e-01 | RNF135:510 TRIM25:1117 OAS3:2368 PHB2:4719 NA NA |
| Plasma Membrane Phospholipid Scrambling | -0.3653594 | 5 | 4.664e-03 | 1.026e-01 | PLSCR3:92 ANO7:360 P2RX7:411 PLSCR5:3087 PLSCR4:7127 NA |
| Organic Hydroxy Compound Catabolic Proce | 0.3555406 | 6 | 2.561e-03 | 7.225e-02 | PDXP:843 FGF23:859 HSD17B6:1256 LCT:1516 CYP2A1:1836 LDHD:7517 |
| Establishment Of Mitotic Sister Chromati | 0.3551057 | 6 | 2.592e-03 | 7.275e-02 | STAG1:824 NIPBL:948 SMC3:1217 RAD21:2361 STAG2:2857 SMC1A:5679 |
| Hepoxilin Biosynthetic Process (GO:00511 | -0.3497193 | 4 | 1.542e-02 | 2.131e-01 | ALOXE3:488 ALOX15B:2296 ALOX12B:2757 ALOX15:4358 NA NA |
| Hepoxilin Metabolic Process (GO:0051121) | -0.3497193 | 4 | 1.542e-02 | 2.131e-01 | ALOXE3:488 ALOX15B:2296 ALOX12B:2757 ALOX15:4358 NA NA |
| Positive Regulation Of DNA Methylation--D | 0.34390984 | 8 | 6.280e-04 | 2.739e-02 | TASOR:349 SETDB2:437 PPHLN1:828 AT7F7P2:1595 TRIM28:2274 MORC2:2819 |
| Cellular Response To UV--A (GO:0071492) | -0.3489810 | 9 | 2.886e-04 | 1.603e-02 | MME:236 OPN1SW:531 PPID:596 MMP9:1060 OPN3:1133 MMP3:1808 |
| Androgen Biosynthetic Process (GO:000670 | 0.3431339 | 7 | 1.667e-03 | 5.397e-02 | MED1:333 HSD3B2:943 HSD17B3:1051 HSD17B6:1256 SRD5A1:4241 SRD5A3:4513 |
| Detection Of Muscle Stretch (GO:003595) | -0.3431090 | 5 | 7.882e-03 | 1.416e-01 | TCAP:388 PTK2:2125 CDH2:2549 CTNNB1:3471 CSRP3:4397 NA |
| Glucocorticoid Biosynthetic Process (GO: | 0.3427544 | 3 | 3.976e-02 | 3.209e-01 | CYP17A1:248 CYP21A2:3245 CYP11A1:4086 NA NA NA |
| Actin--Myosin Filament Sliding (GO:003327 | -0.3420364 | 11 | 8.571e-05 | 6.505e-03 | MYH8:153 MYH2:312 MYH6:664 TPM1:919 MYH4:955 TNNT2:993 |
| Positive Regulation Of Mast Cell Activat | 0.3355274 | 4 | 2.012e-02 | 2.368e-01 | TSLP:186 SPHK2:1020 NECTIN2:3841 NR4A3:5702 NA NA |
| Inhibitory Postsynaptic Potential (GO:00 | -0.3347499 | 6 | 4.549e-03 | 1.009e-01 | GLRA1:402 INSYN2A:1178 NLGN3:2399 NPAS4:2963 INSYN1:3211 INSYN2B:6191 |
| Glucocorticoid Metabolic Process (GO:000 | 0.3324978 | 5 | 1.003e-02 | 1.642e-01 | CYP17A1:248 HSD11B2:2886 YYHAH:2960 CYP21A2:3245 CYP11A1:4086 NA |
| Regulation Of DNA Methylation--Dependent | 0.3323028 | 14 | 1.673e-05 | 2.049e-03 | TASOR:349 TET1:395 SETDB2:437 L3MBTL3:538 PPHLN1:828 SAMD1:981 |
| Positive Regulation Of CD4--positive, CD2 | 0.3297362 | 3 | 4.792e-02 | 3.513e-01 | IFNG:257 HLA--DRA:1240 KHL25:6716 NA NA NA |
| snRNA Modification (GO:0040031) | 0.3294592 | 4 | 2.248e-02 | 2.452e-01 | METTL18:869 NHP2:2194 MPECE:3011 METTL4:4751 NA NA |
| Muscle Filament Sliding (GO:0030049) | -0.3279529 | 10 | 3.281e-04 | 1.786e-02 | MYH8:153 MYH6:664 TPM1:919 MYH4:955 TNNI2:993 MYGB8:1497 |
| Membrane Lipid Catabolic Process (GO:004 | 0.3248545 | 7 | 2.917e-03 | 7.778e-02 | SMPD2:857 MGST2:1147 PPT1:2595 SMPD1:3829 SGPL1:3217 ENPP2:3952 |
| MHC Class II Protein Complex Assembly (G | 0.3240637 | 7 | 2.986e-03 | 7.811e-02 | HLA--DOA:66 GNAO1:967 HLA--DOB:977 HLA--DRA:1240 HLA--DPA1:4273 HLA--DMA:4357 |
| Peptide Antigen Assembly With MHC Class | 0.3240637 | 7 | 2.986e-03 | 7.811e-02 | HLA--DOA:66 GNAO1:967 HLA--DOB:977 HLA--DRA:1240 HLA--DPA1:4273 HLA--DMA:4357 |
| Regulation Of Thymocyte Apoptotic Proces | 0.3231736 | 4 | 2.518e-02 | 2.613e-01 | TP53:1394 BMP4:1773 ZC3H8:2427 JAK3:5719 NA NA |
| Chitin Catabolic Process (GO:0006032) | -0.3224901 | 2 | 1.142e-01 | 4.845e-01 | CTBS:1223 CHIT1:4615 NA NA NA NA |
| Chitin Metabolic Process (GO:0006030) | -0.3224901 | 2 | 1.142e-01 | 4.845e-01 | CTBS:1223 CHIT1:4615 NA NA NA NA |
| Adenylyate Cyclase--Inhibiting Serotonin R | -0.3203648 | 6 | 6.575e-03 | 1.284e-01 | HTR1B:18 HTR1D:144 HTR1F:1671 HTR5A:4324 HTR1E:4268 HTR1A:8224 |
| Positive Regulation Of Chemokine (C--X--C | 0.3321099 | 4 | 2.660e-02 | 2.681e-01 | TNF:1142 MHGB1:2063 TLR4:2553 LCP1:5752 NA NA |
| Ventricular Cardiac Muscle Cell Membrane | -0.3198836 | 7 | 3.380e-03 | 8.591e-02 | KCNJ3:1219 KCNQ1:1341 KCNJ5:1985 KCNE1:2854 KCNE2:3086 KCNH2:4475 |
| Positive Regulation Of Heterochromatin F | 0.3197136 | 11 | 2.411e-04 | 1.412e-02 | TASOR:349 SETDB2:437 PPHLN1:828 AT7F7P2:1595 TRIM28:2274 MORC2:2819 |

EnrichmentHsSymbolsFile2 Top pathways by permulation

| Geneset | stat | num_genes | pval | p.adj | gene.vals |
|--|------------|-----------|-----------|-----------|---|
| REACTOME_SPERM_MOTILITY_AND_TAXES | 0.4327112 | 8 | 2.250e-05 | 8.743e-04 | CATSPER2:12 CATSPERG:43 CATSPERB:79 CATSPERD:380 CATSPERF:812 KCNU1:1183 |
| WP_AFLATOXIN_B1_METABOLISM | -0.4113276 | 2 | 4.392e-02 | 2.285e-01 | EPHX1:1046 CYP1A2:1817 NA NA NA NA |
| MIKHAYLOVA_OXIDATIVE_STRESS_RESPONSE_VIA | 0.3978723 | 6 | 7.373e-04 | 1.454e-02 | PGAM1:38 HSPB1:317 CTSD:404 CALU:907 OAT:3537 AKR1B1:4722 |
| REACTOME_ESTABLISHMENT_OF_SISTER_CHROMAT | 0.39277351 | 11 | 6.468e-06 | 3.019e-04 | ESCO1:1302 PDS5B:653 WAPL:762 STAG1:824 SMC3:1217 PDS5A:1375 |
| WP_NIPBL_ROLE_IN_DNA_DAMAGE_CORNELIA_DE | 0.3677627 | 7 | 7.524e-04 | 1.470e-02 | RNF2:477 RNF168:327 H2AX:541 NIPBL:948 CBX3:3253 ATR:3509 |
| REACTOME_MINERALOCORTICOID_BIOSYNTHESIS | 0.3674805 | 4 | 1.091e-02 | 9.969e-02 | CGA:456 HSD3B2:943 CYP21A2:3245 HSD18A:3927 NA NA |
| REACTOME_GLUCCORTICOID_BIOSYNTHESIS | 0.3662302 | 6 | 1.891e-03 | 3.014e-02 | CYP17A1:248 HSD3B2:943 HSD11B1:1291 HSD11B2:2886 CYP21A2:3245 SERPINA6:4378 |
| REACTOME_PREDNISONE_ADME | 0.3621584 | 5 | 5.036e-03 | 5.940e-02 | ALB:1283 HSD11B1:1291 ABCB1:1314 HSD11B2:2886 SERPINA6:4378 NA |
| WP_PILOCYTIC_ASTROCYTOMA | 0.3612640 | 6 | 2.179e-03 | 3.313e-02 | SOS1:445 RAF1:861 GRB2:1307 BRAF:2046 NF1:2736 PTPN11:6081 |
| NIKOLSKY_BREAST_CANCER_17P11_AMPLICON | 0.3479529 | 10 | 1.388e-04 | 3.865e-03 | ALDH3A2:267 LSC2:368 SLCA7A1:477 EPN2:706 RNF112:2016 SLC47A2:2297 |
| MYLLYKANGAS_AMPLIFICATION_HOT_SPOT_1 | 0.3402176 | 3 | 3.712e-02 | 2.096e-01 | GATA1:1199 WAS:1974 TFE3:4230 NA NA NA |
| CHOL_ATL_ACUTE_STAGE | 0.3402176 | 4 | 1.844e-02 | 1.383e-01 | MBD1:237 MET:833 LHX2:4603 ETV1:4666 NA NA |
| REACTOME_MET_ACTIVATES_PTPN11 | 0.3369180 | 5 | 9.074e-03 | 8.830e-02 | GAB1:418 MET:833 GRB2:1307 HGF:4558 PTPN11:6081 NA |
| REACTOME_FORMYL_PEPTIDE_RECEPTORS_BIND_F | -0.3347935 | 4 | 2.039e-02 | 1.457e-01 | APP:255 HEBP1:375 ANXA1:3526 FPR2:6566 NA NA |
| NIKOLSKY_BREAST_CANCER_21Q22_AMPLICON | -0.3307171 | 14 | 1.831e-05 | 7.379e-04 | PCBP3:248 COL6A1:436 DIP2A:843 SPATC1L:1211 YBEY:2156 COL6A2:2530 |
| OHASHI_AURKA_TARGETS | 0.3250838 | 4 | 2.433e-02 | 1.645e-01 | DLGAP5:1246 TP53:1394 CDC25B:3713 MBD3:4967 NA NA |
| REACTOME_ELECTRIC_TRANSMISSION_ACROSS_GA | -0.3242662 | 5 | 1.203e-02 | 1.066e-01 | PANX1:220 GJA10:1151 GJC1:1769 PANX2:5803 GJD2:5805 NA |
| REACTOME_LEUKOTRIENE_RECEPTORS | -0.3234565 | 5 | 1.224e-02 | 1.075e-01 | LTBR4:528 LTBAR:1002 CYS1LTR2:1390 GPR17:3658 CYS1LTR1:7742 NA |
| BERGER_MBD2_TARGETS | -0.3225602 | 2 | 1.141e-01 | 3.839e-01 | TFE2:552 CEL2A2:530 NA NA NA NA |
| REACTOME_COHESIN_LOADING_ONTO_CHROMATIN | 0.3191736 | 10 | 4.738e-04 | 1.032e-02 | PDS5B:653 WAPL:762 STAG1:824 NIPBL:948 SMC3:1217 PDS5A:1375 |
| HEIDENBLAD_AMPLIFIED_IN_BONE_CANCER | 0.3168598 | 7 | 3.692e-03 | 4.810e-02 | MDM2:392 TSPAN31:763 FGF23:859 CCND2:2187 CDK4:3471 STK38L:3663 |
| WALLACE_PROSTATE_CANCER_DN | -0.3147394 | 5 | 1.479e-02 | 1.208e-01 | GJA1:638 GPM6B:2592 LAMA4:2750 CA2V:3045 RAP1B:5993 NA |
| CROSBY_E2F4_TARGETS | 0.3139116 | 6 | 7.744e-03 | 8.000e-02 | CENPE:1016 CDC6:1475 BUB1B:2075 NDC80:2206 PTTG1:2529 CHEK1:8772 |
| REACTOME_BIOSYNTHESIS_OF_MARESIN_LIKE_SP | -0.3129467 | 2 | 1.253e-01 | 4.054e-01 | CYP1A2:1817 CYP2E1:4240 NA NA NA NA |
| WP_STEROID_HORMONE_PRECURSOR_BIOSYNTHESI | 0.3119430 | 7 | 4.259e-03 | 5.300e-02 | CYP17A1:248 HSD3B2:943 AKR1D1:3241 CYP21A2:3245 CYP11A1:4086 SRD5A1:4241 |
| REACTOME_NEGATIVE_FEEDBACK_REGULATION_OF | 0.3064465 | 6 | 9.330e-03 | 9.008e-02 | MAP2K2:485 RAF1:861 MAP2K1:882 BRAF:2046 MAPK1:5771 MAPK3:8759 |
| REACTOME_TYPE_I_HEMIDESMOSOMES_ASSEMBLY | -0.3063766 | 11 | 4.337e-04 | 9.637e-03 | PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 KRT14:721 ITGA6:2177 |
| TURASHVILI_BREAST_NORMAL_DUCTAL_VS_LOBUL | 0.3056030 | 6 | 9.527e-03 | 9.143e-02 | EHBP1:203 RHOB1B3:725 TSPAN5:835 DCN:3763 MBTPS2:5057 ARHGEF9:8301 |
| WP_IRINOTECAN_PATHWAY | 0.3039092 | 4 | 3.527e-02 | 2.034e-01 | SLC01B1:372 ABCB1:1613 BCHE:2914 UGT1A1:8804 NA NA |
| REACTOME_ANDROGEN_BIOSYNTHESIS | 0.3027715 | 9 | 1.658e-03 | 2.723e-02 | CYP17A1:248 CGA:456 HSD3B2:943 HSD17B3:1051 LHB:3927 SRD5A1:4241 |
| REACTOME_ESTROGEN_STIMULATED_SIGNALING_T | 0.3024543 | 4 | 3.616e-02 | 2.071e-01 | PDPK1:1180 NRAS:1780 KRAS:4052 MAPK1:5771 NA NA |
| REACTOME_ACTIVATION_OF_NOXA_AND_TRANSLOC | 0.3013315 | 4 | 3.686e-02 | 2.090e-01 | TP53:1394 E2F1:1942 TDFP1:2573 TDFP2:6958 NA NA |
| JL_CARCINOGENESIS_BY_KRAS_AND_STK11_UP | -0.2987281 | 10 | 1.071e-03 | 1.940e-02 | TIAM1:143 BNC1:420 PKP1:972 KRT5:2486 LYPD3:3453 TP63:3845 |
| REACTOME_BIOSYNTHESIS_OF_MARESIN | -0.2981846 | 4 | 3.887e-02 | 2.154e-01 | ALOX5:278 CYP1A2:1817 CYP2E1:4240 EPHX2:6751 NA NA |
| SMID_BREAST_CANCER_ERBB2_DN | -0.2963027 | 4 | 4.012e-02 | 2.189e-01 | NPY1R:566 FGFR2:1822 GABRP:3916 SOX10:6899 NA NA |
| REACTOME_SARS_COV_1_MODULES_HOST_TRANS | 0.2944289 | 31 | 1.403e-08 | 1.423e-06 | RPS24:210 RPS5:836 RPS27L:539 RPS27:719 RPS15:945 RPS6:1023 |
| CHEN_HOXA5_TARGETS_6HR_DN | 0.2941549 | 5 | 2.272e-02 | 1.571e-01 | ZBED8:1034 NPTXR:1397 TUBA1A:3257 FXJ1:3829 PRPF31:7140 NA |
| REACTOME_ROLE_OF_SECOND_MESSENGERS_IN_NE | -0.2940138 | 10 | 1.284e-03 | 2.215e-02 | TRPC4:303 DCC:614 TRPC5:886 TRPC6:1366 NTN1:1634 TRPC3:2302 |
| KUMAMOTO_RESPONSE_TO_NUTLIN_3A_DN | 0.2927550 | 7 | 7.308e-03 | 7.735e-02 | CNGB1:160 SPAG5:343 KIFC1:961 KIF2C:1664 CCNA2:5872 CDKN3:6861 |
| WP_GLUCCORTICOID_BIOSYNTHESIS | 0.2919065 | 6 | 1.327e-02 | 1.129e-01 | HSD11B1:1291 HSD11B2:2886 AKR1D1:3241 CYP21A2:3245 SRD5A1:4241 SRD5A2:5297 |

DisGeNET Top pathways by permulation

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|---|------------|---|-----------|-----------|--|
| Human metapneumovirus infection | 0.4345238 | 2 | 3.330e-02 | 3.243e-01 | CYP17A1:248 CYP2A1:1836 NA NA NA NA |
| Acute postoperative pain | 0.4289714 | 4 | 2.898e-03 | 1.245e-01 | TAOK3:191 COMT:1229 ABCB1:1314 OPRM1:1717 NA NA |
| Monilethrix | -0.4286487 | 2 | 3.576e-02 | 3.341e-01 | KRT80:161 DSG4:2109 NA NA NA NA |
| Junctional split | -0.4238195 | 6 | 3.241e-04 | 4.076e-02 | PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 ITGA6:2177 LAMA3:4062 NA |
| Rheumatoid Vasculitis | 0.4141543 | 2 | 2.429e-02 | 3.533e-01 | CD28:935 RBMA5:1802 NA NA NA NA |
| Sequiosis | 0.4131107 | 2 | 4.301e-02 | 3.557e-01 | GNAO1:967 RBMA5:1802 NA NA NA NA |
| Central nervous system depression (disor | 0.4105528 | 3 | 1.378e-02 | 2.303e-01 | COMT:1229 ABCB1:1314 OPRM1:1717 NA NA NA |
| Human metapneumovirus infection | 0.4103988 | 5 | 1.482e-03 | 9.693e-02 | TSLP:18 PIPPSK1:40 TNF:1142 NCR1:2359 ISYNA1:3676 NA |
| Herlitz Disease | -0.4086677 | 5 | 1.552e-03 | 9.895e-02 | ITGB4:192 LAMB3:361 LAMC2:492 ITGA6:2177 LAMA3:4062 NA |
| Localized vitiligo | 0.4076994 | 2 | 4.582e-02 | 3.643e-01 | TNF:1142 RBMA5:1802 NA NA NA NA |
| Congenital pyloric atresia | -0.4069048 | 5 | 1.626e-03 | 1.006e-01 | PLEC:16 ITGB4:192 LAMC2:492 ITGA6:2177 COL17A1:4556 NA |
| Bulla of lung | -0.3992733 | 2 | 5.049e-02 | 3.773e-01 | EPHX1:1046 TIMP2:2139 NA NA NA NA |
| Plantar hyperkeratosis | -0.3991391 | 6 | 7.095e-04 | 6.446e-02 | PLEC:16 ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 |
| Ineffective erythropoiesis | 0.3958478 | 5 | 2.173e-03 | 1.099e-01 | RPL26:98 COX4I2:995 KLF1:1184 GATA1:1199 SEC23B:5003 NA |
| Opticospinal Multiple Sclerosis | 0.3894387 | 4 | 6.984e-03 | 1.730e-01 | CD2AP:590 RBMA5:1802 AQP4:1987 PLA2G7:2673 NA NA |
| T-lymphocyte immunodeficiency | -0.3890736 | 6 | 9.651e-04 | 7.910e-02 | RAG1:15 CD3E:1383 LBR:1431 SFTPA1:1491 SMARCA1:12365 SIPA1:3895 |
| Abnormality of finger | 0.3884336 | 4 | 7.132e-03 | 1.749e-01 | SIL1:679 INPP5K:699 NRAS:1780 KRAS:4052 NA NA |
| Epidermolysis bullosa inversa dystrophic | -0.3836865 | 6 | 1.135e-03 | 8.419e-02 | ITGB4:192 LAMB3:361 LAMC2:492 LAMC1:1461 LAMA3:4062 COL17A1:4556 |
| Candidiasis of the esophagus | -0.3795516 | 3 | 2.279e-02 | 2.815e-01 | ADAM17:771 NFKB1:946 IL1B:4040 NA NA NA |
| EPIDERMOLYSIS BULLOSA_JUNCTIONAL_LOCAL | -0.3790536 | 5 | 3.331e-03 | 3.181e-01 | ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA |
| Adult junctional epidermolysis bullosa (| -0.3790536 | 5 | 3.331e-03 | 3.181e-01 | ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA |
| Epidermolysis Bullosa Progressiva | -0.3790536 | 5 | 3.331e-03 | 3.181e-01 | ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA |
| JEB-I | -0.3790536 | 5 | 3.331e-03 | 3.181e-01 | ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA |
| Palmar hyperhidrosis | -0.3790536 | 5 | 3.331e-03 | 3.181e-01 | ITGB4:192 LAMB3:361 LAMC2:492 LAMA3:4062 COL17A1:4556 NA |
| Benign neoplasm of thyroid gland | -0.3777993 | 3 | 3.242e-02 | 2.841e-01 | APP:255 IQGAP1:1885 ALK:3706 NA NA NA |
| Microcystic stromal tumor | -0.3733318 | 5 | 3.838e-03 | 1.396e-01 | MME:236 VIM:309 DICER1:1249 CTNNB1:3471 FOXL2:4831 NA |
| Papillary and follicular adenocarcinoma | 0.3701925 | 5 | 4.146e-03 | 1.437e-01 | EGF:390 TP53:1394 BRAF:2046 EDNR4:2564 KRAS:4052 NA |
| Papillary transitional cell carcinoma | 0.3692013 | 4 | 1.055e-02 | 2.037e-01 | EGF:390 ERBB2:944 TP53:1394 VEGFA:5779 NA NA |
| Empyema, Pleural | 0.3680663 | 6 | 1.794e-03 | 1.012e-01 | NFKBIA:451 NFKB1:1433 SMCA2:2352 SMCA2:2417 TNFRSF6B:4687 |
| Intestinal obstruction co-occurrent and | -0.3677232 | 3 | 2.738e-02 | 3.046e-01 | CTFR:773 MUC1:1021 SLC26A9:4520 NA NA NA |
| Congenital muscular hypertrophy-cerebral | 0.3669450 | 5 | 4.488e-03 | 1.477e-01 | BRD4:571 NIPBL:948 SMCA3:1217 RAD21:2361 SMCA1A:5679 NA |
| Cornelia de Lange Syndrome 3 | 0.3669450 | 5 | 4.488e-03 | 1.477e-01 | BRD4:571 NIPBL:948 SMCA3:1217 RAD21:2361 SMCA1A:5679 NA |
| Liver Abcess | -0.3646718 | 5 | 4.742e-03 | 1.501e-01 | NCF1:687 NCF2:1364 DECR1:1756 CYBB:3242 CYBA:3741 NA |
| Myelodysplastic syndrome, no ICD-O subty | 0.3633493 | 6 | 2.054e-03 | 2.066e-01 | TET2:791 PAFH1A1:1010 SF3B1:1469 YYW4E:1922 SETBP1:3122 FANCB:4755 |
| Myopathy, Centronuclear, Autosomal Reces | -0.3604260 | 4 | 1.254e-02 | 1.177e-01 | SPEG:898 AMPH:1398 BIN1:2934 DHM2:3668 NA NA |
| Phocomelia | 0.3598469 | 5 | 5.325e-03 | 1.586e-01 | GNASB6: NIPBL:948 SMCA3:1217 ESCO2:1631 WNT7A:6675 NA |
| Serosus cystadenoma, borderline malignanc | 0.3597696 | 5 | 5.334e-03 | 1.586e-01 | ERBB2:944 DRLR2:1888 BRAF:2046 MYC:2342 KRAS:4052 NA |
| Small anterior fontanelle | 0.3561526 | 3 | 3.263e-02 | 3.238e-01 | ORC1:107 MYCN:3411 ATR:3509 NA NA NA |
| Anterior Horn Cell Disease | -0.3558228 | 6 | 2.541e-03 | 1.170e-01 | VIM:309 PNPLA6:476 SOD1:722 GLE1:806 PRDX3:2870 SMN1:8655 |
| Acanthomabaga Keratitis | 0.3542440 | 2 | 8.270e-02 | 4.464e-01 | ARSA:2902 TLR4:2553 NA NA NA NA |