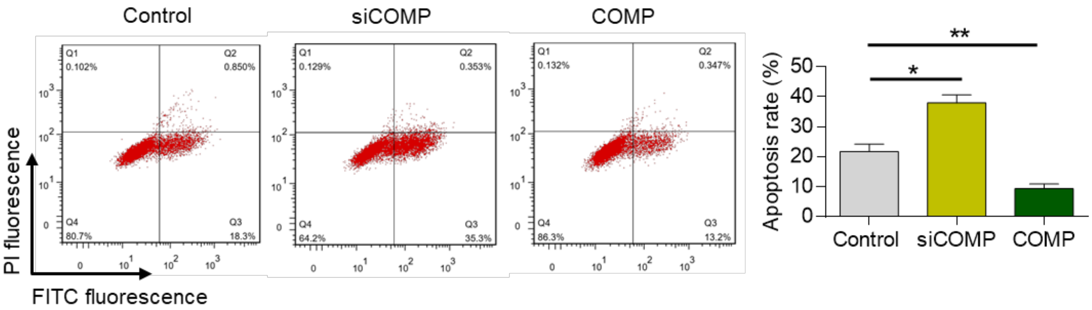

**Figure S1.** COMP protects from cell apoptosis. Apoptosis was induced in the SW620 cells by a 48-h incubation with brefeldin A. The experimental results showed that overexpression of COMP inhibited the apoptosis induced by Brefeldin A of SW620, while COMP knockdown promoted the apoptosis of SW620.

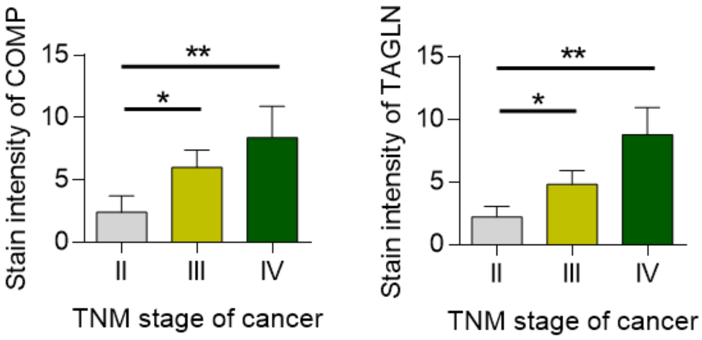

**Figure S2.** Patients with high expression of COMP and TAGLN had higher clinical staging.

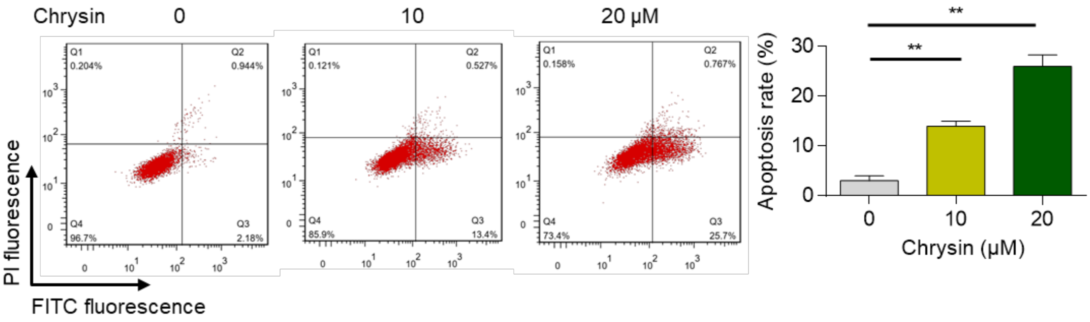

**Figure S3.** Chrysin can induce apoptosis of SW620 cells in a dose-dependent manner.

**Table S1. Unregulated genes in colon cancer.**

| Genes | logFC | PValue | FDR |
|---|---|---|---|
| KLK6 | 2.905 | 1.54E-87 | 2.20E-84 |
| CST1 | 2.287 | 3.47E-72 | 2.24E-69 |
| FEZF1 | 3.752 | 1.18E-71 | 7.19E-69 |
| SFTA2 | 3.107 | 2.13E-63 | 9.27E-61 |
| KLK8 | 3.770 | 5.27E-62 | 2.03E-59 |
| SPERT | 3.854 | 5.71E-59 | 1.85E-56 |
| KLK7 | 2.712 | 5.28E-56 | 1.43E-53 |
| COL10A1 | 1.810 | 3.29E-55 | 8.34E-53 |
| NOTUM | 1.840 | 6.04E-55 | 1.48E-52 |
| MMP7 | 1.575 | 3.39E-54 | 7.99E-52 |
| CASC21 | 2.661 | 4.00E-53 | 8.91E-51 |
| ZIC5 | 3.292 | 7.35E-52 | 1.55E-49 |
| DKK4 | 2.819 | 9.01E-50 | 1.72E-47 |
| KRT80 | 1.421 | 4.71E-49 | 8.51E-47 |
| SOX14 | 3.151 | 4.68E-48 | 8.22E-46 |
| CST2 | 2.528 | 5.68E-48 | 9.90E-46 |
| AC123023 | 2.744 | 4.03E-47 | 6.73E-45 |
| KRT75 | 2.993 | 7.75E-47 | 1.27E-44 |
| SERPINA4 | 2.862 | 4.75E-46 | 7.56E-44 |
| C6orf15 | 3.069 | 5.05E-46 | 7.97E-44 |
| OTX1 | 1.903 | 8.69E-45 | 1.27E-42 |
| IBSP | 2.917 | 8.38E-44 | 1.14E-41 |
| ESM1 | 1.581 | 1.16E-43 | 1.55E-41 |
| WNT2 | 1.509 | 3.68E-42 | 4.64E-40 |
| KLC3 | 2.477 | 4.59E-42 | 5.72E-40 |
| FGF19 | 2.519 | 6.33E-42 | 7.82E-40 |
| CST4 | 3.508 | 9.63E-42 | 1.16E-39 |
| DMBX1 | 2.763 | 9.22E-41 | 1.05E-38 |
| IGFL4 | 1.909 | 5.41E-40 | 5.92E-38 |
| AC005256 | 3.497 | 1.24E-39 | 1.31E-37 |
| C5orf46 | 3.080 | 1.94E-38 | 1.89E-36 |
| BLACAT1 | 1.520 | 3.00E-38 | 2.88E-36 |
| WNT7B | 2.188 | 5.98E-38 | 5.73E-36 |
| FOXQ1 | 1.188 | 6.03E-38 | 5.76E-36 |
| IGFL1 | 3.983 | 9.20E-38 | 8.73E-36 |
| CDH3 | 1.077 | 1.66E-37 | 1.57E-35 |
| KRT6A | 2.076 | 4.61E-37 | 4.25E-35 |
| AKR1C4 | 2.389 | 1.31E-36 | 1.18E-34 |
| ELF5 | 2.549 | 1.35E-36 | 1.20E-34 |
| TCN1 | 1.521 | 1.92E-36 | 1.69E-34 |
| CASC19 | 1.881 | 3.77E-36 | 3.24E-34 |
| AC007128 | 1.998 | 7.36E-36 | 6.19E-34 |

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|---|---|---|---|
| FIRRE | 1.967 | 1.01E-35 | 8.38E-34 |
| EPYC | 2.515 | 1.14E-35 | 9.33E-34 |
| KRT6B | 1.521 | 1.63E-35 | 1.32E-33 |
| COL11A1 | 1.185 | 5.22E-35 | 4.15E-33 |
| C8orf74 | 3.745 | 6.87E-35 | 5.38E-33 |
| ADAM20P3 | 3.877 | 7.90E-35 | 6.14E-33 |
| SP8 | 2.498 | 2.44E-33 | 1.77E-31 |
| CLDN2 | 1.014 | 2.91E-33 | 2.10E-31 |
| KRT23 | 1.145 | 3.21E-33 | 2.30E-31 |
| GAD1 | 1.547 | 4.91E-33 | 3.47E-31 |
| MMP13 | 1.947 | 5.30E-33 | 3.74E-31 |
| SLCO1B3 | 1.750 | 6.08E-33 | 4.28E-31 |
| COMP | 1.287 | 2.39E-32 | 1.64E-30 |
| LY6G6E | 2.954 | 5.69E-32 | 3.84E-30 |
| KRT16 | 1.972 | 1.01E-31 | 6.73E-30 |
| GBX2 | 2.978 | 1.86E-31 | 1.23E-29 |
| AC007099 | 3.504 | 1.95E-31 | 1.28E-29 |
| MAGEA3 | 3.471 | 2.56E-31 | 1.68E-29 |
| LEMD1 | 1.984 | 3.56E-31 | 2.31E-29 |
| SPRR2D | 3.037 | 3.91E-31 | 2.52E-29 |
| SPRR1A | 3.274 | 4.32E-31 | 2.77E-29 |
| AP000697 | 3.704 | 7.11E-31 | 4.55E-29 |
| LY6G6F | 3.081 | 1.45E-30 | 9.05E-29 |
| C6orf223 | 1.026 | 2.09E-30 | 1.30E-28 |
| C2orf61 | 1.707 | 3.52E-30 | 2.15E-28 |
| LY6G6D | 1.487 | 6.99E-30 | 4.19E-28 |
| SPRR1B | 3.032 | 8.47E-30 | 5.03E-28 |
| RAET1L | 1.637 | 8.77E-30 | 5.18E-28 |
| AMELX | 2.596 | 4.26E-29 | 2.41E-27 |
| CPNE7 | 1.031 | 4.96E-29 | 2.77E-27 |
| DDN | 1.313 | 6.33E-29 | 3.50E-27 |
| PRSS56 | 2.941 | 1.24E-28 | 6.74E-27 |
| STRA6 | 1.174 | 1.74E-28 | 9.30E-27 |
| C14orf105 | 2.878 | 2.20E-28 | 1.18E-26 |
| UCN2 | 1.887 | 4.60E-28 | 2.43E-26 |
| PIWIL1 | 1.369 | 1.56E-27 | 8.01E-26 |
| CCAT1 | 1.090 | 1.57E-27 | 8.05E-26 |
| SALL4 | 1.269 | 2.21E-27 | 1.12E-25 |
| PAEP | 2.395 | 4.96E-27 | 2.43E-25 |
| PDX1 | 1.284 | 6.64E-27 | 3.23E-25 |
| PAH | 1.528 | 7.97E-27 | 3.85E-25 |
| MCIDAS | 1.484 | 8.79E-27 | 4.22E-25 |
| FABP6 | 1.124 | 9.63E-27 | 4.59E-25 |
| AC079466 | 2.842 | 1.94E-26 | 9.07E-25 |

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|---|---|---|---|
| AC142293 | 2.736 | 3.19E-26 | 1.46E-24 |
| EN2 | 1.793 | 3.71E-26 | 1.69E-24 |
| FGB | 2.103 | 4.94E-26 | 2.23E-24 |
| MSLNL | 2.773 | 5.51E-26 | 2.47E-24 |
| AC007277 | 1.844 | 6.20E-26 | 2.76E-24 |
| SPRR2A | 2.606 | 6.64E-26 | 2.94E-24 |
| CRNDE | 1.187 | 8.01E-26 | 3.53E-24 |
| TCF24 | 2.320 | 8.61E-26 | 3.78E-24 |
| MAGEA6 | 3.056 | 1.63E-25 | 7.00E-24 |
| IRX5 | 1.516 | 3.19E-25 | 1.35E-23 |
| HABP2 | 1.885 | 3.21E-25 | 1.36E-23 |
| OBP2B | 2.942 | 4.19E-25 | 1.74E-23 |
| TNNI3 | 1.488 | 7.57E-25 | 3.10E-23 |
| HTR1D | 1.061 | 8.60E-25 | 3.51E-23 |
| KRT17 | 1.009 | 1.10E-24 | 4.45E-23 |
| EPHX4 | 1.052 | 1.34E-24 | 5.43E-23 |
| ZNF280A | 2.851 | 1.38E-24 | 5.56E-23 |
| PRR9 | 3.240 | 1.71E-24 | 6.78E-23 |
| AC068121 | 2.831 | 4.24E-24 | 1.67E-22 |
| CNTD2 | 1.109 | 4.83E-24 | 1.89E-22 |
| FAM195CP | 2.047 | 7.57E-24 | 2.92E-22 |
| NPSR1 | 1.612 | 1.99E-23 | 7.50E-22 |
| VGLL1 | 2.971 | 2.54E-23 | 9.56E-22 |
| AC018359 | 2.736 | 4.40E-23 | 1.64E-21 |
| GOLGA6L2 | 3.311 | 4.63E-23 | 1.72E-21 |
| PCAT2 | 3.055 | 1.82E-22 | 6.64E-21 |
| ULBP1 | 1.415 | 2.13E-22 | 7.73E-21 |
| ZIC2 | 1.231 | 3.42E-22 | 1.22E-20 |
| C1orf105 | 1.826 | 3.60E-22 | 1.28E-20 |
| CXCL17 | 1.688 | 4.14E-22 | 1.46E-20 |
| DUSP27 | 1.068 | 5.12E-22 | 1.80E-20 |
| C3P1 | 2.718 | 5.73E-22 | 2.01E-20 |
| NCAPD2P1 | 1.832 | 6.07E-22 | 2.12E-20 |
| TPSP2 | 2.655 | 7.56E-22 | 2.63E-20 |
| IL11 | 1.065 | 7.44E-21 | 2.43E-19 |
| FGF20 | 2.007 | 1.14E-20 | 3.69E-19 |
| NEUROG2 | 2.295 | 1.27E-20 | 4.08E-19 |
| LPO | 1.618 | 1.28E-20 | 4.11E-19 |
| MMP8 | 1.862 | 1.30E-20 | 4.17E-19 |
| GJB4 | 1.048 | 1.51E-20 | 4.82E-19 |
| ERVMER61 | 2.946 | 2.13E-20 | 6.68E-19 |
| SLC26A9 | 1.762 | 2.13E-20 | 6.70E-19 |
| ONECUT3 | 1.605 | 2.18E-20 | 6.84E-19 |
| SMKR1 | 1.150 | 3.27E-20 | 1.01E-18 |

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|---|---|---|---|
| SPRR3 | 2.278 | 5.99E-20 | 1.82E-18 |
| TLX1 | 1.022 | 6.31E-20 | 1.91E-18 |
| NXPH1 | 2.751 | 8.81E-20 | 2.65E-18 |
| ULBP2 | 1.134 | 9.72E-20 | 2.91E-18 |
| DUSP5P1 | 2.332 | 1.47E-19 | 4.32E-18 |
| SLCO1B1 | 2.758 | 1.90E-19 | 5.54E-18 |
| LY6D | 1.664 | 2.15E-19 | 6.24E-18 |
| ARHGAP40 | 2.087 | 3.08E-19 | 8.83E-18 |
| MYBPHL | 2.057 | 3.09E-19 | 8.86E-18 |
| FGA | 1.544 | 3.37E-19 | 9.64E-18 |
| DSG3 | 1.013 | 4.03E-19 | 1.14E-17 |
| SIX1 | 1.348 | 4.84E-19 | 1.37E-17 |
| MIR31HG | 2.402 | 5.02E-19 | 1.42E-17 |
| CNN2P4 | 2.385 | 5.23E-19 | 1.47E-17 |
| ASCL5 | 1.156 | 5.45E-19 | 1.53E-17 |
| BTBD16 | 1.160 | 5.67E-19 | 1.59E-17 |
| AC012501 | 2.476 | 1.00E-18 | 2.75E-17 |
| SPATA12 | 1.121 | 1.23E-18 | 3.37E-17 |
| AL162759 | 2.682 | 1.41E-18 | 3.84E-17 |
| PLA2G3 | 1.265 | 2.55E-18 | 6.79E-17 |
| MAGEA12 | 2.696 | 2.60E-18 | 6.92E-17 |
| TRIM71 | 1.878 | 2.80E-18 | 7.44E-17 |
| AC093732 | 1.796 | 3.71E-18 | 9.76E-17 |
| AC093850 | 2.162 | 3.82E-18 | 1.01E-16 |
| SNORA74A | 2.875 | 4.07E-18 | 1.06E-16 |
| AC012512 | 2.077 | 4.24E-18 | 1.11E-16 |
| SERPINB7 | 1.682 | 5.88E-18 | 1.53E-16 |
| PLAC4 | 1.372 | 6.92E-18 | 1.78E-16 |
| AC004593 | 1.570 | 7.08E-18 | 1.82E-16 |
| APELA | 1.469 | 9.16E-18 | 2.33E-16 |
| NXPH4 | 1.015 | 1.01E-17 | 2.56E-16 |
| KRT83 | 1.838 | 1.02E-17 | 2.58E-16 |
| DMRTA2 | 1.337 | 1.23E-17 | 3.09E-16 |
| AKAP4 | 2.473 | 1.30E-17 | 3.24E-16 |
| AC140076 | 2.023 | 1.51E-17 | 3.75E-16 |
| CPA4 | 1.543 | 1.70E-17 | 4.22E-16 |
| DUSP9 | 1.381 | 1.96E-17 | 4.82E-16 |
| DCSTAMP | 1.517 | 2.00E-17 | 4.93E-16 |
| SLAMF9 | 1.368 | 2.94E-17 | 7.17E-16 |
| AC133785 | 2.235 | 3.67E-17 | 8.83E-16 |
| AC019100 | 1.962 | 3.76E-17 | 9.02E-16 |
| SBSN | 1.886 | 3.77E-17 | 9.03E-16 |
| PPBP | 1.123 | 4.96E-17 | 1.18E-15 |
| CYP4F23P | 1.476 | 5.40E-17 | 1.28E-15 |

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|---|---|---|---|
| LUCAT1 | 1.342 | 8.28E-17 | 1.95E-15 |
| DMRT3 | 1.890 | 9.20E-17 | 2.16E-15 |
| MIR3189 | 1.334 | 9.94E-17 | 2.33E-15 |
| FAM150A | 1.024 | 1.47E-16 | 3.41E-15 |
| SNORA71A | 1.303 | 1.49E-16 | 3.45E-15 |
| HOXC11 | 1.442 | 1.55E-16 | 3.57E-15 |
| S100A11P1 | 2.353 | 2.43E-16 | 5.55E-15 |
| PTF1A | 2.578 | 2.99E-16 | 6.79E-15 |
| MMP20 | 1.915 | 3.21E-16 | 7.25E-15 |
| BAAT | 1.451 | 3.47E-16 | 7.82E-15 |
| CCAT2 | 1.973 | 7.52E-16 | 1.65E-14 |
| APOA2 | 1.731 | 8.72E-16 | 1.91E-14 |
| SLC22A11 | 1.027 | 1.10E-15 | 2.40E-14 |
| CHST4 | 1.108 | 1.17E-15 | 2.53E-14 |
| AC004988 | 1.653 | 1.41E-15 | 3.04E-14 |
| SPATA20P1 | 2.221 | 2.23E-15 | 4.75E-14 |
| KDELC1P1 | 1.545 | 2.65E-15 | 5.62E-14 |
| PGC | 1.109 | 3.00E-15 | 6.31E-14 |
| CLDN16 | 1.053 | 4.07E-15 | 8.45E-14 |
| XIRP1 | 1.191 | 4.13E-15 | 8.57E-14 |
| WFDC10A | 2.036 | 5.41E-15 | 1.11E-13 |
| IFNWP19 | 2.151 | 5.51E-15 | 1.12E-13 |
| DUXAP10 | 1.619 | 5.91E-15 | 1.20E-13 |
| KRT6C | 2.151 | 8.02E-15 | 1.61E-13 |
| TMEM40 | 1.615 | 8.78E-15 | 1.76E-13 |
| KRT87P | 1.811 | 1.00E-14 | 1.99E-13 |
| AHSG | 1.581 | 1.15E-14 | 2.29E-13 |
| PRSS41 | 1.553 | 1.25E-14 | 2.47E-13 |
| RHBG | 1.778 | 1.67E-14 | 3.24E-13 |
| RNA5SP18 | 2.390 | 1.67E-14 | 3.24E-13 |
| CYCSP6 | 1.275 | 2.48E-14 | 4.74E-13 |
| PRDM12 | 1.223 | 2.74E-14 | 5.22E-13 |
| IFITM5 | 2.192 | 2.85E-14 | 5.43E-13 |
| BBOX1 | 1.123 | 3.05E-14 | 5.79E-13 |
| PGLYRP3 | 2.181 | 3.53E-14 | 6.64E-13 |
| CSF2 | 1.151 | 3.98E-14 | 7.43E-13 |
| RAET1K | 1.331 | 4.35E-14 | 8.08E-13 |
| BHLHA9 | 2.133 | 4.38E-14 | 8.13E-13 |
| SNORD12B | 1.343 | 4.50E-14 | 8.35E-13 |
| SH2D5 | 1.230 | 5.46E-14 | 1.01E-12 |
| IFNE | 2.188 | 6.26E-14 | 1.15E-12 |
| CSTL1 | 1.586 | 7.13E-14 | 1.30E-12 |
| SNORA71D | 2.183 | 7.23E-14 | 1.32E-12 |
| AC064834 | 1.800 | 7.52E-14 | 1.37E-12 |

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|---|---|---|---|
| RPS18P1 | 1.945 | 7.57E-14 | 1.38E-12 |
| MAGEB17 | 1.137 | 8.14E-14 | 1.47E-12 |
| SNORD12C | 2.028 | 8.35E-14 | 1.51E-12 |
| ATP6V0A4 | 1.695 | 9.72E-14 | 1.75E-12 |
| AC005264 | 1.787 | 1.04E-13 | 1.86E-12 |
| PTTG3P | 1.953 | 1.14E-13 | 2.03E-12 |
| FOXI3 | 2.292 | 1.17E-13 | 2.09E-12 |
| PCMTD1P3 | 1.928 | 1.27E-13 | 2.24E-12 |
| IGFL1P1 | 1.994 | 1.97E-13 | 3.43E-12 |
| CALCA | 1.184 | 2.32E-13 | 4.02E-12 |
| OFCC1 | 1.887 | 2.79E-13 | 4.80E-12 |
| AC105399 | 2.090 | 2.83E-13 | 4.86E-12 |
| AL589743 | 1.422 | 3.26E-13 | 5.58E-12 |
| VTCN1 | 1.414 | 3.26E-13 | 5.58E-12 |
| AC002331 | 1.561 | 3.58E-13 | 6.13E-12 |
| TDGF1P3 | 1.651 | 3.64E-13 | 6.21E-12 |
| SNORD48 | 1.886 | 4.01E-13 | 6.82E-12 |
| GSDMC | 1.132 | 4.29E-13 | 7.29E-12 |
| RPL37AP8 | 1.163 | 4.62E-13 | 7.84E-12 |
| TMEM75 | 1.548 | 6.48E-13 | 1.09E-11 |
| IL36RN | 1.804 | 8.41E-13 | 1.40E-11 |
| SPDYC | 1.050 | 9.32E-13 | 1.55E-11 |
| BEST3 | 1.318 | 1.21E-12 | 1.99E-11 |
| AFP | 1.385 | 1.50E-12 | 2.46E-11 |
| SNORA71C | 1.088 | 1.63E-12 | 2.66E-11 |
| SEC14L4 | 1.291 | 1.70E-12 | 2.76E-11 |
| F2 | 1.157 | 1.79E-12 | 2.91E-11 |
| OACYLP | 1.136 | 1.84E-12 | 2.98E-11 |
| HSPE1P5 | 1.906 | 2.40E-12 | 3.86E-11 |
| PPP1R14BP2 | 1.242 | 2.41E-12 | 3.86E-11 |
| RPL18P13 | 1.143 | 3.99E-12 | 6.25E-11 |
| ALOXE3 | 1.243 | 4.02E-12 | 6.29E-11 |
| GAST | 2.035 | 4.13E-12 | 6.46E-11 |
| DIRC1 | 1.984 | 4.82E-12 | 7.49E-11 |
| CAMKV | 1.030 | 7.10E-12 | 1.09E-10 |
| MAGEA11 | 1.378 | 7.78E-12 | 1.18E-10 |
| TECRP2 | 1.617 | 8.32E-12 | 1.26E-10 |
| RPL35AP21 | 1.519 | 9.20E-12 | 1.39E-10 |
| TAS2R38 | 1.127 | 9.30E-12 | 1.40E-10 |
| PRDM13 | 1.292 | 1.35E-11 | 2.00E-10 |
| RFX8 | 1.128 | 2.39E-11 | 3.48E-10 |
| SNRPFP1 | 1.518 | 2.55E-11 | 3.70E-10 |
| MAGOH3P | 1.538 | 2.63E-11 | 3.80E-10 |
| NAT16 | 1.324 | 3.57E-11 | 5.09E-10 |

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|---|---|---|---|
| TPT1P12 | 1.262 | 3.91E-11 | 5.55E-10 |
| FGG | 1.787 | 4.18E-11 | 5.91E-10 |
| RPS3AP46 | 1.465 | 4.34E-11 | 6.13E-10 |
| ORM1 | 1.269 | 4.38E-11 | 6.18E-10 |
| S100A7 | 1.698 | 4.51E-11 | 6.35E-10 |
| CSAG1 | 1.711 | 4.84E-11 | 6.79E-10 |
| AC009362 | 1.070 | 5.03E-11 | 7.04E-10 |
| MIR7111 | 1.214 | 5.74E-11 | 7.98E-10 |
| HULC | 1.595 | 6.41E-11 | 8.87E-10 |
| SMCO2 | 1.081 | 6.42E-11 | 8.87E-10 |
| AC018641 | 1.325 | 7.08E-11 | 9.73E-10 |
| METTL11B | 1.879 | 7.20E-11 | 9.88E-10 |
| SAA4 | 1.666 | 7.76E-11 | 1.06E-09 |
| HBE1 | 1.652 | 7.97E-11 | 1.09E-09 |
| CST5 | 1.906 | 9.07E-11 | 1.23E-09 |
| AC009410 | 1.212 | 9.91E-11 | 1.34E-09 |
| AC104297 | 1.093 | 1.14E-10 | 1.53E-09 |
| MIOX | 1.116 | 1.15E-10 | 1.54E-09 |
| IL17C | 1.084 | 1.21E-10 | 1.62E-09 |
| AC112721 | 1.666 | 1.50E-10 | 1.99E-09 |
| SCDP1 | 1.332 | 1.52E-10 | 2.02E-09 |
| GRK1 | 1.073 | 1.66E-10 | 2.19E-09 |
| SNORA23 | 1.517 | 1.66E-10 | 2.19E-09 |
| LRRN4 | 1.017 | 2.21E-10 | 2.89E-09 |
| ATP5G1P6 | 1.667 | 2.71E-10 | 3.51E-09 |
| SNORD88A | 1.611 | 3.15E-10 | 4.05E-09 |
| HIST1H2AH | 1.286 | 3.23E-10 | 4.14E-09 |
| UBE2SP2 | 1.032 | 3.28E-10 | 4.19E-09 |
| SLCO1A2 | 1.225 | 3.39E-10 | 4.32E-09 |
| C9orf57 | 1.865 | 3.52E-10 | 4.48E-09 |
| SNORA80B | 1.370 | 3.63E-10 | 4.61E-09 |
| SNORD72 | 1.648 | 3.63E-10 | 4.61E-09 |
| RPL36P16 | 1.415 | 3.98E-10 | 5.03E-09 |
| RYKP1 | 1.129 | 4.30E-10 | 5.42E-09 |
| AQP2 | 1.740 | 4.58E-10 | 5.76E-09 |
| RPS24P16 | 1.436 | 4.77E-10 | 5.98E-09 |
| SCARNA5 | 1.265 | 5.63E-10 | 7.03E-09 |
| TMEM249 | 1.019 | 5.96E-10 | 7.42E-09 |
| AC118754 | 1.378 | 6.44E-10 | 7.98E-09 |
| FAR2P1 | 1.176 | 6.59E-10 | 8.14E-09 |
| PCAT14 | 1.042 | 7.25E-10 | 8.93E-09 |
| CLLU1 | 1.576 | 7.56E-10 | 9.29E-09 |
| HIST1H4B | 1.317 | 8.18E-10 | 1.00E-08 |
| HCRT | 1.408 | 8.37E-10 | 1.02E-08 |

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|---|---|---|---|
| GTF2F2P1 | 1.359 | 8.50E-10 | 1.04E-08 |
| AKR1C8P | 1.598 | 1.03E-09 | 1.25E-08 |
| UPK2 | 1.161 | 1.19E-09 | 1.43E-08 |
| POU3F2 | 1.286 | 1.36E-09 | 1.63E-08 |
| WASIR2 | 1.196 | 1.55E-09 | 1.85E-08 |
| GNGT1 | 1.067 | 1.58E-09 | 1.88E-08 |
| AC144450 | 1.183 | 1.70E-09 | 2.01E-08 |
| HIST1H3J | 1.115 | 2.42E-09 | 2.82E-08 |
| AC092573 | 1.012 | 2.45E-09 | 2.85E-08 |
| DDX3P1 | 1.166 | 2.73E-09 | 3.17E-08 |
| RPL7AP4 | 1.135 | 2.79E-09 | 3.23E-08 |
| PRDX2P4 | 1.295 | 2.94E-09 | 3.40E-08 |
| IZUMO2 | 1.065 | 3.39E-09 | 3.89E-08 |
| HIST1H2AB | 1.418 | 3.41E-09 | 3.91E-08 |
| PDCD5P1 | 1.254 | 3.57E-09 | 4.09E-08 |
| EIF3IP1 | 1.399 | 4.29E-09 | 4.87E-08 |
| MRPL40P1 | 1.652 | 4.41E-09 | 5.01E-08 |
| HIST1H2BI | 1.453 | 4.73E-09 | 5.34E-08 |
| AC013439 | 1.270 | 4.77E-09 | 5.38E-08 |
| TCAM1P | 1.330 | 5.05E-09 | 5.68E-08 |
| SULT1C2P1 | 1.246 | 5.14E-09 | 5.77E-08 |
| LRP2 | 1.281 | 5.58E-09 | 6.21E-08 |
| HES7 | 1.213 | 6.94E-09 | 7.63E-08 |
| PPEF1 | 1.208 | 1.00E-08 | 1.08E-07 |
| ERHP1 | 1.178 | 1.30E-08 | 1.38E-07 |
| HIST1H3I | 1.334 | 1.67E-08 | 1.75E-07 |
| AC105009 | 1.517 | 1.72E-08 | 1.80E-07 |
| RN7SL28P | 1.475 | 1.73E-08 | 1.81E-07 |
| HSPD1P2 | 1.395 | 2.40E-08 | 2.49E-07 |
| MIR6797 | 1.282 | 3.02E-08 | 3.09E-07 |
| TEX19 | 1.130 | 3.42E-08 | 3.48E-07 |
| FGF8 | 1.300 | 3.49E-08 | 3.54E-07 |
| AC005592 | 1.153 | 3.92E-08 | 3.96E-07 |
| C15orf54 | 1.407 | 4.02E-08 | 4.04E-07 |
| UROC1 | 1.399 | 4.02E-08 | 4.04E-07 |
| AL022326 | 1.154 | 4.16E-08 | 4.18E-07 |
| RPL31P2 | 1.203 | 4.25E-08 | 4.26E-07 |
| AC079145 | 1.043 | 4.41E-08 | 4.41E-07 |
| POLD2P1 | 1.263 | 4.78E-08 | 4.76E-07 |
| IFNL3P1 | 1.090 | 5.09E-08 | 5.03E-07 |
| PCBP2P1 | 1.262 | 5.86E-08 | 5.76E-07 |
| PKMP5 | 1.045 | 5.92E-08 | 5.81E-07 |
| BHMG1 | 1.433 | 6.03E-08 | 5.91E-07 |
| RPS8P3 | 1.249 | 6.49E-08 | 6.32E-07 |

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|---|---|---|---|
| KLK5 | 1.440 | 7.65E-08 | 7.38E-07 |
| ANKRD33 | 1.253 | 8.66E-08 | 8.29E-07 |
| SEPHS1P4 | 1.160 | 9.99E-08 | 9.49E-07 |
| EPHA8 | 1.343 | 1.06E-07 | 1.00E-06 |
| EEF1DP5 | 1.193 | 1.08E-07 | 1.02E-06 |
| IGFL3 | 1.078 | 1.09E-07 | 1.03E-06 |
| ANKRD1 | 1.091 | 1.31E-07 | 1.22E-06 |
| ARF1P2 | 1.296 | 1.48E-07 | 1.37E-06 |
| SNRPD2P1 | 1.238 | 1.86E-07 | 1.71E-06 |
| FDPSP8 | 1.166 | 1.88E-07 | 1.72E-06 |
| AC064850 | 1.009 | 2.15E-07 | 1.96E-06 |
| SNRPCP2 | 1.033 | 2.21E-07 | 2.01E-06 |
| AP000577 | 1.258 | 2.22E-07 | 2.01E-06 |
| ANKRD20A19P | 1.360 | 2.31E-07 | 2.09E-06 |
| SUPT4H1P | 1.412 | 2.63E-07 | 2.36E-06 |
| AC092415 | 1.410 | 2.86E-07 | 2.56E-06 |
| SLC25A24P1 | 1.157 | 2.90E-07 | 2.59E-06 |
| OBP2A | 1.301 | 3.11E-07 | 2.77E-06 |
| RPL37P1 | 1.267 | 3.56E-07 | 3.14E-06 |
| SERPINH1P1 | 1.163 | 4.45E-07 | 3.88E-06 |
| MUCL1 | 1.006 | 4.72E-07 | 4.10E-06 |
| TREML3P | 1.194 | 5.35E-07 | 4.62E-06 |
| AC012066 | 1.003 | 5.87E-07 | 5.04E-06 |
| ILF2P1 | 1.167 | 6.32E-07 | 5.41E-06 |
| AC019129 | 1.001 | 6.73E-07 | 5.74E-06 |
| MPP4 | 1.051 | 7.88E-07 | 6.66E-06 |
| AC007790 | 1.209 | 8.94E-07 | 7.50E-06 |
| RNU4ATAC | 1.056 | 9.05E-07 | 7.58E-06 |
| EN1 | 1.215 | 9.58E-07 | 8.00E-06 |
| FDPSP5 | 1.240 | 9.72E-07 | 8.11E-06 |
| KAAG1 | 1.179 | 1.06E-06 | 8.83E-06 |
| FKBP4P6 | 1.268 | 1.11E-06 | 9.15E-06 |
| PRDX2P1 | 1.146 | 1.13E-06 | 9.30E-06 |
| EIF5AP3 | 1.184 | 1.22E-06 | 1.01E-05 |
| AC005102 | 1.098 | 1.57E-06 | 1.27E-05 |
| HIST2H2AB | 1.145 | 1.61E-06 | 1.30E-05 |
| RPS7P15 | 1.075 | 1.76E-06 | 1.41E-05 |
| NUFIP1P | 1.216 | 1.97E-06 | 1.57E-05 |
| AC007750 | 1.195 | 1.97E-06 | 1.57E-05 |
| GCM1 | 1.023 | 2.01E-06 | 1.59E-05 |
| EPGN | 1.288 | 2.03E-06 | 1.61E-05 |
| CHRNA6 | 1.024 | 2.10E-06 | 1.66E-05 |
| HBQ1 | 1.014 | 2.20E-06 | 1.74E-05 |
| ACTBL2 | 1.209 | 2.44E-06 | 1.91E-05 |

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|---|---|---|---|
| PMCH | 1.191 | 2.71E-06 | 2.10E-05 |
| MIR6835 | 1.041 | 2.82E-06 | 2.18E-05 |
| SLED1 | 1.081 | 2.84E-06 | 2.19E-05 |
| HNRNPH1P3 | 1.180 | 3.55E-06 | 2.70E-05 |
| KLF2P1 | 1.186 | 4.39E-06 | 3.30E-05 |
| OR7E85P | 1.176 | 4.40E-06 | 3.31E-05 |
| AC073326 | 1.208 | 5.15E-06 | 3.82E-05 |
| AC024995 | 1.100 | 5.32E-06 | 3.93E-05 |
| IFIT1P1 | 1.166 | 5.60E-06 | 4.12E-05 |
| ZDHHC4P1 | 1.114 | 6.46E-06 | 4.70E-05 |
| PARP1P1 | 1.045 | 6.62E-06 | 4.82E-05 |
| TMEM213 | 1.012 | 6.83E-06 | 4.96E-05 |
| GPRC6A | 1.004 | 7.03E-06 | 5.09E-05 |
| GAPDHP67 | 1.019 | 7.09E-06 | 5.13E-05 |
| SCARNA8 | 1.111 | 7.29E-06 | 5.27E-05 |
| RPL7P33 | 1.102 | 8.08E-06 | 5.79E-05 |
| SIX3 | 1.185 | 8.28E-06 | 5.92E-05 |
| SNORD1B | 1.089 | 1.55E-05 | 0.000107 |
| EGOT | 1.099 | 1.74E-05 | 0.000119 |
| SEPW1P | 1.063 | 1.81E-05 | 0.000124 |
| CD300LD | 1.143 | 1.86E-05 | 0.000127 |
| AC012354 | 1.021 | 3.15E-05 | 0.000207 |
| RNY1 | 1.030 | 3.48E-05 | 0.000226 |
| AC023672 | 1.042 | 3.82E-05 | 0.000247 |
| NPM1P40 | 1.010 | 5.37E-05 | 0.000337 |
| IRG1 | 1.006 | 0.000113 | 0.000664 |

**Table S2. Downregulated genes in colon cancer.**

| Genes | logFC | PValue | FDR |
|---|---|---|---|
| OTOP2 | -2.658 | 2.42E-179 | 4.84E-175 |
| CLDN8 | -2.102 | 1.11E-110 | 1.11E-106 |
| MYOC | -2.397 | 2.53E-109 | 1.69E-105 |
| CD177P1 | -2.668 | 4.33E-109 | 2.17E-105 |
| TMIGD1 | -1.849 | 5.71E-107 | 2.29E-103 |
| LGI1 | -2.586 | 7.85E-103 | 2.62E-99 |
| GUCA2B | -1.752 | 5.08E-96 | 1.45E-92 |
| SLC17A8 | -2.557 | 1.87E-95 | 4.67E-92 |
| PCSK2 | -2.198 | 7.00E-94 | 1.56E-90 |
| DAO | -2.296 | 2.98E-90 | 5.96E-87 |
| PYY | -1.719 | 2.76E-89 | 5.02E-86 |
| MS4A10 | -2.597 | 7.42E-88 | 1.24E-84 |
| GCG | -1.800 | 1.17E-87 | 1.80E-84 |
| RERGL | -2.144 | 5.87E-87 | 7.84E-84 |
| CA1 | -1.459 | 7.26E-87 | 9.09E-84 |

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|---|---|---|---|
| SLC30A10 | -1.886 | 2.17E-86 | 2.56E-83 |
| NPY2R | -2.466 | 8.85E-85 | 9.85E-82 |
| NGB | -2.563 | 3.14E-84 | 3.32E-81 |
| PHOX2B | -2.284 | 1.80E-83 | 1.80E-80 |
| INSL5 | -2.149 | 3.75E-83 | 3.58E-80 |
| RN7SKP127 | -2.595 | 8.55E-83 | 7.78E-80 |
| HSD3B2 | -1.951 | 2.34E-81 | 2.04E-78 |
| SST | -1.860 | 3.07E-80 | 2.56E-77 |
| AQP8 | -1.364 | 1.86E-76 | 1.49E-73 |
| VSTM2A | -2.338 | 3.74E-76 | 2.88E-73 |
| PMP2 | -2.251 | 2.04E-74 | 1.51E-71 |
| CMTM5 | -2.347 | 1.94E-73 | 1.39E-70 |
| KHDRBS2 | -2.403 | 9.27E-73 | 6.40E-70 |
| FEV | -2.039 | 2.29E-72 | 1.53E-69 |
| FAM180B | -2.385 | 3.82E-72 | 2.39E-69 |
| BRINP3 | -1.714 | 4.01E-71 | 2.36E-68 |
| NRXN1 | -1.763 | 1.26E-70 | 7.23E-68 |
| FAM135B | -1.930 | 7.83E-70 | 4.36E-67 |
| STMN4 | -2.170 | 1.34E-69 | 7.24E-67 |
| C14orf180 | -2.377 | 1.52E-68 | 8.00E-66 |
| SGCG | -2.228 | 5.32E-68 | 2.73E-65 |
| ASB5 | -2.155 | 1.47E-66 | 7.37E-64 |
| TMEFF2 | -2.131 | 1.94E-66 | 9.50E-64 |
| ANGPTL7 | -1.886 | 2.79E-66 | 1.33E-63 |
| PLP1 | -1.536 | 4.65E-66 | 2.17E-63 |
| SCGN | -1.528 | 6.41E-65 | 2.92E-62 |
| CMA1 | -1.840 | 1.58E-63 | 7.02E-61 |
| SLC5A7 | -2.080 | 2.22E-63 | 9.46E-61 |
| SLC7A14 | -1.942 | 2.79E-63 | 1.16E-60 |
| SPOCK3 | -2.109 | 1.38E-62 | 5.64E-60 |
| SLC6A19 | -1.471 | 2.42E-62 | 9.58E-60 |
| AC007182 | -1.737 | 2.44E-62 | 9.58E-60 |
| SLITRK3 | -1.878 | 8.03E-62 | 3.04E-59 |
| NEUROD1 | -1.905 | 1.33E-61 | 4.92E-59 |
| ABCB11 | -1.738 | 1.37E-60 | 4.98E-58 |
| CA7 | -1.276 | 1.53E-60 | 5.48E-58 |
| MS4A12 | -1.248 | 1.74E-60 | 6.13E-58 |
| SYT10 | -2.233 | 8.37E-60 | 2.89E-57 |
| AC106869 | -2.021 | 1.07E-59 | 3.63E-57 |
| SEMA3E | -1.651 | 1.14E-59 | 3.81E-57 |
| BMP3 | -1.338 | 2.25E-59 | 7.38E-57 |
| GALR1 | -2.207 | 1.10E-58 | 3.50E-56 |
| XKR4 | -1.757 | 2.65E-58 | 8.29E-56 |
| TCEAL5 | -2.136 | 3.40E-58 | 1.05E-55 |

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|---|---|---|---|
| GABRG2 | -2.150 | 6.72E-58 | 2.04E-55 |
| CHST9 | -2.157 | 8.18E-58 | 2.44E-55 |
| SCN7A | -1.425 | 2.55E-57 | 7.52E-55 |
| PI16 | -1.411 | 2.98E-57 | 8.65E-55 |
| CLCA4 | -1.129 | 7.32E-57 | 2.09E-54 |
| P2RX2 | -1.960 | 2.14E-56 | 6.04E-54 |
| ASTN1 | -1.843 | 2.40E-56 | 6.67E-54 |
| RIMS4 | -1.779 | 3.37E-56 | 9.26E-54 |
| TUSC5 | -1.942 | 1.01E-55 | 2.71E-53 |
| CDH19 | -1.552 | 1.16E-55 | 3.06E-53 |
| MGAT4C | -2.049 | 1.60E-55 | 4.17E-53 |
| ST8SIA3 | -2.123 | 2.65E-55 | 6.81E-53 |
| PRIMA1 | -1.411 | 3.53E-55 | 8.84E-53 |
| HS3ST6 | -2.170 | 4.09E-55 | 1.01E-52 |
| PHOX2A | -2.003 | 9.40E-55 | 2.27E-52 |
| HTR3C | -2.078 | 1.07E-54 | 2.56E-52 |
| C2orf40 | -1.530 | 4.40E-54 | 1.02E-51 |
| NPY6R | -1.507 | 4.94E-54 | 1.14E-51 |
| NPY | -1.917 | 1.74E-53 | 3.97E-51 |
| SYT4 | -1.760 | 2.53E-53 | 5.68E-51 |
| PIRT | -1.533 | 7.48E-53 | 1.65E-50 |
| RXRG | -1.672 | 1.55E-52 | 3.37E-50 |
| CD177 | -1.075 | 3.48E-52 | 7.50E-50 |
| CA4 | -1.118 | 5.79E-52 | 1.23E-49 |
| HMP19 | -1.512 | 7.69E-52 | 1.61E-49 |
| MORN5 | -1.890 | 8.01E-52 | 1.66E-49 |
| MUSK | -1.661 | 1.50E-51 | 3.07E-49 |
| BEST4 | -1.182 | 1.63E-51 | 3.29E-49 |
| CHGA | -1.119 | 1.36E-50 | 2.72E-48 |
| ADCYAP1R1 | -1.551 | 1.38E-50 | 2.73E-48 |
| FIGF | -1.537 | 1.88E-50 | 3.70E-48 |
| PCAT18 | -2.089 | 2.31E-50 | 4.50E-48 |
| GPM6A | -1.419 | 3.34E-50 | 6.44E-48 |
| OLFM3 | -1.880 | 9.25E-50 | 1.75E-47 |
| MYOT | -1.585 | 1.29E-49 | 2.42E-47 |
| ELANE | -1.837 | 1.38E-49 | 2.56E-47 |
| TCEAL2 | -1.547 | 2.11E-49 | 3.87E-47 |
| CNTN2 | -1.541 | 4.47E-49 | 8.15E-47 |
| LMX1A | -1.870 | 6.18E-49 | 1.10E-46 |
| DPP6 | -1.451 | 1.27E-48 | 2.25E-46 |
| SFRP5 | -1.557 | 7.07E-48 | 1.22E-45 |
| ZG16 | -1.012 | 9.04E-48 | 1.55E-45 |
| AC074363 | -2.029 | 2.69E-47 | 4.57E-45 |
| GBA3 | -1.271 | 3.38E-47 | 5.69E-45 |

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|---|---|---|---|
| RSPO2 | -1.365 | 5.31E-47 | 8.79E-45 |
| ADH1B | -1.108 | 2.27E-46 | 3.70E-44 |
| CHRM2 | -1.418 | 3.30E-46 | 5.32E-44 |
| CASR | -1.963 | 3.49E-46 | 5.60E-44 |
| AMPD1 | -1.399 | 7.39E-46 | 1.16E-43 |
| ATP1A2 | -1.193 | 1.06E-45 | 1.65E-43 |
| B4GALNT2 | -1.092 | 1.21E-45 | 1.87E-43 |
| CTNND2 | -1.517 | 2.56E-45 | 3.92E-43 |
| SERPINA9 | -1.928 | 3.88E-45 | 5.88E-43 |
| CD300LG | -1.744 | 5.00E-45 | 7.54E-43 |
| SLC18A3 | -1.990 | 6.13E-45 | 9.16E-43 |
| CLVS2 | -1.883 | 8.04E-45 | 1.19E-42 |
| CWH43 | -1.173 | 8.23E-45 | 1.21E-42 |
| ABCB5 | -1.720 | 8.85E-45 | 1.28E-42 |
| UGT1A8 | -1.231 | 1.05E-44 | 1.51E-42 |
| ELAVL3 | -1.810 | 1.24E-44 | 1.77E-42 |
| ABCA8 | -1.132 | 1.35E-44 | 1.92E-42 |
| NRSN1 | -1.884 | 2.64E-44 | 3.73E-42 |
| KIAA2022 | -1.477 | 3.48E-44 | 4.85E-42 |
| AL928768 | -1.519 | 3.49E-44 | 4.85E-42 |
| DMRTA1 | -1.439 | 4.07E-44 | 5.62E-42 |
| CNGB1 | -1.692 | 4.50E-44 | 6.18E-42 |
| WISP2 | -1.244 | 8.74E-44 | 1.18E-41 |
| SCNN1G | -1.417 | 1.74E-43 | 2.33E-41 |
| SFRP1 | -1.104 | 1.83E-43 | 2.43E-41 |
| AC004947 | -1.760 | 5.45E-43 | 7.18E-41 |
| SNAP91 | -1.566 | 6.23E-43 | 8.15E-41 |
| KRT9 | -1.940 | 8.30E-43 | 1.08E-40 |
| MAB21L1 | -1.605 | 1.04E-42 | 1.35E-40 |
| BCHE | -1.229 | 1.30E-42 | 1.67E-40 |
| GSG1L | -1.870 | 2.22E-42 | 2.83E-40 |
| ATCAY | -1.571 | 3.56E-42 | 4.51E-40 |
| CASQ2 | -1.225 | 3.84E-42 | 4.80E-40 |
| PLCXD3 | -1.513 | 6.88E-42 | 8.43E-40 |
| SLC27A6 | -1.627 | 6.90E-42 | 8.43E-40 |
| OGN | -1.122 | 8.12E-42 | 9.86E-40 |
| ANGPTL5 | -1.969 | 1.02E-41 | 1.23E-39 |
| NUS1P2 | -1.964 | 1.17E-41 | 1.39E-39 |
| TAGLN3 | -1.507 | 1.53E-41 | 1.81E-39 |
| BAI3 | -1.430 | 1.60E-41 | 1.88E-39 |
| ATP2B3 | -1.870 | 2.87E-41 | 3.37E-39 |
| UG0898H09 | -1.571 | 3.78E-41 | 4.40E-39 |
| FRRS1L | -1.486 | 6.83E-41 | 7.90E-39 |
| LHFPL4 | -1.510 | 7.46E-41 | 8.59E-39 |

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|---|---|---|---|
| CADM3 | -1.299 | 8.34E-41 | 9.55E-39 |
| NEFM | -1.498 | 1.12E-40 | 1.26E-38 |
| GPR15 | -1.227 | 1.97E-40 | 2.22E-38 |
| BEST2 | -1.124 | 2.51E-40 | 2.80E-38 |
| NEFL | -1.295 | 3.41E-40 | 3.80E-38 |
| PKHD1L1 | -1.320 | 3.50E-40 | 3.87E-38 |
| CNR1 | -1.244 | 5.33E-40 | 5.87E-38 |
| SLC30A8 | -1.888 | 5.65E-40 | 6.15E-38 |
| SORCS1 | -1.239 | 1.05E-39 | 1.14E-37 |
| EPHA6 | -1.702 | 1.11E-39 | 1.19E-37 |
| SPIB | -1.030 | 1.23E-39 | 1.31E-37 |
| SLC4A10 | -1.270 | 1.82E-39 | 1.92E-37 |
| CNGA3 | -1.380 | 2.33E-39 | 2.43E-37 |
| CTNNA3 | -1.390 | 3.10E-39 | 3.21E-37 |
| RASGEF1C | -1.583 | 3.55E-39 | 3.67E-37 |
| MEP1B | -1.165 | 4.36E-39 | 4.48E-37 |
| FOXD3 | -1.657 | 5.20E-39 | 5.32E-37 |
| SCN2B | -1.337 | 6.12E-39 | 6.22E-37 |
| PRPH | -1.209 | 7.88E-39 | 7.98E-37 |
| NAP1L2 | -1.264 | 9.43E-39 | 9.49E-37 |
| COL19A1 | -1.659 | 1.24E-38 | 1.24E-36 |
| FMN2 | -1.319 | 1.35E-38 | 1.35E-36 |
| MAPK4 | -1.341 | 1.42E-38 | 1.41E-36 |
| P2RY4 | -1.586 | 1.50E-38 | 1.48E-36 |
| SLAMF6P1 | -1.409 | 1.62E-38 | 1.60E-36 |
| CTSG | -1.207 | 1.70E-38 | 1.67E-36 |
| SCN11A | -1.373 | 2.35E-38 | 2.27E-36 |
| SPINK2 | -1.389 | 2.03E-37 | 1.91E-35 |
| PCDH10 | -1.495 | 3.03E-37 | 2.84E-35 |
| KCTD4 | -1.534 | 3.33E-37 | 3.11E-35 |
| HSPB3 | -1.435 | 4.27E-37 | 3.96E-35 |
| HRK | -1.520 | 5.66E-37 | 5.20E-35 |
| NR1H4 | -1.164 | 7.46E-37 | 6.82E-35 |
| LCN6 | -1.660 | 8.99E-37 | 8.18E-35 |
| LONRF2 | -1.243 | 9.29E-37 | 8.42E-35 |
| ANGPTL1 | -1.095 | 1.15E-36 | 1.04E-34 |
| DPYSL5 | -1.547 | 1.35E-36 | 1.20E-34 |
| AGTR1 | -1.254 | 1.44E-36 | 1.28E-34 |
| SLCO4C1 | -1.231 | 2.01E-36 | 1.77E-34 |
| KCNB1 | -1.270 | 2.17E-36 | 1.90E-34 |
| NPTX1 | -1.160 | 2.26E-36 | 1.97E-34 |
| HAND1 | -1.325 | 2.31E-36 | 2.00E-34 |
| SCG3 | -1.266 | 3.50E-36 | 3.02E-34 |
| PTPRZ1 | -1.294 | 3.81E-36 | 3.26E-34 |

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| SLC6A15 | -1.576 | 5.00E-36 | 4.26E-34 |
| CA10 | -1.585 | 5.22E-36 | 4.43E-34 |
| TMEM179 | -1.389 | 6.35E-36 | 5.37E-34 |
| IGLJ1 | -1.825 | 7.70E-36 | 6.45E-34 |
| ADH1A | -1.844 | 8.50E-36 | 7.10E-34 |
| C20orf166 | -1.335 | 9.61E-36 | 7.98E-34 |
| HMX2 | -1.764 | 1.08E-35 | 8.89E-34 |
| KCNA1 | -1.737 | 1.32E-35 | 1.08E-33 |
| ASPA | -1.146 | 1.36E-35 | 1.11E-33 |
| IGKV1OR10 | -1.801 | 1.65E-35 | 1.34E-33 |
| SH2D7 | -1.179 | 2.03E-35 | 1.64E-33 |
| IGHV3OR16 | -1.556 | 3.26E-35 | 2.61E-33 |
| ZMAT4 | -1.797 | 3.77E-35 | 3.01E-33 |
| GRIN2A | -1.419 | 5.37E-35 | 4.25E-33 |
| TEX11 | -1.174 | 5.70E-35 | 4.49E-33 |
| C11orf86 | -1.035 | 5.81E-35 | 4.56E-33 |
| MEP1AP4 | -1.542 | 7.76E-35 | 6.05E-33 |
| C16orf89 | -1.103 | 8.34E-35 | 6.45E-33 |
| TMEM100 | -1.081 | 9.41E-35 | 7.25E-33 |
| TNFRSF13B | -1.207 | 1.24E-34 | 9.53E-33 |
| ENPP6 | -1.236 | 1.89E-34 | 1.44E-32 |
| SYT9 | -1.804 | 2.13E-34 | 1.62E-32 |
| SVOPL | -1.342 | 2.47E-34 | 1.87E-32 |
| FCER2 | -1.250 | 2.82E-34 | 2.13E-32 |
| ADRA1A | -1.572 | 4.60E-34 | 3.47E-32 |
| UNC5D | -1.455 | 6.29E-34 | 4.70E-32 |
| SLITRK2 | -1.535 | 1.02E-33 | 7.61E-32 |
| TMEM151B | -1.343 | 1.16E-33 | 8.61E-32 |
| BEX1 | -1.312 | 1.18E-33 | 8.73E-32 |
| ENAM | -1.364 | 1.36E-33 | 9.99E-32 |
| HMGCLL1 | -1.429 | 1.61E-33 | 1.18E-31 |
| PCOLCE2 | -1.092 | 2.00E-33 | 1.46E-31 |
| PROKR1 | -1.754 | 2.15E-33 | 1.57E-31 |
| CNTFR | -1.381 | 3.07E-33 | 2.21E-31 |
| IGKV1OR22 | -1.451 | 3.36E-33 | 2.40E-31 |
| KIF1A | -1.096 | 3.49E-33 | 2.48E-31 |
| MOBP | -1.410 | 8.71E-33 | 6.10E-31 |
| TUBB4A | -1.173 | 9.15E-33 | 6.39E-31 |
| UGT1A1 | -1.259 | 9.18E-33 | 6.39E-31 |
| HTR4 | -1.133 | 1.51E-32 | 1.05E-30 |
| ANO5 | -1.026 | 2.02E-32 | 1.39E-30 |
| GLP2R | -1.025 | 2.06E-32 | 1.41E-30 |
| ADRB3 | -1.604 | 3.01E-32 | 2.05E-30 |
| ALK | -1.469 | 3.03E-32 | 2.06E-30 |

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| CALY | -1.352 | 3.44E-32 | 2.33E-30 |
| CELA3B | -1.607 | 7.04E-32 | 4.73E-30 |
| INA | -1.193 | 7.83E-32 | 5.25E-30 |
| AP001627 | -1.413 | 1.56E-31 | 1.04E-29 |
| FCRL4 | -1.413 | 1.68E-31 | 1.11E-29 |
| ZBTB16 | -1.136 | 2.84E-31 | 1.85E-29 |
| FXYD1 | -1.176 | 2.87E-31 | 1.87E-29 |
| PDZRN4 | -1.081 | 3.58E-31 | 2.32E-29 |
| GFRA2 | -1.035 | 7.83E-31 | 4.99E-29 |
| GAP43 | -1.079 | 8.13E-31 | 5.17E-29 |
| TPH1 | -1.024 | 1.28E-30 | 8.07E-29 |
| IGKV3OR2 | -1.401 | 1.30E-30 | 8.16E-29 |
| HTR3A | -1.270 | 1.43E-30 | 9.00E-29 |
| LCN10 | -1.631 | 1.56E-30 | 9.73E-29 |
| HAND2 | -1.002 | 1.87E-30 | 1.17E-28 |
| CPB1 | -1.551 | 2.74E-30 | 1.69E-28 |
| CLEC4G | -1.315 | 3.41E-30 | 2.10E-28 |
| IGHJ3P | -1.269 | 3.52E-30 | 2.15E-28 |
| MAL | -1.078 | 4.11E-30 | 2.50E-28 |
| POU3F3 | -1.409 | 4.39E-30 | 2.66E-28 |
| DIRAS2 | -1.396 | 4.67E-30 | 2.83E-28 |
| ELAVL4 | -1.133 | 4.94E-30 | 2.98E-28 |
| IGHV6 | -1.094 | 5.96E-30 | 3.59E-28 |
| SEZ6L | -1.271 | 7.71E-30 | 4.61E-28 |
| SVOP | -1.298 | 7.97E-30 | 4.75E-28 |
| SNTG2 | -1.503 | 8.68E-30 | 5.15E-28 |
| CCL23 | -1.152 | 9.32E-30 | 5.49E-28 |
| IGKV6D | -1.351 | 1.03E-29 | 6.08E-28 |
| AQPEP | -1.245 | 1.07E-29 | 6.25E-28 |
| ZNF536 | -1.128 | 1.14E-29 | 6.65E-28 |
| KLHL34 | -1.173 | 1.23E-29 | 7.14E-28 |
| TNNT3 | -1.462 | 1.43E-29 | 8.31E-28 |
| HPSE2 | -1.039 | 1.75E-29 | 1.01E-27 |
| DUSP26 | -1.173 | 2.20E-29 | 1.26E-27 |
| GNG13 | -1.250 | 2.77E-29 | 1.59E-27 |
| SYNDIG1L | -1.475 | 3.52E-29 | 2.00E-27 |
| HTR3E | -1.714 | 3.53E-29 | 2.00E-27 |
| CDH22 | -1.522 | 4.21E-29 | 2.38E-27 |
| AICDA | -1.614 | 4.33E-29 | 2.44E-27 |
| GLRA4 | -1.157 | 4.56E-29 | 2.56E-27 |
| ZNF676 | -1.570 | 4.59E-29 | 2.57E-27 |
| CUX2 | -1.454 | 5.15E-29 | 2.87E-27 |
| FAM181B | -1.296 | 6.16E-29 | 3.42E-27 |
| SLC17A1 | -1.428 | 7.00E-29 | 3.86E-27 |

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| FAM163B | -1.248 | 7.03E-29 | 3.87E-27 |
| OMD | -1.076 | 9.09E-29 | 4.99E-27 |
| WSCD2 | -1.173 | 1.23E-28 | 6.68E-27 |
| CXCR5 | -1.410 | 1.34E-28 | 7.27E-27 |
| TMEM59L | -1.099 | 1.46E-28 | 7.88E-27 |
| AMER3 | -1.411 | 1.54E-28 | 8.32E-27 |
| ANO3 | -1.453 | 1.72E-28 | 9.24E-27 |
| RPH3A | -1.385 | 3.26E-28 | 1.74E-26 |
| RIC3 | -1.140 | 3.81E-28 | 2.02E-26 |
| SMYD1 | -1.225 | 5.23E-28 | 2.75E-26 |
| PCP4L1 | -1.154 | 5.28E-28 | 2.77E-26 |
| BEND4 | -1.225 | 6.96E-28 | 3.64E-26 |
| P2RY12 | -1.147 | 7.34E-28 | 3.83E-26 |
| UGT1A9 | -1.650 | 7.73E-28 | 4.02E-26 |
| GNG8 | -1.437 | 9.48E-28 | 4.91E-26 |
| C10orf105 | -1.637 | 9.49E-28 | 4.91E-26 |
| ACSM5 | -1.191 | 1.19E-27 | 6.17E-26 |
| GP2 | -1.045 | 1.20E-27 | 6.20E-26 |
| WDR17 | -1.186 | 1.23E-27 | 6.32E-26 |
| CBLN2 | -1.101 | 2.16E-27 | 1.10E-25 |
| DPEP3 | -1.442 | 2.41E-27 | 1.22E-25 |
| FGFBP2 | -1.186 | 2.84E-27 | 1.43E-25 |
| IGHV4OR15 | -1.646 | 2.84E-27 | 1.43E-25 |
| CHST8 | -1.484 | 3.01E-27 | 1.51E-25 |
| KCNE2 | -1.294 | 3.27E-27 | 1.64E-25 |
| KCNK3 | -1.014 | 3.85E-27 | 1.91E-25 |
| GFI1B | -1.145 | 4.00E-27 | 1.98E-25 |
| TCL1A | -1.150 | 4.05E-27 | 1.99E-25 |
| CRHBP | -1.257 | 6.31E-27 | 3.08E-25 |
| CLEC9A | -1.189 | 6.65E-27 | 3.23E-25 |
| SFTA1P | -1.289 | 7.63E-27 | 3.69E-25 |
| NRG2 | -1.190 | 8.25E-27 | 3.97E-25 |
| SH3GL2 | -1.220 | 8.93E-27 | 4.28E-25 |
| ERVH | -1.328 | 9.63E-27 | 4.59E-25 |
| IGKV1OR2 | -1.448 | 1.17E-26 | 5.55E-25 |
| KCNK2 | -1.230 | 1.26E-26 | 5.96E-25 |
| NTNG1 | -1.275 | 1.37E-26 | 6.45E-25 |
| DRD5 | -1.414 | 1.78E-26 | 8.37E-25 |
| COL6A5 | -1.270 | 2.17E-26 | 1.01E-24 |
| ANKS1B | -1.144 | 2.45E-26 | 1.14E-24 |
| NOVA1 | -1.090 | 2.51E-26 | 1.17E-24 |
| METTL24 | -1.106 | 2.90E-26 | 1.34E-24 |
| CLCA2 | -1.155 | 2.96E-26 | 1.36E-24 |
| FLJ38122 | -1.459 | 2.99E-26 | 1.38E-24 |

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| MAMDC2 | -1.016 | 3.13E-26 | 1.44E-24 |
| RPL15P21 | -1.390 | 3.39E-26 | 1.55E-24 |
| PPP1R1A | -1.035 | 3.83E-26 | 1.74E-24 |
| ASCL1 | -1.618 | 4.09E-26 | 1.85E-24 |
| CACNG7 | -1.627 | 4.68E-26 | 2.12E-24 |
| SEZ6 | -1.264 | 4.86E-26 | 2.19E-24 |
| CELF4 | -1.189 | 5.28E-26 | 2.37E-24 |
| TMEM229A | -1.466 | 5.54E-26 | 2.48E-24 |
| IGHV3OR15 | -1.141 | 6.00E-26 | 2.68E-24 |
| VWC2 | -1.212 | 9.07E-26 | 3.98E-24 |
| AKR1B10P1 | -1.345 | 9.09E-26 | 3.98E-24 |
| PENK | -1.173 | 1.28E-25 | 5.57E-24 |
| TRDV1 | -1.389 | 1.41E-25 | 6.13E-24 |
| IGLV5 | -1.137 | 1.45E-25 | 6.26E-24 |
| ZNF492 | -1.349 | 1.46E-25 | 6.28E-24 |
| SCGB2A1 | -1.045 | 2.11E-25 | 9.06E-24 |
| VIT | -1.055 | 2.56E-25 | 1.10E-23 |
| SLC17A7 | -1.049 | 2.81E-25 | 1.20E-23 |
| LIPC | -1.023 | 3.25E-25 | 1.37E-23 |
| LRAT | -1.273 | 3.64E-25 | 1.52E-23 |
| IGKV2OR22 | -1.226 | 3.67E-25 | 1.54E-23 |
| ERBB4 | -1.550 | 3.91E-25 | 1.63E-23 |
| DNER | -1.022 | 4.28E-25 | 1.78E-23 |
| KCNS2 | -1.352 | 4.72E-25 | 1.94E-23 |
| RFX6 | -1.199 | 4.74E-25 | 1.95E-23 |
| GRIA1 | -1.280 | 7.83E-25 | 3.20E-23 |
| TMEM72 | -1.065 | 9.55E-25 | 3.88E-23 |
| CASC18 | -1.373 | 1.02E-24 | 4.13E-23 |
| OR2W3 | -1.206 | 1.41E-24 | 5.64E-23 |
| NPY5R | -1.392 | 1.59E-24 | 6.35E-23 |
| UNC80 | -1.341 | 1.68E-24 | 6.72E-23 |
| IGKV5 | -1.019 | 2.19E-24 | 8.69E-23 |
| NAP1L6 | -1.577 | 2.56E-24 | 1.01E-22 |
| KCNG3 | -1.126 | 2.88E-24 | 1.14E-22 |
| LGI3 | -1.233 | 4.78E-24 | 1.87E-22 |
| ZIC1 | -1.523 | 4.86E-24 | 1.89E-22 |
| NOS1 | -1.055 | 5.47E-24 | 2.13E-22 |
| HNRNPA1P33 | -1.560 | 5.48E-24 | 2.13E-22 |
| CRABP1 | -1.075 | 6.12E-24 | 2.37E-22 |
| KRT1 | -1.182 | 7.48E-24 | 2.89E-22 |
| HMX3 | -1.339 | 7.91E-24 | 3.05E-22 |
| C1orf177 | -1.107 | 8.97E-24 | 3.45E-22 |
| KIAA1045 | -1.197 | 9.21E-24 | 3.54E-22 |
| FCRL1 | -1.091 | 9.64E-24 | 3.69E-22 |

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| TMEM132C | -1.036 | 9.77E-24 | 3.73E-22 |
| OR2S1P | -1.123 | 1.05E-23 | 3.99E-22 |
| CPNE4 | -1.192 | 1.06E-23 | 4.02E-22 |
| GRIA4 | -1.071 | 1.26E-23 | 4.78E-22 |
| HS6ST3 | -1.293 | 1.57E-23 | 5.95E-22 |
| RSPO1 | -1.109 | 1.68E-23 | 6.35E-22 |
| SCRG1 | -1.075 | 2.23E-23 | 8.39E-22 |
| GPR88 | -1.257 | 2.75E-23 | 1.03E-21 |
| NLGN1 | -1.492 | 4.35E-23 | 1.62E-21 |
| CNTNAP3 | -1.035 | 1.29E-22 | 4.74E-21 |
| SSTR3 | -1.147 | 1.33E-22 | 4.86E-21 |
| ZNF727 | -1.327 | 1.75E-22 | 6.37E-21 |
| IGKV1D | -1.165 | 2.16E-22 | 7.80E-21 |
| SIGLEC6 | -1.042 | 2.36E-22 | 8.51E-21 |
| NWD2 | -1.029 | 2.40E-22 | 8.63E-21 |
| AC104699 | -1.138 | 2.71E-22 | 9.71E-21 |
| SULT4A1 | -1.052 | 3.13E-22 | 1.12E-20 |
| PRAMENP | -1.252 | 3.71E-22 | 1.32E-20 |
| DPP10 | -1.306 | 3.89E-22 | 1.38E-20 |
| CCDC129 | -1.087 | 4.92E-22 | 1.73E-20 |
| HTR7 | -1.044 | 5.15E-22 | 1.81E-20 |
| IGHV1OR21 | -1.184 | 5.37E-22 | 1.89E-20 |
| CYP4B1 | -1.002 | 7.61E-22 | 2.64E-20 |
| RBFOX1 | -1.075 | 7.79E-22 | 2.70E-20 |
| C8orf46 | -1.199 | 8.71E-22 | 3.01E-20 |
| FADS6 | -1.040 | 8.91E-22 | 3.07E-20 |
| GRIA2 | -1.485 | 1.14E-21 | 3.93E-20 |
| ABCC8 | -1.016 | 1.31E-21 | 4.47E-20 |
| GPR142 | -1.382 | 1.36E-21 | 4.65E-20 |
| KCNB2 | -1.351 | 1.43E-21 | 4.87E-20 |
| SLC5A11 | -1.032 | 1.69E-21 | 5.74E-20 |
| NRAP | -1.070 | 2.22E-21 | 7.51E-20 |
| RPL10L | -1.026 | 2.25E-21 | 7.58E-20 |
| PLA2G2C | -1.422 | 2.65E-21 | 8.92E-20 |
| FAM218A | -1.186 | 2.68E-21 | 9.02E-20 |
| SLC5A8 | -1.300 | 2.94E-21 | 9.85E-20 |
| MT1DP | -1.104 | 3.04E-21 | 1.01E-19 |
| GRIA3 | -1.019 | 4.22E-21 | 1.40E-19 |
| CRYBA2 | -1.017 | 4.77E-21 | 1.58E-19 |
| FAR2P2 | -1.117 | 5.77E-21 | 1.90E-19 |
| NLRP7 | -1.087 | 8.40E-21 | 2.74E-19 |
| TMEM132D | -1.125 | 1.07E-20 | 3.48E-19 |
| TAS1R1 | -1.236 | 1.15E-20 | 3.71E-19 |
| NPAS4 | -1.242 | 1.30E-20 | 4.16E-19 |

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| FNDC9 | -1.238 | 1.30E-20 | 4.16E-19 |
| PTCHD1 | -1.205 | 1.74E-20 | 5.53E-19 |
| SNCB | -1.418 | 1.95E-20 | 6.17E-19 |
| MT1P3 | -1.480 | 2.10E-20 | 6.62E-19 |
| ACADL | -1.398 | 2.12E-20 | 6.67E-19 |
| DKFZp779M0652 | -1.328 | 2.21E-20 | 6.91E-19 |
| SPX | -1.325 | 2.99E-20 | 9.28E-19 |
| AF131217 | -1.061 | 3.14E-20 | 9.71E-19 |
| KCNIP1 | -1.218 | 3.71E-20 | 1.14E-18 |
| KCNJ16 | -1.147 | 4.30E-20 | 1.32E-18 |
| CSMD1 | -1.172 | 4.45E-20 | 1.36E-18 |
| CLCNKB | -1.218 | 4.59E-20 | 1.40E-18 |
| CLEC17A | -1.060 | 5.22E-20 | 1.59E-18 |
| DACH2 | -1.373 | 5.76E-20 | 1.75E-18 |
| TAT | -1.174 | 6.08E-20 | 1.84E-18 |
| KLRF1 | -1.079 | 6.39E-20 | 1.93E-18 |
| IL1RAPL1 | -1.420 | 7.79E-20 | 2.35E-18 |
| STXBP5L | -1.077 | 8.08E-20 | 2.43E-18 |
| CYP11A1 | -1.056 | 1.30E-19 | 3.86E-18 |
| MIR8071 | -1.373 | 1.35E-19 | 3.97E-18 |
| SLC8A3 | -1.047 | 1.44E-19 | 4.25E-18 |
| TRIM55 | -1.426 | 1.51E-19 | 4.43E-18 |
| SCTR | -1.027 | 1.78E-19 | 5.18E-18 |
| LIX1 | -1.266 | 2.48E-19 | 7.16E-18 |
| GALNT13 | -1.046 | 2.63E-19 | 7.56E-18 |
| AARD | -1.056 | 2.89E-19 | 8.32E-18 |
| CCDC178 | -1.159 | 6.58E-19 | 1.83E-17 |
| AC096579 | -1.191 | 7.09E-19 | 1.97E-17 |
| LEP | -1.162 | 7.18E-19 | 1.99E-17 |
| NOL4 | -1.051 | 1.22E-18 | 3.35E-17 |
| CYP4F29P | -1.050 | 1.30E-18 | 3.56E-17 |
| MYO3A | -1.062 | 1.83E-18 | 4.98E-17 |
| IL5RA | -1.008 | 1.88E-18 | 5.11E-17 |
| AF186192 | -1.295 | 2.23E-18 | 6.02E-17 |
| CPEB1 | -1.116 | 2.42E-18 | 6.46E-17 |
| CELA3A | -1.301 | 2.74E-18 | 7.28E-17 |
| UTS2B | -1.107 | 3.27E-18 | 8.64E-17 |
| CLEC4F | -1.062 | 3.27E-18 | 8.65E-17 |
| IGKV7 | -1.122 | 3.93E-18 | 1.03E-16 |
| FOXI2 | -1.258 | 4.13E-18 | 1.08E-16 |
| RPL7AP28 | -1.333 | 5.17E-18 | 1.35E-16 |
| LILRP2 | -1.142 | 6.02E-18 | 1.56E-16 |
| IGHV1OR15 | -1.269 | 6.76E-18 | 1.75E-16 |
| IGSF11 | -1.372 | 7.34E-18 | 1.89E-16 |

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| RGS22 | -1.048 | 8.44E-18 | 2.15E-16 |
| LRRTM4 | -1.145 | 1.00E-17 | 2.55E-16 |
| KCNC1 | -1.085 | 1.12E-17 | 2.83E-16 |
| AF064860 | -1.349 | 1.20E-17 | 3.01E-16 |
| CYP8B1 | -1.240 | 1.39E-17 | 3.47E-16 |
| TRGV4 | -1.201 | 1.52E-17 | 3.79E-16 |
| BRINP2 | -1.197 | 1.66E-17 | 4.10E-16 |
| SNAP25 | -1.080 | 1.82E-17 | 4.50E-16 |
| KRT14 | -1.110 | 2.24E-17 | 5.50E-16 |
| CETN4P | -1.333 | 2.40E-17 | 5.87E-16 |
| NCAN | -1.303 | 2.67E-17 | 6.53E-16 |
| TRGV2 | -1.255 | 3.19E-17 | 7.76E-16 |
| ANXA8L1 | -1.011 | 4.03E-17 | 9.64E-16 |
| DDX25 | -1.263 | 4.42E-17 | 1.05E-15 |
| AC002511 | -1.004 | 5.13E-17 | 1.22E-15 |
| SEC14L6 | -1.008 | 5.85E-17 | 1.39E-15 |
| FAM187B2P | -1.208 | 8.26E-17 | 1.94E-15 |
| HCN4 | -1.176 | 1.08E-16 | 2.52E-15 |
| SFTPD | -1.062 | 1.09E-16 | 2.54E-15 |
| hsa | -1.349 | 1.37E-16 | 3.18E-15 |
| AC004637 | -1.325 | 1.45E-16 | 3.35E-15 |
| CCDC169 | -1.324 | 1.57E-16 | 3.62E-15 |
| MIR133A1HG | -1.227 | 2.09E-16 | 4.79E-15 |
| TRIM50 | -1.205 | 2.95E-16 | 6.71E-15 |
| STAC2 | -1.002 | 3.40E-16 | 7.68E-15 |
| HCG4 | -1.114 | 3.64E-16 | 8.18E-15 |
| TPPP2 | -1.214 | 4.38E-16 | 9.83E-15 |
| PCDH8 | -1.085 | 4.58E-16 | 1.03E-14 |
| CARTPT | -1.033 | 5.43E-16 | 1.21E-14 |
| LRP1B | -1.097 | 5.80E-16 | 1.29E-14 |
| TRPC7 | -1.143 | 6.39E-16 | 1.41E-14 |
| AC246787 | -1.251 | 7.00E-16 | 1.54E-14 |
| PAX4 | -1.095 | 7.40E-16 | 1.63E-14 |
| CYP4F24P | -1.186 | 7.65E-16 | 1.68E-14 |
| TMEM155 | -1.014 | 8.77E-16 | 1.92E-14 |
| WDR64 | -1.288 | 1.42E-15 | 3.06E-14 |
| GRIK1 | -1.049 | 2.64E-15 | 5.60E-14 |
| EFCAB1 | -1.019 | 2.84E-15 | 6.00E-14 |
| IGKV2 | -1.150 | 3.13E-15 | 6.58E-14 |
| GP9 | -1.126 | 3.14E-15 | 6.60E-14 |
| TCF23 | -1.058 | 3.86E-15 | 8.05E-14 |
| KIR3DL2 | -1.290 | 4.33E-15 | 8.97E-14 |
| AMHR2 | -1.234 | 4.72E-15 | 9.73E-14 |
| HIGD1AP1 | -1.174 | 5.34E-15 | 1.09E-13 |

| | | | |
|---|---|---|---|
| NPPC | -1.080 | 6.14E-15 | 1.24E-13 |
| ZNF812 | -1.142 | 6.52E-15 | 1.32E-13 |
| ZFR2 | -1.130 | 1.13E-14 | 2.25E-13 |
| FAM216B | -1.041 | 1.30E-14 | 2.55E-13 |
| SYT15 | -1.038 | 1.36E-14 | 2.68E-13 |
| MAP1LC3C | -1.032 | 1.39E-14 | 2.73E-13 |
| GCSAML | -1.002 | 1.42E-14 | 2.77E-13 |
| AC016995 | -1.064 | 1.45E-14 | 2.83E-13 |
| WFIKKN2 | -1.029 | 1.62E-14 | 3.14E-13 |
| SLC7A3 | -1.167 | 1.65E-14 | 3.19E-13 |
| IGLL1 | -1.055 | 1.67E-14 | 3.24E-13 |
| AL161668 | -1.039 | 1.87E-14 | 3.61E-13 |
| C1QTNF9 | -1.229 | 2.21E-14 | 4.24E-13 |
| CAMP | -1.097 | 2.55E-14 | 4.87E-13 |
| OPN4 | -1.184 | 3.04E-14 | 5.77E-13 |
| TRGV3 | -1.089 | 3.15E-14 | 5.96E-13 |
| TRBV27 | -1.226 | 3.19E-14 | 6.03E-13 |
| IGLL3P | -1.202 | 3.23E-14 | 6.09E-13 |
| C16orf96 | -1.176 | 3.49E-14 | 6.57E-13 |
| RIMS2 | -1.034 | 3.99E-14 | 7.46E-13 |
| TRIM63 | -1.106 | 4.25E-14 | 7.93E-13 |
| IGKV2D | -1.163 | 4.27E-14 | 7.95E-13 |
| ELL2P1 | -1.045 | 5.02E-14 | 9.28E-13 |
| CCNA1 | -1.074 | 5.38E-14 | 9.94E-13 |
| PCDHA1 | -1.173 | 1.14E-13 | 2.03E-12 |
| SYT6 | -1.068 | 1.21E-13 | 2.14E-12 |
| CHODL | -1.002 | 1.37E-13 | 2.41E-12 |
| UGT3A2 | -1.059 | 1.55E-13 | 2.72E-12 |
| LGSN | -1.057 | 1.87E-13 | 3.26E-12 |
| UGT1A7 | -1.128 | 2.52E-13 | 4.35E-12 |
| ABHD17AP6 | -1.186 | 6.02E-13 | 1.02E-11 |
| GSTA2 | -1.009 | 1.13E-12 | 1.86E-11 |
| PEBP4 | -1.116 | 1.14E-12 | 1.88E-11 |
| GPR31 | -1.108 | 2.05E-12 | 3.31E-11 |
| DCX | -1.015 | 2.22E-12 | 3.57E-11 |
| C5orf17 | -1.009 | 3.79E-12 | 5.95E-11 |
| LRRC37A7P | -1.051 | 4.49E-12 | 7.01E-11 |
| DIRC3 | -1.069 | 4.69E-12 | 7.30E-11 |
| PKD1L2 | -1.076 | 9.23E-12 | 1.39E-10 |
| CNTN5 | -1.074 | 9.44E-12 | 1.42E-10 |
| AC078941 | -1.006 | 1.28E-11 | 1.90E-10 |
| RPL7P60 | -1.084 | 1.89E-11 | 2.78E-10 |
| BFSP2 | -1.015 | 4.47E-11 | 6.30E-10 |
| AC013264 | -1.111 | 4.90E-11 | 6.87E-10 |

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|---|---|---|---|
| ANKRD20A4 | -1.040 | 6.87E-11 | 9.48E-10 |
| CALHM1 | -1.015 | 7.04E-11 | 9.69E-10 |
| SLC4A1 | -1.073 | 1.74E-10 | 2.30E-09 |
| AC005235 | -1.063 | 2.22E-10 | 2.90E-09 |
| PVALB | -1.010 | 2.71E-10 | 3.50E-09 |
| HDAC1P1 | -1.031 | 3.11E-10 | 3.99E-09 |

**Table S3. Unfavorable genes in colon cancer**

| Gene names | UniProtKB | Length | Protein names |
|---|---|---|---|
| LRCH4 | O75427 | 683 | Leucine-rich repeat and calponin homology domain-containing protein 4 |
| POFUT2 | Q9Y2G5 | 429 | GDP-fucose protein O-fucosyltransferase 2 |
| CLK3 | P49761 | 638 | Dual specificity protein kinase CLK3 |
| EGFL7 | Q9UHF1 | 273 | Epidermal growth factor-like protein 7 |
| DPP7 | Q9UHL4 | 492 | Dipeptidyl peptidase 2 |
| HSH2D | Q96JZ2 | 352 | Hematopoietic SH2 domain-containing protein |
| ASB6 | Q9NWX5 | 421 | Ankyrin repeat and SOCS box protein 6 |
| SPAG4 | Q9NPE6 | 437 | Sperm-associated antigen 4 protein |
| EXOC3L4 | Q17RC7 | 722 | Exocyst complex component 3-like protein 4 |
| HSPA1A | P0DMV8 | 641 | Heat shock 70 kDa protein 1A |
| PAQR6 | Q6TCH4 | 344 | Membrane progestin receptor delta |
| FAM69B | Q5VUD6 | 431 | Divergent protein kinase domain 1B |
| CRACR2B | Q8N4Y2 | 399 | EF-hand calcium-binding domain-containing protein 4A |
| ARHGAP4 | P98171 | 946 | Rho GTPase-activating protein 4 |
| NPDC1 | Q9NQX5 | 325 | Neural proliferation differentiation and control protein 1 |
| DAPK1 | P53355 | 1430 | Death-associated protein kinase 1 |
| CNPY3 | Q9BT09 | 278 | Protein canopy homolog 3 |
| ARL8A | Q96BM9 | 186 | ADP-ribosylation factor-like protein 8A |
| INAFM1 | C9JVW0 | 142 | Putative transmembrane protein INAFM1 |
| RHBDD2 | Q6NTF9 | 364 | Rhomboid domain-containing protein 2 |
| SEMA4C | Q9C0C4 | 833 | Semaphorin-4C |
| GDI1 | P31150 | 447 | Rab GDP dissociation inhibitor alpha |
| SLC10A3 | P09131 | 477 | P3 protein |
| PI4K2A | Q9BTU6 | 479 | Phosphatidylinositol 4-kinase type 2-alpha |
| HOMER3 | Q9NSC5 | 361 | Homer protein homolog 3 |
| HSD17B14 | Q9BPX1 | 270 | 17-beta-hydroxysteroid dehydrogenase 14 |
| NPC2 | P61916 | 151 | NPC intracellular cholesterol transporter 2 |
| CRYAB | P02511 | 175 | Alpha-crystallin B chain |
| LIMK1 | P53667 | 647 | LIM domain kinase 1 |
| PYCR2 | Q96C36 | 320 | Pyrroline-5-carboxylate reductase 2 |
| RRNAD1 | Q96FB5 | 475 | Protein RRNAD1 |
| CALB2 | P22676 | 271 | Calretinin |
| GPC1 | P35052 | 558 | Glypican-1 [Cleaved into: Secreted glypican-1] |
| VAMP1 | P23763 | 118 | Vesicle-associated membrane protein 1 |

| | | | |
|---|---|---|---|
| PPP1R3E | Q9H7J1 | 279 | Protein phosphatase 1 regulatory subunit 3E |
| HOXD13 | P35453 | 343 | Homeobox protein Hox-D13 |
| ALAD | P13716 | 330 | Delta-aminolevulinic acid dehydratase |
| ADARB1 | P78563 | 741 | Double-stranded RNA-specific editase 1 |
| HSF4 | Q9ULV5 | 492 | Heat shock factor protein 4 |
| ARHGEF17 | Q96PE2 | 2063 | Rho guanine nucleotide exchange factor 17 |
| JDP2 | Q8WYK2 | 163 | Jun dimerization protein 2 |
| MGEA5 | O60502 | 916 | Protein O-GlcNAcase |
| COMP | P49747 | 757 | Cartilage oligomeric matrix protein |
| AMH | P03971 | 560 | Muellerian-inhibiting factor |
| GPRC5B | Q9NZH0 | 403 | G-protein coupled receptor family C group 5 member B |
| KCNE4 | Q8WWG9 | 221 | Potassium voltage-gated channel subfamily E member 4 |
| FAM50A | Q14320 | 339 | Protein FAM50A |
| TMEM106A | Q96A25 | 262 | Transmembrane protein 106A |
| PHF1 | O43189 | 567 | PHD finger protein 1 |
| PRELP | P51888 | 382 | Prolargin |
| MTHFSD | Q2M296 | 383 | Methenyltetrahydrofolate synthase domain-containing protein |
| HSPB1 | P04792 | 205 | Heat shock protein beta-1 |
| AGAP9 | Q5VTM2 | 703 | Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 9 |
| DNAJB2 | P25686 | 324 | DnaJ homolog subfamily B member 2 |
| LMBR1L | Q6UX01 | 489 | Protein LMBR1L |
| WBP1 | Q96G27 | 269 | WW domain-binding protein 1 |
| CYHR1 | Q6ZMK1 | 362 | Cysteine and histidine-rich protein 1 |
| IGFBP3 | P17936 | 291 | Insulin-like growth factor-binding protein 3 |
| FAM167B | Q9BTA0 | 163 | Protein FAM167B |
| TMEM184A | Q6ZMB5 | 413 | Transmembrane protein 184A |
| TMEM88 | Q6PEY1 | 159 | Transmembrane protein 88 |
| ALDH3B1 | P43353 | 468 | Aldehyde dehydrogenase family 3 member B1 |
| FKBP8 | Q14318 | 412 | Peptidyl-prolyl cis-trans isomerase FKBP8 |
| S1PR3 | Q99500 | 378 | Sphingosine 1-phosphate receptor 3 |
| GATAD2B | Q8WXI9 | 593 | Transcriptional repressor p66-beta |
| SEZ6L2 | Q6UXD5 | 910 | Seizure 6-like protein 2 |
| WWC3 | Q9ULE0 | 1092 | Protein WWC3 |
| THAP3 | Q8WTV1 | 239 | THAP domain-containing protein 3 |
| VSIG4 | Q9Y279 | 399 | V-set and immunoglobulin domain-containing protein 4 |
| TBC1D10B | Q4KMP7 | 808 | TBC1 domain family member 10B |
| DENND6B | Q8NEG7 | 585 | Protein DENND6B |
| INHBB | P09529 | 407 | Inhibin beta B chain |
| GAS1 | P54826 | 345 | Growth arrest-specific protein 1 |
| GPR137B | O60478 | 399 | Integral membrane protein GPR137B |
| GOLGA2 | Q08379 | 1002 | Golgin subfamily A member 2 |
| CRY2 | Q49AN0 | 593 | Cryptochrome-2 |

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|---|---|---|---|
| DEF6 | Q01524 | 100 | Defensin-6 |
| WBSCR27 | Q8N6F8 | 245 | Methyltransferase-like protein 27 |
| FAM219B | Q5XKK7 | 198 | Protein FAM219B |
| FAM3A | P98173 | 230 | Protein FAM3A |
| CCM2 | Q9BSQ5 | 444 | Cerebral cavernous malformations 2 protein |
| RHOG | P84095 | 191 | Rho-related GTP-binding protein RhoG |
| ADAMTSL4 | Q6UY14 | 1074 | ADAMTS-like protein 4 |
| DVL3 | Q92997 | 716 | Segment polarity protein dishevelled homolog DVL-3 |
| SPOCK1 | Q08629 | 439 | Testican-1 |
| AIP | O00170 | 330 | AH receptor-interacting protein |
| NR1D1 | P20393 | 614 | Nuclear receptor subfamily 1 group D member 1 |
| TIMP1 | P01033 | 207 | Metalloproteinase inhibitor 1 |
| RNF32 | Q9H0A6 | 362 | RING finger protein 32 |
| PNMA5 | Q96PV4 | 448 | Paraneoplastic antigen-like protein 5 |
| ANKRD39 | Q53RE8 | 183 | Ankyrin repeat domain-containing protein 39 |
| BCAM | P50895 | 628 | Basal cell adhesion molecule |
| PTGES | O14684 | 152 | Prostaglandin E synthase |
| KRTAP5-1 | Q6L8H4 | 278 | Keratin-associated protein 5-1 |
| TNS1 | Q9HBL0 | 1735 | Tensin-1 |
| THBS3 | P49746 | 956 | Thrombospondin-3 |
| CHD3 | Q12873 | 2000 | Chromodomain-helicase-DNA-binding protein 3 |
| CTSD | P07339 | 412 | Cathepsin D |
| USP20 | Q9Y2K6 | 914 | Ubiquitin carboxyl-terminal hydrolase 20 |
| CUL9 | Q8IWT3 | 2517 | Cullin-9 |
| RBP7 | Q96R05 | 134 | Retinoid-binding protein 7 |
| TAOK2 | Q9UL54 | 1235 | Serine/threonine-protein kinase TAO2 |
| SLC39A13 | Q96H72 | 371 | Zinc transporter ZIP13 |
| TPM2 | P07951 | 284 | Tropomyosin beta chain |
| TSC22D4 | Q9Y3Q8 | 395 | TSC22 domain family protein 4 |
| PBXIP1 | Q96AQ6 | 731 | Pre-B-cell leukemia transcription factor-interacting protein 1 |
| KDM4B | O94953 | 1096 | Lysine-specific demethylase 4B |
| SERPINE1 | P05121 | 402 | Plasminogen activator inhibitor 1 |
| RNF187 | Q5TA31 | 235 | E3 ubiquitin-protein ligase RNF187 |
| AFAP1L1 | Q8TED9 | 768 | Actin filament-associated protein 1-like 1 |
| MIER2 | Q8N344 | 545 | Mesoderm induction early response protein 2 |
| HIST2H2BE | Q16778 | 126 | Histone H2B type 2-E |
| PRNP | F7VJQ1 | 73 | Alternative prion protein |
| C8G | P07360 | 202 | Complement component C8 gamma chain |
| FSTL3 | O95633 | 263 | Follistatin-related protein 3 |
| OLFM2 | O95897 | 454 | Noelin-2 |
| MEGF6 | O75095 | 1541 | Multiple epidermal growth factor-like domains protein 6 |
| DNAJC4 | Q9NNZ3 | 241 | DnaJ homolog subfamily C member 4 |
| IDUA | P35475 | 653 | Alpha-L-iduronidase |

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|---|---|---|---|
| PPP2R2D | Q66LE6 | 453 | Serine/threonine-protein phosphatase 2A 55 kDa regulatory subunit B delta isoform |
| TSPYL2 | Q9H2G4 | 693 | Testis-specific Y-encoded-like protein 2 |
| PLOD3 | O60568 | 738 | Multifunctional procollagen lysine hydroxylase and glycosyltransferase LH3 |
| PARP6 | Q2NL67 | 630 | Protein mono-ADP-ribosyltransferase PARP6 |
| NUMBL | Q9Y6R0 | 609 | Numb-like protein |
| AKAP8L | Q9ULX6 | 646 | A-kinase anchor protein 8-like |
| PLEKHG2 | Q9H7P9 | 1386 | Pleckstrin homology domain-containing family G member 2 |
| FOXC1 | Q12948 | 553 | Forkhead box protein C1 |
| TRIP10 | Q15642 | 601 | Cdc42-interacting protein 4 |
| PXDC1 | Q5TGL8 | 231 | PX domain-containing protein 1 |
| TMPRSS3 | P57727 | 454 | Transmembrane protease serine 3 |
| PRKRIP1 | Q9H875 | 184 | PRKR-interacting protein 1 |
| AOC3 | Q16853 | 763 | Membrane primary amine oxidase |
| SCT | P09683 | 121 | Secretin |
| CBX7 | O95931 | 251 | Chromobox protein homolog 7 |
| LMNTD2 | Q8IXW0 | 634 | Lamin tail domain-containing protein 2 |
| CLK2 | P49760 | 499 | Dual specificity protein kinase CLK2 |
| PABPC1L | Q4VXU2 | 614 | Polyadenylate-binding protein 1-like |
| HIST1H2BD | P58876 | 126 | Histone H2B type 1-D |
| NFKB2 | Q00653 | 900 | Nuclear factor NF-kappa-B p100 subunit |
| PPP1R26 | Q5T8A7 | 1209 | Protein phosphatase 1 regulatory subunit 26 |
| SPARCL1 | Q14515 | 664 | SPARC-like protein 1 |
| PLEC | Q15149 | 4684 | Plectin |
| EPHB4 | P54760 | 987 | Ephrin type-B receptor 4 |
| ENDOV | Q8N8Q3 | 282 | Endonuclease V |
| EPS8L1 | Q8TE68 | 723 | Epidermal growth factor receptor kinase substrate 8-like protein 1 |
| TNFRSF25 | Q93038 | 417 | Tumor necrosis factor receptor superfamily member 25 |
| PCGF2 | P35227 | 344 | Polycomb group RING finger protein 2 |
| SHC2 | P98077 | 582 | SHC-transforming protein 2 |
| TNNT1 | P13805 | 278 | Troponin T, slow skeletal muscle |
| PPP1R18 | Q6NYC8 | 613 | Phostensin |
| FASTK | Q14296 | 549 | Fas-activated serine/threonine kinase |
| SNAI1 | O95863 | 264 | Zinc finger protein SNAI1 |
| DNAJB12 | Q9NXW2 | 375 | DnaJ homolog subfamily B member 12 |
| HYI | Q5T013 | 277 | Putative hydroxypyruvate isomerase |
| ADAMTSL2 | Q86TH1 | 951 | ADAMTS-like protein 2 |
| MFNG | O00587 | 321 | Beta-1,3-N-acetylglucosaminyltransferase manic fringe |
| TFPT | P0C1Z6 | 253 | TCF3 fusion partner |
| ZNF385A | Q96PM9 | 386 | Zinc finger protein 385A |
| ADAP1 | O75689 | 374 | Arf-GAP with dual PH domain-containing protein 1 |
| ABHD8 | Q96I13 | 439 | Protein ABHD8 |

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|---|---|---|---|
| MOGS | Q13724 | 837 | Mannosyl-oligosaccharide glucosidase |
| PTPN6 | P29350 | 595 | Tyrosine-protein phosphatase non-receptor type 6 |
| GAL3ST4 | Q96RP7 | 486 | Galactose-3-O-sulfotransferase 4 |
| TMEM185B | Q9H7F4 | 350 | Transmembrane protein 185B |
| COQ10A | Q96MF6 | 247 | Coenzyme Q-binding protein COQ10 homolog A, mitochondrial |
| SMARCD3 | Q6STE5 | 483 | SWI/SNF-related matrix-associated actin-dependent regulator of chromatin subfamily D member 3 |
| UBTD1 | Q9HAC8 | 227 | Ubiquitin domain-containing protein 1 |
| TLN1 | Q9Y490 | 2541 | Talin-1 |
| NEXN | Q0ZGT2 | 675 | Nexilin |
| RGCC | Q9H4X1 | 137 | Regulator of cell cycle RGCC |
| ADAP2 | Q9NPF8 | 381 | Arf-GAP with dual PH domain-containing protein 2 |
| CRTC2 | Q53ET0 | 693 | CREB-regulated transcription coactivator 2 |
| FES | P07332 | 822 | Tyrosine-protein kinase Fes/Fps |
| FLOT1 | O75955 | 427 | Flotillin-1 |
| NFATC4 | Q14934 | 902 | Nuclear factor of activated T-cells, cytoplasmic 4 |
| DNAJC17 | Q9NVM6 | 304 | DnaJ homolog subfamily C member 17 |
| HSD3B7 | Q9H2F3 | 369 | 3 beta-hydroxysteroid dehydrogenase type 7 |
| STK25 | O00506 | 426 | Serine/threonine-protein kinase 25 |
| GPSM1 | Q86YR5 | 675 | G-protein-signaling modulator 1 |
| RAB3IL1 | Q8TBN0 | 382 | Guanine nucleotide exchange factor for Rab-3A |
| PHF21A | Q96BD5 | 680 | PHD finger protein 21A |
| GBGT1 | Q8N5D6 | 347 | Globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 |
| PTRF | Q6NZI2 | 390 | Caveolae-associated protein 1 |
| PLPPR2 | Q96GM1 | 343 | Phospholipid phosphatase-related protein type 2 |
| TOR4A | Q9NXH8 | 423 | Torsin-4A |
| SOX13 | Q9UN79 | 622 | Transcription factor SOX-13 |
| EBF4 | Q9BQW3 | 602 | Transcription factor COE4 |
| PTOV1 | Q86YD1 | 416 | Prostate tumor-overexpressed gene 1 protein |
| RUBCN | Q92622 | 972 | Run domain Beclin-1-interacting and cysteine-rich domain-containing protein |
| TPBG | Q13641 | 420 | Trophoblast glycoprotein |
| TBC1D8 | O95759 | 1140 | TBC1 domain family member 8 |
| BCL7A | Q4VC05 | 210 | B-cell CLL/lymphoma 7 protein family member A |
| ATG4B | Q9Y4P1 | 393 | Cysteine protease ATG4B |
| ZFYVE27 | Q5T4F4 | 411 | Protrudin |
| ENO2 | P09104 | 434 | Gamma-enolase |
| NEK8 | Q86SG6 | 692 | Serine/threonine-protein kinase Nek8 |
| STAC3 | Q96MF2 | 364 | SH3 and cysteine-rich domain-containing protein 3 |
| ABCA7 | Q8IZY2 | 2146 | Phospholipid-transporting ATPase ABCA7 |
| TLX1 | P31314 | 330 | T-cell leukemia homeobox protein 1 |
| ENO3 | P13929 | 434 | Beta-enolase |
| FLNA | P21333 | 2647 | Filamin-A |

|  |  |  |  |
|---|---|---|---|
| SHANK3 | Q9BYB0 | 1731 | SH3 and multiple ankyrin repeat domains protein 3 |
| PKD1 | P98161 | 4303 | Polycystin-1 |
| ANGPTL4 | Q9BY76 | 406 | Angiopoietin-related protein 4 |
| CD81 | P60033 | 236 | CD81 antigen |
| STAB1 | Q9NY15 | 2570 | Stabilin-1 |
| RRAGB | Q5VZM2 | 374 | Ras-related GTP-binding protein B |
| GAA | P10253 | 952 | Lysosomal alpha-glucosidase |
| C1orf35 | Q9BU76 | 263 | Multiple myeloma tumor-associated protein 2 |
| G0S2 | P27469 | 103 | G0/G1 switch protein 2 |
| FAM134A | Q8NC44 | 543 | Reticulophagy regulator 2 |
| NRIP2 | Q9BQI9 | 281 | Nuclear receptor-interacting protein 2 |
| KCTD7 | Q96MP8 | 289 | BTB/POZ domain-containing protein KCTD7 |
| UCN | P55089 | 124 | Urocortin |
| LZTS2 | Q9BRK4 | 669 | Leucine zipper putative tumor suppressor 2 |
| HOXD9 | P28356 | 352 | Homeobox protein Hox-D9 |
| BATF | Q16520 | 125 | Basic leucine zipper transcriptional factor ATF-like |
| PLIN4 | Q96Q06 | 1357 | Perilipin-4 |
| ZNF653 | Q96CK0 | 615 | Zinc finger protein 653 |
| FOLR2 | P14207 | 255 | Folate receptor beta |
| ITGA5 | P08648 | 1049 | Integrin alpha-5 |
| LCAT | P04180 | 440 | Phosphatidylcholine-sterol acyltransferase |
| NR2C2AP | Q86WQ0 | 139 | Nuclear receptor 2C2-associated protein |
| KCTD13 | Q8WZ19 | 329 | BTB/POZ domain-containing adapter for CUL3-mediated RhoA degradation protein 1 |
| SLC2A3 | P11169 | 496 | Solute carrier family 2, facilitated glucose transporter member 3 |
| SF3A2 | Q15428 | 464 | Splicing factor 3A subunit 2 |
| RUNX3 | Q13761 | 415 | Runt-related transcription factor 3 |
| OAZ2 | O95190 | 189 | Ornithine decarboxylase antizyme 2 |
| KCNJ8 | Q15842 | 424 | ATP-sensitive inward rectifier potassium channel 8 |
| TRAF2 | Q12933 | 501 | TNF receptor-associated factor 2 |
| PHF2 | O75151 | 1096 | Lysine-specific demethylase PHF2 |
| KRI1 | Q8N9T8 | 703 | Protein KRI1 homolog |
| SIPA1 | Q96FS4 | 1042 | Signal-induced proliferation-associated protein 1 |
| CSAD | Q9Y600 | 493 | Cysteine sulfinic acid decarboxylase |
| TUT1 | Q9H6E5 | 874 | Speckle targeted PIP5K1A-regulated poly |
| AGAP3 | Q96P47 | 875 | Arf-GAP with GTPase, ANK repeat and PH domain-containing protein 3 |
| SCAF1 | Q9H7N4 | 1312 | Splicing factor, arginine/serine-rich 19 |
| CLASRP | Q8N2M8 | 674 | CLK4-associating serine/arginine rich protein |
| NR1H2 | P55055 | 460 | Oxysterols receptor LXR-beta |
| C9orf16 | Q9BUW7 | 83 | UPF0184 protein C9orf16 |
| PHKG2 | P15735 | 406 | Phosphorylase b kinase gamma catalytic chain, liver/testis isoform |

|  |  |  |  |
|---|---|---|---|
| SERPING1 | P05155 | 500 | Plasma protease C1 inhibitor |

**Table S4. In all modules of WGCNA, the genes ranked in the top 1000 in connectivity**

| fromNode | toNode | weight |
|---|---|---|
| ABCC9 | DDR2 | 0.28393497 |
| AC018738 | RPL41P1 | 0.318344881 |
| AC026271 | RPL41P1 | 0.287650075 |
| AC107983 | HNRNPCP2 | 0.347219912 |
| ACSS3 | DDR2 | 0.262884034 |
| ACTC1 | MSRB3 | 0.272329137 |
| ACTG2 | LMOD1 | 0.306304734 |
| ADAM12 | COL5A2 | 0.277567183 |
| ADAMTS12 | COL5A2 | 0.298899887 |
| ADAMTS16 | DDR2 | 0.277805673 |
| ADAMTS2 | COL3A1 | 0.283151826 |
| ADCY2 | MSRB3 | 0.276771399 |
| AKAP12 | DDR2 | 0.270114221 |
| AL158801 | RPL41P1 | 0.272151583 |
| AMOTL1 | DDR2 | 0.274032367 |
| ANTXR1 | DDR2 | 0.28602415 |
| AOC3 | CNN1 | 0.282239887 |
| ARHGEF25 | MSRB3 | 0.264466426 |
| ASB5 | LMOD1 | 0.263268793 |
| ASPN | DDR2 | 0.298157265 |
| BEND6 | DDR2 | 0.274523683 |
| BGN | COL1A2 | 0.291674197 |
| BNC2 | DDR2 | 0.282499264 |
| BOC | MSRB3 | 0.262587294 |
| BTF3L4P2 | RPL41P1 | 0.278675854 |
| C11orf98 | RPL41P1 | 0.313183097 |
| C20orf194 | SGCD | 0.268879679 |
| CACNA2D1 | DDR2 | 0.281039235 |
| CALD1 | DDR2 | 0.289600596 |
| CARTPT | LMOD1 | 0.274913361 |
| CASQ2 | LMOD1 | 0.277796732 |
| CCDC8 | DDR2 | 0.269132005 |
| CCDC80 | DDR2 | 0.268863758 |
| CD3G | IKZF1 | 0.272566082 |
| CD79A | IGHJ3 | 0.288620599 |
| CDH2 | DDR2 | 0.289700785 |
| CDK14 | DDR2 | 0.271640276 |
| CHCHD2P9 | RPL41P1 | 0.318939837 |
| CHRDL2 | LMOD1 | 0.277457789 |
| CHRM2 | LMOD1 | 0.281077216 |

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|---|---|---|
| CLMP | DDR2 | 0.273467177 |
| CNN1 | LMOD1 | 0.295713673 |
| COL10A1 | SULF1 | 0.296699008 |
| COL11A1 | SULF1 | 0.296839853 |
| COL12A1 | FBN1 | 0.269049988 |
| COL1A1 | COL1A2 | 0.311159138 |
| COL1A2 | PPAPDC1A | 0.287323169 |
| COL24A1 | DDR2 | 0.262213365 |
| COL3A1 | PPAPDC1A | 0.284489342 |
| COL5A2 | PPAPDC1A | 0.285482178 |
| COL6A3 | DDR2 | 0.267786672 |
| COL8A1 | CORIN | 0.277262786 |
| COL8A2 | DDR2 | 0.270499579 |
| COMP | THBS2 | 0.272014828 |
| CORIN | SULF1 | 0.277585322 |
| CPXM2 | MSRB3 | 0.265523688 |
| CRISPLD1 | DDR2 | 0.282331425 |
| CRYAB | LMOD1 | 0.261519028 |
| CSDC2 | MSRB3 | 0.277465041 |
| CTAGE8 | RPL41P1 | 0.27966984 |
| CTHRC1 | SULF1 | 0.288265066 |
| CXCR2P1 | IKZF1 | 0.266589011 |
| CYP27C1 | DDR2 | 0.269529323 |
| CYP7B1 | DDR2 | 0.264748738 |
| DCN | DDR2 | 0.261814596 |
| DDR2 | SGCD | 0.297013854 |
| DDT | RPL41P1 | 0.275469477 |
| DES | LMOD1 | 0.306551002 |
| DGKI | MSRB3 | 0.265299952 |
| DKK2 | FBN1 | 0.266865489 |
| DPYSL3 | MSRB3 | 0.274032222 |
| EEF1A1P16 | RPL6P27 | 0.28238306 |
| EEF1A1P6 | HNRNPCP2 | 0.331056042 |
| EEF1B2P6 | RPL6P27 | 0.342943793 |
| EEF1G | RPL41P1 | 0.308771101 |
| EIF4BP3 | RPL41P1 | 0.263048004 |
| EIF4BP6 | HNRNPCP2 | 0.297702396 |
| EIF4BP7 | RPL41P1 | 0.302502284 |
| EVC | MSRB3 | 0.264778878 |
| FABP5P7 | HNRNPCP2 | 0.287412204 |
| FAM180A | MSRB3 | 0.274821484 |
| FAM92B | IGHV3 | 0.278847327 |
| FAP | SULF1 | 0.275440723 |
| FBN1 | ITGA11 | 0.280509336 |

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|---|---|---|
| FGF1 | MSRB3 | 0.274427527 |
| FIBIN | MSRB3 | 0.28272229 |
| FLNA | TNS1 | 0.262443312 |
| FLRT2 | MSRB3 | 0.264762482 |
| FST | MSRB3 | 0.271093449 |
| GBP5 | PTPRC | 0.266078819 |
| GDF5 | LMOD1 | 0.276533795 |
| GDF6 | MSRB3 | 0.26669247 |
| GLI3 | MSRB3 | 0.273755954 |
| GLRB | MSRB3 | 0.282552368 |
| GNAO1 | HAND1 | 0.273579154 |
| GREM1 | MSRB3 | 0.267053962 |
| GTF2IP1 | HNRNPA1P38 | 0.266084151 |
| GUCY1A3 | MSRB3 | 0.281209235 |
| HAND1 | LMOD1 | 0.307465138 |
| HAND2 | MSRB3 | 0.268903131 |
| HIST1H2AB | HIST1H4C | 0.263212959 |
| HIST1H2AH | HIST1H4C | 0.264904105 |
| HIST1H3I | HIST1H4C | 0.263317065 |
| HIST1H4A | HIST1H4C | 0.26269903 |
| HIST1H4B | HIST1H4C | 0.268327915 |
| HMGB1P10 | RPL41P1 | 0.307147171 |
| HMGB1P5 | HNRNPA1P38 | 0.309882851 |
| HMGN1P37 | RPL41P1 | 0.291073368 |
| HMGN2P17 | RPL41P1 | 0.29255908 |
| HMGN2P3 | RPL41P1 | 0.324351272 |
| HMGN2P41 | RPL41P1 | 0.329462886 |
| HNRNPA1P10 | HNRNPCP2 | 0.309048406 |
| HNRNPA1P38 | RPL41P1 | 0.342180459 |
| HNRNPCP2 | RPL35P1 | 0.341861466 |
| HOXB5 | HOXB6 | 0.336688595 |
| HOXB6 | HOXB8 | 0.329970781 |
| HOXB8 | HOXB9 | 0.266303066 |
| HSPB6 | LMOD1 | 0.268577364 |
| HSPB7 | LMOD1 | 0.293227231 |
| HSPB8 | MSRB3 | 0.263443577 |
| IFNWP19 | MIR31HG | 0.298076444 |
| IGFBP5 | MSRB3 | 0.273042202 |
| IGHA1 | IGHV3 | 0.333031668 |
| IGHA2 | IGHV3 | 0.281741868 |
| IGHG2 | IGKV1 | 0.277392957 |
| IGHG4 | IGKV1 | 0.291867493 |
| IGHJ1 | IGHV3 | 0.365425495 |
| IGHJ2 | IGHV3 | 0.399820121 |

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|---|---|---|
| IGHJ3 | IGHV3 | 0.405914847 |
| IGHM | IGHV3 | 0.277765637 |
| IGHV1 | IGLC2 | 0.343472762 |
| IGHV1OR21 | IGHV3 | 0.291250938 |
| IGHV2 | IGLC2 | 0.278493482 |
| IGHV3 | IGLC2 | 0.364506351 |
| IGHV3OR15 | IGKV1 | 0.279832655 |
| IGHV4 | IGLC2 | 0.341359654 |
| IGHV5 | IGLC2 | 0.286208235 |
| IGHV6 | IGKV1 | 0.277716281 |
| IGJ | IGKV1 | 0.265331767 |
| IGKC | IGLC2 | 0.315162526 |
| IGKJ5 | IGKV1 | 0.337604936 |
| IGKV1 | IGLC2 | 0.362930611 |
| IGKV2OR22 | IGLV1 | 0.28889708 |
| IGKV4 | IGLV1 | 0.304432248 |
| IGKV6 | IGLV1 | 0.267582133 |
| IGKV7 | IGLV1 | 0.299606167 |
| IGLC2 | IGLV1 | 0.3388089 |
| IGLC3 | IGLV1 | 0.290989675 |
| IGLC7 | IGLV1 | 0.287793824 |
| IGLL1 | IGLV1 | 0.311130561 |
| IGLL5 | IGLV1 | 0.301152999 |
| IGLV1 | IGLV6 | 0.317745316 |
| IGLV2 | IGLV6 | 0.299013986 |
| IGLV4 | MZB1 | 0.269218665 |
| IGLV6 | MZB1 | 0.294121639 |
| IGLV8 | MZB1 | 0.273469489 |
| IGLV9 | MZB1 | 0.276461469 |
| IKZF1 | SH2D1A | 0.273646452 |
| JPH2 | LMOD1 | 0.272437755 |
| KAL1 | SULF1 | 0.274238703 |
| KCNMB1 | LMOD1 | 0.272610108 |
| KIAA1462 | MSRB3 | 0.262130208 |
| KIF26B | SULF1 | 0.266041728 |
| KLHL4 | MSRB3 | 0.262768929 |
| LIMS2 | LMOD1 | 0.264774686 |
| LMOD1 | MORN5 | 0.286902283 |
| LRRC4C | MSRB3 | 0.268897032 |
| LSM12P1 | RPL41P1 | 0.305330649 |