**Supplementary Tables**

**Supplementary Table 1.** A total of 1113 genes were identified to be differentially expressed in early CRC compared with the non-tumoral colorectal tissues.

|  |  |  |
| --- | --- | --- |
| **Gene symbol** | **FDR** | **Log2 FC** |
| FOXQ1 | 5.77E-08 | 4.54 |
| TACSTD2 | 3.09E-06 | 4.52 |
| CLDN1 | 7.89E-09 | 4.37 |
| MMP7 | 5.07E-05 | 4.24 |
| CEMIP | 3.24E-11 | 4.09 |
| DUSP27 | 5.77E-04 | 3.85 |
| COL11A1 | 3.47E-05 | 3.85 |
| KRT23 | 7.97E-04 | 3.78 |
| SRPX2 | 5.69E-10 | 3.62 |
| CXCL8 | 3.94E-05 | 3.25 |
| TESC | 5.07E-05 | 3.24 |
| CTHRC1 | 1.00E-04 | 3.24 |
| COL10A1 | 1.86E-04 | 3.21 |
| NFE2L3 | 5.17E-09 | 3.16 |
| CHI3L1 | 6.91E-05 | 3.10 |
| MMP11 | 1.54E-06 | 3.07 |
| CRNDE | 3.41E-05 | 3.03 |
| COL1A1 | 4.26E-05 | 2.87 |
| TRIB3 | 2.88E-10 | 2.86 |
| LGR5 | 3.15E-04 | 2.86 |
| FAP | 4.93E-04 | 2.83 |
| ASCL2 | 3.54E-08 | 2.82 |
| CDH3 | 3.86E-11 | 2.80 |
| TGFBI | 3.02E-06 | 2.80 |
| FABP6 | 5.80E-06 | 2.78 |
| FCGR3A | 7.26E-04 | 2.72 |
| CXCL1 | 1.18E-05 | 2.68 |
| GNG4 | 2.71E-05 | 2.66 |
| UBE2C | 3.08E-06 | 2.66 |
| SLC7A5 | 8.52E-09 | 2.63 |
| SLC6A6 | 2.70E-07 | 2.63 |
| TPX2 | 2.22E-06 | 2.61 |
| INHBA | 1.23E-05 | 2.59 |
| DPEP1 | 1.19E-04 | 2.52 |
| CXCL3 | 3.88E-04 | 2.49 |
| GDF15 | 2.48E-04 | 2.46 |
| MTHFD1L | 1.65E-07 | 2.45 |
| SLCO4A1 | 5.07E-08 | 2.45 |
| COL1A2 | 3.71E-05 | 2.42 |
| TDGF1 | 3.12E-04 | 2.41 |
| S100A9 | 9.76E-04 | 2.32 |
| PHLDA1 | 1.58E-04 | 2.32 |
| BMP7 | 2.42E-04 | 2.31 |
| MKI67 | 5.53E-06 | 2.28 |
| OLR1 | 8.92E-04 | 2.27 |
| TRIP13 | 1.64E-06 | 2.26 |
| AZGP1 | 1.66E-05 | 2.23 |
| NOX4 | 5.63E-04 | 2.20 |
| APOC1 | 6.45E-04 | 2.20 |
| GTF2IRD1 | 3.36E-10 | 2.17 |
| ENC1 | 8.74E-07 | 2.15 |
| PPM1H | 1.52E-06 | 2.14 |
| PLAU | 8.62E-06 | 2.12 |
| CEP55 | 1.19E-04 | 2.11 |
| CDK1 | 1.27E-04 | 2.11 |
| S100A11 | 4.29E-08 | 2.10 |
| SLC39A10 | 1.35E-09 | 2.10 |
| BUB1 | 2.98E-05 | 2.10 |
| CKS2 | 8.71E-05 | 2.10 |
| TNFRSF12A | 4.07E-08 | 2.09 |
| SOX9 | 2.83E-05 | 2.08 |
| LRRC8E | 5.53E-09 | 2.06 |
| PMEPA1 | 3.89E-04 | 2.04 |
| TOP2A | 4.63E-04 | 2.03 |
| TIMP1 | 1.01E-04 | 2.01 |
| FERMT1 | 3.06E-04 | 1.99 |
| GRHL1 | 1.14E-05 | 1.99 |
| ETV4 | 2.72E-08 | 1.98 |
| ITGA2 | 1.36E-05 | 1.97 |
| PSAT1 | 5.91E-04 | 1.97 |
| HILPDA | 2.22E-07 | 1.96 |
| CDKN2A | 4.29E-04 | 1.96 |
| NEBL | 8.41E-05 | 1.96 |
| CELSR1 | 6.27E-05 | 1.95 |
| SOX4 | 4.67E-05 | 1.94 |
| CYP2S1 | 5.56E-06 | 1.94 |
| GABRE | 9.57E-06 | 1.93 |
| EPHX4 | 6.92E-05 | 1.93 |
| GINS1 | 4.05E-04 | 1.93 |
| ANLN | 3.78E-05 | 1.92 |
| TOP1MT | 1.77E-06 | 1.92 |
| RNF43 | 7.61E-05 | 1.91 |
| C2 | 1.92E-06 | 1.91 |
| TTK | 2.25E-04 | 1.91 |
| ZAK | 3.29E-07 | 1.90 |
| AXIN2 | 9.10E-07 | 1.90 |
| KIAA1549 | 8.24E-09 | 1.90 |
| ECT2 | 4.71E-06 | 1.90 |
| CENPF | 6.38E-06 | 1.89 |
| NEK2 | 1.52E-04 | 1.89 |
| GDPD5 | 6.37E-05 | 1.88 |
| KIF20A | 2.20E-06 | 1.88 |
| DSCC1 | 9.57E-06 | 1.88 |
| GPT2 | 1.80E-06 | 1.87 |
| HOMER1 | 1.10E-05 | 1.87 |
| CDCA5 | 2.95E-04 | 1.86 |
| SLC5A6 | 1.46E-06 | 1.86 |
| SLC7A11 | 1.77E-04 | 1.85 |
| ATP11A | 2.20E-06 | 1.84 |
| GALNT6 | 7.15E-05 | 1.84 |
| BOP1 | 1.73E-07 | 1.84 |
| ARID3A | 1.75E-05 | 1.82 |
| SCD | 3.30E-06 | 1.82 |
| CCNB1 | 2.80E-04 | 1.82 |
| CCDC113 | 5.95E-05 | 1.81 |
| SLC22A3 | 4.40E-04 | 1.81 |
| TMEM97 | 5.49E-04 | 1.80 |
| SIM2 | 4.88E-04 | 1.80 |
| LDLRAD3 | 4.28E-05 | 1.78 |
| NUSAP1 | 5.50E-04 | 1.78 |
| C2CD4A | 6.73E-04 | 1.77 |
| PALD1 | 2.30E-04 | 1.77 |
| UHRF1 | 4.47E-05 | 1.76 |
| RAD54B | 2.38E-06 | 1.76 |
| SPC25 | 9.44E-04 | 1.75 |
| ASPM | 1.19E-04 | 1.75 |
| NCAPG | 1.53E-04 | 1.74 |
| PABPC1L | 9.48E-05 | 1.73 |
| SHROOM4 | 1.17E-06 | 1.72 |
| SQLE | 8.92E-05 | 1.72 |
| CDC6 | 2.19E-04 | 1.72 |
| ATAD2 | 8.20E-05 | 1.71 |
| PTTG1 | 7.81E-04 | 1.70 |
| MACC1 | 2.18E-04 | 1.70 |
| PMAIP1 | 2.53E-04 | 1.70 |
| THY1 | 8.16E-04 | 1.69 |
| ORC6 | 8.91E-06 | 1.69 |
| AURKA | 2.53E-04 | 1.66 |
| CENPA | 9.18E-04 | 1.65 |
| LRP8 | 9.59E-06 | 1.65 |
| MND1 | 3.67E-04 | 1.65 |
| MTFR2 | 4.57E-04 | 1.64 |
| RNF183 | 2.01E-04 | 1.63 |
| BGN | 4.65E-04 | 1.63 |
| LIF | 1.44E-04 | 1.62 |
| ZDHHC9 | 1.91E-06 | 1.62 |
| NUF2 | 3.73E-05 | 1.61 |
| RPS14 | 2.03E-05 | 1.60 |
| KIF14 | 3.82E-05 | 1.60 |
| KRT80 | 1.75E-04 | 1.57 |
| PCSK9 | 2.06E-04 | 1.56 |
| HJURP | 2.58E-06 | 1.55 |
| PRRC2C | 4.58E-04 | 1.55 |
| SERPINE2 | 5.58E-04 | 1.55 |
| TGIF2 | 2.28E-05 | 1.55 |
| SORD | 3.51E-04 | 1.55 |
| SLC39A4 | 4.47E-04 | 1.54 |
| ESM1 | 1.96E-05 | 1.54 |
| NPM1 | 1.34E-05 | 1.54 |
| DLGAP5 | 9.35E-04 | 1.54 |
| FXYD5 | 2.56E-07 | 1.54 |
| SNTB1 | 2.76E-04 | 1.54 |
| CPNE1 | 8.09E-07 | 1.53 |
| BYSL | 9.26E-08 | 1.53 |
| SAPCD2 | 4.22E-05 | 1.53 |
| GOLT1A | 6.05E-04 | 1.53 |
| ZFAS1 | 1.92E-04 | 1.53 |
| RFC3 | 2.50E-05 | 1.52 |
| MYOM3 | 2.92E-04 | 1.51 |
| TM4SF1 | 4.67E-04 | 1.50 |
| LAMC2 | 5.31E-04 | 1.50 |
| KIF4A | 4.28E-04 | 1.50 |
| AHCY | 1.42E-04 | 1.49 |
| RNASEH2A | 1.47E-04 | 1.49 |
| HELLS | 2.60E-04 | 1.49 |
| IMPDH1 | 5.91E-08 | 1.48 |
| NME1 | 8.48E-04 | 1.48 |
| LAMP2 | 9.32E-04 | 1.48 |
| GRAMD1A | 7.85E-08 | 1.48 |
| AJUBA | 5.67E-06 | 1.47 |
| OSBPL3 | 2.22E-05 | 1.47 |
| SLC12A8 | 6.38E-05 | 1.47 |
| SHMT2 | 1.09E-04 | 1.47 |
| LOXL2 | 5.06E-04 | 1.47 |
| UBE2T | 3.21E-04 | 1.46 |
| PCID2 | 7.26E-04 | 1.46 |
| PLEKHA8P1 | 3.77E-06 | 1.46 |
| MYC | 3.24E-04 | 1.46 |
| HSPH1 | 1.22E-05 | 1.46 |
| SKA3 | 3.33E-05 | 1.46 |
| PAICS | 2.75E-05 | 1.45 |
| DTL | 6.04E-04 | 1.44 |
| CMTM7 | 4.14E-06 | 1.43 |
| CMSS1 | 1.93E-04 | 1.43 |
| KIF2C | 9.81E-04 | 1.43 |
| LZTS3 | 3.18E-04 | 1.43 |
| NELFCD | 1.09E-05 | 1.43 |
| C17orf96 | 2.19E-05 | 1.43 |
| SALL4 | 1.90E-04 | 1.43 |
| FAM83H | 2.47E-04 | 1.42 |
| PAQR4 | 4.62E-05 | 1.42 |
| EVA1A | 4.59E-05 | 1.42 |
| DLEU2 | 1.75E-04 | 1.41 |
| VEGFA | 2.24E-04 | 1.41 |
| C10orf2 | 4.04E-06 | 1.41 |
| TPM4 | 7.32E-05 | 1.41 |
| DGAT2 | 4.48E-06 | 1.41 |
| FANCI | 1.79E-04 | 1.40 |
| PSPH | 3.66E-05 | 1.40 |
| CBX2 | 7.36E-05 | 1.40 |
| SYT7 | 5.98E-04 | 1.40 |
| ANXA3 | 1.80E-05 | 1.39 |
| MEST | 4.34E-04 | 1.39 |
| PHF19 | 4.54E-05 | 1.39 |
| RPP40 | 1.59E-04 | 1.39 |
| CAD | 1.68E-07 | 1.39 |
| TIGD1 | 2.61E-04 | 1.39 |
| DDX27 | 5.56E-06 | 1.39 |
| TMEM206 | 2.11E-07 | 1.38 |
| PUS7 | 1.52E-05 | 1.38 |
| CDC25B | 2.78E-06 | 1.38 |
| E2F5 | 4.39E-04 | 1.38 |
| CCND1 | 2.19E-05 | 1.37 |
| TCF7 | 5.98E-05 | 1.37 |
| CCNF | 1.20E-04 | 1.37 |
| HAUS6 | 1.20E-05 | 1.36 |
| NOP56 | 1.69E-05 | 1.36 |
| PTP4A3 | 6.71E-05 | 1.36 |
| BORA | 6.24E-04 | 1.36 |
| CSE1L | 1.66E-04 | 1.36 |
| CDC27 | 8.81E-04 | 1.36 |
| FAM60A | 4.69E-06 | 1.36 |
| FAM89A | 4.77E-05 | 1.35 |
| NOP2 | 3.88E-07 | 1.35 |
| SNORA25 | 4.37E-05 | 1.35 |
| TRIM59 | 6.07E-04 | 1.35 |
| NUDCD1 | 1.18E-04 | 1.35 |
| PPAT | 3.53E-05 | 1.34 |
| NUFIP1 | 1.95E-06 | 1.34 |
| WDR74 | 2.76E-05 | 1.34 |
| GTF3A | 5.83E-06 | 1.34 |
| RIPK2 | 9.42E-05 | 1.34 |
| TP53RK | 2.17E-04 | 1.34 |
| POLR1C | 2.59E-07 | 1.34 |
| RRS1 | 6.30E-05 | 1.33 |
| CDC20 | 5.37E-04 | 1.33 |
| CKAP2 | 8.10E-05 | 1.33 |
| SH3PXD2B | 4.30E-04 | 1.33 |
| FAM84B | 9.03E-04 | 1.32 |
| C4orf48 | 9.41E-05 | 1.32 |
| MMP14 | 4.77E-04 | 1.32 |
| TMEM132A | 1.97E-05 | 1.32 |
| U2SURP | 3.16E-06 | 1.32 |
| PAFAH1B3 | 1.40E-05 | 1.32 |
| ALDH4A1 | 2.81E-04 | 1.32 |
| P4HA1 | 5.81E-05 | 1.31 |
| MFAP2 | 8.76E-04 | 1.31 |
| UBE2S | 4.83E-05 | 1.31 |
| COL7A1 | 8.99E-04 | 1.31 |
| GNL3 | 1.21E-05 | 1.31 |
| PFDN4 | 1.10E-04 | 1.31 |
| DKC1 | 1.14E-04 | 1.30 |
| S100A2 | 3.65E-04 | 1.30 |
| HS2ST1 | 5.72E-05 | 1.29 |
| MSL3P1 | 1.16E-04 | 1.29 |
| KCTD14 | 9.30E-04 | 1.29 |
| RAE1 | 2.99E-06 | 1.29 |
| LYAR | 2.10E-05 | 1.28 |
| PRPF4 | 1.43E-05 | 1.28 |
| TAF1D | 1.19E-07 | 1.28 |
| DNAJC2 | 6.23E-08 | 1.27 |
| MTHFD2 | 1.00E-04 | 1.27 |
| NCAPG2 | 3.59E-04 | 1.27 |
| FUT1 | 5.14E-07 | 1.27 |
| XPOT | 7.34E-06 | 1.27 |
| MTIF3 | 1.26E-05 | 1.27 |
| STRA6 | 6.83E-04 | 1.27 |
| RUVBL1 | 3.87E-04 | 1.27 |
| XKRX | 9.15E-05 | 1.27 |
| BIRC5 | 7.36E-04 | 1.26 |
| TRPM2 | 2.29E-05 | 1.26 |
| LRRC6 | 3.26E-04 | 1.26 |
| NMB | 1.73E-05 | 1.26 |
| POLR1B | 1.74E-06 | 1.25 |
| NIFK | 2.13E-08 | 1.25 |
| MCM10 | 2.52E-06 | 1.25 |
| ADGRG1 | 6.01E-04 | 1.24 |
| PUS1 | 8.89E-06 | 1.24 |
| IER5L | 4.45E-05 | 1.24 |
| NEK6 | 4.90E-05 | 1.23 |
| HM13 | 7.86E-06 | 1.23 |
| PLEKHG4 | 1.60E-04 | 1.23 |
| RPL37A | 3.91E-06 | 1.23 |
| HMMR | 9.30E-04 | 1.23 |
| MRGBP | 1.33E-05 | 1.23 |
| RAD51AP1 | 9.57E-04 | 1.23 |
| ARMC10 | 8.96E-05 | 1.23 |
| SLC35E4 | 3.24E-04 | 1.22 |
| SFXN3 | 5.66E-05 | 1.22 |
| DCAF13 | 5.16E-04 | 1.22 |
| LRP11 | 4.44E-06 | 1.22 |
| NOP16 | 1.82E-05 | 1.22 |
| ASXL1 | 3.56E-05 | 1.22 |
| ANKRD10 | 4.19E-04 | 1.22 |
| MZT1 | 2.60E-04 | 1.22 |
| PBX4 | 1.65E-05 | 1.21 |
| WDR77 | 1.82E-05 | 1.21 |
| GYLTL1B | 9.68E-04 | 1.21 |
| MTAP | 3.18E-04 | 1.21 |
| ZC3HAV1L | 2.89E-05 | 1.21 |
| UNC5CL | 2.09E-04 | 1.21 |
| RNF24 | 3.09E-05 | 1.21 |
| SLC7A6 | 4.83E-06 | 1.21 |
| CENPN | 4.36E-05 | 1.20 |
| ASAP1 | 4.88E-05 | 1.20 |
| SNORA40 | 7.19E-05 | 1.20 |
| SULT2B1 | 5.95E-04 | 1.20 |
| TRIM24 | 3.58E-05 | 1.20 |
| BRIX1 | 1.72E-05 | 1.20 |
| TEAD4 | 1.67E-06 | 1.20 |
| CBX4 | 1.97E-07 | 1.20 |
| NPM3 | 8.90E-05 | 1.19 |
| NOP14 | 8.71E-06 | 1.19 |
| WDR43 | 2.60E-08 | 1.19 |
| CCNE1 | 9.03E-04 | 1.19 |
| ABCC1 | 1.08E-04 | 1.19 |
| MRPS17 | 2.75E-04 | 1.19 |
| ANGPT2 | 6.84E-06 | 1.19 |
| PLEKHA8 | 2.38E-06 | 1.18 |
| CENPP | 1.10E-04 | 1.18 |
| ADRM1 | 3.16E-07 | 1.18 |
| NKRF | 1.91E-04 | 1.18 |
| IL1RAP | 1.35E-04 | 1.18 |
| MCM8 | 5.39E-04 | 1.18 |
| INADL | 2.62E-04 | 1.17 |
| CHPF | 6.43E-06 | 1.17 |
| MORC4 | 1.24E-04 | 1.17 |
| DSN1 | 1.59E-04 | 1.17 |
| DBF4 | 5.00E-04 | 1.17 |
| CFAP97 | 8.51E-06 | 1.17 |
| CDK4 | 7.04E-05 | 1.17 |
| PYCR1 | 9.18E-05 | 1.17 |
| ZMYND8 | 6.23E-04 | 1.16 |
| TTPAL | 1.89E-05 | 1.16 |
| AUNIP | 1.60E-05 | 1.16 |
| CMTM8 | 3.09E-05 | 1.16 |
| TCF3 | 8.09E-07 | 1.16 |
| HSPD1 | 4.83E-05 | 1.16 |
| JADE3 | 3.18E-04 | 1.16 |
| C6orf223 | 2.03E-05 | 1.16 |
| SLC7A1 | 8.57E-04 | 1.16 |
| FAM122B | 2.31E-04 | 1.16 |
| CLPB | 2.00E-05 | 1.15 |
| DDX21 | 4.59E-05 | 1.15 |
| NOP58 | 1.42E-08 | 1.15 |
| WDR12 | 7.37E-06 | 1.15 |
| GGCT | 3.98E-05 | 1.15 |
| SNORA72 | 1.30E-04 | 1.15 |
| CTNNBIP1 | 3.97E-06 | 1.15 |
| MSH5 | 2.21E-04 | 1.15 |
| NANP | 1.15E-04 | 1.15 |
| SNORA33 | 1.72E-04 | 1.14 |
| SLC11A2 | 1.05E-05 | 1.14 |
| TOMM34 | 2.34E-04 | 1.14 |
| UFM1 | 6.12E-04 | 1.14 |
| SNORA32 | 5.37E-04 | 1.14 |
| GART | 2.29E-05 | 1.14 |
| CALU | 6.68E-04 | 1.14 |
| PROSER1 | 1.59E-04 | 1.14 |
| PDRG1 | 3.80E-05 | 1.14 |
| CHD7 | 5.75E-04 | 1.13 |
| CHCHD7 | 3.72E-04 | 1.13 |
| TEX10 | 8.47E-06 | 1.13 |
| FANCD2 | 4.72E-04 | 1.13 |
| CCT6A | 1.49E-06 | 1.12 |
| EXOSC4 | 5.86E-04 | 1.12 |
| HTR1D | 6.84E-05 | 1.12 |
| COMT | 6.64E-06 | 1.12 |
| NOLC1 | 9.70E-04 | 1.12 |
| IRAK1 | 3.23E-04 | 1.12 |
| CNPY3 | 6.38E-05 | 1.12 |
| CCDC34 | 4.25E-04 | 1.12 |
| PNO1 | 4.97E-06 | 1.11 |
| ARFGAP1 | 2.50E-04 | 1.11 |
| GMPS | 1.65E-05 | 1.11 |
| HEATR1 | 1.18E-05 | 1.11 |
| ASUN | 3.42E-04 | 1.11 |
| SNRPB | 5.07E-04 | 1.11 |
| FIGNL1 | 6.17E-04 | 1.11 |
| LY6E | 5.37E-04 | 1.11 |
| RRP12 | 9.76E-07 | 1.11 |
| SLC1A5 | 7.47E-04 | 1.11 |
| PDCD2L | 7.80E-05 | 1.11 |
| SMC4 | 1.17E-04 | 1.10 |
| MCM7 | 3.18E-05 | 1.10 |
| H2AFX | 5.29E-04 | 1.10 |
| PUM3 | 8.62E-05 | 1.10 |
| XPO5 | 4.36E-06 | 1.10 |
| CXXC5 | 1.27E-05 | 1.10 |
| UTP4 | 6.10E-06 | 1.10 |
| SLC7A7 | 6.38E-04 | 1.10 |
| IQGAP3 | 3.94E-04 | 1.09 |
| CBFB | 4.78E-05 | 1.09 |
| C16orf13 | 1.96E-05 | 1.09 |
| SPRY4 | 5.43E-04 | 1.09 |
| MRE11A | 5.27E-05 | 1.09 |
| NOB1 | 5.69E-07 | 1.09 |
| TROAP | 6.57E-04 | 1.08 |
| POLD2 | 1.27E-05 | 1.08 |
| NCBP2 | 3.72E-04 | 1.08 |
| DARS | 3.81E-05 | 1.08 |
| CD46 | 8.57E-04 | 1.08 |
| PSMG4 | 3.11E-04 | 1.08 |
| DLGAP4 | 3.27E-05 | 1.08 |
| YTHDF1 | 3.38E-06 | 1.08 |
| CSNK2A2 | 4.67E-05 | 1.08 |
| UTP14A | 1.36E-05 | 1.08 |
| PPP1R13L | 4.83E-05 | 1.07 |
| LAMC1 | 1.05E-04 | 1.07 |
| INTS6 | 1.60E-04 | 1.07 |
| RRP1 | 2.62E-06 | 1.07 |
| CPNE7 | 4.03E-04 | 1.07 |
| C19orf48 | 4.23E-04 | 1.07 |
| TGIF1 | 2.94E-05 | 1.07 |
| SYNCRIP | 3.63E-05 | 1.07 |
| TTI1 | 3.95E-05 | 1.07 |
| HAUS7 | 1.00E-05 | 1.06 |
| MIF | 3.77E-06 | 1.06 |
| TAF1A | 1.70E-06 | 1.06 |
| POP1 | 1.32E-04 | 1.06 |
| TMEM41A | 1.52E-06 | 1.06 |
| KPNA2 | 3.54E-05 | 1.06 |
| E2F3 | 1.01E-06 | 1.06 |
| SKIL | 2.56E-04 | 1.06 |
| DESI1 | 1.56E-04 | 1.06 |
| DUS4L | 9.88E-04 | 1.06 |
| NONO | 2.18E-04 | 1.06 |
| WDR75 | 3.33E-07 | 1.06 |
| SLC3A2 | 5.63E-05 | 1.06 |
| NXT1 | 7.93E-04 | 1.06 |
| ANKH | 2.81E-04 | 1.06 |
| PDCD5 | 5.33E-06 | 1.05 |
| SMYD2 | 6.72E-07 | 1.05 |
| CD3EAP | 2.58E-07 | 1.05 |
| ANAPC1 | 7.49E-05 | 1.05 |
| RAD18 | 8.02E-04 | 1.05 |
| KIAA1143 | 2.70E-05 | 1.05 |
| PLXNA1 | 8.60E-06 | 1.05 |
| ATIC | 3.88E-04 | 1.05 |
| CNN2 | 2.90E-04 | 1.04 |
| POLB | 3.04E-04 | 1.04 |
| CEP72 | 2.23E-04 | 1.04 |
| MYBL2 | 1.23E-04 | 1.04 |
| TGS1 | 6.30E-04 | 1.04 |
| PNPT1 | 1.10E-04 | 1.04 |
| ATP6V1F | 2.23E-06 | 1.04 |
| NLE1 | 3.59E-06 | 1.03 |
| NCAPD2 | 7.98E-04 | 1.03 |
| EIF3B | 1.75E-06 | 1.03 |
| GTPBP4 | 7.18E-04 | 1.03 |
| RHPN1 | 3.94E-04 | 1.03 |
| YDJC | 3.11E-04 | 1.03 |
| GARS | 6.47E-05 | 1.03 |
| RAI14 | 8.67E-04 | 1.03 |
| DPY19L1 | 2.39E-04 | 1.03 |
| CENPL | 5.37E-04 | 1.02 |
| BBC3 | 2.53E-04 | 1.02 |
| ZNF263 | 5.82E-05 | 1.02 |
| SNRPF | 1.86E-04 | 1.02 |
| CHTF18 | 1.85E-04 | 1.02 |
| NDE1 | 8.79E-05 | 1.01 |
| GLA | 9.93E-05 | 1.01 |
| LYN | 6.23E-04 | 1.01 |
| EIF4EBP1 | 8.62E-04 | 1.01 |
| CBX3 | 2.67E-05 | 1.01 |
| ABCE1 | 1.24E-05 | 1.01 |
| PPP1R14B | 2.88E-06 | 1.01 |
| TWISTNB | 1.57E-05 | 1.01 |
| LPGAT1 | 2.51E-04 | 1.01 |
| ZMYND19 | 2.14E-06 | 1.01 |
| TCTN1 | 6.12E-05 | 1.01 |
| BCL2L1 | 1.60E-08 | 1.00 |
| SIGMAR1 | 2.08E-05 | 1.00 |
| RANGAP1 | 6.30E-05 | 1.00 |
| ATP6V1G2 | 8.29E-04 | -1.00 |
| CIRBP | 1.77E-04 | -1.00 |
| AGL | 5.36E-04 | -1.01 |
| ABHD5 | 1.48E-04 | -1.01 |
| FAM8A1 | 4.54E-05 | -1.01 |
| AP3S2 | 8.04E-05 | -1.01 |
| PBLD | 7.43E-04 | -1.02 |
| PEX11A | 1.63E-04 | -1.02 |
| ACO2 | 1.20E-04 | -1.02 |
| PCCA | 8.76E-04 | -1.02 |
| MTFR1L | 8.09E-04 | -1.02 |
| FOXP1 | 3.82E-05 | -1.02 |
| CROT | 3.74E-05 | -1.02 |
| ADAMTSL1 | 2.24E-06 | -1.03 |
| BLOC1S1-RDH5 | 1.69E-06 | -1.03 |
| FBLIM1 | 1.80E-06 | -1.03 |
| TMEM50B | 1.20E-04 | -1.03 |
| CDKL2 | 3.55E-04 | -1.03 |
| NDUFV3 | 2.64E-04 | -1.04 |
| SECISBP2L | 2.15E-04 | -1.04 |
| SLCO2A1 | 4.51E-04 | -1.04 |
| ZNF655 | 2.83E-06 | -1.05 |
| DAAM2 | 3.73E-04 | -1.05 |
| BMP5 | 2.63E-05 | -1.05 |
| EDNRB | 2.05E-04 | -1.05 |
| RILP | 1.37E-06 | -1.05 |
| SCYL2 | 8.71E-04 | -1.05 |
| GNB1 | 2.28E-04 | -1.06 |
| NCOA1 | 5.49E-05 | -1.06 |
| MYOC | 3.93E-05 | -1.06 |
| STX12 | 4.40E-06 | -1.06 |
| PNKD | 1.16E-06 | -1.06 |
| ALDH6A1 | 1.56E-04 | -1.06 |
| GAB1 | 8.47E-07 | -1.06 |
| PPM1A | 1.11E-04 | -1.06 |
| ME2 | 1.92E-05 | -1.07 |
| SARAF | 3.61E-04 | -1.07 |
| HPGDS | 5.87E-04 | -1.07 |
| CHMP1B | 7.14E-06 | -1.07 |
| XKR4 | 1.18E-05 | -1.07 |
| SYTL4 | 4.76E-04 | -1.07 |
| UQCRH | 3.38E-07 | -1.07 |
| CALM1 | 1.43E-05 | -1.08 |
| UHRF1BP1L | 6.60E-05 | -1.08 |
| CYCS | 8.77E-06 | -1.08 |
| MOGAT2 | 4.59E-04 | -1.08 |
| ENTPD3 | 7.01E-05 | -1.08 |
| CCPG1 | 1.26E-04 | -1.08 |
| KLF3 | 3.02E-05 | -1.09 |
| TMBIM4 | 7.20E-04 | -1.09 |
| NIT1 | 9.21E-06 | -1.09 |
| MXI1 | 1.92E-04 | -1.09 |
| SLC17A5 | 1.08E-04 | -1.09 |
| KIF5C | 2.24E-04 | -1.10 |
| MYO1C | 2.10E-05 | -1.10 |
| SEC23A | 2.95E-04 | -1.10 |
| FECH | 2.12E-04 | -1.10 |
| MPPE1 | 9.12E-06 | -1.10 |
| SPTSSA | 2.22E-05 | -1.10 |
| CCL14 | 4.31E-05 | -1.10 |
| CFLAR | 1.48E-06 | -1.11 |
| C1orf210 | 3.27E-05 | -1.11 |
| APPL2 | 2.70E-04 | -1.11 |
| PHOX2B | 1.35E-04 | -1.11 |
| CPEB1 | 4.35E-04 | -1.11 |
| NUDT6 | 3.17E-05 | -1.11 |
| FAM149A | 4.22E-04 | -1.11 |
| SMCHD1 | 3.11E-05 | -1.11 |
| FXYD1 | 2.29E-05 | -1.12 |
| INPP5A | 1.00E-04 | -1.12 |
| LGI1 | 1.73E-06 | -1.12 |
| DMXL1 | 4.21E-05 | -1.12 |
| FOSL2 | 6.03E-05 | -1.12 |
| PACSIN2 | 2.89E-05 | -1.12 |
| ADGRB3 | 2.48E-04 | -1.12 |
| MEOX1 | 1.67E-04 | -1.13 |
| REEP5 | 3.29E-04 | -1.13 |
| ADAM28 | 8.96E-05 | -1.13 |
| LTBP4 | 1.78E-05 | -1.13 |
| IDH3A | 2.19E-04 | -1.13 |
| CRADD | 3.39E-05 | -1.13 |
| HDHD2 | 2.91E-07 | -1.13 |
| SDHA | 5.27E-05 | -1.13 |
| VPS4B | 6.84E-08 | -1.13 |
| SCP2 | 1.90E-04 | -1.14 |
| DHRS4 | 2.86E-04 | -1.14 |
| GPA33 | 6.64E-04 | -1.14 |
| C10orf54 | 1.43E-05 | -1.14 |
| SLC22A18AS | 2.69E-04 | -1.14 |
| MAL | 1.03E-06 | -1.14 |
| CADM2 | 4.13E-04 | -1.14 |
| PAFAH2 | 9.29E-05 | -1.14 |
| TEF | 1.64E-06 | -1.14 |
| SNX24 | 1.19E-04 | -1.14 |
| PLPP3 | 1.85E-04 | -1.14 |
| SLC35A1 | 6.63E-04 | -1.14 |
| UQCRFS1 | 1.36E-04 | -1.14 |
| ZADH2 | 2.02E-06 | -1.14 |
| ACVRL1 | 8.23E-04 | -1.15 |
| ZNF658 | 4.14E-06 | -1.15 |
| HEXIM1 | 9.91E-05 | -1.15 |
| NCOA4 | 8.91E-06 | -1.15 |
| GRAMD3 | 9.65E-05 | -1.15 |
| AP5M1 | 2.62E-04 | -1.15 |
| AHRR | 1.10E-04 | -1.15 |
| VPS13D | 2.93E-05 | -1.16 |
| SLC35D1 | 4.36E-04 | -1.16 |
| PTPN21 | 1.20E-04 | -1.16 |
| RBM47 | 6.61E-04 | -1.16 |
| RNASEL | 3.25E-04 | -1.16 |
| ACSL6 | -5.80E-01 | -1.16 |
| LARGE | 1.85E-04 | -1.16 |
| SNCA | 3.23E-05 | -1.16 |
| WNT5B | 8.15E-04 | -1.17 |
| TIMM21 | 1.09E-05 | -1.17 |
| FAM107B | 3.02E-04 | -1.17 |
| MPP5 | 3.55E-06 | -1.17 |
| WDR7 | 3.87E-07 | -1.18 |
| GNAQ | 8.28E-06 | -1.18 |
| ACOX1 | 5.18E-04 | -1.18 |
| SLC4A10 | 6.38E-04 | -1.19 |
| TSHZ1 | 5.93E-05 | -1.19 |
| RHOU | 2.16E-07 | -1.20 |
| EFHC2 | 4.87E-06 | -1.20 |
| SOCS6 | 1.11E-05 | -1.20 |
| ANKRD12 | 4.21E-05 | -1.20 |
| LGR4 | 2.11E-04 | -1.20 |
| KLF6 | 1.23E-04 | -1.20 |
| MIER1 | 4.82E-07 | -1.20 |
| TMEM59 | 5.62E-05 | -1.21 |
| NBPF1 | 5.90E-04 | -1.21 |
| RAP1B | 6.33E-04 | -1.21 |
| TAGLN3 | 2.85E-04 | -1.21 |
| MTM1 | 1.34E-04 | -1.22 |
| PPP1R16B | 5.38E-04 | -1.22 |
| SYNJ2BP | 5.31E-06 | -1.22 |
| CHRNA1 | 6.99E-04 | -1.22 |
| CLEC10A | 2.28E-05 | -1.22 |
| CALCOCO2 | 9.41E-04 | -1.22 |
| SLC22A5 | 2.81E-04 | -1.22 |
| TRAK2 | 6.63E-09 | -1.22 |
| PPP1R12A | 7.86E-04 | -1.23 |
| TRAPPC8 | 1.67E-06 | -1.23 |
| ITGA8 | 6.97E-05 | -1.24 |
| DYNC1LI2 | 1.07E-06 | -1.24 |
| PCSK2 | 6.99E-05 | -1.24 |
| HAPLN1 | 4.91E-05 | -1.24 |
| TNFSF10 | 3.39E-04 | -1.24 |
| CRK | 1.25E-06 | -1.24 |
| SRSF5 | 2.40E-05 | -1.24 |
| TIAM1 | 4.58E-04 | -1.24 |
| HCFC2 | 7.58E-04 | -1.24 |
| MPZ | 1.73E-04 | -1.25 |
| MXD1 | 9.47E-04 | -1.25 |
| FOXN3 | 1.38E-04 | -1.25 |
| FLVCR2 | 3.88E-04 | -1.25 |
| PPP1CB | 1.17E-04 | -1.25 |
| P2RX4 | 7.58E-05 | -1.25 |
| SLC25A34 | 8.32E-06 | -1.25 |
| VAPA | 1.55E-04 | -1.25 |
| ECI2 | 2.05E-04 | -1.25 |
| CDC14A | 4.36E-05 | -1.26 |
| STYK1 | 5.51E-05 | -1.27 |
| KCNMA1 | 1.70E-04 | -1.27 |
| C7orf31 | 4.21E-05 | -1.27 |
| RBM24 | 1.30E-05 | -1.27 |
| ABCC13 | 2.52E-05 | -1.27 |
| SLC9A9 | 8.90E-04 | -1.27 |
| MAB21L1 | 1.61E-05 | -1.28 |
| TMEM54 | 3.87E-04 | -1.28 |
| CCNYL1 | 3.01E-05 | -1.28 |
| RCAN1 | 5.66E-05 | -1.28 |
| NPY | 1.08E-04 | -1.28 |
| DENND5B | 9.63E-04 | -1.28 |
| PDE2A | 4.30E-04 | -1.29 |
| NDUFS1 | 9.53E-04 | -1.29 |
| SLC25A23 | 5.82E-05 | -1.29 |
| SGPP1 | 3.29E-05 | -1.29 |
| KCTD9 | 9.11E-06 | -1.29 |
| GINM1 | 2.31E-07 | -1.29 |
| TXNIP | 7.58E-04 | -1.29 |
| SDHD | 5.99E-04 | -1.30 |
| AHNAK | 9.35E-04 | -1.30 |
| HADHA | 5.71E-04 | -1.30 |
| MGLL | 1.23E-06 | -1.31 |
| IL11RA | 2.38E-05 | -1.31 |
| MAP4 | 1.60E-05 | -1.31 |
| MYZAP | 1.72E-05 | -1.31 |
| CHST5 | 2.39E-04 | -1.31 |
| RAVER2 | 2.10E-04 | -1.31 |
| PLEKHB2 | 4.09E-04 | -1.31 |
| CDHR2 | 9.01E-04 | -1.32 |
| CD27 | 2.09E-04 | -1.33 |
| MS4A1 | 9.81E-04 | -1.33 |
| TEX11 | 1.26E-05 | -1.33 |
| RTN1 | 4.33E-04 | -1.33 |
| SORCS1 | 2.43E-04 | -1.34 |
| CEP85L | 7.75E-04 | -1.34 |
| CPEB4 | 7.27E-06 | -1.34 |
| KIAA2022 | 4.83E-04 | -1.34 |
| SUCLG2 | 3.57E-04 | -1.35 |
| SECTM1 | 1.04E-05 | -1.35 |
| WLS | 1.72E-04 | -1.35 |
| RNF125 | 5.00E-05 | -1.35 |
| HADHB | 3.23E-05 | -1.35 |
| NPTN | 9.54E-05 | -1.36 |
| NOVA1 | 1.99E-04 | -1.36 |
| PTP4A1 | 4.94E-06 | -1.36 |
| CPEB3 | 6.80E-07 | -1.37 |
| TRDC | 4.10E-05 | -1.37 |
| FAM214A | 3.08E-06 | -1.37 |
| ST3GAL4 | 6.25E-04 | -1.37 |
| CNST | 7.67E-10 | -1.38 |
| SPINK2 | 7.41E-06 | -1.38 |
| ARHGAP15 | 8.71E-05 | -1.38 |
| RIMS3 | 9.57E-06 | -1.38 |
| SIPA1L2 | 8.62E-05 | -1.39 |
| RTN4 | 1.34E-04 | -1.39 |
| MAGI2 | 9.30E-05 | -1.39 |
| ZZEF1 | 4.83E-09 | -1.39 |
| NSG1 | 4.90E-06 | -1.39 |
| ATP6V0D1 | 5.65E-06 | -1.39 |
| MPC1 | 1.13E-05 | -1.39 |
| VSTM2A | 1.88E-07 | -1.40 |
| DLST | 1.91E-08 | -1.40 |
| ACAA2 | 4.77E-05 | -1.40 |
| ADCY9 | 1.42E-04 | -1.40 |
| GPD1L | 6.06E-05 | -1.40 |
| C1orf21 | 3.29E-06 | -1.40 |
| CLIC5 | 5.63E-05 | -1.40 |
| USP2 | 1.87E-06 | -1.41 |
| FAM43A | 3.28E-04 | -1.41 |
| TCF21 | 2.54E-05 | -1.41 |
| GNA11 | 2.24E-07 | -1.41 |
| PIRT | 3.86E-05 | -1.41 |
| PPP3CB | 9.22E-04 | -1.42 |
| ENTPD5 | 1.97E-04 | -1.42 |
| ACAT1 | 4.19E-04 | -1.42 |
| SCN3A | 1.95E-07 | -1.42 |
| VWA5A | 5.38E-04 | -1.42 |
| PITPNM3 | 5.28E-07 | -1.42 |
| FCER1A | 6.85E-06 | -1.43 |
| PINK1 | 6.15E-06 | -1.43 |
| MUSTN1 | 1.09E-04 | -1.44 |
| RETSAT | 9.40E-05 | -1.44 |
| CASD1 | 3.97E-09 | -1.44 |
| NDRG2 | 1.57E-06 | -1.44 |
| TLR3 | 4.78E-06 | -1.44 |
| RMDN2 | 4.68E-05 | -1.45 |
| CELF2 | 3.76E-05 | -1.45 |
| KRT24 | 7.91E-06 | -1.45 |
| MTUS1 | 6.07E-05 | -1.46 |
| PRDX6 | 1.32E-07 | -1.46 |
| FOXP2 | 3.80E-04 | -1.46 |
| ANKRD36 | 1.78E-04 | -1.46 |
| FMN2 | 3.42E-04 | -1.47 |
| KITLG | 6.23E-04 | -1.47 |
| DPP10 | 2.01E-05 | -1.47 |
| RET | 7.36E-05 | -1.47 |
| PELI2 | 4.81E-05 | -1.47 |
| GFRA2 | 4.98E-08 | -1.47 |
| GLIPR2 | 1.34E-04 | -1.48 |
| EYA2 | 6.62E-04 | -1.48 |
| RELL1 | 1.01E-06 | -1.48 |
| DCLK1 | 9.81E-06 | -1.48 |
| ACADM | 1.41E-05 | -1.48 |
| PRADC1 | 8.62E-06 | -1.49 |
| AKIRIN1 | 4.66E-08 | -1.49 |
| GALNT12 | 4.85E-04 | -1.50 |
| CBX7 | 1.00E-04 | -1.50 |
| CPT2 | 1.15E-05 | -1.50 |
| SLC22A23 | 5.91E-04 | -1.50 |
| TOX | 6.57E-05 | -1.50 |
| PTPRH | 1.39E-04 | -1.50 |
| KCNN3 | 6.29E-04 | -1.50 |
| CHGB | 4.59E-10 | -1.50 |
| GPT | 4.88E-06 | -1.51 |
| IRF4 | 2.42E-05 | -1.51 |
| PPP2R3A | 2.69E-06 | -1.51 |
| PCDH20 | 6.53E-04 | -1.51 |
| CASP7 | 8.48E-05 | -1.52 |
| MT1E | 2.19E-05 | -1.52 |
| FKBP1B | 4.57E-06 | -1.52 |
| ZNF575 | 1.56E-06 | -1.52 |
| HMP19 | 2.35E-05 | -1.52 |
| NEDD4L | 7.50E-05 | -1.53 |
| DUSP1 | 2.27E-04 | -1.53 |
| ZDHHC2 | 7.60E-04 | -1.53 |
| NR3C1 | 1.83E-04 | -1.54 |
| ST6GALNAC6 | 3.09E-05 | -1.54 |
| MARCH2 | 1.49E-04 | -1.54 |
| ACADSB | 1.81E-06 | -1.54 |
| CIPC | 2.55E-06 | -1.54 |
| SRI | 9.47E-05 | -1.54 |
| PER1 | 4.12E-04 | -1.54 |
| SPPL2A | 1.06E-04 | -1.55 |
| NCAM1 | 1.72E-04 | -1.55 |
| MT1X | 4.98E-05 | -1.55 |
| TRHDE | 4.98E-05 | -1.55 |
| DENND2A | 1.22E-04 | -1.55 |
| IL6R | 1.45E-09 | -1.56 |
| ARHGEF9 | 9.12E-07 | -1.56 |
| PXMP2 | 3.17E-04 | -1.56 |
| SHISA3 | 3.71E-05 | -1.56 |
| PTPRZ1 | 1.59E-04 | -1.56 |
| ELAVL4 | 3.82E-05 | -1.56 |
| ABCD3 | 6.99E-06 | -1.56 |
| EPHX2 | 4.55E-06 | -1.56 |
| BCAR3 | 7.11E-06 | -1.57 |
| ZNF611 | 2.46E-08 | -1.57 |
| FBXL17 | 1.62E-05 | -1.57 |
| CPNE8 | 1.34E-05 | -1.57 |
| COL4A6 | 4.79E-09 | -1.57 |
| PGM1 | 7.74E-04 | -1.57 |
| B3GNT6 | 6.00E-05 | -1.57 |
| LRMP | 5.67E-05 | -1.58 |
| ABCA5 | 2.24E-04 | -1.59 |
| UGP2 | 1.26E-09 | -1.59 |
| RNF152 | 5.70E-08 | -1.59 |
| MIER3 | 1.31E-05 | -1.59 |
| FRMD3 | 7.57E-06 | -1.59 |
| GLTP | 3.93E-08 | -1.59 |
| SLC25A4 | 3.17E-04 | -1.60 |
| MOB3B | 6.07E-06 | -1.61 |
| ATP5A1 | 2.30E-06 | -1.61 |
| MAN1A1 | 2.67E-04 | -1.61 |
| CNTN4 | 4.25E-04 | -1.61 |
| UGDH | 2.35E-05 | -1.61 |
| TMOD2 | 1.39E-04 | -1.61 |
| SLAMF7 | 2.95E-04 | -1.61 |
| BCL2 | 8.72E-08 | -1.61 |
| CCL21 | 6.94E-05 | -1.62 |
| SSBP2 | 1.68E-04 | -1.62 |
| FGFBP2 | 5.24E-05 | -1.62 |
| SEPP1 | 2.17E-06 | -1.62 |
| GNAI1 | 2.48E-04 | -1.62 |
| MT2A | 7.26E-04 | -1.62 |
| RAP1A | 2.57E-05 | -1.62 |
| PRKACB | 1.07E-04 | -1.62 |
| DSC2 | 1.64E-04 | -1.63 |
| CCDC68 | 1.04E-05 | -1.63 |
| PEG3 | 5.62E-04 | -1.63 |
| SCNN1G | 5.63E-05 | -1.63 |
| KL | 8.62E-06 | -1.64 |
| CDKN2B-AS1 | 2.23E-07 | -1.64 |
| FAS | 1.28E-04 | -1.64 |
| GCNT2 | 1.67E-07 | -1.64 |
| HLF | 9.73E-04 | -1.65 |
| HHLA2 | 4.06E-05 | -1.65 |
| SCUBE2 | 1.78E-04 | -1.66 |
| PDCD4 | 6.01E-07 | -1.66 |
| NLGN4X | 2.18E-04 | -1.66 |
| ADGRL3 | 4.37E-08 | -1.67 |
| DNER | 2.63E-05 | -1.67 |
| HOXD1 | 3.14E-08 | -1.67 |
| PDE6A | 2.83E-05 | -1.67 |
| CDHR5 | 7.63E-05 | -1.67 |
| TARP | 1.02E-04 | -1.67 |
| PJA2 | 2.01E-06 | -1.68 |
| SCN9A | 1.50E-09 | -1.68 |
| PLCD1 | 7.29E-08 | -1.69 |
| SMIM6 | 8.28E-05 | -1.69 |
| ACADS | 1.28E-06 | -1.69 |
| SLC2A13 | 1.69E-07 | -1.69 |
| NEFL | 1.90E-04 | -1.70 |
| SLC25A20 | 3.89E-07 | -1.70 |
| THRB | 2.16E-04 | -1.70 |
| ANK3 | 3.77E-07 | -1.70 |
| KCNIP4 | 3.45E-04 | -1.70 |
| NAAA | 4.98E-05 | -1.71 |
| PIP5K1B | 1.77E-04 | -1.71 |
| ZBTB7C | 3.73E-05 | -1.72 |
| ATP2A3 | 1.95E-04 | -1.72 |
| PRPH | 5.69E-07 | -1.73 |
| GDPD2 | 1.10E-06 | -1.73 |
| AKAP5 | 3.98E-04 | -1.73 |
| ETHE1 | 1.55E-04 | -1.73 |
| GSN | 3.34E-05 | -1.74 |
| SMIM5 | 7.94E-08 | -1.74 |
| PER3 | 7.56E-05 | -1.74 |
| TMEM72 | 4.67E-06 | -1.74 |
| AHCYL2 | 5.07E-04 | -1.74 |
| PLCE1 | 6.80E-06 | -1.74 |
| STOX2 | 1.64E-09 | -1.74 |
| TP53INP2 | 1.29E-07 | -1.74 |
| TMEM37 | 5.32E-05 | -1.74 |
| KAT2B | 8.62E-06 | -1.75 |
| ENDOD1 | 1.25E-04 | -1.75 |
| RIOK3 | 1.26E-05 | -1.75 |
| RAB27A | 3.99E-06 | -1.76 |
| PDE4D | 7.61E-06 | -1.76 |
| CCL28 | 3.03E-04 | -1.77 |
| NR1H4 | 7.96E-04 | -1.77 |
| PLPP1 | 4.03E-05 | -1.78 |
| UGT2A3 | 5.76E-05 | -1.78 |
| KIAA1211 | 2.39E-05 | -1.79 |
| FAM107A | 2.97E-08 | -1.79 |
| METTL7A | 1.18E-05 | -1.80 |
| TNXA | 1.24E-07 | -1.81 |
| TSC22D3 | 2.57E-04 | -1.82 |
| ETFDH | 1.31E-08 | -1.82 |
| DHRS11 | 6.01E-06 | -1.82 |
| EML1 | 7.63E-04 | -1.83 |
| COL4A5 | 2.62E-05 | -1.83 |
| RASSF6 | 5.80E-05 | -1.83 |
| CITED2 | 6.68E-06 | -1.83 |
| SOCS2 | 2.08E-05 | -1.84 |
| MAOA | 4.84E-04 | -1.84 |
| ATP8A1 | 1.10E-04 | -1.84 |
| OSBPL1A | 1.76E-04 | -1.84 |
| CNTN3 | 4.70E-07 | -1.85 |
| EPB41L3 | 1.29E-05 | -1.85 |
| FABP2 | 5.51E-05 | -1.85 |
| S100B | 2.34E-05 | -1.85 |
| SLC23A1 | 5.55E-04 | -1.86 |
| TCEAL7 | 5.29E-04 | -1.86 |
| PRKCB | 6.94E-05 | -1.86 |
| EIF4E3 | 3.09E-06 | -1.86 |
| SMIM14 | 9.59E-07 | -1.86 |
| CACNB2 | 7.13E-05 | -1.86 |
| KLRB1 | 9.55E-06 | -1.87 |
| OLFM1 | 1.89E-06 | -1.87 |
| NR5A2 | 2.14E-04 | -1.88 |
| ARHGAP44 | 7.47E-04 | -1.88 |
| TMCC3 | 1.30E-06 | -1.89 |
| MIR22HG | 3.72E-07 | -1.90 |
| CHODL | 5.70E-08 | -1.90 |
| GPM6B | 2.18E-05 | -1.91 |
| PTN | 1.51E-04 | -1.91 |
| EPB41L4A | 1.66E-07 | -1.91 |
| PCK1 | 2.02E-04 | -1.92 |
| CA7 | 1.24E-07 | -1.92 |
| FAM46C | 1.41E-04 | -1.92 |
| CNR1 | 3.73E-04 | -1.93 |
| TMEM56 | 4.75E-04 | -1.93 |
| LPAR1 | 3.88E-07 | -1.93 |
| BEX1 | 1.22E-05 | -1.94 |
| KLF9 | 3.05E-04 | -1.95 |
| ABHD3 | 2.65E-05 | -1.95 |
| NXPE2 | 8.79E-04 | -1.95 |
| RUNDC3B | 4.14E-05 | -1.95 |
| RGS13 | 2.35E-04 | -1.95 |
| PDE7B | 3.64E-07 | -1.95 |
| HRASLS2 | 3.96E-05 | -1.96 |
| TMEM35 | 2.19E-04 | -1.97 |
| SULT1B1 | 4.99E-04 | -1.97 |
| PID1 | 6.12E-04 | -1.97 |
| SETBP1 | 5.13E-04 | -1.98 |
| C3orf70 | 1.52E-04 | -1.98 |
| NAP1L2 | 1.27E-05 | -1.99 |
| GNG2 | 3.70E-05 | -1.99 |
| FUCA1 | 4.42E-06 | -1.99 |
| MT1F | 9.97E-05 | -2.00 |
| IQGAP2 | 3.86E-04 | -2.00 |
| MMP28 | 7.95E-05 | -2.00 |
| XDH | 9.55E-04 | -2.00 |
| PDZD3 | 2.26E-04 | -2.00 |
| PRKAR2B | 1.06E-04 | -2.01 |
| WDR78 | 1.02E-06 | -2.03 |
| SSTR1 | 3.09E-04 | -2.03 |
| PARM1 | 2.14E-04 | -2.03 |
| PLCL2 | 3.91E-08 | -2.04 |
| SEMA6A | 9.34E-05 | -2.04 |
| BMP2 | 5.39E-04 | -2.06 |
| CD69 | 4.32E-04 | -2.06 |
| PPARGC1A | 9.03E-05 | -2.07 |
| RGMA | 8.07E-04 | -2.07 |
| ANGPTL1 | 2.46E-04 | -2.07 |
| RERGL | 4.93E-11 | -2.07 |
| NPY1R | 2.22E-05 | -2.08 |
| ATP1A2 | 5.00E-04 | -2.09 |
| ABI3BP | 1.69E-05 | -2.09 |
| NR3C2 | 1.86E-07 | -2.10 |
| ZC3H12C | 5.23E-06 | -2.10 |
| EMP1 | 4.26E-04 | -2.10 |
| OTOP2 | 2.13E-08 | -2.10 |
| LIFR | 3.38E-07 | -2.10 |
| CA12 | 4.48E-04 | -2.11 |
| TMEM220 | 2.81E-08 | -2.11 |
| FKBP1A-SDCBP2 | 5.83E-05 | -2.11 |
| TSPAN1 | 1.02E-04 | -2.12 |
| SLC1A1 | 5.93E-04 | -2.12 |
| PDE5A | 6.13E-04 | -2.13 |
| PTGS1 | 2.40E-04 | -2.13 |
| SCGN | 5.01E-16 | -2.13 |
| PHLPP2 | 4.88E-07 | -2.13 |
| RSPO2 | 6.37E-06 | -2.14 |
| LYVE1 | 1.26E-04 | -2.14 |
| PTGER4 | 9.59E-06 | -2.14 |
| SMPDL3A | 7.34E-05 | -2.14 |
| NRXN1 | 6.61E-07 | -2.16 |
| ITM2C | 8.69E-05 | -2.17 |
| FGFR2 | 9.87E-07 | -2.18 |
| BCAS1 | 8.21E-05 | -2.18 |
| SLC17A4 | 1.57E-05 | -2.19 |
| SPINK5 | 3.82E-04 | -2.19 |
| HSD11B2 | 3.02E-04 | -2.20 |
| MZB1 | 3.60E-04 | -2.21 |
| LDHD | 2.11E-07 | -2.21 |
| FHL1 | 6.80E-04 | -2.22 |
| RCAN2 | 1.68E-05 | -2.22 |
| C1orf115 | 2.25E-06 | -2.24 |
| IGKV1-12 | 3.09E-04 | -2.24 |
| SELENBP1 | 5.90E-04 | -2.25 |
| AMPD1 | 8.61E-09 | -2.25 |
| ANO5 | 2.08E-09 | -2.26 |
| P2RY14 | 1.05E-09 | -2.27 |
| C11orf86 | 3.07E-08 | -2.27 |
| SST | 8.52E-06 | -2.27 |
| GNG7 | 1.35E-10 | -2.28 |
| SDPR | 3.12E-04 | -2.28 |
| OGN | 4.12E-04 | -2.31 |
| CDKN2B | 1.95E-04 | -2.33 |
| GAP43 | 1.57E-06 | -2.34 |
| PI15 | 7.27E-06 | -2.34 |
| NKX2-3 | 1.42E-06 | -2.34 |
| IGK | 6.98E-04 | -2.35 |
| AKR1B15 | 2.70E-06 | -2.35 |
| ITM2A | 2.20E-06 | -2.35 |
| PLA2G10 | 1.72E-04 | -2.36 |
| TMEM236 | 2.47E-06 | -2.36 |
| ANO7 | 9.81E-06 | -2.37 |
| CHL1 | 1.32E-04 | -2.37 |
| POU2AF1 | 4.66E-04 | -2.37 |
| HIGD1A | 2.20E-06 | -2.38 |
| TSPAN7 | 7.05E-09 | -2.39 |
| NEGR1 | 4.17E-05 | -2.40 |
| TMEM100 | 3.67E-07 | -2.46 |
| FGL2 | 9.89E-06 | -2.46 |
| CLDN23 | 1.35E-05 | -2.47 |
| BTNL8 | 2.16E-04 | -2.48 |
| MATN2 | 1.05E-05 | -2.48 |
| AFF3 | 1.44E-06 | -2.49 |
| FOXF2 | 3.65E-06 | -2.50 |
| SGK1 | 1.07E-05 | -2.51 |
| BTNL3 | 6.82E-06 | -2.51 |
| TRPM6 | 9.84E-07 | -2.53 |
| HPGD | 7.14E-04 | -2.56 |
| CFD | 1.61E-04 | -2.57 |
| MAMDC2 | 4.70E-07 | -2.58 |
| LRRC19 | 8.32E-06 | -2.60 |
| HSPA2 | 1.20E-04 | -2.61 |
| CXCL12 | 3.46E-04 | -2.61 |
| SCIN | 1.36E-04 | -2.62 |
| PLAC8 | 7.85E-04 | -2.64 |
| ANKRD36BP2 | 1.04E-05 | -2.66 |
| TNFRSF17 | 8.80E-06 | -2.66 |
| MMRN1 | 4.91E-09 | -2.67 |
| GBA3 | 2.81E-06 | -2.68 |
| PDK4 | 6.81E-05 | -2.70 |
| KLF4 | 1.27E-07 | -2.70 |
| SLITRK6 | 1.30E-04 | -2.71 |
| EDN3 | 4.64E-08 | -2.71 |
| MFSD4 | 2.34E-05 | -2.72 |
| ABCG2 | 1.49E-08 | -2.72 |
| PYY | 6.64E-06 | -2.74 |
| SCGB2A1 | 1.67E-06 | -2.77 |
| GPAT3 | 4.19E-08 | -2.78 |
| GREM2 | 5.72E-10 | -2.79 |
| BEST4 | 2.29E-11 | -2.80 |
| PRIMA1 | 7.14E-09 | -2.81 |
| ABCA8 | 4.98E-08 | -2.83 |
| FAM150B | 8.65E-10 | -2.85 |
| SEMA6D | 9.26E-08 | -2.85 |
| PDE9A | 7.30E-08 | -2.86 |
| ADAMDEC1 | 4.29E-05 | -2.86 |
| PADI2 | 3.66E-05 | -2.87 |
| STMN2 | 1.62E-07 | -2.88 |
| IGKV2-28 | 3.44E-04 | -2.90 |
| UGT1A1 | 7.51E-05 | -2.91 |
| ANK2 | 6.30E-05 | -2.91 |
| MT1H | 1.64E-06 | -2.92 |
| B3GALT5-AS1 | 7.32E-05 | -2.93 |
| SLC51B | 4.32E-05 | -2.93 |
| CLEC3B | 2.40E-11 | -2.95 |
| SLC4A4 | 3.92E-07 | -2.97 |
| VSIG2 | 1.05E-05 | -2.98 |
| DPT | 1.03E-05 | -3.01 |
| ADTRP | 5.64E-06 | -3.02 |
| DNASE1L3 | 7.38E-09 | -3.03 |
| SCARA5 | 2.22E-11 | -3.03 |
| MT1G | 2.73E-04 | -3.06 |
| NXPE1 | 1.79E-04 | -3.08 |
| CWH43 | 1.30E-05 | -3.10 |
| REP15 | 1.68E-04 | -3.10 |
| MT1JP | 3.65E-07 | -3.12 |
| LAMA1 | 1.39E-05 | -3.17 |
| INSL5 | 1.15E-04 | -3.18 |
| SCNN1B | 7.11E-07 | -3.19 |
| B3GNT7 | 3.92E-05 | -3.20 |
| AKR1B10 | 1.55E-04 | -3.22 |
| ADH1B | 4.98E-04 | -3.24 |
| HSD17B2 | 8.87E-06 | -3.25 |
| PKIB | 2.86E-05 | -3.27 |
| CD177 | 1.02E-06 | -3.27 |
| ANPEP | 2.33E-05 | -3.28 |
| PLP1 | 1.24E-06 | -3.31 |
| CDH19 | 8.53E-09 | -3.31 |
| BMP3 | 2.97E-08 | -3.36 |
| ADH1A | 8.60E-06 | -3.36 |
| C2orf88 | 4.49E-06 | -3.39 |
| SLC26A2 | 4.11E-04 | -3.39 |
| BEST2 | 8.64E-08 | -3.41 |
| DHRS9 | 6.72E-06 | -3.47 |
| LGALS2 | 7.15E-05 | -3.48 |
| IGH | 1.07E-04 | -3.50 |
| LYPD8 | 7.41E-06 | -3.50 |
| GCG | 1.22E-06 | -3.51 |
| CLDN8 | 6.65E-05 | -3.53 |
| JCHAIN | 1.59E-04 | -3.55 |
| IGHA1 | 3.97E-05 | -3.55 |
| MUC4 | 2.02E-04 | -3.56 |
| C2orf40 | 1.07E-06 | -3.57 |
| MYOT | 2.76E-13 | -3.65 |
| PIGR | 2.13E-04 | -3.73 |
| SI | 2.62E-04 | -3.75 |
| CHP2 | 1.48E-06 | -3.82 |
| MUC2 | 1.87E-04 | -3.89 |
| ITLN1 | 3.73E-04 | -3.99 |
| CEACAM7 | 1.57E-04 | -4.00 |
| MT1M | 1.42E-07 | -4.04 |
| ZG16 | 1.89E-07 | -4.25 |
| HEPACAM2 | 1.70E-05 | -4.26 |
| UGT2B15 | 1.47E-04 | -4.28 |
| VIP | 7.24E-07 | -4.30 |
| ADH1C | 1.44E-04 | -4.35 |
| FCGBP | 1.69E-04 | -4.39 |
| CA4 | 3.36E-10 | -4.50 |
| TMIGD1 | 2.22E-11 | -4.74 |
| SLC26A3 | 2.19E-04 | -5.07 |
| CLCA1 | 4.35E-05 | -5.12 |
| GUCA2B | 4.37E-13 | -5.14 |
| CHGA | 2.22E-11 | -5.14 |
| GUCA2A | 4.80E-10 | -5.15 |
| CA2 | 7.52E-08 | -5.22 |
| MS4A12 | 3.33E-07 | -5.46 |
| AQP8 | 2.31E-10 | -5.69 |
| CA1 | 3.49E-09 | -6.25 |
| CLCA4 | 8.04E-11 | -7.07 |

CRC, colorectal cancer.

**Supplementary Table 2.** Several pathways significantly enriched by the modules within the protein interaction map associated with primary CRC.

|  |  |  |  |
| --- | --- | --- | --- |
| **Cluster. No** | **Pathway id** | **Pathway name** | **FDR** |
| 1 | KEGG:04110 | Cell cycle | 1.78E-08 |
| KEGG:04114 | Oocyte meiosis | 2.99E-05 |
| KEGG:04914 | Progesterone-mediated oocyte maturation | 5.70E-03 |
| REAC:R-HSA-1640170 | Cell Cycle | 2.39E-28 |
| REAC:R-HSA-69278 | Cell Cycle, Mitotic | 2.26E-26 |
| REAC:R-HSA-68886 | M Phase | 7.35E-15 |
| REAC:R-HSA-68877 | Mitotic Prometaphase | 1.09E-14 |
| REAC:R-HSA-69620 | Cell Cycle Checkpoints | 4.38E-12 |
| REAC:R-HSA-2500257 | Resolution of Sister Chromatid Cohesion | 1.72E-11 |
| REAC:R-HSA-68882 | Mitotic Anaphase | 6.37E-11 |
| REAC:R-HSA-2555396 | Mitotic Metaphase and Anaphase | 6.76E-11 |
| REAC:R-HSA-2467813 | Separation of Sister Chromatids | 2.83E-09 |
| REAC:R-HSA-69618 | Mitotic Spindle Checkpoint | 5.23E-09 |
| REAC:R-HSA-141444 | Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal | 3.37E-08 |
| REAC:R-HSA-141424 | Amplification of signal from the kinetochores | 3.37E-08 |
| REAC:R-HSA-2514853 | Condensation of Prometaphase Chromosomes | 1.45E-07 |
| REAC:R-HSA-9648025 | EML4 and NUDC in mitotic spindle formation | 2.55E-07 |
| REAC:R-HSA-5663220 | RHO GTPases Activate Formins | 1.14E-06 |
| REAC:R-HSA-174143 | APC/C-mediated degradation of cell cycle proteins | 2.08E-05 |
| REAC:R-HSA-453276 | Regulation of mitotic cell cycle | 2.08E-05 |
| REAC:R-HSA-195258 | RHO GTPase Effectors | 1.72E-04 |
| REAC:R-HSA-176409 | APC/C:Cdc20 mediated degradation of mitotic proteins | 2.07E-04 |
| REAC:R-HSA-176814 | Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins | 2.24E-04 |
| REAC:R-HSA-69275 | G2/M Transition | 3.87E-04 |
| REAC:R-HSA-453274 | Mitotic G2-G2/M phases | 4.18E-04 |
| REAC:R-HSA-176417 | Phosphorylation of Emi1 | 4.35E-04 |
| REAC:R-HSA-194315 | Signaling by Rho GTPases | 6.06E-04 |
| REAC:R-HSA-9716542 | Signaling by Rho GTPases, Miro GTPases and RHOBTB3 | 6.06E-04 |
| REAC:R-HSA-453279 | Mitotic G1 phase and G1/S transition | 7.29E-04 |
| REAC:R-HSA-174048 | APC/C:Cdc20 mediated degradation of Cyclin B | 8.48E-04 |
| REAC:R-HSA-1538133 | G0 and Early G1 | 1.39E-03 |
| REAC:R-HSA-8854518 | AURKA Activation by TPX2 | 3.40E-03 |
| REAC:R-HSA-69306 | DNA Replication | 4.37E-03 |
| REAC:R-HSA-176187 | Activation of ATR in response to replication stress | 5.07E-03 |
| REAC:R-HSA-156711 | Polo-like kinase mediated events | 1.18E-02 |
| REAC:R-HSA-69242 | S Phase | 1.66E-02 |
| REAC:R-HSA-6804114 | TP53 Regulates Transcription of Genes Involved in G2 Cell Cycle Arrest | 1.72E-02 |
| REAC:R-HSA-69481 | G2/M Checkpoints | 2.03E-02 |
| REAC:R-HSA-176412 | Phosphorylation of the APC/C | 2.38E-02 |
| REAC:R-HSA-69239 | Synthesis of DNA | 4.28E-02 |
| 2 | KEGG:03008 | Ribosome biogenesis in eukaryotes | 1.95E-16 |
| REAC:R-HSA-8868773 | rRNA processing in the nucleus and cytosol | 2.11E-29 |
| REAC:R-HSA-72312 | rRNA processing | 5.76E-29 |
| REAC:R-HSA-6791226 | Major pathway of rRNA processing in the nucleolus and cytosol | 8.30E-25 |
| REAC:R-HSA-8953854 | Metabolism of RNA | 5.52E-19 |
| REAC:R-HSA-6790901 | rRNA modification in the nucleus and cytosol | 7.21E-18 |
| 3 | KEGG:00071 | Fatty acid degradation | 3.21E-11 |
| KEGG:01212 | Fatty acid metabolism | 3.55E-10 |
| KEGG:04723 | Retrograde endocannabinoid signaling | 2.99E-08 |
| KEGG:01200 | Carbon metabolism | 1.21E-07 |
| KEGG:04713 | Circadian entrainment | 1.06E-06 |
| KEGG:00020 | Citrate cycle (TCA cycle) | 2.05E-06 |
| KEGG:04725 | Cholinergic synapse | 3.09E-06 |
| KEGG:04724 | Glutamatergic synapse | 3.28E-06 |
| KEGG:00640 | Propanoate metabolism | 3.97E-06 |
| KEGG:04371 | Apelin signaling pathway | 1.11E-05 |
| KEGG:05032 | Morphine addiction | 1.94E-05 |
| KEGG:04727 | GABAergic synapse | 1.94E-05 |
| KEGG:00280 | Valine, leucine and isoleucine degradation | 2.37E-05 |
| KEGG:04714 | Thermogenesis | 2.78E-05 |
| KEGG:04726 | Serotonergic synapse | 7.60E-05 |
| KEGG:04062 | Chemokine signaling pathway | 1.08E-04 |
| KEGG:04926 | Relaxin signaling pathway | 1.74E-04 |
| KEGG:04728 | Dopaminergic synapse | 1.90E-04 |
| KEGG:05163 | Human cytomegalovirus infection | 3.14E-04 |
| KEGG:01100 | Metabolic pathways | 6.50E-04 |
| KEGG:05170 | Human immunodeficiency virus 1 infection | 2.85E-03 |
| KEGG:00650 | Butanoate metabolism | 5.96E-03 |
| KEGG:00410 | beta-Alanine metabolism | 7.35E-03 |
| KEGG:05034 | Alcoholism | 1.84E-02 |
| KEGG:00380 | Tryptophan metabolism | 1.89E-02 |
| REAC:R-HSA-1430728 | Metabolism | 5.90E-13 |
| REAC:R-HSA-392518 | Signal amplification | 3.14E-08 |
| REAC:R-HSA-163685 | Integration of energy metabolism | 3.42E-08 |
| REAC:R-HSA-163359 | Glucagon signaling in metabolic regulation | 3.83E-08 |
| REAC:R-HSA-422356 | Regulation of insulin secretion | 1.61E-07 |
| REAC:R-HSA-991365 | Activation of GABAB receptors | 2.07E-07 |
| REAC:R-HSA-977444 | GABA B receptor activation | 2.07E-07 |
| REAC:R-HSA-418597 | G alpha (z) signalling events | 4.14E-07 |
| REAC:R-HSA-71403 | Citric acid cycle (TCA cycle) | 4.68E-07 |
| REAC:R-HSA-392170 | ADP signalling through P2Y purinoceptor 12 | 4.68E-07 |
| REAC:R-HSA-418592 | ADP signalling through P2Y purinoceptor 1 | 7.52E-07 |
| REAC:R-HSA-428930 | Thromboxane signalling through TP receptor | 7.52E-07 |
| REAC:R-HSA-977443 | GABA receptor activation | 1.66E-06 |
| REAC:R-HSA-202040 | G-protein activation | 1.73E-06 |
| REAC:R-HSA-400042 | Adrenaline,noradrenaline inhibits insulin secretion | 1.73E-06 |
| REAC:R-HSA-1428517 | The citric acid (TCA) cycle and respiratory electron transport | 1.75E-06 |
| REAC:R-HSA-456926 | Thrombin signalling through proteinase activated receptors (PARs) | 2.97E-06 |
| REAC:R-HSA-420092 | Glucagon-type ligand receptors | 4.14E-06 |
| REAC:R-HSA-9660821 | ADORA2B mediated anti-inflammatory cytokines production | 6.94E-06 |
| REAC:R-HSA-381676 | Glucagon-like Peptide-1 (GLP1) regulates insulin secretion | 1.46E-05 |
| REAC:R-HSA-6814122 | Cooperation of PDCL (PhLP1) and TRiC/CCT in G-protein beta folding | 1.46E-05 |
| REAC:R-HSA-432040 | Vasopressin regulates renal water homeostasis via Aquaporins | 1.65E-05 |
| REAC:R-HSA-111885 | Opioid Signalling | 1.96E-05 |
| REAC:R-HSA-8964315 | G beta:gamma signalling through BTK | 2.63E-05 |
| REAC:R-HSA-392851 | Prostacyclin signalling through prostacyclin receptor | 3.33E-05 |
| REAC:R-HSA-8964616 | G beta:gamma signalling through CDC42 | 4.16E-05 |
| REAC:R-HSA-418217 | G beta:gamma signalling through PLC beta | 4.16E-05 |
| REAC:R-HSA-445717 | Aquaporin-mediated transport | 4.39E-05 |
| REAC:R-HSA-500657 | Presynaptic function of Kainate receptors | 5.13E-05 |
| REAC:R-HSA-71406 | Pyruvate metabolism and Citric Acid (TCA) cycle | 5.33E-05 |
| REAC:R-HSA-392451 | G beta:gamma signalling through PI3Kgamma | 1.08E-04 |
| REAC:R-HSA-997272 | Inhibition of voltage gated Ca2+ channels via Gbeta/gamma subunits | 2.01E-04 |
| REAC:R-HSA-1296059 | G protein gated Potassium channels | 2.01E-04 |
| REAC:R-HSA-1296041 | Activation of G protein gated Potassium channels | 2.01E-04 |
| REAC:R-HSA-9662851 | Anti-inflammatory response favouring Leishmania parasite infection | 2.25E-04 |
| REAC:R-HSA-9664433 | Leishmania parasite growth and survival | 2.25E-04 |
| REAC:R-HSA-451326 | Activation of kainate receptors upon glutamate binding | 2.31E-04 |
| REAC:R-HSA-9009391 | Extra-nuclear estrogen signaling | 2.45E-04 |
| REAC:R-HSA-397795 | G-protein beta:gamma signalling | 3.03E-04 |
| REAC:R-HSA-1296065 | Inwardly rectifying K+ channels | 4.38E-04 |
| REAC:R-HSA-373080 | Class B/2 (Secretin family receptors) | 8.21E-04 |
| REAC:R-HSA-390466 | Chaperonin-mediated protein folding | 9.12E-04 |
| REAC:R-HSA-8978868 | Fatty acid metabolism | 9.40E-04 |
| REAC:R-HSA-391251 | Protein folding | 1.30E-03 |
| REAC:R-HSA-9658195 | Leishmania infection | 1.85E-03 |
| REAC:R-HSA-112314 | Neurotransmitter receptors and postsynaptic signal transmission | 1.93E-03 |
| REAC:R-HSA-416476 | G alpha (q) signalling events | 3.03E-03 |
| REAC:R-HSA-4086398 | Ca2+ pathway | 3.66E-03 |
| REAC:R-HSA-76002 | Platelet activation, signaling and aggregation | 9.26E-03 |
| REAC:R-HSA-112315 | Transmission across Chemical Synapses | 9.47E-03 |
| REAC:R-HSA-418594 | G alpha (i) signalling events | 1.09E-02 |
| REAC:R-HSA-416482 | G alpha (12/13) signalling events | 1.23E-02 |
| REAC:R-HSA-418346 | Platelet homeostasis | 1.56E-02 |
| REAC:R-HSA-77350 | Beta oxidation of hexanoyl-CoA to butanoyl-CoA | 1.79E-02 |
| REAC:R-HSA-77289 | Mitochondrial Fatty Acid Beta-Oxidation | 2.99E-02 |
| REAC:R-HSA-611105 | Respiratory electron transport | 3.06E-02 |
| REAC:R-HSA-1296071 | Potassium Channels | 3.31E-02 |
| REAC:R-HSA-9033500 | TYSND1 cleaves peroxisomal proteins | 3.75E-02 |
| REAC:R-HSA-8939211 | ESR-mediated signaling | 4.92E-02 |
| REAC:R-HSA-418555 | G alpha (s) signalling events | 4.97E-02 |
| 6 | KEGG:05146 | Amoebiasis | 5.14E-07 |
| KEGG:04512 | ECM-receptor interaction | 7.73E-06 |
| KEGG:04510 | Focal adhesion | 5.72E-05 |
| KEGG:05222 | Small cell lung cancer | 3.07E-04 |
| KEGG:05414 | Dilated cardiomyopathy | 3.60E-04 |
| KEGG:05200 | Pathways in cancer | 4.76E-04 |
| KEGG:05165 | Human papillomavirus infection | 1.61E-03 |
| KEGG:04151 | PI3K-Akt signaling pathway | 2.43E-03 |
| KEGG:05412 | Arrhythmogenic right ventricular cardiomyopathy | 3.65E-03 |
| KEGG:05410 | Hypertrophic cardiomyopathy | 6.72E-03 |
| KEGG:04064 | NF-kappa B signaling pathway | 1.09E-02 |
| KEGG:04974 | Protein digestion and absorption | 1.13E-02 |
| REAC:R-HSA-1474244 | Extracellular matrix organization | 3.05E-15 |
| REAC:R-HSA-3000178 | ECM proteoglycans | 1.34E-09 |
| REAC:R-HSA-1474228 | Degradation of the extracellular matrix | 5.14E-09 |
| REAC:R-HSA-3000157 | Laminin interactions | 1.65E-08 |
| REAC:R-HSA-1442490 | Collagen degradation | 2.95E-08 |
| REAC:R-HSA-3000171 | Non-integrin membrane-ECM interactions | 1.08E-06 |
| REAC:R-HSA-1474290 | Collagen formation | 1.48E-05 |
| REAC:R-HSA-2022090 | Assembly of collagen fibrils and other multimeric structures | 7.68E-05 |
| REAC:R-HSA-1650814 | Collagen biosynthesis and modifying enzymes | 1.34E-04 |
| REAC:R-HSA-8874081 | MET activates PTK2 signaling | 2.04E-04 |
| REAC:R-HSA-1592389 | Activation of Matrix Metalloproteinases | 3.03E-04 |
| REAC:R-HSA-216083 | Integrin cell surface interactions | 4.18E-04 |
| REAC:R-HSA-8875878 | MET promotes cell motility | 6.69E-04 |
| REAC:R-HSA-422475 | Axon guidance | 7.77E-04 |
| REAC:R-HSA-8948216 | Collagen chain trimerization | 9.87E-04 |
| REAC:R-HSA-9675108 | Nervous system development | 1.12E-03 |
| REAC:R-HSA-2214320 | Anchoring fibril formation | 1.67E-03 |
| REAC:R-HSA-9006934 | Signaling by Receptor Tyrosine Kinases | 3.19E-03 |
| REAC:R-HSA-6806834 | Signaling by MET | 8.87E-03 |
| REAC:R-HSA-419037 | NCAM1 interactions | 4.04E-02 |
| REAC:R-HSA-6783783 | Interleukin-10 signaling | 4.97E-02 |
| 8 | KEGG:04960 | Aldosterone-regulated sodium reabsorption | 3.03E-07 |
| KEGG:04742 | Taste transduction | 1.15E-03 |
| KEGG:05167 | Kaposi sarcoma-associated herpesvirus infection | 5.68E-03 |
| KEGG:04060 | Cytokine-cytokine receptor interaction | 7.09E-03 |
| REAC:R-HSA-418457 | cGMP effects | 4.62E-03 |
| REAC:R-HSA-2672351 | Stimuli-sensing channels | 7.00E-03 |
| REAC:R-HSA-392154 | Nitric oxide stimulates guanylate cyclase | 1.33E-02 |
| 13 | KEGG:00670 | One carbon pool by folate | 5.23E-07 |
| KEGG:01523 | Antifolate resistance | 4.80E-04 |
| REAC:R-HSA-210991 | Basigin interactions | 3.37E-06 |
| REAC:R-HSA-352230 | Amino acid transport across the plasma membrane | 9.54E-06 |
| REAC:R-HSA-5660862 | Defective SLC7A7 causes lysinuric protein intolerance (LPI) | 3.38E-04 |
| REAC:R-HSA-1430728 | Metabolism | 1.04E-03 |
| REAC:R-HSA-425393 | Transport of inorganic cations/anions and amino acids/oligopeptides | 1.21E-03 |
| REAC:R-HSA-202733 | Cell surface interactions at the vascular wall | 1.27E-02 |
| REAC:R-HSA-73817 | Purine ribonucleoside monophosphate biosynthesis | 2.22E-02 |
| REAC:R-HSA-71240 | Tryptophan catabolism | 3.05E-02 |
| REAC:R-HSA-8956320 | Nucleobase biosynthesis | 3.52E-02 |
| REAC:R-HSA-425407 | SLC-mediated transmembrane transport | 3.58E-02 |
| REAC:R-HSA-196757 | Metabolism of folate and pterines | 4.02E-02 |
| 15 | KEGG:04975 | Fat digestion and absorption | 1.32E-04 |
| KEGG:00561 | Glycerolipid metabolism | 3.89E-02 |
| REAC:R-HSA-8979227 | Triglyceride metabolism | 2.66E-05 |
| REAC:R-HSA-556833 | Metabolism of lipids | 3.51E-03 |
| REAC:R-HSA-163560 | Triglyceride catabolism | 4.62E-03 |
| 16 | KEGG:00350 | Tyrosine metabolism | 9.37E-04 |
| KEGG:00982 | Drug metabolism - cytochrome P450 | 6.97E-03 |
| KEGG:00830 | Retinol metabolism | 6.97E-03 |
| KEGG:00980 | Metabolism of xenobiotics by cytochrome P450 | 8.62E-03 |
| KEGG:05204 | Chemical carcinogenesis | 1.17E-02 |
| KEGG:04061 | Viral protein interaction with cytokine and cytokine receptor | 2.06E-02 |
| REAC:R-HSA-211859 | Biological oxidations | 8.99E-03 |
| REAC:R-HSA-2161522 | Abacavir transport and metabolism | 9.77E-03 |
| REAC:R-HSA-71384 | Ethanol oxidation | 1.43E-02 |
| REAC:R-HSA-189483 | Heme degradation | 1.97E-02 |
| REAC:R-HSA-5365859 | RA biosynthesis pathway | 4.98E-02 |

FDR, false discovery rate; CRC, colorectal cancer.

**Supplementary Table 3.** Different biological processes significantly affected by the modules in the protein interaction map associated with primary CRC.

|  |  |  |  |
| --- | --- | --- | --- |
| **Cluster** | **GO id** | **GO name** | **FDR** |
| 1 | GO:0007049 | cell cycle | 9.62E-42 |
| GO:0022402 | cell cycle process | 6.75E-39 |
| GO:1903047 | mitotic cell cycle process | 1.13E-35 |
| GO:0007059 | chromosome segregation | 1.55E-35 |
| GO:0000278 | mitotic cell cycle | 6.81E-35 |
| GO:0000280 | nuclear division | 2.67E-34 |
| GO:0048285 | organelle fission | 6.24E-33 |
| GO:0051301 | cell division | 1.88E-32 |
| GO:0140014 | mitotic nuclear division | 1.98E-30 |
| GO:0000819 | sister chromatid segregation | 7.80E-29 |
| GO:0000070 | mitotic sister chromatid segregation | 1.61E-28 |
| GO:0098813 | nuclear chromosome segregation | 3.59E-27 |
| GO:0051276 | chromosome organization | 3.03E-22 |
| GO:0006996 | organelle organization | 7.80E-19 |
| GO:1902850 | microtubule cytoskeleton organization involved in mitosis | 2.38E-18 |
| GO:0007052 | mitotic spindle organization | 1.83E-17 |
| GO:0007051 | spindle organization | 6.24E-17 |
| GO:0051726 | regulation of cell cycle | 2.51E-16 |
| GO:0000226 | microtubule cytoskeleton organization | 1.09E-15 |
| GO:0007346 | regulation of mitotic cell cycle | 3.69E-15 |
| GO:0010564 | regulation of cell cycle process | 6.43E-15 |
| GO:0051983 | regulation of chromosome segregation | 4.77E-14 |
| GO:0007017 | microtubule-based process | 1.21E-13 |
| GO:1901990 | regulation of mitotic cell cycle phase transition | 1.59E-12 |
| GO:1903046 | meiotic cell cycle process | 1.67E-12 |
| GO:0051321 | meiotic cell cycle | 2.35E-12 |
| GO:0010965 | regulation of mitotic sister chromatid separation | 6.61E-12 |
| GO:0051306 | mitotic sister chromatid separation | 9.21E-12 |
| GO:0044772 | mitotic cell cycle phase transition | 9.25E-12 |
| GO:0051304 | chromosome separation | 9.56E-12 |
| GO:0071103 | DNA conformation change | 1.41E-11 |
| GO:0051783 | regulation of nuclear division | 1.69E-11 |
| GO:0140013 | meiotic nuclear division | 1.77E-11 |
| GO:0033045 | regulation of sister chromatid segregation | 2.02E-11 |
| GO:1905818 | regulation of chromosome separation | 2.02E-11 |
| GO:1901987 | regulation of cell cycle phase transition | 3.65E-11 |
| GO:0007088 | regulation of mitotic nuclear division | 5.05E-11 |
| GO:0016043 | cellular component organization | 8.64E-11 |
| GO:0044770 | cell cycle phase transition | 1.30E-10 |
| GO:0030071 | regulation of mitotic metaphase/anaphase transition | 2.52E-10 |
| GO:0007091 | metaphase/anaphase transition of mitotic cell cycle | 3.46E-10 |
| GO:0071840 | cellular component organization or biogenesis | 3.54E-10 |
| GO:0007010 | cytoskeleton organization | 3.75E-10 |
| GO:1902099 | regulation of metaphase/anaphase transition of cell cycle | 4.04E-10 |
| GO:0044784 | metaphase/anaphase transition of cell cycle | 5.45E-10 |
| GO:0006259 | DNA metabolic process | 7.04E-10 |
| GO:0006323 | DNA packaging | 7.51E-10 |
| GO:0007076 | mitotic chromosome condensation | 7.51E-10 |
| GO:0030261 | chromosome condensation | 8.41E-10 |
| GO:0000910 | cytokinesis | 8.21E-09 |
| GO:0033044 | regulation of chromosome organization | 8.93E-09 |
| GO:0090068 | positive regulation of cell cycle process | 1.10E-08 |
| GO:0045787 | positive regulation of cell cycle | 1.86E-08 |
| GO:0033043 | regulation of organelle organization | 5.61E-08 |
| GO:0033048 | negative regulation of mitotic sister chromatid segregation | 7.80E-08 |
| GO:0033046 | negative regulation of sister chromatid segregation | 7.80E-08 |
| GO:2000816 | negative regulation of mitotic sister chromatid separation | 7.80E-08 |
| GO:0000281 | mitotic cytokinesis | 1.10E-07 |
| GO:0051985 | negative regulation of chromosome segregation | 1.10E-07 |
| GO:1905819 | negative regulation of chromosome separation | 1.10E-07 |
| GO:0051383 | kinetochore organization | 1.10E-07 |
| GO:0033047 | regulation of mitotic sister chromatid segregation | 1.30E-07 |
| GO:2001251 | negative regulation of chromosome organization | 6.49E-07 |
| GO:0010389 | regulation of G2/M transition of mitotic cell cycle | 1.02457E-06 |
| GO:0061640 | cytoskeleton-dependent cytokinesis | 1.49292E-06 |
| GO:1902749 | regulation of cell cycle G2/M phase transition | 1.55998E-06 |
| GO:0007093 | mitotic cell cycle checkpoint signaling | 2.1299E-06 |
| GO:0071174 | mitotic spindle checkpoint signaling | 2.91372E-06 |
| GO:0007094 | mitotic spindle assembly checkpoint signaling | 2.91372E-06 |
| GO:0071173 | spindle assembly checkpoint signaling | 2.91372E-06 |
| GO:0031577 | spindle checkpoint signaling | 3.43534E-06 |
| GO:0045841 | negative regulation of mitotic metaphase/anaphase transition | 4.03201E-06 |
| GO:1902100 | negative regulation of metaphase/anaphase transition of cell cycle | 5.48438E-06 |
| GO:0051303 | establishment of chromosome localization | 1.00001E-05 |
| GO:0000086 | G2/M transition of mitotic cell cycle | 1.14933E-05 |
| GO:0050000 | chromosome localization | 1.18576E-05 |
| GO:0006974 | cellular response to DNA damage stimulus | 1.20422E-05 |
| GO:0045839 | negative regulation of mitotic nuclear division | 1.26486E-05 |
| GO:0000075 | cell cycle checkpoint signaling | 1.4185E-05 |
| GO:0044839 | cell cycle G2/M phase transition | 1.70219E-05 |
| GO:1901992 | positive regulation of mitotic cell cycle phase transition | 1.92832E-05 |
| GO:0051128 | regulation of cellular component organization | 2.0826E-05 |
| GO:0045132 | meiotic chromosome segregation | 2.25035E-05 |
| GO:0051784 | negative regulation of nuclear division | 3.28382E-05 |
| GO:0034508 | centromere complex assembly | 3.28382E-05 |
| GO:0010948 | negative regulation of cell cycle process | 5.55777E-05 |
| GO:0051310 | metaphase plate congression | 8.17779E-05 |
| GO:1901989 | positive regulation of cell cycle phase transition | 0.000100321 |
| GO:0051225 | spindle assembly | 0.000106571 |
| GO:0045931 | positive regulation of mitotic cell cycle | 0.00012733 |
| GO:0008608 | attachment of spindle microtubules to kinetochore | 0.000141778 |
| GO:1901991 | negative regulation of mitotic cell cycle phase transition | 0.000162588 |
| GO:0007127 | meiosis I | 0.000222938 |
| GO:0010639 | negative regulation of organelle organization | 0.000236109 |
| GO:0061982 | meiosis I cell cycle process | 0.000289931 |
| GO:0006281 | DNA repair | 0.000306333 |
| GO:0007096 | regulation of exit from mitosis | 0.000315443 |
| GO:0045786 | negative regulation of cell cycle | 0.000405962 |
| GO:0051382 | kinetochore assembly | 0.000417605 |
| GO:0031145 | anaphase-promoting complex-dependent catabolic process | 0.000474583 |
| GO:0051445 | regulation of meiotic cell cycle | 0.000695588 |
| GO:0007080 | mitotic metaphase plate congression | 0.000771064 |
| GO:0045930 | negative regulation of mitotic cell cycle | 0.000891374 |
| GO:0010458 | exit from mitosis | 0.001037017 |
| GO:0051640 | organelle localization | 0.001039374 |
| GO:1901988 | negative regulation of cell cycle phase transition | 0.00118412 |
| GO:0007143 | female meiotic nuclear division | 0.002730835 |
| GO:0022414 | reproductive process | 0.003059491 |
| GO:0090307 | mitotic spindle assembly | 0.003132534 |
| GO:0000003 | reproduction | 0.00314427 |
| GO:0051129 | negative regulation of cellular component organization | 0.004772279 |
| GO:0070925 | organelle assembly | 0.005891485 |
| GO:0065004 | protein-DNA complex assembly | 0.006310741 |
| GO:0007292 | female gamete generation | 0.00952286 |
| GO:0032506 | cytokinetic process | 0.009621616 |
| GO:0051347 | positive regulation of transferase activity | 0.012097805 |
| GO:0051656 | establishment of organelle localization | 0.01354762 |
| GO:0032465 | regulation of cytokinesis | 0.014561931 |
| GO:0006260 | DNA replication | 0.015133616 |
| GO:0051988 | regulation of attachment of spindle microtubules to kinetochore | 0.017120384 |
| GO:0071824 | protein-DNA complex subunit organization | 0.017939945 |
| GO:0031055 | chromatin remodeling at centromere | 0.020883963 |
| GO:2000241 | regulation of reproductive process | 0.024479468 |
| GO:0051302 | regulation of cell division | 0.027914607 |
| GO:0006271 | DNA strand elongation involved in DNA replication | 0.045078918 |
| GO:0007062 | sister chromatid cohesion | 0.045939167 |
| GO:0051785 | positive regulation of nuclear division | 0.049293145 |
| 2 | GO:0006364 | rRNA processing | 1.90E-39 |
| GO:0042254 | ribosome biogenesis | 2.26E-39 |
| GO:0016072 | rRNA metabolic process | 5.01E-39 |
| GO:0022613 | ribonucleoprotein complex biogenesis | 2.34E-35 |
| GO:0034470 | ncRNA processing | 8.89E-34 |
| GO:0034660 | ncRNA metabolic process | 1.39E-31 |
| GO:0006396 | RNA processing | 1.30E-24 |
| GO:0044085 | cellular component biogenesis | 1.00E-14 |
| GO:0016070 | RNA metabolic process | 1.73E-12 |
| GO:0042273 | ribosomal large subunit biogenesis | 2.76E-12 |
| GO:0090304 | nucleic acid metabolic process | 3.14E-11 |
| GO:0006139 | nucleobase-containing compound metabolic process | 4.27E-10 |
| GO:0046483 | heterocycle metabolic process | 9.85E-10 |
| GO:0006725 | cellular aromatic compound metabolic process | 1.21E-09 |
| GO:0010467 | gene expression | 3.26E-09 |
| GO:1901360 | organic cyclic compound metabolic process | 3.81E-09 |
| GO:0034641 | cellular nitrogen compound metabolic process | 1.71E-08 |
| GO:0071840 | cellular component organization or biogenesis | 5.93E-08 |
| GO:0030490 | maturation of SSU-rRNA | 2.93E-07 |
| GO:0000027 | ribosomal large subunit assembly | 1.1493E-06 |
| GO:0000470 | maturation of LSU-rRNA | 1.6869E-06 |
| GO:0006360 | transcription by RNA polymerase I | 1.97671E-06 |
| GO:0042274 | ribosomal small subunit biogenesis | 3.32378E-06 |
| GO:0000462 | maturation of SSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 6.13738E-06 |
| GO:0000463 | maturation of LSU-rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 1.42562E-05 |
| GO:0043170 | macromolecule metabolic process | 4.32089E-05 |
| GO:0042255 | ribosome assembly | 8.8628E-05 |
| GO:0045943 | positive regulation of transcription by RNA polymerase I | 9.16689E-05 |
| GO:0006807 | nitrogen compound metabolic process | 9.76638E-05 |
| GO:0000466 | maturation of 5.8S rRNA from tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 0.000109881 |
| GO:0000469 | cleavage involved in rRNA processing | 0.000180881 |
| GO:0044238 | primary metabolic process | 0.000388314 |
| GO:0006356 | regulation of transcription by RNA polymerase I | 0.000474297 |
| GO:0000460 | maturation of 5.8S rRNA | 0.000601105 |
| GO:0044237 | cellular metabolic process | 0.000868191 |
| GO:2000234 | positive regulation of rRNA processing | 0.000877485 |
| GO:0071704 | organic substance metabolic process | 0.002841409 |
| GO:0000478 | endonucleolytic cleavage involved in rRNA processing | 0.00330927 |
| GO:0000479 | endonucleolytic cleavage of tricistronic rRNA transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) | 0.00330927 |
| GO:2000232 | regulation of rRNA processing | 0.00330927 |
| GO:0008152 | metabolic process | 0.010327824 |
| GO:0033979 | box H/ACA RNA metabolic process | 0.014819701 |
| GO:0090502 | RNA phosphodiester bond hydrolysis, endonucleolytic | 0.016154743 |
| GO:0022618 | ribonucleoprotein complex assembly | 0.027037942 |
| GO:0071826 | ribonucleoprotein complex subunit organization | 0.032031843 |
| GO:0007000 | nucleolus organization | 0.049300927 |
| 3 | GO:0006635 | fatty acid beta-oxidation | 1.09E-14 |
| GO:0009062 | fatty acid catabolic process | 4.06E-13 |
| GO:0019395 | fatty acid oxidation | 4.48E-13 |
| GO:0034440 | lipid oxidation | 7.18E-13 |
| GO:0016054 | organic acid catabolic process | 1.53E-12 |
| GO:0072329 | monocarboxylic acid catabolic process | 3.60E-12 |
| GO:0046395 | carboxylic acid catabolic process | 4.09E-11 |
| GO:0019752 | carboxylic acid metabolic process | 1.38E-10 |
| GO:0043436 | oxoacid metabolic process | 2.24E-10 |
| GO:0006082 | organic acid metabolic process | 3.54E-10 |
| GO:0030258 | lipid modification | 5.46E-10 |
| GO:0044282 | small molecule catabolic process | 7.19E-10 |
| GO:0044242 | cellular lipid catabolic process | 1.12E-09 |
| GO:0044281 | small molecule metabolic process | 8.59E-09 |
| GO:0006631 | fatty acid metabolic process | 1.04E-08 |
| GO:0016042 | lipid catabolic process | 6.52E-08 |
| GO:0032787 | monocarboxylic acid metabolic process | 1.90623E-06 |
| GO:0045333 | cellular respiration | 2.59336E-06 |
| GO:0006099 | tricarboxylic acid cycle | 3.12303E-06 |
| GO:0006091 | generation of precursor metabolites and energy | 5.11377E-06 |
| GO:0009060 | aerobic respiration | 2.27892E-05 |
| GO:0015980 | energy derivation by oxidation of organic compounds | 3.45289E-05 |
| GO:0007188 | adenylate cyclase-modulating G protein-coupled receptor signaling pathway | 7.12501E-05 |
| GO:0007189 | adenylate cyclase-activating G protein-coupled receptor signaling pathway | 0.000118696 |
| GO:0044255 | cellular lipid metabolic process | 0.000294136 |
| GO:0055114 | obsolete oxidation-reduction process | 0.000518478 |
| GO:0033540 | fatty acid beta-oxidation using acyl-CoA oxidase | 0.002285931 |
| GO:0006629 | lipid metabolic process | 0.005445936 |
| GO:0002861 | regulation of inflammatory response to antigenic stimulus | 0.028198272 |
| GO:0006550 | isoleucine catabolic process | 0.03675142 |
| GO:0006104 | succinyl-CoA metabolic process | 0.03675142 |
| GO:0022904 | respiratory electron transport chain | 0.044509103 |
| 6 | GO:0030198 | extracellular matrix organization | 6.35E-14 |
| GO:0043062 | extracellular structure organization | 6.56E-14 |
| GO:0045229 | external encapsulating structure organization | 7.02E-14 |
| GO:0030199 | collagen fibril organization | 1.18709E-05 |
| GO:0016043 | cellular component organization | 2.21148E-05 |
| GO:0001704 | formation of primary germ layer | 2.58252E-05 |
| GO:0071840 | cellular component organization or biogenesis | 4.49458E-05 |
| GO:0033627 | cell adhesion mediated by integrin | 8.22061E-05 |
| GO:0022617 | extracellular matrix disassembly | 0.000157447 |
| GO:0048729 | tissue morphogenesis | 0.000279291 |
| GO:0007369 | gastrulation | 0.000299224 |
| GO:0007155 | cell adhesion | 0.000336458 |
| GO:0022610 | biological adhesion | 0.000354067 |
| GO:0033628 | regulation of cell adhesion mediated by integrin | 0.000939089 |
| GO:0009790 | embryo development | 0.001119534 |
| GO:0009888 | tissue development | 0.001516293 |
| GO:0048598 | embryonic morphogenesis | 0.00163663 |
| GO:0038065 | collagen-activated signaling pathway | 0.001863532 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 0.003892139 |
| GO:0007166 | cell surface receptor signaling pathway | 0.005302618 |
| GO:0009653 | anatomical structure morphogenesis | 0.006707477 |
| GO:0007492 | endoderm development | 0.007409731 |
| GO:0007275 | multicellular organism development | 0.009751778 |
| GO:0032501 | multicellular organismal process | 0.012062707 |
| GO:0042060 | wound healing | 0.012916535 |
| GO:0019538 | protein metabolic process | 0.019382883 |
| GO:0032502 | developmental process | 0.023131334 |
| GO:0048333 | mesodermal cell differentiation | 0.024088087 |
| GO:0032963 | collagen metabolic process | 0.030291332 |
| GO:0006928 | movement of cell or subcellular component | 0.034612116 |
| GO:0006935 | chemotaxis | 0.037537852 |
| GO:0048856 | anatomical structure development | 0.038234254 |
| GO:0042330 | taxis | 0.038662331 |
| GO:0009611 | response to wounding | 0.048247768 |
| 8 | GO:0071310 | cellular response to organic substance | 0.000111977 |
| GO:0046069 | cGMP catabolic process | 0.000171211 |
| GO:0008015 | blood circulation | 0.000380065 |
| GO:0070887 | cellular response to chemical stimulus | 0.000701768 |
| GO:0042221 | response to chemical | 0.000722487 |
| GO:0010033 | response to organic substance | 0.000755246 |
| GO:0097529 | myeloid leukocyte migration | 0.000807534 |
| GO:0030595 | leukocyte chemotaxis | 0.000997272 |
| GO:0003013 | circulatory system process | 0.001405547 |
| GO:0014070 | response to organic cyclic compound | 0.001779475 |
| GO:0050900 | leukocyte migration | 0.002271531 |
| GO:0032872 | regulation of stress-activated MAPK cascade | 0.006412643 |
| GO:0070302 | regulation of stress-activated protein kinase signaling cascade | 0.0070124 |
| GO:0071345 | cellular response to cytokine stimulus | 0.007227265 |
| GO:0009214 | cyclic nucleotide catabolic process | 0.007671644 |
| GO:0060326 | cell chemotaxis | 0.007929848 |
| GO:0046068 | cGMP metabolic process | 0.011430249 |
| GO:0002688 | regulation of leukocyte chemotaxis | 0.011961381 |
| GO:0009605 | response to external stimulus | 0.015632207 |
| GO:0071495 | cellular response to endogenous stimulus | 0.015799469 |
| GO:0034097 | response to cytokine | 0.016208635 |
| GO:0050920 | regulation of chemotaxis | 0.017181233 |
| GO:0009719 | response to endogenous stimulus | 0.018036957 |
| GO:1901700 | response to oxygen-containing compound | 0.020458993 |
| GO:0006814 | sodium ion transport | 0.023001129 |
| GO:1904045 | cellular response to aldosterone | 0.024534323 |
| GO:0050918 | positive chemotaxis | 0.025795839 |
| GO:0065007 | biological regulation | 0.027421472 |
| GO:0032501 | multicellular organismal process | 0.030485999 |
| GO:0043408 | regulation of MAPK cascade | 0.042542775 |
| GO:0050926 | regulation of positive chemotaxis | 0.048419883 |
| GO:0051403 | stress-activated MAPK cascade | 0.048590784 |
| 13 | GO:0046653 | tetrahydrofolate metabolic process | 4.53E-07 |
| GO:0019752 | carboxylic acid metabolic process | 1.5621E-06 |
| GO:0043436 | oxoacid metabolic process | 2.06463E-06 |
| GO:0006760 | folic acid-containing compound metabolic process | 2.20837E-06 |
| GO:0006082 | organic acid metabolic process | 2.68345E-06 |
| GO:0042558 | pteridine-containing compound metabolic process | 1.08576E-05 |
| GO:1902475 | L-alpha-amino acid transmembrane transport | 8.13607E-05 |
| GO:0015807 | L-amino acid transport | 9.26029E-05 |
| GO:0006575 | cellular modified amino acid metabolic process | 0.000156488 |
| GO:0044281 | small molecule metabolic process | 0.000371162 |
| GO:0003333 | amino acid transmembrane transport | 0.000385822 |
| GO:0043648 | dicarboxylic acid metabolic process | 0.000541881 |
| GO:0015823 | phenylalanine transport | 0.000543133 |
| GO:0006865 | amino acid transport | 0.002301594 |
| GO:1905039 | carboxylic acid transmembrane transport | 0.002864192 |
| GO:1903825 | organic acid transmembrane transport | 0.003019502 |
| GO:0009069 | serine family amino acid metabolic process | 0.004187043 |
| GO:0042398 | cellular modified amino acid biosynthetic process | 0.005097825 |
| GO:0015827 | tryptophan transport | 0.005425335 |
| GO:0098713 | leucine import across plasma membrane | 0.005425335 |
| GO:1903801 | L-leucine import across plasma membrane | 0.005425335 |
| GO:0006189 | 'de novo' IMP biosynthetic process | 0.008135009 |
| GO:1901605 | alpha-amino acid metabolic process | 0.01049187 |
| GO:0072522 | purine-containing compound biosynthetic process | 0.011312651 |
| GO:0006564 | L-serine biosynthetic process | 0.011384823 |
| GO:0046654 | tetrahydrofolate biosynthetic process | 0.011384823 |
| GO:0003360 | brainstem development | 0.011384823 |
| GO:0015820 | leucine transport | 0.015174179 |
| GO:0009396 | folic acid-containing compound biosynthetic process | 0.019502482 |
| GO:0015803 | branched-chain amino acid transport | 0.019502482 |
| GO:0006188 | IMP biosynthetic process | 0.024369134 |
| GO:0009113 | purine nucleobase biosynthetic process | 0.024369134 |
| GO:0035999 | tetrahydrofolate interconversion | 0.024369134 |
| GO:0006563 | L-serine metabolic process | 0.029773539 |
| GO:0046942 | carboxylic acid transport | 0.033834163 |
| GO:0015801 | aromatic amino acid transport | 0.042193231 |
| GO:0042559 | pteridine-containing compound biosynthetic process | 0.049207327 |
| GO:1990822 | basic amino acid transmembrane transport | 0.049207327 |
| 15 | GO:0006641 | triglyceride metabolic process | 0.015024035 |
| GO:0006639 | acylglycerol metabolic process | 0.029174457 |
| GO:0006638 | neutral lipid metabolic process | 0.029797928 |
| 16 | GO:1904995 | negative regulation of leukocyte adhesion to vascular endothelial cell | 0.000108654 |
| GO:0042573 | retinoic acid metabolic process | 0.001617121 |
| GO:0034754 | cellular hormone metabolic process | 0.002366987 |
| GO:1904994 | regulation of leukocyte adhesion to vascular endothelial cell | 0.002920732 |
| GO:1903237 | negative regulation of leukocyte tethering or rolling | 0.003256399 |
| GO:2000107 | negative regulation of leukocyte apoptotic process | 0.004187043 |
| GO:2000669 | negative regulation of dendritic cell apoptotic process | 0.008135009 |
| GO:0061756 | leukocyte adhesion to vascular endothelial cell | 0.008595197 |
| GO:0002548 | monocyte chemotaxis | 0.01401982 |
| GO:0002692 | negative regulation of cellular extravasation | 0.015174179 |
| GO:0042445 | hormone metabolic process | 0.016149324 |
| GO:2000106 | regulation of leukocyte apoptotic process | 0.026729742 |
| GO:2000668 | regulation of dendritic cell apoptotic process | 0.029773539 |
| GO:0097048 | dendritic cell apoptotic process | 0.029773539 |
| GO:0070098 | chemokine-mediated signaling pathway | 0.03078975 |
| GO:0006069 | ethanol oxidation | 0.035715103 |
| GO:1990869 | cellular response to chemokine | 0.042669273 |
| GO:1990868 | response to chemokine | 0.042669273 |
| GO:1903236 | regulation of leukocyte tethering or rolling | 0.049207327 |

FDR, false discovery rate; CRC, colorectal cancer.

**Supplementary Table 4.** A total of 15 molecular functions significantly enriched by DEGs associated with primary CRC.

|  |  |  |
| --- | --- | --- |
| **Term id** | **Term name** | **FDR** |
| GO:0005515 | protein binding | 2.38E-11 |
| GO:0005488 | binding | 1.01E-04 |
| GO:0008509 | anion transmembrane transporter activity | 1.78E-03 |
| GO:0016616 | oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor | 2.54E-03 |
| GO:0022804 | active transmembrane transporter activity | 2.79E-03 |
| GO:0005201 | extracellular matrix structural constituent | 3.52E-03 |
| GO:0003988 | acetyl-CoA C-acyltransferase activity | 4.43E-03 |
| GO:0016614 | oxidoreductase activity, acting on CH-OH group of donors | 9.43E-03 |
| GO:0070696 | transmembrane receptor protein serine/threonine kinase binding | 1.22E-02 |
| GO:0030515 | snoRNA binding | 1.76E-02 |
| GO:0008514 | organic anion transmembrane transporter activity | 1.89E-02 |
| GO:0005102 | signaling receptor binding | 2.97E-02 |
| GO:0051861 | glycolipid binding | 3.18E-02 |
| GO:0042578 | phosphoric ester hydrolase activity | 4.20E-02 |
| GO:0015291 | secondary active transmembrane transporter activity | 4.81E-02 |

FDR, false discovery rate.

**Supplementary Table 5.** A total of 33 cellular components significantly enriched by DEGs associated with primary CRC.

|  |  |  |
| --- | --- | --- |
| **Term id** | **Term name** | **FDR** |
| GO:0070013 | intracellular organelle lumen | 1.29E-07 |
| GO:0043233 | organelle lumen | 1.29E-07 |
| GO:0031974 | membrane-enclosed lumen | 1.29E-07 |
| GO:0045177 | apical part of cell | 2.80E-06 |
| GO:0016324 | apical plasma membrane | 8.93E-06 |
| GO:0005737 | cytoplasm | 9.96E-06 |
| GO:0070062 | extracellular exosome | 1.59E-05 |
| GO:1903561 | extracellular vesicle | 5.18E-05 |
| GO:0065010 | extracellular membrane-bounded organelle | 5.50E-05 |
| GO:0043230 | extracellular organelle | 5.50E-05 |
| GO:0005819 | spindle | 7.31E-05 |
| GO:0098590 | plasma membrane region | 1.54E-04 |
| GO:0005730 | nucleolus | 1.90E-04 |
| GO:0043226 | organelle | 2.44E-04 |
| GO:0043227 | membrane-bounded organelle | 6.82E-04 |
| GO:0000775 | chromosome, centromeric region | 1.21E-03 |
| GO:0005654 | nucleoplasm | 1.49E-03 |
| GO:0031981 | nuclear lumen | 2.05E-03 |
| GO:0030054 | cell junction | 2.08E-03 |
| GO:0005576 | extracellular region | 2.38E-03 |
| GO:0030684 | preribosome | 6.15E-03 |
| GO:0005615 | extracellular space | 7.00E-03 |
| GO:0071944 | cell periphery | 8.39E-03 |
| GO:0031253 | cell projection membrane | 8.96E-03 |
| GO:0005829 | cytosol | 1.40E-02 |
| GO:0062023 | collagen-containing extracellular matrix | 1.57E-02 |
| GO:0016020 | membrane | 1.98E-02 |
| GO:0043231 | intracellular membrane-bounded organelle | 2.64E-02 |
| GO:0045121 | membrane raft | 2.90E-02 |
| GO:0098857 | membrane microdomain | 2.90E-02 |
| GO:0043005 | neuron projection | 3.19E-02 |
| GO:0000779 | condensed chromosome, centromeric region | 3.22E-02 |
| GO:0012505 | endomembrane system | 3.73E-02 |

FDR, false discovery rate.

**Supplementary Table 6.** Seventy-five nodes were considered hub genes in the protein interaction map associated with the primary colorectal cancer.

|  |  |  |
| --- | --- | --- |
| **Gene symbol** | **Degree** | **Betweenness** |
| MYC | 134 | 0.1197 |
| VEGFA | 76 | 0.0469 |
| CCND1 | 80 | 0.0363 |
| CDK1 | 113 | 0.0268 |
| PAICS | 55 | 0.0242 |
| CXCL8 | 59 | 0.0238 |
| NPM1 | 64 | 0.0237 |
| CCNB1 | 105 | 0.0236 |
| H2AFX | 64 | 0.0220 |
| HSPD1 | 43 | 0.0187 |
| GART | 56 | 0.0180 |
| GMPS | 59 | 0.0171 |
| CDKN2A | 49 | 0.0167 |
| ASPM | 80 | 0.0166 |
| COL1A1 | 38 | 0.0161 |
| TOP2A | 91 | 0.0156 |
| SOX9 | 41 | 0.0152 |
| RUVBL1 | 49 | 0.0147 |
| MKI67 | 76 | 0.0146 |
| BCL2L1 | 40 | 0.0141 |
| AURKA | 94 | 0.0131 |
| CDC20 | 90 | 0.0130 |
| NME1 | 30 | 0.0128 |
| NCAPG | 76 | 0.0116 |
| TRIP13 | 72 | 0.0107 |
| MCM7 | 79 | 0.0106 |
| CDC6 | 87 | 0.0104 |
| TTK | 71 | 0.0098 |
| NEK2 | 65 | 0.0097 |
| ABCE1 | 48 | 0.0094 |
| ANLN | 65 | 0.0092 |
| UBE2C | 78 | 0.0086 |
| KIF2C | 69 | 0.0085 |
| KPNA2 | 65 | 0.0080 |
| CDC27 | 36 | 0.0077 |
| RPS14 | 40 | 0.0075 |
| NOP56 | 61 | 0.0075 |
| IQGAP3 | 35 | 0.0075 |
| TPX2 | 73 | 0.0073 |
| DDX21 | 54 | 0.0071 |
| CCT6A | 35 | 0.0068 |
| ECT2 | 60 | 0.0068 |
| GTPBP4 | 52 | 0.0065 |
| THY1 | 29 | 0.0058 |
| BRIX1 | 51 | 0.0057 |
| SMC4 | 73 | 0.0056 |
| POLR1B | 53 | 0.0056 |
| ATAD2 | 53 | 0.0054 |
| RFC3 | 61 | 0.0054 |
| HJURP | 61 | 0.0052 |
| SHMT2 | 29 | 0.0051 |
| DKC1 | 56 | 0.0050 |
| CYCS | 51 | 0.0276 |
| PRKACB | 39 | 0.0197 |
| HPGDS | 34 | 0.0193 |
| PPARGC1A | 38 | 0.0188 |
| NRXN1 | 29 | 0.0178 |
| NCAM1 | 39 | 0.0158 |
| CALM1 | 31 | 0.0156 |
| SNCA | 29 | 0.0150 |
| ACO2 | 42 | 0.0128 |
| NR3C1 | 30 | 0.0126 |
| KITLG | 29 | 0.0117 |
| SUCLG2 | 31 | 0.0115 |
| GPT | 31 | 0.0113 |
| ACADM | 39 | 0.0110 |
| ETFDH | 33 | 0.0100 |
| ACAT1 | 30 | 0.0099 |
| GNAQ | 30 | 0.0097 |
| ATP5A1 | 34 | 0.0095 |
| KAT2B | 32 | 0.0090 |
| GCG | 31 | 0.0077 |
| ACOX1 | 36 | 0.0066 |
| CXCL12 | 38 | 0.0064 |
| SDHA | 34 | 0.0060 |

**Supplementary Table 7.** A total of 19 hub genes in primary CRC were demonstrated prognostic impact in COAD and READ based on the GEPIA2 database.

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **A, Single gene** | | | | | |  |  |  |
| **Gene symbol (label)** | **HR** | **Log-rank *P*** | ***P* (HR)** | | **Log2 FC, Primary CRC/Normal** | **Direction of change based on the GEPIA2 database, COAD/Normal** | **Direction of change based on the GEPIA2 database, READ/Normal** | **Validated** |
| SUCLG2 (A) | 0.5 | 0.0016 | 0.002 | | -1.346 | Up | Up | No |
| KPNA2 (B) | 0.51 | 0.0024 | 0.0029 | | 1.063 | Up | Up | Yes |
| ABCE1 (C) | 0.52 | 0.0043 | 0.005 | | 1.009 | Up | Up | Yes |
| AURKA (D) | 0.53 | 0.0041 | 0.0047 | | 1.662 | Up | Up | Yes |
| PAICS (E) | 0.53 | 0.0039 | 0.0045 | | 1.447 | Up | Up | Yes |
| NPM1 (F) | 0.54 | 0.0056 | 0.0064 | | 1.540 | Up | Up | Yes |
| GCG (G) | 0.54 | 0.0063 | 0.0073 | | -3.512 | Down | Down | Yes |
| DDX21 (H) | 0.57 | 0.013 | 0.014 | | 1.152 | Up | Up | Yes |
| ACOX1 (I) | 0.57 | 0.011 | 0.012 | | -1.184 | Down | Down | Yes |
| ACADM (J) | 0.59 | 0.02 | 0.022 | | -1.483 | Down | Down | Yes |
| GART (K) | 0.6 | 0.023 | 0.025 | | 1.140 | Up | Up | Yes |
| CYCS (L) | 0.6 | 0.022 | 0.024 | | -1.076 | Up | Up | No |
| NCAPG (M) | 0.61 | 0.024 | 0.026 | | 1.743 | Up | Up | Yes |
| GMPS (N) | 0.61 | 0.025 | 0.027 | | 1.112 | Up | Up | Yes |
| CXCL8 (O) | 0.62 | 0.032 | 0.034 | | 3.252 | Up | Up | Yes |
| PPARGC1A (P) | 0.62 | 0.029 | 0.03 | | -2.067 | Down | Down | Yes |
| ACO2 (Q) | 0.64 | 0.043 | 0.044 | | -1.018 | Not significant | | |
| ETFDH (R) | 0.65 | 0.047 | 0.049 | | -1.816 | Down | Down | Yes |
| CDKN2A (S) | 1.7 | 0.021 | 0.022 | | 1.960 | Up | Up | Yes |
| **B, Signature** | | | | |  |  |  |  |
| **Prognostic panel** | **HR** | **Logrank *P*** | | ***P* (HR)** |  |  |  |  |
| A+B | 0.43 | 0.00014 | | 0.00021 |  |  |  |  |
| A to C | 0.53 | 0.0041 | | 0.0048 |  |  |  |  |
| A to D | 0.48 | 0.00096 | | 0.0012 |  |  |  |  |
| A to E | 0.5 | 0.0017 | | 0.002 |  |  |  |  |
| A to F | 0.49 | 0.0015 | | 0.0018 |  |  |  |  |
| A to G | 0.48 | 0.00091 | | 0.0012 |  |  |  |  |
| A to H | 0.5 | 0.002 | | 0.0024 |  |  |  |  |
| A to I | 0.45 | 0.00047 | | 0.00066 |  |  |  |  |
| A to J | 0.49 | 0.0016 | | 0.002 |  |  |  |  |
| A to K | 0.47 | 0.0008 | | 0.0011 |  |  |  |  |
| A to L | 0.54 | 0.0057 | | 0.0066 |  |  |  |  |
| A to M | 0.56 | 0.0094 | | 0.01 |  |  |  |  |
| A to M | 0.53 | 0.0043 | | 0.005 |  |  |  |  |
| A to O | 0.44 | 0.00024 | | 0.00036 |  |  |  |  |
| A to P | 0.44 | 0.00023 | | 0.00035 |  |  |  |  |
| A to Q | 0.47 | 0.00097 | | 0.0013 |  |  |  |  |
| A to R | 0.47 | 0.00083 | | 0.0011 |  |  |  |  |

CRC, colorectal cancer; COAD, colon adenocarcinoma; READ, rectum adenocarcinoma.