# Supplementary tables

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## Supplementary Table S1. Summary of primers of each gene

| Gene | Primner direction | Sequence |
|---|---|---|
| F2 | Forward primer | 5’-AGATCGGCATGTCACCTTGG-3’ |
| | Reverse primer | 5’-TGAAGTTCTTGTCCCAGGGC-3’ |
| GPX3 | Forward primer | 5’-AAGAGCTTGCACCATTCGGT-3’ |
| | Reverse primer | 5’-CTCCACCTGGTCGGACATAC-3’ |
| BCL2L10 | Forward primer | 5’-CCCTTTCCACTGGCTTTTTGG-3’ |
| | Reverse primer | 5’-TTAGTTGGTCACAGTTGGGCA-3’ |
| BTG2 | Forward primer | 5’-CACCTGCAAGAACCAAGTGC-3’ |
| | Reverse primer | 5’-AGGTATGTGGTGGCCTGTTG-3’ |
| KRT18 | Forward primer | 5’-GGCTCTGGTTCCCGGATCTC-3’ |
| | Reverse primer | 5’-GTCGTTCAGGCTTTGCATGG-3’ |
| GCLC | Forward primer | 5’-TAAGCCCCCTCCTCCAAACT-3’ |
| | Reverse primer | 5’-GGATCACTCTGGTGAGCAGT-3’ |
| ITGB4 | Forward primer | 5’-GACATCCGGGCCCTAGACA-3’ |
| | Reverse primer | 5’-GTCCCATCCACGTGCTCAAG-3’ |
| SLC7A11 | Forward primer | 5’-ATGCTGGCAGCCATCTCTTT-3’ |
| | Reverse primer | 5’-TAGACCAAACCCACGATGCC-3’ |
| GAPDH | Forward primer | 5’-AAATCAAGTGGGGCGATGCT-3’ |
| | Reverse primer | 5’-CAAATGAGCCCCAGCCTTCT-3’ |
| BIRC5 | Forward primer | 5’-GGTGATGTGGATCTCGGCTT-3’ |
| | Reverse primer | 5’-TTTAAGGAAAGGCCGTGGCA-3’ |
| ACTB | Forward primer | 5’-TGGAACGGTGAAGGTGACAG-3’ |
| | Reverse primer | 5’-AACAACGCATCTCATATTTGGAA-3’ |

## Supplementary Table S2. Clinical information of patients with LUAD in this study

| **Cohorts** | **TCGA-LUAD** | **GSE68465** | **GSE72094** | **GSE135222** |
|---|---|---|---|---|
| **Number of patients** | 490 | 439 | 386 | 27 |
| **Age(Mean±SD)** | 65±10.01 | 64±10.08 | 69±9.41 | 62±8.95 |
| **Follow up time (Mean±SD)(years)** | 2.54±2.46 | 4.41±3.01 | 2.24±1.05 | 0.35±0.40 |
| **Follow up status** | | | | |
| Alive(or Non-progress) | 178(36.33%) | 206(46.92%) | 277(71.76%) | 6(22.2%) |
| Dead(or Progression) | 312(63.67%) | 233(53.08%) | 109(28.24%) | 21(77.8%) |
| **Gender** | | | | |
| Male | 228(46.53%) | 221(50.34%) | 168(43.52%) | 22(81.2%) |

| | | | | |
|---|---|---|---|---|
| Female | 262(53.47%) | 218(49.66%) | 218(56.48%) | 5(18.5%) |
| **Tumor stage** | | | | |
| Stage I | 263(53.67%) | — | 246(63.73%) | — |
| Stage II | 115(23.47%) | — | 65(16.84%) | — |
| Stage III | 79(16.12%) | — | 56(14.51%) | — |
| Stage IV | 25(5.1%) | — | 14(3.63%) | — |
| Unknown | 8(1.63%) | — | 5(1.3%) | — |
| **T stage** | | | | |
| T1 | 163(33.27%) | — | — | — |
| T2 | 263(53.67%) | — | — | — |
| T3 | 43(8.78%) | — | — | — |
| T4 | 18(3.67%) | — | — | — |
| Unknown | 3(0.61%) | — | — | — |
| **M stage** | | | | |
| M0 | 324(66.12%) | — | — | — |
| M1 | 24(4.9%) | — | — | — |
| Unknown | 142(28.98%) | — | — | — |
| **N stage** | | | | |
| N0 | 317(64.69%) | — | — | — |
| N1 | 92(18.78%) | — | — | — |
| N2 | 68(13.88%) | — | — | — |
| N3 | 2(0.41%) | — | — | — |
| Unknown | 11(2.24%) | — | — | — |

LUAD: Lung Adenocarcinoma

## Supplementary Table S3. Summary of apoptosis-related differentially expressed genes

| Genes | Normal mean | Tumor mean | logFC | FDR |
|---|---|---|---|---|
| ERBB2 | 53.95151 | 115.5234 | 1.09845 | 8.24E-12 |
| TOP2A | 4.100736 | 65.2725 | 3.992521 | 1.01E-32 |
| DCN | 263.5448 | 98.50812 | -1.41973 | 3.82E-22 |
| CASP6 | 21.29729 | 42.91521 | 1.010819 | 1.13E-23 |
| BRCA1 | 2.243802 | 6.602468 | 1.55706 | 3.15E-16 |
| PAK1 | 19.37819 | 45.42825 | 1.229156 | 8.33E-27 |
| GSR | 62.57321 | 130.0547 | 1.055502 | 1.76E-07 |
| FEZ1 | 16.18518 | 3.800841 | -2.09028 | 1.41E-31 |
| CCND2 | 43.69996 | 20.0543 | -1.12372 | 9.79E-23 |
| EMP1 | 187.8912 | 58.30875 | -1.68811 | 3.39E-18 |
| H1-0 | 194.3844 | 455.7345 | 1.229281 | 6.43E-21 |
| IL6 | 90.02395 | 12.87702 | -2.80551 | 2.40E-14 |
| JUN | 404.5419 | 196.337 | -1.04296 | 9.07E-14 |
| BMP2 | 74.08091 | 22.55298 | -1.71578 | 2.29E-23 |
| SMAD7 | 53.89011 | 25.83579 | -1.06065 | 6.90E-22 |
| NEDD9 | 135.5231 | 47.35134 | -1.51706 | 1.94E-24 |
| F2 | 0.014541 | 2.342485 | 7.331734 | 1.08E-08 |
| CTH | 4.491548 | 10.27525 | 1.193888 | 5.11E-13 |
| GPX3 | 977.0999 | 213.3145 | -2.19552 | 5.95E-31 |
| BIK | 6.323503 | 25.78731 | 2.027865 | 4.46E-20 |
| TGFBR3 | 35.20263 | 6.301537 | -2.48191 | 4.23E-31 |
| PMAIP1 | 9.753947 | 32.16271 | 1.721331 | 5.06E-12 |
| BCL2L10 | 0.101511 | 1.922282 | 4.24311 | 4.57E-21 |
| IER3 | 104.2548 | 209.0634 | 1.003827 | 1.75E-08 |
| CD69 | 28.71894 | 13.30273 | -1.11028 | 2.54E-14 |
| HMOX1 | 237.1725 | 85.0041 | -1.48033 | 2.58E-08 |
| DAP | 122.6047 | 252.4932 | 1.04223 | 9.07E-22 |
| PRF1 | 49.4246 | 20.57506 | -1.26433 | 1.19E-16 |
| CCNA1 | 4.1513 | 1.830098 | -1.18164 | 7.08E-09 |
| EGR3 | 19.82495 | 6.080861 | -1.70497 | 1.01E-11 |
| ATF3 | 147.5042 | 44.3293 | -1.73442 | 1.27E-15 |
| GADD45B | 295.7206 | 90.89111 | -1.70202 | 8.87E-19 |
| CAV1 | 1122.195 | 108.187 | -3.37473 | 1.86E-33 |
| TIMP3 | 29.2944 | 8.180837 | -1.8403 | 1.17E-23 |
| BTG2 | 431.0148 | 178.6295 | -1.27077 | 3.50E-18 |
| TIMP1 | 337.2161 | 1000.811 | 1.569425 | 1.22E-21 |
| BMF | 14.24 | 28.74405 | 1.013314 | 4.60E-12 |
| KRT18 | 341.9933 | 781.8987 | 1.193013 | 3.57E-16 |

## Supplementary Table S4. Summary of ferroptosis-related differentially expressed genes

| Genes | Normal mean | Tumor mean | logFC | FDR |
|---|---|---|---|---|
| GOT1 | 38.15677 | 77.73569 | 1.026638 | 5.47E-16 |
| G6PD | 61.07184 | 160.4975 | 1.393972 | 0.001302 |
| GCLC | 9.032639 | 45.41128 | 2.329831 | 5.61E-11 |
| NQO1 | 36.12424 | 301.9941 | 3.063481 | 1.21E-21 |
| FANCD2 | 2.065724 | 6.343254 | 1.618576 | 7.09E-28 |
| CRYAB | 43.11565 | 11.48605 | -1.90833 | 5.70E-28 |
| ALOX15 | 33.00706 | 7.94942 | -2.05385 | 5.32E-13 |
| DPP4 | 35.54338 | 91.14569 | 1.358594 | 0.00305 |
| HMOX1 | 237.1725 | 85.0041 | -1.48033 | 2.02E-08 |
| GCLM | 15.61372 | 33.44879 | 1.09914 | 6.63E-07 |
| ZEB1 | 22.1229 | 9.016497 | -1.2949 | 1.26E-22 |
| NOX1 | 0.971572 | 2.753516 | 1.502881 | 2.31E-15 |
| SLC7A11 | 1.732222 | 15.42726 | 3.154786 | 7.39E-17 |
| ALOX5 | 148.4852 | 44.46523 | -1.73957 | 5.70E-28 |
| CBS | 0.217825 | 0.566942 | 1.38003 | 0.001302 |

## Supplementary Table S5. Summary of autophagy-related differentially expressed genes

| Genes | Normal mean | Tumor mean | logFC | FDR |
|---|---|---|---|---|
| ERBB2 | 53.95151 | 115.5234 | 1.09845 | 1.02E-11 |
| ITGB4 | 36.24137 | 117.294 | 1.69442 | 9.64E-10 |
| PTK6 | 9.83288 | 32.77381 | 1.736858 | 1.48E-14 |
| PARP1 | 44.00246 | 89.43756 | 1.023297 | 9.86E-22 |
| P4HB | 356.6344 | 790.1354 | 1.147654 | 1.11E-26 |
| DRAM1 | 226.9468 | 112.6859 | -1.01005 | 1.97E-19 |
| ATIC | 33.51486 | 81.9049 | 1.289149 | 5.71E-29 |
| BNIP3 | 23.99594 | 54.96109 | 1.19562 | 4.69E-16 |
| TMEM74 | 0.12045 | 0.63766 | 2.404354 | 0.000189 |
| GAPDH | 698.9194 | 2370.165 | 1.76179 | 3.21E-27 |
| CDKN2A | 1.612464 | 19.09732 | 3.566031 | 9.02E-13 |
| NLRC4 | 15.4004 | 3.922144 | -1.97325 | 4.52E-31 |
| GRID1 | 2.475573 | 0.964091 | -1.36052 | 1.90E-22 |
| NRG3 | 1.304533 | 0.240737 | -2.438 | 7.72E-28 |
| NRG1 | 3.313373 | 1.234046 | -1.4249 | 1.14E-24 |
| DAPK2 | 17.94294 | 4.777742 | -1.90902 | 8.40E-29 |
| DLC1 | 108.9355 | 23.80691 | -2.19402 | 8.42E-29 |
| IFNG | 1.069693 | 2.512608 | 1.231989 | 0.02111 |
| IKBKE | 7.507105 | 17.43193 | 1.215404 | 1.97E-23 |
| FOS | 1019.161 | 323.7209 | -1.65456 | 1.02E-13 |
| BIRC5 | 2.568249 | 35.12886 | 3.7738 | 2.09E-30 |
| EIF4EBP1 | 42.02699 | 131.569 | 1.646431 | 1.92E-16 |
| DAPK1 | 69.01759 | 33.90928 | -1.02528 | 7.44E-20 |
| PRKCQ | 13.95012 | 4.852202 | -1.52357 | 1.02E-26 |
| PPP1R15A | 307.433 | 87.01793 | -1.82089 | 3.98E-26 |
| MAP1LC3C | 15.95419 | 6.511978 | -1.29277 | 6.15E-18 |
| ATG9B | 0.98434 | 3.64945 | 1.89045 | 8.46E-10 |
| CCL2 | 195.8406 | 73.54487 | -1.41298 | 1.99E-07 |
| HSPB8 | 114.4183 | 30.23852 | -1.91986 | 1.75E-30 |

## Supplementary Table S6. Summary of the differentially expressed genes between high and low programmed cell death score group

| Genes | low-score Mean | high-score Mean | logFC | FDR |
|---|---|---|---|---|
| AC007906.2 | 30.12636 | 12.97571 | -1.21521 | 8.93E-05 |
| AC236972.3 | 2.988329 | 0.803269 | -1.89538 | 4.81E-20 |
| FIBCD1 | 1.653714 | 3.712865 | 1.166823 | 0.015642 |
| BAIAP2L2 | 6.236154 | 12.80714 | 1.038219 | 5.19E-05 |
| TTC29 | 1.714596 | 0.771667 | -1.15182 | 3.69E-06 |
| CFAP43 | 4.278484 | 2.066878 | -1.04965 | 0.000314 |
| AC068228.2 | 0.697439 | 1.587665 | 1.186767 | 1.48E-13 |
| DNMT3B | 3.215286 | 7.063384 | 1.135412 | 2.27E-12 |
| RGS20 | 1.032654 | 2.790593 | 1.434215 | 9.31E-07 |
| AC129926.1 | 0.979258 | 2.071938 | 1.08122 | 0.000114 |
| ZBTB16 | 4.368185 | 1.775123 | -1.29912 | 3.99E-16 |
| TREML3P | 1.158166 | 3.986908 | 1.783428 | 5.75E-06 |
| HLF | 14.9668 | 6.789203 | -1.14045 | 7.05E-17 |
| SLC25A47P1 | 1.689881 | 0.579889 | -1.54307 | 0.009695 |
| SHOX2 | 0.874055 | 2.612878 | 1.579844 | 3.99E-08 |
| DEPDC1B | 4.134563 | 9.151023 | 1.146198 | 1.43E-22 |
| TOP2A | 39.9043 | 85.07975 | 1.092272 | 2.51E-21 |
| CPA6 | 2.575996 | 1.127669 | -1.19179 | 0.015249 |
| CDIPTOSP | 1.481906 | 3.173093 | 1.098436 | 0.001599 |
| DES | 22.56672 | 9.036754 | -1.32032 | 1.51E-12 |
| ARTN | 1.585843 | 4.659709 | 1.55499 | 4.73E-11 |
| PRC1 | 12.53121 | 26.58317 | 1.084987 | 6.71E-27 |
| MGAT5B | 0.505842 | 1.686995 | 1.737696 | 0.000392 |
| CFAP65 | 1.721047 | 0.724446 | -1.24834 | 3.64E-05 |
| PLA2G12B | 14.32034 | 5.634392 | -1.34573 | 1.16E-11 |
| ITGB4 | 72.41687 | 151.7571 | 1.067366 | 7.27E-12 |
| GSTM5 | 2.27234 | 1.134189 | -1.00252 | 1.27E-13 |
| SFTA1P | 122.4424 | 45.66703 | -1.42288 | 1.00E-16 |
| H19 | 76.39964 | 200.4182 | 1.391376 | 0.004911 |
| AC022497.1 | 2.616323 | 1.232791 | -1.08561 | 1.55E-16 |
| SPAG8 | 3.329638 | 1.635674 | -1.02548 | 1.41E-10 |
| GAS2L2 | 4.079846 | 1.846779 | -1.1435 | 1.02E-06 |
| ORM2 | 35.10887 | 15.26698 | -1.20142 | 3.12E-06 |
| FXYD1 | 1.585334 | 0.723727 | -1.13127 | 3.14E-18 |
| MYBL2 | 35.43737 | 87.06983 | 1.296901 | 1.41E-23 |
| TK1 | 61.72472 | 144.8021 | 1.230162 | 3.90E-30 |
| UCK2 | 8.552243 | 19.39536 | 1.181337 | 3.64E-23 |

| | | | | |
|---|---|---|---|---|
| CRYBG2 | 2.608949 | 6.251079 | 1.260637 | 8.26E-11 |
| RN7SL648P | 3.489332 | 0.672245 | -2.37589 | 0.000606 |
| IGKV1OR9-2 | 2.15733 | 1.043328 | -1.04805 | 0.000243 |
| CCNE1 | 7.248255 | 16.25769 | 1.165416 | 2.16E-20 |
| SH3PXD2A-AS1 | 0.79989 | 2.086548 | 1.383245 | 8.63E-07 |
| APCDD1L | 1.066277 | 2.751211 | 1.367485 | 1.55E-09 |
| MIR23A | 5.074661 | 2.395571 | -1.08294 | 1.26E-05 |
| HSPE1P18 | 1.915817 | 0.911041 | -1.07237 | 9.49E-10 |
| RNU5F-1 | 4.075511 | 1.950715 | -1.06298 | 0.042897 |
| CDA | 27.90977 | 79.07832 | 1.502512 | 1.52E-05 |
| TEKT1 | 5.897679 | 2.388904 | -1.3038 | 4.41E-06 |
| PCLAF | 9.891808 | 19.98711 | 1.014764 | 3.39E-22 |
| CGB5 | 0.543925 | 9.208571 | 4.081498 | 0.028367 |
| FOSB | 86.79436 | 35.10427 | -1.30595 | 7.26E-07 |
| IGF2BP2 | 11.06882 | 26.68657 | 1.269613 | 3.75E-14 |
| LINC02253 | 1.047977 | 2.753285 | 1.393547 | 0.001521 |
| CFAP57 | 3.718481 | 1.822314 | -1.02894 | 1.93E-08 |
| CCDC17 | 8.196631 | 4.005914 | -1.0329 | 0.010444 |
| AL669830.1 | 1.91248 | 0.804471 | -1.24933 | 5.52E-07 |
| TCF21 | 7.310376 | 2.58669 | -1.49884 | 1.48E-17 |
| TROAP | 6.73147 | 16.15115 | 1.262644 | 4.65E-25 |
| EDNRB | 14.63079 | 7.073188 | -1.04858 | 2.52E-15 |
| ARHGAP11A | 6.059427 | 12.28199 | 1.019291 | 2.48E-21 |
| FLNC | 6.422032 | 13.97251 | 1.12149 | 0.000935 |
| APOBEC4 | 1.738179 | 0.762769 | -1.18826 | 8.11E-06 |
| MIR3677 | 7.390399 | 3.663046 | -1.01261 | 1.55E-07 |
| PSCA | 34.69956 | 119.5963 | 1.785184 | 0.000284 |
| TRIM15 | 0.882881 | 3.281302 | 1.893977 | 2.76E-06 |
| RETN | 17.61821 | 8.439004 | -1.06192 | 0.003059 |
| CHIAP2 | 2.889467 | 0.943572 | -1.6146 | 1.14E-13 |
| MPHOSPH6P1 | 1.670062 | 0.48261 | -1.79097 | 7.14E-05 |
| RPL26P30 | 4.600689 | 2.045636 | -1.1693 | 3.03E-12 |
| CYP4F3 | 2.650463 | 11.07885 | 2.063492 | 0.020737 |
| IGHV3OR16-6 | 6.255745 | 2.710218 | -1.20677 | 1.69E-05 |
| PTPRN | 0.715808 | 3.622954 | 2.339522 | 1.80E-12 |
| PHACTR1 | 6.147647 | 2.856115 | -1.10598 | 2.72E-23 |
| CRHR2 | 1.724196 | 0.440842 | -1.96759 | 6.20E-05 |
| TPPP3 | 80.77486 | 38.25354 | -1.07831 | 2.67E-09 |
| S100A8 | 76.46546 | 287.3451 | 1.909904 | 0.024047 |
| POPDC3 | 1.798022 | 5.6012 | 1.639325 | 0.000633 |
| TNFSF11 | 1.986297 | 4.07951 | 1.038314 | 0.01761 |
| IGHV4OR15-8 | 1.998383 | 0.996021 | -1.00459 | 0.000229 |
| LINC01765 | 2.626285 | 1.168136 | -1.16881 | 2.39E-06 |

| | | | | |
|---|---|---|---|---|
| TNFRSF13B | 2.163363 | 0.840929 | -1.36322 | 1.43E-13 |
| KIF18B | 5.314455 | 13.28243 | 1.321525 | 3.60E-26 |
| AC103702.2 | 1.80325 | 3.79161 | 1.072211 | 0.004318 |
| SCN4B | 5.236412 | 2.178629 | -1.26516 | 1.60E-17 |
| MIR4538 | 6.88791 | 3.361993 | -1.03475 | 1.70E-05 |
| CSAG1 | 5.744902 | 17.39133 | 1.598014 | 0.008919 |
| C1orf194 | 9.692791 | 4.826487 | -1.00594 | 0.000116 |
| IGKV6-21 | 88.75929 | 38.32328 | -1.21168 | 9.09E-07 |
| SKA1 | 3.91702 | 9.176958 | 1.228259 | 7.91E-26 |
| IGHV2-70D | 88.58826 | 38.52276 | -1.2014 | 0.024389 |
| IGKV1OR1-1 | 1.772891 | 0.625026 | -1.50412 | 0.00127 |
| C9orf24 | 12.8718 | 5.261546 | -1.29065 | 2.89E-06 |
| PI16 | 2.346319 | 0.926574 | -1.34042 | 1.82E-08 |
| ANKRD29 | 12.53812 | 5.649658 | -1.15009 | 3.80E-17 |
| HIGD1B | 13.79066 | 6.859333 | -1.00755 | 3.43E-15 |
| ROBO2 | 2.300689 | 0.954542 | -1.26919 | 1.51E-13 |
| KRT16 | 7.760017 | 32.18923 | 2.052446 | 2.56E-12 |
| SLC14A2 | 6.669537 | 2.393531 | -1.47845 | 2.48E-13 |
| FCER2 | 2.601987 | 0.82178 | -1.66279 | 2.75E-11 |
| NKAIN4 | 1.13353 | 2.465497 | 1.121056 | 0.000378 |
| AFP | 0.107698 | 8.819827 | 6.355688 | 0.012536 |
| AHNAK2 | 11.64323 | 25.62108 | 1.13784 | 3.04E-11 |
| TTK | 4.502476 | 10.62881 | 1.239189 | 2.69E-23 |
| AC246787.2 | 1.467835 | 0.686687 | -1.09597 | 1.27E-06 |
| IGFBP1 | 0.791899 | 13.60015 | 4.102162 | 0.003263 |
| PADI1 | 1.078794 | 5.444916 | 2.335491 | 1.75E-09 |
| AQP4 | 66.74322 | 29.27621 | -1.18889 | 2.10E-11 |
| IFNWP19 | 0.942558 | 2.471857 | 1.390943 | 1.80E-05 |
| CDKN3 | 10.04808 | 22.05759 | 1.134355 | 3.45E-22 |
| HTR3A | 6.061837 | 14.48517 | 1.25675 | 0.007187 |
| ITLN1 | 167.7119 | 3.54727 | -5.56313 | 4.98E-05 |
| STAC2 | 3.81538 | 1.40893 | -1.43723 | 0.017318 |
| EFCAB1 | 3.525138 | 1.610729 | -1.12997 | 4.41E-06 |
| CASC19 | 0.844756 | 2.410954 | 1.512998 | 3.50E-05 |
| TRNP1 | 27.36431 | 58.57509 | 1.097992 | 4.45E-05 |
| NKAIN1 | 0.612337 | 1.947271 | 1.669055 | 9.27E-09 |
| PIH1D3 | 1.579204 | 0.663485 | -1.25106 | 4.31E-06 |
| AC027277.2 | 1.872859 | 0.91098 | -1.03975 | 2.20E-08 |
| PRG4 | 34.90683 | 3.149471 | -3.47033 | 4.18E-13 |
| BUB1 | 8.335733 | 18.02637 | 1.112728 | 3.18E-22 |
| FOLR1 | 448.5498 | 204.596 | -1.13249 | 9.64E-11 |
| TM4SF5 | 4.998029 | 15.4202 | 1.62539 | 0.022763 |
| SLC5A9 | 2.301278 | 1.088279 | -1.08039 | 1.04E-09 |
| MACROD2 | 9.746607 | 3.868912 | -1.33297 | 1.18E-09 |

| | | | | |
|---|---|---|---|---|
| DLEC1 | 3.698797 | 1.498455 | -1.30358 | 1.14E-11 |
| ANXA13 | 0.441931 | 2.681786 | 2.601302 | 0.002791 |
| MMP10 | 7.421345 | 24.37647 | 1.715737 | 0.002025 |
| MIR34C | 3.603008 | 1.457867 | -1.30534 | 2.88E-06 |
| AL021068.1 | 6.791314 | 2.832441 | -1.26165 | 0.003857 |
| THBS4 | 23.0245 | 10.62241 | -1.11606 | 9.77E-10 |
| CAPSL | 8.649137 | 4.259327 | -1.02193 | 0.000166 |
| GREB1L | 0.939555 | 2.128337 | 1.179677 | 9.19E-09 |
| STC2 | 6.901857 | 13.96339 | 1.016593 | 1.88E-07 |
| CA4 | 5.06724 | 1.598374 | -1.6646 | 5.92E-08 |
| SCGB3A2 | 1951.12 | 427.2166 | -2.19126 | 2.22E-16 |
| C15orf48 | 89.92472 | 184.8363 | 1.039459 | 3.04E-11 |
| MIR3671 | 4.780331 | 2.25655 | -1.08299 | 2.41E-09 |
| AC104971.3 | 1.499237 | 0.69236 | -1.11464 | 2.08E-10 |
| IL11 | 1.442437 | 2.912702 | 1.01385 | 1.05E-07 |
| WFDC12 | 19.69248 | 0.585601 | -5.07158 | 2.51E-09 |
| FMO2 | 23.60541 | 10.85311 | -1.12101 | 1.79E-19 |
| CTSG | 4.850927 | 1.903933 | -1.34928 | 3.69E-11 |
| Z83843.1 | 7.51216 | 3.755723 | -1.00014 | 1.44E-06 |
| SCGB3A1 | 2557.132 | 769.504 | -1.73253 | 3.00E-14 |
| KIAA0319 | 2.160721 | 5.061114 | 1.227942 | 0.030399 |
| MTFR2 | 3.326541 | 6.960417 | 1.065151 | 1.24E-21 |
| SCARNA5 | 85.13579 | 9.544475 | -3.15703 | 0.049513 |
| SNORD116-24 | 2.79338 | 1.37989 | -1.01746 | 0.000299 |
| STRA6 | 4.496364 | 9.209055 | 1.034294 | 1.66E-06 |
| RSPH4A | 7.249027 | 3.36722 | -1.10623 | 3.74E-05 |
| RASGRP2 | 5.656198 | 2.699945 | -1.0669 | 9.34E-16 |
| COL7A1 | 4.650821 | 11.77914 | 1.340677 | 1.53E-09 |
| CENPA | 6.000288 | 14.89877 | 1.31209 | 1.08E-26 |
| CDCA5 | 11.2016 | 27.24757 | 1.282423 | 6.87E-27 |
| ARC | 1.949004 | 0.863029 | -1.17526 | 9.24E-09 |
| GFRA1 | 3.233558 | 0.836257 | -1.9511 | 6.51E-25 |
| KCNS1 | 1.884153 | 0.828778 | -1.18486 | 0.007851 |
| AMPD1 | 2.183238 | 0.879658 | -1.31146 | 1.16E-14 |
| LRRC66 | 0.719756 | 1.710371 | 1.248729 | 0.003266 |
| KIF4A | 8.143422 | 20.5444 | 1.335038 | 1.02E-25 |
| IL1R2 | 3.15886 | 8.28692 | 1.391432 | 2.05E-10 |
| FDCSP | 42.49761 | 13.82022 | -1.6206 | 3.04E-08 |
| CXCL5 | 12.73213 | 39.0568 | 1.6171 | 0.001438 |
| LY6G6C | 0.643231 | 1.558752 | 1.276983 | 0.013631 |
| SLC22A3 | 46.33869 | 20.79375 | -1.15607 | 7.73E-16 |
| FAM107A | 10.5804 | 4.220254 | -1.32599 | 1.55E-16 |
| DKK1 | 9.44023 | 39.10557 | 2.05048 | 2.62E-07 |
| INSL4 | 3.607552 | 11.75722 | 1.704455 | 0.006694 |

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| AC087284.1 | 1.550259 | 0.699997 | -1.14709 | 0.041452 |
| MIR30C2 | 1.959062 | 0.848922 | -1.20646 | 2.16E-07 |
| TMEM171 | 2.08031 | 4.630449 | 1.154354 | 1.16E-09 |
| POLQ | 1.470513 | 2.976885 | 1.017484 | 1.14E-16 |
| ASPG | 3.008547 | 1.438357 | -1.06465 | 0.000148 |
| LRRC71 | 2.408686 | 1.007231 | -1.25785 | 3.79E-06 |
| C1orf189 | 6.317447 | 2.932604 | -1.10716 | 6.09E-06 |
| GPR35 | 3.868679 | 7.978854 | 1.044341 | 3.20E-05 |
| APOBEC1 | 1.273664 | 4.506521 | 1.82303 | 7.40E-05 |
| AC058791.1 | 2.556921 | 0.739112 | -1.79054 | 0.004598 |
| CD19 | 8.19762 | 3.824387 | -1.09998 | 4.48E-08 |
| NDC80 | 7.02227 | 15.04186 | 1.098974 | 6.41E-24 |
| GTSE1 | 5.068777 | 11.8272 | 1.222399 | 5.97E-26 |
| MIR6071 | 4.890858 | 2.384859 | -1.03618 | 2.06E-09 |
| NCAPG | 5.990511 | 14.15094 | 1.240147 | 5.38E-24 |
| COL6A6 | 4.159034 | 1.483324 | -1.48741 | 1.82E-18 |
| EFNA2 | 0.814426 | 2.106989 | 1.371328 | 2.75E-05 |
| ATP13A4 | 29.63738 | 13.87364 | -1.09507 | 3.06E-11 |
| AURKB | 11.60939 | 28.489 | 1.295113 | 2.30E-26 |
| AC012651.1 | 2.75744 | 1.204486 | -1.19491 | 3.10E-12 |
| CKAP2L | 4.238616 | 9.198066 | 1.117737 | 6.04E-23 |
| STAP1 | 4.599645 | 2.29762 | -1.00138 | 8.50E-14 |
| LRRN3 | 2.657863 | 1.105656 | -1.26536 | 9.66E-20 |
| MAP3K19 | 1.556502 | 0.66554 | -1.22571 | 3.39E-06 |
| GJB4 | 0.612412 | 1.950086 | 1.670962 | 0.00057 |
| FAM83D | 12.60798 | 26.16224 | 1.053149 | 3.19E-20 |
| PTPRH | 6.92544 | 16.91022 | 1.287918 | 8.87E-15 |
| DNAI1 | 3.556103 | 1.528767 | -1.21793 | 0.000173 |
| AC015722.2 | 2.490173 | 0.958831 | -1.3769 | 0.000227 |
| ABCC2 | 3.021011 | 18.72988 | 2.632239 | 0.003015 |
| ESPL1 | 3.367961 | 7.881438 | 1.226583 | 2.69E-22 |
| KLK6 | 5.500987 | 24.20301 | 2.137424 | 1.59E-06 |
| BCL2L1-AS1 | 2.647571 | 0.97663 | -1.43878 | 9.31E-05 |
| PGM5P4 | 1.761511 | 0.773066 | -1.18815 | 2.17E-14 |
| S100A2 | 51.77986 | 136.8976 | 1.402634 | 0.004284 |
| FAM216B | 9.195493 | 3.377172 | -1.44511 | 9.69E-10 |
| NTSR1 | 0.305978 | 3.580902 | 3.548821 | 0.008779 |
| IL5RA | 1.544857 | 0.629318 | -1.29561 | 1.21E-13 |
| ZBBX | 2.463385 | 1.062744 | -1.21285 | 8.12E-06 |
| ELOVL3 | 1.53711 | 3.430208 | 1.158075 | 0.049192 |
| AL138499.1 | 1.999478 | 0.940553 | -1.08804 | 0.044406 |
| FHL5 | 4.895574 | 2.16202 | -1.1791 | 7.87E-18 |
| ANKRD44-AS1 | 8.329505 | 3.489564 | -1.25518 | 4.51E-11 |
| SPAG5 | 12.2543 | 25.73343 | 1.070356 | 4.40E-23 |

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| GPR18 | 3.070492 | 1.512887 | -1.02117 | 2.41E-08 |
| MS4A2 | 4.936059 | 2.144312 | -1.20284 | 1.76E-13 |
| IGLV5-48 | 7.574431 | 3.264757 | -1.21416 | 1.19E-05 |
| CNIH3-AS2 | 0.912006 | 1.913054 | 1.068763 | 0.029947 |
| MAGEA3 | 9.16992 | 27.04681 | 1.560477 | 7.94E-06 |
| AL513282.1 | 4.731685 | 2.094711 | -1.1756 | 0.000532 |
| LINC01833 | 0.901789 | 1.880923 | 1.060579 | 8.84E-07 |
| IRX1 | 6.087175 | 2.674642 | -1.18643 | 1.28E-10 |
| SP8 | 1.389935 | 2.903688 | 1.062869 | 1.67E-06 |
| IL20RB | 7.063219 | 16.4367 | 1.218523 | 0.000242 |
| PLEKHG6 | 7.084132 | 14.25583 | 1.008889 | 3.16E-17 |
| AC067747.1 | 1.765013 | 0.66425 | -1.40988 | 5.87E-12 |
| TMEM190 | 13.91251 | 6.867461 | -1.01853 | 0.003997 |
| C11orf97 | 3.32745 | 1.404493 | -1.24437 | 0.000362 |
| INHA | 12.09432 | 26.25624 | 1.118331 | 0.006821 |
| INA | 2.211207 | 5.730598 | 1.373852 | 0.000612 |
| HOPX | 221.5441 | 88.39565 | -1.32555 | 4.24E-13 |
| AL645608.3 | 0.50077 | 1.54433 | 1.62476 | 0.030232 |
| RAD51 | 4.731708 | 9.797041 | 1.049985 | 9.32E-24 |
| HMGA1 | 209.2417 | 527.5828 | 1.334227 | 4.42E-28 |
| KHDC1L | 0.666902 | 3.159983 | 2.244369 | 0.00025 |
| IGKV1D-16 | 89.76309 | 21.07151 | -2.09083 | 8.99E-06 |
| DNAI2 | 3.757248 | 1.417771 | -1.40605 | 1.84E-07 |
| AC124947.2 | 1.027433 | 2.115352 | 1.041854 | 2.98E-05 |
| SEC14L6 | 9.191245 | 4.334795 | -1.0843 | 5.45E-10 |
| CCL19 | 138.0797 | 68.35503 | -1.01438 | 3.69E-09 |
| SYBU | 19.83282 | 9.595188 | -1.04751 | 1.25E-05 |
| CASC15 | 1.58416 | 3.344878 | 1.078235 | 0.012706 |
| AC004386.7 | 3.978933 | 1.122876 | -1.82518 | 0.017982 |
| PLA2G4F | 11.3902 | 5.08515 | -1.16343 | 2.52E-14 |
| STX1A | 10.01212 | 20.29665 | 1.019494 | 6.58E-16 |
| LRRK2 | 36.09215 | 14.90763 | -1.27563 | 5.09E-17 |
| KLF15 | 13.27184 | 5.847137 | -1.18257 | 1.01E-16 |
| AC079467.1 | 6.201592 | 2.135398 | -1.53813 | 3.83E-12 |
| ZNF385B | 15.92181 | 4.474094 | -1.83134 | 7.94E-15 |
| LINC00460 | 3.811908 | 11.11602 | 1.544054 | 0.008181 |
| MYEOV | 8.353801 | 25.22542 | 1.594373 | 1.70E-11 |
| SFTPB | 10023.09 | 4414.772 | -1.18292 | 2.15E-15 |
| C11orf88 | 3.050264 | 1.285605 | -1.24649 | 5.25E-06 |
| ANLN | 13.51855 | 37.54167 | 1.473552 | 1.64E-27 |
| IGKV2-26 | 4.769236 | 1.750051 | -1.44636 | 2.29E-07 |
| AQP7 | 4.633278 | 2.315525 | -1.00069 | 9.22E-09 |
| TCN1 | 26.57086 | 84.78464 | 1.673958 | 0.000133 |
| GCLC | 25.02763 | 61.33093 | 1.293093 | 1.52E-07 |

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|---|---|---|---|---|
| CCNA2 | 15.03843 | 32.37974 | 1.106438 | 2.72E-23 |
| NNAT | 28.74679 | 4.530809 | -2.66556 | 0.004136 |
| PTCHD4 | 1.857482 | 0.876254 | -1.08393 | 2.54E-10 |
| RIC3 | 2.07471 | 0.841488 | -1.30189 | 1.25E-17 |
| PIMREG | 4.864509 | 10.53031 | 1.114181 | 2.89E-25 |
| FAM72B | 0.689169 | 1.626546 | 1.238882 | 1.95E-21 |
| RNU6-247P | 5.077192 | 1.80911 | -1.48875 | 7.05E-05 |
| PCSK2 | 72.71552 | 12.86856 | -2.49841 | 1.09E-09 |
| RNU1-38P | 1.937669 | 0.427768 | -2.17942 | 1.05E-12 |
| TCTE1 | 1.599449 | 0.677196 | -1.23993 | 0.000312 |
| OMG | 4.560437 | 2.108911 | -1.11267 | 7.24E-12 |
| C5orf49 | 10.54425 | 5.176001 | -1.02655 | 1.05E-09 |
| PCDH7 | 5.044954 | 10.32613 | 1.033387 | 1.96E-05 |
| EXO1 | 4.408636 | 10.70555 | 1.279955 | 2.18E-24 |
| VWA3B | 2.431903 | 1.187013 | -1.03475 | 7.23E-05 |
| AC103563.1 | 16.306 | 7.945543 | -1.03718 | 0.000303 |
| LYPD3 | 9.610043 | 38.18704 | 1.990468 | 3.03E-14 |
| AC009093.3 | 2.302519 | 0.975824 | -1.23852 | 1.93E-10 |
| BTBD16 | 0.772087 | 1.992252 | 1.367565 | 0.014059 |
| KCNJ8 | 25.31688 | 12.61429 | -1.00504 | 1.52E-06 |
| CEP55 | 13.49616 | 32.1095 | 1.250451 | 1.84E-26 |
| TRAJ3 | 2.582756 | 1.250966 | -1.04587 | 0.000134 |
| CDHR3 | 8.327333 | 4.100875 | -1.02192 | 8.07E-09 |
| C6 | 3.556897 | 1.658739 | -1.10053 | 1.21E-10 |
| AC002563.1 | 3.10904 | 1.198206 | -1.37559 | 3.40E-11 |
| CDC45 | 7.269618 | 17.10243 | 1.23425 | 5.82E-25 |
| PTGFR | 3.357103 | 1.507035 | -1.1555 | 4.53E-07 |
| ARHGEF2-AS1 | 3.545883 | 1.554184 | -1.18999 | 4.24E-09 |
| SLC5A5 | 2.096818 | 6.878094 | 1.713807 | 0.023878 |
| STEAP1B | 1.571113 | 3.310429 | 1.075232 | 0.000412 |
| FHOD3 | 2.064397 | 4.717143 | 1.192193 | 0.000474 |
| ABCA8 | 4.338758 | 1.282303 | -1.75854 | 5.50E-25 |
| PRAC2 | 0.572888 | 1.553326 | 1.439035 | 0.001634 |
| FABP4 | 17.5606 | 7.649511 | -1.1989 | 1.29E-08 |
| CD1B | 3.911625 | 1.857832 | -1.07415 | 1.70E-11 |
| AC013275.1 | 3.557875 | 1.597166 | -1.1555 | 4.37E-11 |
| MAGEA6 | 7.394468 | 20.38867 | 1.463249 | 4.72E-05 |
| GAPDH | 1512.412 | 3088.372 | 1.029995 | 6.24E-36 |
| GJB3 | 6.472019 | 25.79795 | 1.994969 | 7.77E-13 |
| TFAP2A | 3.98398 | 9.255316 | 1.216072 | 1.27E-13 |
| WFDC5 | 21.27598 | 0.716345 | -4.89243 | 0.000264 |
| SUSD2 | 178.3392 | 66.82972 | -1.41606 | 3.80E-16 |
| LINC00942 | 4.96799 | 18.14826 | 1.869097 | 1.09E-05 |
| SCN7A | 9.978635 | 3.871964 | -1.36578 | 6.20E-22 |

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| SCGB2A1 | 30.02677 | 11.76052 | -1.3523 | 0.000539 |
| RHPN2 | 16.84951 | 33.80533 | 1.004544 | 3.81E-16 |
| S100A7 | 3.142628 | 36.6529 | 3.543884 | 2.18E-05 |
| ALDH3B2 | 8.644416 | 17.95923 | 1.054885 | 2.06E-09 |
| AZU1 | 2.579978 | 0.83855 | -1.62139 | 3.53E-06 |
| GPIHBP1 | 9.003329 | 3.454299 | -1.38207 | 6.56E-11 |
| MMRN1 | 7.361767 | 3.513557 | -1.06712 | 1.09E-14 |
| GTF2IP7 | 0.668772 | 1.776353 | 1.409332 | 1.71E-14 |
| UHRF1 | 6.367517 | 13.65051 | 1.100152 | 2.30E-26 |
| MIR4539 | 7.599384 | 3.585417 | -1.08374 | 0.000104 |
| LINC01518 | 0.912574 | 1.933737 | 1.083378 | 5.13E-05 |
| C7 | 92.36984 | 26.97494 | -1.7758 | 1.72E-24 |
| CYP2B7P | 201.6554 | 77.09991 | -1.38709 | 4.67E-19 |
| RPL13AP17 | 2.61042 | 0.764761 | -1.7712 | 3.07E-15 |
| CLGN | 4.00066 | 10.28324 | 1.361985 | 0.004467 |
| KLK8 | 3.284944 | 7.181008 | 1.128318 | 0.003145 |
| MS4A1 | 15.17753 | 5.07532 | -1.58037 | 1.62E-12 |
| CACNA2D2 | 51.40856 | 17.15066 | -1.58374 | 6.48E-21 |
| TNS4 | 9.683906 | 38.13978 | 1.977636 | 4.27E-09 |
| ELANE | 2.526867 | 1.025809 | -1.30059 | 1.71E-09 |
| IGKV6D-21 | 26.90028 | 13.35546 | -1.01019 | 2.84E-05 |
| AL132989.2 | 1.5334 | 0.717436 | -1.09581 | 0.001881 |
| AC079949.2 | 0.843162 | 2.499101 | 1.567527 | 0.004209 |
| PLK1 | 10.79692 | 24.56853 | 1.186191 | 5.41E-27 |
| RGS22 | 1.45336 | 0.678194 | -1.09962 | 5.53E-12 |
| HLA-DRB5 | 1163.306 | 565.8174 | -1.03982 | 5.38E-13 |
| LINC00941 | 0.54758 | 3.005574 | 2.456499 | 7.14E-07 |
| C1orf61 | 0.554039 | 1.35783 | 1.293244 | 0.000615 |
| ANGPT1 | 7.292495 | 3.547506 | -1.03961 | 1.06E-15 |
| CLSPN | 3.13623 | 6.394618 | 1.027827 | 1.21E-16 |
| RRM2 | 20.88585 | 49.07925 | 1.232587 | 1.05E-26 |
| SBSPON | 4.51246 | 1.998715 | -1.17484 | 1.56E-09 |
| NPR1 | 12.23589 | 6.096184 | -1.00514 | 4.63E-11 |
| ECT2 | 20.03594 | 41.9233 | 1.065162 | 5.34E-21 |
| LPL | 59.36259 | 27.2577 | -1.12289 | 5.26E-13 |
| SLPI | 3320.351 | 1136.441 | -1.54681 | 7.09E-05 |
| MIR548V | 3.573166 | 0.881379 | -2.01937 | 0.000275 |
| AC005256.1 | 0.903559 | 2.15698 | 1.255322 | 0.000596 |
| SLC6A4 | 2.328926 | 0.75342 | -1.62814 | 3.44E-10 |
| CDC25A | 2.653962 | 5.951825 | 1.165184 | 1.62E-25 |
| MECOM-AS1 | 2.012927 | 0.720641 | -1.48194 | 8.43E-09 |
| CPA3 | 60.74258 | 29.9068 | -1.02223 | 1.05E-10 |
| DNAAF1 | 3.83722 | 1.496054 | -1.3589 | 7.68E-09 |
| ANKRD36BP2 | 3.681108 | 1.758762 | -1.06558 | 9.28E-07 |

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| KRT6B | 4.40418 | 9.348216 | 1.085817 | 1.06E-07 |
| PLPPR4 | 2.928026 | 1.428553 | -1.03537 | 1.22E-12 |
| SYNGR4 | 0.78586 | 1.705615 | 1.117948 | 3.80E-09 |
| RNF186 | 1.383367 | 3.838316 | 1.47229 | 0.012104 |
| AC010735.2 | 2.029601 | 4.063082 | 1.001378 | 0.000833 |
| SIGLEC17P | 2.317627 | 1.158528 | -1.00036 | 1.29E-12 |
| AL133466.1 | 3.091944 | 1.357833 | -1.18721 | 2.70E-12 |
| CD109 | 8.272416 | 17.85832 | 1.110216 | 1.57E-08 |
| FCRL1 | 2.396542 | 0.793728 | -1.59424 | 7.95E-15 |
| SNORA74B | 13.95959 | 1.580247 | -3.14303 | 0.001008 |
| MIR7152 | 1.563262 | 0.730983 | -1.09665 | 0.000217 |
| IGLV8-61 | 297.5654 | 147.21 | -1.01533 | 2.72E-05 |
| CFLAR-AS1 | 1.986482 | 0.95822 | -1.05179 | 0.000167 |
| CCL14 | 2.100492 | 0.7306 | -1.52357 | 8.08E-21 |
| AL138760.1 | 1.510911 | 3.091754 | 1.033007 | 0.005422 |
| SDCBP2 | 18.45532 | 39.07646 | 1.082263 | 2.15E-05 |
| FAM92B | 8.525472 | 3.533793 | -1.27056 | 6.97E-09 |
| IGHV1-45 | 37.0724 | 16.98088 | -1.12643 | 1.10E-06 |
| KCP | 0.931266 | 2.562473 | 1.460272 | 1.19E-13 |
| CLC | 3.329111 | 1.635605 | -1.02531 | 0.008416 |
| RNU1-67P | 2.69565 | 1.23713 | -1.12364 | 0.034781 |
| AC007878.1 | 2.755275 | 0.956385 | -1.52653 | 0.000756 |
| ACTL8 | 0.703859 | 2.160547 | 1.618038 | 0.000342 |
| OGN | 12.11652 | 3.208397 | -1.91705 | 3.46E-13 |
| TRAJ18 | 1.72017 | 0.770802 | -1.15812 | 5.06E-06 |
| VWA3A | 3.226235 | 1.155865 | -1.48088 | 8.73E-09 |
| HSD17B6 | 54.31985 | 15.38189 | -1.82025 | 9.05E-17 |
| DCDC2B | 2.263449 | 0.956988 | -1.24195 | 1.14E-07 |
| PLAU | 131.8054 | 269.8908 | 1.033967 | 1.09E-08 |
| AKR1C7P | 0.837668 | 1.753082 | 1.065444 | 0.033882 |
| IGLV3-13 | 3.086371 | 1.435865 | -1.10399 | 4.05E-07 |
| KRT20 | 5.886419 | 56.89398 | 3.272814 | 0.006449 |
| DLGAP5 | 8.635376 | 21.16025 | 1.293026 | 2.86E-24 |
| RN7SKP51 | 4.409141 | 2.116633 | -1.05873 | 2.40E-11 |
| AKAP14 | 2.825817 | 1.263757 | -1.16095 | 1.64E-06 |
| PVALB | 2.604741 | 0.968371 | -1.42751 | 1.12E-08 |
| LINC02657 | 1.367436 | 3.487041 | 1.35053 | 4.66E-12 |
| NPW | 6.06538 | 13.71 | 1.176559 | 3.10E-05 |
| CFAP221 | 7.562697 | 3.733609 | -1.01833 | 7.21E-15 |
| CTSV | 2.717283 | 10.11785 | 1.896666 | 2.30E-26 |
| ERVMER34-1 | 3.092294 | 6.349629 | 1.037995 | 1.54E-05 |
| AC112777.1 | 0.967611 | 1.969908 | 1.02563 | 2.07E-17 |
| C8orf34-AS1 | 16.44589 | 7.637198 | -1.10661 | 4.92E-13 |
| CD79B | 17.39882 | 8.608109 | -1.01522 | 7.57E-11 |

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| CASQ2 | 1.675261 | 0.713343 | -1.23172 | 5.80E-17 |
| MAGEC1 | 0.987806 | 3.134571 | 1.665969 | 0.000276 |
| ARL14 | 3.112236 | 13.34928 | 2.100738 | 8.15E-06 |
| FCRL3 | 2.980965 | 1.362084 | -1.12996 | 4.94E-08 |
| AC079384.1 | 6.020577 | 2.805232 | -1.10178 | 0.000162 |
| LANCL1-AS1 | 1.588105 | 0.579712 | -1.4539 | 1.01E-12 |
| AC061975.6 | 0.782165 | 1.597241 | 1.030037 | 0.000428 |
| LINC00973 | 2.081595 | 7.850736 | 1.915138 | 0.002523 |
| ARNTL2 | 8.817929 | 22.74132 | 1.366804 | 3.27E-15 |
| CASP14 | 0.338668 | 3.429273 | 3.33996 | 5.77E-05 |
| SFTPA2 | 6236.173 | 2422.303 | -1.36428 | 2.62E-12 |
| ITGA8 | 10.25252 | 5.01901 | -1.0305 | 2.02E-18 |
| SAPCD2 | 9.13326 | 18.8512 | 1.045454 | 5.75E-24 |
| AFF3 | 2.918417 | 1.2248 | -1.25264 | 4.17E-18 |
| AC007686.1 | 0.54675 | 1.611031 | 1.55903 | 0.046774 |
| GNG4 | 3.26055 | 10.53363 | 1.691816 | 1.05E-07 |
| VGF | 1.865943 | 12.52622 | 2.746974 | 1.06E-08 |
| LINC01843 | 1.904374 | 4.721051 | 1.309791 | 2.15E-06 |
| CENPF | 9.667578 | 20.299 | 1.070182 | 3.24E-19 |
| RNU6-341P | 3.192721 | 1.193135 | -1.42003 | 0.00251 |
| BCHE | 4.701629 | 2.218952 | -1.08328 | 1.75E-08 |
| CD22 | 7.640213 | 3.331577 | -1.19741 | 2.64E-13 |
| IGHD6-25 | 8.48835 | 3.77182 | -1.17022 | 0.000421 |
| NXPH4 | 5.102134 | 12.2441 | 1.262914 | 0.000548 |
| SCARNA7 | 34.79962 | 5.152097 | -2.75584 | 0.013457 |
| BTLA | 2.247892 | 1.10445 | -1.02524 | 3.25E-14 |
| PEBP4 | 97.85481 | 21.35947 | -2.19577 | 6.47E-16 |
| MFAP4 | 199.7363 | 85.95596 | -1.21643 | 2.31E-17 |
| LINC02577 | 1.732561 | 4.325026 | 1.319803 | 3.21E-10 |
| COL6A5 | 2.534687 | 1.024911 | -1.30631 | 2.11E-15 |
| AC016831.4 | 2.038439 | 0.39613 | -2.36342 | 0.001612 |
| AGER | 192.5813 | 56.07609 | -1.78001 | 1.17E-10 |
| GCNT3 | 16.78493 | 35.14947 | 1.066336 | 0.007471 |
| VEGFD | 12.55879 | 3.277373 | -1.93809 | 5.49E-20 |
| BLK | 3.690211 | 1.445201 | -1.35243 | 1.09E-11 |
| RPS29P11 | 38.48462 | 18.3434 | -1.06902 | 2.25E-11 |
| IGLV1-41 | 33.54742 | 14.71518 | -1.1889 | 0.000124 |
| TCL1A | 3.005503 | 1.449068 | -1.05248 | 3.96E-06 |
| SNRPGP4 | 2.507013 | 0.93648 | -1.42065 | 0.000153 |
| MS4A15 | 46.85656 | 23.14831 | -1.01734 | 7.55E-08 |
| KYNU | 3.639531 | 10.94937 | 1.589023 | 0.010631 |
| DLC1 | 34.2527 | 15.75763 | -1.12017 | 3.92E-20 |
| DNASE1L3 | 4.025935 | 1.504369 | -1.42016 | 1.14E-14 |
| CDK5R2 | 1.391096 | 3.006223 | 1.11173 | 2.14E-07 |

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| IGKV3OR2-5 | 1.886506 | 0.657554 | -1.52054 | 1.52E-06 |
| AL353662.1 | 2.230084 | 0.483289 | -2.20614 | 0.008077 |
| F2 | 0.174587 | 4.320315 | 4.62912 | 4.53E-08 |
| UPK1B | 7.676359 | 28.76747 | 1.905944 | 0.014008 |
| LINC02313 | 0.767503 | 2.314545 | 1.592485 | 7.85E-05 |
| ABCA6 | 2.041797 | 0.999385 | -1.03073 | 2.50E-19 |
| EPS8L3 | 2.988817 | 9.396566 | 1.652559 | 0.000416 |
| CYP2B6 | 2.399033 | 0.993093 | -1.27245 | 0.016053 |
| IGHJ3P | 72.55002 | 31.51723 | -1.20284 | 1.17E-06 |
| PKMYT1 | 4.980827 | 10.3048 | 1.048859 | 4.90E-26 |
| ADH1B | 40.878 | 9.286787 | -2.13807 | 3.38E-27 |
| CYP2F1 | 1.902998 | 0.731988 | -1.37838 | 1.15E-05 |
| LINC01629 | 0.53669 | 1.8016 | 1.747119 | 0.024624 |
| MAGEC2 | 3.508536 | 8.724139 | 1.314144 | 3.69E-05 |
| AC090181.3 | 2.82352 | 1.005224 | -1.48998 | 0.000253 |
| AP005262.1 | 0.623253 | 1.828242 | 1.552568 | 0.004672 |
| FKBP9P1 | 1.661677 | 3.706772 | 1.157523 | 0.000357 |
| CPB2 | 21.69587 | 4.336153 | -2.32293 | 6.34E-09 |
| LHFPL3-AS2 | 13.39634 | 5.103531 | -1.39227 | 2.05E-15 |
| IGLV7-43 | 131.5506 | 65.37405 | -1.00883 | 3.31E-07 |
| SULT2B1 | 9.166691 | 19.53749 | 1.091772 | 1.00E-09 |
| IGHV3-22 | 4.522247 | 1.911141 | -1.24261 | 3.45E-06 |
| AC005077.4 | 1.691246 | 6.010815 | 1.829474 | 1.77E-22 |
| AC114760.2 | 1.780972 | 0.692503 | -1.36277 | 1.54E-06 |
| MCM10 | 3.45869 | 7.756421 | 1.165165 | 5.37E-21 |
| MIR4537 | 7.018049 | 3.261708 | -1.10544 | 3.29E-06 |
| SLC15A1 | 1.516171 | 4.666468 | 1.621899 | 9.83E-05 |
| FOSL1 | 10.41274 | 33.457 | 1.683959 | 1.71E-13 |
| TIMM9P2 | 1.849411 | 0.576429 | -1.68185 | 0.030872 |
| SNORA80B | 7.712322 | 2.157832 | -1.83758 | 0.002082 |
| RHOF | 2.414089 | 4.972344 | 1.042447 | 1.80E-10 |
| SMIM24 | 2.643667 | 7.581899 | 1.520019 | 4.08E-05 |
| ORC1 | 4.591303 | 10.62481 | 1.210462 | 4.80E-24 |
| AC108215.1 | 4.858397 | 1.29413 | -1.9085 | 7.03E-14 |
| MIR553 | 2.864116 | 1.325388 | -1.11168 | 0.018335 |
| SYT13 | 5.850894 | 15.39997 | 1.396198 | 0.027161 |
| AL353804.2 | 1.653289 | 0.793127 | -1.05972 | 0.004134 |
| ANXA8 | 1.110327 | 2.634292 | 1.246431 | 0.04746 |
| AC012213.4 | 0.87165 | 2.464163 | 1.499276 | 3.56E-08 |
| CTSH | 443.8114 | 204.4459 | -1.11823 | 5.81E-14 |
| CLEC17A | 1.526672 | 0.690307 | -1.14508 | 1.04E-10 |
| IGHV3-16 | 1.710171 | 0.648645 | -1.39864 | 2.61E-06 |
| TRIM31 | 4.582804 | 14.27234 | 1.638919 | 0.002738 |
| JCHAIN | 1574.499 | 730.44 | -1.10806 | 1.12E-15 |

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|---|---|---|---|---|
| KRT6A | 49.21032 | 149.8072 | 1.606074 | 1.66E-08 |
| KRT83 | 0.729742 | 1.775345 | 1.282641 | 0.000293 |
| CFAP73 | 6.301577 | 3.017281 | -1.06246 | 0.000205 |
| FOXD1 | 0.88305 | 2.970325 | 1.750053 | 0.001975 |
| GPX3 | 305.1449 | 147.0045 | -1.05363 | 2.67E-13 |
| IGF2BP1 | 1.041387 | 5.690791 | 2.450123 | 4.09E-09 |
| AC011298.1 | 0.447398 | 1.859446 | 2.055241 | 0.004641 |
| AC115989.1 | 1.988744 | 0.682416 | -1.54314 | 1.17E-08 |
| CCDC60 | 1.580013 | 0.738063 | -1.09812 | 6.73E-08 |
| RN7SL8P | 5.888074 | 1.99409 | -1.56206 | 1.27E-12 |
| UCA1 | 3.545838 | 13.84773 | 1.965451 | 0.001079 |
| AC027288.3 | 3.140825 | 1.000236 | -1.6508 | 1.51E-11 |
| LINC02086 | 0.587549 | 1.330399 | 1.179079 | 0.00887 |
| KRT81 | 13.3187 | 66.06621 | 2.31046 | 5.97E-06 |
| SFTPC | 1914.133 | 327.0315 | -2.54919 | 8.50E-14 |
| PBK | 9.745494 | 19.59659 | 1.007796 | 1.55E-17 |
| BUB1B | 6.719478 | 15.71611 | 1.225823 | 1.65E-25 |
| AC010789.1 | 1.430613 | 3.904323 | 1.448439 | 4.41E-06 |
| GALNT14 | 9.65814 | 19.56613 | 1.018541 | 1.44E-08 |
| MIR421 | 3.173761 | 1.225618 | -1.37268 | 2.40E-06 |
| CDC6 | 8.229485 | 19.80915 | 1.267293 | 7.81E-26 |
| CADM3 | 4.288019 | 1.899102 | -1.17499 | 9.97E-12 |
| DUOXA1 | 18.56609 | 7.835841 | -1.24451 | 4.77E-12 |
| IGHV3-42 | 3.433947 | 1.591968 | -1.10906 | 7.45E-06 |
| DNAH9 | 2.043105 | 0.724313 | -1.49608 | 7.17E-08 |
| AL033397.2 | 1.856036 | 4.249282 | 1.194994 | 0.005307 |
| ALOX15 | 11.17049 | 4.624836 | -1.27222 | 2.23E-05 |
| AC007684.1 | 2.494632 | 0.990901 | -1.33202 | 0.018365 |
| MORN5 | 6.777501 | 3.126217 | -1.11634 | 7.30E-05 |
| CYP17A1 | 2.50699 | 0.363588 | -2.78558 | 1.34E-13 |
| LINC01781 | 3.271276 | 1.250035 | -1.38788 | 9.26E-12 |
| AC016813.1 | 3.755547 | 0.425264 | -3.14259 | 6.87E-11 |
| HBQ1 | 0.483902 | 1.677353 | 1.793399 | 0.003464 |
| ACKR1 | 29.06001 | 12.24753 | -1.24654 | 4.29E-16 |
| ATP1A2 | 1.800464 | 0.677584 | -1.4099 | 1.19E-18 |
| AC092071.1 | 11.16652 | 4.754096 | -1.23194 | 2.38E-15 |
| LY6D | 14.013 | 28.19096 | 1.008467 | 0.005984 |
| ERICH3 | 2.688992 | 1.095112 | -1.29599 | 1.53E-05 |
| AC092868.2 | 2.923858 | 10.10564 | 1.789216 | 0.042052 |
| INSYN1 | 1.683708 | 0.766916 | -1.1345 | 8.06E-16 |
| ITGB1-DT | 0.46532 | 2.701732 | 2.537589 | 1.34E-12 |
| PRR15 | 10.60518 | 23.76189 | 1.16388 | 6.95E-07 |
| CASC8 | 0.722115 | 1.730805 | 1.261143 | 2.31E-08 |
| ATP13A4-AS1 | 4.391858 | 0.874079 | -2.329 | 9.58E-11 |

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|---|---|---|---|---|
| PAX8 | 2.059601 | 4.857613 | 1.237883 | 0.042643 |
| ARMC2-AS1 | 1.786108 | 0.687044 | -1.37835 | 0.000337 |
| HMGA2 | 0.989216 | 6.280692 | 2.666567 | 2.20E-10 |
| RANBP20P | 2.023705 | 0.194702 | -3.37766 | 0.003116 |
| AL136452.1 | 3.264339 | 1.514762 | -1.1077 | 1.35E-11 |
| NCAPH | 8.37077 | 19.74018 | 1.237703 | 3.22E-25 |
| CD40LG | 4.867081 | 2.185291 | -1.15523 | 5.67E-20 |
| UBE2S | 14.72247 | 30.51866 | 1.051671 | 2.53E-25 |
| SERPINB5 | 4.374333 | 21.26788 | 2.281541 | 2.11E-08 |
| AL096712.1 | 1.575583 | 0.633767 | -1.31386 | 0.017194 |
| TINAG | 1.003716 | 2.443538 | 1.283621 | 0.001571 |
| SLIT3 | 10.78528 | 4.642902 | -1.21596 | 4.62E-14 |
| LBP | 7.401451 | 18.94909 | 1.356248 | 0.00111 |
| ADGRF4 | 2.991954 | 8.742043 | 1.546882 | 2.75E-15 |
| BTNL9 | 5.995401 | 2.042065 | -1.55383 | 2.41E-18 |
| KREMEN2 | 1.114303 | 2.471001 | 1.148954 | 2.94E-15 |
| CDHR2 | 0.96337 | 4.52852 | 2.232877 | 3.19E-06 |
| AP003119.3 | 1.454181 | 2.995023 | 1.04236 | 1.09E-07 |
| KRT75 | 1.110217 | 2.8226 | 1.346183 | 0.016032 |
| HSD17B13 | 6.018543 | 2.077505 | -1.53456 | 7.15E-15 |
| AL513548.1 | 1.740173 | 0.510289 | -1.76984 | 2.67E-05 |
| REG4 | 5.859474 | 93.167 | 3.990976 | 0.000615 |
| SCUBE1 | 1.509245 | 0.723506 | -1.06075 | 8.51E-08 |
| SLCO4A1 | 5.994444 | 12.49108 | 1.0592 | 1.26E-06 |
| KIF15 | 3.345342 | 6.922264 | 1.04909 | 3.50E-19 |
| F11 | 2.152501 | 0.582898 | -1.8847 | 5.17E-14 |
| LHFPL3 | 2.475909 | 1.083736 | -1.19194 | 2.06E-13 |
| SNORD89 | 9.799351 | 4.764209 | -1.04045 | 0.03175 |
| PTGDS | 131.8706 | 55.85793 | -1.23929 | 1.19E-20 |
| TRGJP2 | 5.568629 | 2.393163 | -1.2184 | 4.93E-06 |
| TRAJ4 | 1.587471 | 0.658118 | -1.27031 | 4.26E-06 |
| C20orf85 | 45.73293 | 19.32169 | -1.24301 | 6.91E-06 |
| AL109914.1 | 2.741052 | 1.18787 | -1.20635 | 2.54E-06 |
| TICRR | 1.359064 | 3.159613 | 1.217134 | 4.47E-23 |
| SNTN | 4.714569 | 2.110014 | -1.15987 | 2.67E-10 |
| DMBT1 | 118.3427 | 55.09919 | -1.10287 | 2.16E-06 |
| SPDYC | 1.043969 | 3.686494 | 1.820171 | 0.00063 |
| FAM83A | 34.94668 | 106.446 | 1.606894 | 2.11E-17 |
| KRT19 | 677.6211 | 1379.245 | 1.025328 | 8.78E-17 |
| PTCSC3 | 12.51849 | 4.838927 | -1.3713 | 4.69E-15 |
| IGKV1-33 | 14.45569 | 6.941819 | -1.05825 | 0.000118 |
| SCGB1A1 | 1429.472 | 378.217 | -1.9182 | 3.85E-08 |
| CNMD | 67.3991 | 8.825194 | -2.93303 | 3.56E-06 |
| LRRC18 | 1.707881 | 0.693777 | -1.29966 | 2.75E-08 |

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| SELENBP1 | 263.7155 | 122.1129 | -1.11077 | 1.07E-17 |
| AC113349.1 | 1.678911 | 0.510386 | -1.71786 | 1.28E-07 |
| MDFI | 21.11861 | 43.76027 | 1.051107 | 1.37E-13 |
| IL23A | 5.028868 | 10.22996 | 1.024495 | 9.71E-06 |
| CD1E | 8.634801 | 4.165104 | -1.05181 | 2.61E-14 |
| GNMT | 3.369482 | 1.637619 | -1.04093 | 1.08E-15 |
| UBE2SP1 | 1.273212 | 2.657205 | 1.061437 | 7.87E-15 |
| CRISP2 | 2.355633 | 1.116861 | -1.07666 | 0.000244 |
| NEK2 | 9.948446 | 22.29321 | 1.164061 | 5.04E-24 |
| AC020978.3 | 2.332244 | 1.112165 | -1.06835 | 1.68E-10 |
| TFF1 | 158.446 | 418.8674 | 1.402503 | 0.000494 |
| CCNB1 | 33.36363 | 69.05826 | 1.049538 | 8.02E-24 |
| BIRC5 | 20.25631 | 47.91212 | 1.242019 | 1.75E-25 |
| PRR11 | 8.296261 | 19.75385 | 1.251601 | 1.08E-26 |
| SGO1 | 2.442726 | 5.351688 | 1.131502 | 2.28E-23 |
| PI3 | 23.0905 | 130.927 | 2.503392 | 0.000489 |
| AF127577.3 | 0.866306 | 1.848885 | 1.093707 | 0.018309 |
| FCRLA | 6.389945 | 2.727922 | -1.228 | 3.12E-10 |
| PKIB | 8.903348 | 18.86151 | 1.083025 | 5.59E-05 |
| AL445493.3 | 2.837463 | 1.015374 | -1.48259 | 2.83E-10 |
| FAM171A2 | 3.641083 | 7.480229 | 1.038715 | 1.30E-05 |
| PSMD10P1 | 2.317778 | 0.862549 | -1.42606 | 0.000138 |
| MYO3B | 0.795125 | 1.807156 | 1.184468 | 0.007214 |
| BCL2L10 | 1.285264 | 2.594944 | 1.013638 | 1.26E-12 |
| CA3 | 5.793391 | 2.60544 | -1.15288 | 1.81E-18 |
| CAPN3 | 2.357066 | 0.994569 | -1.24485 | 1.07E-13 |
| KIF2C | 12.43709 | 29.48267 | 1.245219 | 1.05E-26 |
| AC027288.1 | 3.986161 | 1.475835 | -1.43347 | 9.49E-11 |
| FAM83F | 1.177629 | 3.099396 | 1.396102 | 5.52E-06 |
| OIP5 | 4.273373 | 9.556788 | 1.16115 | 4.42E-22 |
| CFAP77 | 3.304822 | 1.451965 | -1.18657 | 2.61E-06 |
| IGKV1OR2-6 | 19.73712 | 8.019903 | -1.29925 | 1.47E-06 |
| LINC02471 | 5.506104 | 2.001361 | -1.46005 | 3.00E-08 |
| C4BPA | 451.6563 | 225.339 | -1.00313 | 1.07E-10 |
| MUC2 | 0.1847 | 1.886215 | 3.352237 | 6.28E-06 |
| PDX1 | 1.027794 | 2.64954 | 1.366191 | 0.009549 |
| CDHR4 | 5.056094 | 2.142206 | -1.23893 | 0.000284 |
| MIR29B2CHG | 3.253342 | 1.330679 | -1.28976 | 9.69E-14 |
| PRAP1 | 2.562851 | 8.693425 | 1.762175 | 0.004847 |
| AC073149.1 | 2.345478 | 0.881122 | -1.41247 | 4.25E-11 |
| AKR1B10 | 53.44454 | 228.2888 | 2.094746 | 0.004467 |
| MIR374B | 2.165531 | 0.794501 | -1.4466 | 6.84E-08 |
| AC007849.1 | 2.053733 | 0.467732 | -2.13449 | 3.43E-05 |
| SFTPD | 839.5427 | 252.406 | -1.73386 | 9.99E-16 |

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| UGT2B7 | 0.83024 | 2.597854 | 1.64572 | 0.00265 |
| NUS1P2 | 0.778494 | 1.73615 | 1.157134 | 0.003015 |
| AL135999.3 | 23.52224 | 11.12739 | -1.07991 | 5.39E-11 |
| LINC02323 | 0.583152 | 1.869999 | 1.681095 | 8.35E-14 |
| AP005233.2 | 4.20354 | 8.929676 | 1.087003 | 4.08E-10 |
| FCER1A | 24.36783 | 11.90272 | -1.03369 | 4.76E-13 |
| HJURP | 8.082666 | 18.81599 | 1.219056 | 2.82E-26 |
| FA2H | 16.90235 | 36.0465 | 1.092635 | 1.51E-08 |
| CHIA | 18.76661 | 3.674288 | -2.35263 | 4.10E-14 |
| LINC00861 | 2.497357 | 1.209492 | -1.046 | 3.25E-14 |
| TMEM132D | 1.992016 | 0.794259 | -1.32655 | 3.09E-10 |
| SMOX | 10.00744 | 21.25013 | 1.086398 | 3.72E-15 |
| C1QTNF7 | 3.289119 | 1.256725 | -1.38803 | 5.65E-21 |
| ACOXL | 4.10206 | 2.040238 | -1.00761 | 2.10E-16 |
| SKA3 | 4.697849 | 10.31442 | 1.13459 | 1.08E-26 |
| CYCSP6 | 1.547054 | 4.887017 | 1.65943 | 6.87E-06 |
| SPC25 | 5.723549 | 11.52751 | 1.010098 | 1.07E-23 |
| SBSN | 1.682794 | 4.630018 | 1.460159 | 1.81E-09 |
| RAD51AP1 | 7.867304 | 17.1381 | 1.123266 | 2.35E-21 |
| ADAMTS7P3 | 2.021608 | 0.378418 | -2.41745 | 2.93E-14 |
| AL133304.2 | 3.151001 | 0.900415 | -1.80715 | 2.13E-08 |
| GDF10 | 7.058116 | 2.434256 | -1.5358 | 1.38E-14 |
| MIR31HG | 0.797829 | 2.386577 | 1.580791 | 1.82E-05 |
| FAM30A | 2.806819 | 1.282727 | -1.12972 | 2.91E-09 |
| INMT | 42.49677 | 12.58689 | -1.75543 | 6.13E-26 |
| RN7SKP80 | 4.73913 | 2.164498 | -1.13059 | 2.09E-05 |
| RNY4P25 | 1.562712 | 0.632091 | -1.30585 | 0.001697 |
| ZIC2 | 1.127504 | 2.552314 | 1.178674 | 0.000151 |
| FAM83A-AS1 | 4.817085 | 12.82583 | 1.412819 | 9.44E-15 |
| CDCA3 | 3.67124 | 9.146698 | 1.316984 | 1.23E-28 |
| CDC20 | 32.05225 | 78.53096 | 1.292836 | 5.61E-27 |
| SPATA18 | 11.42283 | 5.396363 | -1.08186 | 1.35E-11 |
| PENK | 5.401546 | 1.923216 | -1.48985 | 6.62E-13 |
| RSPO1 | 1.796916 | 0.373276 | -2.26721 | 6.87E-18 |
| AC112722.1 | 1.838605 | 0.804507 | -1.19243 | 3.78E-13 |
| IGHVIII-67-2 | 3.717997 | 1.439517 | -1.36894 | 0.000102 |
| C1orf87 | 1.821356 | 0.707105 | -1.36502 | 9.15E-08 |
| GJB5 | 3.461796 | 8.973945 | 1.374222 | 0.001464 |
| ABI3BP | 12.38963 | 5.329633 | -1.21703 | 7.07E-21 |
| GCKR | 0.6524 | 1.520668 | 1.220876 | 0.001098 |
| PKP2 | 4.843353 | 13.08353 | 1.433674 | 3.13E-10 |
| DUOX1 | 24.40845 | 9.120077 | -1.42026 | 1.93E-12 |
| AL590226.1 | 2.306076 | 0.992151 | -1.21681 | 1.10E-16 |
| PWAR5 | 1.997299 | 0.805131 | -1.31076 | 6.81E-05 |

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|---|---|---|---|---|
| WIF1 | 104.2882 | 13.11947 | -2.9908 | 6.00E-15 |
| RPL32P1 | 2.798415 | 1.281367 | -1.12693 | 2.47E-13 |
| AC006270.1 | 2.485301 | 1.2083 | -1.04044 | 0.02044 |
| HOXA10 | 1.763621 | 4.451047 | 1.335605 | 5.91E-05 |
| LY6K | 5.401648 | 12.67429 | 1.230433 | 4.35E-07 |
| IGKV2D-30 | 7.628288 | 3.392169 | -1.16915 | 0.000196 |
| SLC46A2 | 12.29564 | 4.473104 | -1.4588 | 1.44E-12 |
| AUNIP | 2.225686 | 5.232659 | 1.233294 | 1.35E-24 |
| TUBAL3 | 0.81745 | 1.850231 | 1.178502 | 2.74E-05 |
| AC141273.2 | 2.823299 | 1.302062 | -1.11658 | 1.86E-06 |
| TESMIN | 1.571716 | 4.420508 | 1.491872 | 5.78E-18 |
| IGF2BP3 | 2.781786 | 7.65619 | 1.460616 | 1.72E-11 |
| GAS6-AS1 | 3.85396 | 1.816653 | -1.08506 | 2.43E-11 |
| TPX2 | 29.66551 | 73.95455 | 1.317852 | 1.64E-26 |
| LINC02351 | 2.832997 | 1.198853 | -1.24067 | 1.91E-07 |
| AL157931.1 | 0.676045 | 1.511715 | 1.160996 | 0.000402 |
| TUBA4B | 4.862668 | 2.246025 | -1.11437 | 6.88E-05 |
| SOX14 | 4.462477 | 1.411138 | -1.66099 | 0.000491 |
| NR4A3 | 10.36488 | 4.882988 | -1.08587 | 2.51E-06 |
| UBE2C | 55.68021 | 135.9267 | 1.287593 | 1.86E-23 |
| ALKAL2 | 1.937587 | 0.606299 | -1.67616 | 8.65E-17 |
| SLCO4A1-AS1 | 1.519107 | 3.808106 | 1.32585 | 0.000119 |
| SRGAP3-AS2 | 7.120019 | 2.910336 | -1.2907 | 1.30E-06 |
| AC084375.1 | 10.24172 | 4.120093 | -1.31371 | 1.39E-09 |
| CIDEC | 0.263306 | 2.230019 | 3.082245 | 6.70E-05 |
| PSMD10P2 | 0.593743 | 1.754643 | 1.563267 | 2.81E-15 |
| RNU6-1010P | 3.013917 | 1.379633 | -1.12736 | 0.010558 |
| AC010998.3 | 2.537102 | 1.043352 | -1.28196 | 3.44E-12 |
| SNORA47 | 3.910924 | 0.841245 | -2.21691 | 0.003354 |
| C8orf34 | 1.420363 | 0.683158 | -1.05597 | 5.89E-13 |
| WDR38 | 9.755802 | 4.41326 | -1.14442 | 0.0011 |
| PITX1 | 7.886131 | 19.87179 | 1.333332 | 1.67E-12 |
| TNXB | 8.188685 | 3.015864 | -1.44106 | 1.09E-11 |
| AL161431.1 | 1.252581 | 5.003725 | 1.998099 | 0.033557 |
| DEPDC1 | 3.712578 | 8.406569 | 1.179096 | 2.06E-22 |
| AC120498.2 | 4.688292 | 1.954411 | -1.26233 | 7.20E-06 |
| PLA2G1B | 37.54757 | 10.63232 | -1.82026 | 5.85E-15 |
| RTBDN | 0.727301 | 1.51253 | 1.056339 | 9.36E-05 |
| RNU6ATAC39P | 1.640396 | 0.804639 | -1.02763 | 0.026442 |
| GJB2 | 29.42703 | 68.93861 | 1.22817 | 2.42E-11 |
| EMCN | 10.84049 | 5.312076 | -1.02908 | 1.10E-18 |
| NWD1 | 3.318206 | 1.387772 | -1.25763 | 5.83E-05 |
| AC027288.2 | 5.432964 | 2.353043 | -1.20721 | 7.12E-08 |
| GPR87 | 11.61172 | 27.96544 | 1.268063 | 2.56E-07 |

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|---|---|---|---|---|
| RAD54L | 4.341181 | 8.724251 | 1.006944 | 1.10E-20 |
| HHATL | 3.516812 | 1.042408 | -1.75435 | 2.05E-05 |
| LINC01116 | 2.303507 | 5.479521 | 1.250218 | 0.000121 |
| CHRDL1 | 25.90077 | 9.793252 | -1.40314 | 9.26E-25 |
| TTLL10 | 1.849673 | 0.74429 | -1.31333 | 3.98E-05 |
| HES2 | 1.648139 | 3.594351 | 1.124894 | 0.008065 |
| ECT2L | 2.059156 | 0.881488 | -1.22404 | 2.16E-07 |
| LGI3 | 6.504469 | 1.343596 | -2.27533 | 8.70E-13 |
| F5 | 6.253764 | 12.59212 | 1.009725 | 0.004069 |
| ELFN1-AS1 | 1.525728 | 3.661015 | 1.262746 | 0.000123 |
| LINC02555 | 4.529917 | 1.296628 | -1.80472 | 3.47E-09 |
| SELENOOLP | 0.735347 | 4.307903 | 2.550489 | 0.000787 |
| MIR6124 | 2.392805 | 1.155819 | -1.04979 | 0.02324 |
| BNIP3P40 | 1.694183 | 0.546388 | -1.63259 | 0.00208 |
| ADAMTS8 | 5.909452 | 1.861119 | -1.66685 | 4.44E-20 |
| DYNLRB2 | 4.188629 | 1.853655 | -1.1761 | 1.01E-09 |
| CFAP52 | 4.148708 | 1.685501 | -1.29948 | 2.01E-05 |
| AC053527.1 | 1.697287 | 0.630047 | -1.4297 | 0.00171 |
| MKI67 | 11.7011 | 28.07015 | 1.262393 | 1.09E-23 |
| AC023421.1 | 20.50828 | 6.004021 | -1.77221 | 1.56E-10 |
| C16orf89 | 610.6091 | 182.0099 | -1.74623 | 7.46E-20 |
| AC026347.1 | 7.061783 | 2.652529 | -1.41266 | 4.02E-05 |
| AC022784.1 | 2.031806 | 7.715429 | 1.924984 | 1.05E-07 |
| EIF4EBP1 | 81.76891 | 179.1927 | 1.131888 | 7.58E-22 |
| CDCA8 | 17.18691 | 35.09331 | 1.029886 | 1.28E-25 |
| KIF11 | 11.37947 | 24.40529 | 1.10076 | 7.55E-24 |
| GLYATL2 | 5.077882 | 2.160855 | -1.23262 | 0.036416 |
| TSPAN19 | 1.994755 | 0.791072 | -1.33433 | 0.000157 |
| KIFC1 | 16.47371 | 34.47574 | 1.065416 | 1.86E-25 |
| LINC01612 | 5.184096 | 2.157328 | -1.26485 | 2.26E-09 |
| CYP4Z2P | 3.172137 | 0.593491 | -2.41816 | 7.36E-20 |
| PGC | 4251.697 | 1071.91 | -1.98785 | 1.10E-17 |
| GJB6 | 3.73349 | 9.032147 | 1.274544 | 0.015588 |
| GDA | 0.685673 | 2.055319 | 1.58377 | 0.0014 |
| OIT3 | 2.371857 | 1.132556 | -1.06644 | 3.19E-09 |
| NR4A1AS | 6.753403 | 2.564182 | -1.39712 | 9.01E-11 |
| PRR20G | 0.626355 | 2.817125 | 2.169172 | 1.04E-05 |
| IL22RA1 | 2.782815 | 6.842513 | 1.297981 | 1.13E-07 |
| PNCK | 0.74659 | 1.721133 | 1.204971 | 3.91E-05 |
| FTX | 2.568706 | 1.11792 | -1.20022 | 2.23E-13 |
| NAPSA | 1963.769 | 936.2423 | -1.06867 | 6.10E-16 |
| CYP2A6 | 15.65559 | 1.232675 | -3.66681 | 2.49E-12 |
| CABCOCO1 | 6.293333 | 2.771992 | -1.1829 | 1.04E-09 |
| AC094019.2 | 1.680435 | 0.78818 | -1.09224 | 9.73E-08 |

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|---|---|---|---|---|
| CST5 | 2.787536 | 1.277797 | -1.12533 | 1.37E-10 |
| TMEM100 | 13.59707 | 5.560624 | -1.28998 | 7.10E-12 |
| RNASE1 | 1760.007 | 806.3158 | -1.12616 | 1.73E-17 |
| AC018629.1 | 1.395728 | 4.700321 | 1.751741 | 3.71E-05 |
| CENPE | 2.813607 | 5.868108 | 1.060475 | 1.82E-19 |
| HCN2 | 0.929105 | 2.082052 | 1.164092 | 3.07E-06 |
| STOML3 | 3.512336 | 1.608706 | -1.12653 | 2.72E-05 |
| LINC01108 | 1.686178 | 0.520881 | -1.69473 | 0.000116 |
| HOXA9 | 0.343184 | 1.733479 | 2.336618 | 0.021869 |
| ANGPTL4 | 46.57877 | 93.96277 | 1.012417 | 2.19E-09 |
| SLC16A12 | 3.813724 | 1.807345 | -1.07733 | 1.49E-05 |
| ENTPD2 | 3.416166 | 6.999567 | 1.034888 | 1.31E-06 |
| E2F7 | 1.530202 | 3.285841 | 1.10254 | 2.26E-16 |
| TPSD1 | 7.490365 | 3.620313 | -1.04892 | 0.002102 |
| DTHD1 | 2.418088 | 0.958882 | -1.33444 | 4.75E-09 |
| MALAT1 | 366.4345 | 116.6045 | -1.65193 | 5.50E-05 |
| SOX15 | 2.842533 | 7.803946 | 1.457027 | 9.71E-06 |
| FENDRR | 3.104469 | 1.214536 | -1.35394 | 5.27E-11 |
| DAAM2 | 17.65799 | 8.80031 | -1.0047 | 2.10E-19 |
| AL357093.2 | 5.549662 | 2.366756 | -1.22949 | 1.12E-08 |
| PADI3 | 2.251743 | 7.097982 | 1.656367 | 0.00021 |
| ATP5MC1P4 | 1.325031 | 2.841704 | 1.10073 | 2.02E-17 |
| AC099850.4 | 11.98176 | 27.54461 | 1.20093 | 9.63E-23 |
| LINC02163 | 0.918213 | 2.067372 | 1.170897 | 0.001807 |
| SLC2A1 | 56.00997 | 175.6852 | 1.649237 | 1.70E-26 |
| SFTPA1 | 5175.67 | 1950.477 | -1.40792 | 2.16E-13 |
| FOXM1 | 12.53955 | 34.6769 | 1.467489 | 1.47E-27 |
| PACRG | 2.292913 | 1.131556 | -1.01887 | 2.36E-06 |
| ACADL | 3.81198 | 1.512717 | -1.3334 | 1.00E-12 |
| MGP | 362.3864 | 180.5586 | -1.00506 | 4.70E-19 |
| HTR1D | 2.021742 | 5.434234 | 1.426478 | 7.18E-11 |
| AC133963.1 | 4.253596 | 1.782744 | -1.25458 | 2.46E-11 |
| DEFB1 | 26.35596 | 67.07411 | 1.347627 | 0.002011 |
| DNER | 4.031041 | 8.362641 | 1.052806 | 0.029139 |
| PLEKHH1 | 1.677311 | 3.641956 | 1.118563 | 5.40E-08 |
| UCN2 | 0.467656 | 1.638717 | 1.809049 | 5.32E-13 |
| MAMDC2 | 13.40013 | 4.88614 | -1.45548 | 3.81E-22 |
| ECRG4 | 6.808017 | 2.21642 | -1.619 | 1.48E-16 |
| LOXL2 | 21.29563 | 46.28281 | 1.119919 | 4.13E-13 |
| SERPINB3 | 5.652848 | 20.01034 | 1.823696 | 0.011926 |
| RNU4ATAC | 6.367048 | 1.85484 | -1.77933 | 0.000889 |
| AC079210.1 | 4.006868 | 1.826372 | -1.13349 | 6.11E-10 |
| SLC16A1 | 9.880455 | 23.12857 | 1.227026 | 1.00E-06 |
| SERPINB7 | 1.18444 | 2.739749 | 1.209839 | 0.000149 |

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|---|---|---|---|---|
| LAMP3 | 125.9324 | 61.93325 | -1.02386 | 4.55E-12 |
| FAM83B | 1.466463 | 3.336058 | 1.185804 | 0.001346 |
| CR2 | 12.27057 | 5.435716 | -1.17466 | 1.75E-07 |
| ZNF695 | 0.661107 | 1.419334 | 1.102258 | 1.41E-08 |
| IGKV1D-8 | 30.06496 | 14.39014 | -1.063 | 3.80E-06 |
| AC068587.2 | 5.34372 | 2.440818 | -1.13048 | 1.45E-11 |
| CDH3 | 40.37802 | 86.08774 | 1.092238 | 1.87E-10 |
| HILPDA | 27.98081 | 58.24939 | 1.057805 | 4.12E-12 |
| RNU6-1016P | 10.10295 | 4.956624 | -1.02735 | 0.003179 |
| S100A9 | 1123.01 | 2419.115 | 1.107108 | 0.002455 |
| IGLV3-16 | 22.46537 | 10.08328 | -1.15574 | 5.57E-08 |
| RAB3B | 0.990183 | 3.659387 | 1.885834 | 3.49E-13 |
| SERPINB4 | 1.675159 | 4.945488 | 1.561815 | 4.22E-05 |
| AC116407.1 | 6.067072 | 2.897662 | -1.06611 | 8.19E-12 |
| KIF14 | 2.802096 | 6.207481 | 1.147501 | 2.95E-22 |
| MAGEA12 | 4.830863 | 13.30588 | 1.461711 | 0.005476 |
| SSXP10 | 2.185805 | 0.380235 | -2.5232 | 4.60E-05 |
| AC008268.1 | 26.79318 | 10.20205 | -1.39301 | 2.82E-08 |
| LAMC2 | 88.27186 | 215.2817 | 1.2862 | 1.27E-12 |
| CDT1 | 10.7377 | 22.1511 | 1.044694 | 6.20E-25 |
| FHL1 | 27.69868 | 11.4361 | -1.27622 | 4.98E-19 |
| AL162511.1 | 18.07795 | 5.004872 | -1.85283 | 3.34E-17 |
| AL513008.1 | 2.200413 | 0.845087 | -1.3806 | 1.49E-05 |
| CYP4B1 | 165.18 | 41.57968 | -1.99009 | 6.67E-20 |
| PRSS3 | 2.298637 | 11.62125 | 2.337915 | 1.97E-05 |
| NXF3 | 1.690914 | 0.734821 | -1.20234 | 0.000308 |
| PLOD2 | 33.34029 | 67.35338 | 1.014483 | 8.97E-12 |
| LRRC36 | 5.187012 | 1.483272 | -1.80612 | 3.29E-16 |
| MIR6774 | 1.810678 | 0.785174 | -1.20545 | 3.21E-07 |
| FAM166B | 7.987641 | 3.648466 | -1.13048 | 0.000106 |
| CYP24A1 | 36.98194 | 118.405 | 1.678838 | 1.43E-07 |
| LRRK2-DT | 15.66138 | 6.141302 | -1.3506 | 1.63E-19 |
| AC026785.3 | 3.67881 | 7.641789 | 1.054671 | 0.003379 |
| TRIP13 | 12.74584 | 26.47355 | 1.054525 | 1.25E-20 |
| AC090001.1 | 1.996807 | 0.822338 | -1.27989 | 0.000258 |
| PPP2R2C | 2.320097 | 6.212932 | 1.421089 | 0.002868 |
| MYOZ1 | 6.021326 | 2.926699 | -1.04081 | 5.78E-11 |
| IGKV3D-7 | 4.318645 | 1.86314 | -1.21284 | 1.26E-05 |
| CFAP100 | 2.541304 | 1.002651 | -1.34175 | 8.70E-08 |
| ABCA3 | 151.7635 | 69.77407 | -1.12106 | 8.07E-15 |
| FURIN | 170.3013 | 363.4485 | 1.093661 | 0.000213 |
| AC005076.1 | 2.361963 | 0.496348 | -2.25056 | 2.50E-06 |
| HPDL | 2.592027 | 5.478757 | 1.079768 | 5.38E-11 |
| C22orf15 | 2.224847 | 0.935788 | -1.24945 | 4.06E-06 |

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|---|---|---|---|---|
| AC005722.2 | 2.372514 | 0.993903 | -1.25524 | 7.65E-06 |
| AL049555.1 | 2.428728 | 6.044555 | 1.315435 | 0.000372 |
| GKN2 | 51.45243 | 10.43282 | -2.30211 | 2.73E-10 |
| A2ML1 | 0.711255 | 4.084373 | 2.521675 | 0.029791 |
| MLXP1 | 1.081558 | 3.870386 | 1.839367 | 1.17E-05 |
| AC108451.2 | 0.777674 | 3.882828 | 2.319871 | 0.020624 |
| ST8SIA6-AS1 | 1.161672 | 3.379322 | 1.540531 | 0.049022 |
| LNCAROD | 0.251546 | 1.805005 | 2.843107 | 3.56E-06 |
| NFE4 | 2.824621 | 8.399497 | 1.572246 | 2.46E-05 |
| RHOV | 21.5628 | 93.17061 | 2.111331 | 2.24E-20 |
| IGHV1-24 | 531.7257 | 247.7798 | -1.10162 | 0.003974 |
| IGKV1OR2-108 | 63.6555 | 29.1227 | -1.12814 | 3.31E-06 |
| IGLV1-36 | 167.4023 | 55.27641 | -1.59858 | 3.69E-07 |
| NEIL3 | 3.266827 | 7.131404 | 1.126296 | 1.22E-14 |
| AURKA | 17.40841 | 35.20343 | 1.015932 | 9.73E-20 |
| RXRG | 2.366306 | 1.178037 | -1.00625 | 9.91E-10 |
| CFAP161 | 1.458677 | 0.679888 | -1.10129 | 2.53E-06 |
| AL139041.1 | 3.372377 | 1.41628 | -1.25166 | 2.29E-16 |
| ARHGEF4 | 1.950195 | 4.429152 | 1.183412 | 1.09E-07 |
| GGTLC1 | 68.195 | 24.07578 | -1.50208 | 1.22E-15 |
| LINC00922 | 4.333482 | 1.928899 | -1.16775 | 0.007904 |
| C6orf118 | 2.904622 | 1.178231 | -1.30173 | 7.15E-06 |
| MIR1972-1 | 1.462739 | 0.706184 | -1.05056 | 0.0024 |
| MBL1P | 4.15241 | 1.841131 | -1.17336 | 7.55E-16 |
| IGHV1OR16-3 | 4.826992 | 2.066228 | -1.22412 | 7.37E-06 |
| HSPA6 | 12.86938 | 29.05412 | 1.1748 | 0.00827 |
| AP001011.1 | 2.947323 | 1.219326 | -1.27332 | 3.52E-05 |
| SLC26A9 | 50.58383 | 21.16503 | -1.25699 | 8.04E-09 |
| KCNF1 | 0.973229 | 2.880567 | 1.565502 | 0.00093 |
| BTG2 | 255.636 | 121.2546 | -1.07605 | 2.68E-24 |
| SAXO2 | 4.122966 | 1.941829 | -1.08627 | 1.58E-07 |
| FGF19 | 1.134439 | 5.697938 | 2.328462 | 0.000983 |
| MELTF | 5.329884 | 14.52996 | 1.446855 | 9.51E-14 |
| PTGES | 47.00674 | 101.2999 | 1.107694 | 3.06E-06 |
| LINC00337 | 0.694486 | 1.824404 | 1.393409 | 9.95E-17 |
| AGTR2 | 14.25955 | 3.783653 | -1.91408 | 2.72E-06 |
| SFRP5 | 3.729819 | 1.650143 | -1.17651 | 0.013374 |
| FSCN1 | 65.23657 | 136.7187 | 1.067458 | 2.90E-10 |
| GUCY2C | 1.357873 | 3.773393 | 1.474514 | 0.005616 |
| CNGA4 | 1.898943 | 0.940371 | -1.01389 | 4.08E-06 |
| LPAL2 | 2.402671 | 1.108162 | -1.11647 | 1.55E-16 |
| CHEK1 | 5.309168 | 11.47776 | 1.112284 | 4.42E-26 |
| SLC7A5 | 61.53102 | 125.1215 | 1.023943 | 4.08E-13 |
| MELK | 10.40898 | 22.7779 | 1.129806 | 1.24E-21 |

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|---|---|---|---|---|
| DSG3 | 1.19759 | 3.014855 | 1.331955 | 0.013173 |
| KRT17 | 62.65465 | 242.3194 | 1.951417 | 7.44E-05 |
| LINC01559 | 0.600134 | 3.599053 | 2.584261 | 1.98E-05 |
| KIF23 | 5.850359 | 13.29332 | 1.184105 | 1.18E-26 |
| NCCRP1 | 6.846524 | 18.98493 | 1.471411 | 0.046094 |

**Supplementary Table S7. GO enrichment analysis of differentially expressed genes between high and low programmed cell death score group**

| Category | ID | Description | Counts | qvalue |
|---|---|---|---|---|
| BP | GO:0140014 | mitotic nuclear division | 40 | 2.62E-12 |
| BP | GO:0000070 | mitotic sister chromatid segregation | 30 | 2.62E-12 |
| BP | GO:0007059 | chromosome segregation | 41 | 4.12E-11 |
| BP | GO:0000819 | sister chromatid segregation | 31 | 4.86E-11 |
| BP | GO:0051983 | regulation of chromosome segregation | 22 | 8.36E-10 |
| BP | GO:0000280 | nuclear division | 44 | 1.24E-09 |
| BP | GO:0098813 | nuclear chromosome segregation | 34 | 1.74E-09 |
| BP | GO:0048285 | organelle fission | 46 | 2.52E-09 |
| BP | GO:0030071 | regulation of mitotic metaphase/anaphase transition | 16 | 2.71E-09 |
| BP | GO:0007091 | metaphase/anaphase transition of mitotic cell cycle | 16 | 4.02E-09 |
| BP | GO:1902099 | regulation of metaphase/anaphase transition of cell cycle | 16 | 4.02E-09 |
| BP | GO:0044784 | metaphase/anaphase transition of cell cycle | 16 | 6.52E-09 |
| BP | GO:0010965 | regulation of mitotic sister chromatid separation | 16 | 7.93E-09 |
| BP | GO:0051306 | mitotic sister chromatid separation | 16 | 1.63E-08 |
| BP | GO:1905818 | regulation of chromosome separation | 16 | 2.52E-08 |
| BP | GO:0006959 | humoral immune response | 38 | 2.81E-08 |
| BP | GO:0007088 | regulation of mitotic nuclear division | 24 | 3.89E-08 |
| BP | GO:0019730 | antimicrobial humoral response | 22 | 3.89E-08 |
| BP | GO:0033047 | regulation of mitotic sister chromatid segregation | 16 | 8.07E-08 |
| BP | GO:0051304 | chromosome separation | 18 | 8.33E-08 |
| BP | GO:1902850 | microtubule cytoskeleton organization involved in mitosis | 22 | 8.96E-08 |
| BP | GO:0033045 | regulation of sister chromatid segregation | 17 | 9.38E-08 |
| BP | GO:0007094 | mitotic spindle assembly checkpoint | 11 | 4.34E-07 |
| BP | GO:0031577 | spindle checkpoint | 11 | 4.34E-07 |
| BP | GO:0071173 | spindle assembly checkpoint | 11 | 4.34E-07 |
| BP | GO:0071174 | mitotic spindle checkpoint | 11 | 4.34E-07 |
| BP | GO:0007052 | mitotic spindle organization | 19 | 4.34E-07 |
| BP | GO:0051783 | regulation of nuclear division | 24 | 4.61E-07 |
| BP | GO:0033046 | negative regulation of sister chromatid segregation | 12 | 6.83E-07 |

| | | | | |
|---|---|---|---|---|
| BP | GO:0045841 | negative regulation of mitotic metaphase/anaphase transition | 11 | 7.66E-07 |
| BP | GO:0051985 | negative regulation of chromosome segregation | 12 | 8.47E-07 |
| BP | GO:1902100 | negative regulation of metaphase/anaphase transition of cell cycle | 11 | 9.93E-07 |
| BP | GO:2000816 | negative regulation of mitotic sister chromatid separation | 11 | 1.79E-06 |
| BP | GO:1905819 | negative regulation of chromosome separation | 11 | 2.33E-06 |
| BP | GO:0051310 | metaphase plate congression | 13 | 3.35E-06 |
| BP | GO:0033048 | negative regulation of mitotic sister chromatid segregation | 11 | 3.85E-06 |
| BP | GO:0007093 | mitotic cell cycle checkpoint | 21 | 3.94E-06 |
| BP | GO:0045839 | negative regulation of mitotic nuclear division | 12 | 4.08E-06 |
| BP | GO:0008608 | attachment of spindle microtubules to kinetochore | 10 | 4.40E-06 |
| BP | GO:0007051 | spindle organization | 22 | 4.40E-06 |
| BP | GO:0050000 | chromosome localization | 14 | 9.75E-06 |
| BP | GO:0051303 | establishment of chromosome localization | 14 | 9.75E-06 |
| BP | GO:1901987 | regulation of cell cycle phase transition | 38 | 1.13E-05 |
| BP | GO:0019731 | antibacterial humoral response | 12 | 1.57E-05 |
| BP | GO:0051784 | negative regulation of nuclear division | 12 | 1.87E-05 |
| BP | GO:0000075 | cell cycle checkpoint | 23 | 2.31E-05 |
| BP | GO:1901990 | regulation of mitotic cell cycle phase transition | 35 | 3.35E-05 |
| BP | GO:0090307 | mitotic spindle assembly | 12 | 4.39E-05 |
| BP | GO:1901988 | negative regulation of cell cycle phase transition | 25 | 7.23E-05 |
| BP | GO:0007080 | mitotic metaphase plate congression | 10 | 9.53E-05 |
| BP | GO:0010948 | negative regulation of cell cycle process | 29 | 0.000158 |
| BP | GO:1901991 | negative regulation of mitotic cell cycle phase transition | 23 | 0.000221 |
| BP | GO:0007018 | microtubule-based movement | 29 | 0.000249 |
| BP | GO:0070942 | neutrophil mediated cytotoxicity | 5 | 0.000419 |
| BP | GO:0003341 | cilium movement | 17 | 0.00042 |
| BP | GO:0000076 | DNA replication checkpoint | 6 | 0.000512 |
| BP | GO:0070268 | cornification | 14 | 0.000612 |
| BP | GO:0051225 | spindle assembly | 14 | 0.000738 |
| BP | GO:2001251 | negative regulation of chromosome organization | 16 | 0.00081 |
| BP | GO:0033044 | regulation of chromosome organization | 27 | 0.000954 |
| BP | GO:0042742 | defense response to bacterium | 26 | 0.001728 |

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|---|---|---|---|---|---|
| BP | GO:0051988 | regulation of attachment of spindle microtubules to kinetochore | 5 | 0.001728 | |
| BP | GO:0045787 | positive regulation of cell cycle | 28 | 0.002258 | |
| BP | GO:0051383 | kinetochore organization | 6 | 0.002371 | |
| BP | GO:0045930 | negative regulation of mitotic cell cycle | 25 | 0.003167 | |
| BP | GO:0001578 | microtubule bundle formation | 12 | 0.003483 | |
| BP | GO:0051315 | attachment of mitotic spindle microtubules to kinetochore | 5 | 0.003546 | |
| BP | GO:0000083 | regulation of transcription involved in G1/S transition of mitotic cell cycle | 7 | 0.004384 | |
| BP | GO:0044843 | cell cycle G1/S phase transition | 23 | 0.004921 | |
| BP | GO:0061844 | antimicrobial humoral immune response mediated by antimicrobial peptide | 10 | 0.005064 | |
| BP | GO:0044839 | cell cycle G2/M phase transition | 21 | 0.005793 | |
| BP | GO:0051873 | killing by host of symbiont cells | 6 | 0.00586 | |
| BP | GO:0001909 | leukocyte mediated cytotoxicity | 12 | 0.006073 | |
| BP | GO:0031570 | DNA integrity checkpoint | 15 | 0.006721 | |
| BP | GO:0007568 | aging | | 23 | 0.006941 |
| BP | GO:0034698 | response to gonadotropin | 6 | 0.006955 | |
| BP | GO:0033314 | mitotic DNA replication checkpoint | 4 | 0.007765 | |
| BP | GO:0051231 | spindle elongation | 4 | 0.007765 | |
| BP | GO:0006270 | DNA replication initiation | 7 | 0.007765 | |
| BP | GO:0090068 | positive regulation of cell cycle process | 22 | 0.007813 | |
| BP | GO:0051883 | killing of cells in other organism involved in symbiotic interaction | 6 | 0.008008 | |
| BP | GO:0051384 | response to glucocorticoid | 14 | 0.008008 | |
| BP | GO:0050829 | defense response to Gram-negative bacterium | 10 | 0.008218 | |
| BP | GO:0001906 | cell killing | | 15 | 0.012275 |
| BP | GO:0002697 | regulation of immune effector process | 29 | 0.013149 | |
| BP | GO:0007143 | female meiotic nuclear division | 6 | 0.013783 | |
| BP | GO:0000086 | G2/M transition of mitotic cell cycle | 19 | 0.014171 | |
| BP | GO:0000281 | mitotic cytokinesis | 9 | 0.014782 | |
| BP | GO:0035404 | histone-serine phosphorylation | 4 | 0.015219 | |
| BP | GO:0051255 | spindle midzone assembly | 4 | 0.015219 | |
| BP | GO:0051656 | establishment of organelle localization | 27 | 0.01606 | |
| BP | GO:1902749 | regulation of cell cycle G2/M phase transition | 17 | 0.01606 | |
| BP | GO:0051984 | positive regulation of chromosome segregation | 6 | 0.018206 | |
| BP | GO:0045861 | negative regulation of proteolysis | 24 | 0.018369 | |
| BP | GO:0071459 | protein localization to chromosome, centromeric region | 5 | 0.018369 | |
| BP | GO:0017144 | drug metabolic process | 7 | 0.018491 | |

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|---|---|---|---|---|
| BP | GO:0044774 | mitotic DNA integrity checkpoint | 11 | 0.018704 |
| BP | GO:0097529 | myeloid leukocyte migration | 17 | 0.019418 |
| BP | GO:0031341 | regulation of cell killing | 10 | 0.019418 |
| BP | GO:0002440 | production of molecular mediator of immune response | 21 | 0.019418 |
| BP | GO:0031960 | response to corticosteroid | 14 | 0.020095 |
| BP | GO:0045132 | meiotic chromosome segregation | 10 | 0.020757 |
| BP | GO:0000082 | G1/S transition of mitotic cell cycle | 20 | 0.020986 |
| BP | GO:0007100 | mitotic centrosome separation | 4 | 0.024656 |
| BP | GO:0050930 | induction of positive chemotaxis | 4 | 0.024656 |
| BP | GO:0060707 | trophoblast giant cell differentiation | 4 | 0.024656 |
| BP | GO:1904668 | positive regulation of ubiquitin protein ligase activity | 4 | 0.024656 |
| BP | GO:0010466 | negative regulation of peptidase activity | 19 | 0.026496 |
| BP | GO:0002377 | immunoglobulin production | 16 | 0.026866 |
| BP | GO:0071715 | icosanoid transport | 7 | 0.026866 |
| BP | GO:1901571 | fatty acid derivative transport | 7 | 0.026866 |
| BP | GO:0030595 | leukocyte chemotaxis | 17 | 0.028194 |
| BP | GO:0000910 | cytokinesis | 14 | 0.02881 |
| BP | GO:0051321 | meiotic cell cycle | 18 | 0.029051 |
| BP | GO:1903046 | meiotic cell cycle process | 15 | 0.030189 |
| BP | GO:0051299 | centrosome separation | 4 | 0.030269 |
| BP | GO:0002449 | lymphocyte mediated immunity | 23 | 0.03092 |
| BP | GO:0031145 | anaphase-promoting complex-dependent catabolic process | 9 | 0.03153 |
| BP | GO:0061640 | cytoskeleton-dependent cytokinesis | 10 | 0.03153 |
| BP | GO:0060706 | cell differentiation involved in embryonic placenta development | 5 | 0.032738 |
| BP | GO:0010951 | negative regulation of endopeptidase activity | 18 | 0.032738 |
| BP | GO:0002460 | adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains | 23 | 0.034276 |
| BP | GO:0140013 | meiotic nuclear division | 14 | 0.034973 |
| BP | GO:0006956 | complement activation | 14 | 0.036554 |
| BP | GO:0002523 | leukocyte migration involved in inflammatory response | 4 | 0.036554 |
| BP | GO:0016572 | histone phosphorylation | 6 | 0.038872 |
| BP | GO:0010389 | regulation of G2/M transition of mitotic cell cycle | 15 | 0.039111 |
| BP | GO:0035082 | axoneme assembly | 8 | 0.039111 |
| BP | GO:0042445 | hormone metabolic process | 16 | 0.039111 |
| BP | GO:0031099 | regeneration | 15 | 0.040242 |

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|---|---|---|---|---|---|
| BP | GO:0051382 | kinetochore assembly | 4 | 0.044519 | |
| BP | GO:0045840 | positive regulation of mitotic nuclear division | 7 | 0.048875 | |
| BP | GO:0019835 | cytolysis | 5 | 0.048875 | |
| BP | GO:0050855 | regulation of B cell receptor signaling pathway | 5 | 0.048875 | |
| BP | GO:0071624 | positive regulation of granulocyte chemotaxis | 5 | 0.048875 | |
| BP | GO:0032465 | regulation of cytokinesis | 9 | 0.048927 | |
| BP | GO:1902750 | negative regulation of cell cycle G2/M phase transition | 10 | 0.049346 | |
| CC | GO:0000779 | condensed chromosome, centromeric region | 21 | 4.05E-08 | |
| CC | GO:0005819 | spindle | 36 | 1.24E-07 | |
| CC | GO:0000775 | chromosome, centromeric region | 25 | 1.57E-07 | |
| CC | GO:0000940 | condensed chromosome outer kinetochore | 8 | 1.57E-07 | |
| CC | GO:0000777 | condensed chromosome kinetochore | 18 | 2.17E-07 | |
| CC | GO:0000793 | condensed chromosome | 26 | 2.58E-07 | |
| CC | GO:0000776 | kinetochore | 20 | 3.17E-07 | |
| CC | GO:0042599 | lamellar body | 8 | 5.87E-07 | |
| CC | GO:0062023 | collagen-containing extracellular matrix | 35 | 4.63E-06 | |
| CC | GO:0000780 | condensed nuclear chromosome, centromeric region | 9 | 1.11E-05 | |
| CC | GO:0000922 | spindle pole | 19 | 2.21E-05 | |
| CC | GO:0051233 | spindle midzone | 9 | 2.78E-05 | |
| CC | GO:0005874 | microtubule | 33 | 3.42E-05 | |
| CC | GO:0072686 | mitotic spindle | 16 | 7.35E-05 | |
| CC | GO:0098687 | chromosomal region | 28 | 8.23E-05 | |
| CC | GO:0005876 | spindle microtubule | 11 | 9.74E-05 | |
| CC | GO:0000778 | condensed nuclear chromosome kinetochore | 6 | 0.000149 | |
| CC | GO:0000794 | condensed nuclear chromosome | 13 | 0.000286 | |
| CC | GO:0005875 | microtubule associated complex | 16 | 0.000534 | |
| CC | GO:0019814 | immunoglobulin complex | 16 | 0.000688 | |
| CC | GO:0030496 | midbody | 17 | 0.000717 | |
| CC | GO:0031225 | anchored component of membrane | 16 | 0.001117 | |
| CC | GO:0005771 | multivesicular body | 9 | 0.001546 | |
| CC | GO:0009897 | external side of plasma membrane | 27 | 0.002988 | |
| CC | GO:0005922 | connexin complex | 5 | 0.004704 | |
| CC | GO:0005930 | axoneme | 12 | 0.004704 | |
| CC | GO:0031514 | motile cilium | 16 | 0.005073 | |
| CC | GO:0097014 | ciliary plasm | 12 | 0.005073 | |
| CC | GO:1990023 | mitotic spindle midzone | 4 | 0.008066 | |
| CC | GO:0005871 | kinesin complex | 7 | 0.009881 | |

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|---|---|---|---|---|---|
| CC | GO:0045120 | pronucleus | 4 | 0.013071 | |
| CC | GO:0099568 | cytoplasmic region | 17 | 0.022226 | |
| CC | GO:0032838 | plasma membrane bounded cell projection cytoplasm | 15 | 0.022226 | |
| CC | GO:0031362 | anchored component of external side of plasma membrane | 4 | 0.023608 | |
| CC | GO:0005921 | gap junction | 5 | 0.02624 | |
| CC | GO:0042383 | sarcolemma | 11 | 0.027429 | |
| CC | GO:0036157 | outer dynein arm | 3 | 0.036587 | |
| CC | GO:0005680 | anaphase-promoting complex | 4 | 0.037088 | |
| CC | GO:0014704 | intercalated disc | 6 | 0.039252 | |
| CC | GO:0035371 | microtubule plus-end | 4 | 0.041639 | |
| CC | GO:0031233 | intrinsic component of external side of plasma membrane | 4 | 0.047174 | |
| CC | GO:0045171 | intercellular bridge | 7 | 0.047174 | |
| CC | GO:0030018 | Z disc | 10 | 0.047174 | |
| MF | GO:0008017 | microtubule binding | 28 | 5.70E-06 | |
| MF | GO:0015631 | tubulin binding | 31 | 7.33E-05 | |
| MF | GO:0003777 | microtubule motor activity | 12 | 0.000636 | |
| MF | GO:0004867 | serine-type endopeptidase inhibitor activity | 12 | 0.005646 | |
| MF | GO:0003774 | motor activity | 14 | 0.005646 | |
| MF | GO:0019865 | immunoglobulin binding | 6 | 0.006342 | |
| MF | GO:0046906 | tetrapyrrole binding | 14 | 0.013936 | |
| MF | GO:0005506 | iron ion binding | 14 | 0.013936 | |
| MF | GO:0030414 | peptidase inhibitor activity | 16 | 0.013936 | |
| MF | GO:0020037 | heme binding | 13 | 0.017294 | |
| MF | GO:0005243 | gap junction channel activity | 5 | 0.018614 | |
| MF | GO:0004866 | endopeptidase inhibitor activity | 15 | 0.023075 | |
| MF | GO:0061134 | peptidase regulator activity | 17 | 0.025457 | |
| MF | GO:0004252 | serine-type endopeptidase activity | 14 | 0.025457 | |
| MF | GO:0008201 | heparin binding | 14 | 0.025457 | |
| MF | GO:0061135 | endopeptidase regulator activity | 15 | 0.028572 | |
| MF | GO:0005504 | fatty acid binding | 6 | 0.036967 | |
| MF | GO:0035173 | histone kinase activity | 4 | 0.046468 | |
| MF | GO:0004857 | enzyme inhibitor activity | 23 | 0.046468 | |

**Supplementary Table S8. KEGG enrichment analysis of differentially expressed genes between high and low programmed cell death score group**

| Category | Description | Counts | qvalue |
|---|---|---|---|
| hsa04110 | Cell cycle | 15 | 0.001266 |
| hsa00590 | Arachidonic acid metabolism | 9 | 0.009479 |
| hsa04640 | Hematopoietic cell lineage | 11 | 0.014591 |