Table S7. Comparison between HTC-A and HTC-B.

|  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- |
| HTC-A marker | | | | HTC-B marker | | | |
| Gene | ave\_diff | power | myAUC | Gene | ave\_diff | power | myAUC |
| *CFH* | 5.640 | 0.94 | 0.97 | *COL1A1* | 8.082 | 0.948 | 0.974 |
| *CYTL1* | 4.377 | 0.868 | 0.934 | *COL1A2* | 4.194 | 0.948 | 0.974 |
| *SOD3* | 3.239 | 0.866 | 0.933 | *COL9A1* | 5.380 | 0.892 | 0.946 |
| *FRZB* | 3.605 | 0.864 | 0.932 | *MMP13* | 1.046 | 0.892 | 0.946 |
| *CDO1* | 3.302 | 0.846 | 0.923 | *ALPL* | 5.668 | 0.828 | 0.914 |
| *PLAC9* | 2.568 | 0.846 | 0.923 | *PTH1R* | 3.910 | 0.82 | 0.91 |
| *SERPINA5* | 2.586 | 0.824 | 0.912 | *COL11A1* | 2.519 | 0.806 | 0.903 |
| *NDUFA4L2* | 1.902 | 0.804 | 0.902 | *MMP2* | 2.327 | 0.79 | 0.895 |
| *GDF10* | 2.704 | 0.796 | 0.898 | *EZR* | 3.081 | 0.756 | 0.878 |
| *MT1X* | 2.728 | 0.788 | 0.894 | *TGFBI* | 2.162 | 0.75 | 0.875 |
| *S100B* | 1.840 | 0.77 | 0.885 | *TMSB10* | 2.333 | 0.74 | 0.87 |
| *IFITM1* | 1.839 | 0.76 | 0.88 | *COL6A1* | 1.915 | 0.732 | 0.866 |
| *GPC6* | 1.864 | 0.748 | 0.874 | *AOC2* | 2.840 | 0.726 | 0.863 |
| *TF* | 4.296 | 0.734 | 0.867 | *S100A4* | 1.716 | 0.688 | 0.844 |
| *FIBIN* | 2.736 | 0.726 | 0.863 | *SULF1* | 2.338 | 0.674 | 0.837 |
| *SSR3* | 1.757 | 0.72 | 0.86 | *COL6A2* | 1.551 | 0.674 | 0.837 |
| *USP53* | 3.054 | 0.712 | 0.856 | *IBSP* | 2.626 | 0.67 | 0.835 |
| *SMOC2* | 2.217 | 0.7 | 0.85 | *TXN* | 1.725 | 0.664 | 0.832 |
| *TCEAL2* | 4.531 | 0.69 | 0.845 | *PPIC* | 1.791 | 0.662 | 0.831 |
| *MT1E* | 2.833 | 0.678 | 0.839 | *HMGA1* | 4.720 | 0.66 | 0.83 |
| *PLXDC2* | 2.571 | 0.672 | 0.836 | *LOXL2* | 2.385 | 0.658 | 0.829 |
| *ITM2A* | 2.134 | 0.666 | 0.833 | *COL9A2* | 2.034 | 0.658 | 0.829 |
| *TXNIP* | 3.069 | 0.664 | 0.832 | *TOP1* | 1.989 | 0.658 | 0.829 |
| *BHLHE41* | 3.095 | 0.656 | 0.828 | *ARPC2* | 1.016 | 0.656 | 0.828 |
| *CSGALNACT1* | 2.516 | 0.656 | 0.828 | *SMOX* | 3.844 | 0.652 | 0.826 |
| *IFITM3* | 1.197 | 0.65 | 0.825 | *PPP2CA* | 1.342 | 0.648 | 0.824 |
| *METTL7A* | 3.034 | 0.648 | 0.824 | *GRN* | 1.800 | 0.646 | 0.823 |
| *APOD* | 2.111 | 0.646 | 0.823 | *FHL2* | 4.378 | 0.642 | 0.821 |
| *NFIB* | 3.943 | 0.624 | 0.812 | *COL10A1* | 4.585 | 0.64 | 0.82 |
| *BNIP3* | 1.806 | 0.62 | 0.81 | *COL9A3* | 1.514 | 0.64 | 0.82 |
| *WIF1* | 5.194 | 0.614 | 0.807 | *RGS2* | 3.247 | 0.636 | 0.818 |
| *CFB* | 2.647 | 0.61 | 0.805 | *PDPN* | 1.860 | 0.634 | 0.817 |
| *NEBL* | 2.245 | 0.608 | 0.804 | *TNFRSF12A* | 4.439 | 0.632 | 0.816 |
| *LIMCH1* | 2.381 | 0.606 | 0.803 | *COL6A3* | 1.597 | 0.632 | 0.816 |
| *ISM1* | 2.912 | 0.604 | 0.802 | *TPPP3* | 3.572 | 0.63 | 0.815 |
| *HLA-B* | 1.281 | 0.604 | 0.802 | *WDR1* | 2.163 | 0.63 | 0.815 |
| *ITM2C* | 1.953 | 0.59 | 0.795 | *C7orf73* | 1.134 | 0.63 | 0.815 |
| *NPR2* | 1.684 | 0.588 | 0.794 | *IL11* | 3.522 | 0.628 | 0.814 |
| *PARM1* | 3.431 | 0.584 | 0.792 | *STMN1* | 3.762 | 0.626 | 0.813 |
| *CP* | 3.037 | 0.582 | 0.791 | *ARF4* | 1.123 | 0.624 | 0.812 |
| *SBSPON* | 3.761 | 0.58 | 0.79 | *PLAUR* | 3.221 | 0.618 | 0.809 |
| *P4HA1* | 1.323 | 0.568 | 0.784 | *LMNA* | 2.264 | 0.61 | 0.805 |
| *PPP1R3C* | 2.424 | 0.566 | 0.783 | *FABP5* | 2.779 | 0.606 | 0.803 |
| *TGFBR2* | 2.346 | 0.562 | 0.781 | *PARK7* | 1.185 | 0.586 | 0.793 |
| *NFIA* | 2.514 | 0.56 | 0.78 | *ARID5B* | 1.851 | 0.584 | 0.792 |
| *HSD3BP4* | 1.186 | 0.56 | 0.78 | *EGR2* | 2.819 | 0.582 | 0.791 |
| *CHI3L1* | 6.414 | 0.556 | 0.778 | *CCDC124* | 1.594 | 0.58 | 0.79 |
| *ABCA5* | 1.739 | 0.556 | 0.778 | *MATN4* | 3.771 | 0.578 | 0.789 |
| *NEAT1* | 1.149 | 0.556 | 0.778 | *ABHD2* | 1.761 | 0.576 | 0.788 |
| *EDIL3* | 1.753 | 0.55 | 0.775 | *TIMM8B* | 1.314 | 0.576 | 0.788 |
| *RARRES2* | 4.632 | 0.542 | 0.771 | *EIF2S2* | 1.567 | 0.572 | 0.786 |
| *SULF2* | 2.469 | 0.54 | 0.77 | *CYCS* | 1.344 | 0.572 | 0.786 |
| *TGFBR3* | 2.635 | 0.538 | 0.769 | *LOXL4* | 3.947 | 0.566 | 0.783 |
| *C1S* | 1.636 | 0.538 | 0.769 | *PMP22* | 2.803 | 0.562 | 0.781 |
| *MAP2K6* | 2.508 | 0.53 | 0.765 | *GARS* | 2.181 | 0.562 | 0.781 |
| *LTBP3* | 2.515 | 0.52 | 0.76 | *SNRPD1* | 1.787 | 0.562 | 0.781 |
| *HES1* | 2.237 | 0.518 | 0.759 | *MOXD1* | 2.255 | 0.56 | 0.78 |
| *MT1G* | 4.633 | 0.514 | 0.757 | *UBE2D1* | 1.846 | 0.56 | 0.78 |
| *FXYD1* | 1.524 | 0.514 | 0.757 | *KCNN4* | 3.340 | 0.556 | 0.778 |
| *NKTR* | 2.079 | 0.508 | 0.754 | *BZW2* | 1.351 | 0.556 | 0.778 |
| *LVRN* | 3.951 | 0.504 | 0.752 | *CTSA* | 1.541 | 0.554 | 0.777 |
| *SLC39A8* | 3.240 | 0.494 | 0.747 | *MAP1LC3B* | 1.761 | 0.548 | 0.774 |
| *KMT2C* | 2.126 | 0.494 | 0.747 | *EPYC* | 1.734 | 0.544 | 0.772 |
| *MBNL1* | 1.497 | 0.488 | 0.744 | *PMAIP1* | 3.584 | 0.542 | 0.771 |
| *SLC5A12* | 2.118 | 0.486 | 0.743 | *TMEM119* | 3.279 | 0.54 | 0.77 |
| *NINJ1* | 2.455 | 0.484 | 0.742 | *MRPL47* | 1.968 | 0.54 | 0.77 |
| *CBX5* | 1.171 | 0.48 | 0.74 | *TNFAIP6* | 1.683 | 0.538 | 0.769 |
| *RSPO2* | 3.554 | 0.478 | 0.739 | *RGS3* | 2.060 | 0.536 | 0.768 |
| *FBXO2* | 1.638 | 0.478 | 0.739 | *CAPN6* | 4.079 | 0.534 | 0.767 |
| *ZRANB2* | 1.301 | 0.476 | 0.738 | *P3H2* | 1.747 | 0.534 | 0.767 |
| *ECM2* | 1.919 | 0.474 | 0.737 | *OLFML3* | 3.799 | 0.53 | 0.765 |
| *OSMR* | 2.533 | 0.472 | 0.736 | *RAB31* | 2.579 | 0.53 | 0.765 |
| *VTRNA1-1* | 2.553 | 0.47 | 0.735 | *PHLDA1* | 2.185 | 0.53 | 0.765 |
| *ITPR2* | 2.023 | 0.47 | 0.735 | *MEPE* | 4.176 | 0.528 | 0.764 |
| *ZNF385D* | 2.817 | 0.468 | 0.734 | *SPON2* | 2.904 | 0.528 | 0.764 |
| *GREM1* | 4.780 | 0.466 | 0.733 | *TALDO1* | 1.407 | 0.528 | 0.764 |
| *RELN* | 3.270 | 0.466 | 0.733 | *IL17B* | 4.608 | 0.524 | 0.762 |
| *RERG* | 2.336 | 0.466 | 0.733 | *LRRC8C* | 2.903 | 0.524 | 0.762 |
| *NUCB2* | 1.022 | 0.466 | 0.733 | *RUNX2* | 1.722 | 0.524 | 0.762 |
| *MT1M* | 3.380 | 0.462 | 0.731 | *SDC4* | 1.434 | 0.52 | 0.76 |
| *SRSF5* | 1.344 | 0.454 | 0.727 | *RTN3* | 1.054 | 0.52 | 0.76 |
| *SLC25A37* | 1.462 | 0.446 | 0.723 | *ROPN1* | 3.668 | 0.518 | 0.759 |
| *GLDN* | 2.137 | 0.444 | 0.722 | *CDKN1A* | 3.155 | 0.516 | 0.758 |
| *NR1D1* | 1.773 | 0.444 | 0.722 | *GPC1* | 2.500 | 0.514 | 0.757 |
| *FST* | 3.564 | 0.442 | 0.721 | *EIF4EBP1* | 1.953 | 0.514 | 0.757 |
| *ADGRG6* | 2.426 | 0.44 | 0.72 | *ARRDC3* | 1.785 | 0.514 | 0.757 |
| *TNC* | 1.199 | 0.44 | 0.28 | *ANP32B* | 1.277 | 0.514 | 0.757 |
| *CYBRD1* | 1.252 | 0.438 | 0.719 | *TMSB4X* | 1.246 | 0.512 | 0.756 |
| *KCNAB1* | 3.069 | 0.436 | 0.718 | *SCUBE3* | 2.841 | 0.51 | 0.755 |
| *MTUS1* | 1.419 | 0.436 | 0.718 | *CRNDE* | 2.080 | 0.51 | 0.755 |
| *UTRN* | 1.485 | 0.434 | 0.717 | *EGR3* | 2.866 | 0.508 | 0.754 |
| *RNASE4* | 1.204 | 0.432 | 0.716 | *VPS25* | 1.647 | 0.506 | 0.753 |
| *CHRDL2* | 2.853 | 0.43 | 0.715 | *TMEM50A* | 1.275 | 0.502 | 0.751 |
| *EPB41L2* | 1.290 | 0.428 | 0.714 | *SGMS2* | 2.778 | 0.5 | 0.75 |
| *CPAMD8* | 2.864 | 0.422 | 0.711 | *DCUN1D5* | 1.590 | 0.5 | 0.75 |
| *FAM162A* | 1.253 | 0.422 | 0.711 | *FAM43A* | 2.027 | 0.498 | 0.749 |
| *AK4* | 1.484 | 0.42 | 0.71 | *SERINC5* | 1.310 | 0.498 | 0.749 |
| *MPDZ* | 2.696 | 0.418 | 0.709 | *TIMM13* | 1.222 | 0.498 | 0.749 |
| *PRMT2* | 1.465 | 0.418 | 0.709 | *BMP8A* | 3.249 | 0.494 | 0.747 |
| *TMX4* | 2.481 | 0.416 | 0.708 | *BIN3* | 1.926 | 0.494 | 0.747 |
| *CDR1* | 2.587 | 0.414 | 0.707 | *EEF2* | 1.146 | 0.494 | 0.747 |
| *TPD52* | 2.460 | 0.412 | 0.706 | *BMP1* | 2.503 | 0.492 | 0.746 |
| *EPS8* | 1.738 | 0.41 | 0.705 | *GNPNAT1* | 2.259 | 0.492 | 0.746 |
| *ALKBH5* | 1.224 | 0.408 | 0.704 | *TUBB4B* | 1.755 | 0.492 | 0.746 |
| *TCEAL6* | 3.322 | 0.406 | 0.703 | *RRP7A* | 1.663 | 0.492 | 0.746 |
| *ALDH1A2* | 3.172 | 0.406 | 0.703 | *SEPW1* | 1.079 | 0.492 | 0.746 |
| *SEMA3E* | 1.761 | 0.406 | 0.703 | *HNRNPF* | 1.178 | 0.49 | 0.745 |
| *TPD52L1* | 1.132 | 0.404 | 0.702 | *SPRY2* | 1.961 | 0.484 | 0.742 |
| *AKR1C2* | 1.654 | 0.402 | 0.701 | *PDCD6* | 1.174 | 0.482 | 0.741 |
|  | | | | *GPRC5A* | 2.380 | 0.478 | 0.739 |
| *MLF1* | 2.166 | 0.478 | 0.739 |
| *GJA1* | 1.688 | 0.478 | 0.739 |
| *CTHRC1* | 1.207 | 0.476 | 0.738 |
| *PPP1R15A* | 1.563 | 0.474 | 0.737 |
| *ITGA11* | 1.104 | 0.474 | 0.737 |
| *LOC101928841* | 2.174 | 0.472 | 0.736 |
| *KCTD5* | 2.988 | 0.47 | 0.735 |
| *OSTC* | 1.234 | 0.47 | 0.735 |
| *BYSL* | 1.732 | 0.468 | 0.734 |
| *SRD5A3* | 1.072 | 0.466 | 0.733 |
| *LOC652276* | 2.198 | 0.464 | 0.732 |
| *ZYX* | 1.211 | 0.464 | 0.732 |
| *NINJ2* | 3.073 | 0.462 | 0.731 |
| *DCAF13* | 1.325 | 0.462 | 0.731 |
| *GLIS3* | 2.552 | 0.46 | 0.73 |
| *DDX21* | 1.660 | 0.46 | 0.73 |
| *TNNT3* | 1.510 | 0.46 | 0.73 |
| *BMP6* | 2.668 | 0.458 | 0.729 |
| *TOMM34* | 1.940 | 0.458 | 0.729 |
| *ULBP2* | 1.199 | 0.458 | 0.729 |
| *LMO4* | 1.064 | 0.458 | 0.729 |
| *PAPPA* | 4.275 | 0.456 | 0.728 |
| *OCIAD2* | 1.386 | 0.456 | 0.728 |
| *SERPINH1* | 1.725 | 0.454 | 0.727 |
| *MYADM* | 1.194 | 0.452 | 0.726 |
| *TIMM9* | 1.251 | 0.448 | 0.724 |
| *PNP* | 1.867 | 0.446 | 0.723 |
| *PDE4B* | 1.809 | 0.446 | 0.723 |
| *DDX39A* | 2.111 | 0.444 | 0.722 |
| *ANKRD28* | 1.376 | 0.444 | 0.722 |
| *GLUD1* | 1.272 | 0.444 | 0.722 |
| *SLC31A2* | 1.764 | 0.442 | 0.721 |
| *ADAMTS2* | 1.134 | 0.442 | 0.721 |
| *SNRPB2* | 1.066 | 0.442 | 0.721 |
| *P2RX4* | 2.092 | 0.44 | 0.72 |
| *SNRPB* | 1.215 | 0.44 | 0.72 |
| *CDC42EP3* | 1.006 | 0.44 | 0.72 |
| *TUBB2A* | 1.397 | 0.438 | 0.719 |
| *FAM180A* | 3.475 | 0.436 | 0.718 |
| *SH3KBP1* | 1.245 | 0.436 | 0.718 |
| *FRMD6* | 2.183 | 0.432 | 0.716 |
| *CWC25* | 1.498 | 0.432 | 0.716 |
| *MSANTD3* | 1.468 | 0.432 | 0.716 |
| *FAM32A* | 1.069 | 0.432 | 0.716 |
| *ENPP2* | 1.432 | 0.43 | 0.715 |
| *DUSP14* | 2.039 | 0.428 | 0.714 |
| *TUBA1C* | 1.954 | 0.428 | 0.714 |
| *TSPAN2* | 1.498 | 0.428 | 0.714 |
| *NCBP2* | 1.368 | 0.428 | 0.714 |
| *LRRC15* | 5.051 | 0.424 | 0.712 |
| *CAPN2* | 1.284 | 0.424 | 0.712 |
| *TARS* | 1.267 | 0.424 | 0.712 |
| *LAMA4* | 1.941 | 0.422 | 0.711 |
| *GLRX3* | 1.129 | 0.422 | 0.711 |
| *PTTG1* | 1.104 | 0.422 | 0.711 |
| *SNHG15* | 1.863 | 0.42 | 0.71 |
| *IQCB1* | 1.406 | 0.42 | 0.71 |
| *FOSL1* | 3.206 | 0.418 | 0.709 |
| *PSMC6* | 1.261 | 0.418 | 0.709 |
| *CHAC1* | 2.799 | 0.414 | 0.707 |
| *LOX* | 2.156 | 0.414 | 0.707 |
| *GADD45B* | 1.699 | 0.414 | 0.707 |
| *NID2* | 2.343 | 0.412 | 0.706 |
| *SLC25A39* | 1.222 | 0.412 | 0.706 |
| *MARS* | 1.145 | 0.412 | 0.706 |
| *AKIRIN2* | 1.642 | 0.41 | 0.705 |
| *DNAJB11* | 1.006 | 0.41 | 0.705 |
| *C1QTNF3* | 3.257 | 0.406 | 0.703 |
| *MAST4* | 2.477 | 0.406 | 0.703 |
| *CCDC127* | 1.885 | 0.406 | 0.703 |
| *NEU1* | 1.592 | 0.406 | 0.703 |
| *SLC44A2* | 1.285 | 0.406 | 0.703 |
| *EAF2* | 3.363 | 0.404 | 0.702 |
| *PGAM2* | 2.999 | 0.404 | 0.702 |
| *VEGFC* | 2.520 | 0.404 | 0.702 |
| *AEN* | 2.364 | 0.404 | 0.702 |
| *HMGCR* | 2.092 | 0.404 | 0.702 |
| *NT5E* | 1.145 | 0.404 | 0.702 |
| *SERPINI2* | 2.217 | 0.402 | 0.701 |
| *LECT1* | 2.003 | 0.402 | 0.701 |

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| --- | --- | --- |
| HTC-A GO terms | | |
| ID | Name | *P* value |
| GO:0051216 | cartilage development | 1.20E-08 |
| GO:1990267 | response to transition metal nanoparticle | 2.18E-07 |
| GO:0061448 | connective tissue development | 2.57E-07 |
| GO:0051093 | negative regulation of developmental process | 5.48E-07 |
| GO:0001501 | skeletal system development | 1.30E-06 |
| GO:0060541 | respiratory system development | 1.45E-06 |
| GO:0030324 | lung development | 3.79E-06 |
| GO:0071294 | cellular response to zinc ion | 3.99E-06 |
| GO:0030323 | respiratory tube development | 4.39E-06 |
| GO:0001889 | liver development | 4.46E-06 |
| GO:0061008 | hepaticobiliary system development | 5.07E-06 |
| GO:0010810 | regulation of cell-substrate adhesion | 8.33E-06 |
| GO:0045926 | negative regulation of growth | 1.84E-05 |
| GO:0048732 | gland development | 2.22E-05 |
| GO:0002062 | chondrocyte differentiation | 2.56E-05 |
| GO:0045596 | negative regulation of cell differentiation | 2.80E-05 |
| GO:0042127 | regulation of cell proliferation | 3.17E-05 |
| GO:0010038 | response to metal ion | 3.38E-05 |
| GO:0045444 | fat cell differentiation | 3.56E-05 |
| GO:0045598 | regulation of fat cell differentiation | 5.95E-05 |
| GO:0009719 | response to endogenous stimulus | 6.24E-05 |
| GO:0001503 | ossification | 8.10E-05 |
| GO:0055114 | oxidation-reduction process | 1.11E-04 |
| GO:0007178 | transmembrane receptor protein serine/threonine kinase signaling pathway | 1.21E-04 |
| GO:0048762 | mesenchymal cell differentiation | 1.23E-04 |
| GO:0071276 | cellular response to cadmium ion | 1.26E-04 |
| GO:0045595 | regulation of cell differentiation | 1.26E-04 |
| GO:0031099 | regeneration | 1.31E-04 |
| GO:0001952 | regulation of cell-matrix adhesion | 1.83E-04 |
| GO:0071248 | cellular response to metal ion | 1.93E-04 |
| GO:0030509 | BMP signaling pathway | 1.93E-04 |
| GO:0090092 | regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 2.34E-04 |
| GO:0048863 | stem cell differentiation | 2.79E-04 |
| GO:0071798 | response to prostaglandin D | 3.00E-04 |
| GO:0071799 | cellular response to prostaglandin D stimulus | 3.00E-04 |
| GO:0071773 | cellular response to BMP stimulus | 3.01E-04 |
| GO:0071772 | response to BMP | 3.01E-04 |
| GO:0040007 | growth | 3.13E-04 |
| GO:0010043 | response to zinc ion | 3.18E-04 |
| GO:0001666 | response to hypoxia | 3.40E-04 |
| GO:0090101 | negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 3.63E-04 |
| GO:0010811 | positive regulation of cell-substrate adhesion | 3.78E-04 |
| GO:0035295 | tube development | 4.05E-04 |
| GO:0036293 | response to decreased oxygen levels | 4.11E-04 |
| GO:0031589 | cell-substrate adhesion | 4.19E-04 |
| GO:0060389 | pathway-restricted SMAD protein phosphorylation | 4.35E-04 |
| GO:0061037 | negative regulation of cartilage development | 4.36E-04 |
| GO:0071241 | cellular response to inorganic substance | 4.39E-04 |
| GO:0042985 | negative regulation of amyloid precursor protein biosynthetic process | 4.48E-04 |
| GO:0022603 | regulation of anatomical structure morphogenesis | 4.53E-04 |

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| --- | --- | --- |
| HTC-B GO terms | | |
| ID | Name | *P* value |
| GO:0030198 | extracellular matrix organization | 1.07E-15 |
| GO:0043062 | extracellular structure organization | 1.15E-15 |
| GO:0001503 | ossification | 1.08E-11 |
| GO:0001649 | osteoblast differentiation | 6.97E-11 |
| GO:0044236 | multicellular organism metabolic process | 1.43E-10 |
| GO:0030574 | collagen catabolic process | 9.50E-10 |
| GO:0061448 | connective tissue development | 1.08E-09 |
| GO:0044243 | multicellular organismal catabolic process | 2.59E-09 |
| GO:0032963 | collagen metabolic process | 2.69E-09 |
| GO:0044259 | multicellular organismal macromolecule metabolic process | 4.27E-09 |
| GO:0051216 | cartilage development | 8.78E-09 |
| GO:0001501 | skeletal system development | 5.66E-08 |
| GO:0060350 | endochondral bone morphogenesis | 5.87E-08 |
| GO:0006928 | movement of cell or subcellular component | 8.54E-08 |
| GO:0030199 | collagen fibril organization | 1.82E-07 |
| GO:0036075 | replacement ossification | 4.82E-07 |
| GO:0001958 | endochondral ossification | 4.82E-07 |
| GO:0040011 | locomotion | 6.03E-07 |
| GO:0070208 | protein heterotrimerization | 6.52E-07 |
| GO:0002062 | chondrocyte differentiation | 8.96E-07 |
| GO:0048705 | skeletal system morphogenesis | 2.97E-06 |
| GO:0060349 | bone morphogenesis | 3.30E-06 |
| GO:0016477 | cell migration | 9.13E-06 |
| GO:0070206 | protein trimerization | 1.00E-05 |
| GO:0031214 | biomineral tissue development | 1.09E-05 |
| GO:0009719 | response to endogenous stimulus | 1.17E-05 |
| GO:0071363 | cellular response to growth factor stimulus | 1.83E-05 |
| GO:0060348 | bone development | 2.07E-05 |
| GO:0048870 | cell motility | 2.12E-05 |
| GO:0051674 | localization of cell | 2.12E-05 |
| GO:0070848 | response to growth factor | 3.28E-05 |
| GO:0006469 | negative regulation of protein kinase activity | 3.51E-05 |
| GO:0045669 | positive regulation of osteoblast differentiation | 5.31E-05 |
| GO:0044344 | cellular response to fibroblast growth factor stimulus | 5.79E-05 |
| GO:0009611 | response to wounding | 7.21E-05 |
| GO:0072321 | chaperone-mediated protein transport | 7.39E-05 |
| GO:0071774 | response to fibroblast growth factor | 7.86E-05 |
| GO:0001933 | negative regulation of protein phosphorylation | 7.97E-05 |
| GO:0033673 | negative regulation of kinase activity | 8.59E-05 |
| GO:0022610 | biological adhesion | 9.03E-05 |
| GO:0051348 | negative regulation of transferase activity | 9.16E-05 |
| GO:0030282 | bone mineralization | 9.77E-05 |
| GO:0002063 | chondrocyte development | 1.12E-04 |
| GO:0001944 | vasculature development | 1.19E-04 |
| GO:0071495 | cellular response to endogenous stimulus | 1.22E-04 |
| GO:0043407 | negative regulation of MAP kinase activity | 1.32E-04 |
| GO:0007167 | enzyme linked receptor protein signaling pathway | 1.50E-04 |
| GO:0060351 | cartilage development involved in endochondral bone morphogenesis | 1.73E-04 |
| GO:0007155 | cell adhesion | 1.85E-04 |
| GO:0051240 | positive regulation of multicellular organismal process | 1.97E-04 |