Table S6. Comparison among ProC, preHTC and HTC.

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene | cluster | ave\_diff | power | myAUC |
| *P3H2* | ProC | 1.867 | 0.79 | 0.895 |
| *DDX21* | ProC | 1.954 | 0.776 | 0.888 |
| *TUBA1C* | ProC | 1.761 | 0.75 | 0.875 |
| *HSPA9* | ProC | 1.432 | 0.744 | 0.872 |
| *ATP13A3* | ProC | 2.019 | 0.7 | 0.85 |
| *NOP16* | ProC | 1.383 | 0.682 | 0.841 |
| *LRRFIP1* | ProC | 1.440 | 0.68 | 0.84 |
| *TUBB6* | ProC | 1.536 | 0.666 | 0.833 |
| *ERCC1* | ProC | 2.180 | 0.652 | 0.826 |
| *HBEGF* | ProC | 1.717 | 0.632 | 0.816 |
| *PTPRE* | ProC | 1.511 | 0.622 | 0.811 |
| *GLIS3* | ProC | 1.385 | 0.62 | 0.81 |
| *NOTCH2* | ProC | 1.543 | 0.616 | 0.808 |
| *PTRF* | ProC | 1.750 | 0.612 | 0.806 |
| *ACTN1* | ProC | 1.579 | 0.612 | 0.806 |
| *FOSL1* | ProC | 1.374 | 0.61 | 0.805 |
| *CLCF1* | ProC | 1.341 | 0.606 | 0.803 |
| *TGFBR1* | ProC | 1.346 | 0.6 | 0.8 |
| *METRNL* | ProC | 1.887 | 0.598 | 0.799 |
| *RPF2* | ProC | 1.602 | 0.59 | 0.795 |
| *SFPQ* | ProC | 1.491 | 0.588 | 0.794 |
| *NFATC2* | ProC | 1.491 | 0.584 | 0.792 |
| *MAPKAPK2* | ProC | 1.675 | 0.574 | 0.787 |
| *WDR43* | ProC | 1.489 | 0.574 | 0.787 |
| *MSN* | ProC | 1.154 | 0.57 | 0.785 |
| *SNX9* | ProC | 1.533 | 0.566 | 0.783 |
| *GOT1* | ProC | 1.703 | 0.564 | 0.782 |
| *INHBA-AS1* | ProC | 2.117 | 0.56 | 0.78 |
| *UPP1* | ProC | 1.572 | 0.56 | 0.78 |
| *NOTCH2NL* | ProC | 1.331 | 0.558 | 0.779 |
| *STK40* | ProC | 1.609 | 0.556 | 0.778 |
| *SMOX* | ProC | 1.489 | 0.554 | 0.777 |
| *TXNRD1* | ProC | 1.110 | 0.552 | 0.776 |
| *ITGA2* | ProC | 2.792 | 0.55 | 0.775 |
| *CDV3* | ProC | 1.546 | 0.548 | 0.774 |
| *EIF3J* | ProC | 1.185 | 0.548 | 0.774 |
| *PEA15* | ProC | 1.394 | 0.54 | 0.77 |
| *ASNS* | ProC | 1.181 | 0.54 | 0.77 |
| *KDM6B* | ProC | 1.443 | 0.536 | 0.768 |
| *DCAF13* | ProC | 1.471 | 0.53 | 0.765 |
| *SLC7A1* | ProC | 1.401 | 0.53 | 0.765 |
| *PDLIM4* | ProC | 1.101 | 0.526 | 0.763 |
| *KIAA0020* | ProC | 1.547 | 0.524 | 0.762 |
| *GPATCH4* | ProC | 1.659 | 0.52 | 0.76 |
| *SESN2* | ProC | 1.850 | 0.518 | 0.759 |
| *YBX3* | ProC | 1.071 | 0.518 | 0.759 |
| *SLC38A1* | ProC | 1.021 | 0.516 | 0.758 |
| *ZNF593* | ProC | 1.373 | 0.514 | 0.757 |
| *ST3GAL1* | ProC | 1.301 | 0.514 | 0.757 |
| *ELL2* | ProC | 1.551 | 0.506 | 0.753 |
| *NIFK* | ProC | 1.119 | 0.504 | 0.752 |
| *MYADM* | ProC | 1.319 | 0.5 | 0.75 |
| *PNO1* | ProC | 1.249 | 0.498 | 0.749 |
| *SNHG15* | ProC | 1.443 | 0.494 | 0.747 |
| *FAM101B* | ProC | 1.333 | 0.494 | 0.747 |
| *C1orf198* | ProC | 1.121 | 0.494 | 0.747 |
| *IARS* | ProC | 1.074 | 0.494 | 0.747 |
| *ATP6V0A1* | ProC | 2.009 | 0.492 | 0.746 |
| *PGM3* | ProC | 1.158 | 0.492 | 0.746 |
| *SNHG16* | ProC | 1.063 | 0.492 | 0.746 |
| *MARS* | ProC | 1.056 | 0.492 | 0.746 |
| *BMP6* | ProC | 1.250 | 0.486 | 0.743 |
| *NPR2* | ProC | 2.199 | 0.484 | 0.742 |
| *NOP56* | ProC | 1.232 | 0.482 | 0.741 |
| *CTNNAL1* | ProC | 1.129 | 0.482 | 0.741 |
| *PDCD11* | ProC | 1.627 | 0.48 | 0.74 |
| *ODC1* | ProC | 1.263 | 0.478 | 0.739 |
| *WDR1* | ProC | 1.016 | 0.478 | 0.739 |
| *TUBB4B* | ProC | 1.029 | 0.476 | 0.738 |
| *GREM1* | ProC | 1.677 | 0.468 | 0.734 |
| *EIF4G1* | ProC | 1.288 | 0.466 | 0.733 |
| *UBE3A* | ProC | 1.297 | 0.464 | 0.732 |
| *CCT2* | ProC | 1.041 | 0.464 | 0.732 |
| *VEGFA* | ProC | 1.423 | 0.458 | 0.729 |
| *NOLC1* | ProC | 1.308 | 0.458 | 0.729 |
| *SLC7A5* | ProC | 1.446 | 0.456 | 0.728 |
| *PHLDA1* | ProC | 1.360 | 0.456 | 0.728 |
| *GSPT1* | ProC | 1.092 | 0.456 | 0.728 |
| *EPAS1* | ProC | 1.311 | 0.45 | 0.725 |
| *RYBP* | ProC | 1.303 | 0.45 | 0.725 |
| *C3orf52* | ProC | 1.484 | 0.446 | 0.723 |
| *GTPBP4* | ProC | 1.325 | 0.444 | 0.722 |
| *KLHL21* | ProC | 1.031 | 0.444 | 0.722 |
| *NARS* | ProC | 1.038 | 0.442 | 0.721 |
| *SRSF2* | ProC | 1.018 | 0.442 | 0.721 |
| *CHAC1* | ProC | 1.211 | 0.44 | 0.72 |
| *EIF3B* | ProC | 1.352 | 0.438 | 0.719 |
| *CDC42SE1* | ProC | 1.117 | 0.438 | 0.719 |
| *ACTR3* | ProC | 1.011 | 0.438 | 0.719 |
| *SYNJ2* | ProC | 2.291 | 0.436 | 0.718 |
| *TGFB1* | ProC | 1.175 | 0.436 | 0.718 |
| *NIP7* | ProC | 1.301 | 0.434 | 0.717 |
| *MAT2A* | ProC | 1.185 | 0.434 | 0.717 |
| *DLGAP4* | ProC | 1.268 | 0.432 | 0.716 |
| *DKC1* | ProC | 1.536 | 0.43 | 0.715 |
| *NKX3-1* | ProC | 1.347 | 0.428 | 0.714 |
| *SGMS2* | ProC | 1.062 | 0.428 | 0.714 |
| *ARPC5L* | ProC | 1.381 | 0.426 | 0.713 |
| *RRP12* | ProC | 1.892 | 0.424 | 0.712 |
| *AMOTL1* | ProC | 1.328 | 0.424 | 0.712 |
| *TRIB1* | ProC | 1.302 | 0.424 | 0.712 |
| *ARHGAP21* | ProC | 1.160 | 0.418 | 0.709 |
| *EIF3A* | ProC | 1.068 | 0.418 | 0.709 |
| *B3GNT5* | ProC | 1.561 | 0.416 | 0.708 |
| *STK17A* | ProC | 1.285 | 0.416 | 0.708 |
| *SLC4A7* | ProC | 1.198 | 0.416 | 0.708 |
| *EBNA1BP2* | ProC | 1.109 | 0.416 | 0.708 |
| *HNRNPAB* | ProC | 1.283 | 0.414 | 0.707 |
| *SACS* | ProC | 1.620 | 0.412 | 0.706 |
| *ANKRD11* | ProC | 1.145 | 0.412 | 0.706 |
| *YARS* | ProC | 1.009 | 0.412 | 0.706 |
| *RASSF8* | ProC | 1.618 | 0.41 | 0.705 |
| *JHDM1D-AS1* | ProC | 1.496 | 0.41 | 0.705 |
| *TTPAL* | ProC | 1.706 | 0.408 | 0.704 |
| *THBD* | ProC | 2.060 | 0.406 | 0.703 |
| *RELT* | ProC | 1.901 | 0.406 | 0.703 |
| *PA2G4* | ProC | 1.001 | 0.404 | 0.702 |
| *CLMP* | ProC | 1.783 | 0.402 | 0.701 |
| *PCGF5* | ProC | 1.129 | 0.402 | 0.701 |
| *TGFBI* | PreHTC | 1.824 | 0.73 | 0.865 |
| *S100A4* | PreHTC | 2.182 | 0.722 | 0.861 |
| *TNC* | PreHTC | 1.377 | 0.684 | 0.842 |
| *THY1* | PreHTC | 2.022 | 0.678 | 0.839 |
| *ABI3BP* | PreHTC | 1.572 | 0.642 | 0.821 |
| *TNFAIP6* | PreHTC | 2.569 | 0.622 | 0.811 |
| *CRLF1* | PreHTC | 1.872 | 0.61 | 0.805 |
| *FAP* | PreHTC | 2.205 | 0.586 | 0.793 |
| *DPT* | PreHTC | 2.033 | 0.586 | 0.793 |
| *ASPN* | PreHTC | 2.030 | 0.584 | 0.792 |
| *COL5A1* | PreHTC | 1.365 | 0.548 | 0.774 |
| *DNAJB4* | PreHTC | 1.454 | 0.54 | 0.77 |
| *SEMA3C* | PreHTC | 1.820 | 0.528 | 0.764 |
| *PDGFRL* | PreHTC | 1.111 | 0.528 | 0.764 |
| *AKR1C2* | PreHTC | 2.017 | 0.526 | 0.763 |
| *THBS3* | PreHTC | 1.030 | 0.524 | 0.762 |
| *PPIC* | PreHTC | 1.132 | 0.522 | 0.761 |
| *IGFBP7* | PreHTC | 1.284 | 0.52 | 0.76 |
| *STEAP1* | PreHTC | 1.252 | 0.52 | 0.76 |
| *MXRA5* | PreHTC | 1.330 | 0.518 | 0.759 |
| *COL15A1* | PreHTC | 1.307 | 0.506 | 0.753 |
| *TMEM50A* | PreHTC | 1.014 | 0.496 | 0.748 |
| *TMSB4X* | PreHTC | 1.391 | 0.494 | 0.747 |
| *ZFP36* | PreHTC | 1.347 | 0.494 | 0.747 |
| *ADAMTS5* | PreHTC | 1.855 | 0.486 | 0.743 |
| *GALNT15* | PreHTC | 1.185 | 0.484 | 0.742 |
| *SRPX2* | PreHTC | 1.001 | 0.482 | 0.741 |
| *PROCR* | PreHTC | 1.019 | 0.478 | 0.739 |
| *SLC7A2* | PreHTC | 1.355 | 0.466 | 0.733 |
| *ECM1* | PreHTC | 2.050 | 0.464 | 0.732 |
| *AOC2* | PreHTC | 1.184 | 0.464 | 0.732 |
| *GOLGA7B* | PreHTC | 1.935 | 0.462 | 0.731 |
| *CAPS* | PreHTC | 1.428 | 0.46 | 0.73 |
| *HCFC1R1* | PreHTC | 1.029 | 0.456 | 0.728 |
| *AMTN* | PreHTC | 2.489 | 0.454 | 0.727 |
| *C4orf48* | PreHTC | 1.084 | 0.454 | 0.727 |
| *KDELR3* | PreHTC | 1.019 | 0.454 | 0.727 |
| *F5* | PreHTC | 2.140 | 0.446 | 0.723 |
| *IGFBP5* | PreHTC | 3.139 | 0.432 | 0.716 |
| *EFEMP1* | PreHTC | 1.077 | 0.428 | 0.714 |
| *TPPP3* | PreHTC | 1.717 | 0.42 | 0.71 |
| *SOX11* | PreHTC | 1.279 | 0.418 | 0.709 |
| *GALNT16* | PreHTC | 1.278 | 0.41 | 0.705 |
| *C10orf54* | PreHTC | 1.231 | 0.41 | 0.705 |
| *DKK3* | PreHTC | 1.175 | 0.406 | 0.703 |
| *WWP2* | HTC | 2.122 | 0.704 | 0.852 |
| *RNU6-2* | HTC | 3.310 | 0.632 | 0.816 |
| *BHLHE41* | HTC | 3.986 | 0.574 | 0.787 |
| *COL10A1* | HTC | 7.335 | 0.568 | 0.784 |
| *IBSP* | HTC | 3.583 | 0.562 | 0.781 |
| *CRISPLD1* | HTC | 3.588 | 0.538 | 0.769 |
| *MEF2C* | HTC | 2.829 | 0.514 | 0.757 |
| *PLCG2* | HTC | 1.940 | 0.502 | 0.751 |
| *S100A1* | HTC | 1.641 | 0.5 | 0.75 |
| *RMRP* | HTC | 4.717 | 0.494 | 0.747 |
| *SLC14A1* | HTC | 2.186 | 0.49 | 0.745 |
| *SCIN* | HTC | 1.940 | 0.488 | 0.744 |
| *NFIC* | HTC | 1.595 | 0.432 | 0.716 |
| *TXNIP* | HTC | 2.089 | 0.43 | 0.715 |
| *UTRN* | HTC | 1.617 | 0.42 | 0.71 |
| *ZNF385B* | HTC | 2.698 | 0.414 | 0.707 |
| *KMT2E* | HTC | 1.248 | 0.406 | 0.703 |

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| --- | --- | --- |
| ProC GO terms | | |
| ID | Name | *P* value |
| GO:0022613 | ribonucleoprotein complex biogenesis | 2.85E-09 |
| GO:0034660 | ncRNA metabolic process | 6.89E-09 |
| GO:0016072 | rRNA metabolic process | 7.77E-09 |
| GO:0042254 | ribosome biogenesis | 8.43E-09 |
| GO:0006364 | rRNA processing | 5.46E-08 |
| GO:1901566 | organonitrogen compound biosynthetic process | 3.19E-07 |
| GO:0043604 | amide biosynthetic process | 4.07E-06 |
| GO:0034470 | ncRNA processing | 5.09E-06 |
| GO:0002181 | cytoplasmic translation | 1.80E-05 |
| GO:0010608 | posttranscriptional regulation of gene expression | 2.90E-05 |
| GO:0033341 | regulation of collagen binding | 3.61E-05 |
| GO:0060391 | positive regulation of SMAD protein import into nucleus | 4.48E-05 |
| GO:0045446 | endothelial cell differentiation | 5.06E-05 |
| GO:0043491 | protein kinase B signaling | 5.37E-05 |
| GO:0043489 | RNA stabilization | 7.03E-05 |
| GO:0031334 | positive regulation of protein complex assembly | 7.12E-05 |
| GO:0043043 | peptide biosynthetic process | 7.41E-05 |
| GO:0060390 | regulation of SMAD protein import into nucleus | 1.12E-04 |
| GO:0043603 | cellular amide metabolic process | 1.28E-04 |
| GO:0003158 | endothelium development | 1.29E-04 |
| GO:0006412 | translation | 1.86E-04 |
| GO:0006418 | tRNA aminoacylation for protein translation | 2.13E-04 |
| GO:0051054 | positive regulation of DNA metabolic process | 2.27E-04 |
| GO:0006417 | regulation of translation | 2.49E-04 |
| GO:0043039 | tRNA aminoacylation | 2.69E-04 |
| GO:0043038 | amino acid activation | 2.89E-04 |
| GO:0090190 | positive regulation of branching involved in ureteric bud morphogenesis | 3.00E-04 |
| GO:0007184 | SMAD protein import into nucleus | 3.44E-04 |
| GO:1902966 | positive regulation of protein localization to early endosome | 3.54E-04 |
| GO:1902965 | regulation of protein localization to early endosome | 3.54E-04 |
| GO:1900086 | positive regulation of peptidyl-tyrosine autophosphorylation | 3.54E-04 |
| GO:0075525 | viral translational termination-reinitiation | 3.54E-04 |
| GO:2001252 | positive regulation of chromosome organization | 3.62E-04 |
| GO:0006396 | RNA processing | 3.72E-04 |
| GO:0009790 | embryo development | 4.32E-04 |
| GO:0042273 | ribosomal large subunit biogenesis | 4.37E-04 |
| GO:0061213 | positive regulation of mesonephros development | 4.42E-04 |
| GO:0090189 | regulation of branching involved in ureteric bud morphogenesis | 4.42E-04 |
| GO:0001731 | formation of translation preinitiation complex | 4.42E-04 |
| GO:0043408 | regulation of MAPK cascade | 4.72E-04 |
| GO:0034248 | regulation of cellular amide metabolic process | 4.83E-04 |
| GO:0060393 | regulation of pathway-restricted SMAD protein phosphorylation | 4.97E-04 |
| GO:0012501 | programmed cell death | 4.97E-04 |
| GO:1902946 | protein localization to early endosome | 5.29E-04 |
| GO:1900084 | regulation of peptidyl-tyrosine autophosphorylation | 5.29E-04 |
| GO:0010634 | positive regulation of epithelial cell migration | 5.33E-04 |
| GO:0010631 | epithelial cell migration | 5.49E-04 |
| GO:0006518 | peptide metabolic process | 5.57E-04 |
| GO:0043536 | positive regulation of blood vessel endothelial cell migration | 5.58E-04 |
| GO:0090132 | epithelium migration | 5.92E-04 |

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| --- | --- | --- |
| preHTC GO terms | | |
| ID | Name | *P* value |
| GO:0030198 | extracellular matrix organization | 1.29E-05 |
| GO:0043062 | extracellular structure organization | 1.31E-05 |
| GO:0007155 | cell adhesion | 1.96E-05 |
| GO:0022610 | biological adhesion | 2.13E-05 |
| GO:0051241 | negative regulation of multicellular organismal process | 2.86E-05 |
| GO:0001503 | ossification | 3.01E-05 |
| GO:0071798 | response to prostaglandin D | 4.94E-05 |
| GO:0071799 | cellular response to prostaglandin D stimulus | 4.94E-05 |
| GO:0001568 | blood vessel development | 8.80E-05 |
| GO:0048646 | anatomical structure formation involved in morphogenesis | 1.04E-04 |
| GO:0016477 | cell migration | 1.05E-04 |
| GO:0001944 | vasculature development | 1.16E-04 |
| GO:0009887 | animal organ morphogenesis | 1.50E-04 |
| GO:0051093 | negative regulation of developmental process | 1.64E-04 |
| GO:0030334 | regulation of cell migration | 2.17E-04 |
| GO:0060174 | limb bud formation | 2.21E-04 |
| GO:0070170 | regulation of tooth mineralization | 2.21E-04 |
| GO:0048870 | cell motility | 2.41E-04 |
| GO:0051674 | localization of cell | 2.41E-04 |
| GO:2000145 | regulation of cell motility | 3.40E-04 |
| GO:0030574 | collagen catabolic process | 4.62E-04 |
| GO:0072359 | circulatory system development | 4.85E-04 |
| GO:0072358 | cardiovascular system development | 4.85E-04 |
| GO:0001525 | angiogenesis | 5.68E-04 |
| GO:0051270 | regulation of cellular component movement | 5.84E-04 |
| GO:0040012 | regulation of locomotion | 6.11E-04 |
| GO:0044243 | multicellular organismal catabolic process | 6.19E-04 |
| GO:0048592 | eye morphogenesis | 6.52E-04 |
| GO:0045596 | negative regulation of cell differentiation | 8.38E-04 |
| GO:0070167 | regulation of biomineral tissue development | 8.95E-04 |
| GO:0070168 | negative regulation of biomineral tissue development | 1.12E-03 |
| GO:0009611 | response to wounding | 1.25E-03 |
| GO:0040011 | locomotion | 1.26E-03 |
| GO:0034505 | tooth mineralization | 1.33E-03 |
| GO:0048514 | blood vessel morphogenesis | 1.38E-03 |
| GO:0071379 | cellular response to prostaglandin stimulus | 1.44E-03 |

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| --- | --- | --- |
| HTC GO terms | | |
| ID | Name | *P* value |
| GO:0032412 | regulation of ion transmembrane transporter activity | 3.83E-07 |
| GO:0022898 | regulation of transmembrane transporter activity | 4.33E-07 |
| GO:0032409 | regulation of transporter activity | 6.13E-07 |
| GO:0034765 | regulation of ion transmembrane transport | 2.09E-05 |
| GO:0000122 | negative regulation of transcription from RNA polymerase II promoter | 2.31E-05 |
| GO:0034762 | regulation of transmembrane transport | 2.52E-05 |
| GO:1904062 | regulation of cation transmembrane transport | 3.18E-05 |
| GO:0043269 | regulation of ion transport | 1.31E-04 |
| GO:0010959 | regulation of metal ion transport | 1.83E-04 |
| GO:0045652 | regulation of megakaryocyte differentiation | 2.60E-04 |
| GO:0001958 | endochondral ossification | 2.78E-04 |
| GO:0036075 | replacement ossification | 2.78E-04 |
| GO:0045892 | negative regulation of transcription, DNA-templated | 2.80E-04 |
| GO:1901021 | positive regulation of calcium ion transmembrane transporter activity | 2.96E-04 |
| GO:1903507 | negative regulation of nucleic acid-templated transcription | 3.35E-04 |
| GO:1902679 | negative regulation of RNA biosynthetic process | 3.56E-04 |
| GO:0055085 | transmembrane transport | 4.16E-04 |
| GO:0051253 | negative regulation of RNA metabolic process | 4.33E-04 |
| GO:0051216 | cartilage development | 4.83E-04 |
| GO:0045637 | regulation of myeloid cell differentiation | 5.42E-04 |
| GO:2001259 | positive regulation of cation channel activity | 5.88E-04 |
| GO:2000113 | negative regulation of cellular macromolecule biosynthetic process | 6.01E-04 |
| GO:1901532 | regulation of hematopoietic progenitor cell differentiation | 6.69E-04 |
| GO:0045934 | negative regulation of nucleobase-containing compound metabolic process | 7.37E-04 |
| GO:0007527 | adult somatic muscle development | 8.06E-04 |
| GO:0002316 | follicular B cell differentiation | 8.06E-04 |
| GO:0003138 | primary heart field specification | 8.06E-04 |
| GO:0060025 | regulation of synaptic activity | 8.06E-04 |
| GO:0003185 | sinoatrial valve morphogenesis | 8.06E-04 |
| GO:0003172 | sinoatrial valve development | 8.06E-04 |
| GO:0071228 | cellular response to tumor cell | 8.06E-04 |
| GO:0030219 | megakaryocyte differentiation | 8.15E-04 |
| GO:0010558 | negative regulation of macromolecule biosynthetic process | 8.24E-04 |
| GO:0060350 | endochondral bone morphogenesis | 8.77E-04 |
| GO:0031327 | negative regulation of cellular biosynthetic process | 1.03E-03 |
| GO:0010629 | negative regulation of gene expression | 1.10E-03 |
| GO:0034220 | ion transmembrane transport | 1.12E-03 |
| GO:0009890 | negative regulation of biosynthetic process | 1.13E-03 |
| GO:0051172 | negative regulation of nitrogen compound metabolic process | 1.15E-03 |
| GO:0061448 | connective tissue development | 1.15E-03 |
| GO:0050853 | B cell receptor signaling pathway | 1.22E-03 |
| GO:1904427 | positive regulation of calcium ion transmembrane transport | 1.30E-03 |
| GO:0071300 | cellular response to retinoic acid | 1.50E-03 |
| GO:1901019 | regulation of calcium ion transmembrane transporter activity | 1.58E-03 |
| GO:0007521 | muscle cell fate determination | 1.61E-03 |
| GO:0098662 | inorganic cation transmembrane transport | 1.62E-03 |
| GO:0032414 | positive regulation of ion transmembrane transporter activity | 1.80E-03 |
| GO:0045639 | positive regulation of myeloid cell differentiation | 2.28E-03 |
| GO:0032411 | positive regulation of transporter activity | 2.28E-03 |
| GO:0098655 | cation transmembrane transport | 2.35E-03 |