|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **Term** | **Count** | ***p*‐value** | **Genes** |
| BP | GO:0007165~signal transduction | 10 | 7.3E-2 | CD274, GJA1, HPGDS, STMN1, PDE4B, TRIM13, ZNF217, RASSF9, TRHDE, GNG11 |
|  |  |  |  |  |
| BP | GO:0030198~extracellular matrix organization | 4 | 2.9E-2 | LOX, ABI3BP, ITGA2, SPP1 |
| BP | GO:0048545~response to steroid hormone | 2 | 8.5E-2 | LOX, SPP1 |
| CC | GO:0009897~external side of plasma membrane | 4 | 2.9E-2 | SELP, CD274, ITGA2, FCER1A |
|  | | | | |
| CC | GO:0045177~apical part of cell | 3 | 2.2E-2 | SRR, FAT4, EZR |
| CC | GO:0005925~focal adhesion | 5 | 8.9E-2 | GJA1, CSRP2, ITGA2, EZR, FERMT2 |
| MF | GO:0004871~signal transducer activity | 4 | 2.9E-2 | GJA1, STMN1, TRIM13, GNG11 |
|  |  |  |  |  |
| MF | GO:0004842~ubiquitin-protein transferase activity | 7 | 5.1E-2 | KBTBD6, ZNRF3, TRIM24, TRIM13, FBXL3, KBTBD7, TOPORS |
| MF | GO:0034237~protein kinase A regulatory subunit binding | 2 | 1.4E-2 | C2ORF88, EZR |
| KEGG | hsa00670:One carbon pool by folate | 2 | 9.1E-2 | DHFR2, GART |
|  | | | | |
| BP | GO:0006351~transcription, DNA-templated | 33 | 2.3E-2 | CASZ1, ZNF471, ZBTB20, AHR, ZBTB3, MBTD1, PURB, ZNF827, SCML4, E2F1, CCNL1, TEAD2, SCAI, TCF7L2, RBM39, ZNF483, CHURC1, STAT1, PBX2, TRERF1, SMARCA2, EMSY, ZEB2, ZNF519, NFIA, NFIB, ZNF616, MORF4L2, ZNF614, ZNF678, NANOG, BCOR, ZNF236 |
| BP | GO:0045944~positive regulation of transcription from RNA polymerase II promoter | 18 | 2.3E-2 | TCF7L2, RNASEL, STAT1, PBX2, AHR, SMARCA2, VEGFA, ZEB2, NFIA, NFIB, MORF4L2, TRPS1, NAMPT, E2F1, NANOG, BMPR1B, CCNL1, TEAD2 |

young-old

young-middle

young-old DEGs

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| BP | GO:0051301~cell division | 9 | 4.8E-2 | SGO2, CDK19, NUMA1, PPP2R2D, FIGN, ANAPC5, CDC25A, TRIOBP, CDC14A |
| CC | GO:0005662~DNA replication factor A complex | 3 | 1.2E-2 | PURB, RPA4, ERCC5 |

middle-old

|  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| KEGG | | hsa04110:Cell cycle | | 5 | | 0.38E-2 | | E2F1, ANAPC5, CDC25A, CDC14A, CDC14B | |
| CC | | GO:0005654~nucleoplasm | | 13 | | 2.8E-2 | | NFYB, STAT1, ANKRD23, XIAP, NMD3, AHR, CAND1, ZC3H11A, NAMPT, E2F1, ERCC5, MCTP2, C8ORF44 | |
| CC | | GO:0030992~intraciliary transport  particle B | | 2 | | 4.4E-2 | | TTC30A, IFT27 | |

*Note*. BP: biological process; CC: cell component; GO: gene ontology; KEGG: Kyoto Encyclopedia of Genes and Genomes; MF: molecular function (as ranked by the p-value)