|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Category** | **Term** | **Count** | ***p*‐value** | | **Genes** |
| BP | GO:0033993~response to lipid | 10 | 9.12E-4 | | ANXA3, LOX, GJA1, ITGA2, SPP1, CD274, SRR, PDE4B, KMO, SELP |
|  |  |  |  | |  |
| BP | GO:0014070~response to organic cyclic  compound | 9 | 3.28E-4 | | ANXA3, LOX, IFIT1, GJA1, EZR, ITGA2, SPP1, SRR, PDE4B |
| BP | GO:0051098~regulation of  binding | 6 | 2.21-4 | | LOX, IFIT1, STMN1, PPP3CA, ITGA2, CCPG1 |
| CC | GO:0044444~cytoplasmic part | 48 | 1.21E-4 | | GNG11 , PURA , IFIT1, GOLGA8A ,AP1AR ,CAMSAP2, TRIM24, KBTBD7, PIGM, ITGA2, CD274 ,SPP1,SRR,HCFC2 ,RASSF9, FBXL3,FAH ,ITIH4 KBTBD6, SLC25A37, CEP128, KMO , SELP, ST6GAL2, RNF125, TRIP11, ASPA, SHISA2 , STMN1, YIPF5, PPP3CA ,SLC1A6, EZR ,FERMT2,XIRP2 PPP2R2B, ANXA3, ST8SIA4, HPGDS, ZNF217, GJA1, CXADR, FPGT TRIM13 ,GART, CSRP2, TOPORS PDE4B |
|  | | | | | |
| MF | GO:0008092~cytoskeletal protein binding | 7 | 4.28E-4 | | GJA1, STMN1, CAMSAP2, EZR, FERMT2, CSRP2, PDE4B |
| MF | GO:0019904~protein domain specific binding | 5 | 7.35E-4 | | GJA1, MLF1, CXADR, EZR, SRR |
|  | | | |
| MF | GO:0008092~disordered specific domain binding | 2 | 9.58E-4 | | GJA1, EZR |
|  |  |  |  | |  |
| BP | GO:0014070~response to organic cyclic  compound | 9 | 3.28E-4 | | ANXA3, LOX, IFIT1, GJA1, EZR, ITGA2, SPP1, SRR, PDE4B |
| BP | GO:0010769~ regulation of cell morphogenesis involved in differentiation | 9 | 4.77E-4 | | TRIOBP ,PDLIM5, VEGFA, AP1AR, P4HB, ZEB2, PTK2, SPP1, TUBB2B |
| CC | GO:0070062~extracellular exosome | 9 | 7.11E-4 | | HBA2, ITGA4, TPM4, SDF4, TOM1, PP2R1B, DNAJB9, SPP1, RHOJ |
|  | | | | | |
| CC | GO:0044446~intracellular organelle  part | 30 | 2.79E-4 | | TMP4, CASZ1, STAT1, MRPL50, IFT27, DNAJB9, CYP3A5, SLC16A3, SPP1,HBA2,SDF4, SHANK2, WDR63, OAS1, ABCD3, RNF125, SLC37A4, RAD18, TOM1, AAGAB1, DNAJB12, SPACA3, E2F1, TUBB2B, ARGHAP32, GJA1, SDC3, SPIRE2, MS4A3, GJC1 |
| CC | GO:0043233~organelle lumen | 6 | 8.24E-4 | | HBA2, SDF4, SDC3, ABCD3, DNAJB9, SPP1 |

young-old all DEGs

young-middle up DEGs

young-old DEGs

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| MF | GO:0003924~GTPase activity | 4 | 6.07-4 | RASEF, IFT27, RHOJ, TUBB2B |
| KEGG | hsa00350:Tyrosine metabolism | 2 | 9.2E-2 | FAH, COMT |

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| KEGG | hsa00603:Glycosphingolipid biosynthesis - globo series | 2 | 0.38E-2 | FUT, GLA |

*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).

UP-YO