|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **Category** | **Term** | **Count** | ***p*‐value** | **Genes** |
| BP | GO:0048545~response to steroid hormone | 4 | 5.51E−5 | LOX, CASP9, FLT3, SPP1 |
|  |  |  |  |  |
| BP | GO:0014070~response to organic cyclic  compound | 5 | 6.6E−5 | LOX, CASP9, ADA, FLT3, SPP1 |
| BP | GO:0042127~regulation of cell  proliferation | 6 | 9.15E-04 | AGO3 , FUT2 , HPGDS , ADA , FLT3 , NMB |
| BP | GO:0009056~catabolic process | 6 | 9.15E−4 | AGO3 , FUT2, FAH , ADA , GLA , SPP1 |
|  | | | | |
| BP | GO:2000112~regulation of cellular macromolecule biosynthetic process | 9 | 6.16E−5 | TAF15 , IGF2BP2 ,NCOA2 ,USP7 ,CTBP2 ,MED1  ,BCL11A ,PRR16 ,AHR |
| CC | GO:0044424~intracellular part | 38 | 8.08E−6 | NDUFB11 ,PITX2 ,NAGPA ,CAPNS1 ,SHH ,ELK1,STAMBP , STAT1 ,VILL , SRPK3,GAPDHS ,GLO1 ,RFX1, ARPC5 , EIF3C ,FAH ,ATOX1 ,DIAPH1,BUD31, EIF3G, GNG5, PTMA , ZC4H2, INPPL1 , EIF3CL ,DBI ,SULT2A1 ,TACSTD2 ,MUTYH,GNAS ,UCP2 ,SGCB ,HOXD12 ,EMC3 ,RPP38 ,RGS3 ,GAR1, ARHGAP29 |
|  | | | | |

CC GO:0070062~extracellular exosome 10 4.55E-5 GNG5, ARPC5, RALB, FAH, CAPNS1, DBI, STAMBP, TACSTD2, GNAS, GLO1

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| CC | GO:0005578~proteinaceous extracellular matrix | 12 | 1.45E−4 | ASPN, FLRT3, CTHRC1, COL9A1, CRISP3, SMOC2, SPOCK3, CRISPLD2, VEGFA, EFEMP1, COL4A6, MUC4 |
| CC | GO:0031012~extracellular matrix | 12 | 3.42E−4 | ASPN, FGFR2, LGALS3, SPOCK3, SLC25A6, EFEMP1, THSD4, |
|  |  |  |  | COL12A1, TGM4, EEF2, CSTA, ANXA2 |
| CC | GO:0016323~basolateral plasma membrane | 9 | 7.01E−4 | EPCAM, CLDN8, ATP1B1, CHRM3, ANXA1, ABCC4, SLC14A1, AQP3, ANXA2 |
| MF | GO:0008201~heparin binding | 9 | 3.73E−4 | FGFR2, SMOC2, CRISPLD2, LXN, NAV2, VEGFA, LTF, PTN, |
|  |  |  |  | AOC1 |
| MF GO:0019834~phospholipase A2 3 6.99E−4 ANXA1, SCGB1A1, ANXA2  inhibitor activity | | | | |
| MF | GO:0005198~structural molecule activity | 10 | 1.58E−3 | CLDN8, LAMB3, KRT17, KRT5, KRT15, KRT14, ANXA1, NEFH, CSTA, KRT23 |
| MF | GO:0005506~iron ion binding | 7 | 6.66E−3 | P3H2, CYP3A5, MSMO1, ALOX15B, AOX1, LTF, CYP4B1 |
| MF | GO:0005200~structural constituent | 6 | 7.09E−3 | KRT17, KRT5, KRT15, KRT14, NEFH, BICD1 |
|  | of cytoskeleton |  |  |  |
| KEGG hsa04974: Protein digestion and 6 1.77E−3 COL9A1, ATP1B1, COL27A1, COL12A1, MME, COL4A6  absorption | | | | |
| KEGG | hsa04970: Salivary secretion | 4 | 5.42E−2 | CD38, ATP1B1, ADRB1, CHRM3 |
| KEGG | hsa04960: Aldosterone-regulated | 3 | 5.74E−2 | ATP1B1, SFN, SCNN1A |
| sodium reabsorption | | | | |

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KEGG hsa04973: Carbohydrate digestion and absorption

1. 6.55E−2 ATP1B1, SLC2A5, CACNA1D

*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).