

| ID | Description | GeneRatio | BgRatio | pvalue | p.adjust | qvalue | geneID | Count |
|------------|---|-----------|-----------|----------|----------|----------|-----------------------------|-------|
| GO:0008544 | epidermis development | 33/397 | 464/18670 | 1.49E-09 | 5.54E-06 | 5.05E-06 | FA2H/ELF3/IRF6/PKP3/PRSS8/O | 33 |
| GO:0043588 | skin development | 29/397 | 419/18670 | 2.77E-08 | 5.15E-05 | 4.70E-05 | FA2H/IRF6/PKP3/PRSS8/OVOL2 | 29 |
| GO:0007586 | digestion | 16/397 | 139/18670 | 4.52E-08 | 5.59E-05 | 5.10E-05 | PLS1/TFF1/CAPN9/VSIG1/KCNN | 16 |
| GO:0022600 | digestive system process | 13/397 | 100/18670 | 1.99E-07 | 0.000185 | 0.000169 | PLS1/TFF1/VSIG1/KCNN4/MUC: | 13 |
| GO:0048732 | gland development | 27/397 | 434/18670 | 7.05E-07 | 0.000524 | 0.000478 | SOX3/FA2H/ELF3/IRF6/ESRP2/S | 27 |
| GO:0048565 | digestive tract development | 14/397 | 134/18670 | 1.04E-06 | 0.000643 | 0.000587 | PTK6/KLF5/AGR2/OVOL2/SHH/I | 14 |
| GO:0042634 | regulation of hair cycle | 7/397 | 28/18670 | 1.50E-06 | 0.000797 | 0.000727 | FA2H/EPS8L3/FERMT1/SPINK5/ | 7 |
| GO:0006805 | xenobiotic metabolic process | 13/397 | 125/18670 | 2.66E-06 | 0.001201 | 0.001096 | AOC1/HNF4A/CYP3A5/CYP2C18 | 13 |
| GO:0055123 | digestive system development | 14/397 | 146/18670 | 2.91E-06 | 0.001201 | 0.001096 | PTK6/KLF5/AGR2/OVOL2/SHH/I | 14 |
| GO:0032530 | regulation of microvillus organization | 5/397 | 13/18670 | 4.74E-06 | 0.001601 | 0.001461 | PLS1/KLF5/CDHR5/USH1C/CDHI | 5 |
| GO:0032536 | regulation of cell projection size | 5/397 | 13/18670 | 4.74E-06 | 0.001601 | 0.001461 | PLS1/CDHR5/USH1C/CDHR2/XK | 5 |
| GO:0002064 | epithelial cell development | 16/397 | 207/18670 | 9.62E-06 | 0.002761 | 0.00252 | RAB25/KLF5/GRHL2/VSIG1/IHH, | 16 |
| GO:0006721 | terpenoid metabolic process | 12/397 | 120/18670 | 9.66E-06 | 0.002761 | 0.00252 | SDR16C5/SDC1/BCO1/CYP3A5/I | 12 |
| GO:0048706 | embryonic skeletal system development | 12/397 | 126/18670 | 1.59E-05 | 0.004224 | 0.003855 | GRHL2/SHH/IHH/IRX5/TBX15/H | 12 |
| GO:0048754 | branching morphogenesis of an epithelial tube | 13/397 | 150/18670 | 1.97E-05 | 0.004877 | 0.004451 | ESRP2/SHH/IHH/EPHA2/MET/Fc | 13 |
| GO:0042303 | molting cycle | 11/397 | 112/18670 | 2.69E-05 | 0.005869 | 0.005357 | FA2H/EPS8L3/SHH/FERMT1/SPI | 11 |
| GO:0042633 | hair cycle | 11/397 | 112/18670 | 2.69E-05 | 0.005869 | 0.005357 | FA2H/EPS8L3/SHH/FERMT1/SPI | 11 |
| GO:0009913 | epidermal cell differentiation | 21/397 | 358/18670 | 2.95E-05 | 0.005978 | 0.005456 | FA2H/IRF6/PKP3/PRSS8/OVOL2 | 21 |
| GO:0043616 | keratinocyte proliferation | 7/397 | 43/18670 | 3.10E-05 | 0.005978 | 0.005456 | IRF6/SDR16C5/OVOL2/FERMT1, | 7 |
| GO:0071466 | cellular response to xenobiotic stimulus | 14/397 | 180/18670 | 3.22E-05 | 0.005978 | 0.005456 | AOC1/HNF4A/CYP3A5/CYP2C18 | 14 |
| GO:0061138 | morphogenesis of a branching epithelium | 14/397 | 182/18670 | 3.64E-05 | 0.006433 | 0.005872 | ESRP2/GRHL2/SHH/IHH/EPHA2, | 14 |
| GO:0031016 | pancreas development | 9/397 | 78/18670 | 4.05E-05 | 0.006584 | 0.006009 | SHH/IHH/HNF4A/MET/HNF1A/I | 9 |
| GO:0042445 | hormone metabolic process | 16/397 | 233/18670 | 4.14E-05 | 0.006584 | 0.006009 | SDR16C5/SHH/IYD/BCO1/CYP3A | 16 |
| GO:0006720 | isoprenoid metabolic process | 12/397 | 139/18670 | 4.25E-05 | 0.006584 | 0.006009 | SDR16C5/SDC1/BCO1/CYP3A5/I | 12 |
| GO:0051797 | regulation of hair follicle development | 5/397 | 20/18670 | 5.05E-05 | 0.007497 | 0.006842 | FERMT1/SPINK5/DKK4/MSX2/T | 5 |
| GO:0038127 | ERBB signaling pathway | 12/397 | 142/18670 | 5.25E-05 | 0.007497 | 0.006842 | PTK6/CBLC/ERBB3/AGR2/GRB7, | 12 |
| GO:0030277 | maintenance of gastrointestinal epithelium | 5/397 | 21/18670 | 6.51E-05 | 0.008961 | 0.008179 | TFF1/VSIG1/MUC13/TFF2/MUC | 5 |
| GO:0003382 | epithelial cell morphogenesis | 6/397 | 34/18670 | 7.23E-05 | 0.009543 | 0.008709 | RAB25/GRHL2/VSIG1/IHH/MET, | 6 |
| GO:0001523 | retinoid metabolic process | 10/397 | 104/18670 | 7.45E-05 | 0.009543 | 0.008709 | SDR16C5/SDC1/BCO1/CYP3A5/I | 10 |
| GO:0001763 | morphogenesis of a branching structure | 14/397 | 196/18670 | 8.15E-05 | 0.009854 | 0.008994 | ESRP2/GRHL2/SHH/IHH/EPHA2, | 14 |
| GO:0030324 | lung development | 13/397 | 172/18670 | 8.22E-05 | 0.009854 | 0.008994 | ESRP2/AGR2/GRHL2/SHH/SPDE | 13 |
| GO:0060541 | respiratory system development | 14/397 | 198/18670 | 9.09E-05 | 0.010549 | 0.009628 | ESRP2/AGR2/GRHL2/SHH/SPDE | 14 |

| | | | | | | | | |
|------------|---|--------|-----------|----------|----------|----------|-----------------------------|----|
| GO:0034754 | cellular hormone metabolic process | 11/397 | 129/18670 | 9.87E-05 | 0.011004 | 0.010043 | SDR16C5/SHH/BCO1/CYP3A5/C | 11 |
| GO:0030216 | keratinocyte differentiation | 18/397 | 305/18670 | 0.000101 | 0.011004 | 0.010043 | IRF6/PKP3/PRSS8/OVOL2/GRHL | 18 |
| GO:0030323 | respiratory tube development | 13/397 | 176/18670 | 0.000104 | 0.011023 | 0.01006 | ESRP2/AGR2/GRHL2/SHH/SPDE | 13 |
| GO:0016101 | diterpenoid metabolic process | 10/397 | 110/18670 | 0.00012 | 0.012205 | 0.011139 | SDR16C5/SDC1/BCO1/CYP3A5/I | 10 |
| GO:0001894 | tissue homeostasis | 15/397 | 229/18670 | 0.000122 | 0.012205 | 0.011139 | ZG16B/TFF1/VSIG1/IHH/USH1C, | 15 |
| GO:0032528 | microvillus organization | 5/397 | 24/18670 | 0.000129 | 0.012619 | 0.011517 | PLS1/KLF5/CDHR5/USH1C/CDHI | 5 |
| GO:0048568 | embryonic organ development | 22/397 | 428/18670 | 0.000135 | 0.012902 | 0.011775 | OVOL2/GRHL2/SHH/EFNA1/PLC | 22 |
| GO:0070268 | cornification | 10/397 | 112/18670 | 0.000139 | 0.012909 | 0.011781 | PKP3/PRSS8/KRT18/PERP/SPINI | 10 |
| GO:0048562 | embryonic organ morphogenesis | 17/397 | 288/18670 | 0.000156 | 0.013935 | 0.012718 | OVOL2/GRHL2/SHH/EFNA1/IHH | 17 |
| GO:0048704 | embryonic skeletal system morphogenesis | 9/397 | 93/18670 | 0.000162 | 0.013935 | 0.012718 | GRHL2/IRX5/TBX15/TFAP2A/HC | 9 |
| GO:1901184 | regulation of ERBB signaling pathway | 9/397 | 93/18670 | 0.000162 | 0.013935 | 0.012718 | PTK6/CBLC/AGR2/GPRC5A/PTPI | 9 |
| GO:0050673 | epithelial cell proliferation | 22/397 | 434/18670 | 0.000165 | 0.013935 | 0.012718 | IRF6/ESRP2/SDR16C5/MARVELL | 22 |
| GO:1903078 | positive regulation of protein localization to pl | 7/397 | 56/18670 | 0.000176 | 0.014247 | 0.013002 | PLS1/ARHGEF16/AGR2/EPHA2/I | 7 |
| GO:1990778 | protein localization to cell periphery | 18/397 | 319/18670 | 0.000176 | 0.014247 | 0.013002 | PLS1/PKP3/ARHGEF16/AGR2/CI | 18 |
| GO:0007173 | epidermal growth factor receptor signaling pa | 10/397 | 119/18670 | 0.000229 | 0.018113 | 0.016531 | PTK6/CBLC/AGR2/GRB7/GPRC5 | 10 |
| GO:0022612 | gland morphogenesis | 10/397 | 120/18670 | 0.000245 | 0.018988 | 0.01733 | ELF3/ESRP2/SERPINB5/SHH/EPI | 10 |
| GO:1905477 | positive regulation of protein localization to m | 10/397 | 122/18670 | 0.000281 | 0.021274 | 0.019416 | PLS1/ARHGEF16/AGR2/EPHA2/I | 10 |
| GO:0016540 | protein autoprocessing | 4/397 | 16/18670 | 0.000299 | 0.022047 | 0.020122 | MYRF/TMPRSS2/CTSE/F12 | 4 |
| GO:0016266 | O-glycan processing | 7/397 | 61/18670 | 0.000303 | 0.022047 | 0.020122 | B3GNT3/MUC1/GALNT5/MUC1 | 7 |
| GO:0010669 | epithelial structure maintenance | 5/397 | 29/18670 | 0.00033 | 0.023609 | 0.021547 | TFF1/VSIG1/MUC13/TFF2/MUC | 5 |
| GO:1904377 | positive regulation of protein localization to ce | 7/397 | 63/18670 | 0.00037 | 0.025945 | 0.023679 | PLS1/ARHGEF16/AGR2/EPHA2/I | 7 |
| GO:0019731 | antibacterial humoral response | 6/397 | 46/18670 | 0.000406 | 0.027945 | 0.025504 | SLPI/SPINK5/H2BC11/DMBT1/H | 6 |
| GO:0072659 | protein localization to plasma membrane | 15/397 | 260/18670 | 0.000477 | 0.031181 | 0.028458 | PLS1/PKP3/ARHGEF16/AGR2/CI | 15 |
| GO:0045683 | negative regulation of epidermis development | 4/397 | 18/18670 | 0.000486 | 0.031181 | 0.028458 | GRHL2/FERMT1/DKK4/MSX2 | 4 |
| GO:0001942 | hair follicle development | 8/397 | 86/18670 | 0.000487 | 0.031181 | 0.028458 | SHH/FERMT1/SPINK5/DKK4/SO | 8 |
| GO:0042058 | regulation of epidermal growth factor recepto | 8/397 | 86/18670 | 0.000487 | 0.031181 | 0.028458 | PTK6/CBLC/AGR2/GPRC5A/PTPI | 8 |
| GO:0042573 | retinoic acid metabolic process | 5/397 | 32/18670 | 0.000532 | 0.031872 | 0.029088 | CYP3A5/CYP2C18/CYP3A4/UGT | 5 |
| GO:0061572 | actin filament bundle organization | 11/397 | 157/18670 | 0.000547 | 0.031872 | 0.029088 | BAIAP2L1/PLS1/BAIAP2L2/MET, | 11 |
| GO:0022404 | molting cycle process | 8/397 | 88/18670 | 0.000568 | 0.031872 | 0.029088 | SHH/FERMT1/SPINK5/DKK4/SO | 8 |
| GO:0022405 | hair cycle process | 8/397 | 88/18670 | 0.000568 | 0.031872 | 0.029088 | SHH/FERMT1/SPINK5/DKK4/SO | 8 |
| GO:0061097 | regulation of protein tyrosine kinase activity | 8/397 | 88/18670 | 0.000568 | 0.031872 | 0.029088 | PTK6/CBLC/ERBB3/EFNA1/GPRC | 8 |
| GO:0098773 | skin epidermis development | 8/397 | 88/18670 | 0.000568 | 0.031872 | 0.029088 | SHH/FERMT1/SPINK5/DKK4/SO | 8 |
| GO:0060562 | epithelial tube morphogenesis | 17/397 | 322/18670 | 0.000569 | 0.031872 | 0.029088 | ESRP2/OVOL2/GRHL2/SHH/IHH, | 17 |

| | | | | | | | | |
|------------|---|--------|-----------|----------|----------|----------|-----------------------------|----|
| GO:0035094 | response to nicotine | 6/397 | 49/18670 | 0.000575 | 0.031872 | 0.029088 | KCNK1/CHRNA5/SLC7A11/TNF/ | 6 |
| GO:0048546 | digestive tract morphogenesis | 6/397 | 49/18670 | 0.000575 | 0.031872 | 0.029088 | AGR2/OVOL2/SHH/IHH/EPHB3/ | 6 |
| GO:0035115 | embryonic forelimb morphogenesis | 5/397 | 33/18670 | 0.000616 | 0.033651 | 0.030711 | SHH/MSX2/TFAP2A/HOXA11/CI | 5 |
| GO:0048705 | skeletal system morphogenesis | 14/397 | 239/18670 | 0.000629 | 0.033844 | 0.030888 | GRHL2/IHH/IRX5/RFLNA/TBX15, | 14 |
| GO:0060425 | lung morphogenesis | 6/397 | 50/18670 | 0.000642 | 0.034053 | 0.031079 | ESRP2/GRHL2/SHH/FOXA1/ID1/ | 6 |
| GO:0048871 | multicellular organismal homeostasis | 22/397 | 486/18670 | 0.000771 | 0.040323 | 0.036801 | FA2H/ZG16B/TFF1/CLDN4/VSIG | 22 |
| GO:1904375 | regulation of protein localization to cell periph | 9/397 | 115/18670 | 0.000785 | 0.040528 | 0.036988 | PLS1/ARHGEF16/AGR2/MISP/SA | 9 |
| GO:0016042 | lipid catabolic process | 17/397 | 333/18670 | 0.000827 | 0.042075 | 0.0384 | LIPH/PLA2G10/PLA2G4F/PLCD3 | 17 |
| GO:0060428 | lung epithelium development | 5/397 | 36/18670 | 0.000929 | 0.046619 | 0.042547 | AGR2/GRHL2/SHH/SPDEF/FOXA | 5 |
| GO:0048608 | reproductive structure development | 20/397 | 431/18670 | 0.000979 | 0.04851 | 0.044273 | OVOL2/SERPINB5/GRHL2/SHH/I | 20 |