

7c

| Term ID | Biological Process (GO) | Gene Count | Genes | False Discovery Rate |
|------------|---|------------|---|----------------------|
| GO:0050789 | regulation of biological process | 25 | AFGF,ANG1,ANGPT1,CCL2,CSF2,DPP4,EDN1,EGF,ENG,FGF7,HBEGF,IGFBP1,IGFBP2,IGFBP3,IL8,INHBA,LEP,PF4,PLG,PRL,SERPINE1,SR-PSOX,TGFB1,TIMP1,VEGFA | 1.84E-21 |
| GO:0009966 | regulation of signal transduction | 18 | AFGF,CCL2,CSF2,EGF,FGF7,HBEGF,IGFBP1,IGFBP2,IGFBP3,IL8,INHBA,LEP,PF4,PRL,SR-PSOX,TGFB1,TIMP1,VEGFA | 2.93E-20 |
| GO:0042127 | regulation of cell population proliferation | 15 | AFGF,CCL2,CSF2,DPP4,HBEGF,IGFBP2,IGFBP3,IL8,INHBA,LEP,PF4,PRL,TGFB1,TIMP1,VEGFA | 4.82E-20 |
| GO:0050794 | regulation of cellular process | 23 | AFGF,ANG1,ANGPT1,CCL2,CSF2,DPP4,EGF,ENG,FGF7,HBEGF,IGFBP1,IGFBP2,IGFBP3,IL8,INHBA,LEP,PF4,PRL,SERPINE1,SR-PSOX,TGFB1,TIMP1,VEGFA | 4.82E-20 |
| GO:0032502 | developmental process | 16 | AFGF,ANG1,ANGPT1,ANGPT2,CCL2,EGF,ENG,HBEGF,IGFBP3,IL8,INHBA,LEP,PRL,SERPINE1,TGFB1,VEGFA | 5.85E-16 |
| GO:0048856 | anatomical structure development | 14 | AFGF,ANG1,ANGPT1,ANGPT2,CCL2,EGF,ENG,HBEGF,IL8,INHBA,LEP,PRL,TGFB1,VEGFA | 1.47E-13 |
| GO:0030334 | regulation of cell migration | 9 | AFGF,CCL2,HBEGF,IGFBP3,IL8,PF4,SR-PSOX,TGFB1,VEGFA | 4.91E-13 |
| GO:0032879 | regulation of localization | 11 | AFGF,CCL2,HBEGF,IGFBP3,IL8,INHBA,LEP,PF4,SR-PSOX,TGFB1,VEGFA | 7.69E-12 |
| GO:0071363 | cellular response to growth factor stimulus | 7 | AFGF,CCL2,ENG,FGF7,IL8,TGFB1,VEGFA | 4.74E-11 |
| GO:0001525 | angiogenesis | 6 | AFGF,ANG1,ANGPT1,ANGPT2,ENG,VEGFA | 1.67E-10 |
| GO:0035295 | tube development | 7 | AFGF,ANG1,ANGPT1,ANGPT2,ENG,IL8,VEGFA | 3.84E-10 |
| GO:0030154 | cell differentiation | 10 | AFGF,ANG1,ANGPT1,ANGPT2,CCL2,IGFBP3,INHBA,LEP,TGFB1,VEGFA | 5.25E-10 |
| GO:0060326 | cell chemotaxis | 6 | CCL2,HBEGF,IL8,PF4,SR-PSOX,VEGFA | 9.99E-10 |
| GO:0040008 | regulation of growth | 7 | CSF2,IGFBP1,IGFBP2,IGFBP3,INHBA,SR-PSOX,TGFB1 | 1.11E-09 |
| GO:0006950 | response to stress | 10 | AFGF,CCL2,HBEGF,IL8,PF4,PLG,PRL,SR-PSOX,TGFB1,VEGFA | 2.03E-09 |

| Term ID | Cellular Component (GO) | Gene Count | Genes | False Discovery Rate |
|------------|--------------------------------|------------|---|----------------------|
| GO:0005576 | extracellular region | 25 | AFGF,ANG1,ANGPT1,ANGPT2,CCL2,CSF2,DPP4,EDN1,FGF7,HBEGF,IGFBP1,IGFBP2,IGFBP3,IL8,INHBA,LEP,PF4,PLAU,PLG,PRL,SERPINE1,SR-PSOX,TGFB1,TIMP1,VEGFA | 6.24E-29 |
| GO:0009986 | cell surface | 4 | DPP4,HBEGF,TGFB1,VEGFA | 3.82E-05 |
| GO:0005622 | intracellular | 11 | AFGF,ANG1,CCL2,CSF2,DPP4,IGFBP3,IL8,INHBA,LEP,TGFB1,VEGFA | 4.84E-05 |
| GO:0071944 | cell periphery | 5 | AFGF,DPP4,EGF,ENG,HBEGF | 0.0083 |
| GO:0016021 | integral component of membrane | 5 | DPP4,EGF,ENG,HBEGF,SR-PSOX | 0.0098 |
| GO:0016020 | membrane | 6 | DPP4,EGF,ENG,HBEGF,SR-PSOX,VEGFA | 0.0122 |
| GO:0005634 | nucleus | 4 | AFGF,ANG1,IGFBP3,TGFB1 | 0.0197 |
| GO:0031410 | cytoplasmic vesicle | 3 | ANG1,DPP4,VEGFA | 0.0197 |
| GO:0043227 | membrane-bounded organelle | 6 | AFGF,ANG1,DPP4,IGFBP3,TGFB1,VEGFA | 0.0197 |

| Term ID | Molecular Function (GO) | Gene Count | Genes | False Discovery Rate |
|------------|---------------------------------------|------------|--|----------------------|
| GO:0005102 | signaling receptor binding | 19 | AFGF,ANGPT1,ANGPT2,CCL2,CSF2,DPP4,EGF,ENG,FGF7,HBEGF,IL8,INHBA,LEP,PF4,PRL,SR-PSOX,TGFB1,TIMP1,VEGFA | 1.50E-24 |
| GO:0005515 | protein binding | 23 | AFGF,ANG1,ANGPT1,ANGPT2,CCL2,CSF2,DPP4,EGF,ENG,FGF7,HBEGF,IGFBP1,IGFBP2,IGFBP3,IL8,INHBA,LEP,PF4,PRL,SR-PSOX,TGFB1,TIMP1,VEGFA | 1.50E-24 |
| GO:0048018 | receptor ligand activity | 15 | AFGF,CCL2,CSF2,EGF,FGF7,HBEGF,IL8,INHBA,LEP,PF4,PRL,SR-PSOX,TGFB1,TIMP1,VEGFA | 2.83E-20 |
| GO:0008083 | growth factor activity | 9 | AFGF,CSF2,EGF,FGF7,HBEGF,INHBA,TGFB1,TIMP1,VEGFA | 6.11E-15 |
| GO:0005125 | cytokine activity | 9 | CCL2,CSF2,IL8,INHBA,PF4,SR-PSOX,TGFB1,TIMP1,VEGFA | 2.35E-13 |
| GO:0005539 | glycosaminoglycan binding | 6 | AFGF,ENG,FGF7,HBEGF,PF4,VEGFA | 1.87E-09 |
| GO:0008201 | heparin binding | 5 | AFGF,FGF7,HBEGF,PF4,VEGFA | 6.47E-08 |
| GO:0008009 | chemokine activity | 4 | CCL2,IL8,PF4,SR-PSOX | 3.34E-07 |
| GO:0031994 | insulin-like growth factor I binding | 3 | IGFBP1,IGFBP2,IGFBP3 | 4.10E-06 |
| GO:0031995 | insulin-like growth factor II binding | 3 | IGFBP1,IGFBP2,IGFBP3 | 4.10E-06 |

| Term ID | KEGG Pathway | Gene Count | Genes | False Discovery Rate |
|----------|--|------------|---|----------------------|
| ssc04151 | PI3K-Akt signaling pathway | 14 | AFGF,ANGPT1,ANGPT2,AREG,EGF,FGF4,FGF7,HGF,PDGFA,PGF,PRL,THBS1,THBS2,VEGFA | 4.92E-13 |
| ssc04060 | Cytokine-cytokine receptor interaction | 12 | CCL2,CSF2,EGF,HGF,IL8,LEP,PDGFA,PF4,PRL,SR-PSOX,TGFB1,VEGFA | 3.18E-12 |
| ssc04015 | Rap1 signaling pathway | 11 | AFGF,ANGPT1,ANGPT2,EGF,FGF4,FGF7,HGF,PDGFA,PGF,THBS1,VEGFA | 1.53E-11 |
| ssc04010 | MAPK signaling pathway | 12 | AFGF,ANGPT1,ANGPT2,AREG,EGF,FGF4,FGF7,HGF,PDGFA,PGF,TGFB1,VEGFA | 1.63E-11 |
| ssc04014 | Ras signaling pathway | 10 | AFGF,ANGPT1,ANGPT2,EGF,FGF4,FGF7,HGF,PDGFA,PGF,VEGFA | 7.16E-10 |
| ssc04066 | HIF-1 signaling pathway | 7 | ANGPT1,ANGPT2,EDN1,EGF,SERPINE1,TIMP1,VEGFA | 2.67E-08 |
| ssc04933 | AGE-RAGE signaling pathway in diabetic complications | 7 | CCL2,EDN1,F3,IL8,SERPINE1,TGFB1,VEGFA | 2.67E-08 |
| ssc04510 | Focal adhesion | 7 | EGF,HGF,PDGFA,PGF,THBS1,THBS2,VEGFA | 1.01E-06 |
| ssc04115 | p53 signaling pathway | 4 | IGFBP3,SERPINE1,SERPINE1,THBS1 | 6.74E-05 |
| ssc04630 | Jak-STAT signaling pathway | 5 | CSF2,EGF,LEP,PDGFA,PRL | 8.16E-05 |