**SUPPLEMENTARY DATA**

**Supplementary Table S1. Differentially expressed KEGG pathways in detrusor PDGFRα+ cells**

|  |  |  |
| --- | --- | --- |
|  | KEGG pathway | Adjusted *P* |
| Upregulated | Pathways in cancer | 1.1E-02 |
|  | Protein processing in endoplasmic reticulum | 1.5E-06 |
|  | Lysosome | 2.2E-04 |
|  | Osteoclast differentiation | 4.5E-02 |
|  | ECM-receptor interaction | 5.0E-02 |
|  | Protein digestion and absorption | 2.4E-03 |
|  | Basal cell carcinoma | 1.1E-02 |
|  | N-Glycan biosynthesis | 2.3E-02 |
|  | Amino sugar and nucleotide sugar metabolism | 2.3E-02 |
|  | Hedgehog signaling pathway | 4.6E-02 |
|  | Antigen processing and presentation | 4.6E-02 |
|  |  |  |
| Downregulated | Pyruvate metabolism | 4.7E-02 |
|  | Valine, leucine and isoleucine degradation | 2.3E-02 |
|  | Glycolysis / Gluconeogenesis | 7.2E-03 |
|  | Proteasome | 1.2E-04 |
|  | Arrhythmogenic right ventricular cardiomyopathy (ARVC) | 4.6E-02 |
|  | Cardiac muscle contraction | 9.2E-04 |
|  | Tight junction | 4.6E-02 |
|  | Ribosome | 9.4E-09 |
|  | Parkinson's disease | 2.5E-10 |
|  | Oxidative phosphorylation | 3.2E-10 |
|  | Alzheimer's disease | 4.5E-08 |
|  | Huntington's disease | 1.1E-09 |
|  | Metabolic pathways | 4.6E-02 |

**Supplementary Table S2. Differentially expressed KEGG pathways in suburothelial PDGFRα+ cells**

|  |  |  |
| --- | --- | --- |
|  | KEGG pathway | Adjusted P |
| Upregulated | Focal adhesion | 2.9E-03 |
|  | Protein processing in endoplasmic reticulum | 1.1E-02 |
|  | Wnt signaling pathway | 2.1E-02 |
|  | Cytokine-cytokine receptor interaction | 3.7E-02 |
|  | Jak-STAT signaling pathway | 2.7E-02 |
|  | ECM-receptor interaction | 4.5E-03 |
|  | Dilated cardiomyopathy | 2.9E-03 |
|  | Amoebiasis | 2.6E-02 |
|  | Hypertrophic cardiomyopathy (HCM) | 1.1E-02 |
|  | Protein digestion and absorption | 2.6E-02 |
|  |  |  |
| Downregulated | Oxidative phosphorylation | 3.1E-02 |
|  | Parkinson's disease | 2.6E-02 |
|  | Alzheimer's disease | 3.7E-02 |
|  | Ribosome | 5.3E-13 |

**Supplementary Table S3. Differentially expressed GO biological process terms in detrusor PDGFRα+ cells**

|  | GO term | Adjusted *P* |
| --- | --- | --- |
| Upregulated | GO:0065007~biological regulation | 1.5E-03 |
|  | GO:0050789~regulation of biological process | 9.4E-04 |
|  | GO:0050794~regulation of cellular process | 6.4E-04 |
|  | GO:0050896~response to stimulus | 4.2E-03 |
|  | GO:0051716~cellular response to stimulus | 3.9E-03 |
|  | GO:0032502~developmental process | 2.7E-04 |
|  | GO:0032501~multicellular organismal process | 5.4E-03 |
|  | GO:0007275~multicellular organismal development | 2.8E-05 |
|  | GO:0007154~cell communication | 6.7E-03 |
|  | GO:0007165~signal transduction | 1.2E-03 |
|  | GO:0048856~anatomical structure development | 1.7E-04 |
|  | GO:0023052~signaling | 1.0E-02 |
|  | GO:0048731~system development | 1.7E-05 |
|  | GO:0048518~positive regulation of biological process | 3.8E-03 |
|  | GO:0080090~regulation of primary metabolic process | 4.6E-02 |
|  | GO:0048522~positive regulation of cellular process | 3.8E-03 |
|  | GO:0048519~negative regulation of biological process | 5.1E-03 |
|  | GO:0006351~transcription, DNA-dependent | 1.2E-03 |
|  | GO:0019219~regulation of nucleobase-containing compound metabolic process | 4.9E-03 |
|  | GO:0048523~negative regulation of cellular process | 2.9E-03 |
|  | GO:0048869~cellular developmental process | 4.0E-04 |
|  | GO:0009889~regulation of biosynthetic process | 6.7E-03 |
|  | GO:0031326~regulation of cellular biosynthetic process | 6.7E-03 |
|  | GO:0048583~regulation of response to stimulus | 1.7E-05 |
|  | GO:0030154~cell differentiation | 3.0E-04 |
|  | GO:0010556~regulation of macromolecule biosynthetic process | 5.9E-03 |
|  | GO:2000112~regulation of cellular macromolecule biosynthetic process | 5.3E-03 |
|  | GO:0006355~regulation of transcription, DNA-dependent | 1.4E-03 |
|  | GO:0051171~regulation of nitrogen compound metabolic process | 3.2E-02 |
|  | GO:0051252~regulation of RNA metabolic process | 3.3E-03 |
|  | GO:0010468~regulation of gene expression | 2.0E-02 |
|  | GO:2001141~regulation of RNA biosynthetic process | 2.6E-03 |
|  | GO:0048513~organ development | 3.4E-04 |
|  | GO:0007166~cell surface receptor signaling pathway | 1.5E-03 |
|  | GO:0023051~regulation of signaling | 2.2E-04 |
|  | GO:0042221~response to chemical stimulus | 2.2E-02 |
|  | GO:0009966~regulation of signal transduction | 7.7E-05 |
|  | GO:0009653~anatomical structure morphogenesis | 1.2E-03 |
|  | GO:0010033~response to organic substance | 2.4E-03 |
|  | GO:0050793~regulation of developmental process | 4.2E-06 |
|  | GO:0007399~nervous system development | 1.4E-03 |
|  | GO:0051239~regulation of multicellular organismal process | 1.2E-03 |
|  | GO:0008283~cell proliferation | 1.3E-03 |
|  | GO:0009888~tissue development | 3.5E-05 |
|  | GO:0006366~transcription from RNA polymerase II promoter | 3.3E-03 |
|  | GO:0070887~cellular response to chemical stimulus | 2.1E-02 |
|  | GO:0010646~regulation of cell communication | 1.4E-02 |
|  | GO:2000026~regulation of multicellular organismal development | 4.7E-05 |
|  | GO:0051173~positive regulation of nitrogen compound metabolic process | 1.4E-03 |
|  | GO:0009891~positive regulation of biosynthetic process | 3.6E-03 |
|  | GO:0031328~positive regulation of cellular biosynthetic process | 3.3E-03 |
|  | GO:0045935~positive regulation of nucleobase-containing compound metabolic process | 2.6E-03 |
|  | GO:0010628~positive regulation of gene expression | 1.2E-03 |
|  | GO:0010557~positive regulation of macromolecule biosynthetic process | 2.5E-03 |
|  | GO:0009605~response to external stimulus | 1.5E-02 |
|  | GO:0042127~regulation of cell proliferation | 4.8E-03 |
|  | GO:0006357~regulation of transcription from RNA polymerase II promoter | 4.0E-03 |
|  | GO:0071310~cellular response to organic substance | 9.4E-03 |
|  | GO:0071704~organic substance metabolic process | 1.4E-02 |
|  | GO:0045595~regulation of cell differentiation | 1.9E-04 |
|  | GO:1901135~carbohydrate derivative metabolic process | 1.0E-02 |
|  | GO:0040011~locomotion | 2.2E-02 |
|  | GO:0045893~positive regulation of transcription, DNA-dependent | 2.4E-03 |
|  | GO:0051254~positive regulation of RNA metabolic process | 6.7E-03 |
|  | GO:0007167~enzyme linked receptor protein signaling pathway | 1.0E-03 |
|  | GO:0031327~negative regulation of cellular biosynthetic process | 3.2E-03 |
|  | GO:0022008~neurogenesis | 1.8E-02 |
|  | GO:0009890~negative regulation of biosynthetic process | 5.6E-03 |
|  | GO:0009790~embryo development | 4.9E-04 |
|  | GO:0010558~negative regulation of macromolecule biosynthetic process | 5.1E-03 |
|  | GO:0048584~positive regulation of response to stimulus | 2.8E-02 |
|  | GO:2000113~negative regulation of cellular macromolecule biosynthetic process | 4.8E-03 |
|  | GO:0009887~organ morphogenesis | 1.8E-05 |
|  | GO:0040007~growth | 6.4E-04 |
|  | GO:0051094~positive regulation of developmental process | 4.9E-06 |
|  | GO:0051172~negative regulation of nitrogen compound metabolic process | 1.3E-02 |
|  | GO:0048699~generation of neurons | 4.7E-02 |
|  | GO:0072358~cardiovascular system development | 2.9E-03 |
|  | GO:0072359~circulatory system development | 2.9E-03 |
|  | GO:0045934~negative regulation of nucleobase-containing compound metabolic process | 1.5E-02 |
|  | GO:0051253~negative regulation of RNA metabolic process | 6.7E-03 |
|  | GO:0010629~negative regulation of gene expression | 1.9E-02 |
|  | GO:0048870~cell motility | 2.3E-02 |
|  | GO:0051674~localization of cell | 2.3E-02 |
|  | GO:0045892~negative regulation of transcription, DNA-dependent | 6.7E-03 |
|  | GO:0018193~peptidyl-amino acid modification | 1.5E-03 |
|  | GO:0005975~carbohydrate metabolic process | 5.9E-03 |
|  | GO:0016477~cell migration | 2.8E-02 |
|  | GO:0048585~negative regulation of response to stimulus | 2.3E-02 |
|  | GO:0023056~positive regulation of signaling | 2.8E-02 |
|  | GO:0010647~positive regulation of cell communication | 3.5E-02 |
|  | GO:0001944~vasculature development | 6.4E-04 |
|  | GO:0045944~positive regulation of transcription from RNA polymerase II promoter | 8.7E-03 |
|  | GO:0009967~positive regulation of signal transduction | 4.6E-02 |
|  | GO:0060429~epithelium development | 9.4E-04 |
|  | GO:0001568~blood vessel development | 1.7E-03 |
|  | GO:0008284~positive regulation of cell proliferation | 1.1E-02 |
|  | GO:0009100~glycoprotein metabolic process | 1.3E-07 |
|  | GO:0009968~negative regulation of signal transduction | 4.2E-02 |
|  | GO:0001501~skeletal system development | 4.5E-08 |
|  | GO:1901137~carbohydrate derivative biosynthetic process | 4.9E-06 |
|  | GO:0045597~positive regulation of cell differentiation | 8.9E-04 |
|  | GO:0035295~tube development | 1.7E-04 |
|  | GO:0009792~embryo development ending in birth or egg hatching | 3.1E-03 |
|  | GO:0043009~chordate embryonic development | 3.8E-03 |
|  | GO:0034097~response to cytokine stimulus | 2.4E-02 |
|  | GO:0009101~glycoprotein biosynthetic process | 1.8E-06 |
|  | GO:0048598~embryonic morphogenesis | 2.8E-03 |
|  | GO:0051093~negative regulation of developmental process | 1.8E-02 |
|  | GO:0000122~negative regulation of transcription from RNA polymerase II promoter | 1.5E-02 |
|  | GO:0048514~blood vessel morphogenesis | 2.2E-02 |
|  | GO:0051270~regulation of cellular component movement | 2.3E-02 |
|  | GO:0040012~regulation of locomotion | 3.0E-02 |
|  | GO:2000145~regulation of cell motility | 2.2E-02 |
|  | GO:0051347~positive regulation of transferase activity | 5.0E-02 |
|  | GO:0051960~regulation of nervous system development | 1.2E-02 |
|  | GO:0030334~regulation of cell migration | 3.0E-02 |
|  | GO:0048729~tissue morphogenesis | 3.2E-02 |
|  | GO:0070085~glycosylation | 1.2E-05 |
|  | GO:0051056~regulation of small GTPase mediated signal transduction | 3.3E-02 |
|  | GO:0006486~protein glycosylation | 2.4E-05 |
|  | GO:0043413~macromolecule glycosylation | 2.4E-05 |
|  | GO:0001503~ossification | 7.7E-05 |
|  | GO:0007423~sensory organ development | 1.2E-02 |
|  | GO:0045596~negative regulation of cell differentiation | 4.2E-02 |
|  | GO:0048011~nerve growth factor receptor signaling pathway | 1.4E-03 |
|  | GO:0002009~morphogenesis of an epithelium | 2.0E-02 |
|  | GO:0007389~pattern specification process | 2.8E-02 |
|  | GO:0035239~tube morphogenesis | 2.9E-03 |
|  | GO:0051090~regulation of sequence-specific DNA binding transcription factor activity | 3.7E-02 |
|  | GO:0048568~embryonic organ development | 1.3E-03 |
|  | GO:0001655~urogenital system development | 1.4E-03 |
|  | GO:0043687~post-translational protein modification | 1.8E-06 |
|  | GO:0051241~negative regulation of multicellular organismal process | 2.4E-02 |
|  | GO:0051272~positive regulation of cellular component movement | 1.0E-02 |
|  | GO:0050673~epithelial cell proliferation | 1.3E-02 |
|  | GO:0048589~developmental growth | 1.8E-02 |
|  | GO:2000147~positive regulation of cell motility | 1.1E-02 |
|  | GO:0040017~positive regulation of locomotion | 1.5E-02 |
|  | GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway | 4.1E-03 |
|  | GO:0043062~extracellular structure organization | 1.8E-06 |
|  | GO:0030198~extracellular matrix organization | 1.7E-06 |
|  | GO:0030855~epithelial cell differentiation | 2.0E-02 |
|  | GO:0003002~regionalization | 1.8E-02 |
|  | GO:0030335~positive regulation of cell migration | 2.5E-02 |
|  | GO:0072001~renal system development | 3.3E-03 |
|  | GO:0001822~kidney development | 2.0E-03 |
|  | GO:0061448~connective tissue development | 6.8E-04 |
|  | GO:0048705~skeletal system morphogenesis | 4.5E-05 |
|  | GO:0060562~epithelial tube morphogenesis | 2.0E-02 |
|  | GO:0060541~respiratory system development | 5.7E-04 |
|  | GO:0008544~epidermis development | 1.9E-02 |
|  | GO:0050678~regulation of epithelial cell proliferation | 2.0E-02 |
|  | GO:0048193~Golgi vesicle transport | 2.1E-02 |
|  | GO:0001654~eye development | 4.7E-02 |
|  | GO:0006986~response to unfolded protein | 1.0E-03 |
|  | GO:0051052~regulation of DNA metabolic process | 4.1E-02 |
|  | GO:0035966~response to topologically incorrect protein | 3.4E-03 |
|  | GO:0001763~morphogenesis of a branching structure | 2.1E-02 |
|  | GO:0048562~embryonic organ morphogenesis | 1.0E-03 |
|  | GO:0030278~regulation of ossification | 1.4E-03 |
|  | GO:0030323~respiratory tube development | 1.6E-03 |
|  | GO:0051091~positive regulation of sequence-specific DNA binding transcription factor activity | 2.3E-02 |
|  | GO:0030324~lung development | 2.8E-03 |
|  | GO:0006487~protein N-linked glycosylation | 1.1E-05 |
|  | GO:0007179~transforming growth factor beta receptor signaling pathway | 1.1E-03 |
|  | GO:0051216~cartilage development | 2.9E-03 |
|  | GO:0018196~peptidyl-asparagine modification | 2.2E-05 |
|  | GO:0018279~protein N-linked glycosylation via asparagine | 1.8E-05 |
|  | GO:0005976~polysaccharide metabolic process | 3.3E-03 |
|  | GO:0006984~ER-nucleus signaling pathway | 3.6E-04 |
|  | GO:0034976~response to endoplasmic reticulum stress | 2.3E-03 |
|  | GO:0048754~branching morphogenesis of an epithelial tube | 3.2E-02 |
|  | GO:0090092~regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 2.5E-02 |
|  | GO:0007219~Notch signaling pathway | 3.6E-02 |
|  | GO:0050679~positive regulation of epithelial cell proliferation | 5.9E-03 |
|  | GO:0009306~protein secretion | 1.9E-02 |
|  | GO:0043583~ear development | 3.8E-02 |
|  | GO:0048736~appendage development | 2.8E-02 |
|  | GO:0060173~limb development | 2.8E-02 |
|  | GO:0021915~neural tube development | 7.6E-03 |
|  | GO:0001649~osteoblast differentiation | 4.2E-02 |
|  | GO:0035967~cellular response to topologically incorrect protein | 4.7E-03 |
|  | GO:0030968~endoplasmic reticulum unfolded protein response | 1.6E-03 |
|  | GO:0034620~cellular response to unfolded protein | 1.6E-03 |
|  | GO:0042445~hormone metabolic process | 1.4E-02 |
|  | GO:0048706~embryonic skeletal system development | 6.2E-04 |
|  | GO:0051604~protein maturation | 1.1E-02 |
|  | GO:0016485~protein processing | 2.7E-03 |
|  | GO:0045787~positive regulation of cell cycle | 3.3E-02 |
|  | GO:0014075~response to amine stimulus | 6.7E-03 |
|  | GO:0035107~appendage morphogenesis | 4.0E-02 |
|  | GO:0035108~limb morphogenesis | 4.0E-02 |
|  | GO:0051656~establishment of organelle localization | 4.2E-02 |
|  | GO:0006275~regulation of DNA replication | 6.7E-03 |
|  | GO:0031214~biomineral tissue development | 5.6E-03 |
|  | GO:0032075~positive regulation of nuclease activity | 6.2E-04 |
|  | GO:0032069~regulation of nuclease activity | 1.6E-03 |
|  | GO:0060348~bone development | 2.0E-03 |
|  | GO:0006987~activation of signaling protein activity involved in unfolded protein response | 4.5E-04 |
|  | GO:0000271~polysaccharide biosynthetic process | 6.3E-03 |
|  | GO:0006766~vitamin metabolic process | 2.2E-02 |
|  | GO:0001890~placenta development | 4.2E-02 |
|  | GO:0010466~negative regulation of peptidase activity | 2.3E-02 |
|  | GO:0008217~regulation of blood pressure | 4.2E-02 |
|  | GO:0001101~response to acid | 8.6E-03 |
|  | GO:0006022~aminoglycan metabolic process | 1.4E-03 |
|  | GO:0051054~positive regulation of DNA metabolic process | 1.5E-02 |
|  | GO:0010951~negative regulation of endopeptidase activity | 3.2E-02 |
|  | GO:0045667~regulation of osteoblast differentiation | 3.4E-02 |
|  | GO:0030509~BMP signaling pathway | 4.1E-02 |
|  | GO:0001657~ureteric bud development | 3.9E-02 |
|  | GO:0035270~endocrine system development | 2.6E-02 |
|  | GO:0030902~hindbrain development | 3.1E-02 |
|  | GO:0030282~bone mineralization | 8.7E-03 |
|  | GO:0002526~acute inflammatory response | 6.7E-03 |
|  | GO:0007088~regulation of mitosis | 5.0E-02 |
|  | GO:0051783~regulation of nuclear division | 5.0E-02 |
|  | GO:0030203~glycosaminoglycan metabolic process | 3.8E-03 |
|  | GO:0051648~vesicle localization | 1.8E-02 |
|  | GO:0007224~smoothened signaling pathway | 3.9E-03 |
|  | GO:0043200~response to amino acid stimulus | 1.1E-02 |
|  | GO:0017015~regulation of transforming growth factor beta receptor signaling pathway | 1.9E-02 |
|  | GO:0002062~chondrocyte differentiation | 2.3E-02 |
|  | GO:0035282~segmentation | 1.3E-02 |
|  | GO:0001656~metanephros development | 3.4E-02 |
|  | GO:0006888~ER to Golgi vesicle-mediated transport | 2.0E-02 |
|  | GO:0042471~ear morphogenesis | 4.4E-02 |
|  | GO:0042058~regulation of epidermal growth factor receptor signaling pathway | 3.8E-02 |
|  | GO:1901184~regulation of ERBB signaling pathway | 3.8E-02 |
|  | GO:0060349~bone morphogenesis | 1.6E-02 |
|  | GO:0051650~establishment of vesicle localization | 2.6E-03 |
|  | GO:0048864~stem cell development | 3.2E-02 |
|  | GO:0060021~palate development | 3.4E-02 |
|  | GO:0090101~negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 4.1E-02 |
|  | GO:0009798~axis specification | 1.6E-02 |
|  | GO:0010469~regulation of receptor activity | 3.6E-02 |
|  | GO:0045598~regulation of fat cell differentiation | 4.4E-02 |
|  | GO:0009953~dorsal/ventral pattern formation | 3.4E-02 |
|  | GO:0070167~regulation of biomineral tissue development | 8.2E-03 |
|  | GO:0006029~proteoglycan metabolic process | 3.2E-03 |
|  | GO:0019827~stem cell maintenance | 2.2E-02 |
|  | GO:0048704~embryonic skeletal system morphogenesis | 2.1E-02 |
|  | GO:0030510~regulation of BMP signaling pathway | 2.4E-02 |
|  | GO:0030500~regulation of bone mineralization | 1.1E-02 |
|  | GO:0044236~multicellular organismal metabolic process | 3.2E-02 |
|  | GO:0071417~cellular response to organic nitrogen | 4.4E-02 |
|  | GO:0006903~vesicle targeting | 2.4E-03 |
|  | GO:0021549~cerebellum development | 3.9E-02 |
|  | GO:0071418~cellular response to amine stimulus | 3.4E-02 |
|  | GO:0042059~negative regulation of epidermal growth factor receptor signaling pathway | 1.6E-02 |
|  | GO:1901185~negative regulation of ERBB signaling pathway | 1.6E-02 |
|  | GO:0007030~Golgi organization | 2.8E-02 |
|  | GO:0006023~aminoglycan biosynthetic process | 2.0E-03 |
|  | GO:0006040~amino sugar metabolic process | 2.4E-03 |
|  | GO:0044259~multicellular organismal macromolecule metabolic process | 4.1E-02 |
|  | GO:0071229~cellular response to acid | 4.3E-02 |
|  | GO:0006900~membrane budding | 2.1E-02 |
|  | GO:0019233~sensory perception of pain | 4.4E-02 |
|  | GO:0008589~regulation of smoothened signaling pathway | 9.4E-03 |
|  | GO:0006901~vesicle coating | 1.1E-02 |
|  | GO:0043588~skin development | 3.9E-02 |
|  | GO:0016266~O-glycan processing | 1.8E-02 |
|  | GO:0045778~positive regulation of ossification | 3.1E-02 |
|  |  |  |
| Downregulated | GO:0031032~actomyosin structure organization | 4.6E-02 |
|  | GO:0051187~cofactor catabolic process | 1.6E-02 |
|  | GO:0043648~dicarboxylic acid metabolic process | 1.4E-03 |
|  | GO:0006754~ATP biosynthetic process | 3.5E-03 |
|  | GO:0006626~protein targeting to mitochondrion | 4.9E-02 |
|  | GO:0072655~establishment of protein localization to mitochondrion | 4.3E-02 |
|  | GO:0006096~glycolysis | 1.3E-02 |
|  | GO:0009145~purine nucleoside triphosphate biosynthetic process | 5.1E-03 |
|  | GO:0009206~purine ribonucleoside triphosphate biosynthetic process | 2.9E-03 |
|  | GO:0006120~mitochondrial electron transport, NADH to ubiquinone | 5.3E-05 |
|  | GO:0070585~protein localization to mitochondrion | 3.3E-02 |
|  | GO:0009060~aerobic respiration | 6.6E-04 |
|  | GO:0006007~glucose catabolic process | 4.3E-02 |
|  | GO:0009201~ribonucleoside triphosphate biosynthetic process | 2.9E-03 |
|  | GO:0009142~nucleoside triphosphate biosynthetic process | 1.0E-02 |
|  | GO:0015992~proton transport | 5.5E-03 |
|  | GO:0006818~hydrogen transport | 6.9E-03 |
|  | GO:0009152~purine ribonucleotide biosynthetic process | 2.3E-02 |
|  | GO:0006084~acetyl-CoA metabolic process | 4.9E-04 |
|  | GO:0006813~potassium ion transport | 1.1E-02 |
|  | GO:0042773~ATP synthesis coupled electron transport | 1.2E-05 |
|  | GO:0042775~mitochondrial ATP synthesis coupled electron transport | 1.2E-05 |
|  | GO:0009260~ribonucleotide biosynthetic process | 3.2E-02 |
|  | GO:0006200~ATP catabolic process | 1.6E-02 |
|  | GO:0006521~regulation of cellular amino acid metabolic process | 5.7E-04 |
|  | GO:0006977~DNA damage response, signal transduction by p53 class mediator resulting in cell cycle arrest | 4.8E-03 |
|  | GO:0072401~signal transduction involved in DNA integrity checkpoint | 4.8E-03 |
|  | GO:0072413~signal transduction involved in mitotic cell cycle checkpoint | 4.8E-03 |
|  | GO:0072422~signal transduction involved in DNA damage checkpoint | 4.8E-03 |
|  | GO:0072431~signal transduction involved in mitotic cell cycle G1/S transition DNA damage checkpoint | 4.8E-03 |
|  | GO:0072474~signal transduction involved in mitotic cell cycle G1/S checkpoint | 4.8E-03 |
|  | GO:0072395~signal transduction involved in cell cycle checkpoint | 4.7E-03 |
|  | GO:0072404~signal transduction involved in G1/S transition checkpoint | 4.7E-03 |
|  | GO:0071158~positive regulation of cell cycle arrest | 2.3E-02 |
|  | GO:0033238~regulation of cellular amine metabolic process | 1.6E-03 |
|  | GO:0050792~regulation of viral reproduction | 3.6E-02 |
|  | GO:0000216~M/G1 transition of mitotic cell cycle | 1.3E-02 |
|  | GO:0006119~oxidative phosphorylation | 1.5E-05 |
|  | GO:0031571~mitotic cell cycle G1/S transition DNA damage checkpoint | 1.4E-03 |
|  | GO:0031575~mitotic cell cycle G1/S transition checkpoint | 2.9E-03 |
|  | GO:0071779~G1/S transition checkpoint | 3.9E-03 |
|  | GO:2000045~regulation of G1/S transition of mitotic cell cycle | 1.3E-02 |
|  | GO:0022618~ribonucleoprotein complex assembly | 1.0E-02 |
|  | GO:0071826~ribonucleoprotein complex subunit organization | 1.5E-02 |
|  | GO:0046034~ATP metabolic process | 7.8E-03 |
|  | GO:0006364~rRNA processing | 1.1E-02 |
|  | GO:0016072~rRNA metabolic process | 1.3E-02 |
|  | GO:0007093~mitotic cell cycle checkpoint | 4.7E-02 |
|  | GO:0030330~DNA damage response, signal transduction by p53 class mediator | 7.6E-03 |
|  | GO:0010565~regulation of cellular ketone metabolic process | 3.4E-02 |
|  | GO:0072331~signal transduction by p53 class mediator | 1.3E-02 |
|  | GO:0000084~S phase of mitotic cell cycle | 3.8E-02 |
|  | GO:0006839~mitochondrial transport | 2.2E-04 |
|  | GO:2000602~regulation of interphase of mitotic cell cycle | 2.3E-02 |
|  | GO:0042770~signal transduction in response to DNA damage | 1.8E-02 |
|  | GO:0044106~cellular amine metabolic process | 1.1E-02 |
|  | GO:0000077~DNA damage checkpoint | 1.1E-03 |
|  | GO:0009308~amine metabolic process | 2.5E-02 |
|  | GO:0031570~DNA integrity checkpoint | 1.2E-03 |
|  | GO:0000209~protein polyubiquitination | 4.6E-02 |
|  | GO:0006415~translational termination | 7.5E-08 |
|  | GO:0015672~monovalent inorganic cation transport | 1.9E-02 |
|  | GO:0000082~G1/S transition of mitotic cell cycle | 4.9E-02 |
|  | GO:0044282~small molecule catabolic process | 2.1E-02 |
|  | GO:0042254~ribosome biogenesis | 2.9E-03 |
|  | GO:0006614~SRP-dependent cotranslational protein targeting to membrane | 1.3E-07 |
|  | GO:0022904~respiratory electron transport chain | 2.6E-10 |
|  | GO:0006613~cotranslational protein targeting to membrane | 1.3E-07 |
|  | GO:0045047~protein targeting to ER | 1.3E-07 |
|  | GO:0072599~establishment of protein localization to endoplasmic reticulum | 1.3E-07 |
|  | GO:0006732~coenzyme metabolic process | 2.1E-02 |
|  | GO:0034470~ncRNA processing | 4.9E-02 |
|  | GO:0007005~mitochondrion organization | 4.2E-02 |
|  | GO:0006414~translational elongation | 2.1E-08 |
|  | GO:0070972~protein localization to endoplasmic reticulum | 1.1E-06 |
|  | GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 1.3E-07 |
|  | GO:0018130~heterocycle biosynthetic process | 4.5E-02 |
|  | GO:0034220~ion transmembrane transport | 1.7E-02 |
|  | GO:0051186~cofactor metabolic process | 1.4E-02 |
|  | GO:0043624~cellular protein complex disassembly | 1.0E-07 |
|  | GO:0022900~electron transport chain | 2.1E-10 |
|  | GO:0043241~protein complex disassembly | 1.1E-07 |
|  | GO:0006612~protein targeting to membrane | 2.1E-06 |
|  | GO:0006936~muscle contraction | 3.4E-04 |
|  | GO:0034623~cellular macromolecular complex disassembly | 1.3E-07 |
|  | GO:0032984~macromolecular complex disassembly | 1.3E-07 |
|  | GO:0019080~viral genome expression | 1.3E-08 |
|  | GO:0019083~viral transcription | 1.3E-08 |
|  | GO:0045333~cellular respiration | 4.3E-12 |
|  | GO:0003012~muscle system process | 2.8E-04 |
|  | GO:0000956~nuclear-transcribed mRNA catabolic process | 4.0E-07 |
|  | GO:0034660~ncRNA metabolic process | 1.9E-02 |
|  | GO:0006413~translational initiation | 4.7E-10 |
|  | GO:0006402~mRNA catabolic process | 8.0E-07 |
|  | GO:0022613~ribonucleoprotein complex biogenesis | 6.0E-04 |
|  | GO:0006401~RNA catabolic process | 2.9E-06 |
|  | GO:0071843~cellular component biogenesis at cellular level | 2.0E-04 |
|  | GO:0072594~establishment of protein localization to organelle | 7.5E-08 |
|  | GO:0071845~cellular component disassembly at cellular level | 7.9E-05 |
|  | GO:0022411~cellular component disassembly | 1.1E-04 |
|  | GO:0006812~cation transport | 4.6E-02 |
|  | GO:0019058~viral infectious cycle | 1.3E-07 |
|  | GO:0034622~cellular macromolecular complex assembly | 3.2E-02 |
|  | GO:0022415~viral reproductive process | 1.0E-06 |
|  | GO:0015980~energy derivation by oxidation of organic compounds | 5.1E-08 |
|  | GO:0033365~protein localization to organelle | 3.6E-03 |
|  | GO:0006605~protein targeting | 2.3E-03 |
|  | GO:0048610~cellular process involved in reproduction | 9.4E-06 |
|  | GO:0006396~RNA processing | 2.4E-02 |
|  | GO:0016032~viral reproduction | 1.1E-07 |
|  | GO:0006091~generation of precursor metabolites and energy | 1.5E-10 |
|  | GO:0006412~translation | 2.4E-02 |
|  | GO:0055114~oxidation-reduction process | 2.5E-07 |
|  | GO:0034621~cellular macromolecular complex subunit organization | 5.4E-07 |
|  | GO:0071822~protein complex subunit organization | 3.3E-04 |
|  | GO:0009057~macromolecule catabolic process | 8.9E-04 |
|  | GO:0044265~cellular macromolecule catabolic process | 4.3E-06 |
|  | GO:0016071~mRNA metabolic process | 4.5E-08 |
|  | GO:0044085~cellular component biogenesis | 4.7E-02 |
|  | GO:0043933~macromolecular complex subunit organization | 2.4E-05 |
|  | GO:0044248~cellular catabolic process | 2.3E-05 |
|  | GO:0044281~small molecule metabolic process | 1.4E-03 |
|  | GO:0009056~catabolic process | 1.1E-04 |

**Supplementary Table S4. Differentially expressed GO biological process terms in suburothelial PDGFRα+ cells**

|  | GO term | Adjusted *P* |
| --- | --- | --- |
| Upregulated | GO:0050896~response to stimulus | 6.8E-03 |
|  | GO:0051716~cellular response to stimulus | 1.4E-02 |
|  | GO:0007154~cell communication | 9.2E-03 |
|  | GO:0023052~signaling | 7.9E-03 |
|  | GO:0032501~multicellular organismal process | 3.6E-02 |
|  | GO:0007165~signal transduction | 9.6E-03 |
|  | GO:0032502~developmental process | 1.2E-02 |
|  | GO:0007275~multicellular organismal development | 5.5E-03 |
|  | GO:0048856~anatomical structure development | 2.1E-02 |
|  | GO:0048731~system development | 3.8E-03 |
|  | GO:0042221~response to chemical stimulus | 8.0E-04 |
|  | GO:0048869~cellular developmental process | 6.8E-03 |
|  | GO:0030154~cell differentiation | 3.7E-03 |
|  | GO:0009653~anatomical structure morphogenesis | 1.3E-03 |
|  | GO:0048513~organ development | 7.3E-03 |
|  | GO:0010033~response to organic substance | 2.7E-04 |
|  | GO:0007399~nervous system development | 5.9E-04 |
|  | GO:0070887~cellular response to chemical stimulus | 6.5E-04 |
|  | GO:0050793~regulation of developmental process | 2.3E-03 |
|  | GO:0048468~cell development | 2.3E-03 |
|  | GO:0051239~regulation of multicellular organismal process | 4.4E-02 |
|  | GO:0071310~cellular response to organic substance | 2.8E-03 |
|  | GO:0022008~neurogenesis | 1.1E-03 |
|  | GO:0040011~locomotion | 9.2E-03 |
|  | GO:0003008~system process | 4.1E-02 |
|  | GO:0048699~generation of neurons | 3.0E-03 |
|  | GO:0009605~response to external stimulus | 4.2E-02 |
|  | GO:0030182~neuron differentiation | 8.2E-04 |
|  | GO:0000902~cell morphogenesis | 1.7E-02 |
|  | GO:0032989~cellular component morphogenesis | 3.2E-02 |
|  | GO:2000026~regulation of multicellular organismal development | 3.6E-02 |
|  | GO:0022610~biological adhesion | 1.2E-02 |
|  | GO:0007155~cell adhesion | 1.4E-02 |
|  | GO:0045595~regulation of cell differentiation | 1.7E-02 |
|  | GO:0072358~cardiovascular system development | 3.0E-03 |
|  | GO:0072359~circulatory system development | 3.0E-03 |
|  | GO:0040007~growth | 2.3E-03 |
|  | GO:0048666~neuron development | 2.5E-03 |
|  | GO:0048870~cell motility | 4.0E-02 |
|  | GO:0051674~localization of cell | 4.0E-02 |
|  | GO:0031175~neuron projection development | 3.8E-03 |
|  | GO:0016477~cell migration | 4.3E-02 |
|  | GO:0009628~response to abiotic stimulus | 2.0E-02 |
|  | GO:0000904~cell morphogenesis involved in differentiation | 1.2E-02 |
|  | GO:0048858~cell projection morphogenesis | 2.2E-02 |
|  | GO:0032990~cell part morphogenesis | 4.4E-02 |
|  | GO:0007417~central nervous system development | 1.0E-02 |
|  | GO:0048812~neuron projection morphogenesis | 2.6E-02 |
|  | GO:0040008~regulation of growth | 7.3E-03 |
|  | GO:0001944~vasculature development | 2.2E-02 |
|  | GO:0048667~cell morphogenesis involved in neuron differentiation | 2.4E-02 |
|  | GO:0061061~muscle structure development | 6.5E-04 |
|  | GO:0006935~chemotaxis | 4.0E-02 |
|  | GO:0042330~taxis | 4.0E-02 |
|  | GO:0007409~axonogenesis | 2.2E-02 |
|  | GO:0001568~blood vessel development | 4.4E-02 |
|  | GO:0040012~regulation of locomotion | 2.0E-02 |
|  | GO:0051270~regulation of cellular component movement | 3.0E-02 |
|  | GO:0007610~behavior | 4.9E-03 |
|  | GO:2000145~regulation of cell motility | 4.2E-02 |
|  | GO:0001501~skeletal system development | 4.9E-03 |
|  | GO:0007507~heart development | 7.5E-03 |
|  | GO:0016049~cell growth | 1.8E-02 |
|  | GO:0007411~axon guidance | 1.7E-02 |
|  | GO:0001503~ossification | 1.9E-04 |
|  | GO:0007517~muscle organ development | 9.2E-03 |
|  | GO:0060537~muscle tissue development | 3.1E-03 |
|  | GO:0001558~regulation of cell growth | 4.0E-02 |
|  | GO:0014706~striated muscle tissue development | 1.3E-02 |
|  | GO:0042692~muscle cell differentiation | 1.6E-02 |
|  | GO:0003012~muscle system process | 1.5E-02 |
|  | GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway | 1.9E-03 |
|  | GO:0043062~extracellular structure organization | 3.5E-08 |
|  | GO:0030198~extracellular matrix organization | 4.4E-08 |
|  | GO:0006936~muscle contraction | 7.4E-03 |
|  | GO:0061448~connective tissue development | 2.3E-03 |
|  | GO:0006986~response to unfolded protein | 3.3E-03 |
|  | GO:0035966~response to topologically incorrect protein | 7.7E-03 |
|  | GO:0051146~striated muscle cell differentiation | 4.0E-02 |
|  | GO:0051216~cartilage development | 1.9E-03 |
|  | GO:0030278~regulation of ossification | 4.1E-02 |
|  | GO:0090092~regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 1.7E-02 |
|  | GO:0034976~response to endoplasmic reticulum stress | 3.8E-03 |
|  | GO:0001649~osteoblast differentiation | 2.2E-02 |
|  | GO:0006984~ER-nucleus signaling pathway | 9.8E-03 |
|  | GO:0035967~cellular response to topologically incorrect protein | 7.5E-03 |
|  | GO:0030968~endoplasmic reticulum unfolded protein response | 5.0E-03 |
|  | GO:0034620~cellular response to unfolded protein | 5.0E-03 |
|  | GO:0048738~cardiac muscle tissue development | 9.3E-03 |
|  | GO:0050890~cognition | 4.3E-02 |
|  | GO:0030178~negative regulation of Wnt receptor signaling pathway | 4.3E-02 |
|  | GO:0007611~learning or memory | 2.7E-02 |
|  | GO:0050795~regulation of behavior | 4.3E-02 |
|  | GO:0032102~negative regulation of response to external stimulus | 3.6E-02 |
|  | GO:0032075~positive regulation of nuclease activity | 5.6E-03 |
|  | GO:0032069~regulation of nuclease activity | 1.2E-02 |
|  | GO:0006987~activation of signaling protein activity involved in unfolded protein response | 7.3E-03 |
|  | GO:0030509~BMP signaling pathway | 4.4E-02 |
|  | GO:0090090~negative regulation of canonical Wnt receptor signaling pathway | 2.0E-02 |
|  | GO:0007498~mesoderm development | 2.1E-02 |
|  | GO:0090101~negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 2.7E-02 |
|  | GO:0032846~positive regulation of homeostatic process | 4.7E-02 |
|  | GO:0055007~cardiac muscle cell differentiation | 2.2E-02 |
|  | GO:0006900~membrane budding | 1.9E-02 |
|  | GO:0006901~vesicle coating | 8.6E-03 |
|  |  |  |
| Downregulated | GO:0042787~protein ubiquitination involved in ubiquitin-dependent protein catabolic process | 4.3E-02 |
|  | GO:0030216~keratinocyte differentiation | 7.7E-03 |
|  | GO:0022904~respiratory electron transport chain | 3.2E-02 |
|  | GO:0006364~rRNA processing | 9.4E-03 |
|  | GO:0016072~rRNA metabolic process | 1.7E-02 |
|  | GO:0022900~electron transport chain | 2.4E-02 |
|  | GO:0032318~regulation of Ras GTPase activity | 4.2E-02 |
|  | GO:0045333~cellular respiration | 3.6E-02 |
|  | GO:0042254~ribosome biogenesis | 4.7E-03 |
|  | GO:0006415~translational termination | 2.3E-13 |
|  | GO:0006614~SRP-dependent cotranslational protein targeting to membrane | 3.0E-13 |
|  | GO:0006613~cotranslational protein targeting to membrane | 3.1E-13 |
|  | GO:0045047~protein targeting to ER | 3.0E-13 |
|  | GO:0072599~establishment of protein localization to endoplasmic reticulum | 3.0E-13 |
|  | GO:0006414~translational elongation | 2.4E-14 |
|  | GO:0007265~Ras protein signal transduction | 3.9E-02 |
|  | GO:0034470~ncRNA processing | 7.3E-03 |
|  | GO:0070972~protein localization to endoplasmic reticulum | 1.2E-12 |
|  | GO:0022613~ribonucleoprotein complex biogenesis | 3.0E-02 |
|  | GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 2.4E-14 |
|  | GO:0071843~cellular component biogenesis at cellular level | 3.0E-02 |
|  | GO:0046578~regulation of Ras protein signal transduction | 1.1E-02 |
|  | GO:0043624~cellular protein complex disassembly | 1.5E-14 |
|  | GO:0043241~protein complex disassembly | 1.1E-14 |
|  | GO:0006612~protein targeting to membrane | 3.3E-11 |
|  | GO:0019080~viral genome expression | 2.4E-14 |
|  | GO:0019083~viral transcription | 2.4E-14 |
|  | GO:0006413~translational initiation | 2.4E-14 |
|  | GO:0034623~cellular macromolecular complex disassembly | 1.1E-14 |
|  | GO:0051056~regulation of small GTPase mediated signal transduction | 3.6E-02 |
|  | GO:0032984~macromolecular complex disassembly | 1.1E-14 |
|  | GO:0000956~nuclear-transcribed mRNA catabolic process | 2.4E-14 |
|  | GO:0006402~mRNA catabolic process | 9.1E-14 |
|  | GO:0072594~establishment of protein localization to organelle | 3.8E-11 |
|  | GO:0006091~generation of precursor metabolites and energy | 4.1E-02 |
|  | GO:0006401~RNA catabolic process | 1.4E-13 |
|  | GO:0019058~viral infectious cycle | 2.3E-13 |
|  | GO:0071845~cellular component disassembly at cellular level | 2.1E-11 |
|  | GO:0022411~cellular component disassembly | 1.8E-11 |
|  | GO:0055114~oxidation-reduction process | 3.1E-02 |
|  | GO:0022415~viral reproductive process | 3.0E-13 |
|  | GO:0033365~protein localization to organelle | 9.4E-03 |
|  | GO:0006605~protein targeting | 6.5E-04 |
|  | GO:0006886~intracellular protein transport | 4.1E-02 |
|  | GO:0006396~RNA processing | 3.3E-02 |
|  | GO:0048610~cellular process involved in reproduction | 4.9E-09 |
|  | GO:0016032~viral reproduction | 3.1E-09 |
|  | GO:0034621~cellular macromolecular complex subunit organization | 5.6E-07 |
|  | GO:0016071~mRNA metabolic process | 2.8E-07 |
|  | GO:0071822~protein complex subunit organization | 8.2E-05 |
|  | GO:0000003~reproduction | 4.7E-03 |
|  | GO:0046907~intracellular transport | 4.3E-02 |
|  | GO:0044265~cellular macromolecule catabolic process | 4.6E-07 |
|  | GO:0022414~reproductive process | 3.5E-03 |
|  | GO:0006412~translation | 7.5E-07 |
|  | GO:0009057~macromolecule catabolic process | 3.3E-05 |
|  | GO:0043933~macromolecular complex subunit organization | 1.6E-03 |
|  | GO:0051649~establishment of localization in cell | 3.0E-02 |
|  | GO:0032774~RNA biosynthetic process | 4.2E-02 |
|  | GO:0044248~cellular catabolic process | 6.0E-07 |
|  | GO:0009056~catabolic process | 5.3E-07 |
|  | GO:0016070~RNA metabolic process | 2.0E-02 |
|  | GO:0034645~cellular macromolecule biosynthetic process | 3.6E-02 |
|  | GO:0009059~macromolecule biosynthetic process | 4.0E-02 |
|  | GO:0090304~nucleic acid metabolic process | 1.3E-02 |
|  | GO:0006139~nucleobase-containing compound metabolic process | 3.0E-02 |
|  | GO:0034641~cellular nitrogen compound metabolic process | 2.9E-02 |
|  | GO:0006807~nitrogen compound metabolic process | 3.0E-02 |
|  | GO:0044249~cellular biosynthetic process | 3.3E-03 |
|  | GO:0009058~biosynthetic process | 2.6E-03 |
|  | GO:0044237~cellular metabolic process | 4.4E-02 |

Supplementary Table S5. PDGFRα-mediated GO biological process terms

|  |  | Adjusted *P* | |
| --- | --- | --- | --- |
|  | GO term | Detrusor | Suburothelium |
| Upregulated | GO:0050896~response to stimulus | 4.2E-03 | 6.8E-03 |
|  | GO:0051716~cellular response to stimulus | 3.9E-03 | 1.4E-02 |
|  | GO:0032502~developmental process | 2.7E-04 | 1.2E-02 |
|  | GO:0032501~multicellular organismal process | 5.4E-03 | 3.6E-02 |
|  | GO:0007275~multicellular organismal development | 2.8E-05 | 5.5E-03 |
|  | GO:0007154~cell communication | 6.7E-03 | 9.2E-03 |
|  | GO:0007165~signal transduction | 1.2E-03 | 9.6E-03 |
|  | GO:0048856~anatomical structure development | 1.7E-04 | 2.1E-02 |
|  | GO:0023052~signaling | 1.0E-02 | 7.9E-03 |
|  | GO:0048731~system development | 1.7E-05 | 3.8E-03 |
|  | GO:0048869~cellular developmental process | 4.0E-04 | 6.8E-03 |
|  | GO:0030154~cell differentiation | 3.0E-04 | 3.7E-03 |
|  | GO:0048513~organ development | 3.4E-04 | 7.3E-03 |
|  | GO:0042221~response to chemical stimulus | 2.2E-02 | 8.0E-04 |
|  | GO:0009653~anatomical structure morphogenesis | 1.2E-03 | 1.3E-03 |
|  | GO:0010033~response to organic substance | 2.4E-03 | 2.7E-04 |
|  | GO:0050793~regulation of developmental process | 4.2E-06 | 2.3E-03 |
|  | GO:0007399~nervous system development | 1.4E-03 | 5.9E-04 |
|  | GO:0051239~regulation of multicellular organismal process | 1.2E-03 | 4.4E-02 |
|  | GO:0070887~cellular response to chemical stimulus | 2.1E-02 | 6.5E-04 |
|  | GO:2000026~regulation of multicellular organismal development | 4.7E-05 | 3.6E-02 |
|  | GO:0009605~response to external stimulus | 1.5E-02 | 4.2E-02 |
|  | GO:0071310~cellular response to organic substance | 9.4E-03 | 2.8E-03 |
|  | GO:0045595~regulation of cell differentiation | 1.9E-04 | 1.7E-02 |
|  | GO:0040011~locomotion | 2.2E-02 | 9.2E-03 |
|  | GO:0022008~neurogenesis | 1.8E-02 | 1.1E-03 |
|  | GO:0040007~growth | 6.4E-04 | 2.3E-03 |
|  | GO:0048699~generation of neurons | 4.7E-02 | 3.0E-03 |
|  | GO:0072358~cardiovascular system development | 2.9E-03 | 3.0E-03 |
|  | GO:0072359~circulatory system development | 2.9E-03 | 3.0E-03 |
|  | GO:0048870~cell motility | 2.3E-02 | 4.0E-02 |
|  | GO:0051674~localization of cell | 2.3E-02 | 4.0E-02 |
|  | GO:0016477~cell migration | 2.8E-02 | 4.3E-02 |
|  | GO:0001944~vasculature development | 6.4E-04 | 2.2E-02 |
|  | GO:0001568~blood vessel development | 1.7E-03 | 4.4E-02 |
|  | GO:0001501~skeletal system development | 4.5E-08 | 4.9E-03 |
|  | GO:0051270~regulation of cellular component movement | 2.3E-02 | 3.0E-02 |
|  | GO:0040012~regulation of locomotion | 3.0E-02 | 2.0E-02 |
|  | GO:2000145~regulation of cell motility | 2.2E-02 | 4.2E-02 |
|  | GO:0001503~ossification | 7.7E-05 | 1.9E-04 |
|  | GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway | 4.1E-03 | 1.9E-03 |
|  | GO:0043062~extracellular structure organization | 1.8E-06 | 3.5E-08 |
|  | GO:0030198~extracellular matrix organization | 1.7E-06 | 4.4E-08 |
|  | GO:0061448~connective tissue development | 6.8E-04 | 2.3E-03 |
|  | GO:0006986~response to unfolded protein | 1.0E-03 | 3.3E-03 |
|  | GO:0035966~response to topologically incorrect protein | 3.4E-03 | 7.7E-03 |
|  | GO:0030278~regulation of ossification | 1.4E-03 | 4.1E-02 |
|  | GO:0051216~cartilage development | 2.9E-03 | 1.9E-03 |
|  | GO:0006984~ER-nucleus signaling pathway | 3.6E-04 | 9.8E-03 |
|  | GO:0034976~response to endoplasmic reticulum stress | 2.3E-03 | 3.8E-03 |
|  | GO:0090092~regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 2.5E-02 | 1.7E-02 |
|  | GO:0001649~osteoblast differentiation | 4.2E-02 | 2.2E-02 |
|  | GO:0035967~cellular response to topologically incorrect protein | 4.7E-03 | 7.5E-03 |
|  | GO:0030968~endoplasmic reticulum unfolded protein response | 1.6E-03 | 5.0E-03 |
|  | GO:0034620~cellular response to unfolded protein | 1.6E-03 | 5.0E-03 |
|  | GO:0032075~positive regulation of nuclease activity | 6.2E-04 | 5.6E-03 |
|  | GO:0032069~regulation of nuclease activity | 1.6E-03 | 1.2E-02 |
|  | GO:0006987~activation of signaling protein activity involved in unfolded protein response | 4.5E-04 | 7.3E-03 |
|  | GO:0030509~BMP signaling pathway | 4.1E-02 | 4.4E-02 |
|  | GO:0090101~negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway | 4.1E-02 | 2.7E-02 |
|  | GO:0006900~membrane budding | 2.1E-02 | 1.9E-02 |
|  | GO:0006901~vesicle coating | 1.1E-02 | 8.6E-03 |
|  |  |  |  |
| Downregulated | GO:0006364~rRNA processing | 1.1E-02 | 9.4E-03 |
|  | GO:0016072~rRNA metabolic process | 1.3E-02 | 1.7E-02 |
|  | GO:0006415~translational termination | 7.5E-08 | 2.3E-13 |
|  | GO:0042254~ribosome biogenesis | 2.9E-03 | 4.7E-03 |
|  | GO:0006614~SRP-dependent cotranslational protein targeting to membrane | 1.3E-07 | 3.0E-13 |
|  | GO:0022904~respiratory electron transport chain | 2.6E-10 | 3.2E-02 |
|  | GO:0006613~cotranslational protein targeting to membrane | 1.3E-07 | 3.1E-13 |
|  | GO:0045047~protein targeting to ER | 1.3E-07 | 3.0E-13 |
|  | GO:0072599~establishment of protein localization to endoplasmic reticulum | 1.3E-07 | 3.0E-13 |
|  | GO:0034470~ncRNA processing | 4.9E-02 | 7.3E-03 |
|  | GO:0006414~translational elongation | 2.1E-08 | 2.4E-14 |
|  | GO:0070972~protein localization to endoplasmic reticulum | 1.1E-06 | 1.2E-12 |
|  | GO:0000184~nuclear-transcribed mRNA catabolic process, nonsense-mediated decay | 1.3E-07 | 2.4E-14 |
|  | GO:0043624~cellular protein complex disassembly | 1.0E-07 | 1.5E-14 |
|  | GO:0022900~electron transport chain | 2.1E-10 | 2.4E-02 |
|  | GO:0043241~protein complex disassembly | 1.1E-07 | 1.1E-14 |
|  | GO:0006612~protein targeting to membrane | 2.1E-06 | 3.3E-11 |
|  | GO:0034623~cellular macromolecular complex disassembly | 1.3E-07 | 1.1E-14 |
|  | GO:0032984~macromolecular complex disassembly | 1.3E-07 | 1.1E-14 |
|  | GO:0019080~viral genome expression | 1.3E-08 | 2.4E-14 |
|  | GO:0019083~viral transcription | 1.3E-08 | 2.4E-14 |
|  | GO:0045333~cellular respiration | 4.3E-12 | 3.6E-02 |
|  | GO:0000956~nuclear-transcribed mRNA catabolic process | 4.0E-07 | 2.4E-14 |
|  | GO:0006413~translational initiation | 4.7E-10 | 2.4E-14 |
|  | GO:0006402~mRNA catabolic process | 8.0E-07 | 9.1E-14 |
|  | GO:0022613~ribonucleoprotein complex biogenesis | 6.0E-04 | 3.0E-02 |
|  | GO:0006401~RNA catabolic process | 2.9E-06 | 1.4E-13 |
|  | GO:0071843~cellular component biogenesis at cellular level | 2.0E-04 | 3.0E-02 |
|  | GO:0072594~establishment of protein localization to organelle | 7.5E-08 | 3.8E-11 |
|  | GO:0071845~cellular component disassembly at cellular level | 7.9E-05 | 2.1E-11 |
|  | GO:0022411~cellular component disassembly | 1.1E-04 | 1.8E-11 |
|  | GO:0019058~viral infectious cycle | 1.3E-07 | 2.3E-13 |
|  | GO:0022415~viral reproductive process | 1.0E-06 | 3.0E-13 |
|  | GO:0033365~protein localization to organelle | 3.6E-03 | 9.4E-03 |
|  | GO:0006605~protein targeting | 2.3E-03 | 6.5E-04 |
|  | GO:0048610~cellular process involved in reproduction | 9.4E-06 | 4.9E-09 |
|  | GO:0006396~RNA processing | 2.4E-02 | 3.3E-02 |
|  | GO:0016032~viral reproduction | 1.1E-07 | 3.1E-09 |
|  | GO:0006091~generation of precursor metabolites and energy | 1.5E-10 | 4.1E-02 |
|  | GO:0006412~translation | 2.4E-02 | 7.5E-07 |
|  | GO:0055114~oxidation-reduction process | 2.5E-07 | 3.1E-02 |
|  | GO:0034621~cellular macromolecular complex subunit organization | 5.4E-07 | 5.6E-07 |
|  | GO:0071822~protein complex subunit organization | 3.3E-04 | 8.2E-05 |
|  | GO:0009057~macromolecule catabolic process | 8.9E-04 | 3.3E-05 |
|  | GO:0044265~cellular macromolecule catabolic process | 4.3E-06 | 4.6E-07 |
|  | GO:0016071~mRNA metabolic process | 4.5E-08 | 2.8E-07 |
|  | GO:0043933~macromolecular complex subunit organization | 2.4E-05 | 1.6E-03 |
|  | GO:0044248~cellular catabolic process | 2.3E-05 | 6.0E-07 |
|  | GO:0009056~catabolic process | 1.1E-04 | 5.3E-07 |