

Table S4. Enriched gene ontology (GO) categories for commonly regulated genes by both $1\alpha,25(\text{OH})_2\text{D}_3$ and $25(\text{OH})\text{D}_3$ in mouse *Cyp27b1*^{-/-} fibroblasts generated by DAVID.

| Genes regulated by both 10 nM $1\alpha,25(\text{OH})_2\text{D}_3$ and 500 nM $25(\text{OH})\text{D}_3$ | | |
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| Category | Term | <i>p</i> -Value |
| Annotation Cluster 1 | Enrichment Score: 12.950718485029892 | |
| SP_PIR_KEYWORDS | glycoprotein | 0.000 |
| SP_PIR_KEYWORDS | signal | 0.000 |
| SP_PIR_KEYWORDS | disulfide bond | 0.000 |
| UP_SEQ_FEATURE | glycosylation site:N-linked (GlcNAc...) | 0.000 |
| SP_PIR_KEYWORDS | Secreted | 0.000 |
| UP_SEQ_FEATURE | disulfide bond | 0.000 |
| UP_SEQ_FEATURE | signal peptide | 0.000 |
| GOTERM_CC_FAT | GO:0005576~extracellular region | 0.000 |
| Annotation Cluster 2 | Enrichment Score: 3.3579824639576437 | |
| GOTERM_CC_FAT | GO:0005578~proteinaceous extracellular matrix | 0.000 |
| GOTERM_CC_FAT | GO:0031012~extracellular matrix | 0.000 |
| SP_PIR_KEYWORDS | collagen degradation | 0.000 |
| GOTERM_BP_FAT | GO:0030574~collagen catabolic process | 0.000 |
| GOTERM_BP_FAT | GO:0044243~multicellular organismal catabolic process | 0.000 |
| GOTERM_BP_FAT | GO:0032963~collagen metabolic process | 0.000 |
| GOTERM_BP_FAT | GO:0044259~multicellular organismal macromolecule metabolic process | 0.000 |
| GOTERM_MF_FAT | GO:0004222~metalloendopeptidase activity | 0.000 |
| GOTERM_BP_FAT | GO:0044236~multicellular organismal metabolic process | 0.000 |
| INTERPRO | IPR016293:Peptidase M10A, matrix metallopeotidase | 0.000 |
| INTERPRO | IPR006025:Peptidase M, neutral zinc metallopeptidases, zinc-binding site | 0.000 |
| INTERPRO | IPR002477:Peptidoglycan binding-like | 0.000 |
| PIR_SUPERFAMILY | PIRSF001191:Peptidase_M10A_matrix | 0.000 |
| GOTERM_MF_FAT | GO:0008237~metallopeptidase activity | 0.000 |
| INTERPRO | IPR000585:Hemopexin/matrixin | 0.000 |
| INTERPRO | IPR018486:Hemopexin/matrixin, conserved site | 0.000 |
| INTERPRO | IPR018487:Hemopexin/matrixin, repeat | 0.000 |
| UP_SEQ_FEATURE | domain:Hemopexin-like 3 | 0.000 |
| UP_SEQ_FEATURE | domain:Hemopexin-like 4 | 0.000 |
| GOTERM_MF_FAT | GO:0004175~endopeptidase activity | 0.000 |
| UP_SEQ_FEATURE | domain:Hemopexin-like 1 | 0.000 |
| UP_SEQ_FEATURE | domain:Hemopexin-like 2 | 0.000 |
| SMART | SM00120:HX | 0.000 |
| SP_PIR_KEYWORDS | extracellular matrix | 0.000 |
| INTERPRO | IPR006026:Peptidase, metallopeptidases | 0.000 |
| SMART | SM00235:ZnMc | 0.000 |

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| PIR_SUPERFAMILY | PIRSF001191:matrix metalloproteinase, stromelysin type | 0.000 |
| INTERPRO | IPR001818:Peptidase M10A and M12B, matrixin and adamalysin | 0.001 |
| GOTERM_MF_FAT | GO:0070011~peptidase activity, acting on L-amino acid peptides | 0.001 |
| GOTERM_MF_FAT | GO:0008233~peptidase activity | 0.002 |
| UP_SEQ_FEATURE | short sequence motif:Cysteine switch | 0.002 |
| SP_PIR_KEYWORDS | metalloprotease | 0.002 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 3; via carbonyl oxygen | 0.003 |
| UP_SEQ_FEATURE | propeptide:Activation peptide | 0.004 |
| SP_PIR_KEYWORDS | metalloproteinase | 0.007 |
| UP_SEQ_FEATURE | metal ion-binding site:Zinc 2; in inhibited form | 0.008 |
| SP_PIR_KEYWORDS | zymogen | 0.011 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 2; via carbonyl oxygen | 0.014 |
| GOTERM_BP_FAT | GO:0006508~proteolysis | 0.014 |
| UP_SEQ_FEATURE | metal ion-binding site:Zinc 2; catalytic | 0.015 |
| UP_SEQ_FEATURE | metal ion-binding site:Zinc; catalytic | 0.022 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 1 | 0.023 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium 2 | 0.040 |
| SP_PIR_KEYWORDS | Protease | 0.045 |
| Annotation Cluster 3 | Enrichment Score: 3.24116791784555 | |
| INTERPRO | IPR018097:EGF-like calcium-binding, conserved site | 0.000 |
| INTERPRO | IPR006210:EGF-like | 0.000 |
| INTERPRO | IPR001881:EGF-like calcium-binding | 0.000 |
| INTERPRO | IPR000152:EGF-type aspartate/asparagine hydroxylation conserved site | 0.000 |
| INTERPRO | IPR006209:EGF | 0.000 |
| SMART | SM00181:EGF | 0.000 |
| SMART | SM00179:EGF_CA | 0.000 |
| INTERPRO | IPR013032:EGF-like region, conserved site | 0.000 |
| SP_PIR_KEYWORDS | egf-like domain | 0.000 |
| INTERPRO | IPR000742:EGF-like, type 3 | 0.000 |
| UP_SEQ_FEATURE | domain:EGF-like 6 | 0.002 |
| UP_SEQ_FEATURE | domain:EGF-like 1 | 0.003 |
| UP_SEQ_FEATURE | domain:EGF-like 2 | 0.004 |
| UP_SEQ_FEATURE | domain:EGF-like 4 | 0.005 |
| SP_PIR_KEYWORDS | notch signaling pathway | 0.011 |
| UP_SEQ_FEATURE | domain:EGF-like 3 | 0.012 |
| UP_SEQ_FEATURE | domain:EGF-like 5 | 0.016 |
| INTERPRO | IPR001438:EGF-like, type 2 | 0.024 |
| GOTERM_BP_FAT | GO:0007219~Notch signaling pathway | 0.028 |
| INTERPRO | IPR013091:EGF calcium-binding | 0.046 |
| Annotation Cluster 4 | Enrichment Score: 2.4497729172410354 | |

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| GOTERM_BP_FAT | GO:0008544~epidermis development | 0.000 |
| GOTERM_BP_FAT | GO:0007398~ectoderm development | 0.001 |
| GOTERM_BP_FAT | GO:0060429~epithelium development | 0.002 |
| GOTERM_BP_FAT | GO:0009913~epidermal cell differentiation | 0.003 |
| GOTERM_BP_FAT | GO:0030855~epithelial cell differentiation | 0.017 |
| GOTERM_BP_FAT | GO:0030216~keratinocyte differentiation | 0.020 |
| Annotation Cluster 5 | Enrichment Score: 2.058239137874073 | |
| INTERPRO | IPR000884:Thrombospondin, type 1 repeat | 0.000 |
| SMART | SM00209:TSP1 | 0.001 |
| Annotation Cluster 6 | Enrichment Score: 1.949896685297675 | |
| GOTERM_BP_FAT | GO:0018149~peptide cross-linking | 0.001 |
| INTERPRO | IPR001102:Transglutaminase, N-terminal | 0.004 |
| INTERPRO | IPR013808:Transglutaminase, conserved site | 0.004 |
| INTERPRO | IPR008958:Transglutaminase, C-terminal | 0.004 |
| GOTERM_MF_FAT | GO:0003810~protein-glutamine gamma-glutamyltransferase activity | 0.005 |
| INTERPRO | IPR002931:Transglutaminase-like | 0.006 |
| SMART | SM00460:TGc | 0.008 |
| GOTERM_MF_FAT | GO:0016755~transferase activity, transferring amino-acyl groups | 0.018 |
| UP_SEQ_FEATURE | metal ion-binding site:Calcium | 0.050 |
| Annotation Cluster 7 | Enrichment Score: 1.9182723957765455 | |
| SP_PIR_KEYWORDS | growth factor | 0.000 |
| GOTERM_MF_FAT | GO:0008083~growth factor activity | 0.002 |
| KEGG_PATHWAY | mmu04060:Cytokine-cytokine receptor interaction | 0.002 |
| GOTERM_CC_FAT | GO:0005615~extracellular space | 0.003 |
| SP_PIR_KEYWORDS | cytokine | 0.020 |
| GOTERM_MF_FAT | GO:0005125~cytokine activity | 0.023 |
| BIOCARTA | m_erythPathway:Erythrocyte Differentiation Pathway | 0.023 |
| Annotation Cluster 8 | Enrichment Score: 1.721763277599938 | |
| GOTERM_MF_FAT | GO:0043167~ion binding | 0.000 |
| GOTERM_MF_FAT | GO:0046872~metal ion binding | 0.001 |
| GOTERM_MF_FAT | GO:0043169~cation binding | 0.002 |
| SP_PIR_KEYWORDS | metal-binding | 0.007 |
| Annotation Cluster 9 | Enrichment Score: 1.6587981525703623 | |
| GOTERM_BP_FAT | GO:0007411~axon guidance | 0.007 |
| GOTERM_BP_FAT | GO:0000902~cell morphogenesis | 0.013 |
| GOTERM_BP_FAT | GO:0006928~cell motion | 0.014 |
| GOTERM_BP_FAT | GO:0007409~axonogenesis | 0.015 |
| GOTERM_BP_FAT | GO:0000904~cell morphogenesis involved in differentiation | 0.015 |
| GOTERM_BP_FAT | GO:0030030~cell projection organization | 0.016 |
| GOTERM_BP_FAT | GO:0031175~neuron projection development | 0.017 |
| GOTERM_BP_FAT | GO:0048812~neuron projection morphogenesis | 0.020 |

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| GOTERM_BP_FAT | GO:0048667~cell morphogenesis involved in neuron differentiation | 0.024 |
| GOTERM_BP_FAT | GO:0032989~cellular component morphogenesis | 0.028 |
| GOTERM_BP_FAT | GO:0048858~cell projection morphogenesis | 0.037 |
| GOTERM_BP_FAT | GO:0032990~cell part morphogenesis | 0.045 |
| Annotation Cluster 10 | Enrichment Score: 1.6264123345827333 | |
| KEGG_PATHWAY | mmu04360:Axon guidance | 0.002 |
| INTERPRO | IPR003659:Plexin/semaphorin/integrin | 0.016 |
| SMART | SM00423:PSI | 0.026 |
| INTERPRO | IPR001627:Semaphorin/CD100 antigen | 0.050 |
