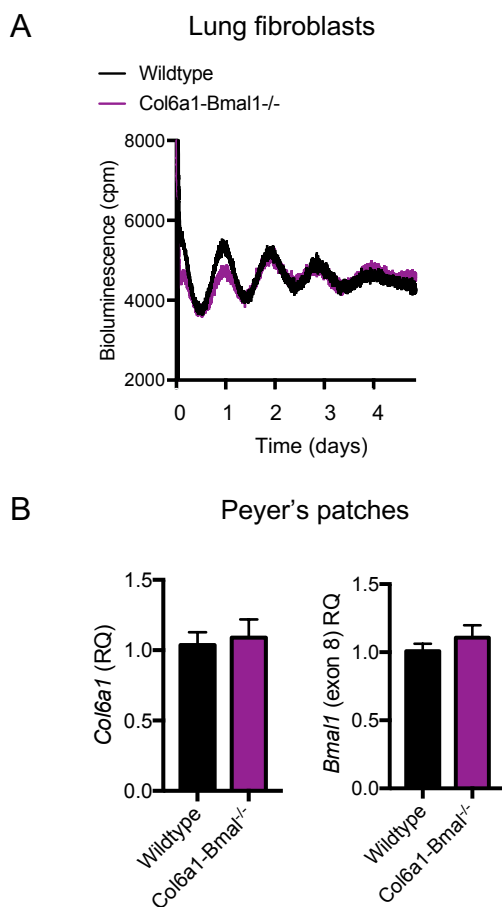
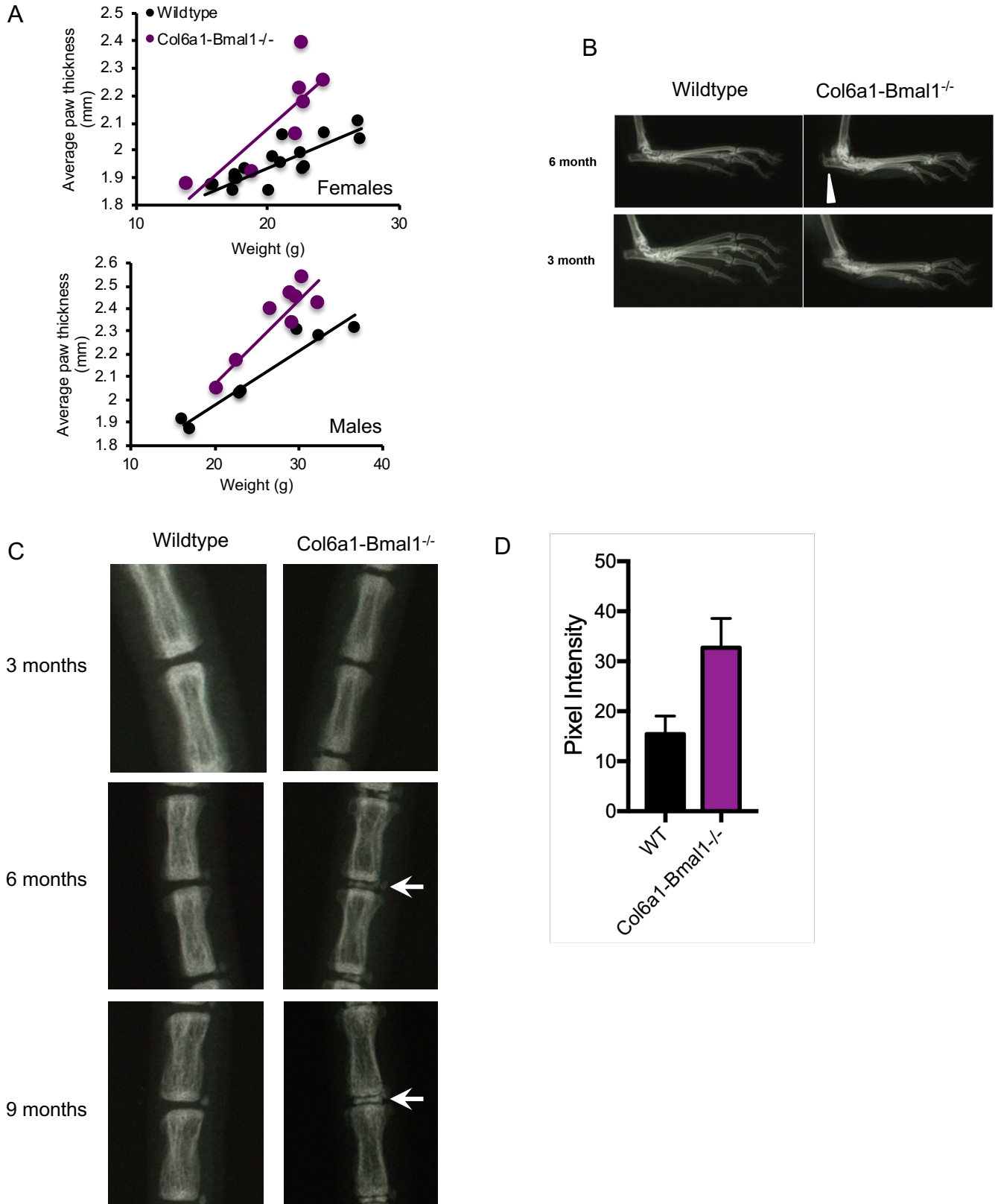


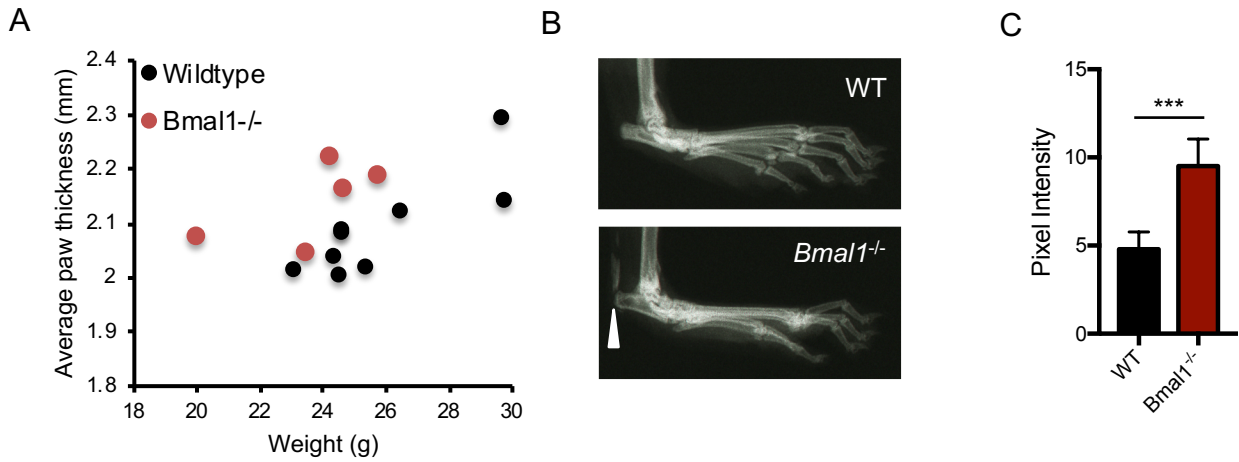
Supplementary Figure 1: (A) Bioluminescence recording from lung fibroblasts cultured from *Col6a1-Bmal1^{-/-}* and wildtype animals on a *PER2::luc* background. (B) QPCR analysis of *Col6a1* and *Bmal1* expression in Peyer's patches isolated from wildtype (n=5) and *Col6a1-Bmal1^{-/-}* (n=3) animals.



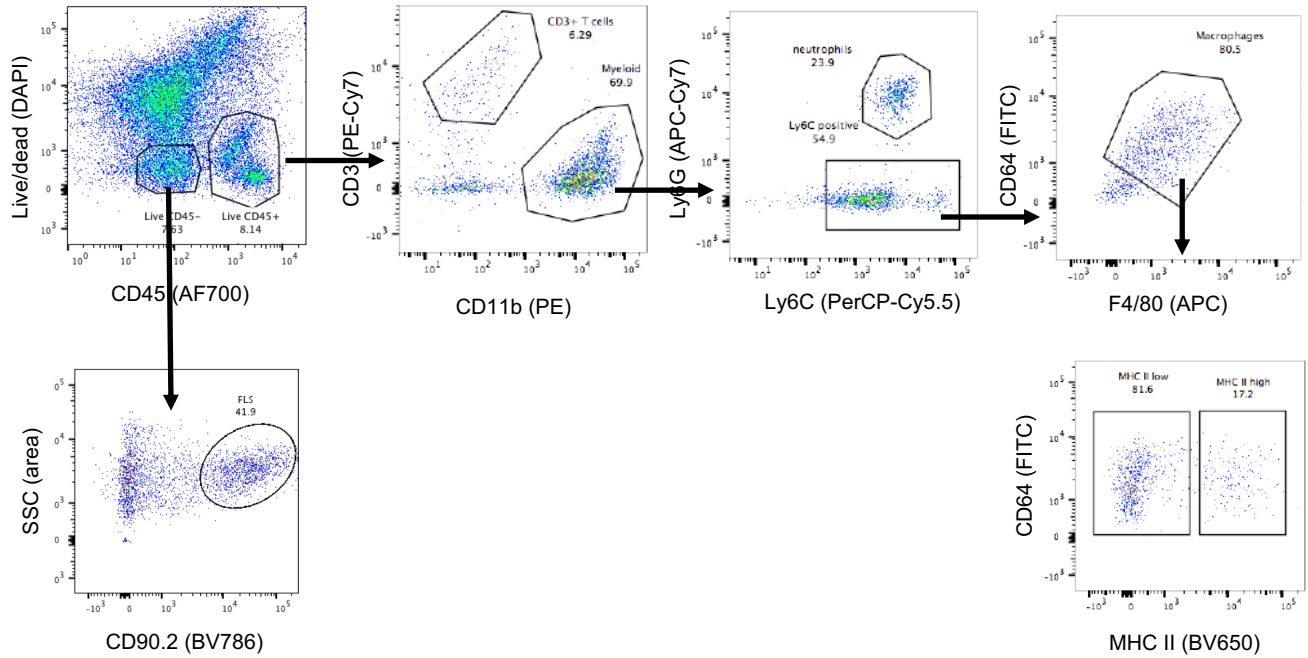
Supplementary Figure 2: (A) Hind paw thickness (mm) plotted against animal weight (g) measured in female (top) and male (bottom) *Col6a1-Bmal1^{-/-}* and WT mice (pooled data shown in Figure 2a). (B) X-rays of hind limbs from *Col6a1-Bmal1^{-/-}* mice and WT littermates age 3 and 6 months, representative of n=3 animals/genotype. Arrow indicates location of a calcaneal spur. (C) X-ray images of the tails of *Col6a1-Bmal1^{-/-}* mice and WT littermates age 3, 6 and 9 months, arrows indicate areas of calcification within the intervertebral disks. (D) Pixel intensity in a defined region of interest encompassing the intervertebral disk space was quantified in 9 month old mice, n=3/genotype.



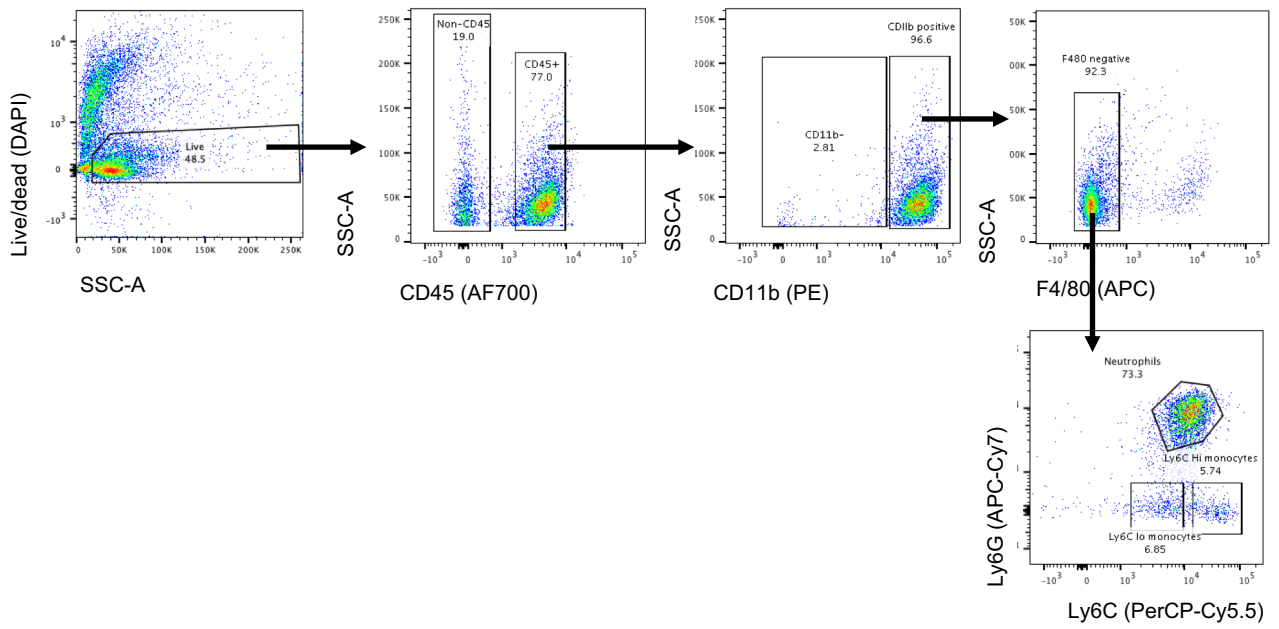
Supplementary Figure 3: (A) Comparison of paw thickness in male wildtype ($Bmal1^{+/+}$, n=9) and KO ($Bmal1^{-/-}$, n=5) mice. Paw thickness (mm) and weights (g) are plotted against one another. (B) X-rays of hind limbs from male $Bmal1^{-/-}$ and wildtype littermates, age 4-5 months. A spur protruding from the calcaneum of the $Bmal1^{-/-}$ is marked by an arrow, representative of n=3-4 animals/genotype. (C) Quantification of pixel intensity from X-ray images in a region of interest superior to the calcaneus, n=6-8 limbs, unpaired T test.



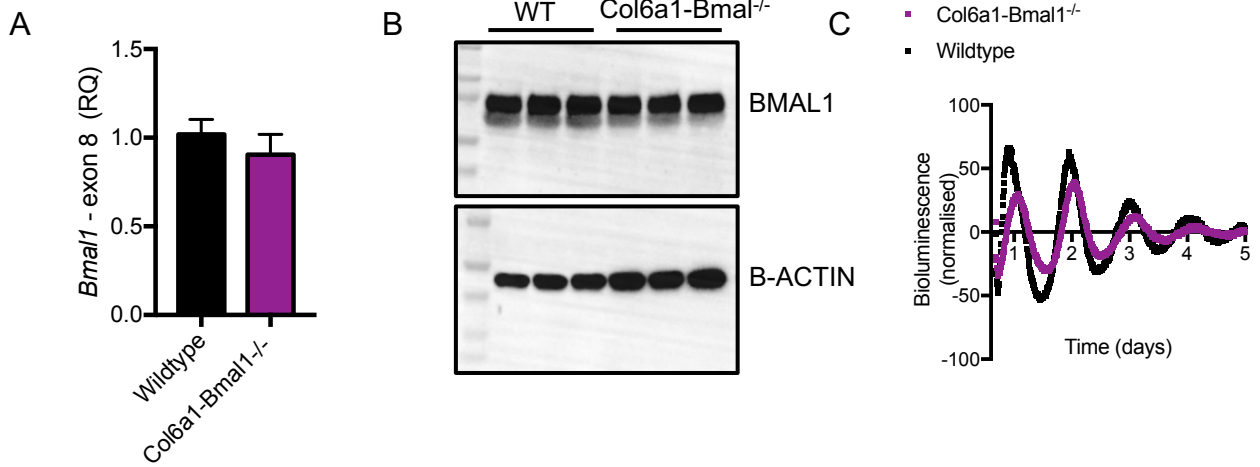
Supplementary Figure 4: Gating strategy for identification of cells digested from the hind limbs of naïve animals. Single cells were gated as shown below to identify populations of FLS (CD45⁻CD90.2⁺), T cells (CD45⁺CD11b⁻CD3⁺), neutrophils (CD45⁺CD11b⁺Ly6C⁺Ly6G⁺) and MHCII^{high} and MHCII^{low} macrophages (CD45⁺CD11b⁺Ly6C⁺CD64⁺F4/80⁺)



Supplementary Figure 5: Gating strategy for identification of cells digested from the hind limbs of arthritic animals. Single cells were gated as shown below to identify populations of neutrophils ($CD45^+CD11b^+F4/80^-Ly6C^+Ly6G^+$) and $Ly6C^{hi}$ and $Ly6C^{low}$ monocytes ($CD45^+CD11b^+F4/80^-Ly6G^-$).



Supplementary Figure 6: Expression of BMAL1 is unaffected in macrophages. (A) Expression of *Bmal1* (exon 8) was quantified from peritoneal macrophages harvested from *Col6a1-Bmal1^{-/-}* (3 male and 3 female) and wildtype (4 male and 3 female) mice using QPCR, *gapdh* was utilized as a housekeeping gene and levels were normalized to wildtype expression. (B) Western blot of BMAL1 and β -ACTIN protein levels in bone marrow derived macrophages harvested from *Col6a1-Bmal1^{-/-}* and wildtype animals. (C) Bioluminescence analysis of PER2::luciferase activity in peritoneal macrophages from *Col6a1-Bmal1^{-/-}* mice and wildtype counterparts, representative of n=3-4 males/genotype.



Supplementary Table 1: Antibodies utilized for flow cytometric assessment of cells digested from naïve limbs

| Antibody | Fluorophore | Clone | Supplier |
|-----------------|--------------------|--------------|-----------------|
| CD45 | AF700 | 30-F11 | BD Biosciences |
| CD3 | Pe-Cy7 | 145-2C11 | Biolegend |
| CD11b | PE | M1/70 | Biolegend |
| Ly6G | APC-Cy7 | IA8 | BD Biosciences |
| Ly6C | PerCP-Cy5.5 | AL-21 | Biolegend |
| CD64 | FITC | XS4-5/7.1 | Biolegend |
| F4/80 | APC | BM8 | eBioscience |
| MHC II | BV650 | M5/114.15.2 | BD Biosciences |
| CD90.2 | BV786 | 30-H12 | Biolegend |

Supplementary Table 2: Antibodies utilized for flow cytometric assessment of cells digested from arthritic limbs.

| Antibody | Fluorophore | Clone | Supplier |
|-----------------|--------------------|--------------|-----------------|
| CD45 | AF700 | 30-F11 | BD Biosciences |
| CD11b | PE | M1/70 | Biolegend |
| F4/80 | APC | BM8 | eBiosciences |
| Ly6G | APC-Cy7 | IA8 | Biolegend |
| Ly6C | PerCP-Cy5.5 | AL-21 | BD Biosciences |

Supplementary Table 3: Primers utilized for QPCR analysis. *Indicates where TaqMan gene expression assays (ThermoFisher Scientific) were utilized with the relevant product code.

| | Forward | Reverse | Probe (Fam-Tamra) |
|-----------------------|--------------------------|----------------------------|---------------------------------|
| <i>Gapdh</i> | CAATGTGTCCGTCGTCGATCT | GTCCTCAGTGTAGCCCAAGATG | CGTGCCGCCTGGAGAAACCTGCC |
| <i>Per2</i> | GCCTTCAGACTCATGATGACA GA | TTTGTGTGCGTCAGCTTTGG | ACTGCTCACTACTGCAGCCGCTCGT |
| <i>Bmal1 (exon 8)</i> | CGTCGGGACAAAATGAACAG | GAACAGCCATCCTTAGCAC | TACCAACATGCAATGCAATGTCCAGGAA |
| <i>Cry1</i> | CTGGCGTGGAAGTCATCGT | CTGTCCGCCATTGAGTTCTATG | CGCATTTCACATACACTGTATGACCTGGACA |
| <i>Dbp</i> | CCGTGGAGGTGCTAATGACCT | CCTCTGAGAAGCGGTGCCT | TGAACCTGATCCGGCTGATCTTGCC |
| <i>Il6</i> | CTATACCACTTCACAAGTCGGAGG | TGCACAACCTCTTTTCTCATTTC | TTAATTACACATGTTCTCTGGGAAATCG |
| <i>Cxcl1</i> | CTGCACCCAAACCGAAGTC | AGCTTCAGGGTCAAGGCAAG | CACTCAAGAATGGTCGCGAGGC |
| <i>Ccl2</i> | TTCTGGGCCTGCTGTTCA | CCAGCCTACTCATTGGGATCA | CTCAGCCAGATGCAGTTAACGCCCC |
| <i>lfn gamma</i> | TCAAGTGGCATAGATGTGGAAGAA | TGGCTCTGCAGGATTTTCATG | TCACCATCCTTTTGCCAGTTCCTCCAG |
| <i>Rankl</i> | GCACACCTCACCATCAATGCT | GGTACCAAGAGGACAGAGTGACTTTA | CCAGCATCCCATCGGGTTCCC |
| <i>Rev-erb α *</i> | Mm00520708_m1 | | |
| <i>Col2a1 *</i> | Mm01309565_m1 | | |
| <i>Col6a1*</i> | Mm00487160_m1 | | |
| <i>Aggrecan *</i> | Mm00545794_m1 | | |
| <i>Prg4 *</i> | Mm01284582_m1 | | |
| <i>Ihh *</i> | Mm00439613_m1 | | |
| <i>Cxcl5 *</i> | Mm00436451_g1 | | |
| <i>Il10 *</i> | Mm01288386_m1 | | |
| <i>Il13 *</i> | Mm00434204_m1 | | |

Supplementary Table 4: Cytokine secretion by cultured FLS. Cell supernatants were assayed by Bioplex or ELISA (CXCL5 and M-CSF), n=4-6. Data was analyzed using two way ANOVA and post hoc Bonferroni's test (black asterix) or unpaired T test (grey asterix). Effects of genotype are shown within each treatment group (control and + TNF α). Secretion of IL1 α , IL1 β , IL2, IL3, IL4, IL5, IL12p40, IL17, CCL11, G-CSF and CCL3 were minimal and thus data are not shown.

| | Control | | + TNF α | |
|-------------------------------|-----------------|-------------------------------------|---------------------|-------------------------------------|
| | WT (pg/ml) | Col6a1-Bmal1 ^{-/-} (pg/ml) | WT (pg/ml) | Col6a1-Bmal1 ^{-/-} (pg/ml) |
| IL6 | 2.3 \pm 0.1 | 3.7 \pm 0.2 | 13.9 \pm 0.5 | 52.6 \pm 1.2*** |
| IL9 | 3.5 \pm 0.9 | 2.4 \pm 0.4 | 11.2 \pm 0.8 | 6.4 \pm 0.9** |
| IL10 | 1.3 \pm 0.4 | 1.0 \pm 0.3 | 12.3 \pm 0.6 | 2.7 \pm 0.5*** |
| IL12 p70 | 5.8 \pm 1.6 | 5.5 \pm 1.3 | 33.3 \pm 2.3 | 24.1 \pm 0.8** |
| IL13 | ND | ND | 150.4 \pm 12.1 | 51.7 \pm 7.2*** |
| GM-CSF | ND | ND | 15.1 \pm 0.8 | 11.2 \pm 0.7** |
| IFNγ | 0.2 \pm 0.06 | 0.2 \pm 0.05 | 5.8 \pm 0.3 | 1.1 \pm 0.1*** |
| CXCL1 | 6.7 \pm 0.7 | 11.7 \pm 0.4 | 170.7 \pm 19.0 | 716.7 \pm 22.1*** |
| CCL2 | 138.0 \pm 6.6 | 303.7 \pm 14.5 | 1447.7 \pm 194.4 | 7586.9 \pm 298.4*** |
| CCL4 | 1.3 \pm 0.072 | 3.9 \pm 0.3*** | 5.2 \pm 0.3 | 11.1 \pm 0.3*** |
| CCL5 | 29.4 \pm 2.3 | 29.6 \pm 3.3 | 387.6 \pm 39.1 | 1574.5 \pm 54.7*** |
| TNFα | 7.2 \pm 0.3 | 4.9 \pm 0.2 | 13777.5 \pm 587.2 | 14762.7 \pm 449.9 |
| CXCL5 | 1.1 \pm 0.2 | 32.9 \pm 2.8 | 22.6 \pm 4.3 | 430.6 \pm 19.1*** |
| M-CSF | ND | 15.9 \pm 3.0 | 2.4 \pm 1.0 | 18.5 \pm 6.7* |