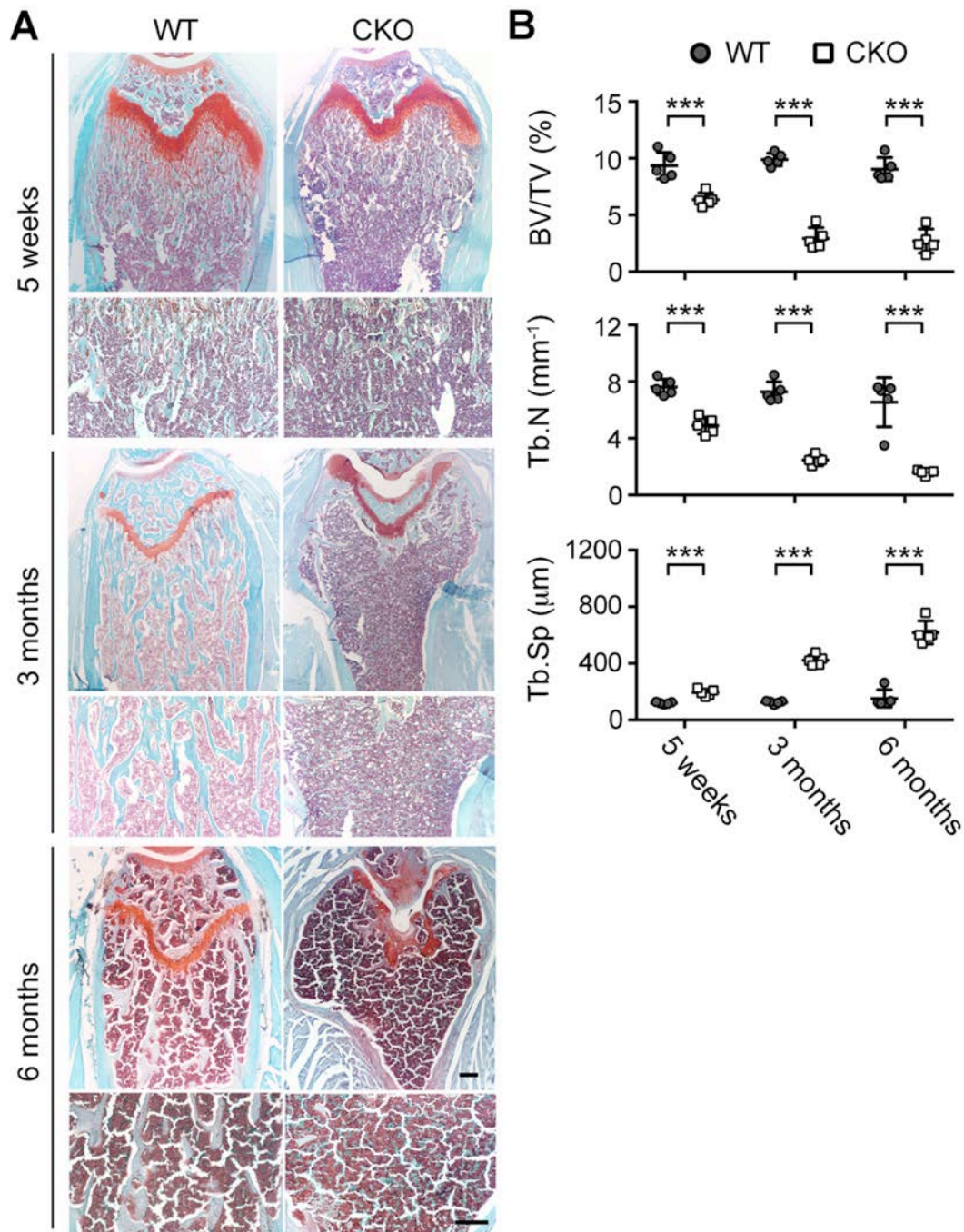
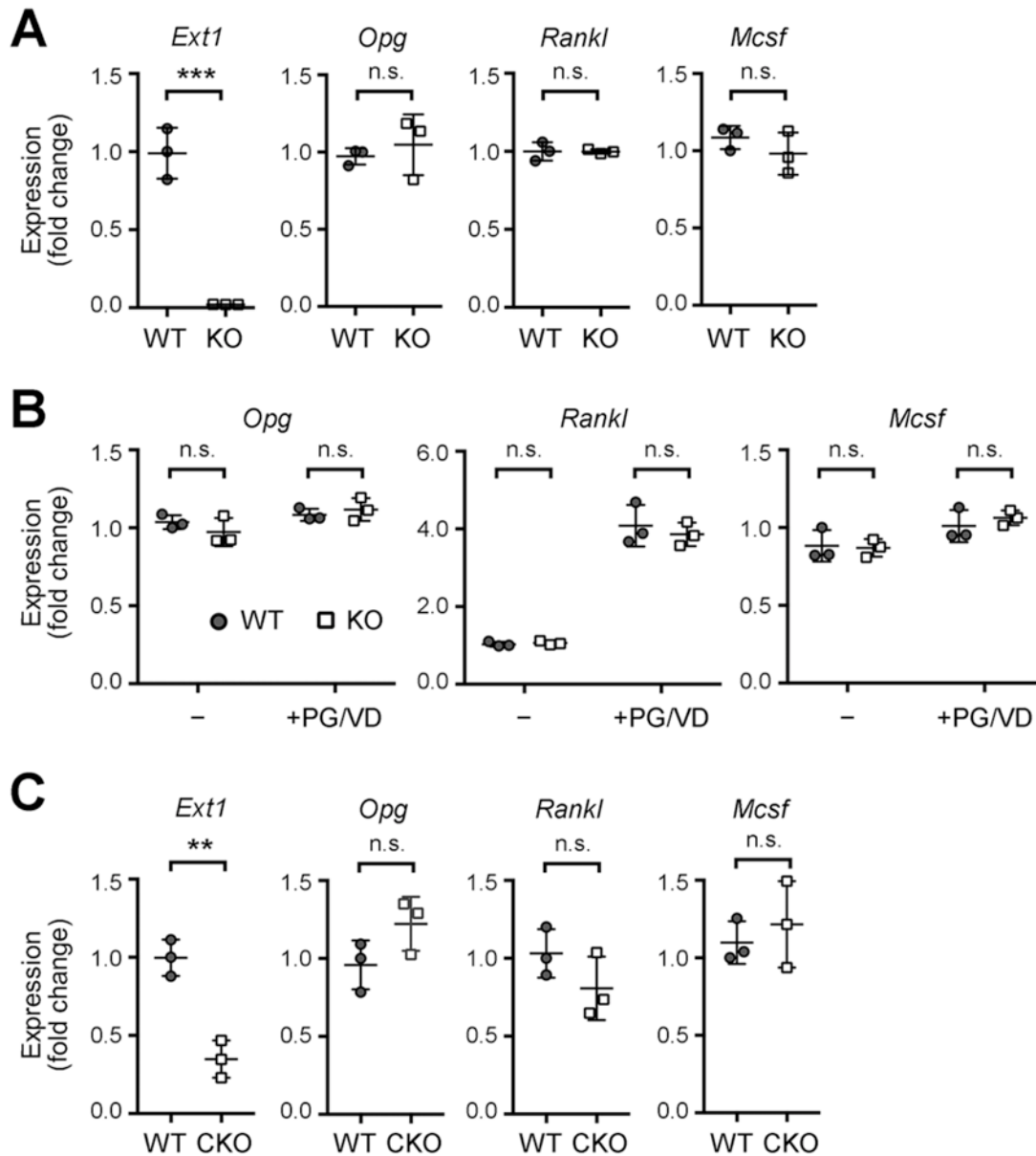


**Supplemental Figure 1. (A) Appearance of an *Oc-Cre;Ext1<sup>lox/lox</sup>* (CKO) and a control littermate (WT) at P60. (B) Body weight of *Oc-Cre;Ext1<sup>lox/lox</sup>* (CKO) and a control littermate (WT) at P60. Data represent the mean  $\pm$  SD of 5 mice per genotype. *n.s.*, not significant by Student's *t* test. (C) PCR analysis of Cre-mediated *Ext1* ablation. PCR was performed with a primer combination specific for the recombined *Ext1* allele on DNA samples harvested from indicated organs of P60 *Oc-Cre;Ext1<sup>lox/lox</sup>* mice.**



**Supplemental Figure 2. Osteoblast-targeted *Ext1* ablation induces osteopenia in long bones.** (A) Safranin O staining of the proximal end of the femur at 5-weeks, 3-months, and 6-months of age. *CKO*, *Oc-Cre;Ext1<sup>flx/flx</sup>* mice; *WT*, wild-type control mice. (B) Histomorphometric analysis of bone mass in the proximal end of the femur at 5-week, 3-months, and 6-months of age. *BV/TV*, bone volume over tissue volume; *Tb.N*, trabecular number; *Tb.Sp*, trabecular separation. Data represent the mean  $\pm$  SD of 5 mice per genotype. \*\*\* $p < 0.001$  by Student's *t* test. Scale bars, 0.2 mm.



**Supplemental Figure 3. Expression of *Opg*, *Rankl*, and *Mcsf* in *Ext1*-deficient osteoblasts and the femur of *Oc-Cre;Ext1<sup>flox/flox</sup>* mice.** (A) Osteoblasts were isolated from the calvaria of *Ext1<sup>flox/flox</sup>* mice and treated with or without Cre-expressing adenovirus to ablate *Ext1* as described in *Methods*. qRT-PCR was performed on total RNA isolated from wild-type (i.e., non-ablated; *WT*) and *Ext1*-ablated (*KO*) osteoblasts. (B) Wild-type (*WT*) and *Ext1*-ablated (*KO*) osteoblasts were treated without (–) or with prostaglandin E2 and 1 $\alpha$ ,25(OH) $_2$ D $_3$  (+*PG/VD*) for 5 days. qRT-PCR was performed on total RNA isolated from these cultures. (C) qRT-PCR was performed on total RNA isolated from homogenates of 5-week old femurs. *WT*, wild-type mice; *CKO*, *Oc-Cre;Ext1<sup>flox/flox</sup>* mice. qRT-PCR was performed by using the TaqMan Gene Expression Master Mix specific for respective genes. Data represent the mean  $\pm$  SD (n = 3). \*\*p<0.01 and \*\*\*p<0.001; n.s., not significant, by Student's *t* test.