

Fig. S1. Comparison of the *Osx-GFP::Cre* transgene to wild type mice on skeletal growth in a C57BL/6J; 129X1 mixed genetic background.

A. Growth curve of wild type and *Osx-GFP::Cre* (*Osx-Cre*) mice showing near normal growth of *Osx-Cre* mice. B and C. Micro CT analysis of the distal femur showing normal trabecular and cortical bone formation (B), and quantitation showing similar BV/TV and BMD values for wild type and *Osx-Cre* mice at P21 (C). D. Histology (H&E) of the proximal tibia showing similar growth plate histology in P21 wild type and *Osx-Cre* mice. E. *In situ* hybridization showing similar intensity of *Fgfr3* expression in the growth plate of P21 wild type and *Osx-Cre* mice. Scale bars: 100 μ m.

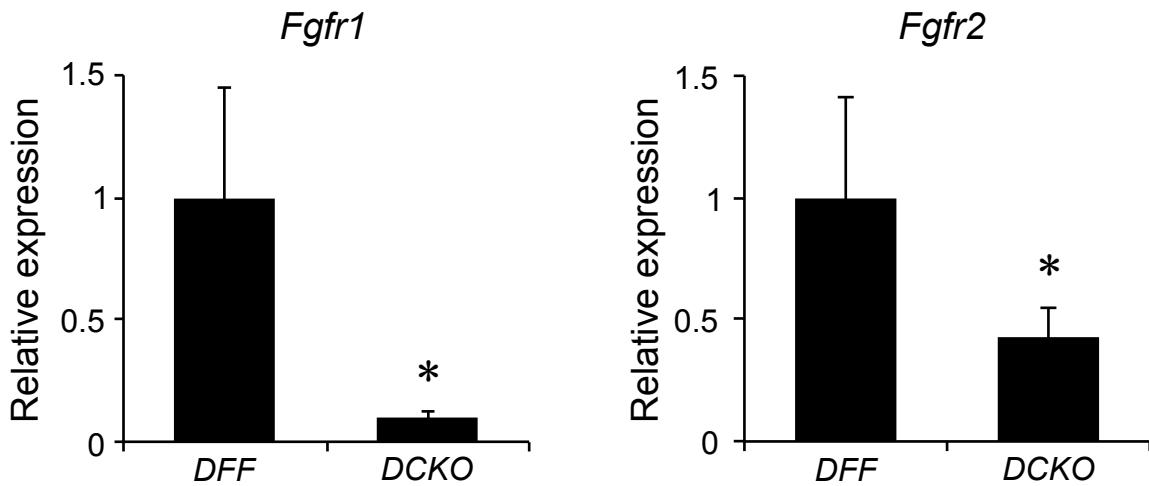


Fig. S2. Reduced *Fgfr1* and *Fgfr2* gene expression in skeletal tissue from *Osx-Cre;DCKO* mice.

Quantitative RT-PCR for *Fgfr1* and *Fgfr2* in cortical bone isolated from P21 *DFF* and *Osx-Cre;DCKO* mice.

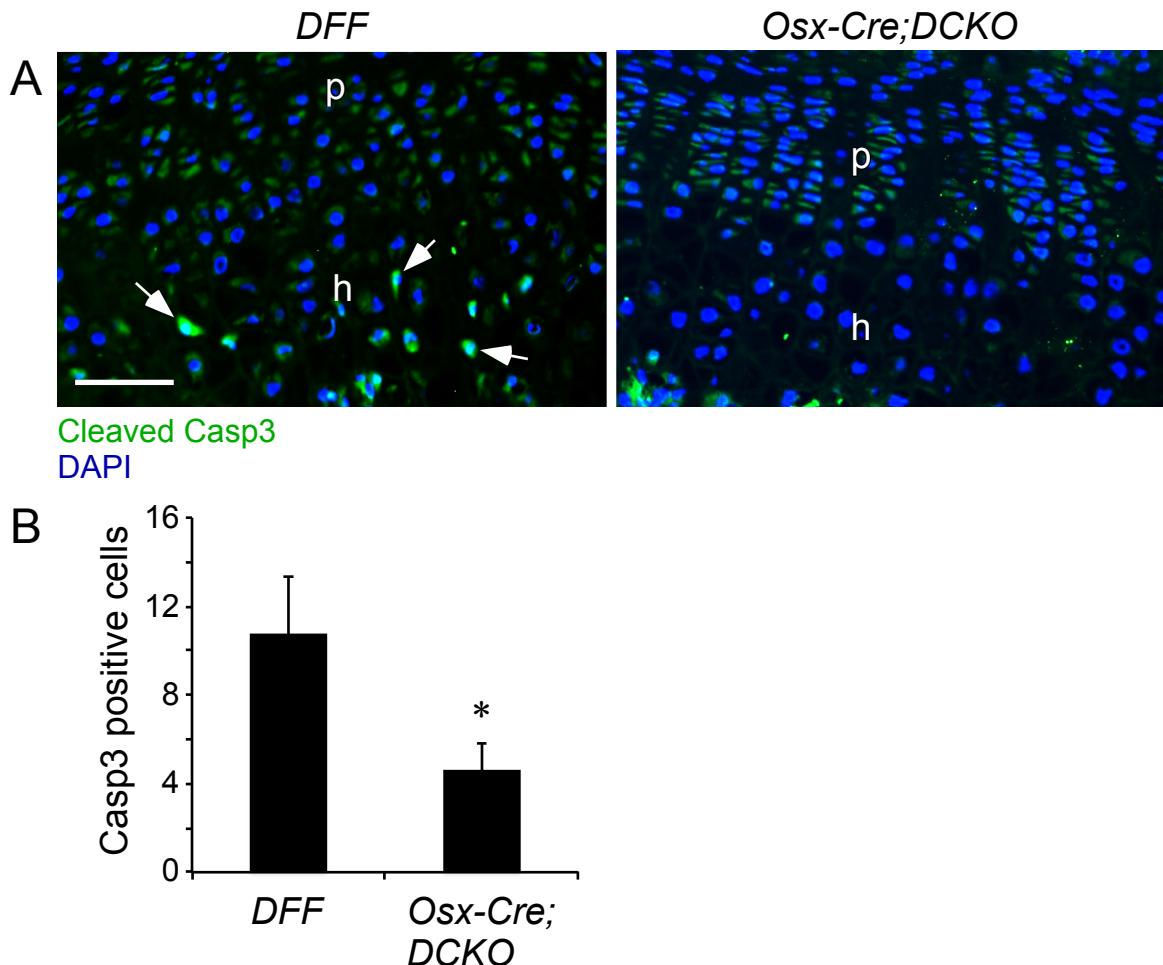


Fig. S3. Decreased cell death in distal hypertrophic chondrocytes of Osx-Cre;DCKO mice.

A. Immunostaining for activated Caspase 3 showing fewer stained cells (arrow) in the distal hypertrophic chondrocyte zone of P21 Osx-Cre;DCKO compared to *DFF* mice. B. Quantification of cells expressing activated Caspase 3 in the distal hypertrophic zone ($n=3-4$). p, proliferating chondrocytes; h, hypertrophic chondrocytes. $*P<0.02$. Scale bar: 50 μ m.