

Supplementary Figure Legends

Figure S1. Gene expression changes in the bones of Prx1-Cre; Notch2^{f/f} (PN2) over Notch2 (N2) littermate mice. Fold changes were calculated from RT-qPCR results after normalization to 18S rRNA. *: $p < 0.05$, $n = 3$. Statistical method: two-tailed Student's t test.

Figure S2. RT-qPCR analyses of osteoblast marker genes. Primary BMSC from 2-month-old N2 (control) or PN2 (mutant) mice were cultured on Fc- or Jag1-coated plates in osteogenic media for 4 days with or without 3PO (20 μ M). Hey1 serves as readout for Notch signaling. *: $p < 0.05$, $n = 3$. Statistical method: two-way ANOVA.

Figure S3. RT-qPCR analyses of mRNA levels in NICD2-ST2 cells with or without Dox induction for 24 hrs. Upper row: glycolytic genes; lower row: mitochondrial ETC genes. *: $p < 0.05$, $n = 3$. Statistical method: two-tailed Student's t test.

Figure S4. RT-qPCR analyses of mRNA levels in NICD2-ST2 cells to detect shRNA knockdown efficiency. Two independent shRNA used from each gene and shLuc used as negative control. RNA was harvested after 48 hrs of Dox or control treatment following shRNA lentiviral infections. Note that Tcf7l2 was no longer induced by NICD2 after 48 hrs even though it was at 24 hrs. *: $p < 0.05$, $n = 3$. Statistical method: two-way ANOVA.

Fig. S1

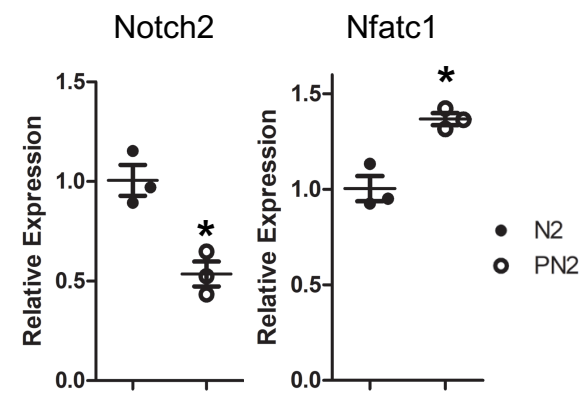


Fig. S2

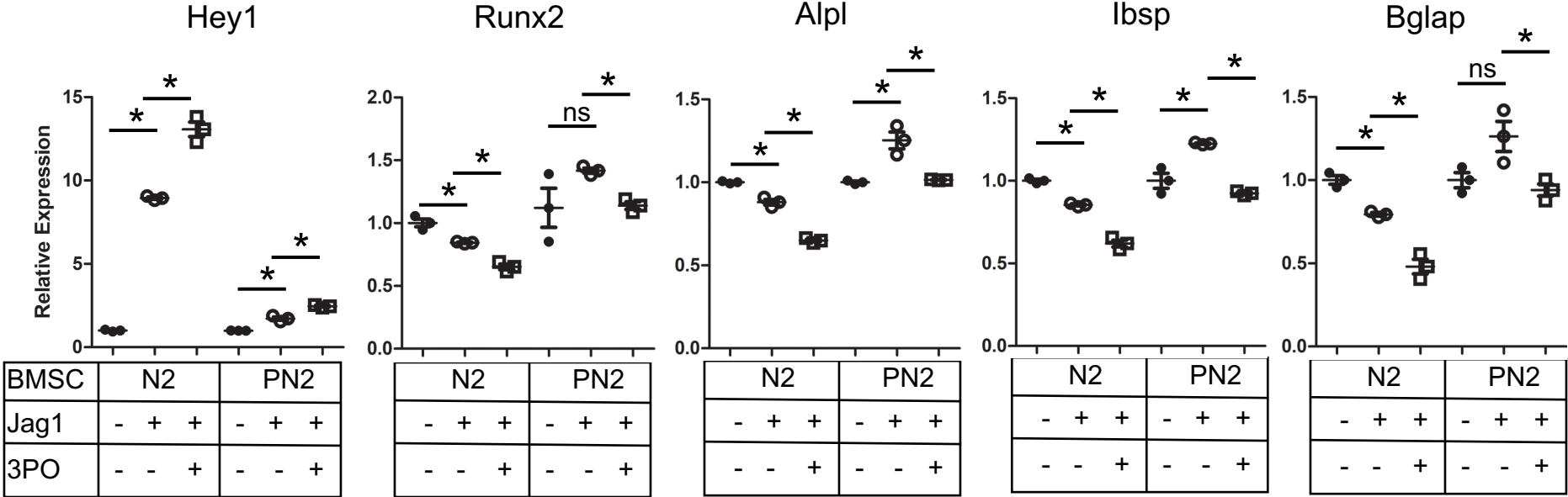


Fig. S3

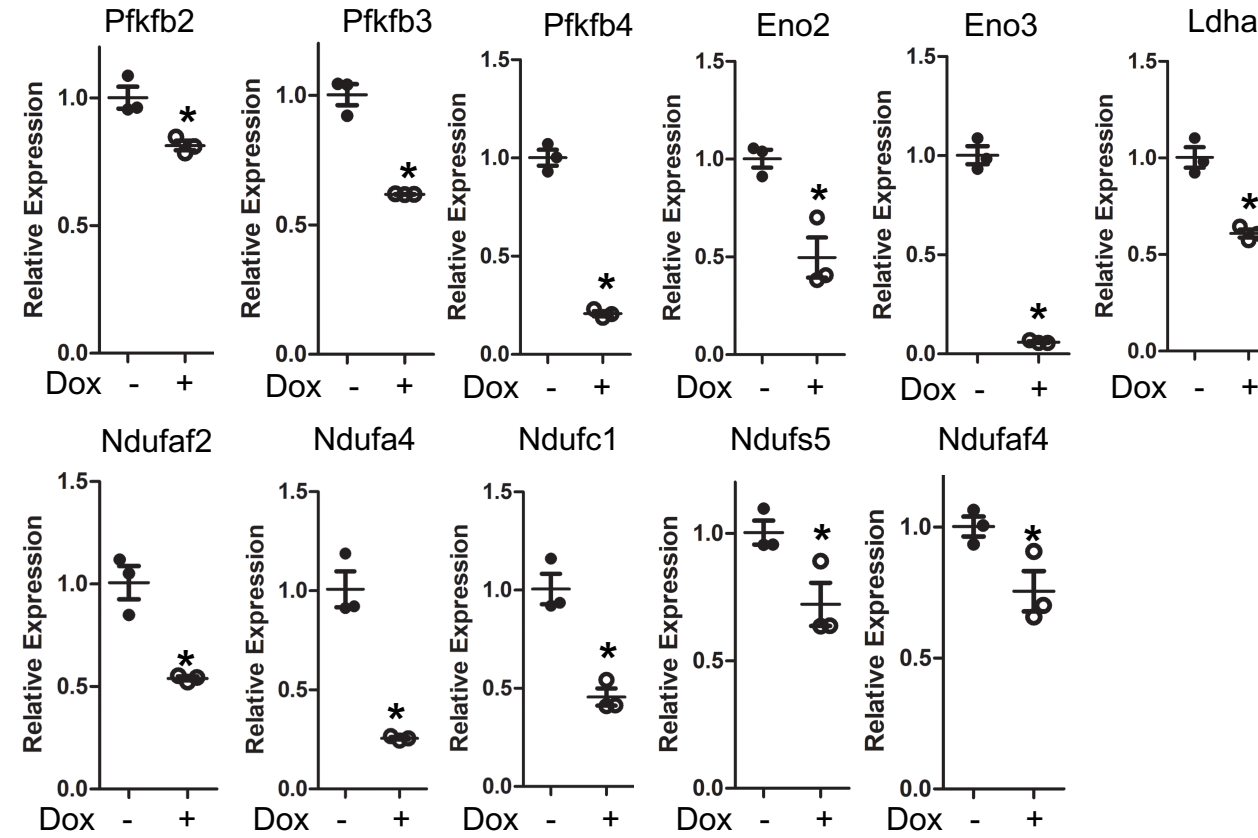


Fig. S4

