

Khavandgar et al., <http://www.jcb.org/cgi/content/full/jcb.201102051/DC1>

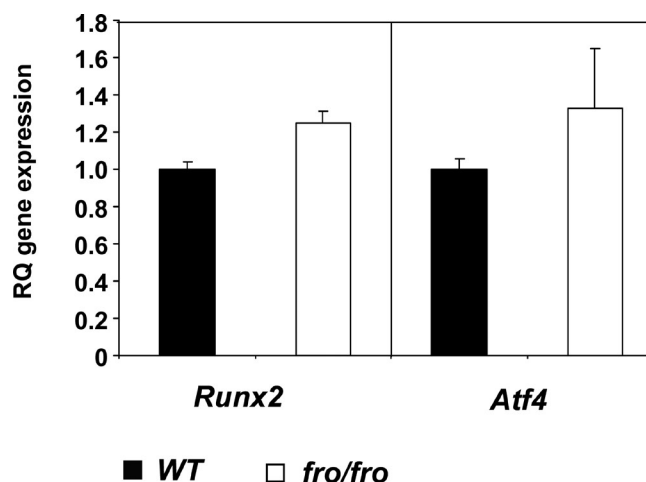


Figure S1. qRT-PCR analysis of *Runx2* and *Atf4* expression in newborn *fro/fro* bones. The qRT-PCR expression analysis of total RNA shows that *Runx2* and *Atf4* expression in the bones from newborn *fro/fro* mice are normal. Error bars represent standard deviations. RQ, relative quantification.

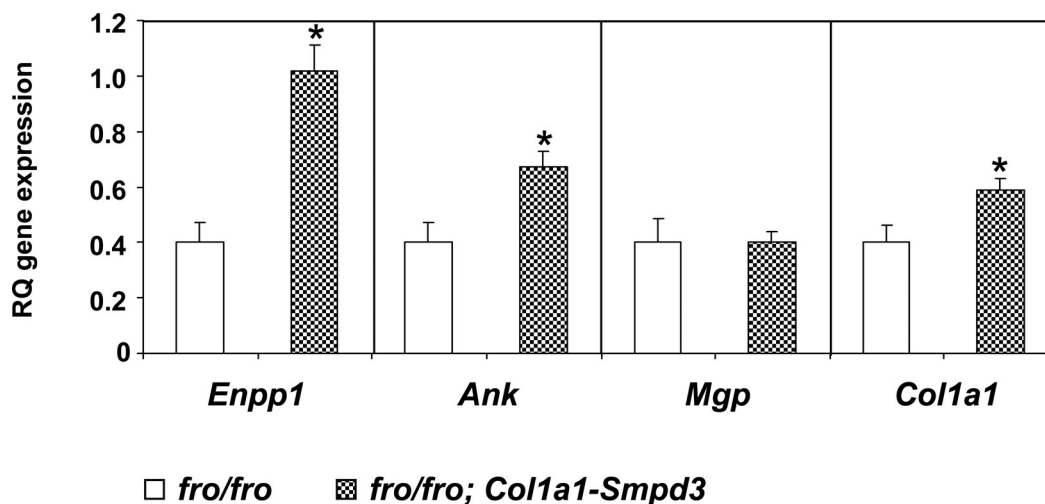


Figure S2. The comparative expression analysis of *Enpp1*, *Ank*, *Mgp*, and *Col1a1* by qRT-PCR in the parietal bones of *fro/fro* and *fro/fro; Col1a1-Smpd3* mice. *Enpp1* expression is ~2.5-fold up-regulated, whereas there is a mild but significant up-regulation of *Ank* and *Col1a1* expression in the bones from newborn *fro/fro; Col1a1-Smpd3* mice in comparison with that of their *fro/fro* littermates. *Mgp* expression remains unchanged. Error bars represent standard deviations. *, $P < 0.05$. RQ, relative quantification.

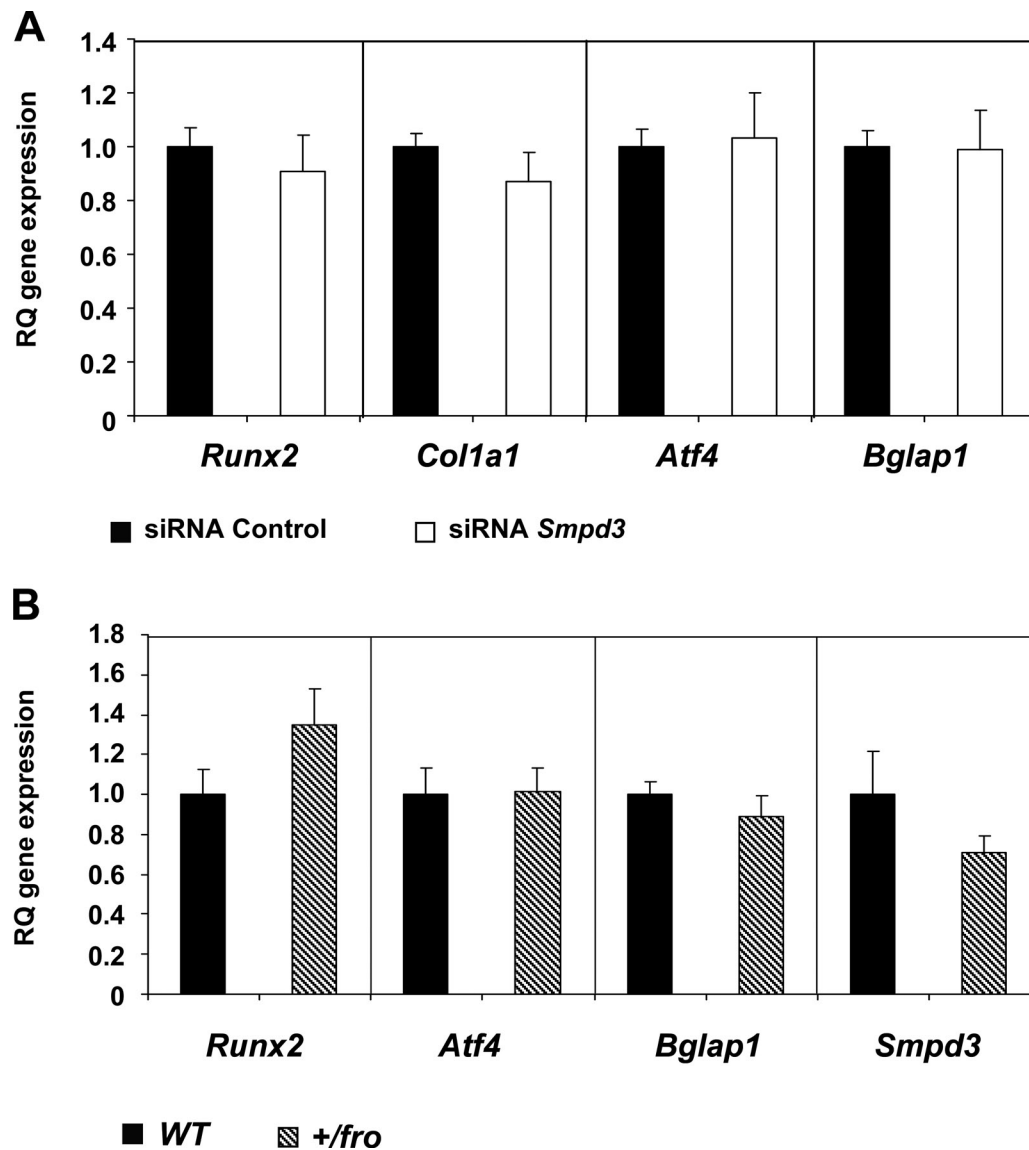


Figure S3. qRT-PCR analysis of *Runx2*, *Col1a1*, *Atf4*, and *Bglap1* expression in the control and *Smpd3* siRNA-treated MC3T3-E1 cells and *Runx2*, *Atf4*, *Bglap1*, and *Smpd3* expression in WT and *+/-*ro mice. (A) *Runx2*, *Col1a1*, *Atf4*, and *Bglap1* expressions are not altered in *Smpd3* siRNA-transfected MC3T3-E1 cells, in comparison with the control siRNA-transfected cells. (B) No significant alteration of *Runx2*, *Atf4*, *Bglap1*, and *Smpd3* expression was seen in the *+/-*ro bones when compared with those from their WT littermates. The qRT-PCR expression analysis was performed on the total RNA extracted from the parietal bones of the newborn mice. Error bars represent standard deviations. RQ, relative quantification.