SUPPLEMENTARY FIGURES

WNT16 is robustly increased by Oncostatin M and acts as a negative feed-back regulator of periosteal osteoclast formation induced by Oncostatin M

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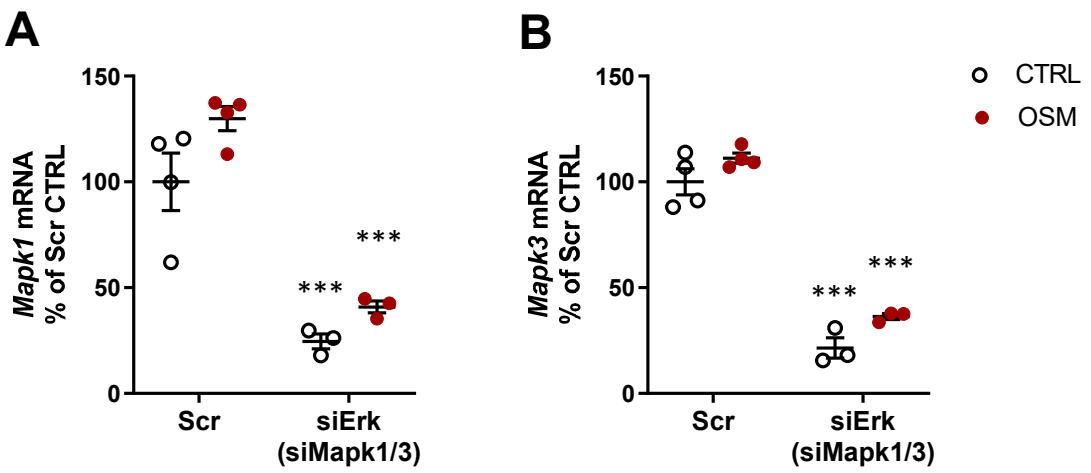
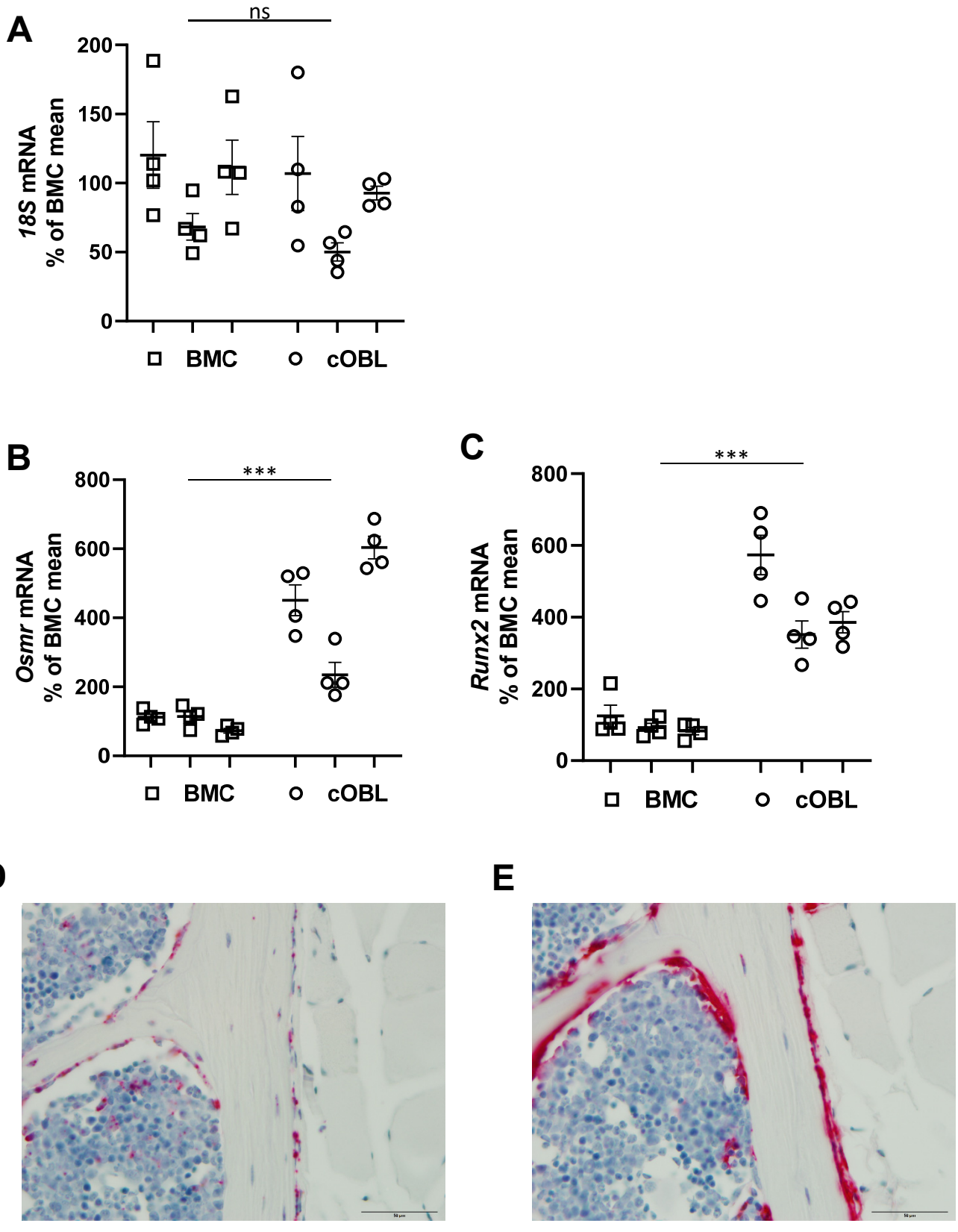
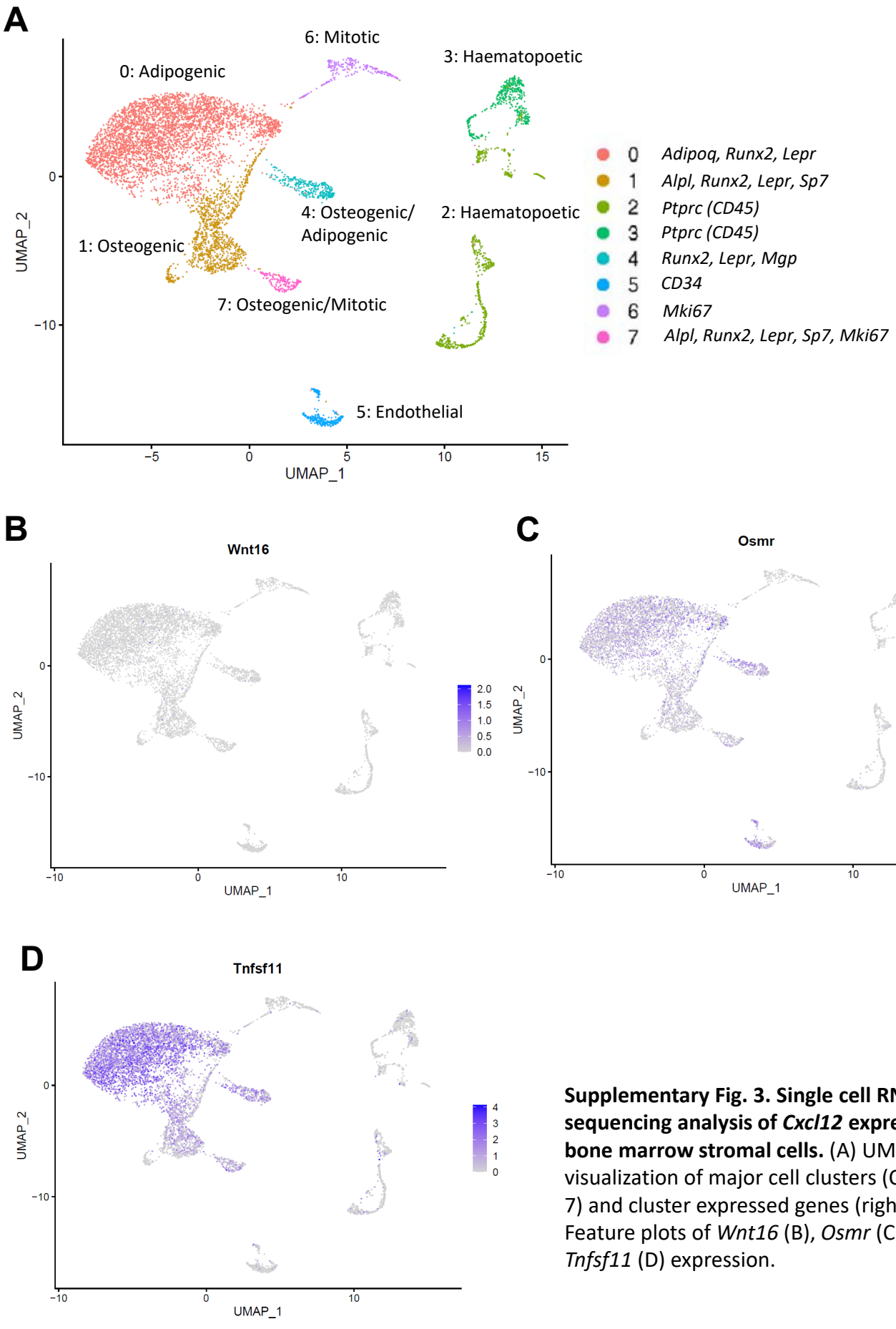


Supplementary Fig. 1. Expression of *Mapk1* and *Mapk3* mRNA in calvarial periosteal osteoblast cultures after silencing using siRNA.

The expression of *Mapk1* and *Mapk3* was simultaneously silenced in primary calvarial osteoblast cultures using siRNA. Cells were treated with 100 ng/ml mOSM for 24 h and thereafter *Mapk1* and *Mapk3* expression was analyzed. Scrambled siRNA (Scr) was used as control. Individual values are presented in all graphs with the mean presented as horizontal lines and ±SEM as vertical lines. ***P<0.001 vs. respective Scr, two-way ANOVA followed by Sidak's multiple comparison test.



Supplementary Fig. 2. Gene expression in bone marrow cells vs. periosteal cells analyzed by PCR and *in situ* hybridization. Expression of *18S* (A), *Osmr* (B) and *Runx2* (C) in three bone marrow cell (BMC) cultures and three calvarial periosteal cell (cOBL) cultures cultured in osteogenic media for 7 and 6-8 days, respectively. Individual values are presented in all graphs with the mean presented as horizontal lines and ±SEM as vertical lines. ***P<0.001 BMC vs. cOBL, two-way ANOVA. RNAscope of *Runx2* (D) and *Col1a1* (E) expression (red) in L5 vertebrae. Scale bar, 50 µm.



Supplementary Fig. 3. Single cell RNA sequencing analysis of *Cxcl12* expressing bone marrow stromal cells. (A) UMAP-based visualization of major cell clusters (Cluster 0-7) and cluster expressed genes (right). Feature plots of *Wnt16* (B), *Osmr* (C) and *Tnfsf11* (D) expression.