

Supplemental Table 1

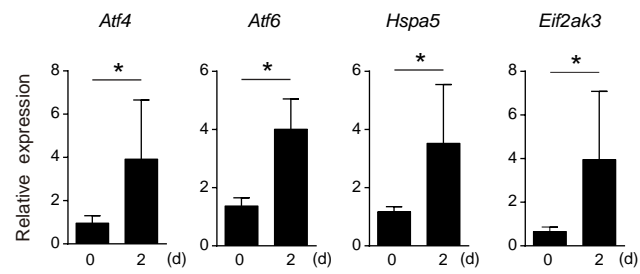
List of oligonucleotides used for quantitative PCR analysis

Gene	Strand	Sequence
<i>Xbp1s</i>	Fwd	CTG AGT CCG AAT CAG GTG CAG
	Rev	GTC CAT GGG AAG ATG TTC TGG
<i>Xbp1u</i>	Fwd	GGT CTG CTG AGT CCG CAG CAC TC
	Rev	AGG CTT GGT GTA TAC ATG G
Total <i>Xpb1</i>	Fwd	GAA CCA GGA GTT AAG AAC ACG
	Rev	AGG CAA CAG TGT CAG AGT C
<i>Nfatc1</i>	Fwd	AAC GCC CTG CTG ACC ACC GAT AGC A
	Rev	CCC GGG TGC CTT CCG TCT CAT A
<i>Fos</i>	Fwd	CCA AGC GGA GAC AGA TCA ACT T
	Rev	TCC AGT TTT TCC TTC TCT TTC AGC AGA T
<i>Rela</i>	Fwd	GCT TTC GCA GGA GCA TTA AC
	Rev	CCG AAG CAG GAG CTA TCA AC
<i>jund</i>	Fwd	GCC TCA CGC TCT GCC TTT CC
	Rev	CAC ACT CAA CAC GCA ACC AAC G
<i>Spi1</i>	Fwd	GCT ATA CCA ACG TCC AAT GC
	Rev	GTT GTT GTG GAC ATG GTG TG
<i>Hspa5</i>	Fwd	TTC AGC CAA TTA TCA GCA AAC TCT
	Rev	TTT TCT GAT GTA TCC TCT TCA CCA GT
<i>Eif2ak3</i>	Fwd	GCC ACA GAG AAC AGC GTG TA
	Rev	CGG CAG AGG AAT AAT TGC AT
<i>Actb</i>	Fwd	CTG AAC CCT AAG GCC AAC CGT G
	Rev	GGC ATA CAG GGA CAG CAC AGC C
<i>Atf4</i>	Fwd	CGA GAT GAG CTT CCT GAA CAG C
	Rev	GGA AAA GGC ATC CTC CTT GC
<i>Ern1</i>	Fwd	AAG CAG CTC CAG TTT TTC CA
	Rev	CTC TCC AAC TGC CGT ACG AT
<i>Ctsk</i>	Fwd	ACG GAG GCA TTG ACT CTG AAG ATG
	Rev	GGA AGC ACC AAC GAG AGG AGA AAT
<i>Acp5</i>	Fwd	CCA ATG CCA AAG AGA TCG CC
	Rev	TCT GTG CAG AGA CGT TGC CAA G

Supplemental Table 2

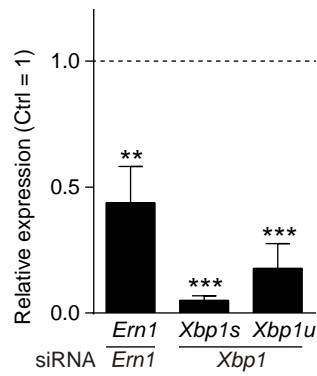
List of oligonucleotides used for chromatin immunoprecipitation assays in Figure 7

Location	Strand	Sequence
-764~561	Fwd	CCG GGA CGC CCA TGC AAT CTG TTA GTA ATT
	Rev	GCG GGT GCC CTG AGA AAG CTA CTC TCC CTT
-942~811	Fwd	TAC AAA GCA CCC TAT GGT CC
	Rev	TGG ATT GCT TGC TGT ACG AG



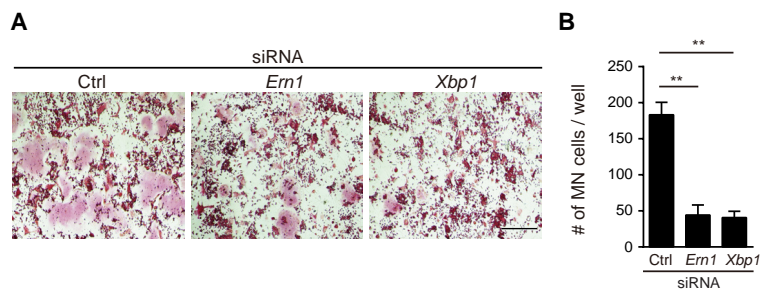
Supplemental Figure 1

ER stress related genes are induced in BMMs after RANKL stimulation. BMMs collected from WT mice were incubated in with sRANKL (50 ng/ml). The expression levels of *Atf4*, *Atf6*, *Hspa5*, and *Eif2ak3* transcripts were quantitatively analyzed after 0 and 2 days. n = 3 repeats. Values are means \pm SD. *p < 0.05. Statistical analysis was performed using Student's *t*-test.



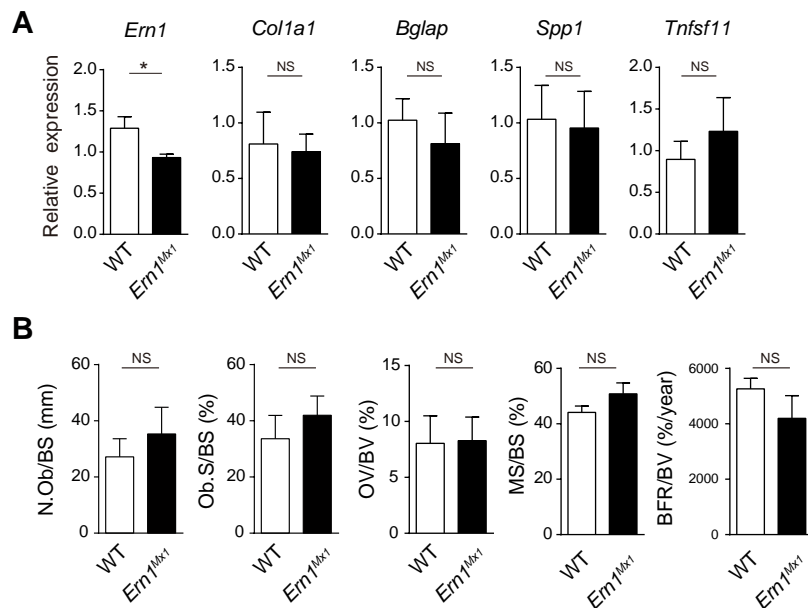
Supplemental Figure 2

siRNA-mediated gene silencing of *Ern1* and *Xbp1* transcripts in BMMs. BMMs collected from WT mice were transfected with siRNA against *Ern1* or *Xbp1*. The relative expression levels of *Ern1*, *Xbp1s*, and *Xbp1u* mRNA were quantitatively analyzed. The expression levels of each transcript in control siRNA-transfected BMM are set to 1. n = 4 repeats. Values are means \pm SD. **p < 0.005, ***p < 0.0005. Statistical analysis was performed using Student's *t*-test.



Supplemental Figure 3

Gene silencing of *Ern1* or *Xbp1* in RAW264.7 cells suppresses RANKL-induced osteoclastogenesis. **(A)** Representative photomicrographs of RAW264.7 cells treated with control (Ctrl) siRNA or with siRNA against *Ern1* or *Xbp1*. The cells were incubated with sRANKL (50 ng/ml) for 4 days and stained for TRAP. Bar, 200 μ m. **(B)** The number of TRAP-positive multi-nucleated (MN) cells in each well. n = 3 repeats. Values are means \pm SD. **p < 0.005. Statistical analysis was performed using Student's *t*-test.



Supplemental Figure 4

No significant changes in bone formation in *Ern1^{Mx1}* mice. **(A)** Relative transcript expression levels of *Ern1*, *Col1a1*, *Bglap* (encodes osteocalcin), *Spp1* (encodes osteopontin), and *Tnfsf11* (encodes RANKL) in osteoblasts in WT and *Ern1^{Mx1}* mice. $n = 4$ mice/group. **(B)** Histomorphometric analysis of the tibial metaphysis ($n = 3-7$ mice/group). N.Ob/BS, osteoblast number/bone surface; Ob.S/BS, osteoblast surface/bone surface, OV/BV, osteoid volume/bone volume; MS/BS, mineralizing surface/bone surface; BFR/BV, bone formation rate/bone volume. Values are means \pm SD. * $p < 0.05$. NS, not significant. Statistical analysis was performed using Student's *t*-test.