Supporting Information

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SI Materials and Methods

Animal Experimentation. All animal experimentation was carried out according to the legal requirements of the Association for Assessment and Accreditation of the Laboratory Animal Care International and the University of Alabama at Birmingham Institutional Animal Care and Use Committee. We used *CCAAT/enhancer binding protein α double-negative* (*C/EBPα*$^{-/-}$) mice, which were a gift from Gretchen J. Darlington (1). Heterozygous C/EBPα$^{+/-}$ male mice were crossed with C/EBPα$^{+/-}$ female mice to obtain C/EBPα$^{-/-}$ and C/EBPα$^{+/+}$ (control) mice. Mice were bred in-house and killed by CO_2 asphyxiation. Samples of organs and tissues were obtained from newborn mice, including mouse bone marrow (MBM), bone, brain, kidney, liver, and muscle.

Cells and Cell Culture. Mature osteoclasts (OCs) in primary culture were generated from MBM as described (2–4). Briefly, MBM was obtained from the tibiae and femora of 6-wk-old female WT *C/EBPα*$^{+/+}$ mice as described (5, 6). Although constitutive *C/EBPα* deletion results in mortality within a few hours of birth (1), we were able to extract MBM from newborn *C/EBPα*$^{+/+}$ and *C/EBPα*$^{-/-}$ mice. Some MBM cells ($1–2 \times 10^5$) were seeded into the wells of a 24-well plate, and other MBM cells (1×10^6) were seeded into the wells of 6-well plate. MBM cells were cultured in α-modified MEM (GIBCO-BRL) with 10% (vol/vol) FBS (GIBCO-BRL) containing 20 ng/mL macrophage colony-stimulating factor (M-CSF; R&D Systems). After 24 h, cells were cultured in the presence of 10 ng/mL receptor activator of NF-κB ligand (RANKL; R&D Systems) and 10 ng/mL M-CSF for an additional 96 h to generate OCs.

To generate mature OCs from the coculture system, MBM and calvarial osteoblasts from *C/EBPα*$^{+/+}$ and *C/EBPα*$^{-/-}$ mice were cultured in the presence of 10^{-8} M $1,25(OH)_2$ vitamin D_3 and 10^{-6} M dexamethasone as described previously (7). Primary calvarial osteoblasts were isolated from C/*EBPα*$^{+/+}$ and *C/EBPα*$^{-/-}$ mice on postnatal day 1 as we previously described (7).

C/EBPα$^{+/+}$ and *C/EBPα*$^{-/-}$ spleen cells were cultured with M-CSF (20 ng/mL) alone for 48 h and were then stimulated with M-CSF (10 ng/mL)/RANKL (10 ng/mL) to generate OC-like cells as we previously described (4, 7–9). Alternatively, spleen cells were stimulated with 20 ng/mL M-CSF alone to generate monocyte/macrophage-like cells as described previously (4, 7–9).

C/EBPα$^{+/+}$ and *C/EBPα*$^{-/-}$ livers were harvested on embryonic days 17.5–18 and cut to small pieces and lysised with 0.05% 1X trypsin/EDTA (Invitrogen) to harvest single cells. Harvested single cells were reseeded in culture dishes and cultured with RANKL/M-CSF as described above to induce OC differentiation. The mouse OC precursor cell line RAW264.7 obtained from the American Type Culture Collection was treated with M-CSF/RANKL to induce OC differentiation as we previously described (4).

Rat osteoblast cells were derived from calvaria as described previously (7). Giant cell tumors (GCTs) of bone contain human stromal cells (hSCs), OC-like precursors, and OC-like giant cells. Because OC-like giant cells from GCTs of bone are effectively the same as OCs in bone, we used GCTs and hSCs obtained from GCTs as previously described (10). The human macrophage (U-937) cell line was purchased from the American Type Culture Collection.

***Cathepsin K* Promoter CAT Constructs.** We characterized the *Cathepsin K* (*Ctsk*) promoter as described (11). The XbaI/EcoRI fragment was subcloned into a pBluescript KS vector (Stratagene) and digested with KpnI/SmaI before insertion of the gene-vector fragment into pCAT-3 Basic Reporter Vector (Promega) to produce pCCAT-1474. The pCCAT-1474 was digested with KpnI and EcoRV, and the product was subjected to controlled 5′ → 3′ digestion with exonuclease III using Erase-a-Base Systems (Promega). The sizes of series of 5′ deletions generated were approximated by electrophoresis in a 3:1 NuSieve-agarose gel (Lonza) or, in selected cases, by DNA sequence analysis with the dideoxy chain termination method.

Cell Transfection and CAT Assay. To determine 5′-flanking regulatory activity, constructs were transfected into RANKL-induced RAW264.7 cells using lipofectamine reagent (BRL) as described (12). The transfected RAW264.7 cells induced to OCs were tested for differential expression of CAT activity as described (13). CAT activity in transfected cultures is standardized by normalization to β-gal activity and the protein concentration of cell extracts using a protein assay kit (BioRad) as described (10, 14). In all experiments, constructs were tested in duplicate or triplicate.

Site-Directed Mutagenesis. Site-directed mutant constructs were created as previously described (10, 14). In brief, a SpeI restriction site was introduced into pCCAT-137 in the mutant fusion gene as indicated in Fig. 1*B*. The SpeI fragment from the mutant gene was isolated and cloned into the identical site in pCCAT-137.

Electrophoretic Mobility Shift Assay. Nuclear extracts were prepared as previously described (15). Gel retardation assays were carried out as described with slight modification (10, 14). For the electrophoretic mobility shift assay, double-stranded oligonucleotides encoding the −53 to −30 region of the *Ctsk* promoter were end-labeled with ^{32}P and used as probes. Competition experiments were performed with a mixture of nuclear extract, and the ^{32}P-labeled −53 to −30 WT *Ctsk* promoter oligonucleotide probe was incubated with unlabeled competitors (e.g., −53 to −30 WT *Ctsk* promoter oligonucleotide, mutant oligonucleotides, activator protein-1 oligonucleotide). Ten mutant oligonucleotides (shown in Fig. 1*D*) were synthesized with 2-bp substitutions of the −53 to −30 WT *Ctsk* promoter sequence AGTTGACTTCCG-CAATCCTTACCG. Mixtures were incubated for 20 min on ice, loaded onto a 4% (vol/vol) nondenaturing polyacrylamide gel, and subjected to electrophoresis. Supershift mobility assays were carried out with antibodies against C/*EBPα,* C/*EBPβ*, or C/*EBPδ* (Santa Cruz Biotechnology) in order to define the factor that binds the critical *cis*-regulatory element recognition site.

DNase I Footprint Analysis. We performed a DNase I footprint analysis as previously described (14). Nuclear extracts from RANKL-induced RAW264.7 cells were prepared by the method of Dignam et al. (16). A 234-bp probe was prepared by PCR assay. The PCR product was purified with the Magic PCR Preps DNA purification system (Promega) and was end-labeled with ^{32}P. The labeled PCR product was digested with DNase I restriction endonuclease. Approximately 104 cpm of end-labeled, polyacrylamide gel-purified probe was incubated with RANKL-induced RAW264.7 cell nuclear extracts for 15 min on ice and then for 2 min at 25 °C. DNase I (1 U/mL) was added for 1 min at 25 °C and separated on an 8% (vol/vol) sequencing gel.

Northern Blotting Analysis. Northern blotting was performed as described previously (10, 17). Total RNA (15 μg per lane) was isolated using TRIzol reagent (Life Technologies) (4). Human

C/*EBPα* transcript (2.4 kb) and mouse C/*EBPα* transcript (2.7 kb) were used as C/*EBPα*-cDNA probes. Blots were stripped and rehybridized with 28S and GAPDH cDNA for normalization purposes.

Western Blotting Analysis. Western blotting was performed as described (4, 17) and visualized and quantified using a Fluor-S Multi-Imager and Multi-Analyst software (Bio-Rad). We used rabbit anti-Ctsk polyclonal antibody, which was previously generated in our laboratory (11). We also used antibodies for C/EBPα, proviral integration 1 (PU.1), Finkel-Biskis-Jinkins osteosarcoma oncogene (*c-fos*), and nuclear factor of activated T cells cytoplasmic 1 (NFATc1) purchased from Santa Cruz Biotechnology. We performed a time-course Western blot analysis using antibodies for inhibitor of κBα (IκBα), phosphorylated (p)-IκBα, p38, p-p38, Iκκα, and p-Iκκαβ (Cell Signaling) in C/*EBPα*$^{+/+}$ and C/*EBPα*$^{-/-}$ MBM cells cultured with M-CSF/RANKL for 0–60 min. We also performed a time-course Western blot analysis of C/EBPα expression in MBM after 0–120 h of M-CSF/RANKL induction. β-actin, GAPDH, and β-tubulin were used as controls.

Histological and Radiographic Procedures. Histological analyses were performed as described ($n > 50$) (7). TNF receptor-associated protein 1 (TRAP) was used as a marker for OCs using a commercial kit (Sigma) according to the manufacturer's instructions. Multinucleated (more than three nuclei) TRAP$^+$ cells appear as dark purple cells and were counted by light microscopy ($n > 50$). Tibiae from C/*EBPα*$^{+/+}$ and C/*EBPα*$^{-/-}$ mice were stained with Goldner's trichrome ($n = 3$); bright blue regions indicate mineralized tissue. For X-ray analysis, radiography was performed using a high-resolution soft X-ray system at 30 kV and high-speed holographic film (Kodak) ($n = 5$). Microcomputed tomography analysis was performed to determine the bone mass of fixed femora as described (18) by the University of Alabama at Birmingham Small Animal Bone Phenotyping Core associated with the Center for Metabolic Bone Disease ($n = 3$).

Immunostaining. Immunostaining was carried out as described (4). Two specific antibodies, F4/80 (Biosource International) and CD11b (Pharmingen), were used as markers of monocyte/macrophage precursors as described previously ($n > 9$) (12, 19). In addition, we used antibodies for C/EBPα, C/EBPβ, and C/EBPδ purchased from Santa Cruz Biotechnology, as well as antibodies for Ctsk as described above.

Immunofluorescence Analysis. We performed immunofluorescence analysis as we have previously described (3), with the exception that we used anti-C/EBPα and anti-Ctsk as the primary antibodies purchased from Santa Cruz Biotechnology, and observations were performed by epifluorescence in a Zeiss axioplan microscope in the Developmental Neurobiology Imaging and Tissue Processing Core at the University of Alabama at Birmingham Intellectual and Disabilities Research Center. Nuclei were visualized with 1 μg/mL DAPI (Sigma). To visualize filamentous (F-actin) rings, MBM was stained with 2 U/mL Alexa Fluor 546-phalloidin (Molecular Probes) as previously described (20). The experiments were set in triplicate on three independent occasions.

Real-Time Quantitative PCR and Semiquantitative PCR. Real-time (RT) quantitative PCR (qPCR) was performed as described (21, 22) using TaqMan probes purchased from Applied Biosystems as listed in Table S1. Briefly, cDNA fragments were amplified by TaqMan Fast Advanced Master Mix (Applied Biosystems). Fluorescence from each TaqMan probe was detected by a Step-One RT-PCR system (Applied Biosystems). RNA samples were obtained from transduced MBM cultured with M-CSF alone, MBM-derived OC-like cells, MBM-derived monocyte/macrophage-like cells, or transfected uninduced RAW264.7 cells. The mRNA expression level of the housekeeping gene *hypoxanthine-guanine phosphoribosyl transferase* (*Hprt*) was used as an endogenous control and enabled calculation of specific mRNA expression levels as a ratio of *Hprt*. Primer sequences used for semi-qPCR are listed in Table S1. PCR conditions are available on request. Experiments were repeated at least three times.

Histomorphometric Analysis. Histomorphometric samples were processed as non-decalcified hard-tissue sections as described (7, 8). Briefly, for quantitative bone volume histomorphometry, 5-μm sections of newborn C/*EBPα*$^{-/-}$ and C/*EBPα*$^{+/+}$ mice were stained with Goldner's trichrome. For histomorphometric analysis of OC size and number, 10-μm sections of newborn C/EBPα$^{-/-}$ and C/EBPα$^{+/+}$ mice were TRAP-stained without counterstaining. Histomorphometric analysis of these sections was performed using the National Institutes of Health ImageJ program. Eight parameters studied in this analysis are presented: bone volume relative to tissue volume, the percentage of OC surface area to total bone surface area of the tibiae, the percentage of osteoblast surface area to total bone surface area of the tibiae, OC numbers per bone perimeter, osteoblast numbers per bone perimeter, distal hypertrophic growth plate thickness, proximal hypertrophic growth plate thickness, and trabecular thickness. Large multinucleated cells with cytoplasmic vesicles and intimate contact to bone were considered as OCs, and cuboidal mononuclear cells in intimate contact with osteoid or bone were identified as osteoblasts.

Flow Cytometry. Alexa Fluor 488-conjugated anti-mouse F4/80 antigen antibody for flow cytometry was purchased from eBioscience. Cells were washed in ice-cold flow cytometry buffer [2% (vol/vol) FCS and 2 mM EDTA in PBS, pH 7.5] and then incubated with antibody for 15 min and washed twice with flow cytometry buffer. Cells were fixed with 4% (wt/vol) paraformaldehyde before acquiring data using a FACSCalibur flow cytometer (BD Biosciences) and performing analysis with FlowJo (TreeStar).

Forced Expression. MBM cells (5×10^5) were seeded into the wells of a 12-well plate (without blood cells) and stimulated with 20 ng/mL M-CSF for 24 h. The attached cell number was confirmed to 60–70% of the total cell number. We used a retrovirus system to express *C/EBPα* ectopically in M-CSF–induced C/*EBPα*$^{+/+}$ MBM cells as described (7). We constructed a retrovirus vector (pBMN-*C/EBPα*) that was engineered to express both *C/EBPα* and GFP. The mouse C/EBPα cDNA was amplified and cloned into the pBMN retroviral vector (purchased from Addgene). We achieved retrovirus packaging by transducing pBMN into phoenix cells using the phoenix independent helper system. The viral supernatant was collected 52 h later. MBM cells were then transduced with the *C/EBPα*-expressing virus (pBMN-*C/EBPα*) or with a control virus (pBMN-GFP) overnight at 37 °C as described (19) and stimulated with 20 ng/mL M-CSF for 24 h. Medium was replaced with fresh α-MEM with 10% (vol/vol) FBS and additionally stimulated with 20 ng/mL M-CSF for 96 h.

We similarly used a retrovirus system to express *c-fos* ectopically, as described previously (7), in C/*EBPα*$^{-/-}$ myeloid cells cultured with M-CSF/RANKL to induce osteoclastogenesis. We then quantified the number of multinucleated OCs as a percentage of the number of GFP$^+$ cells as described (7, 23).

C/EBPα was also overexpressed in uninduced RAW264.7 cells by plasmid stable transfection as described (12, 14). *C/EBPα* cDNA (full-length cDNA from Open Biosystems) was cloned into the pCDNA3.1 expression vector (Invitrogen). RAW264.7 cells were transfected with pcDNA3.1-C/*EBPα* or with the vector control pcDNA3.1. RAW264.7 cells carrying pcDNA3.1-C/*EBPα* or the vector control pcDNA3.1 were passaged three times.

Promoter Analyses. For *c-fos* promoter luciferase promoter analyses, we used RAW264.7 cells maintained in DMEM high glucose containing 10% (vol/vol) FBS. Cells were cotransfected with increasing amounts of pcDNA3.1 (+) C/EBPα (0, 10, 30, or 100 ng per well), pSV-β-Galactosidase control vector (Promega) (50 ng per well), and GL3B, *c-fos* 1.1 kb, *c-fos* 0.48 kb, or *c-fos* 0.22 kb (50 ng per well) using the Lipofectamine transfection 2000 reagent (Invitrogen) and incubated for 6–8 h. Culture medium was replaced with fresh 10% (vol/vol) DMEM with M-CSF (10 ng/mL) and RANKL (10 ng/mL) and cultured for 3 d. Luciferase activity was measured using a Steady-Glo luciferase assay system (Promega). PGL3 basic reporter vectors were used as controls (Promega). Luminescence was detected with a luminometer (BioTek Synergy 2). For ChIP analyses, MBM-derived monocytes and macrophages were differentiated in M-CSF (20 ng/mL) for 24 h. Cells were further cultured for an additional 96 h in the presence of M-CSF (10 ng/mL)/RANKL (10 ng/mL) and C/EBPα-specific antibodies (Santa Cruz Biotechnology). The output of ChIP assays was measured by qPCR and normalized by 10% (vol/vol) input. All assays were repeated at least three times.

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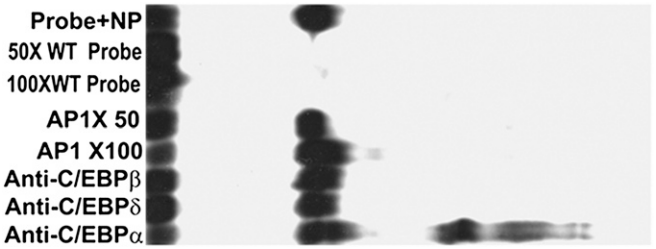

Fig. S1. *Ctsk* critical *cis*-regulatory element (CCRE) contains a specific protein complex binding site that only binds to OC-like cell nuclear proteins (NPs). A gel mobility shift experiment was conducted using a 0- to 100-fold molar excess of ^{32}P-labeled −53 to −30 WT *Ctsk* promoter oligonucleotide probe in nuclear extracts prepared from RANKL-induced RAW264.7 cells. The WT *Ctsk* probe and RANKL-induced RAW264.7 cell nuclear extracts were incubated with unlabeled activator protein 1 (AP-1) at a 50- or 100-fold molar excess. The WT *Ctsk* probe and RANKL-induced RAW264.7 cell nuclear extracts were incubated with antibodies against C/EBPβ, C/EBPδ, or C/EBPα.

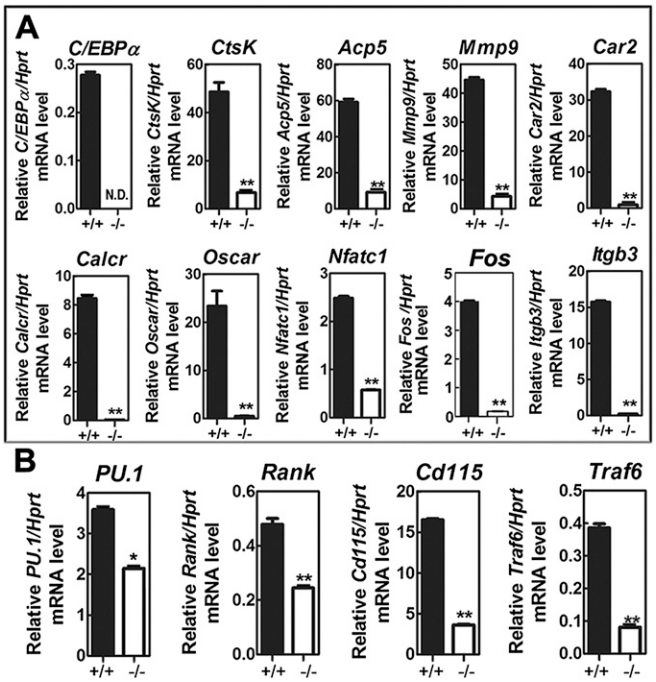

Fig. S2. *C/EBPα* is essential for the induction of OC-specific genes but not essential for the induction of macrophage-specific genes. (*A*) RT-qPCR assay of genes important for osteoclastogenesis and OC-specific functional genes in MBM cells cultured with M-CSF/RANKL. KO of *C/EBPα* dramatically reduced the expression of both RANKL-induced OC transcription factors [*c-fos* and nuclear factor of activated cells cytoplasmic 1 (*Nfatc1*)]. *Acp5, tartrate-resistant acid phosphatase; Calcr, calcitonin receptor; Car2, carbonic anhydrase 2; Itgb3, integrin beta 3; Mmp9, matrix metallopeptidase 9;* N.D., not detected; *Oscar, osteoclast associated receptor*. (*B*) RT-qPCR assay of genes common to both macrophages and OCs in MBM cells cultured with M-CSF/RANKL. KO of *C/EBPα* resulted in a relatively less severe decrease in the expression of genes that are common to macrophages and OCs, including transcription factor *SFFV proviral integration 1 (PU.1), receptor activator of NF-κB* (*RANK*), *colony stimulating factor 1 receptor (CD115 or M-CSF receptor*), and *TNF receptor-associated factor 6* (*Traf6*). $*P < 0.05$; $**P < 0.01$.

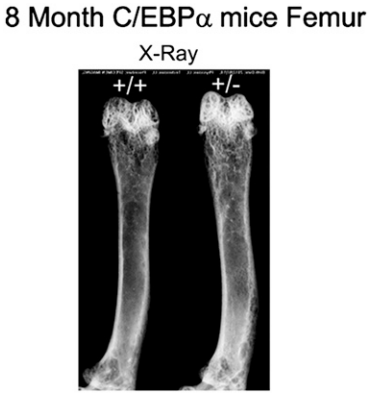

Fig. S3. Heterozygous $C/EBP\alpha^{+/-}$ femora exhibit increased bone density. X-ray analysis of femora indicates increased bone density in 8-mo-old $C/EBP\alpha^{+/-}$ mice compared with $C/EBP\alpha^{+/+}$ mice of the same age ($n = 3$, repeated three times).

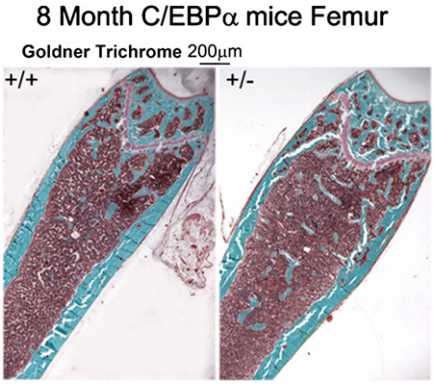

Fig. S4. Heterozygous *C/EBPα*$^{+/-}$ femora have increased trabecular number. Goldner's trichrome stain of femora from 8-mo-old *C/EBPα*$^{+/-}$ or *C/EBPα*$^{+/+}$ mice.

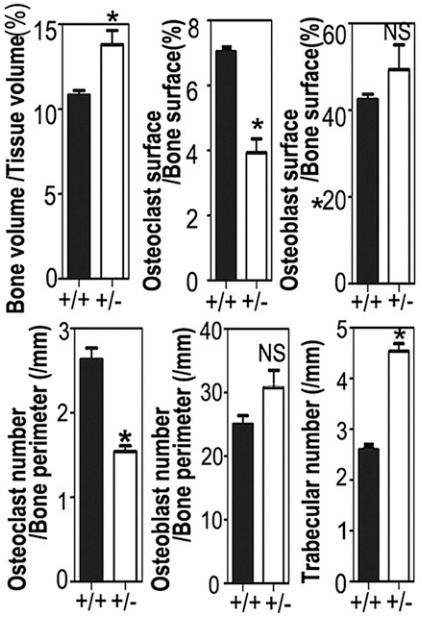

Fig. S5. Histomorphometric analysis of femora from 8-mo-old *C/EBPα*$^{+/+}$ and heterozygous *C/EBPα*$^{+/-}$ mice. Histomorphometric analysis indicates that *C/EBPα*$^{+/-}$ femora have an increase in bone volume/tissue volume and trabecular number and a decrease in osteoclast surface/bone surface and osteoclast number/bone perimeter. *$P < 0.05$. NS, not significant.

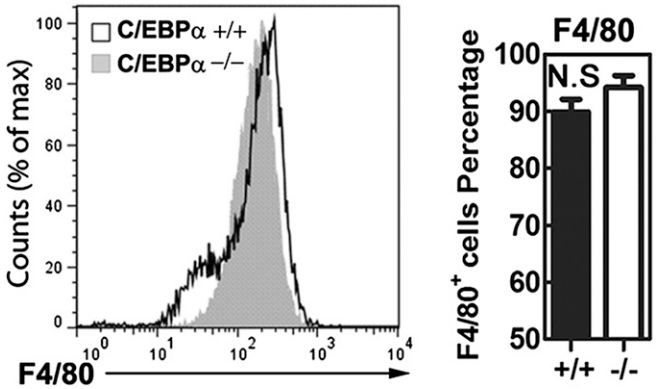

Fig. S6. Flow cytometry analyses with a mature macrophage marker F4/80. Embryonic day 17.5–18 livers were used as a source of myeloid cells, which were then stimulated with M-CSF alone for macrophage differentiation analysis. No significant difference in the percentage of F4/80^{+} cells was observed between the *C/EBPα*$^{+/+}$ and *C/EBPα*$^{-/-}$ groups. max, maximum; N.S, not significant.

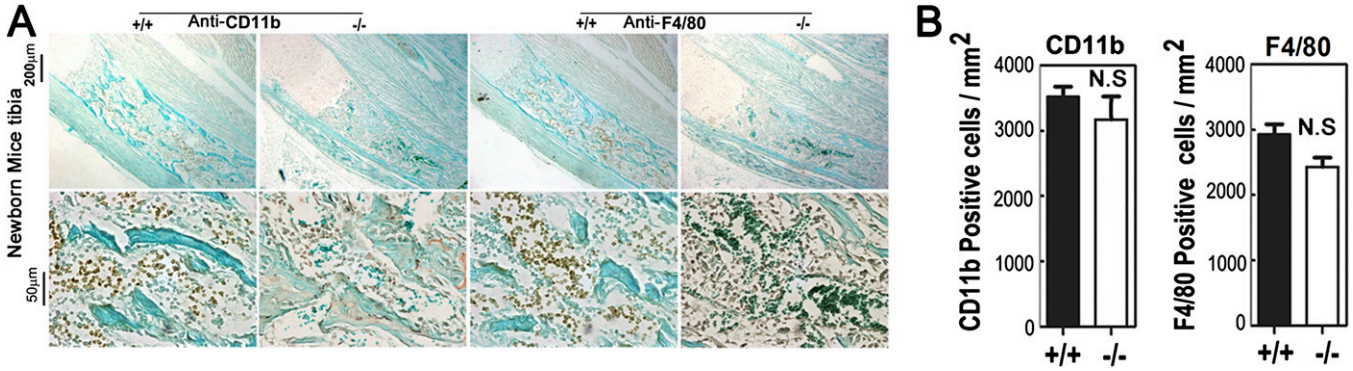

Fig. S7. Immunostaining for monocyte markers (CD11b and F4/80). (*A*) Immunostaining for a monocyte marker [integrin αM (CD11b)] and the mature macrophage marker F4/80 in C/*EBPα*$^{+/+}$ and C/*EBPα*$^{-/-}$ tibiae. (*B*) Quantification of CD11b^{+} and F4/80^{+} cells. There was no significant difference in the number of CD11b^{+} or F4/80^{+} cells in C/*EBPα*$^{-/-}$ tibiae compared with the C/*EBPα*$^{+/+}$ control.

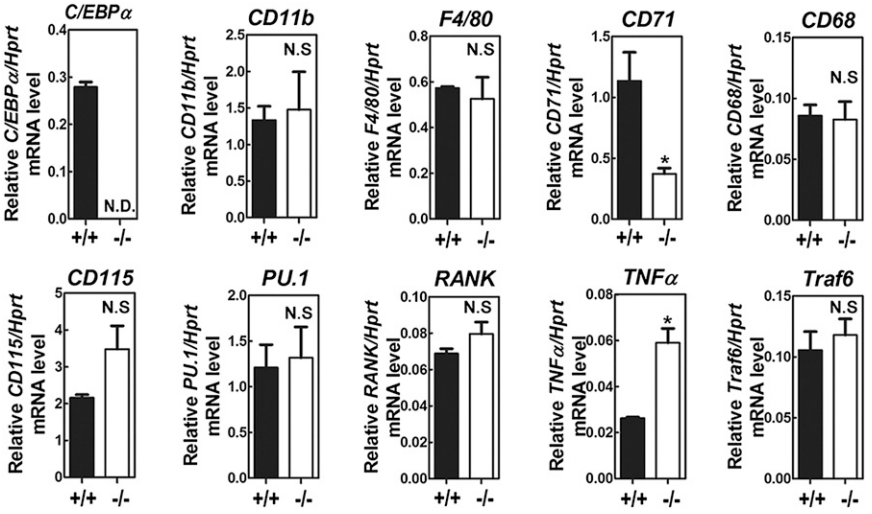

Fig. S8. qPCR analysis of genes important for macrophage differentiation in C/*EBPα*$^{+/+}$ and C/*EBPα*$^{-/-}$ MBM-derived monocyte/macrophage-like cells. RT-qPCR was used to examine the expression of genes important for macrophage differentiation in C/*EBPα*$^{+/+}$ and C/*EBPα*$^{-/-}$ MBM cells cultured with M-CSF alone to generate monocyte/macrophage-like cells. Consistent with our findings in M-CSF cultured MBM cells and mouse tibiae, there was no significant change in the expression of F4/80 between C/*EBPα*$^{+/+}$ and C/*EBPα*$^{-/-}$ MBM-derived monocyte/macrophage-like cells. In addition, there was no significant difference in the expression of genes common to macrophages and OCs (e.g., *PU.1*, *RANK*, *Traf6*, *CD11b*, *CD115*, *CD68*]. Interestingly, C/*EBPα*$^{-/-}$ MBM-derived monocyte/macrophage-like cells did have a significant decrease in the expression of *transferring receptor* (*CD71*) and a significant increase in the expression of the mature macrophage-related gene *TNFα*. The loss of C/*EBPα* expression was confirmed, because C/*EBPα* expression was not detected (N.D.) in C/*EBPα*$^{-/-}$ MBM-derived monocyte/macrophage-like cells. *$P < 0.05$.

Table S1. Primers and Taqman probes used for qPCR

Gene symbol	Applied Biosystems Taqman assay ID	Primers used for semi-qPCR	
		Forward primers (5′-3′)	Reverse primers (5′-3′)
Acp5	Mm00475698_m1	CAGCAGCCCAAAATGCCT	TTTTGAGCCAGGACAGCTGA
Calcr	Mm00432271_m1		
Car2	Mm00501572_m1		
Cd68	Mm03047340_m1		
Cebpa (C/EBPα)	Mm00514283_s1		
Cebpb (C/EBPβ)	Mm00843434_s1		
Csf1r (CD115)	Mm01266652_m1		
Ctsk	Mm00484039_m1	GGGCTCAAGGTTCTGCTGC	TGGGTGTCCAGCATTTCCTC
Emr1 (F4/80)	Mm00802529_m1		
Fos (c-Fos)	Mm00487425_m1	CGGGTTTCAACGCCGACTA	TTGGCACTAGAGACGGACAGA
Hprt	Mm01545399_m1	GGTGGAGATGATCTCTCAACTTTAA	AGGAAAGCAAAGTCTGCATTGTT
Itgam (CD11b)	Mm00434455_m1		
Itgb3	Mm00443980_m1		
Mmp14	Mm00485054_m1		
Mmp9	Mm00442991_m1		
Mst1r	Mm00436365_m1		
Myo1D	Mm01296373_m1		
Nfatc1	Mm00479445_m1	TGCCTTTTGCGAGCAGTATCT	CAGGCAAGGATGGGCTCATAT
Oscar	Mm00558665_m1		
Pparg	Mm01184322_m1		
Rcan2	Mm00472671_m1		
Runx2	Mm00501584_m1		
Sfpi1 (PU.1)	Mm00488142_m1		
Tfrc (CD71)	Mm00441941_m1		
Tnf (TNF-α)	Mm00443260_g1		
Tnfrsf11a (Rank)	Mm00437135_m1		
Traf6	Mm00493836_m1		

The right column lists the probes for qRT-PCR while the left column lists the primer for semi-qPCR. The definitions for the gene symbols are as follows: *Acp5*: *acid phosphatase 5, tartrate resistant*; *Calcr*: *calcitonin receptor*; *Car2*: *carbonic anhydrase 2*; *Cd68*: *CD68 antigen*; *Cebpa*: *CCAAT/enhancer binding protein (C/EBP), alpha*; *Cebpb*: *CCAAT/enhancer binding protein (C/EBP), beta*; *Csf1r (CD115)*: *colony stimulating factor 1 receptor*; *Ctsk*: *cathepsin K*; *Emr1 (F4/80)*: *EGF-like module containing, mucin-like, hormone receptor-like sequence 1*; *Fos (c-Fos)*: *FBJ osteosarcoma oncogene*; *Hprt*: *hypoxanthine guanine phosphoribosyl transferase*; *Itgam (CD11b)*: *integrin alpha M*; *Itgb3*: *integrin beta 3*; *MMP14*: *matrix metallopeptidase 14*; *Mmp9*: *matrix metallopeptidase 9*; *Mst1r*: *macrophage stimulating 1 receptor (c-met-related tyrosine kinase)*; *Myo1D*: *myosin ID*; *Nfatc1*: *nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 1*; *Oscar*: *osteoclast associated receptor*; *Pparg*: *peroxisome proliferator activated receptor gamma*; *Rcan2*: *regulator of calcineurin 2*; *Runx2: runt related transcription factor 2*; *Sfpi1 (PU.1)*: SFFV *proviral integration 1*; *Tfrc (CD71)*: *transferrin receptor*; *TNFalpha*: *tumor necrosis factor*; *Tnfrsf11a*: *tumor necrosis factor receptor superfamily, member 11a*; *Traf6*: *TNF receptor-associated factor 6*.