Supplemental Table 1: Primers used in this study.

	Real-time RT-PCR primers	
Gene (mouse)	Forward	Reverse
CA II	AATGTGTGACCTGGATCGTGC	ACGCTTTGATCTTTCTATTCTTTAGCGG
c-fms	CACGGCCACCATGAACTTCC	GTCCAGTTGTAATGCTGTATGCTAGGGTA
CLCN7	CAATGCCAAAGAGATCGCCA	GGAGGAGGAAAGACGAATCAACCA
Ctsk	ATCTTGTGGACTGTGTGACTGAGAATTA	GCCGTGGCGTTATACATACAACTT
CTR	CCTATCAGCACTGCCCTGACTAC	TTGCAGTTTCTCAGAAGTGAAAGCG
Oscar	CTGGAACTGCTGGTAACGGAT	CCAGGGCTGCACAGAGTCAATA
Ostm1	AGTCGAACCTTCAACTGTTCGG	GACGTTTGGGTAGAATGAGTTTGCG
RANK	ATAGAATTCGCCATGGCCCCGCGCGCC	GCGAGATCTTCATTCTGCACATTGTCC
GAPDH	CTGGTGCTGCCAAGGCT	CTGCTTCACCACCTTCTTGATGTCATCATA

	Semi-qRT-PCR Primers for cell cultures	
Gene (Human)	Forward	Reverse
Mitf-A	Ref (Hershey and Fisher, 2005)	TGCTTCAGACTCTGTGGGAAAAAT
Mitf-B		
Mitf-C		
Mitf-D		
Mitf-E		
Mitf-H		
Mitf-J		
Mitf-M		
Mitf-CM	Ref (Shiohara et al., 2008)	
Mitf-total	Ref (Hershey and Fisher, 2005)	Ref (Hershey and Fisher, 2005)
Gene (Mouse)		
Mitf-A	ATGCAGTCCGAATCGGGAAT	TTGCTTCAGACTCTGTGGGGAAAA
Mitf-B	Ref (Hershey and Fisher, 2005)	
Mitf-C		
Mitf-D		
Mitf-E		
Mitf-H		
Mitf-J		
Mitf-M		
Mitf-Mc		
Mitf-total		Ref (Hershey and Fisher, 2005)

Gene (human)	Semi-qRT-PCR Primers for FFPE tissues	
Mitf-A	CGAACTCAAAAGTCAACCG CTG	TCATACTGGAGGAGCTTATCGGAG
Mitf-E	CTATAGGATGGCTTCCCAGG AGTT	
Mitf-total	CCAGCCAACCTTCCCAACAT	GGCCAGTGCTCTTGCTTCAG
CD68	CTACCTGAGCTACATGGCGG	GAATGTCCACTGTGCTGCGT
c-fms	CCCGGAACAACCTGCAGT	TCCACCACCTTCCCAAAGGC

	Cloning Primers: gene sequences underlined	
Gene (Mouse)	Forward	Reverse
Mitf-A	(1) ATGCAGTCCGAATCGGGA	For MSCViG vector: (contains an HA tag) TAAGTCGACCACACGCATGCTCCGT TTCT For pcDNA6.2 vector: (no tag) GCGAATTCCTAACACGCATGCTCCG TTTCTT
	(2) AGATCTACCATGGCGATGCA GTCCGA	
Mitf-E	(1) ATGACATCACGCATCTTGCT ACGC	
	(2) AGATCTACCATGGTGATGAC ATCACGCATCTTG	
Mitf-B	(1) ATGCTGTGTGCCTTCTGG	
	(2) AGATCTACCATGGTGATGCT GTGTGCCTTCTGG	
Mitf-H	(1) ATGGAGGCGCTTAGATTT	
	(2) AGATCTAAGATGGAGGCGC TTAGATTTGAGATG	

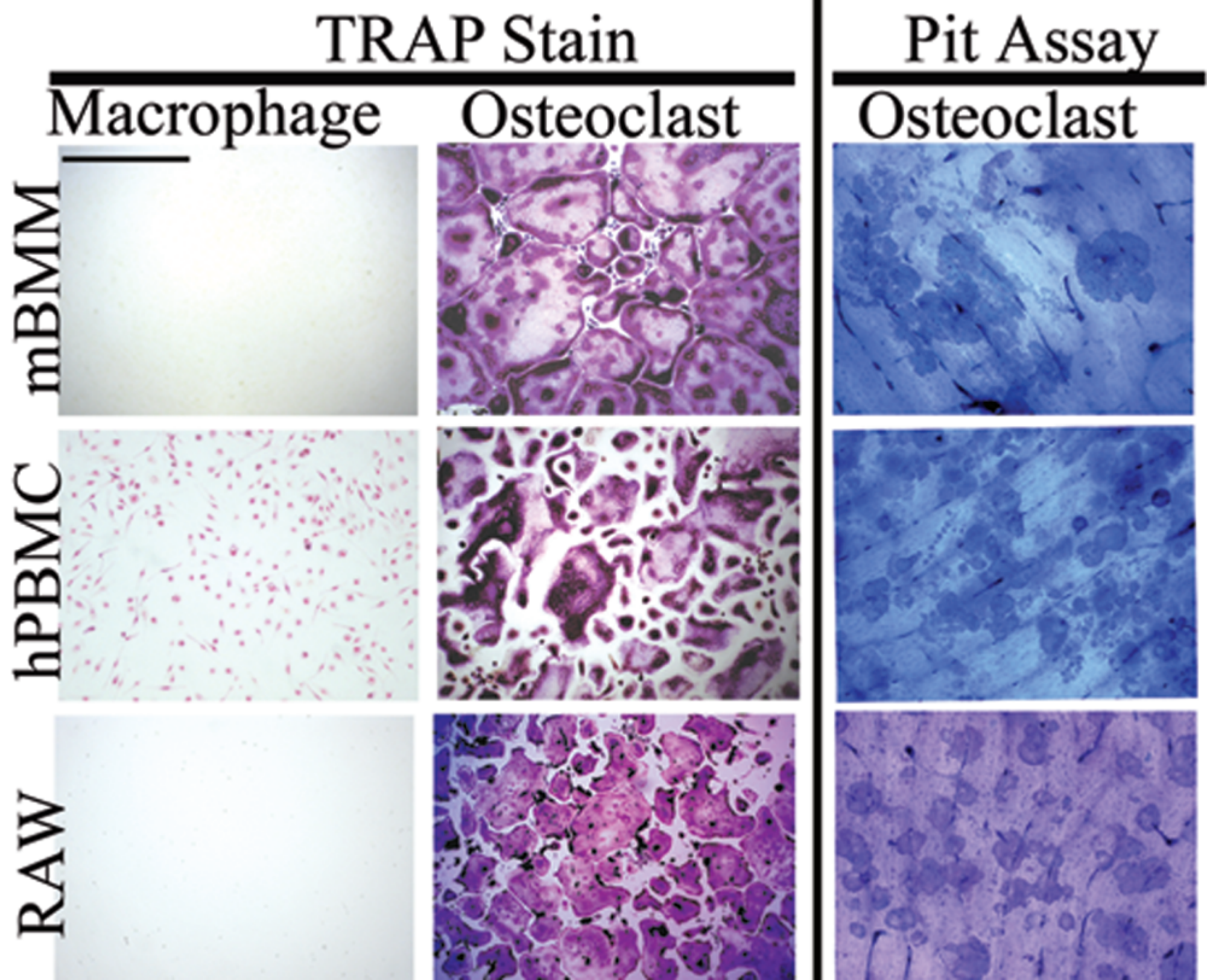
NOTE: Mitf sequences were amplified from mouse osteoclast derived cDNA with two overlapping forward primers to provide a Kozak sequence. The resulting PCR products were cloned into pCR-Blunt II- TOPO (invitrogen) before subsequently cut with BglII and SalI and inserted into MSCViG linearized by the same restriction enzymes. The PCR products were cloned into pCDNA6.2 by TOPO cloning.

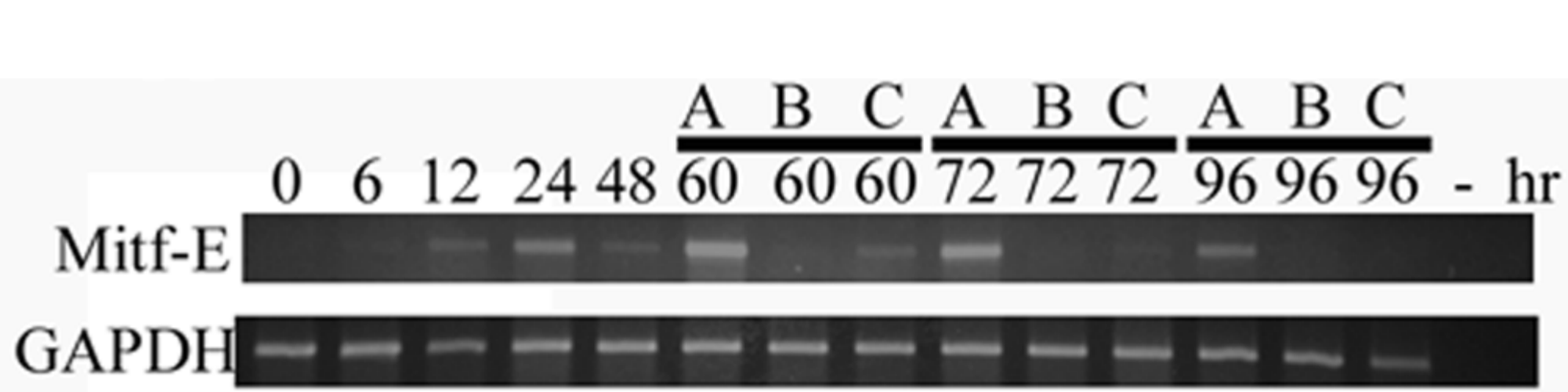
Figure Legends For Supplement Data

Supplemental Table 1. Primers used in this study.

Supplemental Figure 1. Verification of proper differentiation by mBMM, hPBMC and RAW264.7 cells cultured under macrophage or osteoclast conditions. RAW264.7 cells were plated in media with or without RANKL (100 ng/ml) for osteoclast or macrophage cultures, respectively. Left panel: TRAP staining of cell cultures. Right panel: Toluidine blue stain of resorption areas. Scale bar, 500 μm.

Supplemental Figure 2. Mitf-E signal declines in the absence of RANKL replenish. Time course of Mitf-E transcript by semi-qRT-PCR in RAW264.7 cells incubated in media containing 100 ng/mL. GAPDH serves as a cDNA loading control. A: Replenish media with RANKL 100 ng/mL on 48h. B: Replenish media without RANKL on 48h. C: No media change on 48h.


TRAP Stain
Pit Assay
Macrophage
Osteoclast
Osteoclast
mBMM
hPBMC
RAW


A B C A B C A B C
0 6 12 24 48 60 60 60 72 72 72 96 96 96 - hr
Mitf-E
GAPDH