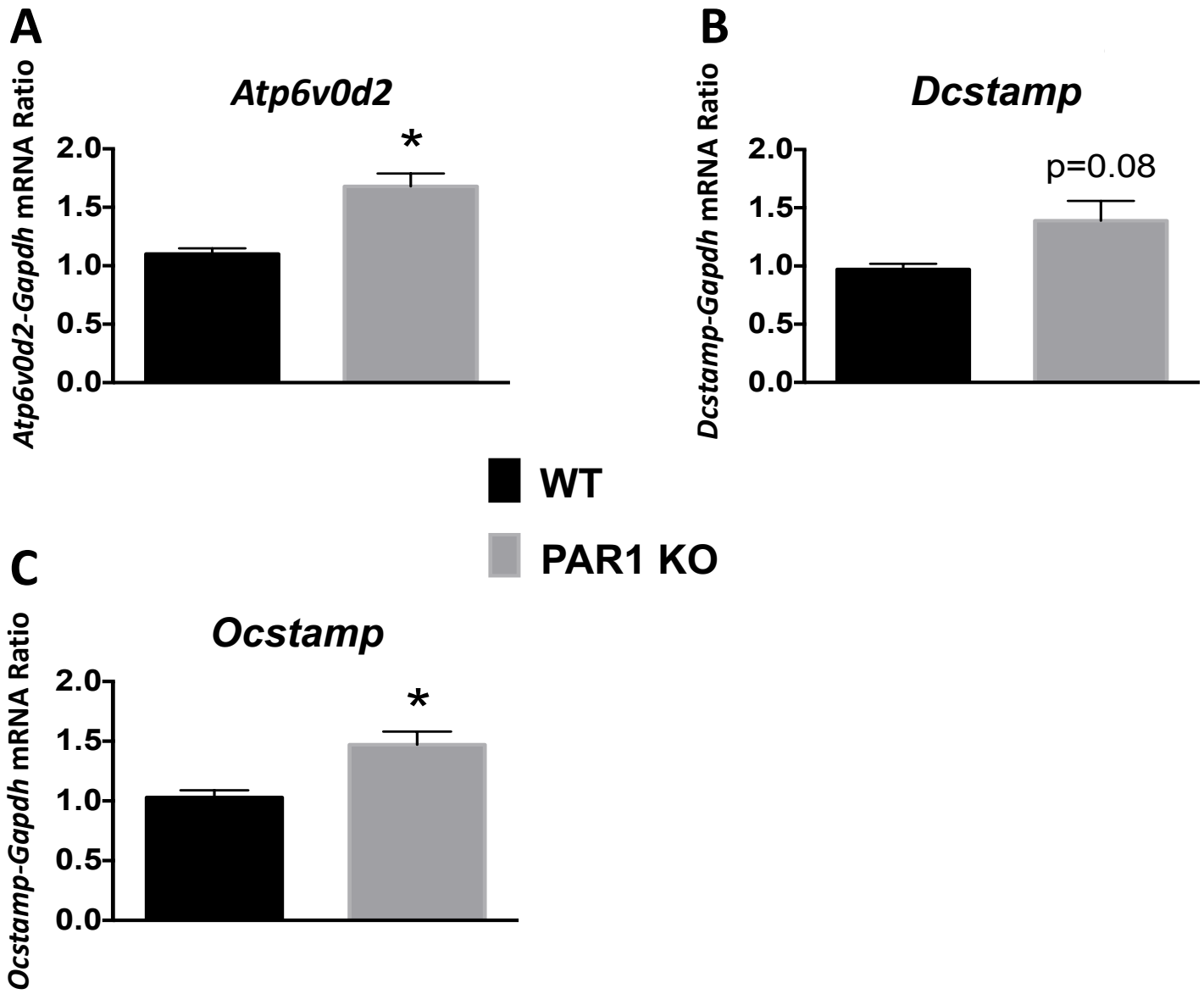
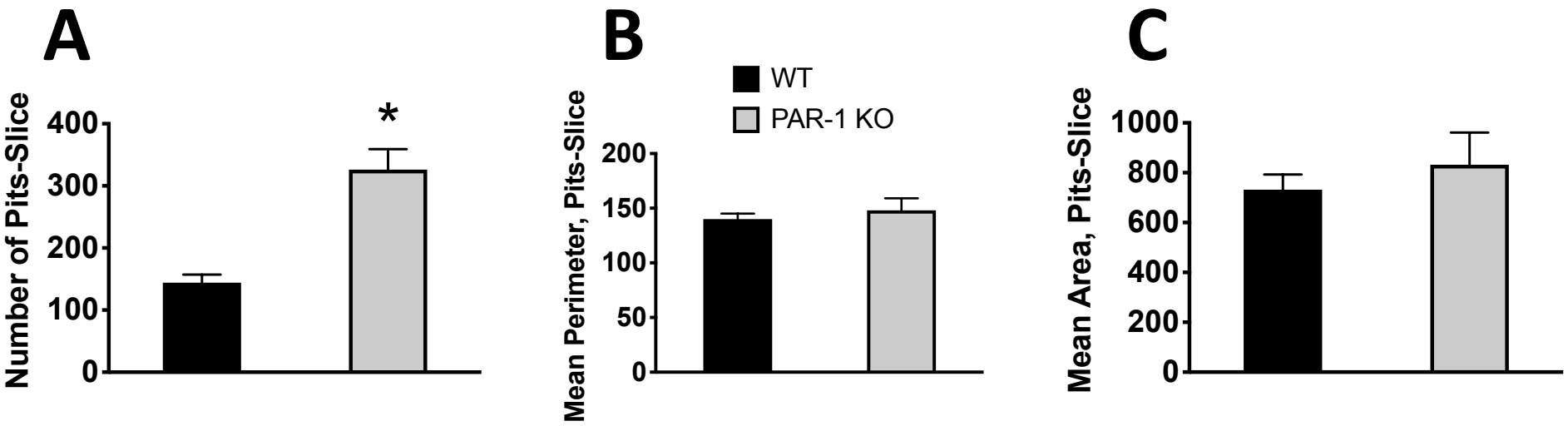


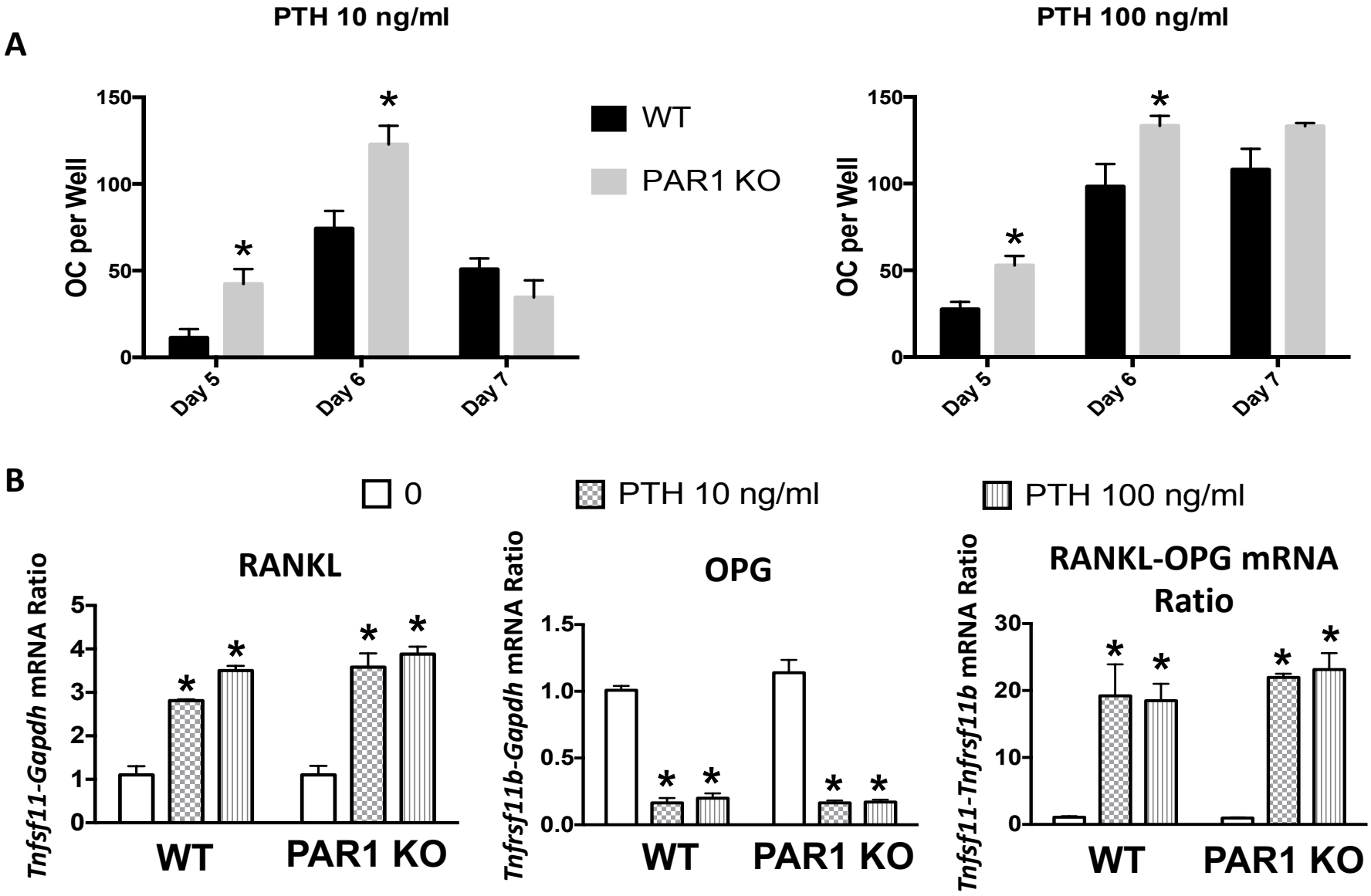
Supplemental Figure 1

BMM cultures from WT and PAR1 KO mice were treated with M-CSF + RANKL (30 ng/ml for both) for 3 days and then extracted for RNA expression by qRT-PCR of A) v-ATPase V0 subunit d2 (*Atp6v0d2*), B) dendritic cell-specific transmembrane protein (*Dcstamp*) and C) OC-stimulatory transmembrane protein (*Ocstamp*). N = 3 for each group. * Significantly different from WT, $p < 0.05$.



Supplemental Figure 2

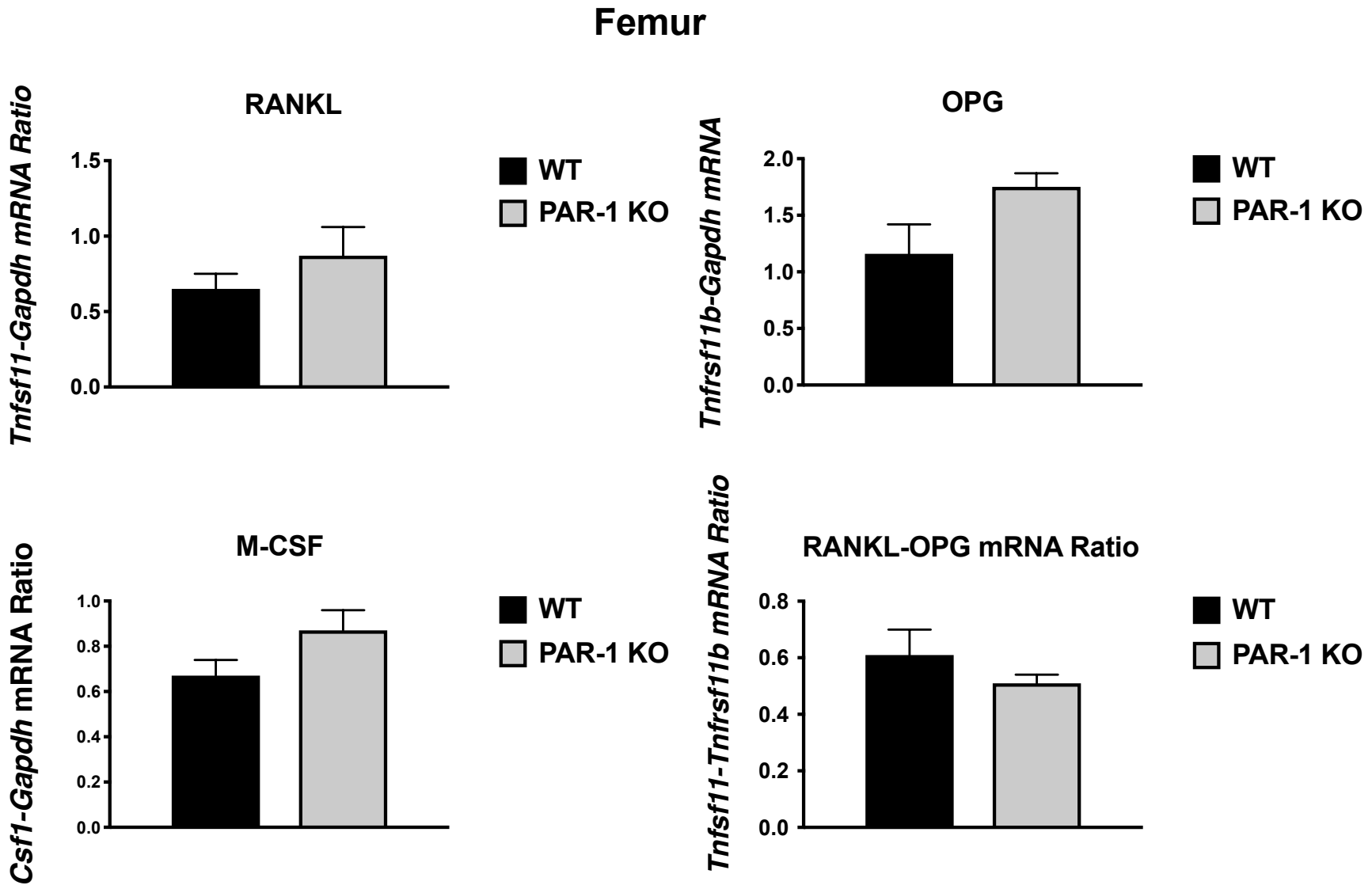
Equal number (5000/well) of BMM from WT and PAR1 KO mice were incubated with M-CSF + RANKL (30 ng/ml for both) on bovine cortical bone slices for 14 days and then stained for pits with toluidine blue. Values are: A) the number of pits per bone slice, B) mean perimeter of each pit per bone slice and C) mean area of each pit per bone slice. N = 3 for each group. *Significantly different from WT, $p < 0.01$.



Supplemental Figure 3

A) Time course for OC formation in WT and PAR1 KO whole bone marrow cultures that were treated with b-PTH 1-34 (PTH) at a concentration of 10 or 100 ng/ml for 5, 6 or 7 days. N = 4 for each group. * Significantly different from WT, $p < 0.05$.

B) mRNA levels of RANKL (*Tnfsf11*), OPG (*Tnfrsf11b*), and the RANKL/OPG mRNA ratio were assayed by qRT-PCR in whole bone marrow cultures that were stimulated with b-PTH 1-34 (PTH) at a concentration of 100 ng/ml for 3 days. N = 4 for each group. * Significantly different from respective group treated without PTH, $p < 0.05$.



Supplemental Figure 4

A) Freshly isolated femurs from WT and PAR1 KO mice were flushed of marrow and then extracted for RNA. Expression levels of RANKL (*Tnfsf11*), OPG (*Tnfrsf11b*), their ratio and M-CSF (*Csf1*) were assayed by qRT-PCR. N = 3 for each group.