Supplemental Figure 1. Flow cytometric analysis of bone marrow cells derived from BLT1<sup>++</sup> and BLT1<sup>-/-</sup> mice stimulated with GFP or IL-23 MC.

Flow cytometric analysis of bone marrow cells from (A) BLT1<sup>++</sup> mice and (B) BLT1<sup>-/-</sup> mice injected with GFP or IL-23 MC. Cells are first visualized on FSC and SSC, followed by exclusion of doublets. Representative dot plots showing the gating strategy that was used to identify monocytes (upper row in a and b), Ly-6C<sup>low</sup> (a) Ly-6C<sup>hi</sup> (b) monocytes and neutrophils (lower row in c). (C) Absolute cell counts of bone marrow monocytes including Ly-6C<sup>high</sup> and Ly-6C<sup>low</sup> monocytes and neutrophils (D) in BLT1<sup>++</sup> mice after GFP (n=5) or IL-23 MC injection (n=6). (E) Absolute cell counts of bone marrow monocytes including Ly-6C<sup>high</sup> and Ly-6C<sup>low</sup> monocytes and neutrophils (F) in BLT1<sup>-/-</sup> mice injected with GFP MC (n=8) or IL-23 MC (n=6). All data are mean ±s.e.m. *p<0.05, **p<0.01. Statistical analysis was performed using two-tailed Student’s t-test.
Supplemental Figure 2. BLT1 deficient mice show increased osteoclast formation.

qRT–PCR expression analysis for the indicated genes during differentiation of BLT1++ and BLT1−/− bone marrow cells into osteoclasts at day 2 after RANKL stimulation. Data are presented as a relative gene expression normalized to BLT1++ M-CSF treated cells. n=3 mice per group. All data are shown as mean ± SEM. ∗p<0.05, ∗∗p<0.01, ∗∗∗p<0.001, ∗∗∗∗p<0.0001 as determined by a one-way ANOVA with Tukey post hoc test.