Materials and methods S1

Reverse transcription and real-time PCR (Q-PCR)

Total RNAs were extracted from cells using Trizol reagent (Invitrogen), and 1–5 μg of total RNA was reverse-transcribed using random hexamer primers and SuperScript III reverse transcriptase (Invitrogen). cDNA corresponding to 10 ng of total RNA was analyzed by Q-PCR using a QuantStudio3 (Applied Biosystems). Q-PCR was performed through SYBR green (Applied Biosystems). The sequences of the primers for SET1 and SET2 are as follows: SET1 (forward: AGTCTGCGATCCTGCCTCAG, reverse: AGCAGTGCAGACACTTGTGG), SET2 (forward: GCTCAACTCCAATCACGACG, reverse: AGCAGTGCAGACACTTGTGG). Mouse 18S primers (forward: GCCATGCATGTCTAAGTACGC, reverse: TCTGATAAATGCACGCATCC) were used for normalization.

Supplemental S1 legend

Expression profiles of SET isoforms 1 and 2 during osteoclast differentiation. Total RNA was collected from $Pcdh7^{+/+}$ and $Pcdh7^{-/-}$ cultures and the levels of the indicated genes were measured by Q-PCR.