Knockout and Double Knockout of Cathepsin K and Mmp9 reveals a novel

function of Cathepsin K as a regulator of osteoclast gene expression and bone

homeostasis

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Supplemental Material

Primers list for qPCR

gene symbol	Forward primers (5'-3')	Reverse primers (5'-3')
c-Fos	CGGGTTTCAACGCCGACTA	TTGGCACTAGAGACGGACAGA
Hprt	GGTGGAGATGATCTCTCAACTTTAA	AGGAAAGCAAAGTCTGCATTGTT
NFATC1	TGCCTTTTGCGAGCAGTATCT	CAGGCAAGGATGGGCTCATAT
Pu.1	CCCCACACCGGCCTCAGTCACCAG	CCCCCACGGCCCAGCACCTC
Cebpa	CAAGAACAGCAACGAGTACCG	GTCACTGGTCAACTCCAGCAC
ATP6i	CACAGGGTCTGCTTACAACTG	CGTCTACCACGAAGCGTCTC

Supplemental Figures and Figure Legends



Supplemental Figure 1. Double deletion of *Mmp9* and *Ctsk* causes increased bone mass and severe osteopetrosis in mice. (a) PCR was used to determine the genotypes of the mice. (b-d) X-ray analysis of (b) 4-week old (c) 8-week-old, and (d) 10-week-old mouse femurs. Data showed representative images, n=10.



Supplemental Figure 2. RNA-seq analysis of *Ctsk* and *Mmp9* modulated genes. Quantification data from volcano plot illustrating differentially regulated gene expression from RNA-seq analysis between the©ntrol (c) $Ctsk^{-/-}$, (b) $Mmp9^{-/-}$ and (c) $Ctsk^{-/-}/Mmp9^{-/-}$ osteoclasts from Figure 4a. Values are presented as the log2 of tag counts.



Supplemental Figure 3. RNA-seq analysis of Ctsk and Mmp9 modulated genes in

osteoclast signaling. Top upregulated signaling pathways in (a) Ctsk^{-/-} and (b) Mmp9⁻

^{/-} osteoclasts, respectively, as analyzed by KEGG database.



Supplemental Figure 4. ATAC-Seq Profiling of WT, Ctsk-/-, Mmp9-/-, and DKO

osteoclasts. (a-d) Distribution of ATAC-seq THSs relative to genomic features in (a)

WT, (b) $Ctsk^{-/-}$, (c) $Mmp9^{-/-}$, and (d) $Ctsk^{-/-}$; $Mmp9^{-/-}$ osteoclasts.