

Supplemental Information

**The role of CDK8 in mesenchymal stem cells in controlling osteoclasto-
genesis and bone homeostasis**

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1 **Supplementary Table 1. List of primers used for genotyping**

Gene	Forward (5'-3')	Reverse (5'-3')
<i>Cre</i>	GAACCTGATGGACATGTTCAGG	AGTGCGTTCGAACGCTAGAGCCTGT
<i>CDK8</i>	CGTAGGTAGCAATCTGGTCGGGGT	CAGGTACACAGGCTGGATTTGCAC

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3 **Supplementary Table 2. List of primers used for deletion PCR.**

Gene	Forward (5'-3')	Reverse (5'-3')
<i>CDK8</i>	CTTCCCTCTTCCCAGAGGAC	CAACCCCTTTTGAGGTTGAA

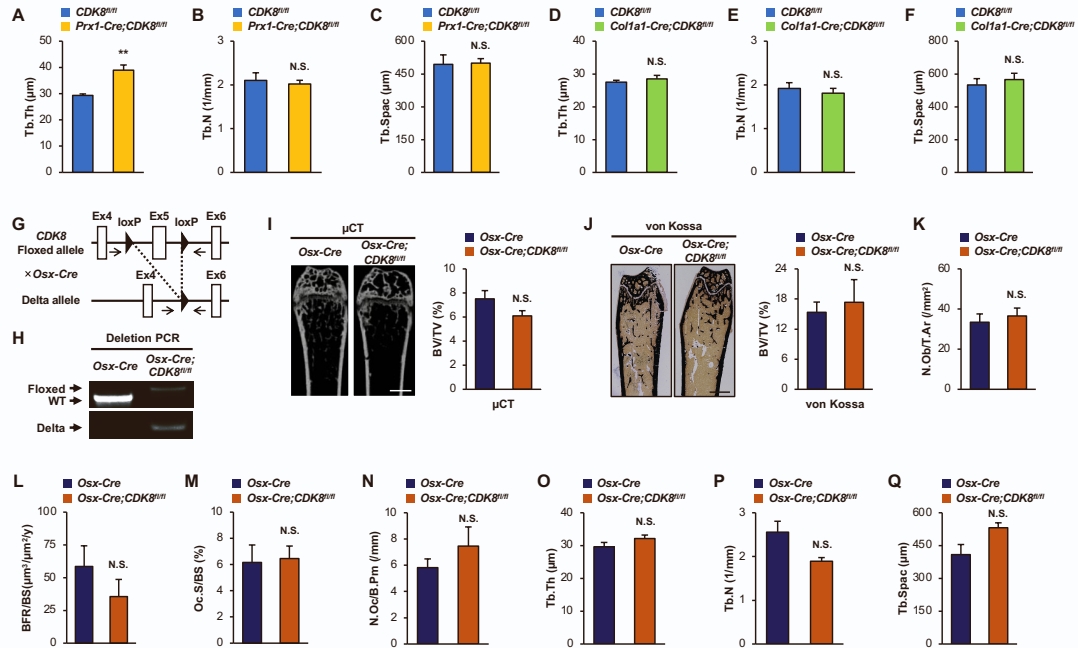
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5 **Supplementary Table 3. List of primers used for real-time PCR.**

Gene	Forward (5'-3')	Reverse (5'-3')
<i>Acp5</i>	AGCTTCTCTGCCCTGGTACTC	TGGCTGTGGGATCAGTTGGTG
<i>Cdkn1a</i>	TCGCTGTCTTGCACTCTGGTGT	CCAATCTGCGCTTGGAGTGATAG
<i>Ctsk</i>	CAACTCTACTCCCTTCTCTCTGC	GAGGACTCCAATGTCTACCAGC
<i>Gapdh</i>	AGGTCGGTGTGAACGGATTTG	TGTAGACCATGTAGTTGAGGTCA
<i>Icam1</i>	TTCACACTGAATGCCAGCTC	GTCTGCTGAGACCCCTCTTG
<i>Ifi204</i>	GGAAAGAGACAACCAAGAGC	TGGCTTGTAGTTGATGTAGG
<i>Irf1</i>	TCCAAGTCCAGCCGAGACACTA	ACTGCTGTGGTCATCAGGTAGG
<i>Irf8</i>	TCCAAGTCCAGCCGAGACAC	ACTGCTGTGGTCATCAGGTA
<i>Mmp9</i>	TGTGCGTTATGGTTCAGGTCAG	CTGCCAGGAAGACACTTGGTTATC
<i>Smad7</i>	AAGATCGGCTGTGGCATC	CCAACAGCGTCCTGGAGT
<i>Spi1</i>	ATCCAGAAGGGCAACCGCAAG	TCTTGACTTTCTTCACCTCGCCTG
<i>Tap1</i>	GACTCCTTGCTCTCCACTCA	AACGCTGTCACCGTTCAGG
<i>Tnfrsf11b</i>	CTGCAATACACACACTCATCACT	ACCCAGAAACTGGTCATCAGC
<i>Tnfsf11</i>	TGTACTTTCGAGCGCAGATG	CCACAATGTGTTGCAGTTCC

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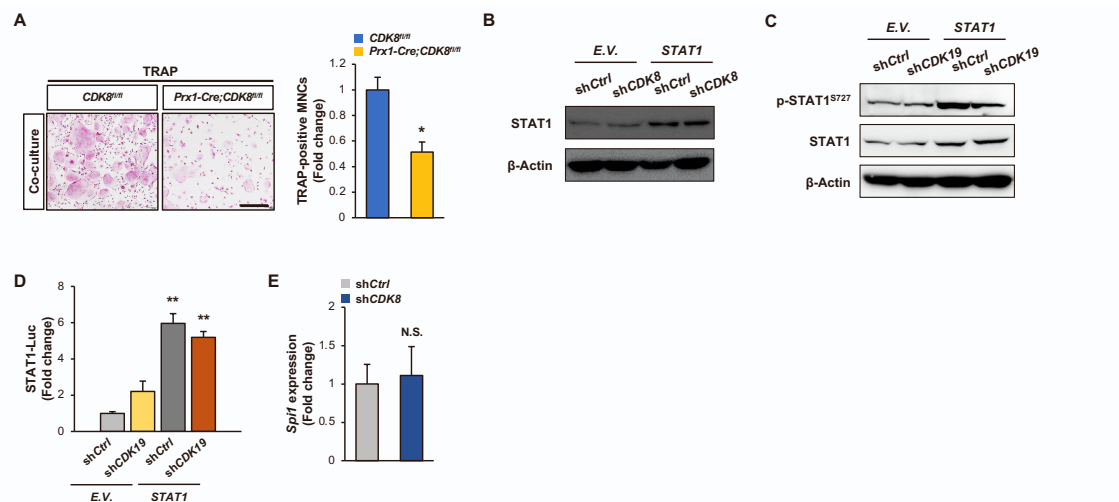
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Supplementary Figure 1. Skeletal phenotype analysis of conditional MSC-specific, osteoblast-specific, and osteoprogenitor-specific *CDK8* knockout mice.

(A-C) Tb.Th (A), Tb.N (B) and Tb.Spac (C) measured by μ CT of femurs from *CDK8^{fl/fl}* and *Prx1-Cre;CDK8^{fl/fl}* mice ($n = 6-7$, ** $P < 0.01$). (D-F) Tb.Th (D), Tb.N (E) and Tb.Spac (F) measured by μ CT of femurs from *CDK8^{fl/fl}* and *Coll1a1-Cre;CDK8^{fl/fl}* mice ($n = 6-7$). (G) Schematic diagram of generation of tissue-specific *CDK8* knockout mice. Black arrows represent primer binding sites. (H) Deletion efficiency of *CDK8* in the marrow-flushed bone of *Osx-Cre;CDK8^{fl/fl}* mice at the genomic DNA level. (I) μ CT analysis and BV/TV measurement of femurs from *Osx-Cre* and *Osx-Cre;CDK8^{fl/fl}* mice ($n = 4-5$). (J to N) BV/TV determined by von Kossa staining (J), N.Ob/T.Ar (K), BFR/BS (L), Oc.S/BS (M) and N.Oc/B.Pm (N) of femur from *Osx-Cre* and *Osx-Cre;CDK8^{fl/fl}* mice ($n = 4-5$). (O-Q) Tb.Th (O), Tb.N (P) and Tb.Spac (Q) measured by μ CT of femurs from *CDK8^{fl/fl}* and *Osx-Cre;CDK8^{fl/fl}* mice ($n = 4-5$). All mice used in this study were female. Scale bars, 1 mm (I and J). μ CT, micro-computed tomography; Tb.Th, Trabecular thickness; Tb.N, Trabecular number; Tb.Spac; Trabecular spacing; BV/TV, bone volume/tissue volume; N.Ob/T.Ar, number of osteoblasts/tissue area; BFR/BS, bone formation rate/bone surface; Oc.S/BS, osteoclast surface/bone surface; N.Oc/B.Pm, number of osteoclasts/bone perimeter; N.S., not significant.

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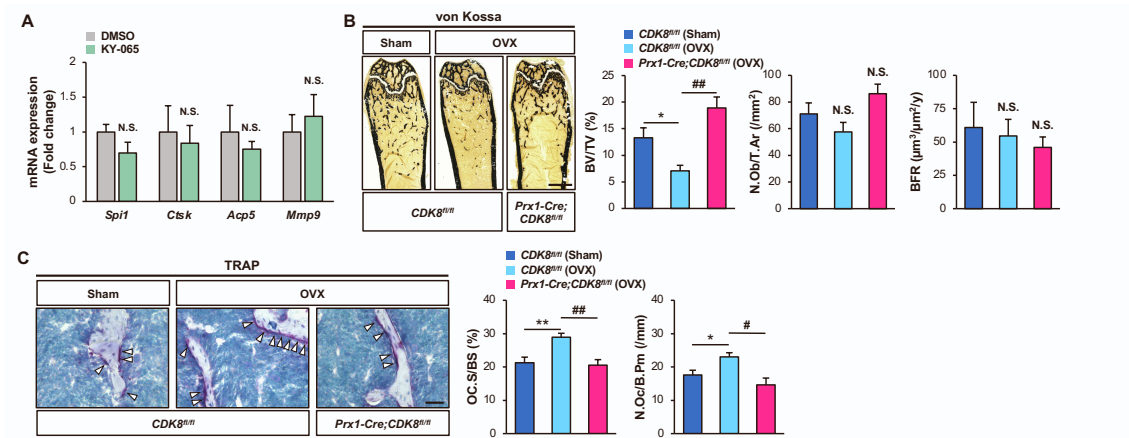


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29 **Supplementary Figure 2. Co-culture of MSCs from *Prx1-Cre;CDK8^{fl/fl}* mice and WT-**
 30 **BMMs, and expression profiles of *CDK8* and *CDK19* knockdown MSCs.**

31 (A) BMMs prepared from WT mice were co-cultured with MSCs from *Prx1-*
 32 *Cre;CDK8^{fl/fl}* mice, followed by TRAP staining ($n = 3$ independent replicates, $*P < 0.05$).
 33 (B) Protein levels of STAT1 in MSCs infected with sh*CDK8* in combination with *STAT1*
 34 expression vector. β -Actin served as a loading control. (C) Protein levels of STAT1 and
 35 p-STAT1^{Ser727} in MSCs infected with sh*CDK19* in combination with *STAT1* expression
 36 vector. β -Actin served as a loading control. (D) GAS-luc activity in MSCs infected with
 37 sh*CDK19* in combination with *STAT1* expression vector ($n = 3$ independent replicates,
 38 $**P < 0.01$). (E) mRNA levels of *Spi1* in MSCs infected with sh*CDK8* ($n = 4$ independent
 39 replicate). Scale bar, 800 μ m (A). BMM, bone marrow macrophage; MSC, mesenchymal
 40 stem cell; TRAP, tartrate-resistant acid phosphatase; sh*Ctrl*, sh*Control*; E.V., empty
 41 vector; N.S., not significant.

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44 **Supplementary Figure 3. Expression levels of osteoclastic marker genes in BMMs**
 45 **treated by KY-065, and the protective effect of MSC-specific CDK8 deficiency on**
 46 **ovariectomy-induced bone loss.**

47 (A) mRNA levels of *Spi1*, *Ctsk*, *Acp5* and *Mmp9* in MSCs treated with 30 nM KY-065 (*n*
 48 = 3 independent replicates). (B) BV/TV measured by von Kossa staining, N.Ob/T. Ar
 49 determined by toluidine blue staining and BFR/BS determined by calcein labeling of
 50 femurs from CDK8^{fl/fl} and Prx1-Cre;CDK8^{fl/fl} mice (*n* = 5-8, **P* < 0.05 (CDK8^{fl/fl} (sham)
 51 vs CDK8^{fl/fl} (OVX)), ###*P* < 0.01 (CDK8^{fl/fl} (OVX) vs Prx1-Cre;CDK8^{fl/fl}(OVX))). (C)
 52 Oc.S/BS and N.Oc/B.Pm determined by TRAP staining of femur (*n* = 5-8, **P* < 0.05
 53 (CDK8^{fl/fl} (sham) vs CDK8^{fl/fl} (OVX)), ***P* < 0.01 (CDK8^{fl/fl} (sham) vs CDK8^{fl/fl} (OVX)),
 54 #*P* < 0.05 (CDK8^{fl/fl} (OVX) vs Prx1-Cre;CDK8^{fl/fl}(OVX)), ###*P* < 0.01 (CDK8^{fl/fl} (OVX)
 55 vs Prx1-Cre;CDK8^{fl/fl}(OVX))). Scale bars, 1 mm (B), 50 μm (C). OVX, ovariectomy;
 56 BV/TV, bone volume/tissue volume; N.Ob/T.Ar, number of osteoblasts/tissue area;
 57 BFR/BS, bone formation rate/bone surface; TRAP, tartrate-resistant acid phosphatase;
 58 Oc.S/BS, osteoclast surface/bone surface; N.Oc/B.Pm, number of osteoclasts/bone
 59 perimeter; N.S., not significant.

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