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**Graphical abstract**

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Lkb1 deletion in periosteal mesenchymal progenitors induces osteogenic tumors through mTORC1 activation

Yujiao Han,1 Heng Feng,1 Jun Sun,1 Xiaoting Liang,2 Zhuo Wang,3 Wenhui Xing,1 Qinggang Dai,4 Yang Yang,1 Anjia Han,3 Zhanying Wei,5 Qing Bi,6 Hongbin Ji,1,7 Tiebang Kang,6 and Weiguo Zou1

1State Key Laboratory of Cell Biology, CAS Center for Excellence in Molecular Cell Sciences, Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences; University of Chinese Academy of Sciences, Shanghai, China. 2State Key Laboratory of Oncology in South China, Collaborative Innovation Center for Cancer Medicine, Sun Yat-sen University Cancer Center, Guangzhou, China. 3Department of Pathology, The First Affiliated Hospital of Sun Yat-sen University, Guangzhou, China. 4The Second Dental Center, Ninth People’s Hospital, Shanghai jiao Tong University School of Medicine, Shanghai, China. 5Department of Osteoporosis and Bone Diseases, Metabolic Bone Disease and Genetics Research Unit, Shanghai jiao Tong University Affiliated Sixth People’s Hospital, Shanghai, China. 6Zhejiang Provincial People’s Hospital, Hangzhou, China. 7School of Life Science and Technology, Shanghai Tech University, Shanghai, China.

Bone osteogenic sarcoma has a poor prognosis, as the exact cell of origin and the signaling pathways underlying tumor formation remain undefined. Here, we report an osteogenic tumor mouse model based on the conditional knockout of liver kinase b1 (Lkb1, also known as Stk11) in Cathepsin K-Cre–expressing (Ctsk-Cre–expressing) cells. Lineage-tracing studies demonstrated that Ctsk-Cre could label a population of periosteal cells. The cells functioned as mesenchymal progenitors with regard to markers and functional properties. LKB1 deficiency increased proliferation and osteoblast differentiation of Ctsk–perosteal cells, while downregulation of mTORC1 activity, using a Raptor genetic mouse model or mTORC1 inhibitor treatment, ameliorated tumor progression of Ctsk-Cre Lkb1+/− mice. Xenograft mouse models using human osteosarcoma cell lines also demonstrated that LKB1 deficiency promoted tumor formation, while mTOR inhibition suppressed xenograft tumor growth. In summary, we identified periosteum-derived Ctsk-Cre–expressing cells as a cell of origin for osteogenic tumor and suggested the LKB1/mTORC1 pathway as a promising target for treatment of osteogenic tumor.

Introduction

Osteogenic tumor is the most common primary tumor of the bone tissue, including benign bone-forming neoplasm, osteoma, osteoblastoma, and a malignant neoplasm called osteogenic sarcoma, also referred to as osteosarcoma (1). The hallmark diagnostic feature of osteogenic tumor is the detection of mineralized bone or osteoid matrix produced by the neoplastic cells, with a very broad spectrum of histological appearances (2). Osteogenic sarcoma arises primarily in children and adolescents, with a second incidence peak in aged people. It confers a poor prognosis, as the survival benefit of traditional chemotherapy treatment remains unsatisfactory. More targeted and personalized therapies for osteogenic sarcoma treatment are urgently required (1). A growing body of evidence indicates that mouse models can recapitulate the fundamental aspects of human osteogenic sarcoma and offer the ability to yield therapeutic targets that will eventually allow customized cancer treatment (3). Furthermore, modeling human cancers using transgenic mice or knockout mice has been proven to further our understanding of the exact cell of origin and the signaling pathways underlying tumor formation (4).

Mutations in p53 and/or Rb genes, as well as other components involved in their pathways, have been identified in human osteosarcoma patients, and mouse models for studying the cell of origin for osteosarcoma have been developed via conditional mesenchymal/osteogenic lineage-restricted knockout of p53 and/or Rb genes (5–9). The disruption of p53/Rb in mesenchymal progenitors (Prx1-Cre), osteoblast precursors (OxS-Cre), and osteoblast committed cells (Col1a1-Cre and OCN-Cre) leading to osteogenic sarcoma confirmed that cells with mesenchymal origin and osteogenic lineage were responsible for osteogenic tumor formation (4, 10–12). Moreover, NOTCH activation in committed osteoblasts (Col1a1-Cre) was sufficient to induce osteogenic sarcoma, also suggesting committed osteoblasts as the potential sources of osteogenic tumor (13). However, the exact cell of origin with distinct genetic mutations that is responsible for the individual subtypes remains to be described (14, 15).

Liver kinase b1 (Lkb1, also known as Stk11), is a master serine/threonine kinase that links energy homeostasis and cell growth through the mTORC1 pathway (16). Loss of Lkb1 in a variety of organs has been reported to initiate both hyperplasia and tumorigenesis (17). Cancers with Lkb1 inactivation tend to exhibit aggressive clinical characteristics, and their therapeutic sensitivity differs from those without Lkb1 inactivation (18–21). Previous studies indicated that Lkb1 may also be involved in bone cancer. Lkb1 heterozygous germine mutant (Lkb1+/-) mice develop gastrointestinal polyps and multifocal osteogenic tumors (22, 23). A recent study showed that 41% of osteosarcoma patients lost LKB1 protein expression and that most of them showed mTORC1 activation.
Although the loss of Lkb1 has been suggested as correlating with osteogenic tumor, the involved cell type and the underlying pathway remain unclear; however, these details are central for a complete understanding of osteogenic tumor formation.

Cathepsin K (CTSK) is a cysteine protease secreted by osteoclasts and is essential for the degradation of matrix collagen during bone resorption (25). The Ctsk promoter has been suggested as being active in osteoclasts only (26), and Ctsk-Cre mice have been widely used to study osteoclast function (27). A recent study demonstrated that Ctsk-Cre–expressing cells can be chondroprogenitor cells, as Ptpn11 deletion in Ctsk-Cre–expressing cells resulted in metachondromatosis by activating Hedgehog signaling (28). Lack of Lkb1 within chondrocytes (Col2a1-Cre) of the endochondral skeleton caused a dramatic disruption of the skeletal growth plate and formation of cartilage tumors (29). This suggests that Lkb1 deletion in Ctsk-Cre–expressing cells causes cartilage tumors. Interestingly, in this study, we found that deletion of Lkb1 in Ctsk-Cre–expressing cells caused an osteogenic tumor–like phenotype, but not cartilage tumors. The features included an overall disruption of cortical bones as well as increased osteoid formation and bone turnover. Lineage tracing indicated that Ctsk-Cre could label a population of peristomium–derived cells, which could function as mesenchymal progenitors in terms of markers and functional properties.

In this study, we identified a cell of origin for osteogenic tumor and suggested Lkb1 as a tumor suppressor in the primary bone tumor, thus advancing our knowledge of both the cell of origin and the molecular genetics of osteogenic tumor. Furthermore, our data supported that Ctsk-Cre–expressing cells could serve as progenitors of both cartilage tumor and osteogenic tumor under the regulatory effects of different signaling. Moreover, these results indicated the therapeutic potential of mTORC1 inhibitors for the treatment of osteogenic sarcoma.

Results

Lkb1 deficiency in Ctsk-Cre–expressing cells causes osteogenic tumor–like phenotype. To investigate the role of Lkb1 in Ctsk-Cre–expressing cells, we generated Ctsk-Cre; Lkb1fl/fl mice (hereinafter named Ctsk-CKO). Lack of Lkb1 within chondrocytes (Col2a1-Cre) of the endochondral skeleton caused cartilage tumors (29), and Ctsk-Cre–expressing cells were identified as the source of metachondroma (28); therefore, Lkb1 loss in Ctsk–cells was supposed to lead to cartilage tumors. Strikingly, Ctsk-CKO mice did not display cartilage tumors, as indicated by H&E staining and safranin O (SO) staining of tibiae from Ctsk-CKO mice before tumor formation, we did a quantitative μCT analysis showed disorganized bone architecture and the presence of ossified spicules outside the periosteum in both axial and appendicular skeletons of Ctsk-CKO mice (Figure 1, C and D). H&E staining of tibiae from Ctsk-CKO mice showed progressive histopathological features of osteogenic tumor: expansive osteoid lesions with mushroom-shaped appearance located in the cortical bone and beginning of invasion of the medullary cavity from the age of 20 weeks (Figure 1E). The tumor gradually formed a large mass, transgressing the cortex and invading into adjacent muscle and fat tissues at the age of 40 weeks (Figure 1E, F, and G, and Supplemental Figure 2C), mimicking malignant human osteogenic sarcoma. Nuclear atypia of cells that compose the osteoid matrix gradually increased from mild to severe with age (Figure 1E). The tumor presented a high proliferation rate, measured via elevated cell proliferation marker Ki67 (Figure 1G).

As lack of Lkb1 in Ctsk–cells led to a tumor–like mass in the cortical bone, the expression levels of genes involved in the cell cycle, including Ccnd1, Cdkn1a, Cdkn2a, and Cdkn2b, were determined to characterize the tumor and it was found that they were significantly increased in Ctsk-CKO tibiae at the age of 20 weeks (Figure 1H). We furthermore observed increased expression of the osteogenic sarcoma oncogene Mdm2 and Notch target gene Hey1 in Ctsk-CKO mice, which were frequently upregulated in osteosarcoma patients or mouse models (13, 30). The expression levels of the tumor suppressors Rb and Bub3 were decreased in Ctsk-CKO mice as expected, while decreased expression levels of the tumor suppressor genes p53, Wif, and Fgfr2 were not detected in Ctsk-CKO mice (8, 11, 31, 32) (Figure 1H). We also examined expression of these genes between control and mutant mice before the tumor mass appeared at the age of 5 weeks and found that expression levels of cell cycle–related genes showed more moderate changes (Supplemental Figure 2D). Interestingly, we found an obvious elevated expression of Fgfr2 at the age of 5 weeks (Supplemental Figure 2D), which was highly involved in cell fate, cell proliferation, and tumor induction, prompting us to trace the phenotype and gene expression of Ctsk-CKO mice before tumor formation.

Lkb1 deletion in Ctsk-Cre–expressing cells results in enhanced bone formation in mice. To examine bone architecture of Ctsk-CKO mice before tumor formation, we did a quantitative μCT analysis and found an increase in the cortical bone thickness and heterotopic bone formation within the cortex in Ctsk-CKO mice (Figure 2, A and B). However, the percentage of bone volume per tissue volume (BV/TV) within the cortical bone of Ctsk-CKO mice was decreased (Figure 2, A and B). von Kossa staining confirmed the mineralization of the heterotopic bone within the cortex (Figure 2C). The thickened diaphyseal cortex then prompted us to test the bone formation rate (BFR) in Ctsk-CKO mice. To determine the BFR, dynamic histomorphometry analysis was performed by double labeling with calcine and alizarin red, which are markers of newly formed bone. Compared with Ctsk-Ctrl mice, Ctsk-CKO mice displayed more heterotopic newly synthesized osteoid in the cortical bones (Figure 2D). The mineral apposition rate (MAR) and BFR at the periosteal surface of the tibiae of 5-week-old Ctsk-CKO mice were significantly increased compared with those of Ctsk-Ctrl mice (Figure 2, D and E). Moreover, higher mRNA levels of marker genes, representing stages of osteoblast differentiation.
Lkb1 deletion in Ctsk-Cre–expressing cells causes osteogenic tumor–like phenotype. (A) Body weight plots of Ctsk-Ctrl (n = 10) and Ctsk-CKO (n = 8) male mice. (B) Kaplan-Meier survival plots of Ctsk-Ctrl (n = 31) and Ctsk-CKO (n = 21) mice. (C and D) X-ray images and μCT scans of the spines (C) and tibiae (D) of 20-week-old Ctsk-Ctrl and Ctsk-CKO mice. (E) H&E staining of tibia from 4-, 20-, 30-, and 40-week-old Ctsk-CKO mice showed a progressive histopathological feature. Scale bar: 1 mm (upper panels); 20 μm (lower panels). (F) Tumor in the tibiae of Ctsk-CKO mice was composed of fibroblastic and osteoblastic cells with abundant blood vessels. It invaded into the adjacent muscle and fat tissues at an age of 40 week. Scale bars: 50 μm. (G) Immunostaining of KI67 in the tumor osteoid displayed a hyperproliferative characteristic. Scale bar: 50 μm. Similar results were obtained from analyses of both male and female mice for each genotype. (H) Gene expression of human osteosarcoma-related genes in the cortical bone of tibiae from 20-week-old female Ctsk-CKO mice (n = 3) compared with normal Ctsk-Ctrl mice (n = 4). Data are represented as mean ± SEM. *P < 0.05; **P < 0.01; ***P < 0.001, unpaired Student’s t test.

(9), were detected in tumors of 20-week-old Ctsk-CKO mice compared with the cortical bone of tibiae from Ctsk-Ctrl mice (Figure 2F). The osteoblast markers were also examined at the age of 2 weeks. The results showed that preosteoblast markers Alp and Colla1 were specifically increased, indicating activation of bone formation in Ctsk-CKO mice (Supplemental Figure 2E). In accordance with observed increased osteoblast activity, the tumor was largely composed of osteoblastic cells, as indicated by immunostaining of the osteoblastic markers osterix (OSX) (Figure 2G) and osteopontin (OPN) (Figure 2H).

Lkb1 deficiency in osteoclast precursors does not induce osteogenic tumor–like phenotype. Ctsk-Cre mice have been widely used to study osteoclast function due to the abundant and selective expression of Ctsk in osteoclasts (27). We next assessed whether this increased bone mass in Ctsk-CKO mice was the result of impaired osteoclast activity. We used tartrate-resistant

Figure 1. Lkb1 deletion in Ctsk-Cre–expressing cells causes osteogenic tumor–like phenotype. (A) Body weight plots of Ctsk-Ctrl (n = 10) and Ctsk-CKO (n = 8) male mice. (B) Kaplan-Meier survival plots of Ctsk-Ctrl (n = 31) and Ctsk-CKO (n = 21) mice. (C and D) X-ray images and μCT scans of the spines (C) and tibiae (D) of 20-week-old Ctsk-Ctrl and Ctsk-CKO mice. (E) H&E staining of tibia from 4-, 20-, 30-, and 40-week-old Ctsk-CKO mice showed a progressive histopathological feature. Scale bar: 1 mm (upper panels); 20 μm (lower panels). (F) Tumor in the tibiae of Ctsk-CKO mice was composed of fibroblastic and osteoblastic cells with abundant blood vessels. It invaded into the adjacent muscle and fat tissues at an age of 40 week. Scale bars: 50 μm. (G) Immunostaining of KI67 in the tumor osteoid displayed a hyperproliferative characteristic. Scale bar: 50 μm. Similar results were obtained from analyses of both male and female mice for each genotype. (H) Gene expression of human osteosarcoma-related genes in the cortical bone of tibiae from 20-week-old female Ctsk-CKO mice (n = 3) compared with normal Ctsk-Ctrl mice (n = 4). Data are represented as mean ± SEM. *P < 0.05; **P < 0.01; ***P < 0.001, unpaired Student’s t test.
acid phosphatase (TRAP) staining and found that osteoclast numbers in the periosteum, endosteum, and trabecular bone were increased in Ctsk-CKO mice when compared with the control mice (Figure 3A). We also cultured bone marrow (BM) cells from Ctsk-Ctrl and Ctsk-CKO mice; then the cells were differentiated into osteoclasts in the presence of monocyte/macrophage CSF (M-CSF) and RANKL. Quantification of TRAP activity demonstrated an increased osteoclast formation ability in Ctsk-CKO BM cells (Figure 3, B and C). These data indicate that the increased bone mass of Ctsk-CKO mice was not due to impaired resorption ability. To further rule out that the increased bone mass of Ctsk-CKO mice originated from the extrinsic role of Lkb1-deficient osteoclasts, we generated LysM-Cre; Lkb1 fl/fl mice in which the LysM promoter was active in monocytes, macrophages, and osteoclast precursors (33). LysM-CKO mice did not show a discernible osteogenic tumor–like phenotype at the age of 20 weeks (Figure 3, D–F) and 40 weeks (data not shown), indicating that the osteogenic tumor–like phenotype in Ctsk-CKO mice was not the result of altered osteoclast function.

Ctsk-Cre–expressing peristeal mesenchymal cells are potential sources for osteogenic tumors. In response to the results presented so far, we hypothesized that a Ctsk-Cre–positive but LysM-Cre–negative mesenchymal cell population might cause osteogenic tumor in Ctsk-CKO mice. To identify this cell population, we performed lineage-tracing studies using Rosa 26-mT/mG mice, which constitutively express membrane-targeted Tomato fluorescent protein and membrane-targeted GFP upon Cre-mediated recombination (34) (Figure 4A). As expected, a Ctsk-Cre–positive but LysM-Cre–negative population was found in the periosteum of cortical bone (Figure 4B), although both Ctsk-Cre and LysM-Cre were expressed in osteoclasts on the surface of trabecular bone at the age of 4 weeks (Supplemental Figure 3A). More importantly, Ctsk-Cre–positive cells expanded and filled within the cortical bone of tibiae from Ctsk-CKO mice with age growth (Supplemental Figure 3B). The osteoid tumor area in Ctsk-CKO tibiae was mainly formed by GFP-positive cells by the age of 20 weeks (Figure 4C and Supplemental Figure 3B), indicating that the osteogenic tumor in Ctsk-CKO mice was caused by intrinsic

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**Figure 2. Lkb1 deletion in Ctsk-Cre–expressing cells leads to increased bone formation.** (A) μCT analysis of femurs from 5-week-old female Ctsk-Ctrl and Ctsk-CKO mice. (B) Ct.Th and BV/TV of the cortical bones of femurs from 5-week-old female Ctsk-Ctrl and Ctsk-CKO mice (n = 5 for each group). (C) von Kossa staining of the tibiae from 5-week-old female Ctsk-Ctrl and Ctsk-CKO mice showing MAR and BFR of the periosteum (n = 3 for each group). Scale bars: 100 μm (left); 10 μm (right). (F) Gene expression of markers for osteoblast progenitor (Runx2 and Dlx), preosteoblast (Alp and Colla1), and mature osteoblast (Opn, Bsp, and Ocn) of the cortical bones of 20-week-old female Ctsk-CKO mice (n = 3) compared with Ctsk-Ctrl mice (n = 4) tibiae. (G and H) Immunostaining of OSX (G) and OPN (H) in the tumor osteoid of Ctsk-CKO tibiae. Scale bars: 50 μm. Data are represented as mean ± SEM. *P < 0.05; **P < 0.01, unpaired Student’s t test.
Lkb1 deletion in Ctsk-Cre–expressing cells. To further determine the role of Ctsk+ cells in tumor formation, another mouse reporter strain (Rosa26-Ai9) was used, which conditionally expresses fluorescent protein tdTomato in response to Cre recombinase activation (35) (Figure 4D). The Rosa26-Ai9 reporter mice showed bright single fluorescence that greatly facilitated in vivo imaging. Expansion of Ctsk-Cre–expressing cells was also observed in the cortical bone of Ctsk-CKO; Rosa-Ai9 tibiae at the age of 4 weeks (Figure 4E). We further examined cell identity of Ctsk+ cells through FACS analyses. Three populations, including CD200+CD105−, previously described as skeletal stem cell (SSC), CD200+CD105− pre–bone-cartilage-stromal progenitor (pre-BCSP), and CD105+BCSP (36) were identified from CD31−, CD45−, TER119− (Lin−) CD90.2−CD24− Ctsk-Ai9+ cells (Figure 4F and Supplemental Figure 4B), which is consistent with the recent study showing that Ctsk-Cre labels periosteal mesenchymal cells (37). Furthermore, we also analyzed the expression of common stem cell markers in Ctsk+ cells and found expression of Sca1, CD24, CD44, CD49f, and CD146 in Ctsk+ cells (Supplemental Figure 4C). We next investigated the differentiation potential of periosteal Ctsk+ cells and found that they are capable of differentiating into osteoblast, chondrocyte, and adipocyte in vitro, as demonstrated by alkaline phosphatase (ALP), Alcian blue, and oil red O staining and expression of corresponding differentiation markers (Supplemental Figure 4A), further demonstrating the Ctsk can label a population of mesenchymal stem cells.

We then examined LKB1 expression in the periosteum of Ctsk-positive cells via immunofluorescence. The results confirmed deletion of LKB1 expression in Ctsk+ periosteal cells from Ctsk-CKO; Rosa-Ai9 mice, but not in Ctsk-Ai9 cells from Ctsk-Ctrl; Rosa-Ai9 mice (Figure 4, G and H). FACS analysis further confirmed the percentage of Ctsk+Lkb1+ cells in Ctsk+ periosteal cells. Interestingly, we found a higher percentage of Lin–CD90.2–CD105–CD200+ cells in the Ctsk+Lkb1+ population when compared with Ctsk+Lkb1− cells (Supplemental Figure 4D), indicating the expression of LKB1 within Ctsk+ stem cells and tumorigenesis might occur specifically within this stem cell population.

Next, we asked whether periosteal Ctsk-Ai9 cells have osteogenic tumor initiation potential in Ctsk-CKO mice. We found increased expression levels of osteoblast markers, including OSX, COL1A1, and OPN, in periosteal mesenchymal Ctsk-Ai9 cells of
Figure 4. Ctsk-Cre–expressing periosteal mesenchymal stem cells are potential sources for osteogenic tumor. (A) Schematic of experiments on Rosa26-loxp-mTomato-stop-loxp-GFP (Rosa26-mT/mG) Cre reporter mice. (B) Confocal images of the tibiae of 4-week-old male LysM-Cre; Rosa26-mT/mG and Ctsk-Cre; Rosa26-mT/mG reporter mice showing that Ctsk-Cre; GFP (green), but not LysM-Cre; GFP (green) was expressed in the periosteum of cortical bone (indicated with the white arrow). Right panel: in Ctsk-CKO mice, Ctsk-positive cells at the periosteum expanded within the cortical bone. Scale bar: 50 μm. (C) Confocal images showing that the majority of the cells in the tumor region of 20-week-old male Ctsk-CKO; Rosa26-mT/mG mice are Ctsk-Cre; GFP–expressing cells (green). Scale bars: 300 μm (left); 50 μm (right). (D) Schematic of experiments on Rosa26-loxp-stop-loxp-tdTomato (Rosa26-Ai9) Cre reporter mice. (E) Images of 4-week-old male Ctsk-Ctrl; Rosa26-Ai9 and Ctsk-CKO; Rosa26-Ai9 tibiae showing expansion of Ctsk-Cre–expressing cells (red) in Ctsk-CKO mice. Scale bars: 300 μm (left); 20 μm (right). (F) Flow cytometry of cells from periosteum of 4-week-old male Ctsk-Ctrl; Rosa26-Ai9 mice to identify expression of SSC markers CD105 and CD200 in Lin–CD90.2–6C3–Ctsk-Ai9+ cells. (G and H) Immunostaining of LKB1 showing that LKB1 (green) was conditionally deleted in Ctsk+ periosteal cells (red) from Ctsk-CKO; Rosa-Ai9 mice, but not in Ctsk-Ai9 cells of Ctsk-Ctrl; Rosa-Ai9 mice. Scale bar: 20 μm. (I and J) Immunostaining showing Ctsk-Cre–positive cells (red) in the cortical bone display osteoblast markers OSX (green), COL1A1 (green), and OPN (green) in the tibiae of 4-week-old male Ctsk-Ctrl; Rosa26-Ai9 and Ctsk-CKO; Rosa26-Ai9 mice (white arrow). Scale bar: 20 μm. (K) Ctsk-Ai9 cells isolated from the cortical bone of tibiae from Ctsk-Cre; Rosa26-Ai9 mice showed expression of osteoblastic markers OSX (green), COL1A1 (green), and OPN (green). Scale bar: 10 μm. Data are represented as mean ± SEM. *P < 0.05; **P < 0.01; ***P < 0.001, unpaired Student’s t test.
Ctsk-CKO mice when compared with those in Ctsk-Ctrl mice (Figure 4, I and J). We also examined the non–long bones and found the distribution of Ctsk-positive cells in the periosteum of skull, spine, and sternum (Supplemental Figure 3, C and D). Moreover, these periosseal Ctsk-Ai9 cells also expressed the preosteoblast marker COL1A1 (Supplemental Figure 3, C and D), indicating Ctsk as a marker of osteoblast progenitors that are responsible for bone formation in both long bones and non–long bones. Ctsk-Ai9
cells isolated from the cortical bone of Ctsk-Ctrl; Rosa-Ai9 mice showed expression of osteoblastic markers OSX, COL1A1, and OPN (Figure 4K), suggesting an in vitro osteoblast differentiation ability of Ctsk-Ai9 cells. Combined with the previous findings that Ctsk-positive cells represent a subset of perichondrial cells within the groove of Ranvier (28), we hypothesize that periosteum-derived Ctsk+ cells could act as periosteal mesenchymal stem cells, which can develop into osteoblasts.

Prx1+ cells have been reported as mesenchymal progenitors residing in both the periosteum of cortical bone and the BM (38). To determine whether Lkb1-deficient mesenchymal progenitors could be the origin of osteogenic tumors, we next generated Prx1-Cre; Lkb1flo/flo (Prx1-CKO) mice. At the age of 20 weeks, Prx1-CKO mice showed abnormal nodules in the long bones, hip bones, and calvarial bones, but not in the vertebrae bones (x-ray images; see Supplemental Figure 5A). H&E staining indicated that the osteoid tumor transgressed the cortex and BM cavity (Supplemental Figure 5B) and calcine–alizarin red double-labeled fluorescence showing a large mass of irregular and diffuse fluorochrome labeling, confirming a dramatic increase in new bone formation within the cortical bone of Prx1-CKO tibiae (Supplemental Figure 5C). This was consistent with the observation in Ctsk-CKO mice. Notably, SO staining indicated a profound disorganization of the growth plate in both femur and tibia of Prx1-CKO mice, which displayed an enchondroma-like phenotype (Supplemental Figure 5D). This phenotype had not been observed in Ctsk-CKO mice (Supplemental Figure 4, A and B). We found Prx1+ cells were expanded from the cortex to the marrow cavity in the periosteum and also expanded to form a mass of cartilage in the growth plate of Prx1-CKO mice (Supplemental Figure 5E). We then compared the distributions of Ctsk+ and Prx1+ cells using 4-week-old Ctsk-Cre; Rosa26-mT/mG and Prx1-Cre; Rosa26-mT/mG mice and found that, in the periosteum, both Ctsk and Prx1 can label periosteum cells, but in the growth plate and articular cartilage, only Prx1+ cells but not Ctsk+ cells were seen (Supplemental Figure 5F). This indicated Ctsk and Prx1 might represent 2 subsets of mesenchymal stem cells with different anatomic distributions and functions.

LKB1 inhibits self-renewal and osteoblast differentiation ability of Ctsk+ periosteal mesenchymal stem cells. To investigate the effects of Lkb1 deficiency on Ctsk+ periosteal mesenchymal stem cells, we first assessed the effects of Lkb1 deficiency on self-renewal ability of periosteum Ctsk+ cells. Proliferating cell nuclear antigen (PCNA) staining showed a rapid proliferation of Ctsk+ cells in the periosteum of Ctsk-CKO; Rosa-Ai9 tibiae in vivo (Figure 5, A and B). Consistently, Ctsk-Ai9 cells were isolated via flow cytometry from the cortical bone of both Ctsk-Ctrl; Rosa-Ai9 and Ctsk-CKO; Rosa-Ai9 tibiae and the same number of sorted Ai9-positive cells were seeded. After 7-day culture, the cells from Ctsk-CKO; Rosa-Ai9 mice showed enhanced proliferative ability compared with cells from Ctsk-Ctrl; Rosa-Ai9 mice (Figure 5, C and D).

Based on the report that CD44+ cancer stem cells (CSCs) are responsible for self-renewal and tumor growth in heterogeneous cancer tissue (39) and that CD44 has also been identified as a self-renewal marker in osteosarcoma (40), we examined the expression of CD44 in Ctsk-Ctrl and Ctsk-CKO mice. Immunostaining of CD44 in the periosteum of Ctsk-Ctrl; Rosa-Ai9 and Ctsk-CKO; Rosa-Ai9 mice showed an increased population of CD44 in the inner surface of Ctsk+ periosteal cells (Figure 5, E and F). Reexpression of LKB1 via lentivirus in both Ctsk-Ctrl; Rosa-Ai9 and Ctsk-CKO; Rosa-Ai9 cells reduced the number of CD44-positive cells (Supplemental Figure 3, F and G). We reasoned that loss of Lkb1 in periosteum-derived Ctsk+ cells caused the expansion of CD44-positive cells and drove osteogenic tumor formation.

We next examined the effects of Lkb1 deficiency on osteoblast differentiation. We cultured periosteal cells from Lkb1fl/fl mice and infected these cells with adenovirus expressing EGFP (Adv-EGFP) and Cre (Adv-Cre). Adv-Cre–infected cells showed increased ALP staining (Figure 5G) and higher supernatant ALP activity (Figure 5H) compared with Adv-EGFP–infected cells. Consistently, expression of osteoblast marker genes, including Osx, Colla1 and Opn, increased in Adv-Cre–infected cells (Figure 5I). In summary, these results support the idea that LKB1 deletion could increase the osteoblast differentiation ability of periosteal mesenchymal stem cells.

To further investigate whether Lkb1-deficient cells are sufficient to drive osteogenic tumor formation in normal mice, we transplanted the periosteum-derived cells from Ctsk-Ctrl; Rosa-Ai9 and Ctsk-CKO; Rosa-Ai9 mice to nude mice subcutaneously. Eight weeks after injection, H&E staining and confocal imaging of Ctsk-Ai9 cells demonstrated an osteoid region formed by Ctsk-Cre; Rosa-Ai9 periosteal cells (Figure 5, L and N), which was consistent with the results showing that transplantation of CTSK+ periosteal stem cells under the kidney capsule of WT mice can de novo generate bone organoids (37). Moreover, periosteal cells from Ctsk-CKO; Rosa-Ai9 mice developed larger bone organoids than cells from Ctsk-Ctrl; Rosa-Ai9 mice (Figure 5, J–L). Cellular and nuclear atypia were observed in the osteoid matrix formed by Ctsk-CKO; Rosa-Ai9 cells, but not that formed by control cells, showing features of neoplasia. von Kossa staining and expression of OSX and OPN in the transplanted Ctsk-Ai9+ cells demonstrated that Ctsk-Ai9+ cells have osteogenic potential (Figure 5, M and O). In summary, our data suggested that transplantation of the Lkb1-deficient Ctsk+ periosteal cells was sufficient to drive osteogenic tumor formation in normal mice.

Inhibition of mTORC1 signaling ameliorates tumor progression in Ctsk-CKO mice. To investigate the mechanism with which Lkb1 deletion induces the osteogenic tumor from Ctsk-Cre–positive periosteal mesenchymal stem cells, we focused on the mTORC1 pathway, which is a critical target downstream of LKB1-dependent AMP kinases (AMPKs). Phosphorylation of mTORC1 catalytic subunits ribosomal protein S6 (S6) and eukaryotic translation initiation factor 4E-binding protein 1 (4E-BP1) were increased in Ctsk-CKO mice (Figure 6A), indicating hyperactivation of mTORC1 signaling in Ctsk-CKO mice. We postulated that if LKB1 deletion indeed induces the osteogenic tumor–like phenotype via activation of the mTORC1 pathway, the deletion of Raptor (the core binding factor of mTORC1) in vivo should lead to amelioration of the osteogenic tumor–like phenotype in Lkb1flo/flo; Ctsk-CKO mice. We constructed Ctsk-DKO mice (Ctsk Cre; Lkb1flo/flo; Raptor−/−) and found that delayed tumor progression in Ctsk-DKO mice was indicated by an extended median life span of 42.3 weeks compared with the life span of 23.9 weeks for Lkb1flo/flo; Ctsk-CKO mice (Figure 6B). The disorganized architecture in the tibiae was partially rescued in Ctsk-DKO mice, as indicated by the results of x-ray and μCT analyses (Figure 6C and Supplemental Figure 6A, compare with Figure 5A).
Figure 6. Inhibition of mTOR signaling delays tumor progression of Ctsk-CKO mice. (A) Immunostaining of phosphorylated mTORC1 catalytic substrates ribosomal protein S6 (p-S6) and p-4E-BP1 in sections of 20-week-old Ctsk-Ctrl and Ctsk-CKO tibiae. Scale bar: 20 μm. (B) Survival plots showing an extended median life span of 42.3 weeks for Lkb1fl/fl; Raptorfl/fl; Ctsk-DKO mice (n = 10) compared with 23.9 weeks for Lkb1fl/fl; Ctsk-CKO mice (n = 21). P = 0.0014. (C) X-ray images of spines and tibiae from Ctsk-Ctrl, Raptorfl/fl; Ctsk-CKO, Lkb1fl/fl; Ctsk-CKO, and Lkb1fl/fl; Raptorfl/fl; Ctsk-DKO mice. (D and E) von Kossa staining and the periosteal MAR and BFR via calcine–alizarin red double labeling of tibiae from 5-week-old Ctsk-Ctrl, Raptorfl/fl; Ctsk-CKO, Lkb1fl/fl; Ctsk-CKO and Lkb1fl/fl; Raptorfl/fl; Ctsk-DKO mice. Scale bars: 50 μm (left); 20 μm (middle); 50 μm (right). (F) Immunostaining of CD44 expression in sections of 20-week-old Ctsk-Ctrl, Lkb1fl/fl; Ctsk-CKO, and Lkb1fl/fl; Raptorfl/fl; Ctsk-DKO tibiae. Scale bar: 100 μm. (G and H) Representative x-ray images of spines and tibia showing that treatment of Ctsk-Ctrl and Ctsk-CKO mice with rapamycin twice per week from 2 weeks old to 20 weeks old (G) or daily from 16 weeks old to 20 weeks old (H) delayed the tumor growth of Ctsk-CKO mice. Similar results were obtained from analyses of both male and female mice for each genotype. Data are represented as mean ± SEM. **P < 0.01, unpaired Student’s t test (B) and 2-way ANOVA (E).
Moreover, we examined CD44-positive cells in the section of tibiae and found a robust decline in Ctsk-DKO mice (Figure 6F), indicating a correlation between the frequency of CD44-positive cells and tumor progression. These results suggested that the increased mTORC1 activity in Ctsk-CKO mice suppressed tumor growth in nude mice. H&E staining showed decreased tumor size in Ctsk-DKO tibiae (Supplemental Figure 6B). As expected, both mineralization of the heterotopic bone within the cortical bone by von Kossa staining and increased periosteal MAR and BFR via double labeling were rescued in Ctsk-DKO mice when compared with Ctsk-CKO mice (Figure 6, D and E). Moreover, we examined CD44-positive cells in the section of tibiae and found a robust decline in Ctsk-DKO mice (Figure 6F), indicating a correlation between the frequency of CD44-positive cells and tumor progression. These results suggested that the increased mTORC1 activity in Ctsk-CKO mice suppressed tumor growth in nude mice. H&E staining showed decreased tumor size in Ctsk-DKO tibiae (Supplemental Figure 6B). As expected, both mineralization of the heterotopic bone within the cortical bone by von Kossa staining and increased periosteal MAR and BFR via double labeling were rescued in Ctsk-DKO mice when compared with Ctsk-CKO mice.
could be pathogenic in tumor formation, which prompted us to test to determine whether an mTORC1 signaling inhibitor could slow tumor progression. Rapamycin, an mTORC1 inhibitor, was administered to both Ctsk-Ctrl and Ctsk-CKO mice via intraperitoneal injection twice per week starting at 2 weeks of age, when the cortical bone began to expand in Ctsk-CKO mice (data not shown). X-ray images and H&E staining indicated that rapamycin treatment significantly delayed tumor growth and improved the mobility of Ctsk-CKO mice at the age of 20 weeks (Figure 6G and Supplemental Figure 6C). To further examine the effects of rapamycin on advanced tumor, this drug was intraperitoneally injected daily from the age of 16 weeks. X-ray images and H&E staining indicated that daily rapamycin treatment for 4 weeks significantly relieved symptoms of osteogenic tumors in Ctsk-CKO mice (Figure 6H and Supplemental Figure 6D).

**Inhibition of mTORC1 signaling prevents tumorigenesis in a xenograft model.** To further investigate the clinical relevance of LKB1 loss with osteogenic sarcoma and the therapeutic effects of rapamycin treatment in human osteosarcoma, we used LKB1 shRNA (shLKB1) lentivirus to knock down LKB1 expression in the human osteosarcoma cell line HOS-MNNG cell, which has been reported to express high levels of LKB1 (24, 41). The knockdown efficiency of LKB1 and hyperactivation of the mTORC1 pathway in shLKB1 lentivirus-infected HOS-MNNG cells were confirmed via Western blot analysis (Figure 7A; see complete unedited blots in the supplemental material). We then injected HOS-MNNG cells that expressed either shEGFP or shLKB1 into nude mice. After tumor establishment, the mice were treated daily with either 4 mg/kg rapamycin or vehicle. As shown in Figure 7, B–D, tumor size was significantly enlarged in the shLKB1 group compared with the shEGFP control group. Histologically, shLKB1 tumors displayed an apparent nuclear variability, increased Ki67 expression, decreased OSX expression, and elevated S6 phosphorylation (Figure 7E). Rapamycin treatment was able to decrease the growth rate and tumor volume in both the shLKB1 group and the shEGFP control group (Figure 7, B–D). Rapamycin treatment decreased cell density, nuclear variability, Ki67 expression, OSX expression, and S6 phosphorylation. Immunohistochemical analysis confirmed the lowered expression of LKB1 in the shLKB1 group compared with that in the shEGFP control (Figure 7E). These data demonstrate that LKB1 knockdown promotes tumor formation of human osteosarcoma cells, while rapamycin inhibits tumor growth in established tumors using human osteosarcoma cell xenografts.

**Discussion**

Our results suggest that Lkb1 deletion in Ctsk−/− periosteal cells caused osteogenic tumor–like phenotype by increasing mTORC1 activity. Previous reports demonstrated that Ptpn11 deficiency in Ctsk−/− cells induced metachondroma with decreased ERK activity and more production of the growth stimulators Ihh and Pthrp (28) (Figure 7F). To further understand why Lkb1-deficient mice developed osteogenic tumor, but not cartilage tumor, we examined expression of pErk in Lkb1−/− deficient Ctsk−/− cells by immunostaining and Western blot and found that Lkb1 deletion had no obvious effect on inhibition of Erk signaling (Supplemental Figure 7, A, B, and C; see complete unedited blots in the supplemental material) and production of Ihh and Pthrp (Supplemental Figure 7D). It has been proven that hypoactivation of Erk signaling in Ctsk+ cells could induce cartilage tumor (28). However, Lkb1 deficiency in Ctsk−/− cells could not inhibit Erk/Ihh signaling and induce cartilage tumor. Our study expanded the definition of Ctsk−/− as not only a progenitor of metachondroma, but also a source of osteosarcoma.

Consistent with the recent publication showing that Ctsk−/− cells can function as periosteal stem cells to mediate intramembranous bone formation (37), our data also identified Ctsk−/− periosteal cells as containing a stem cell population (CD31−CD45−Ter119−CD90.2− 6C3 CD105 CD200−) (36). Deletion of Lkb1 in Ctsk−/− cells leading to osteosarcoma formation demonstrated that Ctsk−/− cells cannot only serve as a physiologic precursor of periosteal osteoblasts, but also as a pathological precursor in osteogenic tumor. Regulation of the cell fate of this periosteal stem cell by deleting transcription factor OSX or tumor-suppressor LKB1 can lead to abnormal cortical architecture or even tumor formation, which shows the importance of understanding the cellular basis of skeletal pathology.

To clarify the role of Lkb1 function in human osteosarcoma, we first searched for genetic mutations in Lkb1 in human osteosarcoma patients. However, genetic mutations in Lkb1 have not yet been commonly found in human osteosarcoma, with the exception of one case report (c.937C>A) (42), which might be restricted by the low incidence rate of the disease and the low availability of samples for sequencing. In addition, allelic loss, Lkb1 promoter hypermethylation, or reduced Lkb1 expression is observed in a wide variety of sporadic cancers (43, 44). The study demonstrated that 41% of osteosarcoma patient loss of Lkb1 protein expression was due to posttranslational regulation by SIRT1 deacetylase, but not due to genetic anomalies or loss of Lkb1 mRNA levels (24), suggesting that decreases in Lkb1 expression could also be important for osteosarcoma formation. Our study has proven that loss of Lkb1 in Ctsk−/− cells can lead to osteosarcoma formation in mice and that Lkb1 deficiency in a human osteosarcoma cell line could accelerate tumor formation, suggesting that further examination of mutations in Lkb1 and/or its upstream genes in human osteosarcoma is warranted.

As a known tumor suppressor, LKB1 is inactivated in a wide range of sporadic cancers, most of which show inactivation of AMPKs and a resulting hyperactivation of mTORC1 signaling (18, 19, 45). Another study used Sleeping Beauty transposon–based somatic forward genetic screening and reported that PI3K/AKT/mTOR signaling was involved in enhancing osteosarcomagenesis (46). Our results also suggest treatment of osteosarcoma by targeting LKB1/AMPK/mTORC1 signaling. The selective mTORC1 inhibitors sirolimus (rapamycin) (47, 48), ridaforolimus (49), and everolimus (50) have been studied in clinical trials for their osteosarcoma treatment potential, showing either complete or partial response in a portion of patients (1). Our mouse model can help with interpreting the mechanism of mTORC1 inhibitors for the treatment of osteosarcoma and adopting a targeted therapy through assessing the genetic mutation, epigenetic modification, and expression levels of the genes that are involved in the LKB1/mTORC1 signaling. The recent accelerated development of techniques for the rapid assessment of both the genetic and epigenetic statuses of tumor biopsies has birthed the concept of personalized medicine. Osteosarcoma presents a challenge for personalized medicine due to the absence of pathognomonic mutations combined with the rarity and
heterogeneity of the disease. This may account for the unsatisfactory results reported by recent trials for targeted therapies. Collaborative multicenter, international, deep-sequencing efforts to study this disease might lead to the discovery of new mutations in osteosarcoma patients in the future (51, 52).

It would be helpful to treat osteosarcoma using a combined therapeutic approach targeting different involved pathways to obtain synergistic effects. Angiogenesis is essential for cancer development and growth, and VEGF is a key mediator of angiogenesis in tumor (53). Previous evidence indicates that LKB1 alterations contribute to cancer progression by modulating VEGF production (54, 55). We examined the expression of VEGF in the tumor region of Ctsk-CKO mice and found increased VEGF production in Ctsk-CKO mice (Supplemental Figure 7, E and F; see complete unedited blots in the supplemental material). It might be rational to study combination therapy using rapamycin and anti-VEGF therapy to treat tumorigenesis in osteosarcoma patients with LKB1 loss.

The fact that deletion of Lkb1 in LysM+ cells does not lead to tumor mass formation within the cortical bone confirms that osteoclasts are not involved in the pathogenesis of Lkb1-related osteosarcomas. Actually, both Ctsk-CKO and LysM-CCKO mice showed increased osteoclast formation (Figure 3, B and C, and Supplemental Figure 7, G and H), and the tumor mass in Ctsk-CKO mice contained a large number of osteoclasts and osteoclast precursors (Figure 3A). These data indicate that Lkb1 might play a role in osteoclastogenese. Our previous study demonstrated that mTORC1 signaling plays a determinative role in osteoclast differentiation, as Raptor deficiency in osteoclasts resulted in increased bone mass with decreased bone resorption (56). It is possible that LKB1 deficiency in osteoclasts could also lead to mTORC1 activation. Further study is required to demonstrate the role of Lkb1 in osteoclastogenesis.

Methods

Animals. Lkb1fl/fl mice were obtained as previously described (18, 57). Raptofrflop mice bearing loxP sites flanking exon 6 of the Raptor gene, were from the Jackson Laboratory (catalog 013188). Ctsk-Cre mice were provided by S. Kato (University of Tokyo, Tokyo, Japan) (26). LysM-Cre mice were provided by Ira Tabas (Columbia University, New York, New York, USA) (33). Rosa26-lox-pTomato-stop-lox-pGFP (Rosa26-lox/I/mg) reporter mice and Rosa26-lox-stop-lox-pI/dTomato (Rosa26-Ai9) reporter mice were obtained as previously described (refs. 34, 35, respectively). All utilized mice were maintained on a C57BL/6 background, and sex-matched littermate controls were used for all analyses. Both male and female mice were analyzed. All animals were housed in specific pathogen-free conditions.

Radiographic assessment. For x-ray image analysis, mice were euthanized with CO2 followed by removal of skin and internal organs. The skeletons were then fixed in 70% ethanol and analyzed via whole-body x-ray using an Eagle III Microspot X-ray Fluorescence (Exida Inc., USA) instrument and a Faxitron SR radiograph digital imaging system.

For μCT analysis, tibiae and vertebrae isolated from age- and sex-matched mice were fixed in 70% ethanol and scanned using a SkyScan 1176 (Bruker Biospin) at a 20 μm resolution for qualitative analysis or at a 10 μm resolution for quantitative analysis. 3D images were reconstructed using a fixed threshold. The percentages of trabecular BV/TV and cortical thickness (Ct.Th) were calculated for the cortical bone of diaphysis of the distal femur.

Histology analysis. For dynamic histomorphometry, 4-week-old mice received intraperitoneal injections of 20 mg/kg body weight calcine (MilliporeSigma, CO875) and 25 mg/kg body weight alizarin red (MilliporeSigma, A5533) with an interval of 4 days. The mice were euthanized with CO2 at 3 days after alizarin red injection. Bone MAR and BFR were measured as previously described (58).

For undecalcified bone section, tibiae were fixed in 4% paraformaldehyde (PFA) for 48 hours at 4°C and dehydrated in a gradient of ethanol and acetic acid, followed by resin embedding. The tibiae were then cut into sections of 4 μm thickness using a Leica RM2265 microtome. Calcium deposits in the bone tissue were visualized by von Kossa staining using 4% silver nitrate followed by 5% sodium thiosulfate and Van Gieson’s counterstaining.

For paraffin sectioning, femurs and tibiae were fixed in 4% PFA for 48 hours at 4°C and decalcified in 15% EDTA. Specimens were dehydrated using a gradient ethanol and xylene and embedded with paraffin, and sections of 8 μm thickness were cut using a Leica RM2235 microtome. Sections were dewaxed and rehydrated and then stained with H&E and SO. TRAP (MilliporeSigma, S387A-1KIT) staining was performed according to the manufacturer’s instructions.

For frozen sectioning, freshly dissected tibiae were fixed in 4% PFA for 48 hours at 4°C, decalcified in 15% EDTA, and dehydrated in 30°C sucrose for 48 hours. The tissue samples were then embedded with OCT (Tissue-Tek, 4583), and sections of 8 μm thickness were cut using a Leica CM3050S cryostat.

Immunohistochemistry and immunofluorescence. For immunohistochemical staining, the paraffin sections were first dewaxed and rehydrated. Antigen retrieval was performed either with protease K at 37°C for 30 minutes or with citrate buffer solution (pH 6.0) at 95°C for 15 minutes according to the specific instructions for the primary antibody. After blocking and permeabilization with 3% BSA and 0.2% Triton-X 100 in PBS at room temperature for 45 minutes, the sections were incubated with primary antibodies, including rabbit anti-Ki67 (Leica Novocastra, catalog NCL-Ki67p, 1:500), rabbit anti-OSX (Santa Cruz Biotechnology Inc., catalog sc-133871, 1:400), rabbit anti-p-S6 (Cell Signaling Technology, catalog 4858, 1:400), and rabbit anti-p-4E-BP1 (Cell Signaling Technology, catalog 2855, 1:400) overnight at 4°C. After washing, corresponding biotinylated secondary antibodies were incubated for 45 minutes at room temperature using either a VECTASTAIN ABC Kit (Vector Labs, PK-6100) or a Polink-2 Plus Polymer HRP Detection System (ZSGB-BIO, PV9004). DAB (Vector Labs, SK-4100) was used as substrate. The nuclei were counterstained using hematoxylin, and sections were dehydrated and mounted using neutral balsam.

For immunofluorescence staining, frozen sections were air-dried and rehydrated with PBS and then blocked and permeabilized with 3% BSA and 0.2% Triton-X 100 in PBS at room temperature for 45 minutes. Sections were probed with primary antibodies against rabbit anti-LKB1 (Santa Cruz Biotechnology Inc., catalog sc-28788, 1:300), mouse anti-PCNA (Santa Cruz Biotechnology Inc., catalog sc-28788, 1:300), goat anti-OPN (R&D, catalog AF808, 1:500), rabbit anti-OSX (Santa Cruz Biotechnology Inc., catalog sc-133871, 1:400), rat anti-CD44 (Santa Cruz Biotechnology Inc., catalog sc-18849, 1:300), rabbit anti-Ki67 (Santa Cruz Biotechnology Inc., catalog sc-133871, 1:300), rabbit anti-perilipin A/B (MilliporeSigma, catalog P1873, 1:1000), and rabbit anti-CD44 (Santa Cruz Biotechnology Inc., catalog sc-18849, 1:300), and rabbit anti-VEGF (Santa Cruz Biotechnology Inc., catalog sc-18849, 1:300) were applied to the sections.
rabbit anti-laminin A/B (MilliporeSigma, catalog L9393, 1:1000), rat anti-CD31 (Abcam, catalog ab7388, 1:500), and rabbit anti-COLIA1 (Rockland, catalog RK-600-401-103, 1:200) overnight at 4°C. Fluorescence-labeling secondary antibodies including donkey anti-rabbit Alexa Fluor 488 (Molecular Probes, catalog A21206, 1:1000), donkey anti-goat Alexa Fluor 488 (Molecular Probes, catalog A11055, 1:1000), donkey anti-rat Alexa Fluor 488 (Molecular Probes, catalog A21208, 1:1000), and donkey anti-mouse Alexa Fluor 488 (Molecular Probes, catalog A21202, 1:1000) were incubated for 1 hour at room temperature after washing. Nuclei were counterstained with DAPI (MilliporeSigma, D9542). Sections were mounted using fluorescence mounting medium (Dako, S3023).

**Total RNA preparation and quantitative RT-PCR analysis.** Total RNA was extracted from cortical bone ground in liquid nitrogen using TRIzol (MilliporeSigma, T9424), following the instructions of the manufacturer. An aliquot of 500 ng total RNA was reverse-transcribed to cDNA using TaKaRa PrimeScript Reverse Transcriptase (TaKaRa, RR037A). Quantitative PCR (qPCR) was performed using a SYBR green mixture (Takara) and a Bio-Rad CFX96 Real-Time PCR Detection System (Bio-Rad Laboratories). Primers used for specific transcripts are listed in Supplemental Table I.

**Isolation and culture of cortical bone cells.** Femurs and tibiae were thoroughly cleaned to remove all soft tissues, and the epiphysis and metaphysis were then removed. The BM was flushed out with D-PBS containing 6.5 mM Na₂CO₃, 18.5 mM NaHCO₃, 2 mM MgCl₂, and 1 mg/ml heparin (Corning) for 3 days. Cells were then fixed and stained with 2 mg/ml of either alizarin red S (not used to determine the chondrocyte differentiation ability. Sorted Ctsk-Ai9 cortical bone cells (5 × 10⁶ cells/ml) were seeded as a 10 μl micromass drop in a culture well in a 24-well plate and incubated at 5% CO₂ and 37°C for 2 hours to allow cell attachment. Then, 1 ml of chondrocyte induction medium (10% MEM containing 10% FBS, 1% ITS [Caygen, ITS-S-10201-10], 10 ng/ml TGF-β3 [Peprotech, 100-36E], 100 nM dexamethasone [MilliporeSigma, D1756], 1 mM sodium pyruvate [MilliporeSigma, 25-000-CIR], 40 μg/ml proline [MilliporeSigma, P5607], 50 μg/ml l-ascorbic acid 2-phosphate [MilliporeSigma, A8960], and 1% penicillin/streptomycin) was added and incubated for 4 days. The micromass was acidic with 0.1 N HCl and stained with 1% alcan blue (MilliporeSigma, A5268).

**Adipocyte differentiation, 6 × 10⁶ sorted Ctsk-Ai9 cortical bone cells were plated in a well in a 96-well plate and cultured with adipocyte induction medium (10% MEM containing 10% FBS, 50 mM dexamethasone [MilliporeSigma, D1756], 100 nM rosiglitazone [MilliporeSigma, R2408], 300 nM 3-isobutyl-1-methylxanthine (BMMX) [MilliporeSigma, E5879], 10 mg/ml insulin [MilliporeSigma, 91077c], and 1% penicillin/streptomycin) for 1 day, followed by adipocyte maintenance medium (10% MEM containing 10% FBS, 10 mg/ml insulin, and 1% penicillin/streptomycin) for 3 days. Cells were then fixed and stained with 2 mg/ml of either oil red O (MilliporeSigma, O1391) or Bodipy FL (Invitrogen).

**Osteoclast differentiation, 3 × 10⁶ cells/ml nonadherent BM cells isolated from the femurs and tibiae of mice were seeded in BMM induction medium (10% MEM containing 10% FBS, 10 ng/ml M-CSF, and 1% penicillin/streptomycin) in a 96-well plate for 3 days, then in osteoclast induction medium (10% MEM containing 10% FBS, 20 ng/ml M-CSF,
150 ng/ml RANKL, and 1% penicillin/streptomycin) for 4 days. The cultured supernatant was harvested for detection of TRAP activity following the method previously described (56). TRAP staining of the cell was performed using a TRAP staining kit (MilliporeSigma, S387A-1KIT) following manufacturer’s instructions.

**Rapamycin treatment.** Rapamycin (Selleck, S1039) treatment was conducted in male and female littermates of Ctsk-Ctrl and Ctsk-CKO mice. Rapamycin was dissolved in 2% DMSO and 5% TWEEN-80 in water following the manufacturer’s instructions. Rapamycin and its solvent control were given intraperitoneally at a dose of either 4 mg/kg twice per week beginning at 2 weeks or at 4 mg/kg daily beginning at 16 weeks to an age of 20 weeks. X-ray images of the whole skeleton and H&E staining of the tibiae were obtained to estimate the overall effect on tumor growth.

**Xenograft tumors and drug therapy in nude mice.** Four-week-old female nude mice were subcutaneously injected (close to the groin) with 1 × 10^6 HOS-MNNG cells or 1 × 10^6 total periosteum-derived cells isolated from Ctsk-Ctrl; Rosa-Ai9 and Ctsk-CKO; Rosa-Ai9 mice in 0.1 ml PBS. For drug therapy, as soon as the tumors reached 100 mm³, nude mice were randomly assigned to either vehicle or rapamycin (4 mg/kg) treatment groups and intraperitoneally injected daily. Tumor volume was measured using digital calipers every 2 days. Tumor volume was calculated by the formula: volume = length × (width)^2/2. Data points were expressed as an average tumor volume.

**Statistics.** Data were generated from independently obtained data sets and were expressed as mean ± SEM. Statistical significance was determined using 2-tailed t tests or 2-way ANOVA. P values below 0.05 were considered to indicate statistically significant differences. GraphPad Prism 6 was used for all statistical analyses.

**Study approval.** Animal experiments were approved and conducted in full accordance with protocols that were approved by the Institutional Animal Care and Research Advisory Committee of Shanghai Institute of Biochemistry and Cell Biology.

**Author contributions**

WZ and YH designed experiments and interpreted results. YH carried out most of the experimental work with the help of HJ, WX, and QD. HF, JS, and YY helped with animal experiments. XL, Z Wang, AH, QB, and TK helped with histology analysis. Z Wei helped with μCT analysis. YH and WZ analyzed the data and wrote the manuscript. All authors discussed and commented on the manuscript.

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Address correspondence to: Weiguo Zou, State Key Laboratory of Cell Biology, CAS Center for Excellence in Molecular Cell Sciences, Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences, 320 YueYang Road, Shanghai 200031, China. Phone: 86.21.54921320; Email: zouwg94@sibcb.ac.cn. Or to Tiebang Kang, State Key Laboratory of Oncology in South China, Sun Yat-sen University Cancer Center, 651 Dongfeng Road East, Guangzhou, China, 510060. Phone: 86.20.87343183; E-mail: kangthb@sysucc.org.cn.

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