### Original Article

# Treatment with soluble bone morphogenetic protein type 1A receptor fusion protein alleviates irradiation-induced bone loss in mice through increased bone formation and reduced bone resorption

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Abstract: An increased fracture risk is often observed in cancer patients undergoing radiotherapy (RT), particularly at sites within the field of radiation. Therefore, the development of appropriate therapeutic options to prevent RT-induced bone loss is urgently needed. A soluble form of the BMP receptor type 1A fusion protein (mBMPR1A-mFc) serves as an antagonist to endogenous BMPR1A. Previous studies have shown that mBMPR1A-mFc treatment increases bone mass in both ovary-intact and ovariectomized via promoting osteoblastic bone formation and inhibiting osteoclastic bone resorption. The present study was designed to investigate whether mBMPR1A-mFc administration prevents radiation-induced bone deterioration in mice. We constructed an animal model of radiation-induced osteoporosis by exposure to a 2-Gy dose of X-rays. Micro-CT, histomorphometric, bone-turnover, and mechanical analyses showed that mBMPR1A-mFc administration prevented trabecular microarchitecture deterioration after RT because of a marked increase in bone formation and a decrease in bone resorption. Mechanistic studies indicated that mBMPR1A-mFc administration promoted osteoblastogenesis by activating Wnt/Lrp5/β-catenin signaling while decreasing osteoclastogenesis by inhibiting the RANKL/RANK/OPG pathway. Our novel findings provide solid evidence for the application of mBMPR1A-mFc as a therapeutic treatment for radiation-induced osteoporosis.

**Keywords:** Murine BMP receptor type 1A fusion protein (mBMPR1A-mFc), irradiation-induced osteoporosis, Wnt/Lrp5/β-catenin, RANK/RANKL/OPG

#### Introduction

Ionizing radiation has been used for nearly a century in cancer patients, alone or in combination with chemotherapy [1, 2], and has been proven to be an effective and indispensable treatment modality [2]. Specifically, ionizing radiation damages tumor DNA and induces tumor cell death. The efficacy of radiotherapy (RT), however, comes at the expense of normal tissue injury [3-5]. In vitro and in vivo findings have demonstrated that radiation reduces

osteoblast proliferation and differentiation, induces cell cycle arrest, decreases collagen production, damages or kills osteoblasts, and inhibits bone formation [6, 7]. The loss of bone density, as well as the increased risk of fracture, remains a problematic side effect of RT [8-10].

The area selected for RT often includes the whole tumor and the healthy neighboring tissue. Previous work has demonstrated that a typical treatment regimen of RT for gynecologi-

cal cancers consists of an administration of up to 60 Gy fractionated over a 6-week treatment span [4, 11]. Healthy neighboring tissue, including bone, absorbs approximately 30 Gy [4, 12]. Various strategies have been developed to attenuate the deleterious effect of RT on the nearby tissues, such as precise treatment planning and delivery [13]. Despite these measures, the incidence of pathological fracture in the area selected for RT remains frequent and increases with time in cancer survivors [8, 9, 14-18]. Previous clinical studies have reported that hip fracture rates are up to 20 times higher in breast cancer patients who received RT compared to those of patients without RT [19, 20]. Patients receiving RT for pelvic tumors have an increased risk of hip fracture compared with that of tumor patients undergoing chemotherapy or surgery alone [8, 9, 15-18]. Additionally, a dose-dependent relationship between rib fracture incidence and RT has been observed in breast tumor patients [14].

Anti-resorptive drugs, such as zoledronic acid and risedronate, are clinically used to treat this deleterious effect [21, 22]. Despite their effectiveness, most of these agents have some limitations and side effects, including thromboembolism and esophageal irritation [23]. Therefore, searching for new agents to prevent or treat RT-induced bone loss is of crucial importance.

Bone morphogenetic proteins (BMPs) are an important member of the transforming growth factor-β (TGF-β) gene superfamily. BMPs control cell growth, differentiation, and function [24] and play a key role in regulating physiological functions. BMPs also act as major regulators of bone homeostasis [25]. BMP signaling is mediated by the activation of type-I and type-II receptors. Upon ligand binding, a conserved glycine- and serine-rich domain between the transmembrane and kinase domains in the type-I receptor is phosphorylated and activated. Among the three type-I receptors that recognize BMPs (BMPR1A or ALK3, BMPR1B or ALK6, and ACVRI or ALK2), BMPR1A (or ALK3) is the most effective receptor for transducing canonical BMP ligands BMP2 [26] and BMP4 [27], which is highly expressed in the bone [28].

Previous studies have reported that mice with a postnatal conditional deletion of BMPR1A experience a significant increase in bone mass [29, 30], which is associated with a reduction of the Wnt antagonists, sclerostin (SOST) and dickkopf-1 (Dkk1) [31], as well as a decrease in the receptor activator of the NF-kB ligand (RANKL) and an increase in osteoprotegerin (OPG) expression [29-34]. Additionally, a postnatal conditional BMPR1A deletion in osteoclasts causes an obviously increased bone mass [33]. All these *in vivo* results strongly suggest that inhibition of BMPR1A signaling provides therapeutic benefits for the treatment of osteoporosis.

A soluble murine BMPR1A-fusion protein (mBMPR1A-mFc) acts as an antagonist to endogenous BMPR1A, consisting of the extracellular domain of murine BMPR1A and the Fc portion of murine IgG2a. A previous study showed that mBMPR1A-mFc binds to BMP2/4 specifically and with high affinity [25], which in turn reduces Dkk1 expression in osteoblasts, activates Wnt signaling, and promotes osteoblastic bone formation [35]. Furthermore, mB-MPR1A-mFc treatment markedly decreased RANKL expression in osteoblasts and inhibited bone resorption. Interestingly, treatment of ovary-intact and ovariectomized mice with mBMPR1A-mFc results in improved bone microarchitecture and strength, as well as increased bone mass, via promoting bone formation and inhibiting bone resorption [25]. These findings suggest that inhibition of BMPR1A signaling with mBMPR1A-mFc may have a positive therapeutic benefit for the treatment of pathological bone loss. Little is known, however, about its therapeutic effects on radiation-induced osteoporosis.

In this study, a focal radiation mouse model was used to evaluate the role of mBMPR1A-mFc in radiation-induced osteoporosis. Our data suggest that mBMPR1A-mFc may represent a novel therapeutic agent to treat radiation-induced osteoporosis.

#### Material and methods

Animals, radiation therapy, and drug administration

The Institutional Animal Care and Use Committee of Xuzhou Medical University approved all study procedures. Fifteen-week-old female C57BL/6j mice were purchased from the Experimental Animal Center of Nanjing Medical

University (Nanjing, China) and allowed to acclimate for 5 weeks, until the age of 20 weeks (n=30); commercial rodent diet and water were given ad libitum. At the start of the study, body masses were measured and used to randomize the mice between groups. Two groups were designated to receive irradiation (n=20 total). Under anesthesia (2% isoflurane), mice were irradiated. A small animal image-guided irradiation system (Precision X-Ray, North Branford, CT, USA) was used to precisely irradiate the mid-shaft of the left femur at a single dose of 2 Gy on day 1. This system offers integrated precision irradiation with cone-beam CT guidance and treatment planning systems with dose calculation tools based on the Monte Carlo methods. In brief, a single field of 140-kVp X-rays to a single-fraction mid-plane dose of 2 Gy at a rate of 1.36 Gy/min in the prone position (Philips Medical Systems, Bothell, WA, USA), as previously reported [21]. Radiation was delivered in a circular collimated field with a diameter of 5 mm at a rate of 0.23 Gy/s. A single 2-Gy dose was used in the present study to simulate a clinical radiotherapy setting consistent with that of previous studies on radiationinduced bone loss [36, 37]. One of the irradiated groups was selected for subcutaneous injections of mBMPR1A-mFc (4.5 mg/kg; Acceleron Pharma, Cambridge, MA, USA) twice a week starting immediately following the irradiation procedure (RT + mBMPR1A-mFc; n= 10). Equivalent volumes of PBS were injected as a placebo into the remaining 2-Gy-irradiated (RT + VEH; n=10) mice. One group was exposed to a sham radiation procedure (Control, n=10). In the sham procedure, anesthetized control animals were placed inside the inactive X-ray unit for the same amount of time as the radiated mice. To assess new bone formation, calcein (20 mg/kg) was injected subcutaneously into each mouse at 7 days and 2 days before euthanization. All chemicals were purchased from Sigma-Aldrich (St. Louis, MO, USA) unless indicated otherwise.

#### Tissue collection

At 4 weeks following the initial radiation exposure, all animals were euthanized. Next, blood was isolated by cardiac puncture and was centrifuged at 3000 rpm for 10 min to separate the serum from the blood cells, rapidly frozen in liquid nitrogen, and stored at -80°C until use.

Both the hind limbs and the vertebral column were collected for measurements. Adherent soft tissue was cleaned off, and the tibiae and femora were fixed in a PLP fixative (2% paraformaldehyde containing 0.075-M lysine and 0.01-M sodium periodate) at 4°C. The next day, the bones were placed in 70% ethanol.

#### Serum chemistry

The serum samples were evaluated using ELISA kits for alkaline phosphatase (ALP) (Sigma, St. Louis, MO, USA), procollagen 1 N-terminal peptide (P1NP) (Immunodiagnostic Systems, Fountain Hills, AZ, USA), C-telopeptide fragments of collagen type 1 (CTX-1) (Immunodiagnostic Systems Inc., Gaithersburg, MD, USA), and tartrate-resistant acid phosphatase 5b (TRAP5b) (Immunodiagnostic Systems, London, UK), following the protocols recommended by the manufacturers.

#### Dual-energy X-ray absorptiometry and micro-CT

Areal BMD (aBMD) was measured by a small animal dual-energy X-ray absorptiometer (DXA) (Lunar Corp., Madison, WI, USA). The bone architecture of the distal femur was analyzed using a high-resolution micro-CT (GE Healthcare, Madison, WI, USA) with isotropic voxels of 9 µm/side, as described previously [38]. The bone histomorphometric parameters for the distal metaphysis of the femur were measured as described in the report of the American Society of Bone and Mineral Research (AS-BMR) Histomorphometry Nomenclature Committee [39]. Both trabecular and cortical bone parameters-including trabecular bone volume/ total volume (BV/TV, %), connectivity density (Conn.D, 1/mm<sup>3</sup>), trabecular number (Tb.N, 1/ mm<sup>3</sup>), trabecular thickness (Tb.Th, µm), trabecular separation (Tb.Sp, µm), and structure model index (SMI)-were determined. The cortical bone parameters, including cortical area (Ct.Ar, mm<sup>2</sup>) and cortical thickness (Ct.Th, µm), were also quantified.

#### Three-point bending test

The femoral shaft (n=10, for each group) was subjected to a three-point bending test to detect the whole-bone structural properties, as described previously [40], using a standard mechanical testing device (Bose ElectroForce 3220; Bose Corp., Eden Prairie, MN, USA). The

parameters of structural properties-including maximum load (N), yield load (N), yield displacement ( $\mu$ m), stiffness (N/mm), energy absorption (N × mm), and ultimate displacement ( $\mu$ m)were determined from the load-displacement curve.

#### Nanoindentation

The distal femur was mounted within the Agilent G200 nanoindentation system (Agilent Technologies Inc., Chandler, AZ, USA). The force-displacement curve was automatically recorded, and the trabecular bone elastic modulus (GPa) and contact hardness (GPa) were calculated according to a protocol described previously [40].

#### Bone histomorphometric studies

Static and dynamic histomorphometries were conducted as described previously [41, 42]. In brief, the femurs were decalcified in an EDTA and glycerol solution for 14 days. The decalcified femurs were dehydrated and embedded in paraffin and 5-µm sections were then cut on a rotary microtome. The sections were stained with hematoxylin and eosin (HE), total collagen, toluidine blue, von Kossa, ALP, and tartrateresistant acid phosphatase (TRAP). The static parameters of bone formation and resorption were measured using an Olympus microscope with an OsteoMeasure system (Osteometrics). As the static parameters, Tb.BV/TV (%), total collagen positive areas/tissue area (%), von Kossa positive area/tissue area (%), number of OBs per bone surface (N.Ob/BS, N/mm), percentage of bone surfaces covered by OBs (Ob.S/BS, %), ALP-positive areas/tissue area (%), number of osteoclasts per bone surface (N.Oc/BS, N/mm), eroded bone surface (ES/ BS, %), and bone surface occupied by osteoclasts (Oc.S/BS, %) were measured.

For fluorochrome-based determination of the rates of bone formation by dynamic histomorphometry, 6-µm frozen sections embedded in methyl methacrylate plastic were cut using a Leica RM2265 rotary microtome (Leica, Heidelberg, Germany). Calcein was visualized by fluorescent microscopy, and the distance between labeled layers was used as a measure of the rate of bone formation as determined by the morphometry software. Mineralizing surface per bone surface (MS/BS, %) and the mineral apposition rate (MAR, mm/day) were mea-

sured and used to calculate the bone formation rate (BFR, mm³/mm²/day), as described previously [42]. The terminology and units used were those recommended by the Histomorphometry Nomenclature Committee of the American Society for Bone and Mineral Research [43].

#### Quantitative PCR

Total RNA was isolated from tibia with Trizol reagent (Invitrogen, Carlsbad, CA, USA) according to the manufacturer's protocol. Real-time RT-PCR was performed as described previously [42, 44]. The primers used for the real-time PCR were purchased commercially. All PCRs were performed in triplicate, and the primer sequences used for PCR are shown in **Table 1**.

#### Western blot analysis

Proteins were isolated from the distal tibiae and were measured with a protein assay kit (Bio-Rad, Mississauga, ON, Canada). Protein samples (15  $\mu$ g) were separated by SDS-PAGE and transferred to nitrocellulose membranes. Membranes were blotted with primary antibodies against  $\beta$ -catenin (ab16051, Abcam, Cambridge, MA, USA), and GAPDH (ab8245, Abcam, Cambridge, MA, USA) was used as the loading control. Immunoblotting was carried out as described previously [41]. Bands were visualized and quantitated by ScionImage Beta 4.02 (Scion Corporation, Frederick, MD, USA).

#### Statistical analysis

Data are expressed as the mean  $\pm$  standard error of the mean. All statistical comparisons were conducted using one-way analysis of variance and a Newman-Keuls post-hoc test; the threshold for significance for all tests was set at a 5% probability of a type-I error (P=0.05). Statistical calculations were performed using Prism 4.0c (GraphPad Software, La Jolla, CA, USA).

#### Results

mBMPR1A-Fc treatment prevents radiationinduced bone mass loss

Following RT, the aBMD values of the whole body (Figure 1D), lumbar spine (Figure 1C), distal femoral metaphysis (Figure 1A), and proximal tibial metaphysis (Figure 1B) were obvi-

Table 1. The primer sequence for gRT-PCR

Gene         Primer         Primer sequence (5'-3')           ALP         F         CCTAGACACAAGCACTAACACTA           R         GTCAGTTCAGTTTCCAATTC           RUNX2         F         CTGTGGTTACCGTCATGGCC           R         GGAGCTCGGCGGAGTAGTTC           OCN         F         GCCTTCATGTCCAAGCAGA           R         GCGCCGGAGTTTTCACTA           Osterix         F         CATCTACAGCGGTTGTGC           R         AAGCCTTTGCCCACCTACTTTT           Col-1A         F         CCCTACTCAGCCGTCTGTGC           R         GGGTTCGGGCTGATGTACC           TRAP         F         CACTCCCACCCTGAGATTGC           RAP         F         CACTCCACCCTGAGATTAC           TCTK         F         CTTCCAATCAGTGAAGAGAA           R         TCTTCCAATCAGTGCAGAAAA           R         TCTTCAGAGCCTAGAGAAAAAAAAAAAAAAAAAAAAAAA	Table 1. The primer sequence for qRT-PCR			
R GTCAGTCAGGTTGTTCCGATTC  RUNX2 F CTGTGGTTACCGTCATGGCC R GGAGCTCGGCGGAGTAGTTC  OCN F GCCTTCATGTCCAAGCAGGA R GCGCCGGAGTCTGTTCACTA  Osterix F CATCTAACAGGAGGATTTTGGTTTG R AAGCCTTTGCCCACCTACTTTT  COl-1A F CCCTACTCAGCCGTCTGTGC R GGGTTCGGCGTGTATGTACC  TRAP F CACTCCACCCTGAGATTTGT R CCCCAGAGACATGATGACC  TRAP F CACTCCACCCTGAGATTTGT R CCCCAGAGACATGATGAGACA R TCTTCAGGCGTTTCTCGTTC  NFATC1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GGGACCTCGGCTGTC ACCCCAGCATGCACCCAGCATGACCAGA  ATP6VOd2 F AAGCCTTTGACCTTTAACCT  Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG  AXin2 F CAGTGTGAAGGCCAATGA R TGCCCTTTTTCAACCG  AXin2 F CAGTGTGAAGGCCAATGA R TGCCTTTTTTAGGTC  Nkd2 F AATTTCAGTCCAAGCACCC R CGGGACTCTCTCTCTTTGGA R TGCCCTTTTTTTAGGTC  TagIn F CAGCCCAGACACCGAAGCTA AGGCTTGGTCGTTTTTTGGAC  TGFβ-3 F AGGCTTGGTCGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	Gene	Primer	Primer sequence (5'-3')	
RUNX2 F CTGTGGTTACCGTCATGGCC R GGAGCTCGGCGGAGTAGTTC OCN F GCCTTCATGTCCAAGCAGGA R GCGCCGGAGTCTGTTCACTA Osterix F CATCTAACAGGAGGATTTTGGTTTG R AAGCCTTTGCCCACCCTCGTTTT COl-1A F CCCTACTCAGCCGTCTGTGC R GGGTTCGGCTGATGTACC TRAP F CACTCCACCCTGAGATTTGT R CCCCAGAGACATGATGAC CTSK F CTTCCAATACGTGCAGCAGA R TCTTCAGGCGTTTCTCGTTC NFATC1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GTGATGACCCCAGCATGCACCAGTCACAG ATP6VOd2 F AAGCCTTTGACCTTTTCAACCTGACAGA ATP6VOd2 F CAGTGCGAGCAATAA R CCTTCTGTCTTTTCAACCTGACCAGACACAGACACAGCACAGTCACCAGTCACAGA ANN F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTTCCAACCG AXIN2 F CAGTGGAAGAGCCAATGAC CYr61 F GTGAAGTGCGTCCTTGTGGA R TGCCCTTTTTTAGGCTCTGT Nkd2 F AATTTCAGTCCAAGCACCC R CGGGACTCTCTCTCTCTTGC TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC TGFβ-3 F AGGCTTGGTCGTTTTGTGGAC TCAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTTGTGGAC TCAGCCAGACACCGAAGCTA R AGGCTTGGTCGTTTTGTGGAC TCAGCCAGACACCGAAGCTA R AGGCTTGGTCGTTTTGTGGAC TCAGCCAGAACTCTACACAGCCC R CGGACATCCTCTCCCTTTCC TWISt1 F TCGACTTTCTGTGCACAGTC TWISt1 F TCGACTTCGTGTACCAGC C CCTTCGGAGTACCAGC C CCTTCGGAGTACCAGC TCF C CAGCCAGAAGTTACAGC C CTGCGAGAGTCAACTCTACA R AGCTCCGCGCTCTCCAT TWISt1 F TCGACTTCCTGTACCAGC C C CCTGCGAGAGTACCAGC C CCTGCGAGAGTCACTCTACA R AGCTCCGCGCTCTCCAT TWISt1 F TCGACTTCCTGTACCAGC C CCTGCGAGAGTCACTCTACA C CCTGCGAGAGTGAAGTTCGTG TCF C CAGCTCCCCCATACTGTGAG R TGCTGCTTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTAACCTCT R ACACAGAATGGGCTAACCTCT R ACACAGAATGGGCTAACCTCT C CACCCCCATACTGTGAG R TGCTGCTTATTTCCGCAGGAA  C CACCACTGGCCAAACGGGTAG C CACCACTGGCCAAACGGGTAG C CACCACTGGCCAAACGGGTAG C CACCACTGGCCAAACGGGTAG C CACCACTGGCCAAACGGTAGTGC C CACCACTGGCCAAACGGGTAG C CACCACTGGCCAAACGGTAGTGCC C CACACGAACTGCACACTT	ALP	F	CCTAGACACAAGCACTAACACTA	
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R AAGCCTTTGCCCACCTACTTTT Col-1A F CCCTACTCAGCCGTCTGTGC R GGGTTCGGGCTGATGTACC TRAP F CACTCCCACCCTGAGATTTGT R CCCCAGAGACATGATGAAGTCA CTSK F CTTCCAATACGTGCAGCAGA R TCTTCAGGGCTTTCTCGTTC NFATC1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GCCAGCACTGACACCAGTCACCAGTCACAG ATP6VOd2 F AAGCCTTTGACGCTGT R GCCAGCACATTCATCTGTACC Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCTTTTCCAACCG Axin2 F CAGTGGAAGGCCAATGAC Cyr61 F GTGAAGGCCAATGAC R TGGCTTTTTAGGCTGCT R GCCAGCACATTCATCTGTACC  Nkd2 F AATTTCAGTCCAAGCAGGA R TGCCCTTTTTTAGGCTGCT  Tagln F CAGCCCAGACACCGAAGCC R CGGGACTCTCTCTCTCTTTGC Tagln F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTTGTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTTGTTGTGGAC TGFβ-3 F AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGCCTCGCCCATACTCTACA R AGCTTCGCGGCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCCC R CCGGCAGCACCCGAAGTT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG Wisp1 F ATGCCTGGTGTACCAGC R CCTGCCAGACACCGAGAA  Wht3a F GGCTCCCCCATACTTGTGAG R TGCTGTCTATATCCGCAGGAA  Wht3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTAGC B-Catenin F CCTAGCTGGTGGACTGC CTGCAGAATGGGCCAGAA R CACCACTGGCCAGAATGATGA  R CACCACTGGCCAGAACGGAA R CACCACTGGCCAGAACGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA R CCTGCAGGAGTCAACTGTGTAC R CCTGCAGGAGTCAACTGTCTACA R CCTGCAGGAGTCAACGGTAG R TGAGTCCAGCACACGAACGGAA R CACCACTGGCCAGAATGATGA R CCTGCCCCATACTGTGAG R TGCTGTCTATATCCCGAGGAA R CACCACTGGCCAGAATGATGA R CCTGCCCCATACTGTGAG R TGCTGTCTATATCCCGAGCACA R CACCACTGGCCAGAATGATGA R CACCACTGGCCAGAATGATGA CCTGCAGGAGTCAGGTAGGTGCC CCTGCAGGAGTCAGGTAGGTGCC CCGGTCTCCTTCTTCCTGTACCAGG R TGAGTCCAGGAACTGCACCACACG R TGAGTCAGGCCAAACGGGTAG R TGCTGCTCTCTGTTCCTGTA R CCTGCAGGAGTCAGGTAGTGTGTC COPG F CACCACGAACTGCAGCACATT		R	GCGCCGGAGTCTGTTCACTA	
Col-1A	Osterix	F	CATCTAACAGGAGGATTTTGGTTTG	
R GGGTTCGGGCTGATGTACC  TRAP F CACTCCCACCCTGAGATTTGT R CCCCAGAGACATGATGAAGTCA  CTSK F CTTCCAATACGTGCAGCAGA R TCTTCAGGGCTTTCTCGTTC  NFATC1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GTGATGACCCCAGCATGCACCAGTCACAG  ATP6VOd2 F AAGCCTTTGACGCTGT R GCCAGCACATTCATCTGTACC  Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG  Axin2 F CAGTGTGAAGGCCAATGAC R TGCCTTTTTAGGCTGC R TGGGTTCTCGGAAAATGAGG  Cyr61 F GTGAAGTGCTCCTTGTGGA R TGCCCTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCAGCC R CGGGACTCTCTCTCTCTTTCC  TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGCCTGGTCGTTACACA R AGCCTGGTCCAACTCACA R AGCCTGGTCCAACTCACA R AGCCTCGCGCTCCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGACTGC  β-catenin F CCTAGCTGGTGACCAGC R TGCTGTCTATATCCGCAGGAA  R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGGCCAAACGGTAG R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTGTTCCTGTA  R CCTGCAGGAGTCAGCACATT  OPG F CACACGAACTGCAGCACATT		R	AAGCCTTTGCCCACCTACTTTT	
TRAP  F CACTCCCACCCTGAGATTTGT  R CCCCAGAGACATGATGAAGTCA  CTSK F CTTCCAATACGTGCAGCAGA  R TCTTCAGGGCTTTCTCGTTC  NFATc1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC  R GTGATGACCCCAGCATGCACCAGTCACAG  ATP6vOd2 F AAGCCTTTGACGCTGT  R GCCAGCACATTCATCTGTACC  Ahr F GGGACCTCGGGTGACAATAA  R CCTCTGTCCTTTTCCAACCG  Axin2 F CAGTGGAAGGCCAATGGC  Cyr61 F GTGAAGTGCTCCTTGTGGA  R TGCCCTTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCACCCC  R CGGGACTCTCTCTCTCTTGC  Tagln F CAGCCCAGACACCGAAGCTA  R AGGCTTGGTCGTTTTGTGAC  TGFβ-3 F AGGCTTGGTCGTTTTGTGAC  R AGGCTGGTTTGTGGAC  R AGGCTGGTCGTTTGTGGAC  R AGCTCCGCGCTCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT  R CCATCTTGGAGTCCAGCTCG  Wisp1 F ATGCCTGGCTGTGTACCAGC  R CCTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG  R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG  R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCTCTCTCT  R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGGACTGCAGAA  R CACCACTGGCCAGAATGATGA  R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATTGCCGACCAG  R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA  R CCTGCAGGAGTCAGCTAGTTGC  OPG F CACACGAACTGCAGCACTT	Col-1A	F	CCCTACTCAGCCGTCTGTGC	
R CCCCAGAGACATGATGAAGTCA CTSK F CTTCCAATACGTGCAGCAGA R TCTTCAGGCTTTCTCTTC  NFATc1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GTGATGACCCCAGCATGCACCAGTCACAG  ATP6vOd2 F AAGCCTTTGACGCTGT R GCCAGCACATTCATCTGTACC  Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG  Axin2 F CAGTGTGAAGGCCAATGGC R TGGGTTCTCGGAAAATGAGG  Cyr61 F GTGAAGTGCGTCCTTGTGGA R TGCCCTTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTCTTGC  Tagln F CAGCCCAGACACCGAAGCTA R AGGCTTGGTGGTTTGTGGAC  TGFβ-3 F AGGCTTGGTCGTTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG  Wisp1 F ATGCCTGGCTGTTACCAGC R CCTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCTCTCTC R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATCCCGACCAG R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA R CCTGCAGGAGTCAGTTGTGC  OPG F CACACGAACTGCAGCACTT		R	GGGTTCGGGCTGATGTACC	
CTSKFCTTCCAATACGTGCAGCAGA RNFATc1FGGTAACTCTGTCTTTCTAACCTTAAGCTC RATP6vOd2FAAGCCTTTGACGCTGT RAhrFGGGACCTCGGGTGACAATAA RCCTCTGTCCTTTTCCAACCGAhrFGGGACCTCGGGTGACAATAA RCCTCTGTCCTTTTCCAACCGAxin2FCAGTGTGAAGGCCAATGGC RTGGGTTCTCGGAAAATGAGGCyr61FGTGAAGTGCGTCCTTGTGGA RTGCCTTTTTTAGGCTGCTGNkd2FAATTCAGTCCAAGCACGCC RCGGGACTCTCCTCTCTCTCTTGCTagInFCAGCCCAGACACCGAAGCTA RAGGCTTGGTCGTTTGTGGACTGFβ-3FAGGCTTGGTCGTTTGTGGACThbs1FGGACCGGGCTCAACTCTACA RAGGCTGATTGTGGCCAAGTTTwist1FTCGACTTCCTGTACCAGGTCCTTwist1FTCGACTTCCTGTACCAGGTCCTWisp1FATGCCTGGCTGTGTACCAGC RCCTGCGAGAGTGAAGTTCGTGTCFFCAGCTCCCCCATACTGTGAG RTGCTGCTATATCCGCAGGAALef 1FCAGCTCCCCCATACTGTGAG RTGCTGTCTATATCCGCAGGAAWnt3aFGGCTCCTCTCGGATACCTCT RACAGAGAATGGGCTGAGTGCβ-cateninFCCTAGCTGGTGGACTGCAGAA RCACCACTGGCCAGAATGATGALRP5FCACCATTGATTATGCCGACCAG RTGAGTCAGGCCAAACGGGTAG TGCAGGCCAGAACGGGTAGRANKLFGCAGCATCGCTCTGTTCCTGTA RCCTGCAGGAGTCAGGTAGTGTGTCOPGFCACACGGAACTGCAGCACATT	TRAP	F	CACTCCCACCCTGAGATTTGT	
R TCTTCAGGGCTTTCTGTTC  NFATC1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GTGATGACCCCAGCATGCACCAGTCACAG  ATP6vOd2 F AAGCCTTTGACGTGT R GCCAGCACATTCATCTGTACC  Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG  Axin2 F CAGTGTAAAGGCCAATGAC  Cyr61 F GTGAAGTGCGTCTTTGGA R TGCCCTTTTTTAGGCTGG  Nkd2 F AATTCAGTCCAAGCAC R CGGGACTCTCTCTCTTGC  TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGA R AGGCTTGTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGATTGTGGACAGCTA R AGCTCGCTCTTCTCTCTCTCT  Twist1 F TCGACTTCCTCTCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG  Wisp1 F ATGCCTGGCTGTTACCAGC R CCTGCGAGAGTCAACTCTACA R TGCTTGTCTATACCAGC R CCTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGGACTGCAGAA  R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTTTGCCGACCAG R TGAGTCAGGCCAAACTGTTACCAGC R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA R CCTGCAGGAGTCAGGTAGTGC  OPG F CACACGAACTGCAGCACATT		R	CCCCAGAGACATGATGAAGTCA	
NFATC1 F GGTAACTCTGTCTTTCTAACCTTAAGCTC R GTGATGACCCCAGCATGCACCAGTCACAG ATP6vOd2 F AAGCCTTTGACGCTGT R GCCAGCACATTCATCTGTACC Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG Axin2 F CAGTGTGAAGGCCAATGAG Cyr61 F GTGAAGTGCGTCCTTGTGGA R TGCCCTTTTTTAGGCTGGT Nkd2 F AATTTCAGTCCAAGCACCC R CGGGACTCTCTCTCTCTTGC Tagln F CAGCCCAGACACCGC R AGGCTTGGTCGTTTTTTGGAC R AGGCTTGGTCGTTTTTTGGAC TGFβ-3 F AGGCTTGGTCGTTTTTTTTTTTTTTTTTTTTTTTTTTTT	CTSK	F	CTTCCAATACGTGCAGCAGA	
R GTGATGACCCCAGCATGCACCAGTCACAG ATP6vOd2 F AAGCCTTTGACGCTGT R GCCAGCACATTCATCTGTACC Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG Axin2 F CAGTGTGAAGGCCAATGAGG Cyr61 F GTGAAGTGCGTCCTTGTGGA R TGCCCTTTTTTAGGCTGCTG Nkd2 F AATTTCAGTCCAAGCACGC R CGGGACTCTCTCTCTTGC TagIn F CAGCCCAGACACCGCAGCC R AGGCTTGGTCGTTTTTGGAC R AGGCTTGGTCGTTTTTTGGAC TGFβ-3 F AGGCTTGGTCGTTTTTTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGATTGTGGACAGTC TWist1 F TCGACTTCCTGTACCAGTCCT TWist1 F TCGACTTCCTGTACCAGTCCT R CCATCTTGGAGTCCAGCTCG Wisp1 F ATGCCTGGCTGTTACCAGC R CCTGCGAGAGTCAACTCTGC TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Wnt3a F GGCTCCTCTCTCT R ACAGAGAATGGGCTGAGTCC β-catenin F CCTAGCTGGCTGAGTGC β-catenin F CCTAGCTGGCCAGAATGATGA LRP5 F CACCATTGATTATCCGCAGCACAGAA R CACCACTGGCCAGAATGATGA R TGAGTCAGGCCAAACCGGTAG R TGAGTCAGGCCAAACCGGTAG R TGAGTCAGGCCAAACGGGTAG R TGAGTCAGGCCAAACGGGTAG R TGAGTCAGGCCAAACGGGTAG R TGAGTCAGGCCAAACGGGTAG R TGAGTCAGGCCAAACGGGTAG RANKL F GCAGCATCGCTCTTTTCCTGTA R CCTGCAGGAGTCAAGTGTGTC OPG F CACACGAACTGCAGCACATT		R	TCTTCAGGGCTTTCTCGTTC	
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R GCCAGCACATTCATCTGTACC  Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG  Axin2 F CAGTGTGAAGGCCAATGGC R TGGGTTCTCGGAAAATGAGG  Cyr61 F GTGAAGTGCGTCCTTGTGGA R TGCCCTTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTCTTGC  TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT  Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCCC R CCTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGGACTGC  β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTGTTA R CCTGCAGGAGTCAGGTAGTGC  RANKL F GCAGCATCGCTCTGTTACCTGTA R CCTGCAGGAGTCAGGTAGTGTC  OPG F CACACGAACTGCAGCACATT		R	GTGATGACCCCAGCATGCACCAGTCACAG	
Ahr F GGGACCTCGGGTGACAATAA R CCTCTGTCCTTTTCCAACCG Axin2 F CAGTGTGAAGGCCAATGGC R TGGGTTCTCGGAAAATGAGG Cyr61 F GTGAAGTGCTCCTTGTGGA R TGCCCTTTTTTAGGCTGCTG Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTCTTGC TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGATTGTGGAC R AGCTCGCGCTCTCCAT Twist1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCCC Wisp1 F ATGCCTGGCTGTTACCAGC R CCTGCGAGAGTGAAGTTCGTG TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Wnt3a F GGCTCCTCTCCGGATACCTCT R ACAGAGAATGGGCTGAGTGC β-catenin F CCTAGCTGGTGGACTGCAGAA LRP5 F CACCACTGGCCAGAATGATGA LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGGCCAAACGGGTAG RANKL F GCAGCATCGCTCTGTTA R CCTGCAGGAGTCCTGTTCCTGTA R CCTGCAGGAGTCAGCACATT	ATP6v0d2	F	AAGCCTTTGACGCTGT	
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Axin2 F CAGTGTGAAGGCCAATGGC R TGGGTTCTCGGAAAATGAGG Cyr61 F GTGAAGTGCTCTTTGTGA R TGCCCTTTTTTAGGCTGCTG Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTCTTTGC TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC R AGGCTTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG Wisp1 F ATGCCTGGCTGTACCAGC C CTGCGAGAGTGAAGTTCGTG TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGGCCAAACGGGTAG RANKL F GCAGCATCGCTCTGTTCCTGTA R CCTGCAGGAGTCAGGTAGTGTC OPG F CACACGAACTGCAGCACATT	Ahr	F	GGGACCTCGGGTGACAATAA	
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Cyr61 F GTGAAGTGCGTCCTTGTGGA R TGCCCTTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTCTTGC  TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC  TGFβ-3 F AGGCTTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT  Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGC Wisp1 F ATGCCTGGCTGTGTACCAGC CTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTGTTCCTGTA R CCTGCAGGAGTCAGTGTCC  OPG F CACACGAACTGCAGCACATT	Axin2	F	CAGTGTGAAGGCCAATGGC	
R TGCCCTTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTTGC  TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC  TGFβ-3 F AGGCTTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT  Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGC Wisp1 F ATGCCTGGCTGTACCAGC R CCTGCGAGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGACCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA R CCTGCAGGAGTCAGGTGC  RANKL F GCAGCATCGCTCTGTTCCTGTA R CCTGCAGGAGTCAGGTAGTGC  OPG F CACACGAACTGCAGCACATT		R	TGGGTTCTCGGAAAATGAGG	
R TGCCCTTTTTTAGGCTGCTG  Nkd2 F AATTTCAGTCCAAGCACGCC R CGGGACTCTCTCTCTTGC  TagIn F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC  TGFβ-3 F AGGCTTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT  Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGC Wisp1 F ATGCCTGGCTGTACCAGC R CCTGCGAGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGACCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA R CCTGCAGGAGTCAGGTGC  RANKL F GCAGCATCGCTCTGTTCCTGTA R CCTGCAGGAGTCAGGTAGTGC  OPG F CACACGAACTGCAGCACATT	Cyr61	F	GTGAAGTGCGTCCTTGTGGA	
R CGGGACTCTCTCTCTCTTGC  Tagin F CAGCCCAGACACCGAAGCTA R AGGCTTGGTCGTTTGTGGAC  TGFβ-3 F AGGCTTGGTCGTTTGTGGAC R AGGCTGATTGTGGCCAAGTT  Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT  Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG  Wisp1 F ATGCCTGGCTGTACCAGC CCTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGCCTG  β-catenin F CCTAGCTGGTGACCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTTTCCTGTA R CCTGCAGGAGTCAGGTGC  COPG F CACACGAACTGCAGCACATT		R	TGCCCTTTTTTAGGCTGCTG	
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R AGGCTGATTGTGGCCAAGTT Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG Wisp1 F ATGCCTGGCTGTGTACCAGC R CCTGCGAGAGTGAAGTTCGTG TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGCCAAACGGGTAG RANKL F GCAGCATCGCTGTTCCTGTA R CCTGCAGGAGTCAGGTGC OPG F CACACGAACTGCAGCACATT	_	R	AGGCTTGGTCGTTTGTGGAC	
R AGGCTGATTGTGGCCAAGTT Thbs1 F GGACCGGGCTCAACTCTACA R AGCTCCGCGCTCTCCAT Twist1 F TCGACTTCCTGTACCAGGTCCT R CCATCTTGGAGTCCAGCTCG Wisp1 F ATGCCTGGCTGTGTACCAGC R CCTGCGAGAGTGAAGTTCGTG TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGCCAAACGGGTAG RANKL F GCAGCATCGCTGTTCCTGTA R CCTGCAGGAGTCAGGTGC OPG F CACACGAACTGCAGCACATT	TGFβ-3	F	AGGCTTGGTCGTTTGTGGAC	
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Wisp1 F ATGCCTGGCTGTGTACCAGC R CCTGCGAGAGTGAAGTTCGTG  TCF F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Lef 1 F CAGCTCCCCCATACTGTGAG R TGCTGTCTATATCCGCAGGAA  Wnt3a F GGCTCCTCTCGGATACCTCT R ACAGAGAATGGGCTGAGTGC  β-catenin F CCTAGCTGGTGGACTGCAGAA R CACCACTGGCCAGAATGATGA  LRP5 F CACCATTGATTATGCCGACCAG R TGAGTCAGGCCAAACGGGTAG  RANKL F GCAGCATCGCTCTGTTCCTGTA R CCTGCAGGAGTCAGGTGC  OPG F CACACGAACTGCAGCACATT	Twist1	F	TCGACTTCCTGTACCAGGTCCT	
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Lef 1       F       CAGCTCCCCCATACTGTGAG         R       TGCTGTCTATATCCGCAGGAA         Wnt3a       F       GGCTCCTCTCGGATACCTCT         R       ACAGAGAATGGGCTGAGTGC         β-catenin       F       CCTAGCTGGTGGACTGCAGAA         R       CACCACTGGCCAGAATGATGA         LRP5       F       CACCATTGATTATGCCGACCAG         R       TGAGTCAGGCCAAACGGGTAG         RANKL       F       GCAGCATCGCTCTGTTCCTGTA         R       CCTGCAGGAGTCAGGTAGTGTC         OPG       F       CACACGAACTGCAGCACATT	TCF	F	CAGCTCCCCCATACTGTGAG	
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Wnt3a       F       GGCTCCTCTCGGATACCTCT         R       ACAGAGAATGGGCTGAGTGC         β-catenin       F       CCTAGCTGGTGGACTGCAGAA         R       CACCACTGGCCAGAATGATGA         LRP5       F       CACCATTGATTATGCCGACCAG         R       TGAGTCAGGCCAAACGGGTAG         RANKL       F       GCAGCATCGCTCTGTTCCTGTA         R       CCTGCAGGAGTCAGGTAGTGTC         OPG       F       CACACGAACTGCAGCACATT	Lef 1	F	CAGCTCCCCCATACTGTGAG	
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β-catenin       F       CCTAGCTGGTGGACTGCAGAA         R       CACCACTGGCCAGAATGATGA         LRP5       F       CACCATTGATTATGCCGACCAG         R       TGAGTCAGGCCAAACGGGTAG         RANKL       F       GCAGCATCGCTCTGTTCCTGTA         R       CCTGCAGGAGTCAGGTAGTGTC         OPG       F       CACACGAACTGCAGCACATT	Wnt3a	F	GGCTCCTCTCGGATACCTCT	
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RANKL F GCAGCATCGCTCTGTTCCTGTA R CCTGCAGGAGTCAGGTAGTGTC OPG F CACACGAACTGCAGCACATT	-	-		
R CCTGCAGGAGTCAGGTAGTGTC OPG F CACACGAACTGCAGCACATT	RANKL			
OPG F CACACGAACTGCAGCACATT		-		
	OPG			
		R	TCCACCAAAACACTCAGCCA	

ously reduced. As expected, treatment with mBMPR1A-Fc almost completely prevented the negative effects of RT on bone density (Figure 1A-D).

Representative mCT images of distal femur metaphysis in the three treated groups are shown in Figure 1E. The Ct.Th, Ct.Ar, and Ct.V values were unchanged (data not shown). RT led to a significant decrease in the trabecular microarchitecture. The BV/ TV (Figure 1F), Conn.D (Figure 1G), Tb.N (Figure 1H), Tb.Th (Figure 1I), and BS/BV (Figure 1J) values in the RT + VEH group were significantly lower, while the Tb.Sp, (Figure 1K) and SMI (Figure 1L) values in the RT + VEH group were significantly higher than those in the control. An mBMPR-1A-Fc administration reversed these defects (Figure 1F-L). There was no obvious difference between the RT + mBMPR1A-Fc group and the control group, suggesting that the mBMPR1A-Fc administration completely prevented RT-induced trabecular bone loss.

## mBMPR1A-Fc treatment prevents RT-induced reduction of mechanical properties

The femoral biomechanical structural properties were measured in the three-point bending test (Figure 2A-F). RT led to a significant decrease in biomechanical parameters, including maximum load (Figure 2A), yield load (Figure 2B), yield displacement (Figure 2C), stiffness (Figure 2D), energy absorption (Figure 2E), and ultimate displacement (Figure 2F), compared with these parameters in the control group. The femoral biomechanical material properties were examined in the nanoindentation test (Figure 2G, 2H). RT resulted in obvious reductions in the tissue-level modulus (Figure 2G) and hardness (Figure 2H) as compared to these parameters in the control group. As expected, the mBMPR1A-Fc administration reversed the decrease in these biomechanical structural and material properties. No significant difference was observed between the RT + mBMPR1A-Fc group and the control group.

## mBMPR1A-Fc enhances osteoblastogenesis

Representative static histomorphometric images for each group obtained by HE, total

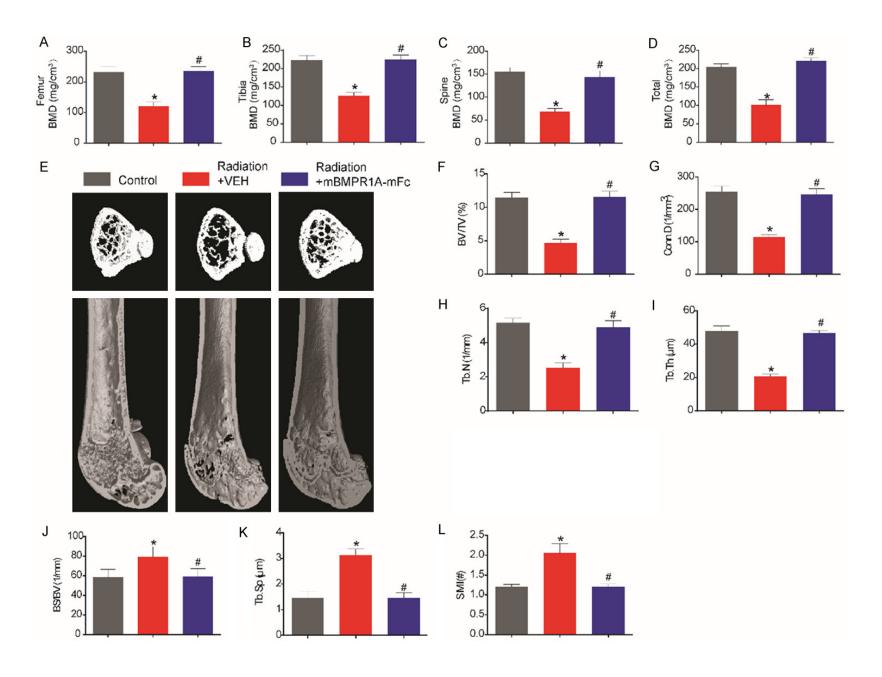


Figure 1. mBMPR1A-mFc treatment protects against radiation-induced bone loss. (A-D) The femur, tibia, spine, and total BMD were measured by DXA. (E) Representative reconstructed  $\mu$ CT images of distal femurs cancellous bone and cortical bone (3D). (F) The trabecular bone volume/total volume (BV/TV), (G) connectivity density (Conn.D), (H) trabecular number (Tb.N), (I) trabecular thickness (Tb.Th), (J) bone surface to bone volume ratio (BS/BV), (K) trabecular separation (Tb.Sp), and (L) structure model index (SMI) from  $\mu$ CT analysis. Values are all expressed as mean  $\pm$  SD, n=10 per group. \*, P<0.05, versus the control group. #, P<0.05, versus the Radiation + VEH group.

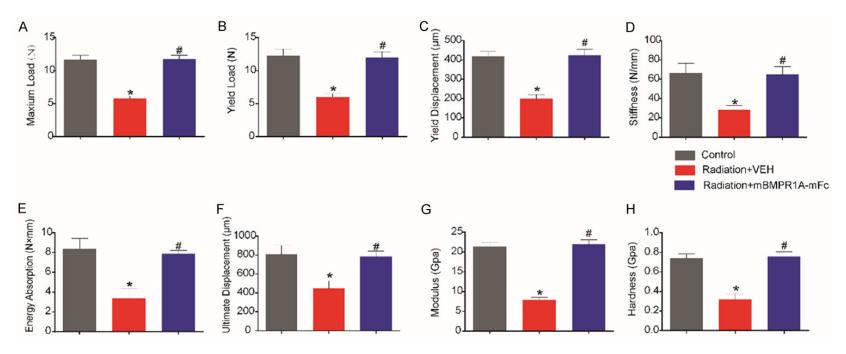


Figure 2. mBMPR1A-mFc treatment protects against radiation-induced reduction of mechanical properties. (A) The maximum load, (B) yield load, (C) yield displacement, (D) stiffness, (E) energy absorption and (F) ultimate displacement through three-point bending test. The (G) moudulus and (H) hardness through the nanoindentation system. Values are all expressed as mean ± SD, n=10 per group. \*, P<0.05, versus the control group. #, P<0.05, versus the Radiation + VEH group.

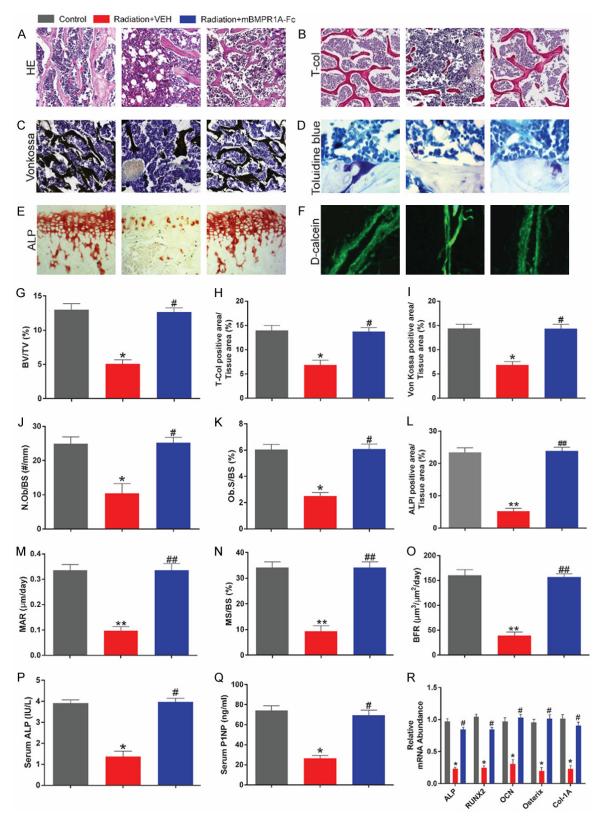
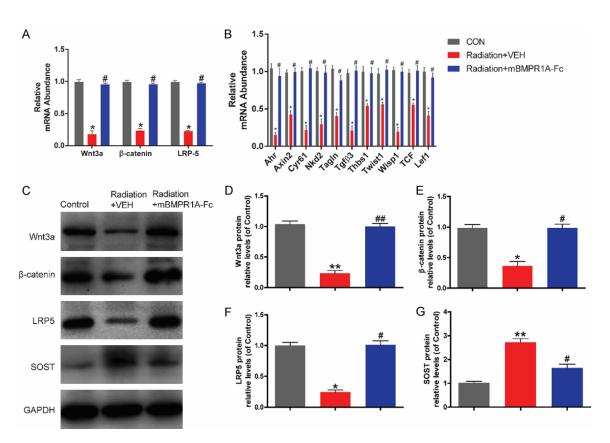


Figure 3. mBMPR1A-mFc treatment protects against the radiation-induced reduction of osteoblastic bone formation. The histomorphometric analysis of distal femur by (A) hematoxylin & eosin (H&E), 400×, (B) total collagen, 400×, (C) von kossa, 400×, (D) toluidine blue, 400×, (E) ALP, 400×, and (F) fluorescent calcein labeling staining, 400×. The histomorphometric analysis of (G) trabecular bone volume/total volume (BV/TV), (H) T-Col positive area/

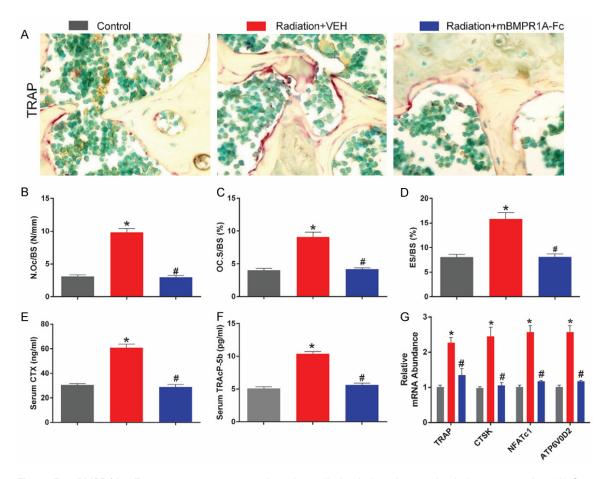
Tissue area, (I) von kossa positive area/tissue area, (J) Number of OBs per bone surface (N.0b/BS), (K) Percentage of bone surfaces covered by OBs (Ob.S/BS), (L) ALP positive area/Tissue area, (M) Mineral apposition rate (MAR), (N) Percentage of bone surfaces covered by mineralized surfaces (MS/BS) and (O) Bone formation rate/bone surface (BFR/BS). Serum bone formation markers (P) ALP, and (Q) PINP were measured by ELISA. (R) The expression of OB-specific genes, including ALP, Runx2, OCN, Osterix, and Col-1A were examined by qRT-PCR in femurs. Values are all expressed as mean  $\pm$  SD, n=10 per group. \*, P<0.05; \*\*, P<0.01, versus the control group. #, P<0.05; ##, P<0.01, versus the Radiation + VEH group.



**Figure 4.** mBMPR1A-mFc treatment alters Wnt/ $\beta$ -catenin signaling. A. RT-PCR of bone tissue extracts for the expression of Wnt3a, LRP5 and  $\beta$ -catenin. B. RT-PCR analysis of mRNA expression of genes specifically upregulated by Wnt signaling in flushed femurs. C. Protein expression of Wnt3a, LRP5,  $\beta$ -catenin and SOST in each group, as assessed by Western blot analysis. D-G. Densitometry results of Wnt3a, LRP5,  $\beta$ -catenin and SOST protein expression in each group. Values are all expressed as mean  $\pm$  SD, n=10 per group. \*, P<0.05; \*\*\*, P<0.01, versus the control group. #, P<0.05; ##, P<0.01, versus the Radiation + VEH group.

collagen, toluidine blue, von Kossa, and ALP staining are shown in Figure 3A-E. RT led to an obvious decrease in the trabecular bone in the femur compared with that of the control group, which was characterized by a significant reduction in the BV/TV (Figure 3G), total collagen positive areas/tissue area (Figure 3H), von Kossa positive area/tissue area (Figure 3I), ALP-positive areas/tissue area (Figure 3L), N.Ob/BS (Figure 3J), and Ob.S/BS (Figure 3K) compared with these parameters in the control group. Next, mBMPR1A-Fc treatment markedly attenuated the RT-induced deterioration of the femur microarchitecture. A dynamic histo-

morphometric (Figure 3F) analysis revealed that mBMPR1A-Fc administration significantly increased new bone formation at the trabecular bone, as reflected by increases in MAR (Figure 3M), BFR (Figure 3N), and MS/BS (Figure 3O), which, otherwise, in the absence of treatment were greatly reduced after RT (Figure 3E, 3M-O). Additionally, significant decreases in serum ALP and P1NP levels were observed in the RT-VEH group compared with those of the control group. After mBMPR1A-Fc treatment, serum ALP and P1NP in the RT-mBMPR1A-Fc group were significantly higher than those in the RT-VEH group (Figure 3P,



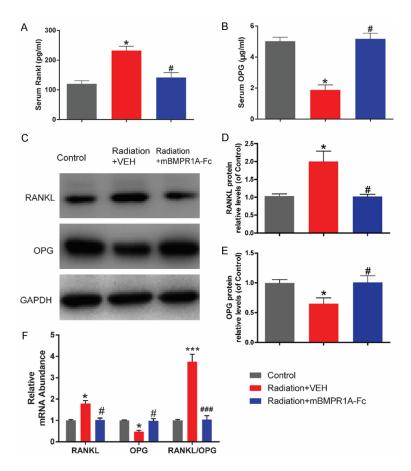
**Figure 5.** mBMPR1A-mFc treatment protects against the radiation-induced osteoclastic bone resorption. (A) Sections of the metaphyseal regions of the distal femurs were performed TRAP staining, 400×. (B) The osteoclast number/bone surface (N.Oc/BS), (C) Osteoclast surface/bone surface (Oc.S/BS) and (D) Eroded surface/bone surface (ES/BS) were analyzed. Serum bone resorption markers (E) CTX and (F) TRAP5b were measured by ELISA. (G) The expression of OC-specific genes, including TRAP, CTSK, NFATc1 and ATP6V0D2 were examined by qRT-PCR in femurs. Values are all expressed as mean ± SD, n=10 per group. \*, P<0.05, versus the control group. #, P<0.05, versus the Radiation + VEH group.

**3Q**). Furthermore, the mRNA levels of ALP, Runx2, OCN, Osterix, and Col-1A were assessed by RT-PCR (**Figure 3R**). RT markedly downregulated the mRNA levels of these osteogenic genes. Expectedly, mBMPR1A-mFc administration significantly increased the expression levels of these osteogenic genes in RT mice (**Figure 3R**).

## mBMPR1A-Fc promotes Wnt3a/Lrp5/β-catenin signaling pathway

Canonical Wnt3a/Lrp5/ $\beta$ -catenin signaling plays a crucial role in regulating the bone mass and the bone strength. In our present study, the mRNA expression levels of Wnt3a, Lrp5, and  $\beta$ -catenin in the three groups are listed in **Figure 4A**. These mRNA expression levels in the RT + VEH group were significantly lower than in the

control group. However, the mRNA expression levels of Wnt3a, β-catenin, and Lrp5 in the RT + mBMPR1A-Fc group were significantly higher than in the RT + VEH group. In addition, we measured the mRNA expression of genes specifically upregulated by the Wnt signaling in flushed femurs. The investigated genes consisted of the following: aryl-hydrocarbon receptor (Ahr), axin2, cysteine-rich protein 61 (Cyr61), naked cuticle 2 homolog (Nkd2), transgelin (tagline), transforming growth factor \$3 (TGFβ3), thrombospondin 1 (Thbs1), twist gene homolog 1 (Twist1), Wnt1-inducible signaling pathway protein 1 (Wisp1), T-cell factor (TCF), and lymphoid enhancer factor-1 (Lef-1). These genes were selected since they are sensitive markers of Wnt signaling activation [45]. The mRNA levels for the 11 studied genes were



**Figure 6.** mBMPR1A-mFc treatment alters RANKL/OPG signaling. (A, B) Serum Rankl and OPG were measured by ELISA. Serum (A) Rankl and (B) OPG. (C) Protein expression of RANKL and OPG in each group, as assessed by Western blot analysis. (D, E) Densitometry results of RANKL and OPG protein expression in each group. (F) qPCR analysis of mRNA expression of RANKL, OPG, and RANKL/OPG ratio in femurs. Values are all expressed as mean ± SD, n=10 per group. \*, P<0.05; \*\*, P<0.01; \*\*\*, P<0.001, versus the control group. #, P<0.05; ##, P<0.01; ###, P<0.001, versus the Radiation + VEH group.

all profoundly reduced by RT compared with those of the control group. However, the mBM-PR1A-Fc treatment significantly increased the mRNA expression of the 11 studied genes in mice belonging to the RT-mBMPR1A-mFc group (Figure 4B). Furthermore, the protein expression levels of Wnt3a,  $\beta$ -catenin, Lrp5 and SOST were reduced significantly in RT-VEH mice compared with that in the control mice; however, the parameters were normalized by mBM-PR1A-mFc administration (Figure 4C-G). These results demonstrated that mBMPR1A-mFc stimulated bone formation by activating Wnt signaling.

#### mBMPR1A-Fc inhibits osteoclastogenesis

Representative TRAP staining (400× magnification) of femurs is shown in **Figure 5A**. A histo-

morphometric analysis revealed a significant increase in the N.Oc/BS (Figure 5B), Oc.S/BS (Figure 5C), and ES/BS (Figure 5D) in the RT-VEH group compared with that of the control mice. Consistent with the increased osteoclast numbers in the RT-VEH group, serum CTX-1 (Figure 5E) and TRAP-5b (Figure 5F) levels were also increased, reflecting increased osteoclastic bone resorption after RT. Additionally, the RT-PCR results revealed that genes related to osteoclastogenesis, such as TRAP, CTSK, NFATc1, and ATP6V0D2, were all significantly increased after RT (Figure 5G). Interestingly, the osteoclast numbers, bone resorption markers, and osteoclastogenic gene expressions were significantly reduced by mBMPR1A-Fc administration. to levels similar to those in the control mice (Figure 5A-G).

#### mBMPR1A-Fc inhibits RANKL/ RANK/OPG signaling pathway

RANKL and OPG are cytokines predominantly secreted by osteoblasts. The relative concentration of RANKL and OPG (RANKL/OPG ratio) plays a critical role in determining bone mass and strength. RT-VEH

mice exhibited a marked elevation of serum RANKL (Figure 6A) and a significant reduction of serum OPG as compared to those in the control (Figure 6B). Additionally, mBMPR1A-Fc administration reversed the adverse effects of RT on these serum markers. Consistent with the serum levels of RANKL and OPG, the protein expression and mRNA levels of OPG were significantly reduced in the RT + VEH group when compared with the control group and were associated with significant elevations in the protein expression and mRNA levels of RANKL (Figure 6C-F). Next, mBMPR1A-Fc administration significantly increased protein expression and mRNA levels of OPG and reduced protein expression and mRNA levels of RANKL (Figure 6C-F), resulting in a significant decrease in the RANKL/OPG ratio in mRNA levels.

#### Discussion

In spite of its efficiency in killing tumor cells, clinical RT causes secondary damage to adjacent bones. Cancer patients treated with RT develop increased fracture risks at the irradiated sites [8-10]. Thus, it is important to find appropriate treatments for RT-induced osteoporosis. In this study, we used an RT-induced osteoporosis mouse model, which revealed that impaired bone formation, as well as accelerated bone resorption, are key mechanisms mediating RT-induced osteoporosis. Furthermore, we demonstrated that mBMPR1A-mFc, an antagonist to endogenous BMPR1A, preserved the skeletal system in mice after RT. We found that mBMPR1A-mFc administration promoted bone formation and inhibited bone resorption, resulting in protection of the integrity and mechanical strength of the trabecular bone after RT. Additionally, the mBMPR1AmFc might regulate the bone via the Wnt3a/ Lrp5/β-catenin and RANKL/RANK/OPG signaling pathways.

Radiation promotes osteoclastogenesis [46]. In this study, Oc.S/BS and Oc.N/BS were obviously increased after radiation. Moreover, the mRNA levels of TRAP, Ctsk, NFATc1, and ATP-6V0D2 in the femurs of the RT-VEH group were considerably higher than those of the control group. TRAP is a critical cytochemical marker enzyme that regulates the growth and differentiation of osteoclasts. As a cysteine protease secreted by osteoclasts. Ctsk is essential for the degradation of matrix collagen [47, 48]. Furthermore, NFATc1 integrates RANKL signaling during terminal differentiation of osteoclasts [49]. Additionally, ATP6V0D2 is a key molecule for osteoclast cell-cell fusion [50]. In the present study, the increases in NFATc1, Ctsk, and ATP6V0D2 mRNA levels were compatible with the histomorphometric findings and bone metabolism markers in the RT + VEH group. Consistent with a previous study [46], the current study demonstrated that the RAN-KL mRNA expression was upregulated, while OPG was downregulated after 4-week RT in mice. As a result, the RANKL/OPG mRNA ratio was markedly higher in the RT-VEH group than that in the control group, which is consistent with the findings of other studies [46].

Our data showed that the Oc.S/BS, Oc.N/BS, serum CTX-1, and TRACP-5b levels in the

RT-mBMPR1A-mFc group were significantly lower than those in the RT-VEH group. Furthermore, mBMPR1A-mFc treatment significantly downregulated mRNA expressions of RANKL and upregulated OPG. The RANKL/OPG mRNA ratio was downregulated by mBMPR1AmFc. Additionally, mBMPR1A-mFc administration downregulated the mRNA levels of TRAP, Ctsk, NFATc1, and ATP6V0D2 in the femur. Our results implied that RT-induced osteoclastogenesis was inhibited by mBMPR1A-mFc, which is consistent with the findings of previous studies [25, 35]. In summary, our study indicated that mBMPR1A-mFc administration regulated the RANKL/RANK/OPG signaling pathway to inhibit bone resorption, leading to improved femoral trabecular bone mass and mechanical strength in RT-treated mice.

The Wnt/Lrp5/β-catenin pathway plays a crucial role in regulating bone formation and bone resorption [51-55]. In accordance with previous studies [46], the major gene expressions in the femurs of the canonical Wnt signaling pathway. including Wnt3a, Lrp5, and β-catenin, were significantly downregulated in the RT-VEH group compared with the control group in this study. Furthermore, we analyzed the mRNA expression of genes specifically upregulated by Wnt signaling in femurs. These genes were chosen as they are sensitive markers of Wnt signaling activation [45]. The results revealed that the levels of mRNA for the 11 tested genes were all dramatically decreased by RT compared with the control group. All of these results indicated that the Wnt3a/Lrp5/β-catenin signaling was downregulated by RT, which is consistent with the findings of a previous study [56]. Interestingly, the expressions of Wnt3a, Lrp5, β-catenin, and the 11 chosen genes were all significantly upregulated after mBMPR1A-mFc administration, indicating the potential activation of the Wnt3a/Lrp5/β-catenin signaling pathway by mBMPR1A-mFc administration. Similar results have also been reported by previous studies [25]. Our study indicated that mBM-PR1A-mFc upregulated the Wnt3a/Lrp5/β-catenin signaling pathway to promote bone formation, resulting in improved femur trabecular bone mass and mechanical strength in RT-induced osteoporosis mice.

A limitation of our present study was that we studied only female mice at a single time point, with a single dosing regimen for mBMPR1A-

mFc administration. Therefore, whether longer treatment at a higher dose or more frequent dosing of mBMPR1A-mFc would have greater osteoprotective effects in RT animal models remains unclear. Additional in-depth experimental work is required to determine the optimal dose and investigate the possible mechanisms responsible for the protective effects of mBMPR1A-mFc against RT-induced osteoporosis.

In conclusion, our study indicated that mBM-PR1A-mFc administration could alleviate radiation-induced osteoporosis in mice, as evidenced by serum biochemical, biomechanical, micro-CT, and histological analyses. The boneprotective effects of mBMPR1A-mFc might be attributed to a combination of promoting bone formation and suppressing bone resorption. Moreover, several signaling pathways may be involved in the underlying mechanisms, including the Wnt3a/Lrp5/β-catenin and RANKL/ RANK/OPG pathways. This observation suggests that mBMPR1A-mFc is a safe and effective dual-action therapeutic agent that may be effective against radiation-induced bone loss by promoting bone formation while inhibiting resorption.

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#### Disclosure of conflict of interest

None.

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