



93 Identification and characterization of Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> Figure S1. mice (*OI.ApoE*<sup>-/-</sup>), 94 hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> mice (hSOST<sup>ki</sup>.Ol.ApoE<sup>-/-</sup>), *Δ*loop3-hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> mice (*Δ*loop3hSOST<sup>ki</sup>.OI.ApoE<sup>-/-</sup>), hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup> mice (hSOST<sup>ki</sup>.OI) and Δloop3-hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup> mice (Δloop3-95 hSOST<sup>ki</sup>.OI), respectively. (A) Representative agarose gel electrophoretic images for PCR genotyping samples from 96 Col1a2+/G610C.ApoE-/- mice. (B) Representative agarose gel electrophoretic images for PCR genotyping samples from 97 hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> mice. (C) Representative agarose gel electrophoretic images for PCR genotyping 98 samples from  $\Delta loop 3$ -hSOST<sup>ki</sup>. Col1a2<sup>+/G610C</sup>. ApoE<sup>-/-</sup> mice. (D) Representative agarose gel electrophoretic images for 99 PCR genotyping samples from  $hSOST^{ki}$ . Col1a2<sup>+/G610C</sup> mice. (E) Representative agarose gel electrophoretic images for 100 PCR genotyping samples from *Δloop3-hSOSTki*. Col1a2<sup>+/G610C</sup> mice. (F) Relative mRNA expression levels of human full-101 length sclerostin (FL hSOST) or loop3 deficient human sclerostin (Δloop3-hSOST) in the aorta and the tibia of Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> mice, hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> mice and Δloop3-hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup> mice (left), 102 as well as Col1a2+/G610C mice, hSOSTki. Col1a2+/G610C mice and Δloop3-hSOSTki. Col1a2+/G610C mice (right), respectively, 103 detected by RT-PCR. No significant difference (ns) were found for comparison between hSOST<sup>ki</sup>.OI.ApoE<sup>-/-</sup> and Δloop3-104 hSOST<sup>ki</sup>.OI.ApoE<sup>-/-</sup>groups, or hSOST<sup>ki</sup>.OI and Δloop3-hSOST<sup>ki</sup>.OI groups, by parried t-test. \*\*\* P < 0.005 and \*\*\*\* P < 105 0.0001 for a comparison vs. OI.ApoE<sup>-/-</sup> group or OI group by one-way ANOVA with Tukey's post-hoc test. (G) Protein 106 expression levels of FL hSOST or Δloop3-hSOST in the serum of Col1a2+'/G610C.ApoE-/- mice, hSOST<sup>ki</sup>.Col1a2+/G610C.ApoE-/- mice and Δloop3-hSOST<sup>ki</sup>.Col1a2+/G610C.ApoE-/- mice (left), as well as Col1a2+/G610C 107 mice, hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup> mice and Δloop3-hSOST<sup>ki</sup>.Col1a2<sup>+/G610C</sup> mice (right), respectively, detected by ELISA. \*\*\* 108 P < 0.005 and \*\*\*\* P < 0.0001 for a comparison vs. OI.ApoE<sup>-/</sup> group or OI group by one-way ANOVA with Tukey's post-109 hoc test. Note: ApoE<sup>-/-</sup> mutant: ~ 245 bp (homozygous); Col1a2+'/G610C mutant: ~ 337 bp (homozygous); hSOSTki: 110 5'arm ~ 1465 bp, 3'arm ~ 1229 bp; *Δloop3-hSOST<sup>ki</sup>*: 5'arm ~ 1465 bp, 3'arm ~ 2149 bp. 111



<sup>43</sup> TNF- $\alpha$ ) and chemokine (MCP-1) in *Col1a2<sup>+/G610C</sup>.ApoE<sup>-/-</sup>* mice with AngII infusion. **(C-F)** Data were expressed as mean ± standard deviation (n = 9). \* *P* < 0.05; \*\* *P* < 0.01; \*\*\* *P* < 0.005 and \*\*\*\* *P* < 0.0001 for a comparison with AngII+veh by one-way ANOVA

<sup>45</sup> with Tukey's post-hoc test. **Note**: AnglI: Angiotensin II; IL-6: interleukin 6; TNF-α: tumor necrosis factor alpha; MCP-1: monocyte

<sup>46</sup> chemoattractant protein-1.



Figure S3. Pharmacokinetic analysis of aptscl56 (black) and Apc001PE (blue) after a single subcutaneous administration in *Col1a2*<sup>+/G610C</sup> mice.





34 Figure S4. Apc001PE had no effect on inflammatory cytokines and chemokines expression, aortic aneurysm (AA) and atherosclerosis progression in 35 Col1a2+/G610C. ApoE-/- mice with AnglI infusion. (A) Schematic diagram showing the experiment design of the study. Briefly, three-month-old Col1a2+/G610C. ApoE-<sup>/</sup> mice were randomly divided into six groups: saline, AngII+veh, AngII+Apc001PE, AngII+antibody, AngII+loop2m, and AngII+antibody+loop2m (n = 9 for each 36 group). For saline group, Col1a2+'G610C.ApoE'- mice were infused with saline for four weeks. For AngII+veh, AngII+Apc001PE, AngII+antibody, AngII+loop2m, and 37 Angll+antibody+loop2m groups, Col1a2+/G610C, ApoE/- mice were infused with angiotensin II (AngII) for four weeks, and were subcutaneously administrated with 38 vehicle (veh, twice per week), Apc001PE (25 mg/kg, twice per week), humanized therapeutic sclerostin antibody (25 mg/kg, twice per week), loop2m (6 mg/kg, 39 twice per week), and therapeutic sclerostin antibody with pretreatment of loop2m (25 mg/kg + 6 mg/kg, twice per week), respectively, for four weeks during AnglI 40 infusion. (B) Representative immunohistochemistry images for the expression of CD68, α-SMA, and cleaved caspase-3 in cross cryo-sections of aortic roots from 41 Col1a2+/G610C. ApoE-/- mice with AnglI infusion (the red circles indicated the locations of atherosclerotic plaque, the black arrows and black squares indicated the locations of positive staining). Scale bars, 100 μm (\*lumen). Note: AnglI: Angiotensin II; CD68: macrophages biomarker; α-SMA: contractile cell biomarker; Cleaved 42 caspase-3: apoptotic cell biomarker. 43











Figure S5. Apc001PE promoted bone formation in Col1a2 +/G610C mice via targeting sclerostin loop3. (A) A schematic diagram showing the experimental design 1 of the study. Briefly, ten six-week-old Col1a2+/G610C mice (OI-Baseline) and ten six-week-old wild-type littermates (WT-Baseline) were euthanized before treatment as 2 baseline, respectively. Another ten six-week-old Col1a2+/G610C mice (Ol-Age matched) and ten six-week-old wild-type littermates (WT-Age matched) were kept 3 untreated for six weeks as the age matched groups, respectively. The remaining Col1a2+/G610C mice were subcutaneously administrated with Apc001PE (12 mg/kg), 4 fatty acid-loop3m (loop3m, 6 mg/kg), Apc001PE+ fatty acid-loop3m (12 mg/kg + 6 mg/kg), and PEG40k-random DNA sequence (RS, 12 mg/kg), respectively, twice 5 per week for six weeks (n = 10 for each group). (B) Representative images showing three-dimensional trabecular bone architecture by micro-CT reconstruction at 6 the fourth lumbar vertebrae. Scale bars, 200 µm. (C) Bar charts of the structural parameters of Tb.BV/TV, Tb.vBMD, Tb.Th, Tb.N, Tb.Sp, Tb.conn.D and Tb.SMI from 7 ex vivo micro-CT examination at the fourth lumbar vertebrae. (D) Representative images showing three-dimensional trabecular architecture by micro-CT reconstruction at the distal femur. Scale bars, 200 µm. (E) Bar charts of the structural parameters of Tb.BV/TV, Tb.vBMD, Tb.Th, Tb.N, Tb.Sp, Tb.conn.D and Tb.SMI 8 from ex vivo micro-CT examination at the distal femur. (F) Representative fluorescent micrographs of the trabecular bone sections showing bone formation at the C fourth lumbar vertebrae visualized by calcein green and xylenol orange labels. Arrows indicated the spaces between calcein green and xylenol orange labeling. Scale 10 bars, 40 µm (the upper panel). Analysis of dynamic bone histomorphometric parameters of Tb.BFR/BS and Tb.MAR at the fourth lumbar vertebrae (the lower panel). 11 (G) Representative fluorescent micrographs of the trabecular bone sections showing bone formation at the distal femur visualized by calcein green and xylenol orange 12 labels. Arrows indicated the spaces between calcein green and xylenol orange labeling. Scale bars, 40 µm (the upper panel). Analysis of dynamic bone histomorphometric parameters of Tb.BFR/BS and Tb.MAR at the distal femur (the lower panel). Note: Tb.BV/TV: trabecular relative bone volume; Tb.vBMD: trabecular 13 volumetric mineral density; Tb.Th: trabecular thickness; Tb.N: trabecular number; Tb.Sp: trabecular spacing; Tb.conn.D: trabecular connect density; Tb.SMI: 14 trabecular structure model index; Tb.BFR/BS: trabecular bone formation rate; Tb.MAR: trabecular mineral apposition rate. Data were expressed as mean ± standard 15 deviation followed by one-way ANOVA with Tukey's post-hoc test vs OI-Baseline, n = 10 per group. \* P < 0.05; \*\* P < 0.01; \*\*\* P < 0.005; \*\*\*\* P < 0.0001. 16



28 Figure S6. Serum levels of liver and kidney function indexes as well as hematologic parameters in healthy C57BL/6 mice after a single or multiple 29 administration(s) of Apc001PE. ALT: alanine aminotransferase; AST: aspartate aminotransferase; BUN: blood urea nitrogen; RBCs: red blood cells; HGB: haemoglobin; WBCs: white blood cells; PLTs: platelets. Data were expressed as mean ± standard deviation followed by one-way ANOVA with Tukey's post-hoc test, 30 n = 10 per group. 31







Figure S7. The sclerostin loop3-specific aptamer did not induce lesions and pathological changes in vital organs of healthy SD rats. Histopathological images of the paraffin sections of the vital organs including brain/cerebellum/cerebral vessels, heart/aortic root, kidneys, livers, lungs/bronchus, spleen, adrenal glands, thymus, thyroid/parathyroid, prostate glands, testicle, ovaries, and uterus/cervix in healthy SD rats, after administration of the sclerostin loop3-specific aptamer at the dosage of 12 mg/kg and 60 mg/kg, respectively, twice per week for six weeks. Differences among three groups were not found (n = 5). Scale bar for brain/cerebellum/cerebral vessels and heart/aortic root: 200 µm. Scale bar for the other organs: 300 µm.

Parameter —	Mean value	
	aptscl56	Apc001PE
AUC <sub>0-t</sub> (mg/L*h)	1336.928	13604.239
AUC₀₋∞ (mg/L*h)	2682.447	28253.472
T <sub>1/2</sub> (h)	0.8	57.798
CL/F (L/h/kg)	0.002	0
V/F (L/kg)	0.015	0.018
T <sub>max</sub> (h)	1	54

Table S1. Pharmacokinetic parameters of aptscl56 and Apc001PE after a single subcutaneous administration in Col1a2 +/G610C mice.