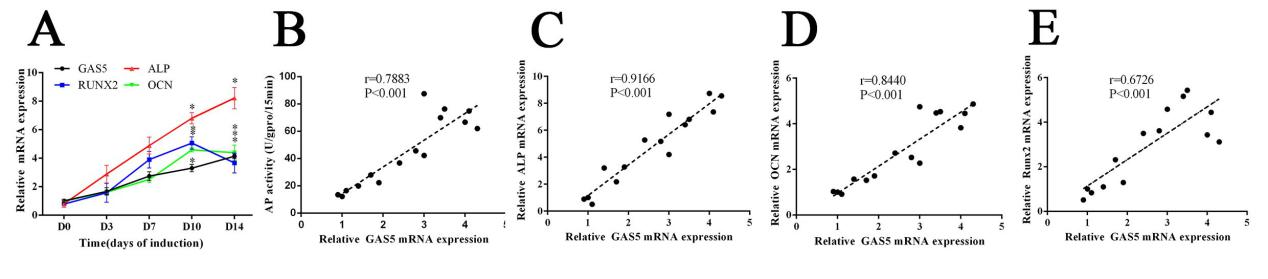
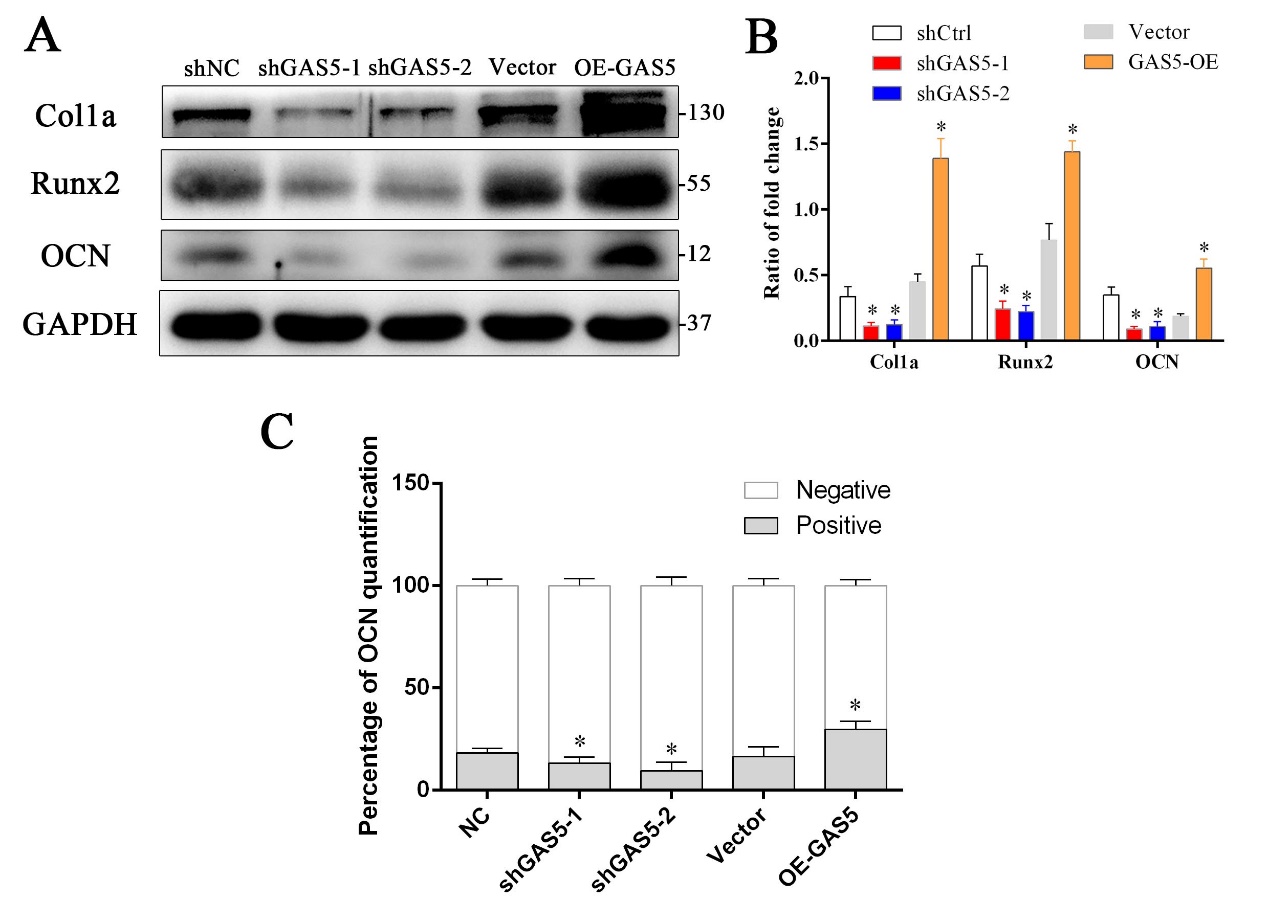
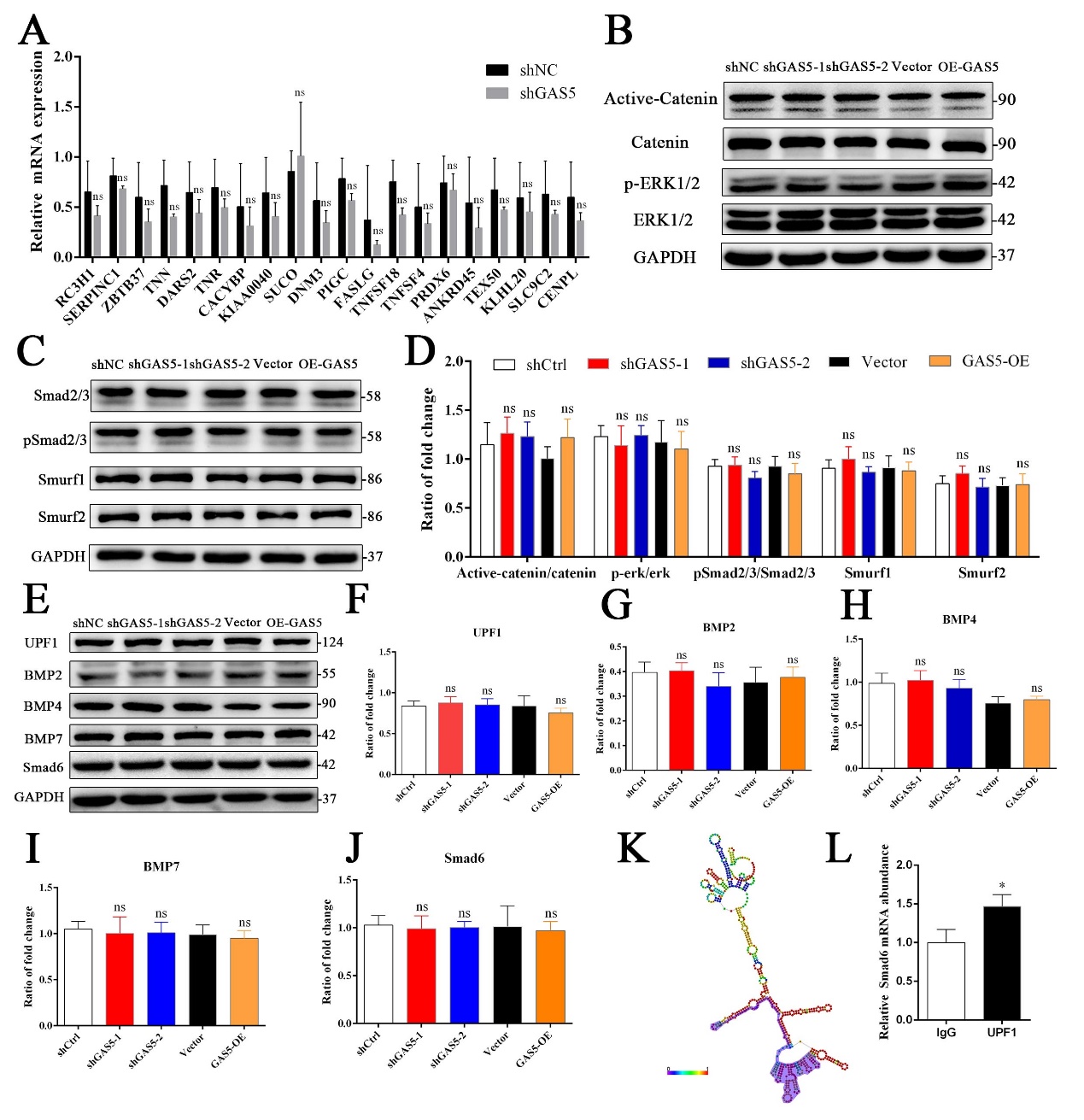
**Supplementary figure**



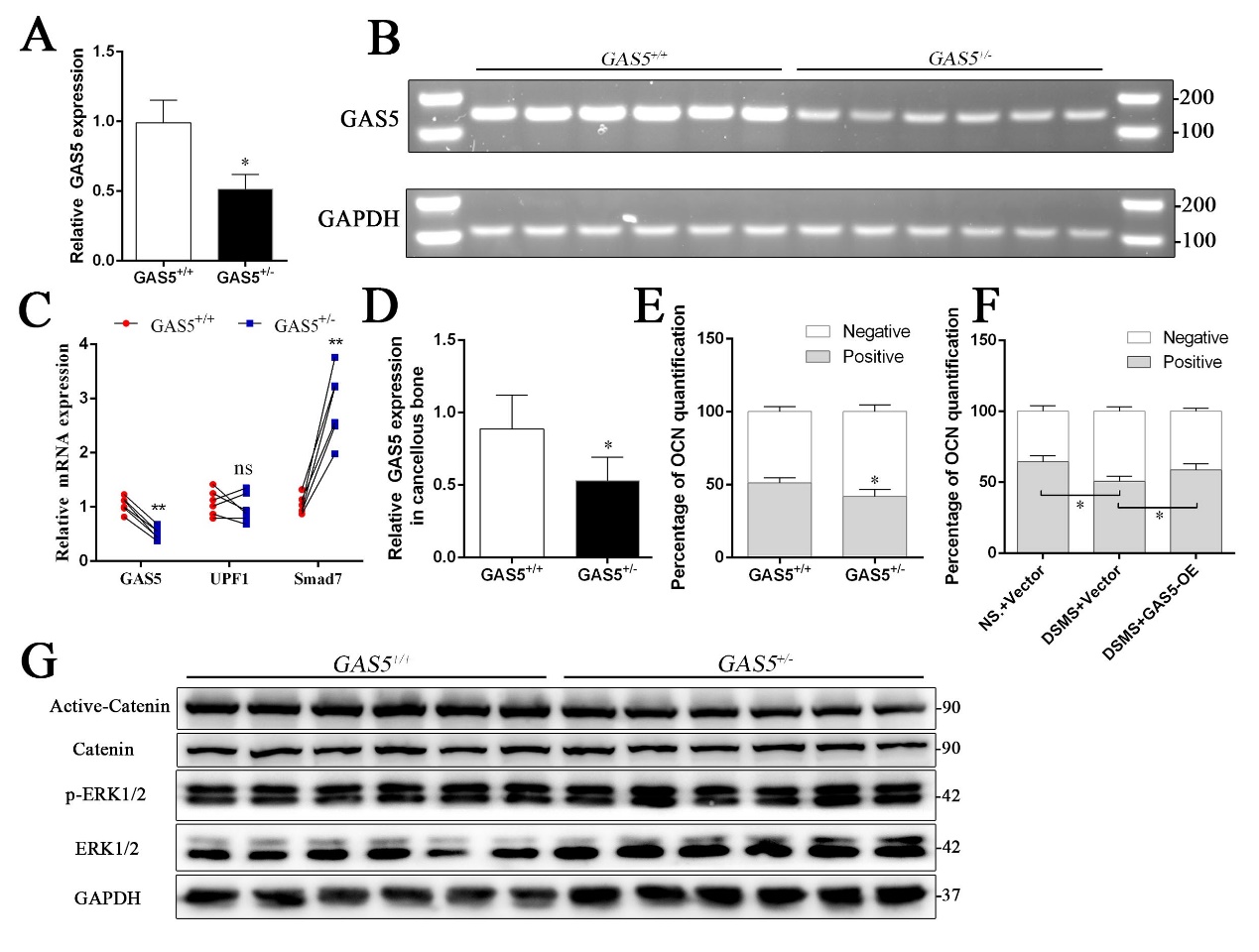
Supplementary figure 1. (A) Relative mRNA expression of GAS5, OCN, ALP, and RUNX2 along with the day of osteogenic differentiation. (B) The correlation of GAS5 and ALP assay during osteogenic differentiation of MSCs (n=15). (C, D, E) The correlation of GAS5 and ALP, OCN, and Runx2 during osteogenic differentiation of MSCs (n=15).



Supplementary figure 2. (A, B) Western blot analysis and quantification of osteogenesis markers (Col1a1, Runx2, OCN) in GAS5 knockdown or overexpression conditions. (C) The quantification of OCN immunohistochemical staining of in vivo bone formation tests in GAS5 knockdown or overexpression treatment.



Supplementary figure 3. (A) qRT-PCR analysis of the GAS5 adjacent genes in GAS5 knockdown conditions. ZBTB37 (zinc finger and BTB domain containing 37), RC3H1 (ring finger and CCCH-type domains 1), SERPINC1 (serpin family C member 1), ZBTB37 (zinc finger and BTB domain containing 37), TNN (tenascin N), DARS2 (aspartyl-tRNA synthetase 2, mitochondrial), TNR (tenascin R), CACYBP (calcyclin binding protein), KIAA0040 (KIAA0040), SUCO (SUN domain containing ossification factor), DNM3 (dynamin 3), PIGC (phosphatidylinositol glycan anchor biosynthesis class C), FASLG (Fas ligand), TNFSF18 (TNF superfamily member 18), TNFSF4 (TNF superfamily member 4), PRDX6 (peroxiredoxin 6), ANKRD45 (ankyrin repeat domain 45), TEX50 (testis expressed 50), KLHL20 (kelch like family member 20), SLC9C2 (solute carrier family 9 member C2 (putative)), CENPL (centromere protein L). (B, C) Western blot analysis of the pathway (catenin, ERK, Smad2/3, Smurf1, Smurf2) in GAS5 knockdown or overexpression conditions. (D) Quantification for Western blot analysis of β-catenin, ERK, Smad2/3, Smurf1 and Smurf2. (E, F, G, H, I, J) Western blot analysis of BMP2, BMP4, BMP7, and Smad6 in GAS5 knockdown or overexpression conditions. (K) RNA fold model of GAS5 predicted on the *RNAfold web server* website (<http://rna.tbi.univie.ac.at//cgi-bin/RNAWebSuite/RNAfold.cgi>). The rainbow color means the base-pair probabilities of the predicted folded RNA. The area of GAS5 combined with UPF1 was painted with lavender. (L) RIP assay with anti-UPF1 showed the binding of UPF1 and Smad6 mRNA.



Supplementary figure 4. (A, B) Relative Gas5 expression in the tails of GAS5+/+ (n=6) and GAS5+/- (n=6) mice analyzed by qRT-PCR and agarose gel electrophoresis. (C) Relative mRNA expression of GAS5, UPF1 and Smad7 in BMSC of GAS5+/- and WT mice (n=6). (D) The mRNA level of GAS5 in cancellous bone of GAS5+/-mice and WT mice. (E) The quantification of OCN immunohistochemical staining of GAS5+/-mice and WT mice. (F) The quantification of OCN immunohistochemical staining of the control mice (n=6), osteoporosis mouse model (n=6) or GAS5-overexpressing adenovirus-treated mice. (G) Western blot analysis of the pathway (catenin, ERK) in the protein from the tibia of GAS5+/+ (n=6) and GAS5+/- mice (n=6).