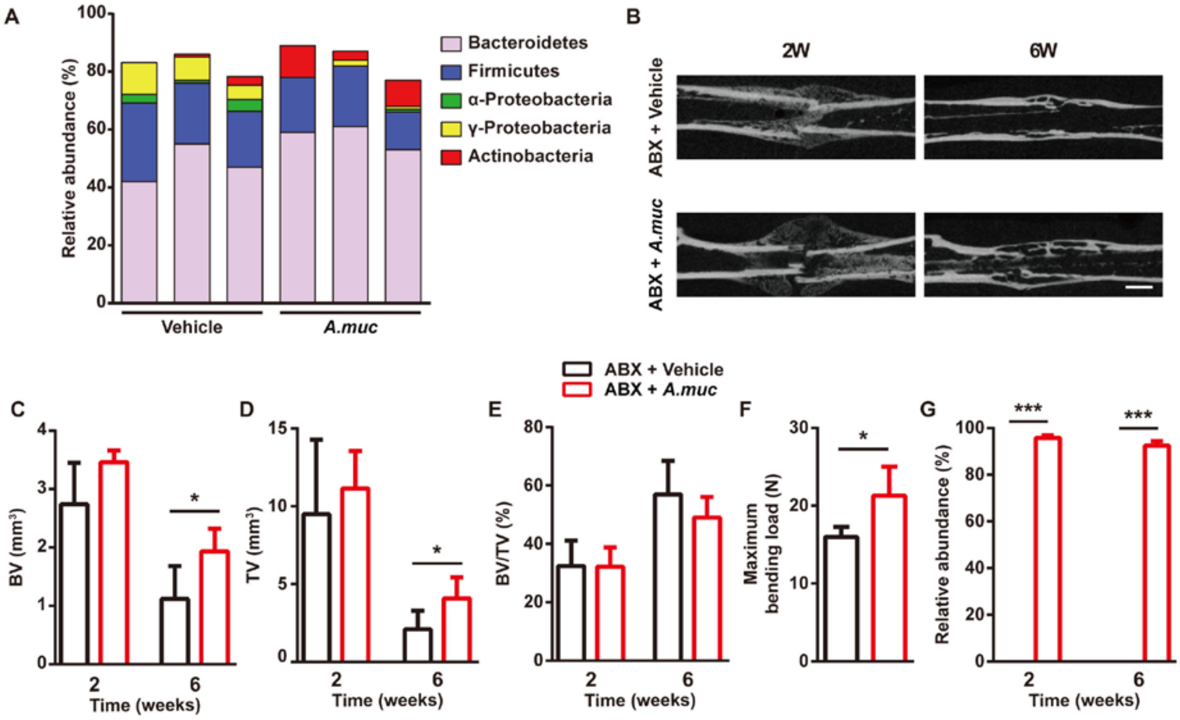

Fig. S1. *A. muc* improves bone repair in gut microbiota-depleted mice. (A) Fecal microbiota composition of vehicle-treated group and *A. muc*-treated group evaluated by 16S rDNA qRT-PCR. n = 3 per group. (B) Representative µCT images of fractured femora from ABX + vehicle and ABX + *A. muc* group mice at 2 and 6 weeks. Scale bar: 1 mm. (C-E) µCT quantitative analyses of BV (C), TV (D) and BV/TV (E) of fractured femora at 2 and 6 WPF. n = 5 per group. (F) Four-point bending measurement of femoral ultimate load at 6 WPF. n = 5 per group. (G) Abundances of *A. muc* in fecal samples of ABX + vehicle and ABX + *A. muc* group mice. n = 5 per group. $^{*}P < 0.05$, $^{***}P < 0.001$ by unpaired two tailed Student's t test.

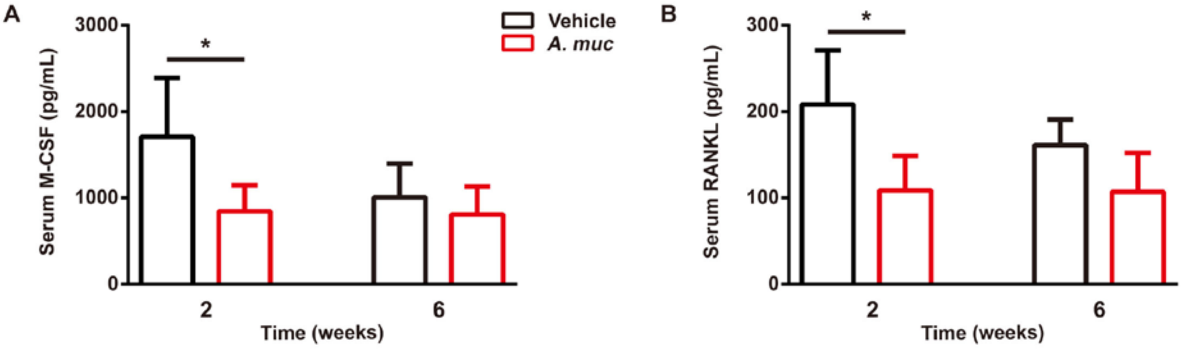

Fig. S2. *A. muc* decreases circulatory levels of M-CSF and RANKL. (A) Serum concentrations of M-CSF (A) and RANKL (B) detected by ELISA at 2 and 6 WPF. *n* = 5 per group. $^{*}P < 0.05$ by unpaired two tailed Student's *t* test.

Table S1: Primers used for 16S rDNA qRT-PCR in Figure S1

Target group	Primer sequence
Universal	AAACTCAAAKGAATTGACGG CTCACRRCACGAGCTGAC
α-Proteobacteria	CIAGTGTAGAGGTGAAATT CCCCGTCAATTCCTTTGAGTT
γ-Proteobacteria	TCGTCAGCTCGTGTYGTGA CGTAAGGGCCATGATG
Bacteroidetes	CRAACAGGATTAGATACCCT GGTAAGGTTCCTCGCGTAT
Firmicutes	TGAAACTYAAAGGAATTGACG ACCATGCACCACCTGTC
Actinobacteria	TACGGCCGCAAGGCTA TCRTCCCCACCTTCCTCCG