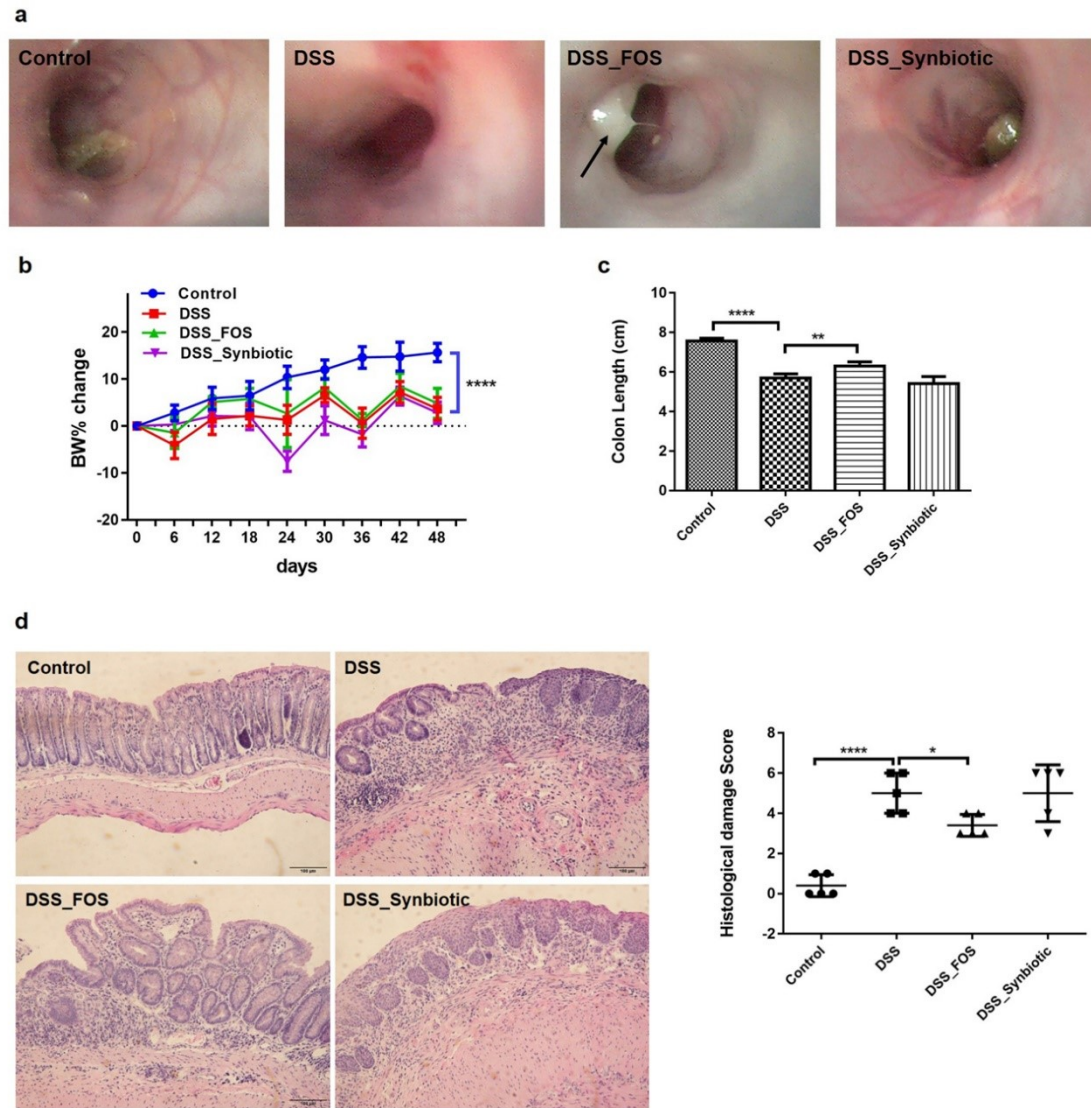


cTable s1 Primer sequences for reference and target genes

Genes	Primer sequences (5' to 3')
GAPDH	forward: TGGTCCTCAGTGTAGCCCAAG
	reverse: CTGCCAGAACATCATCCCT
Claudin	forward: AAAGCACCGGGCAGATACAG
	reverse: ACTAATGTCGCCAGACCTGAA
Occludin	forward: TCTGACTATGCGGAAAGAGTTG
	reverse: TCTAGGTTACCATTGCTGCTGT
ZO-1	forward: CAAAGAAGGCTTAGAGGAAGG
	reverse: TAGGGAGGTCAAGGAGGAAAA
MUC2	forward: GACCTCCACCCCTACAAACA
	reverse: TTGTTCCAGGGGATGATGCT
TNF- α	forward: GCTCCTCCACTTGGTGGTTT
	reverse: AGGCGGTGCCTATGTCTCAG
IL-4	forward: TCATCCTGCTCTTCTTTCTCG
	reverse: CCTTCTCCTGTGACCTCGTT
IL-6	forward: AGTTGTGCAATGGCAATTCTGA
	reverse: TCTGGCTTTGTCTTTCTTGTTATCTTT
IL-17	forward: GAGCTTCATCTGTGTCTCTGAT
	reverse: GCCAAGGGAGTTAAAGACTTTG
IL-10	forward: GCTCTTACTGACTGGCATGAG
	reverse: CGCAGCTCTAGGAGCATGTG



sFig. 1. The effects of FOS and the synbiotic on chronic colitis mice

After 3 rounds of 2% DSS administration, the mice underwent colonoscopy examination (a). “Control” represented the control group for chronic colitis group. “DSS”, “DSS_FOS” and “DSS_Synbiotic” represented the untreated, FOS-treated and Synbiotic-treated chronic colitis groups respectively. The arrow indicated the mucus accumulated at colon mucosa. The colitis activity in each group mice were evaluated through measurement of body weight change (b), colon length (c) and histological analysis (d). *P* values were analyzed by two-tailed unpaired *t*-test (b, c) or two-tailed unpaired Mann-Whitney test (d). * *P* < 0.05, ** *P* < 0.01, **** *P* < 0.0001, *n* ≥ 5.

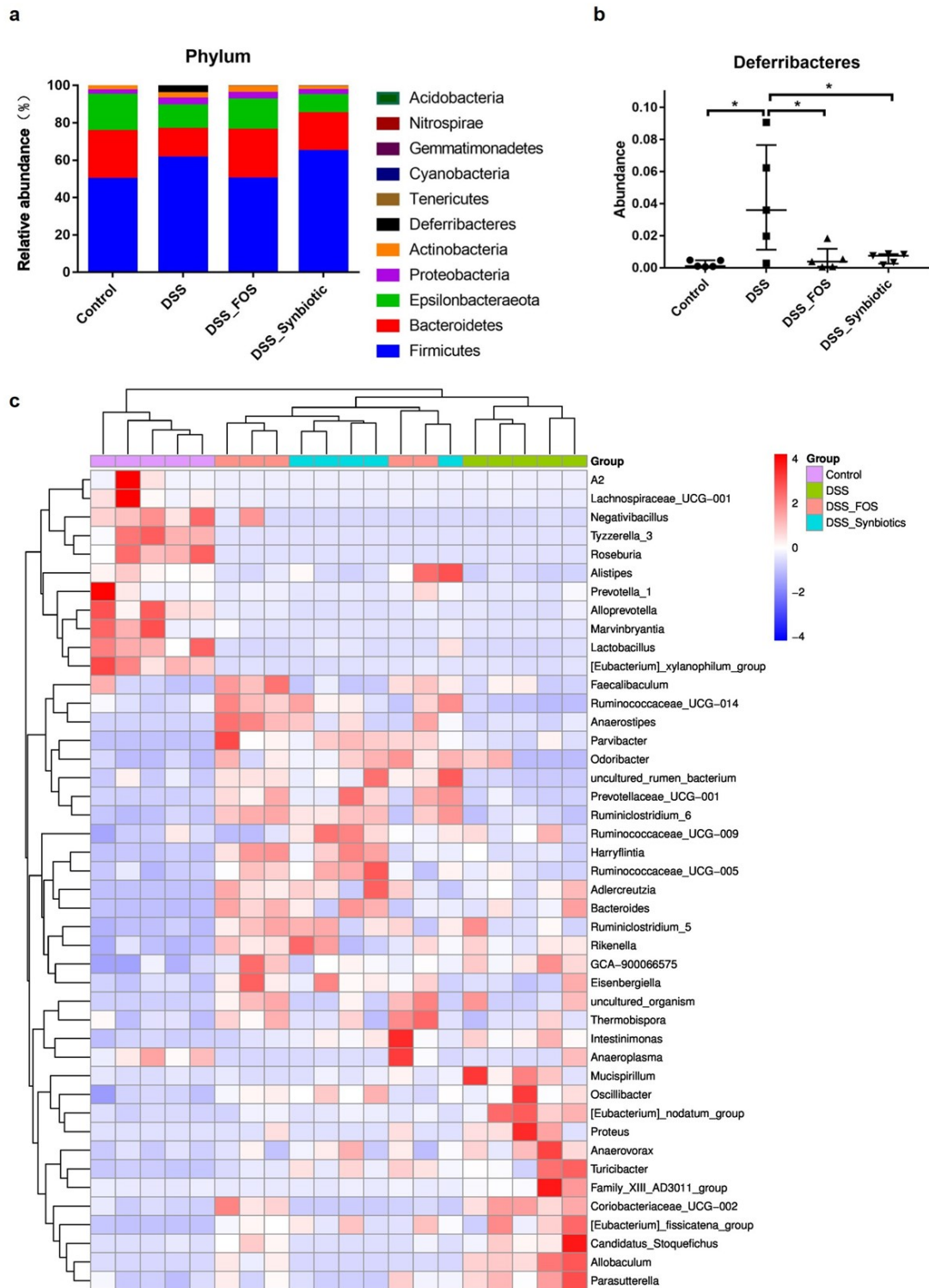
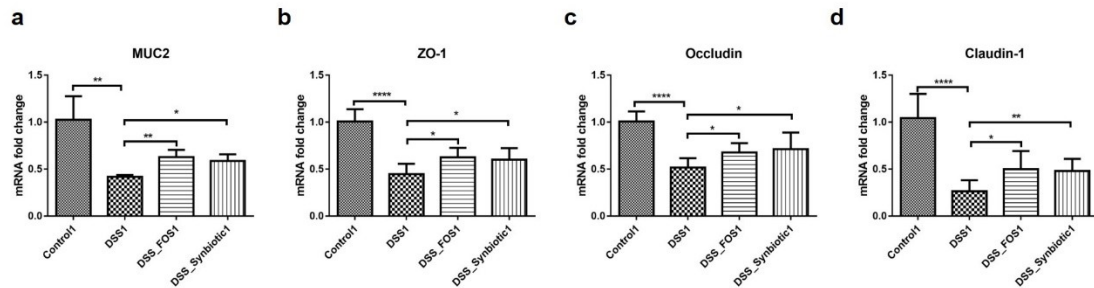


Fig. 2. The alterations of microbial composition in acute colitis mice

The microbial composition of colon mucosa was analyzed by 16s rDNA sequencing in each group mice. “Control” represented the control group for acute colitis group. “DSS”, “DSS_FOS” and “DSS_Synbiotic” represented the untreated, FOS-treated and Synbiotic-treated acute colitis groups respectively. (a) The microbial composition based on relative abundance at phylum level.

(b) Relative abundance of *Deferribacteres*. The pairwise comparisons were performed by Wilcoxon rank sum test. * $P < 0.05$, $n=5$. (c) Heatmap based on relative abundance at genus level.



sFig. 3. mRNA expression of MUC2 and tight junction proteins in acute colitis mice

The colonic expression of MUC2 (a), ZO-1 (b), Occludin (c), and Claudin-1 (d) in each group mice were examined by quantitative PCR. P values were analyzed by two-tailed unpaired t -test (a-d). * $P < 0.05$, ** $P < 0.01$, *** $P < 0.0001$, $n \geq 5$.