

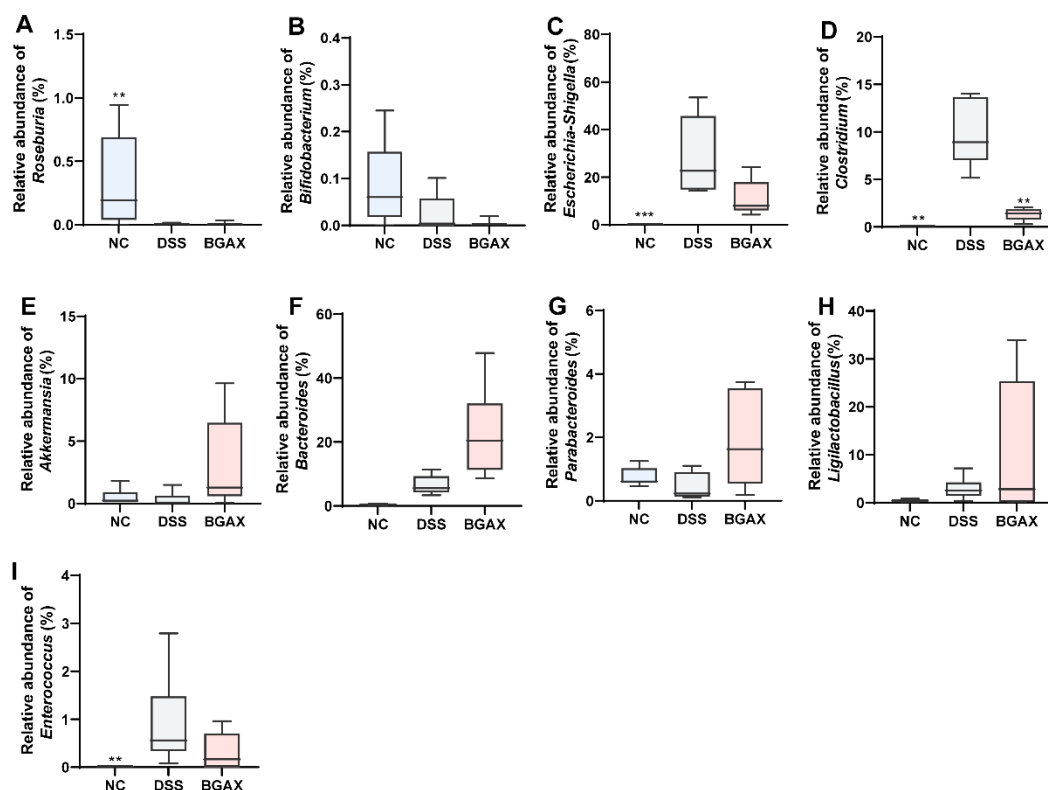


Fig. S1. Changes in the relative abundance at the genus level. Relative abundances of (A) *Roseburia*; (B) *Bifidobacterium*; (C) *Escherichia-Shigella*; (D) *Clostridium*; (E) *Akkermansia*; (F) *Bacteroides*; (G) *Parabacteroides*; (H) *Ligilactobacillus*; (I) *Enterococcus*. Data are expressed as the mean $\pm$ SEM. $n = 6$ mice per group. * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$ were compared with the DSS group.

Table S1 Primer sequence of inflammatory factors genes

Primer Name	Sequence (5' to 3')
<i>Il6</i> -F	TACCACTTCACAAGTCGGAGGC
<i>Il6</i> -R	CTGCAAGTGCATCATCGTTGTTC
<i>Il10</i> -F	CGGGAAGACAATAACTGCACCC
<i>Il10</i> -R	CGGTTAGCAGTATGTTGTCCAGC
<i>Tnfα</i> -F	GGTGCCTATGTCTCAGCCTCTT
<i>Tnfα</i> -R	GCCATAGAACTGATGAGAGGGAG
<i>Il1b</i> -F	TGGACCTTCCAGGATGAGGACA
<i>Il1b</i> -R	GTTCATCTCGGAGCCTGTAGTG
β -actin-F	GGCTGTATTCCCCTCCATCG
β -actin-R	CCAGTTGGTAACAATGCCATG