

Figure S1. Gut microbiota composition at the phylum level. **(A)** Bar plot of gut microbiota composition at the phylum level; **(B)** Relative abundance of Bacteroidetes across each grouped microbiomes; **(C)** Relative abundance of Firmicutes across each grouped microbiomes; **(D)** Relative abundance of Verrucomicrobia across each grouped microbiomes; **(E)** Relative abundance of Proteobacteria across each grouped microbiome. NC, normal control group; MC, model control group; BL, low-dose *B. lactis* XLTG11; BH, high-dose *B. lactis* XLTG11. All data are expressed as mean \pm SD. Different letters indicate statistically significant differences between the groups ($p < 0.05$).

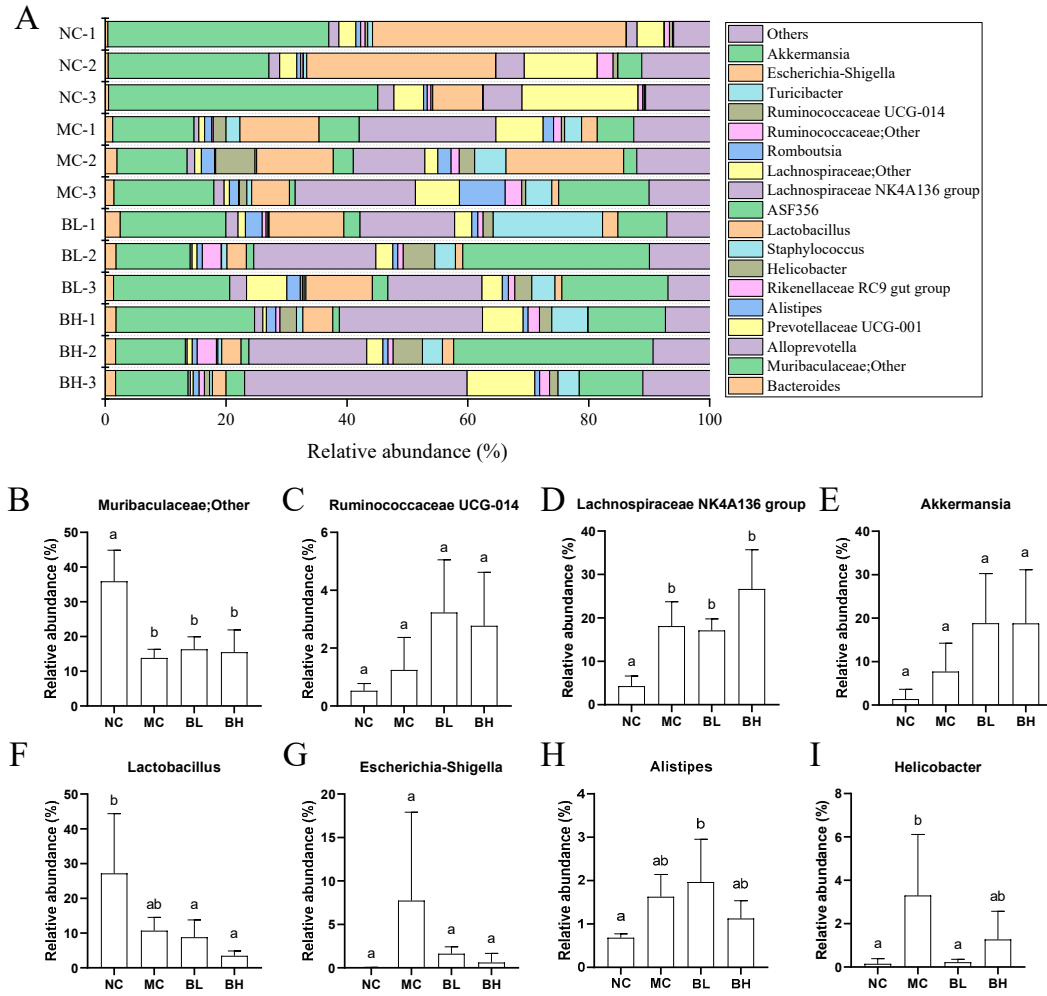


Figure S2. Gut microbiota composition at the genus level. (A) Bar plot of gut microbiota composition at the genus level; (B) Relative abundance of *Muribaculaceae;Other* across each grouped microbiomes; (C) Relative abundance of *Ruminococcaceae UCG-014* across each grouped microbiomes; (D) Relative abundance of *Lachnospiraceae NK4A136 group* across each grouped microbiomes; (E) Relative abundance of *Akkermansia* across each grouped microbiomes; (F) Relative abundance of *Lactobacillus* across each grouped microbiomes; (G) Relative abundance of *Escherichia-Shigella* across each grouped microbiomes; (H) Relative abundance of *Alistipes* across each grouped microbiomes; (I) Relative abundance of *Helicobacter* across each grouped microbiomes. NC, normal control group; MC, model control group; BL, low-dose *B. lactis* XLTG11; BH, high-dose *B. lactis* XLTG11. All data are expressed as mean \pm SD. Different letters indicate statistically significant differences between the groups ($p < 0.05$).