Supporting information for:

Analysis of the key genes of *Lactobacillus reuteri* strains involved in the protection of alcohol-induced intestinal barrier damage

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Method of bacteria suspension preparation:

The bacteria activated to the third generation in MRS liquid culture medium was diluted with physiological saline to obtain four gradient dilutions of 10^{-4},10^{-5},10^{-6},10^{-7}. Take 100ul of each dilution and apply it to the MRS solid plate, with three parallel gradients for each gradient. After incubation at 37°C for 24 hours at a constant humidity, plate counts were performed to determine the final volume of bacterial sludge resuspension. Subsequently, the third-generation strain was inoculated into the same batch of liquid culture medium, and was cultured under the same culture conditions; after 12 h, the bacterial solution was centrifuged at 8000 × g for 10 min at 4°C, and the supernatant was discarded. According to the plate count results, add a certain volume of sterile physiological saline to the obtained bacterial slurry before each gastric administration. Resuspend the strain until the final concentration of the strain suspension is 10^9 CFU/ml.

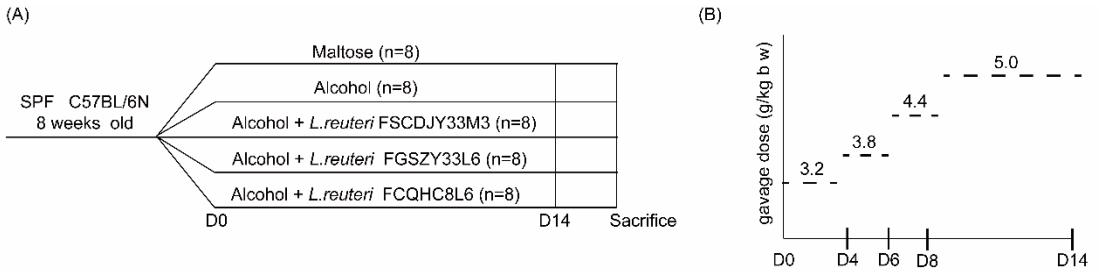

Figure S1. Experimental design of changes of gut microbiota homeostasis in mice after continuous alcohol intake

(A) Animal experimental design. (B) Changes of alcohol intragastric gradient.

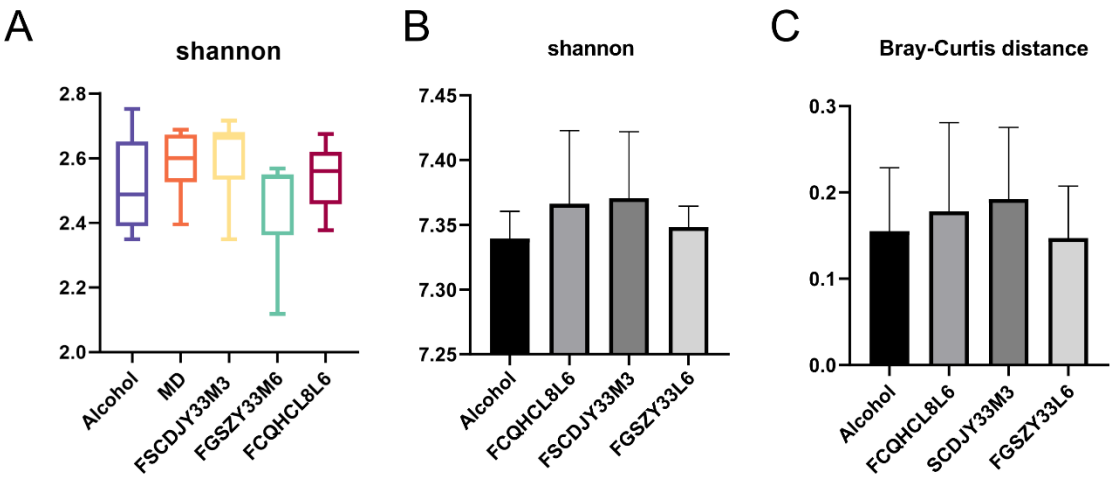

Figure S2. Effects of *Lactobacillus reuteri* FSCDJY33M3, FCQHC8L6, and FYND33L6 on the α diversity and metabolic homeostasis of microbiota.

(A) α diversity of intestinal flora changes in mice after alcohol intake. (B) α diversity changes in the KEGG pathway. (C) β diversity changes in the KEGG pathway.