

Supplementary material

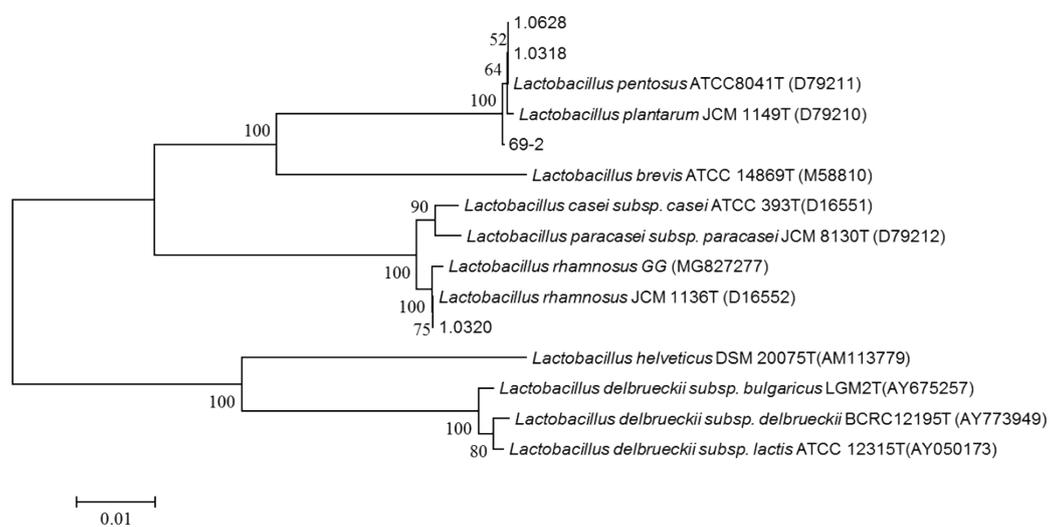


Fig. S1 Phylogenetic tree of *L. rhamnosus* 1.0320 and other strains based on 16S rRNA gene sequences.

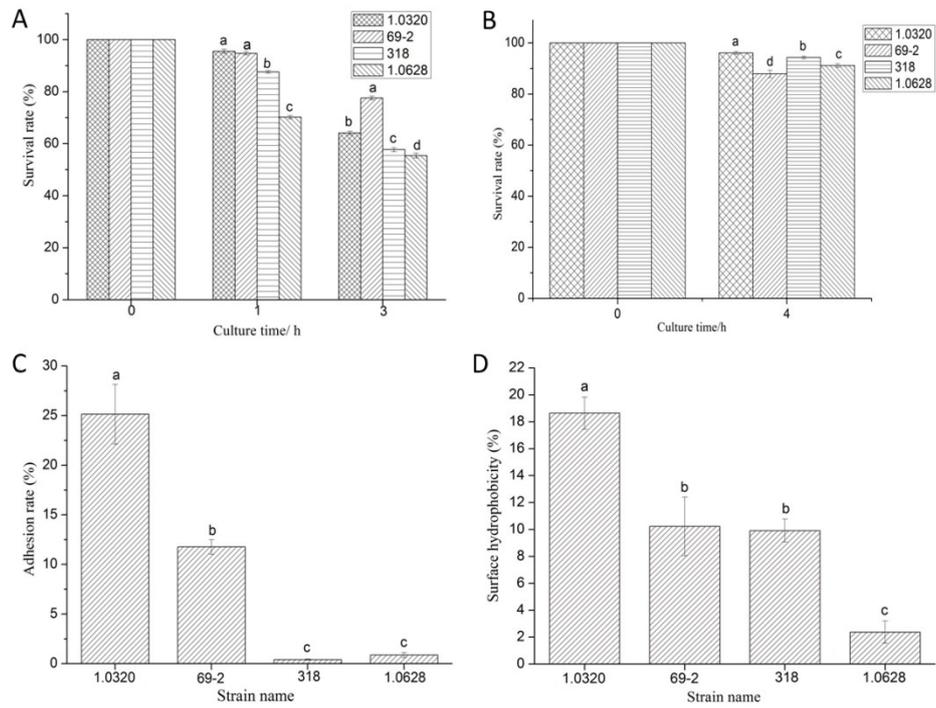
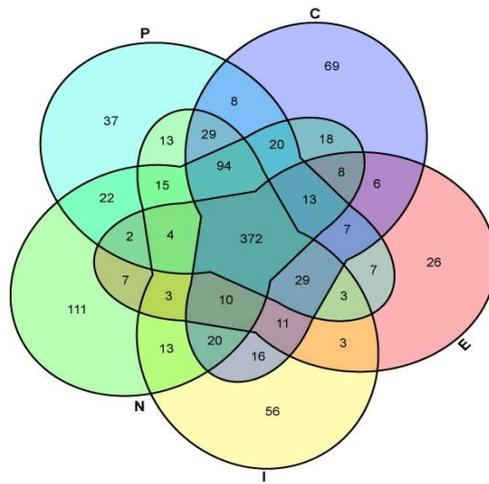
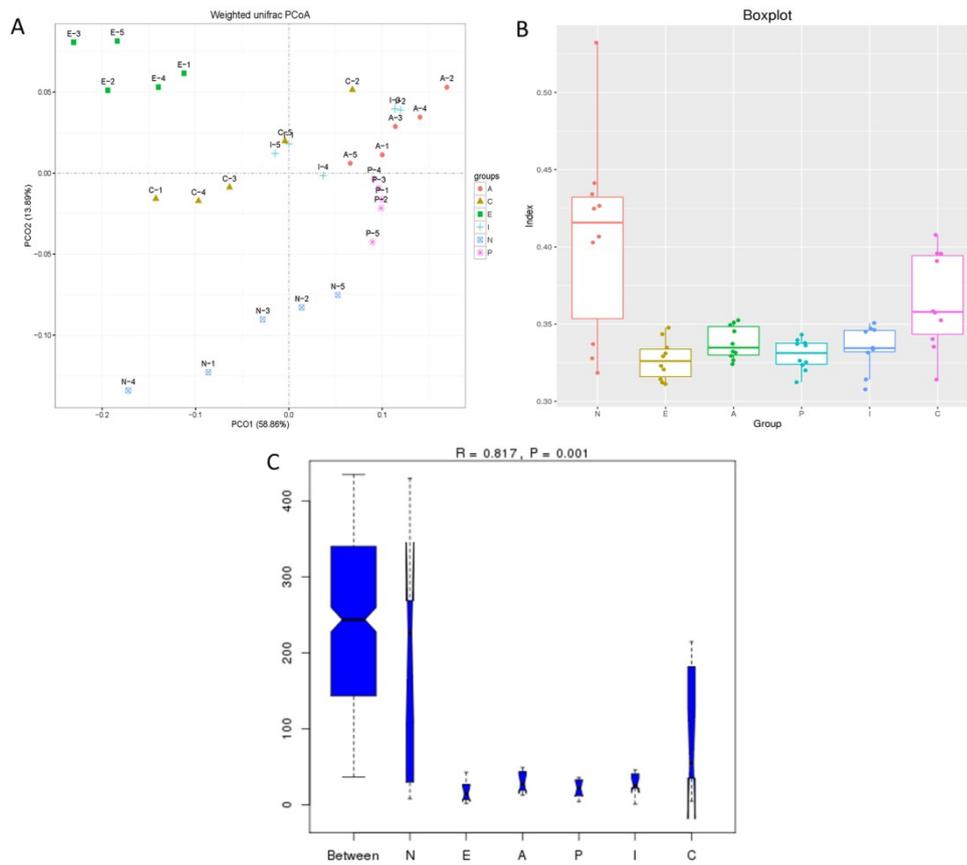


Fig. S2 Determination of probiotic characteristics of *L. rhamnosus* 1.0320. (A) Acid resistance of Lactobacillus strains to pH3; (B) Bile salt resistance of Lactobacillus strains to 0.3% bile salt; (C) Adhesion ability of Lactobacillus strains to Caco-2 cells; (D) Surface hydrophobicity ability of Lactobacillus strains. All data are expressed as mean \pm SD. Different letters indicate significant difference ($P < 0.05$) among groups.



Note: N: Normal group, E: Enteritis group, A: Antibiotic group, P: Probiotics group, I: Inulin group, C: Combination group

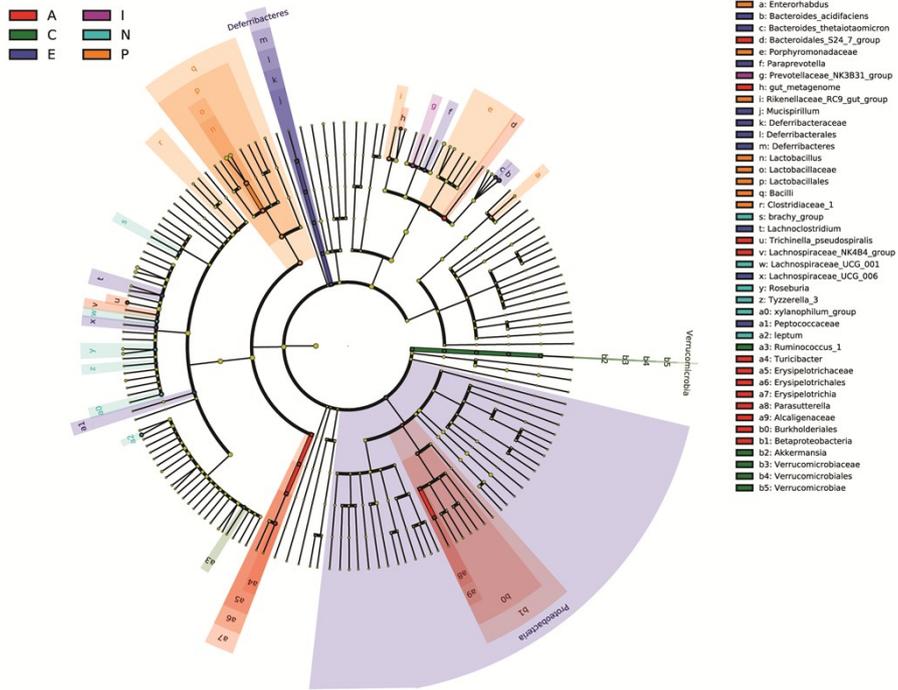
Fig. S3 VEEN diagram representation of the number of OTUs. n = 5 per group.



Note: N: Normal group, E: Enteritis group, A: Antibiotic group, P: Probiotics group, I: Inulin group, C: Combination group

Fig. S4 Influences of *L. rhamnosus* 1.0320 combined with inulin treatment on gut microbiota β -diversity. (A) PCoA analysis; (B) Unifrac distance matrix analysis; (C) ANOSIM analysis. $n = 5$ per group.

Cladogram



Note: N: Normal group, E: Enteritis group, A: Antibiotic group, P: Probiotics group, I: Inulin group, C: Combination group

Fig. S5 Lefse analysis of different samples. n = 5 per group.