

Supplementary Figure

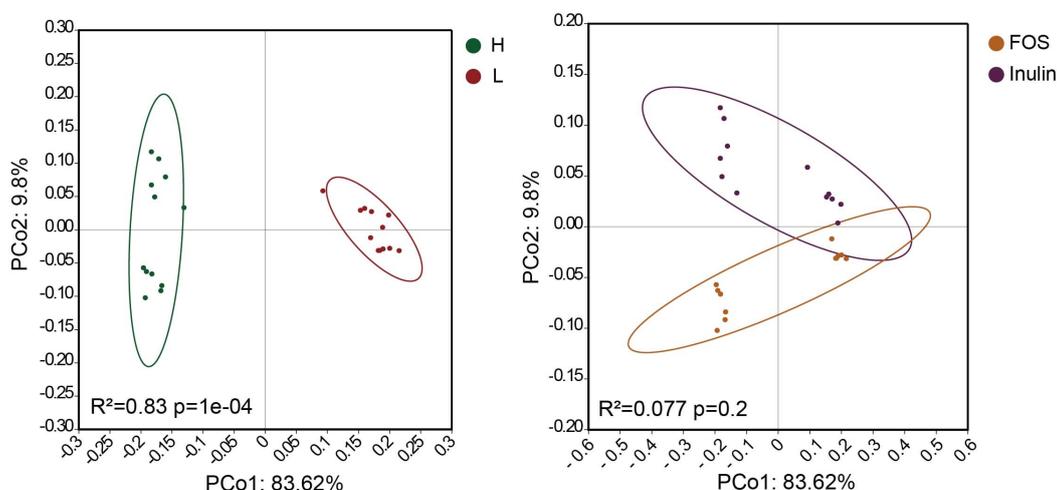


Figure S1. Effect of baseline Ba/Bi ratio and prebiotic species on microbiota β -diversity.

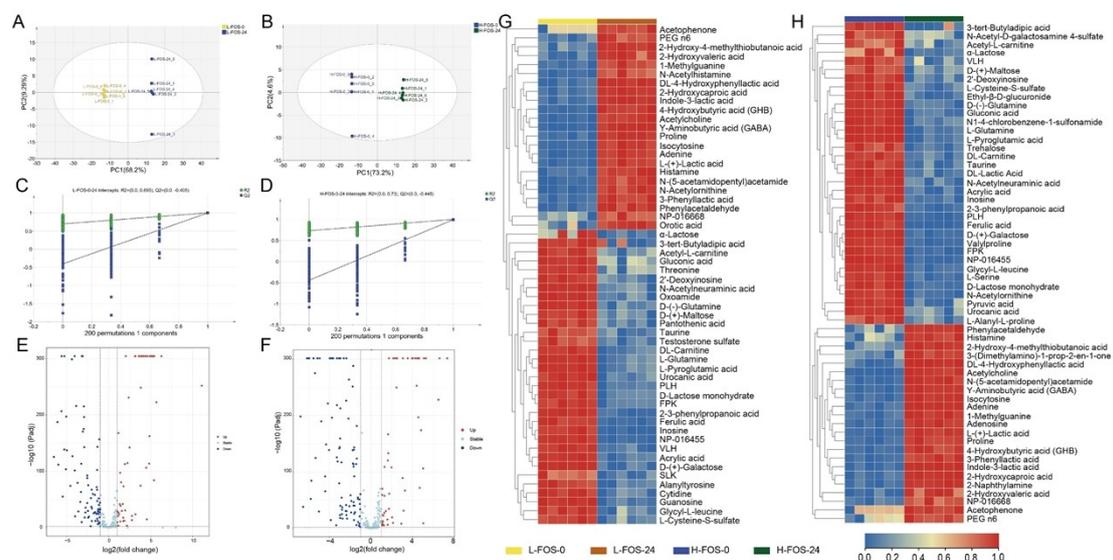


Figure S2. Effect of FOS fermentation on H, L metabolite differences. (A-B) OPLS-DA score plots comparing fermentation broth metabolites before and after FOS intervention in L and H. (C-D) 200-fold cross-validation test for OPLS-DA analysis. (E-F) Volcano plots of differential metabolites. Red dots, significantly up-regulated metabolites. Blue dots, significantly down-regulated genes. Light blue dots, metabolites with no obvious differences. (G-H) Clustered heatmaps of differential metabolites (H: L, H: H). $|FC| > 2.0$, $P < 0.05$, $VIP > 1$).

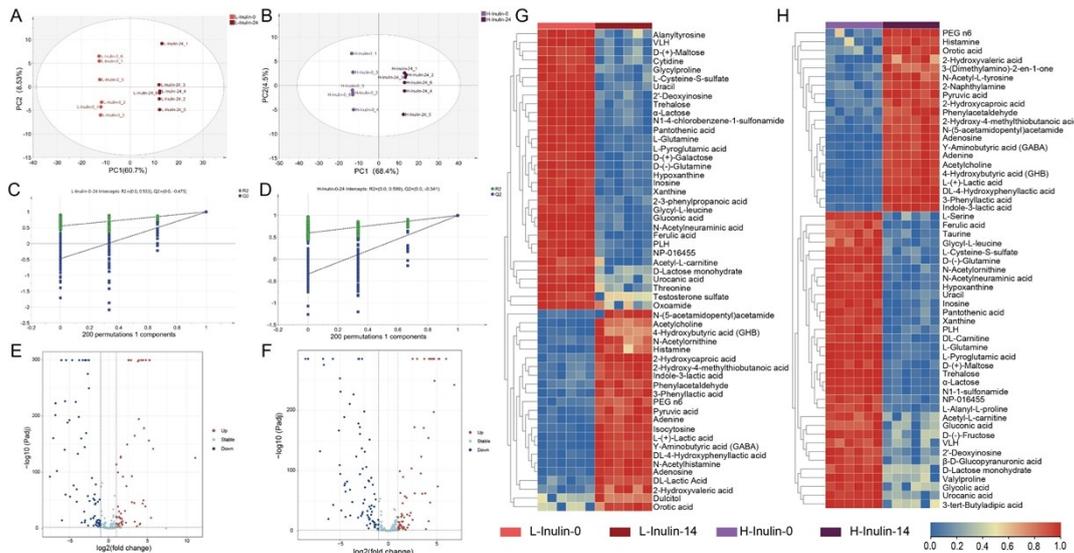


Figure S3. Effect of inulin fermentation on H, L metabolite differences. (A-B) OPLS-DA score plots comparing fermentation broth metabolites before and after inulin intervention in L and H. (C-D) 200-fold cross-validation test for OPLS-DA analysis. (E-F) Volcano plots of differential metabolites. Red dots, significantly up-regulated metabolites. Blue dots, significantly down-regulated genes. Light blue dots, metabolites with no obvious differences. (G-H) Clustered heatmaps of differential metabolites (H-I: L, H. $|FC| > 2.0$, $P < 0.05$, $VIP > 1$).

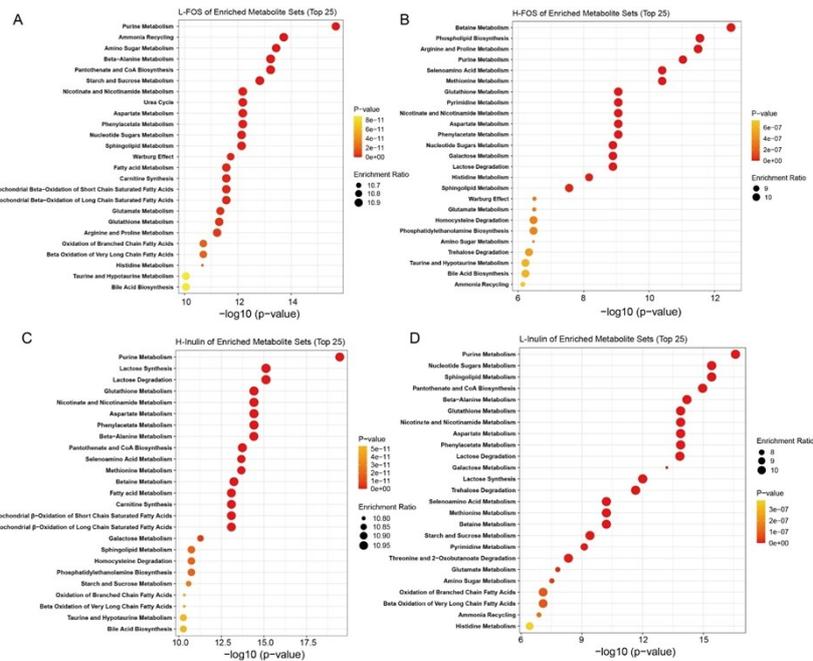


Figure S4. Enrichment of the differential metabolite KEGG pathway. (A) Enrichment

of the differential metabolite KEGG pathway after fermentation with FOS in L; (B) Enrichment of the differential metabolite KEGG pathway after fermentation with FOS in H; (C) Enrichment of the differential metabolite KEGG pathway after fermentation with inulin in L; and (D) Enrichment of the differential metabolite KEGG pathway after fermentation with inulin in H.

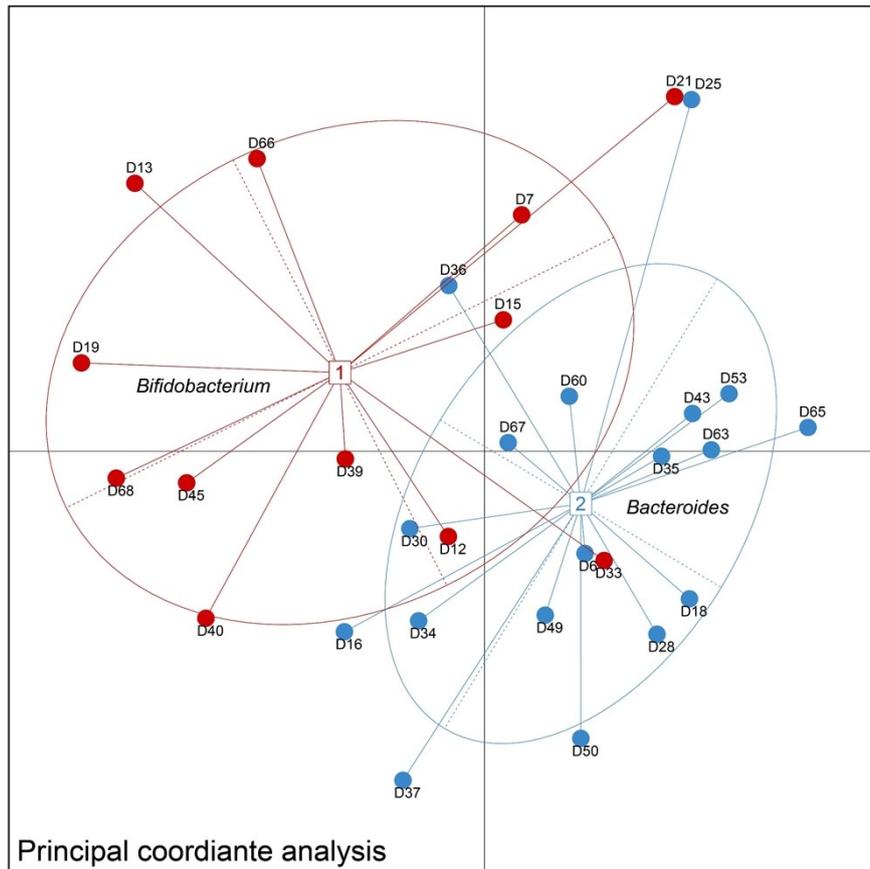


Figure S5. PCoA plot showing two enterotypes.