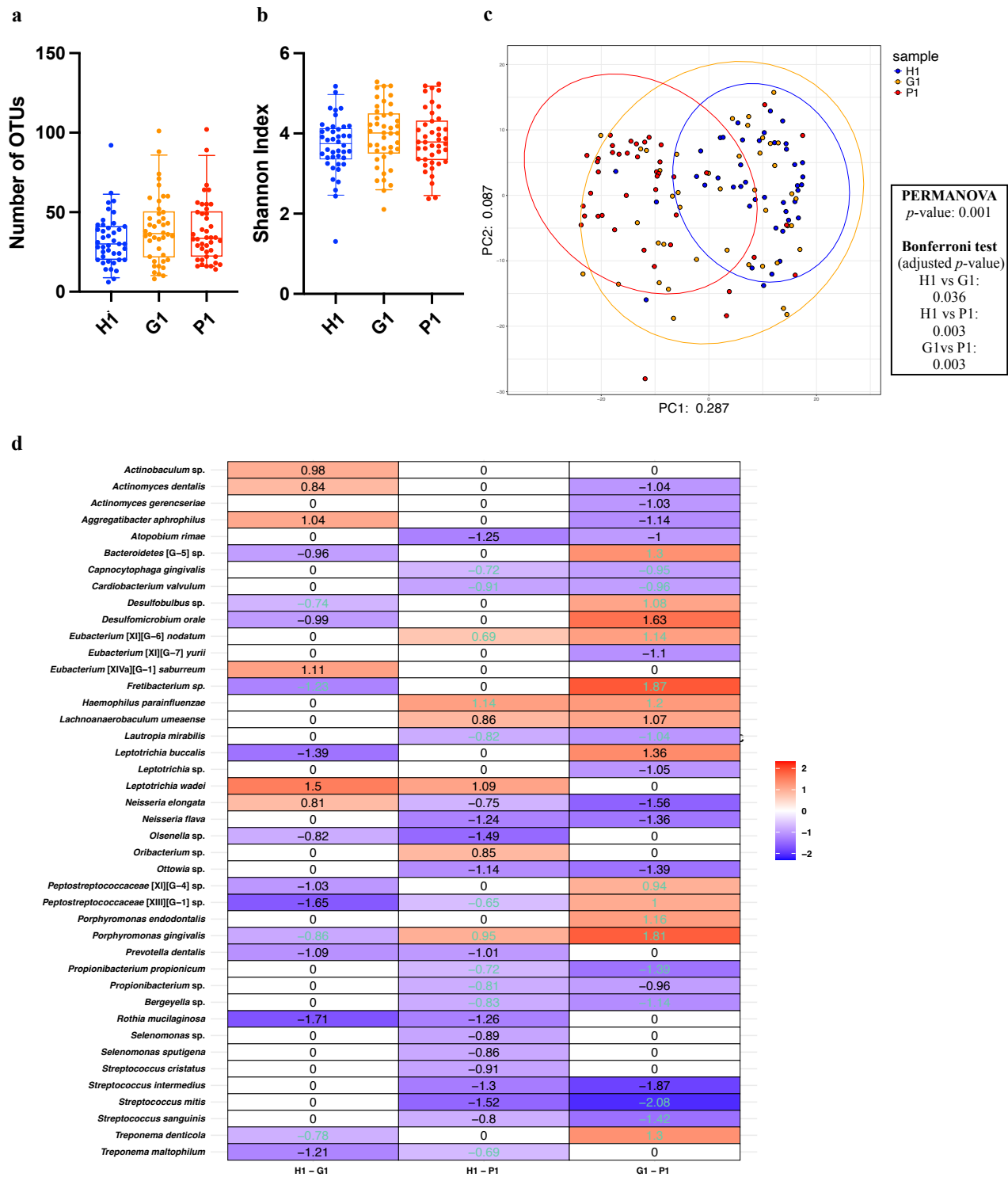


Fig. S1



Supplementary Fig. S1 Bacterial community and differentially abundant taxa analysis of pre-treatment data from 42 subjects. (a, b) α diversity analysis using the number of OTUs and Shannon index. (c) β diversity analysis using PCA and PERMANOVA with Aitchison distance. The plots show each sample, and the ellipses indicate 95% confidence intervals. (d) Differentially abundant taxa between groups were identified using ANCOM-BC2. The log fold changes (LFC) for the right group relative to the left group are shown at the bottom of each column of the heatmap.