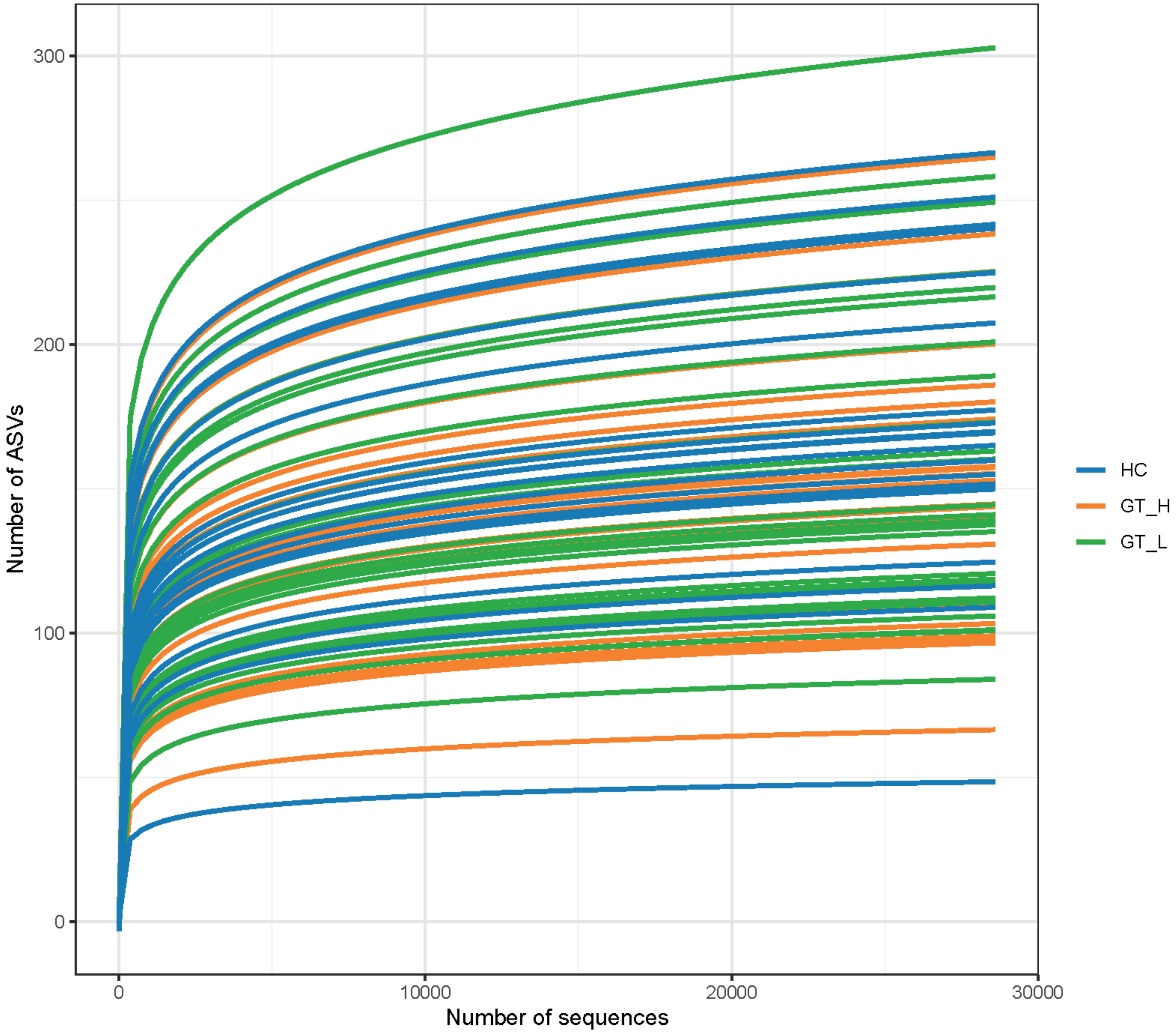

Fig. S1. Rarefaction analysis of bacterial 16S rRNA gene sequences was performed to evaluate whether further sequencing would likely detect additional taxa, indicated by a plateau. Different colors represent different samples.

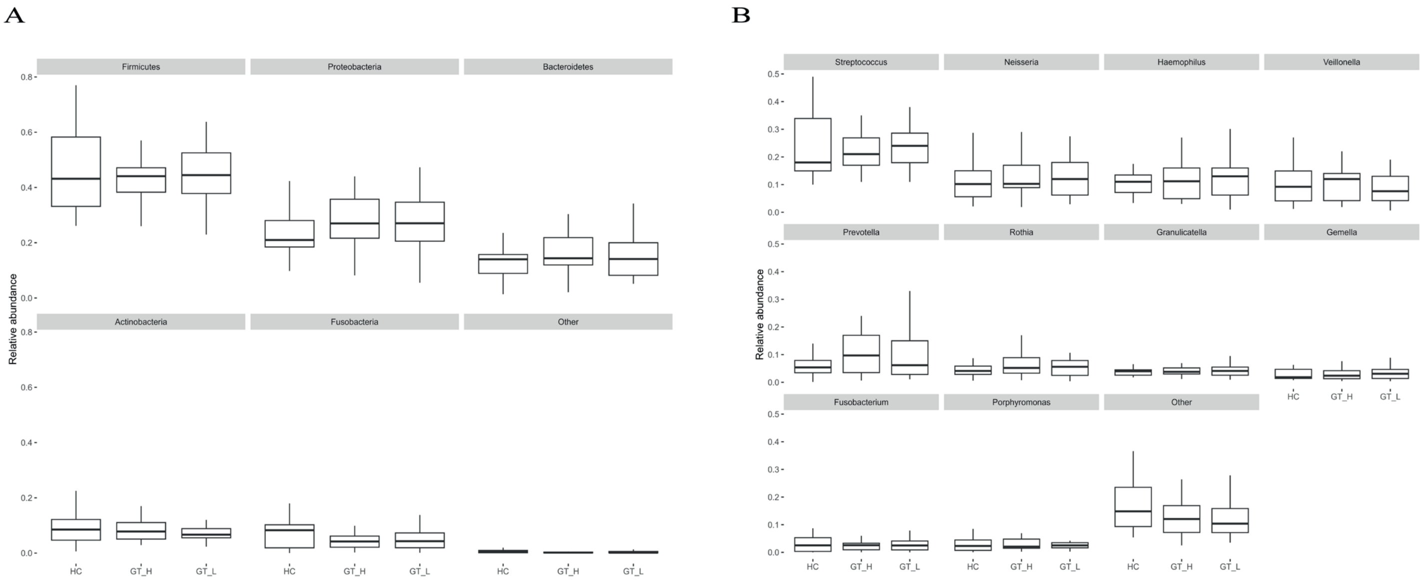

Fig. S2. Composition of bacterial communities in different groups at the phylum and genus levels. A: Relative abundance of bacterial phyla in different groups. B: Relative abundance of bacterial genus in different groups.

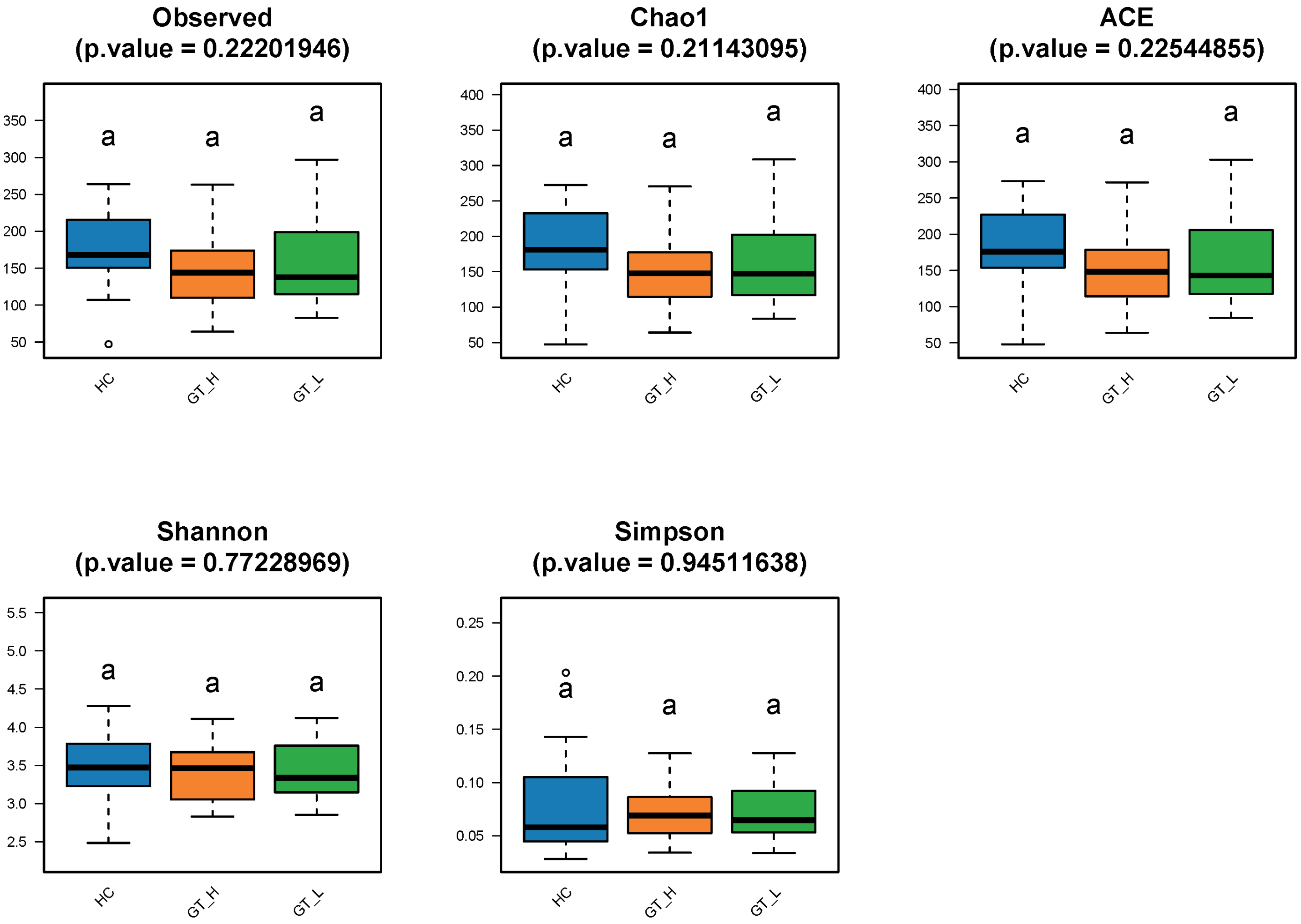

Fig. S3. Phylogenetic diversity of microbiota in different groups. The alpha diversity was estimated by OTUs.

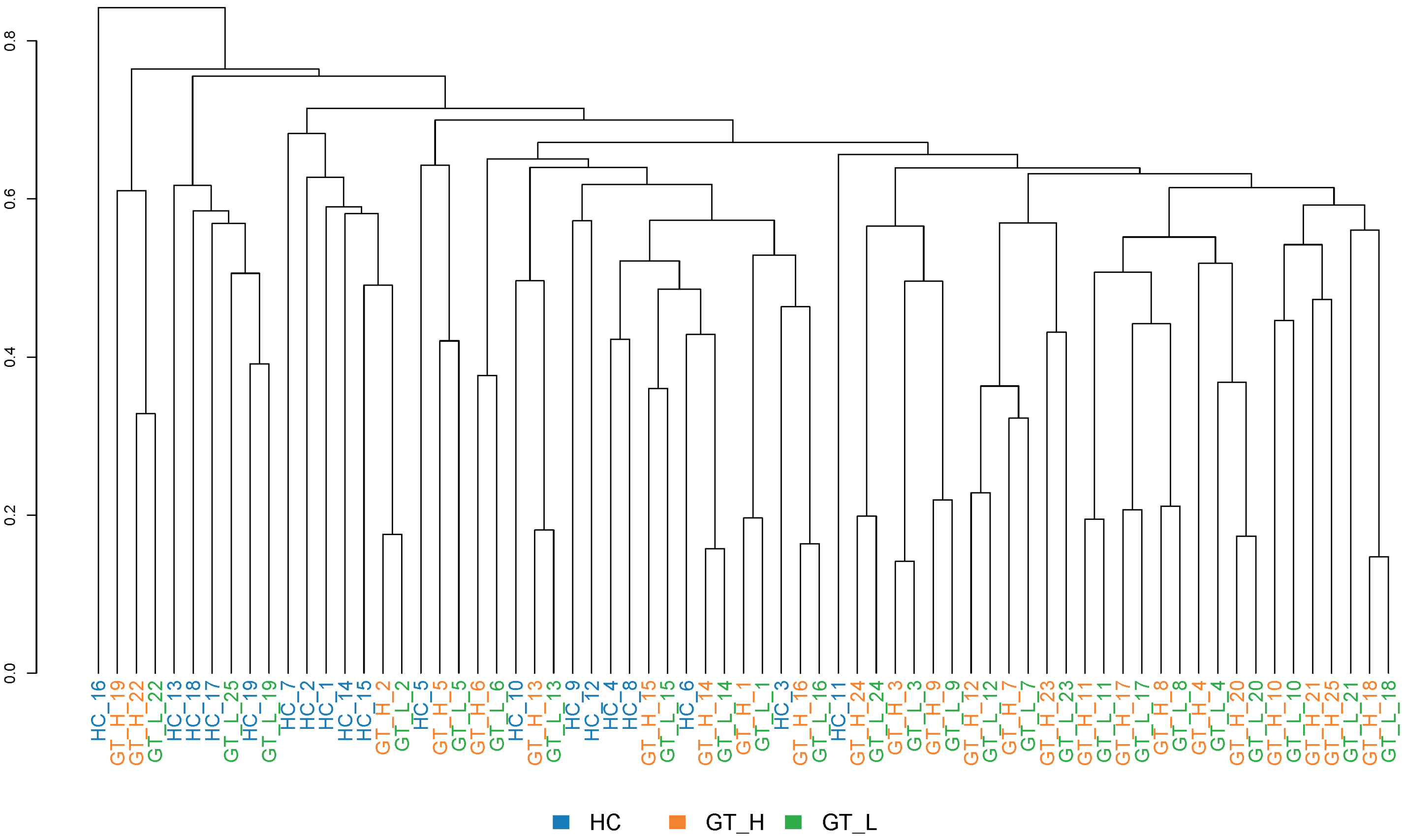

Fig. S4. Cluster of the samples using the abundance of OTUs.

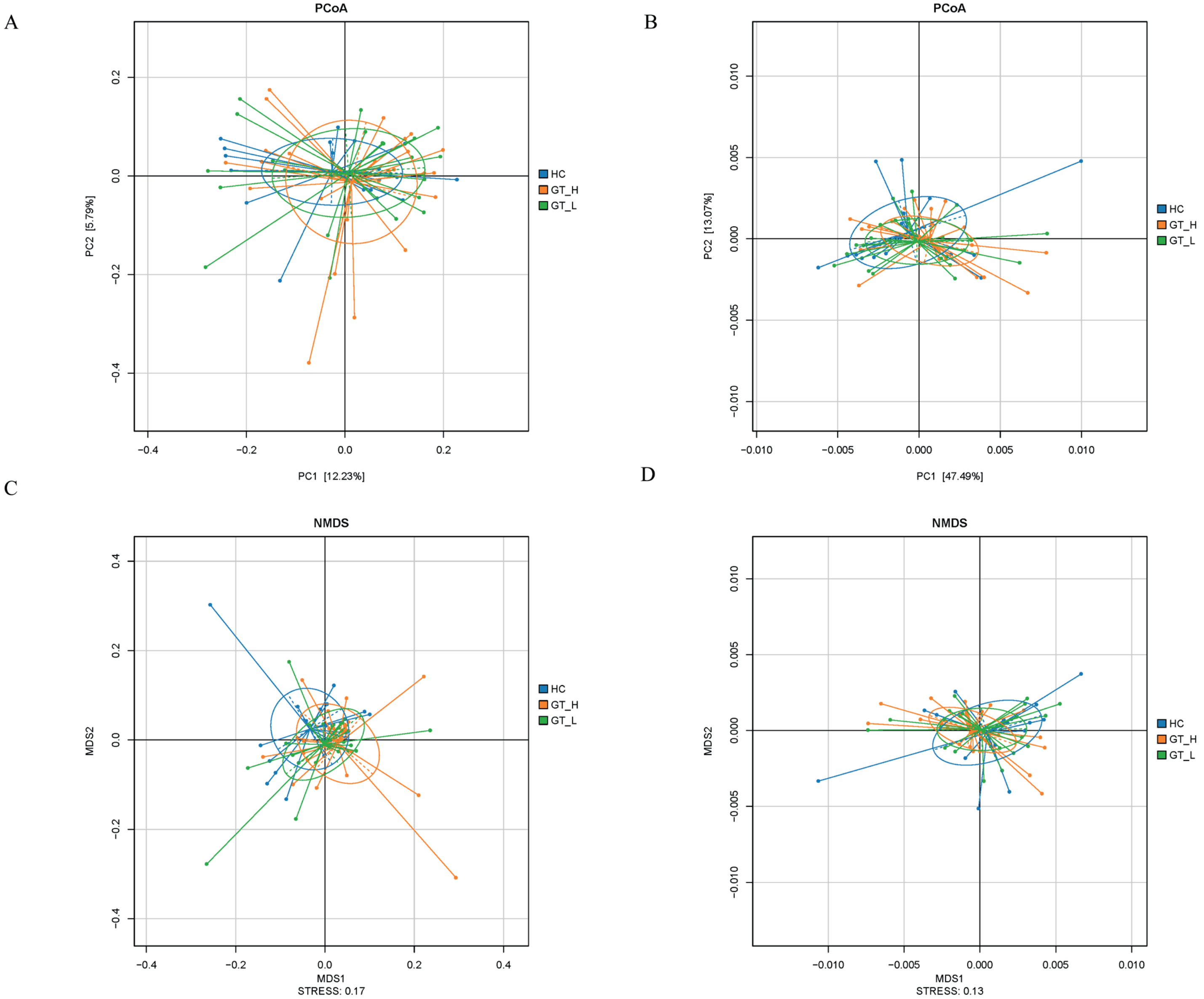

Fig. S5. Beta diversity analysis at different sites. A-B: PCOA analysis for different groups based unweighted or weighted UniFrac distance respectively. C-D: NMDS analysis for different groups based unweighted or weighted UniFrac distance respectively.

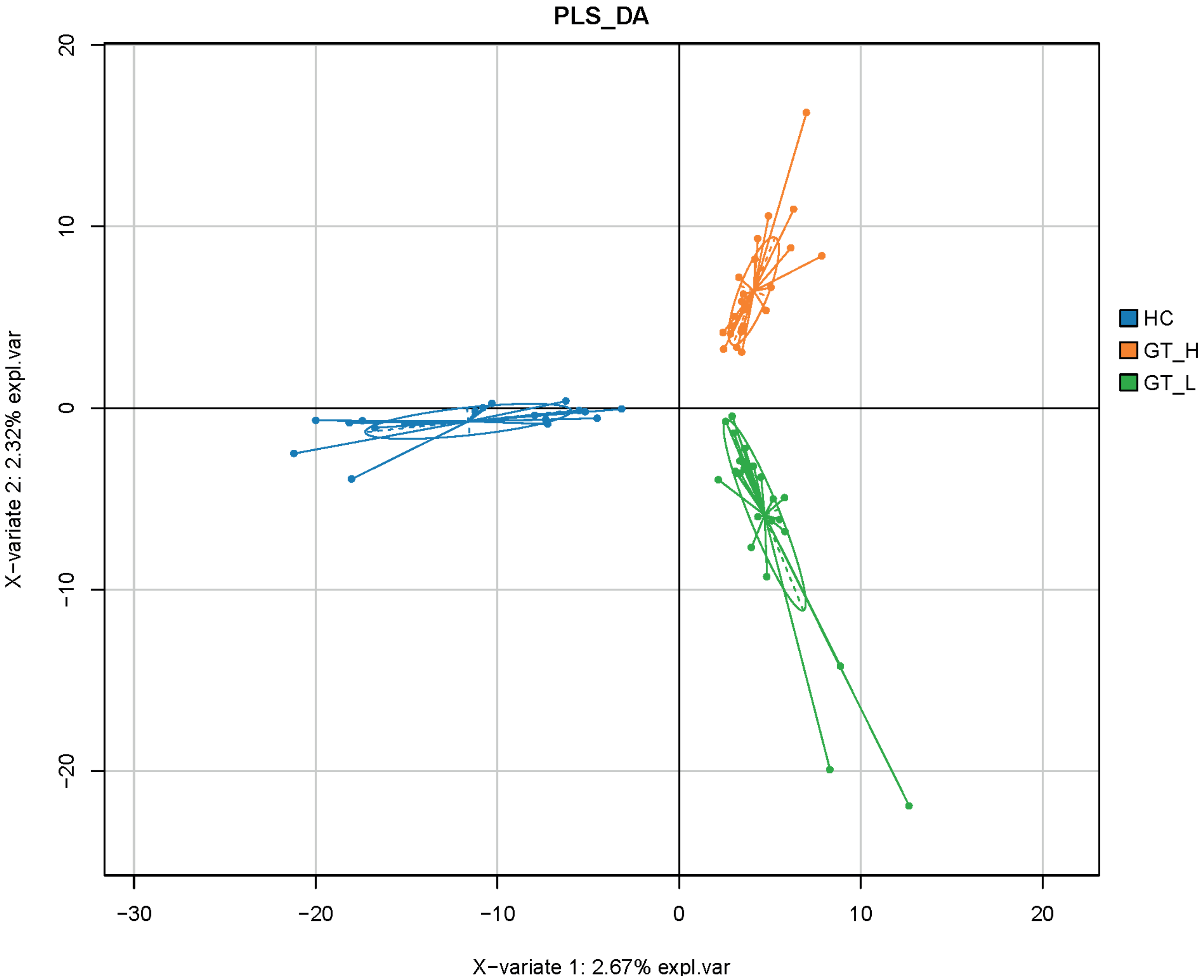

Fig. S6. PLS-DA (Partial Least Squares Discriminant Analysis) analysis.

Fig. S7. The differentially enriched COG function predicted by PICRUSt2 was determined by STAMP. A: Differentially enriched COG function at lingual in heathy controls (HC) and geographic tongue patients (GT-H). B: Differentially enriched COG function at normal lingual (GT-H) or lesion (GT-L) in geographic tongue patients.

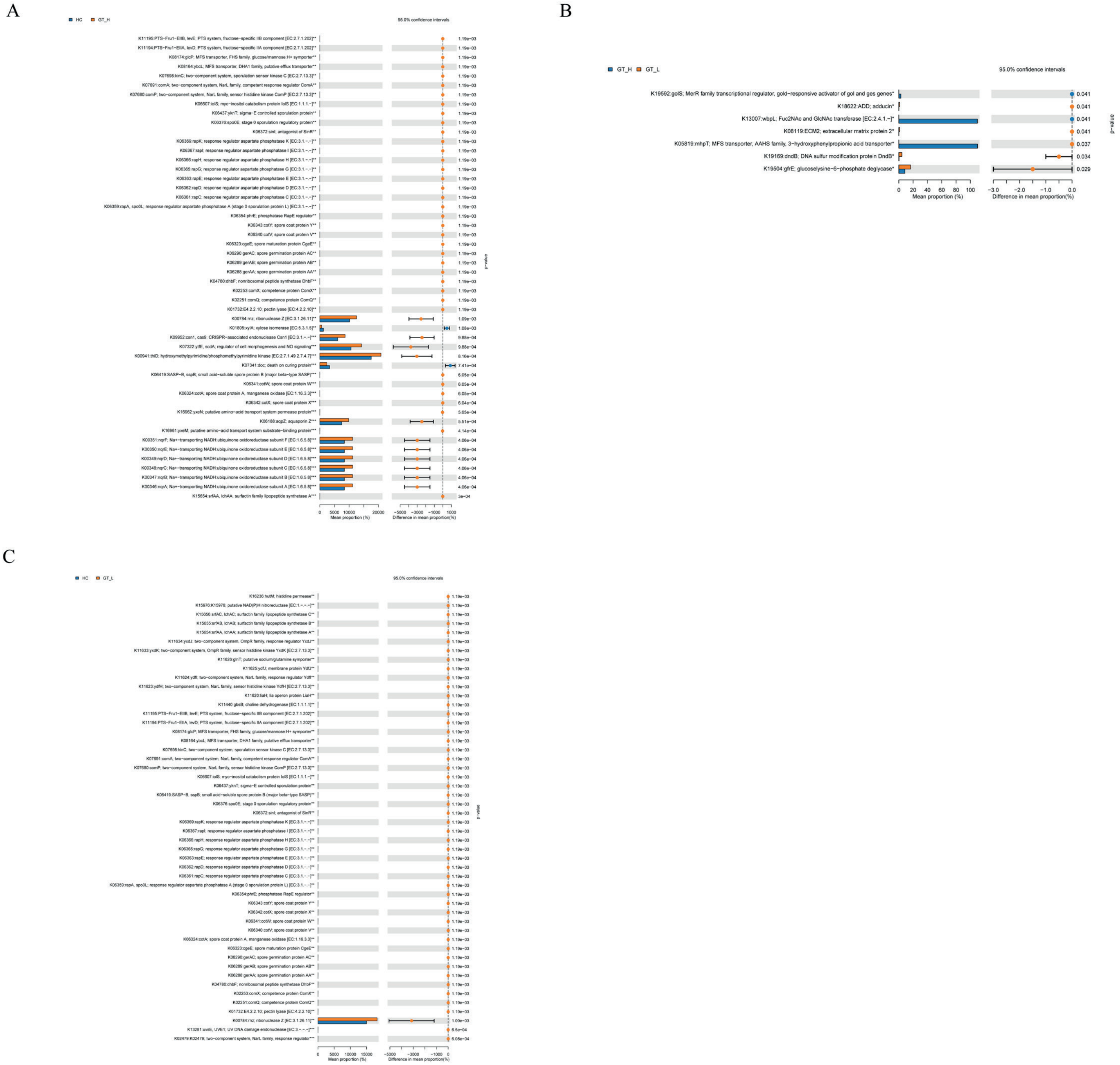

Fig. S8. The differentially enriched KO function predicted by PICRUSt2 was determined by STAMP. A: Differentially enriched KO function at lingual in heathy controls (HC) and geographic tongue patients (GT-H). B: Differentially enriched KO function at normal lingual (GT-H) or lesion (GT-L) in geographic tongue patients.

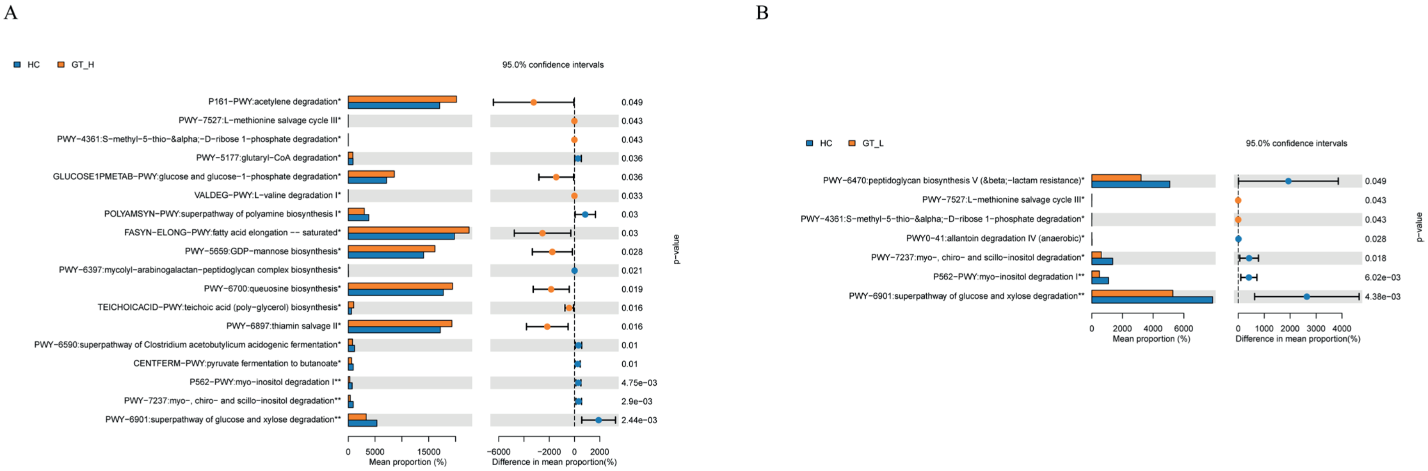

Fig. S9. The differentially enriched METACYC function predicted by PICRUSt2 was determined by STAMP. A: Differentially enriched METACYC function at lingual in heathy controls (HC) and geographic tongue patients (GT-H). B: Differentially enriched METACYC function at normal lingual (GT-H) or lesion (GT-L) in geographic tongue patients.