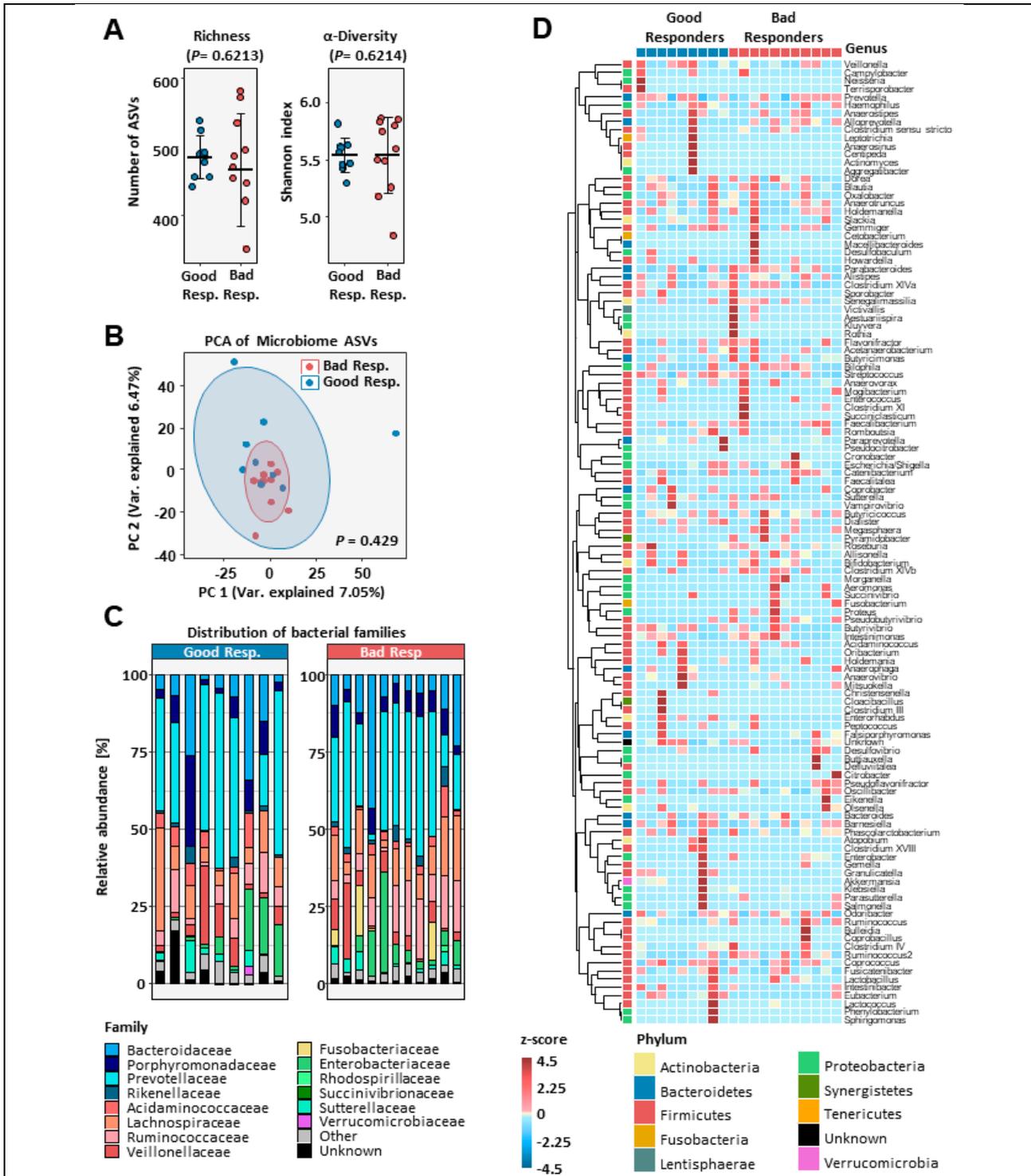


Supplemental Material



Supplemental Figure S1: Analysis of the microbiome taxonomic community structure of good responders and bad responders to RYGB surgery. In panel (A), richness (i.e. number of amplicon sequencing variants /ASV) and alpha-diversity based on the Shannon index calculated using the distribution of ASVs is depicted, with significance calculated by Kruskal-Wallis test. (B) depicts the beta-diversity or diversity between samples using principal component with PERMANOVA to calculate significance of difference between the two groups. (C) reveals the distribution of microbial families in each sample and (D) depicts the relative abundance based on z-scores of microbial genera in each sample.

