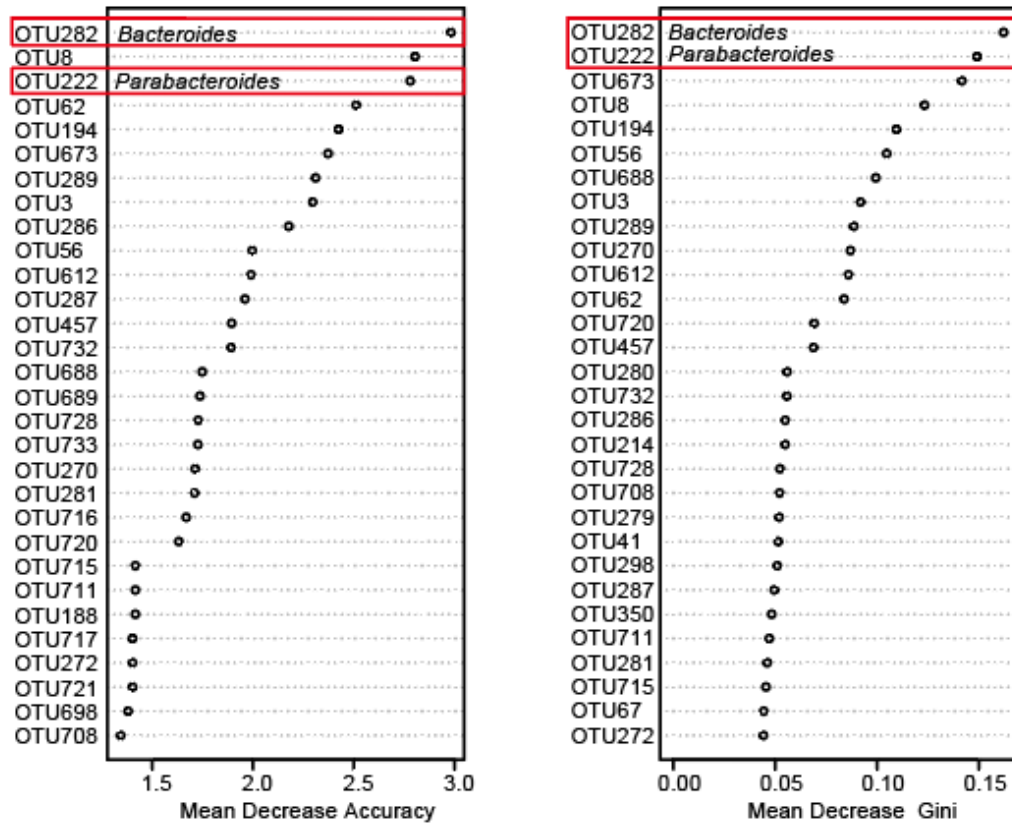


Fig. S1. (A) There are significant differences in the  $\alpha$ -diversity of the microbiome of swab samples from the 2 groups based on the Shannon index and the Simpson index. (B) There are no significant differences in the  $\alpha$ -diversity of the microbiome of feces samples between the two groups based on the Shannon index and the Simpson index. (C) There are no significant differences in the  $\beta$ -diversity of the gut microbiota in feces samples between the two groups based on PCA of Bray-Curtis distances.

A



B

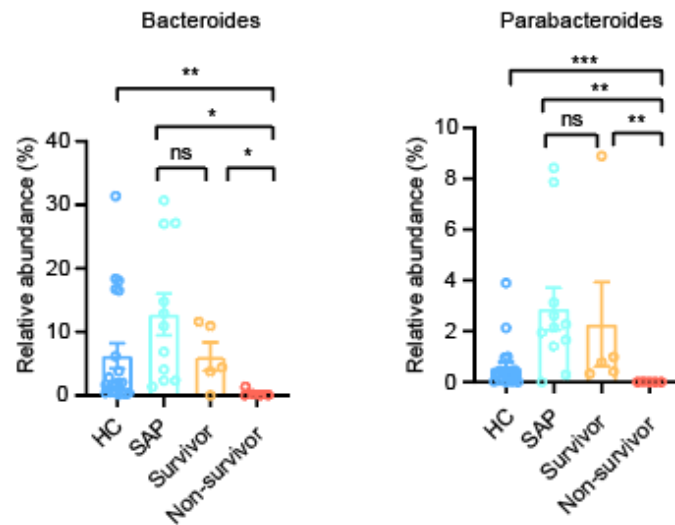


Fig. S2. (A) RandomForest analysis at the OTU level in rectal swab samples, showing Mean Decrease Gini score and Mean Decrease Accuracy as a measure of variable importance. (B) The relative abundance of *Bacteroides* and *Parabacteroides* among Non-survivor, Survivor, SAP, and HC groups in rectal swab samples.

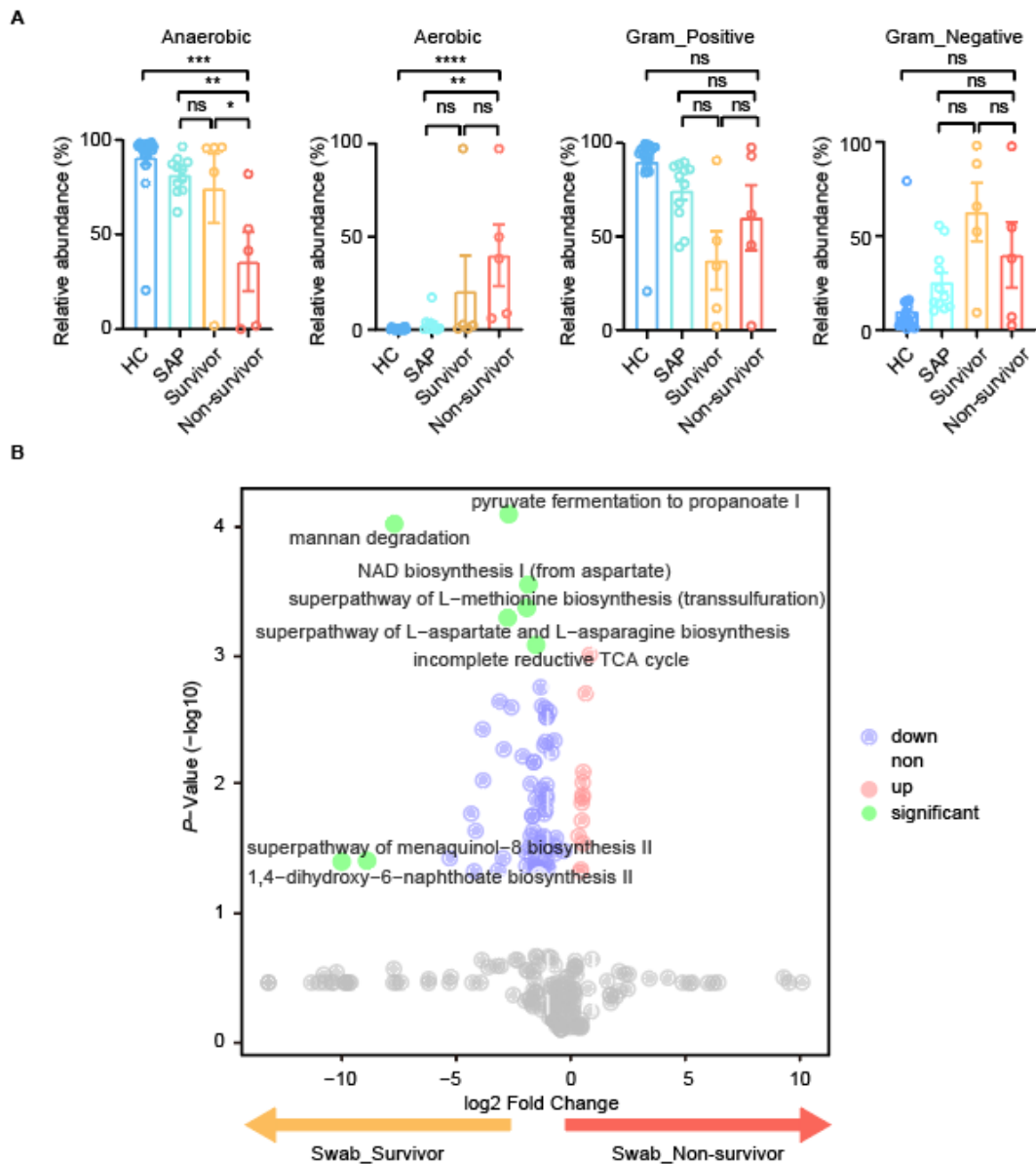


Fig. S3. Bacterial composition comparison in rectal swabs predicted by BugBase in the two groups. (A) Significant differences in anaerobes, aerobes ( $P < 0.05$ ), but no significant differences in gram-negative bacteria, gram-positive bacteria. (B) Volcano plot showing the bacterial MetaCyc pathways that are enriched in COVID-19 patients from survivors ( $n = 5$ ) versus non-survivors ( $n = 5$ ) in rectal swab samples. Green-filled circles indicate pathways with  $P < 0.05$  or  $\text{Log}_2$  Fold Change  $> 5$ .