Figure S1. Rarefaction curves for 16S rRNA gene from penguin fecal samples. Operational taxonomic units (OTUs) in this analysis were defined at 97% sequence identity.
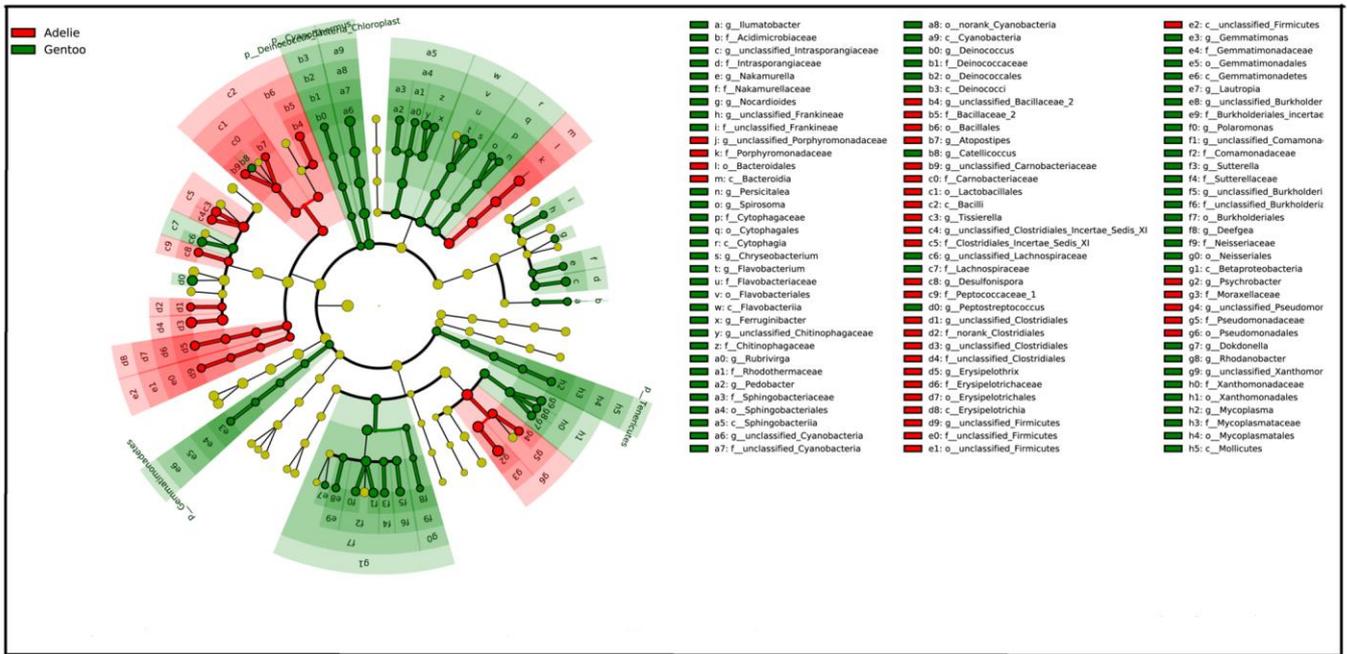
Figure S2. Cladogram indicated the phylogenetic distribution of fecal microbiota associated with Adélie and Gentoo penguin groups. Each dot represented a taxonomic entity and the taxonomic levels ranged from phylum to genus from the inner to outer circles.
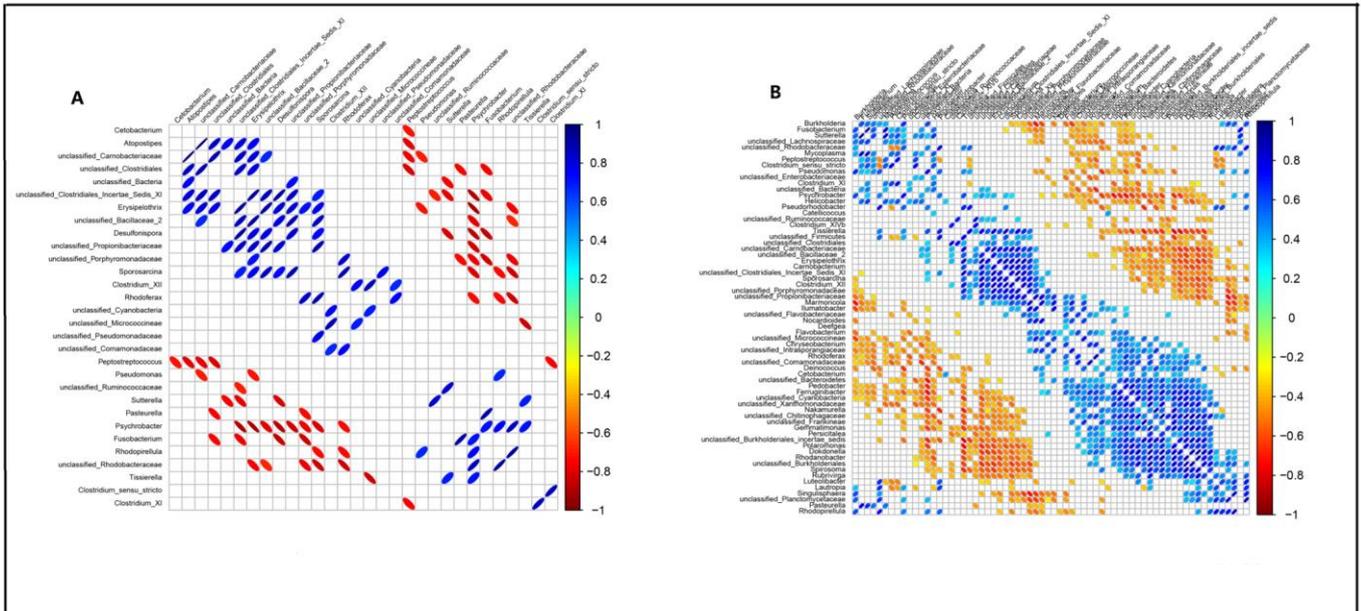
Figure S3. SparCC correlations between gut microbe-microbe at the genus level detected in Adélie (**A**) and Gentoo (**B**) penguin groups. Only correlations of > 0.6 that were statistically significant ($p \leq 0.05$) are shown. The blue color indicates positive correlations, and the red color indicates negative correlations. The color scale on the right indicates the level of the correlation, with darker colors for the strongest positive or negative correlations. Supplemental data for this article can be accessed on the publisher's website.