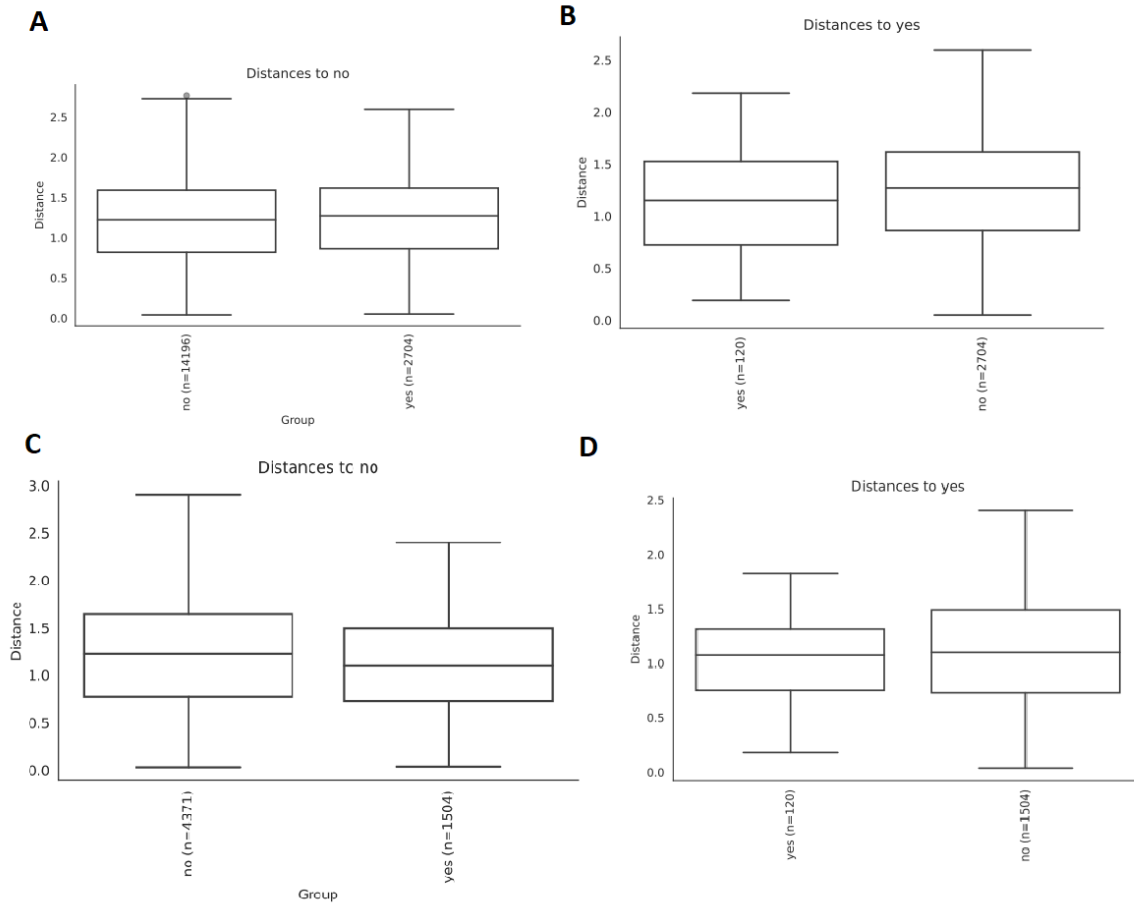
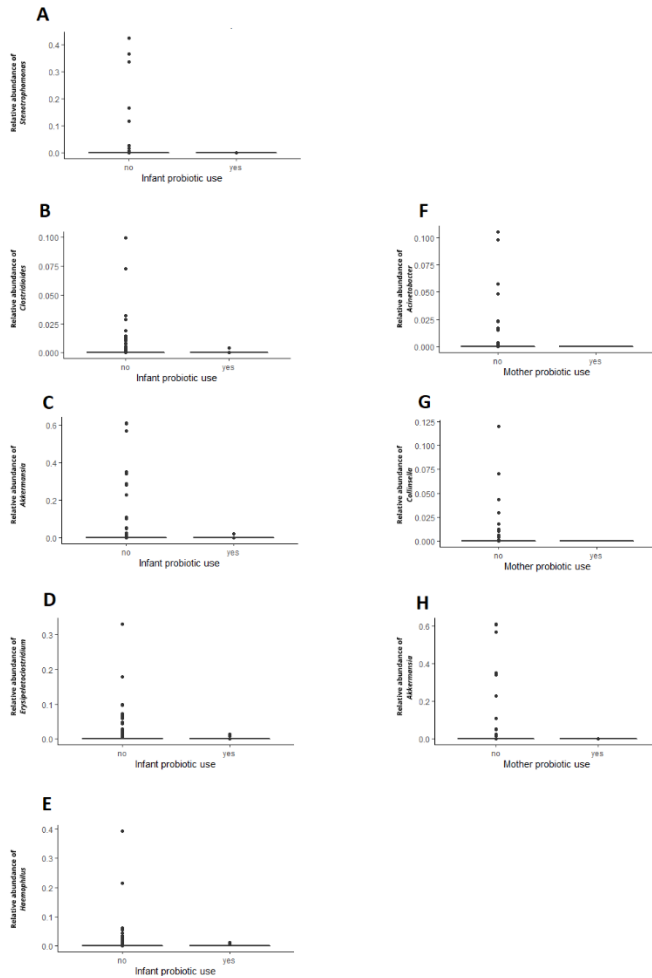


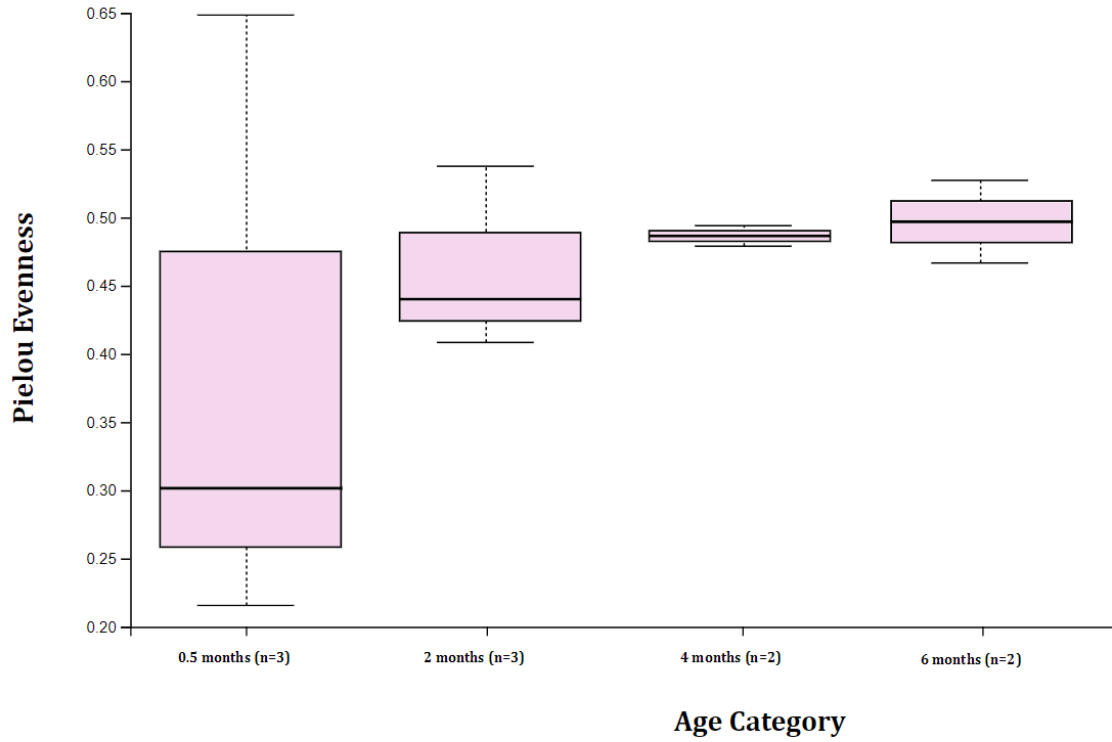
Supplemental Figure 1. Alpha diversity analysis found no significant differences between cohorts that did and did not report probiotic use in analysis of both direct and indirect probiotic use. Boxplots visualizing alpha diversity metrics display no significant differences found between cohorts that reported probiotic use and those that reported no probiotic use. Panels **A** and **B** display measures of Pielou Evenness and Faith's Phylogenetic Diversity respectively for direct (or infant) probiotic use. Panels **C** and **D** display measures of Pielou Evenness and Faith's Phylogenetic Diversity respectively for indirect (or mother) probiotic use



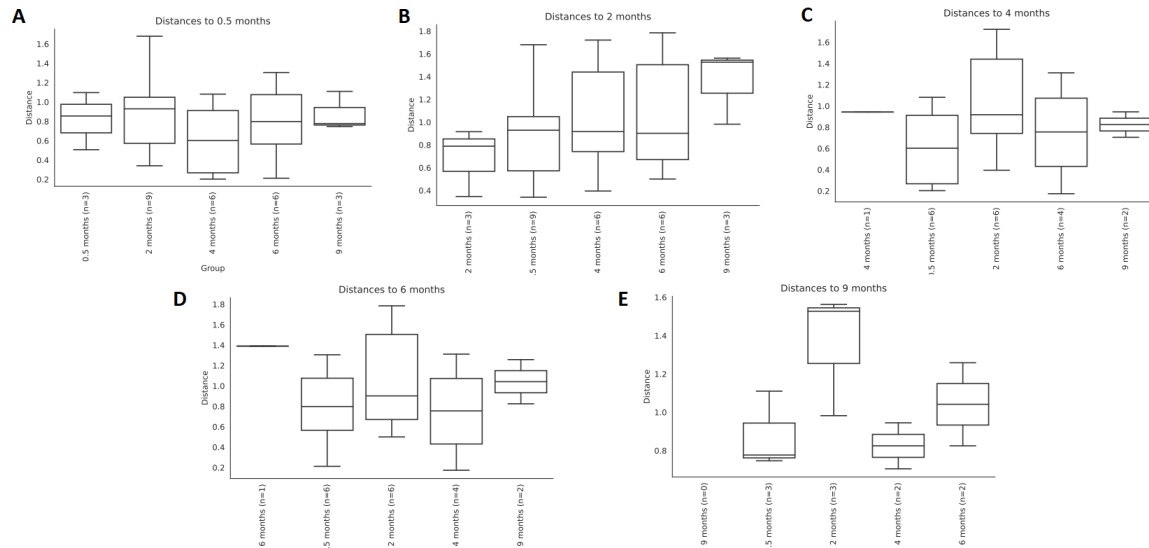
Supplemental Figure 2. Beta diversity analysis found no significant differences between cohorts that did and did not report probiotic use in analysis of both direct and indirect probiotic use. Boxplots visualizing PERMANOVA tests show no significant differences in beta diversity between individuals that reported probiotic use and those that reported no probiotic use. Panels **A** and **B** display results for direct use (p-value = 0.016) and panels **C** and **D** display results for indirect/mother use (p-value = 0.541).



Supplemental Figure 3. Relative abundance plots display various genera are not differentially abundant when comparing probiotic use to no probiotic use. Relative abundance analysis of genera found identified in differential abundance analysis in Figure 2 was conducted to validate the results. Genera listed here were found to not be significantly different and were listed as differentially abundant due to outliers. Panels A-E show plots for genera when assessing direct probiotic use and panels F-H show plots for indirect probiotic use. The genera analyzed per panel are as listed: **A)** *Stenotrophomonas* **B)** *Clostridioides* **C)** *Akkermansia* (Direct use) **D)** *Erysipelatoclostridium* **E)** *Haemophilus* **F)** *Acinetobacter* **G)** *Collinsella* **H)** *Akkermansia* (Indirect use)



Supplemental Figure 4. Alpha diversity analysis reveals no significant difference in gut microbiome among various time points for subjects 1, 14, and 27. Boxplots visualizing measures of Pielou Evenness show no significant differences between samples at different age categories/time points for subjects 70001, 70014 and 70027, all of which had only taken probiotics at the 2 month time point.



Supplemental Figure 5. Supplemental Figure X. Beta diversity analysis reveals no significant difference in gut microbiome among various time points for subjects 1, 14, and 27. Boxplots visualizing measures of PERMANOVA tests show no significant differences in beta diversity between various age categories/time points for subjects 70001, 70014 and 70027, all of which had only taken probiotics at the 2-month time point. Panels **A-E** display Weighted UniFrac distances from each timepoint as designated by graphs.