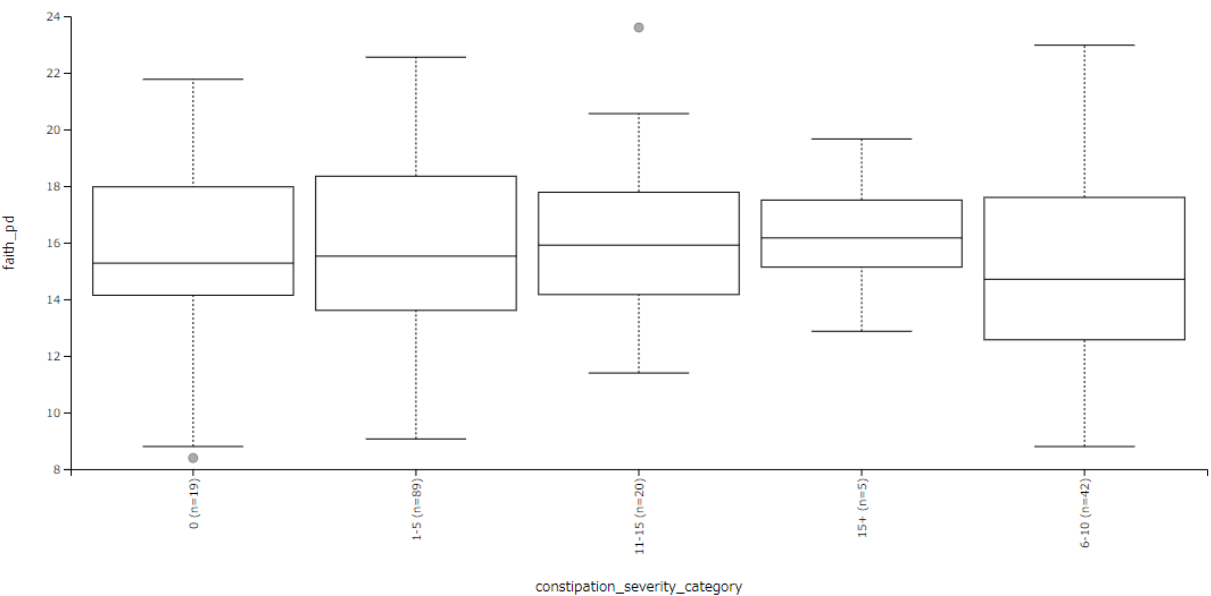


Constipation Severity Affects the Gut Microbiome Composition of Parkinson’s Disease Patients (Supplemental)

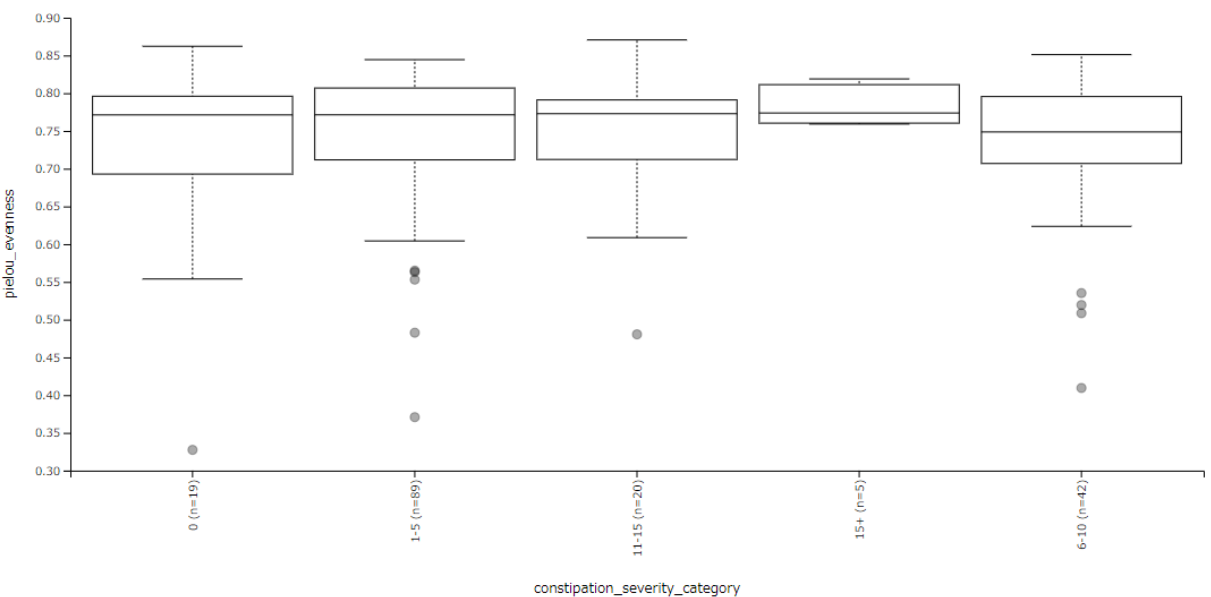
Patricia Balmes, Jack Cheng, Kahori Hirae, Harnoor Kaur

Department of Microbiology and Immunology, University of British Columbia, Canada

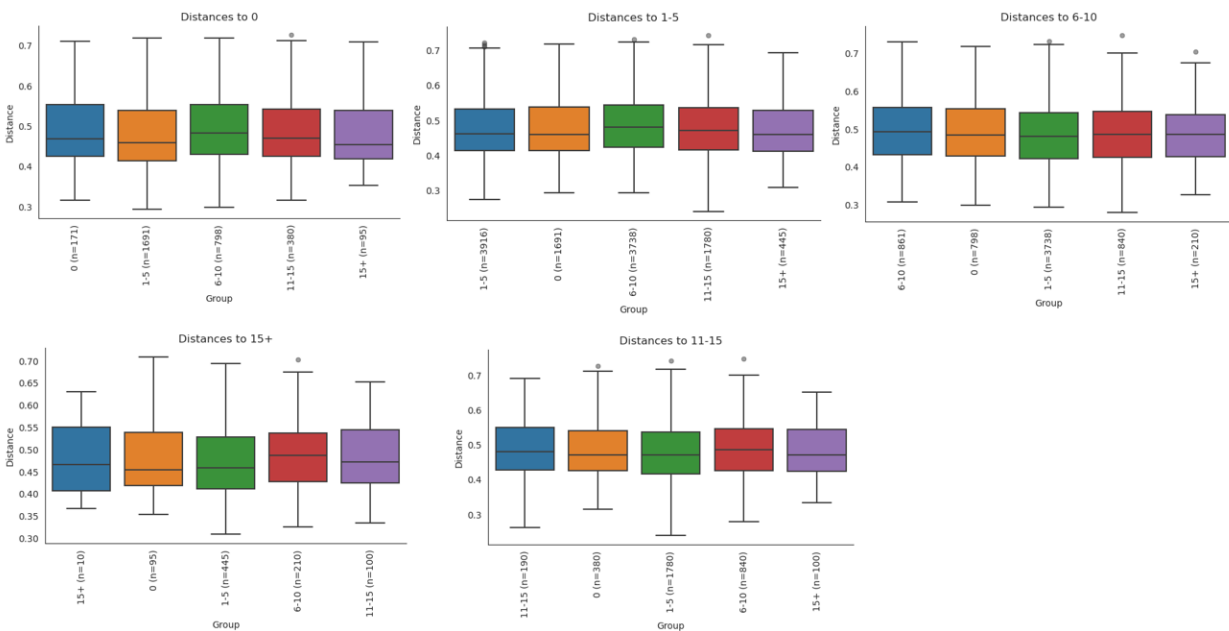
A



B



Supplemental Figure 1. Alpha diversity among the five constipation severity groups showed no statistical significant distinction. **A)** Faith's PD and **B)** Pielou's evenness measure from Shannon alpha diversity analysis showed similar patterns of phylogenetic distance ($p=0.72$) and community richness ($p=0.81$) among constipation severity groups. Total sample size of $n=175$ was divided into five groups ($n=19$ for 0, $n=89$ for 1-5, $n=42$ for 6-10, $n=20$ for 11-15, and $n=5$ for 15+). The statistical analysis was done by all groups and pairwise Kruskal-Wallis test. All the Kruskal-Wallis pairwise tests also showed no statistical significance (all $p > 0.1$) in alpha diversity (Faith's PD, left; Shannon, right).



Supplemental Figure 2. Unweighted UniFrac box plots showed no significance of gut microbial communities at different constipation severity. Unweighted UniFrac distances showed no statistically significant phylogenetic distances ($p=0.73$) overall and pairwise tests (all $p>0.1$). The statistical analysis for unweighted UniFrac distance boxplots was done by PERMANOVA tests.