Supplementary Figure 2: Alpha diversity of rabbit GI tract bacterial microbial communities across different GI tract locations based on 16S rRNA gene amplicon sequencing. The figure compares the number of observed species (Observed), species richness (Chao1), diversity (Shannon), and evenness (Simpson) between the foregut and hindgut. Observed, Chao1, and Shannon diversity were observed to be significantly different ($P < 0.05$) between the sampling groups.