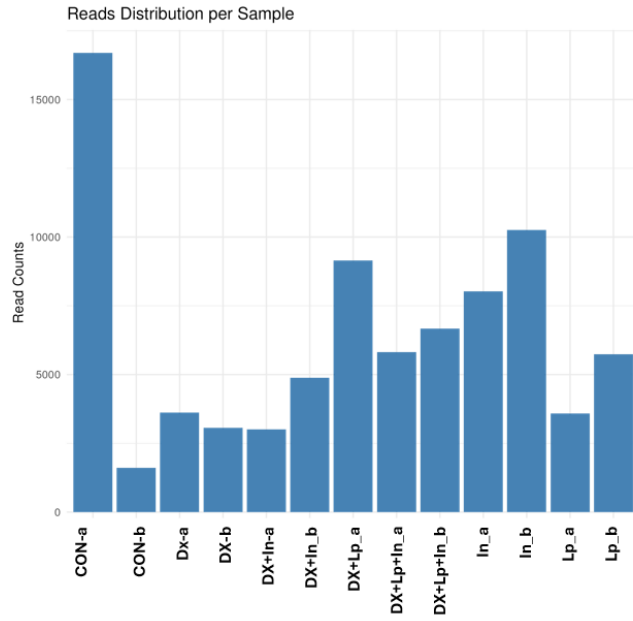
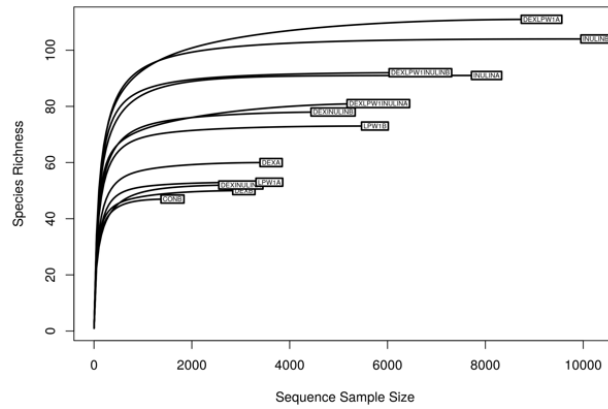


Supplementary materials

A



B



C

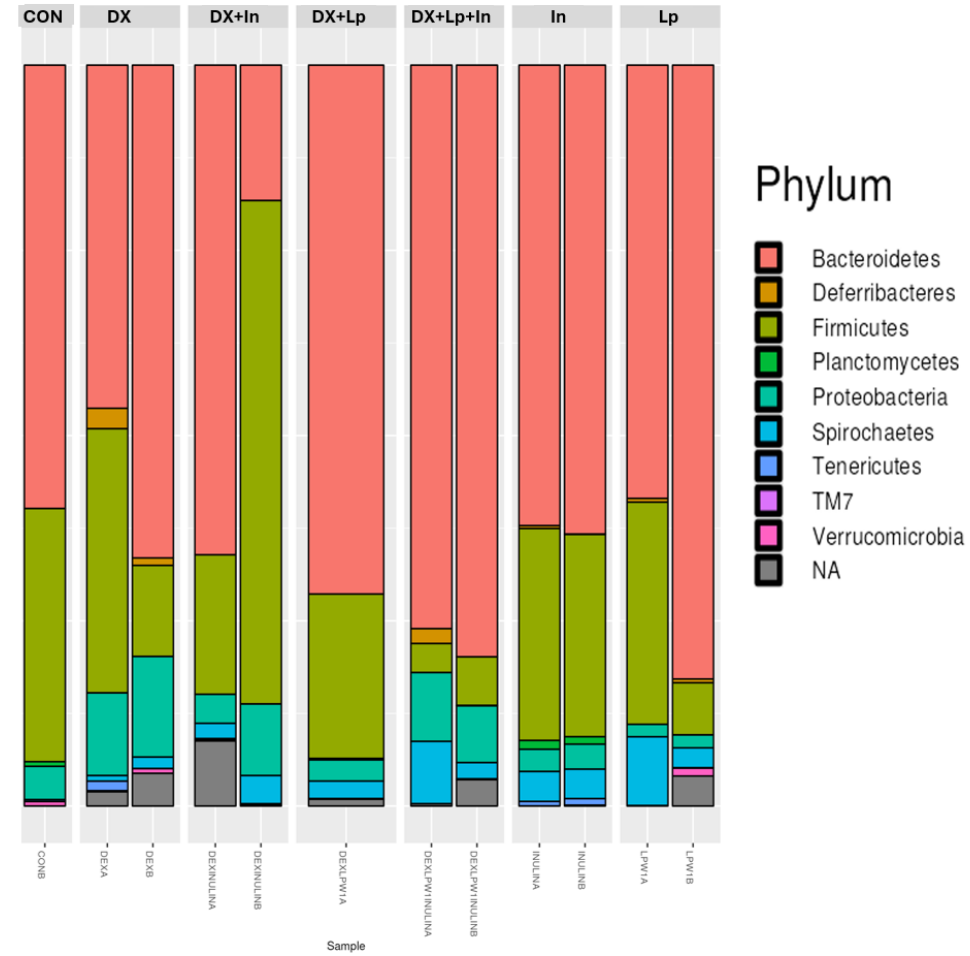


Figure S1. Library Size and Microbiome Analysis Overview. CON (control), DX (dexamethasone), DX-*Lp* (dexamethasone+*Lactiplantibacillus plantarum* W1 - *LpW1*), DX-In (dexamethasone + inulin), and DX-*Lp*-In (dexamethasone + *LpW1*+inulin). Suffixes either a or b denote samples inside the group. (A) The library size overview shows read counts obtained for each group. For the DX+*Lp* group, sequencing resulted in only one successful sample. (B) The rarefaction curve illustrates species richness (y-axis) versus sequence sample size, indicating that the top group samples with the highest species richness (>65) are DX+*Lp* (one sample), inulin group (two samples), DX+*Lp*+In (two samples), DX+In (one sample), and *Lp* (one sample). Additionally, the two samples from the DX group showed an average species richness of 53. (C) The overview of the microbiome structure of the seven groups studied is represented by major phyla, with Bacteroidetes, Firmicutes, and Proteobacteria being predominant. TM7 refers to *Saccharibacteria*, a rare or uncultured phylum, NA refers unclassified bacterial sequences.