

Supplementary Figures

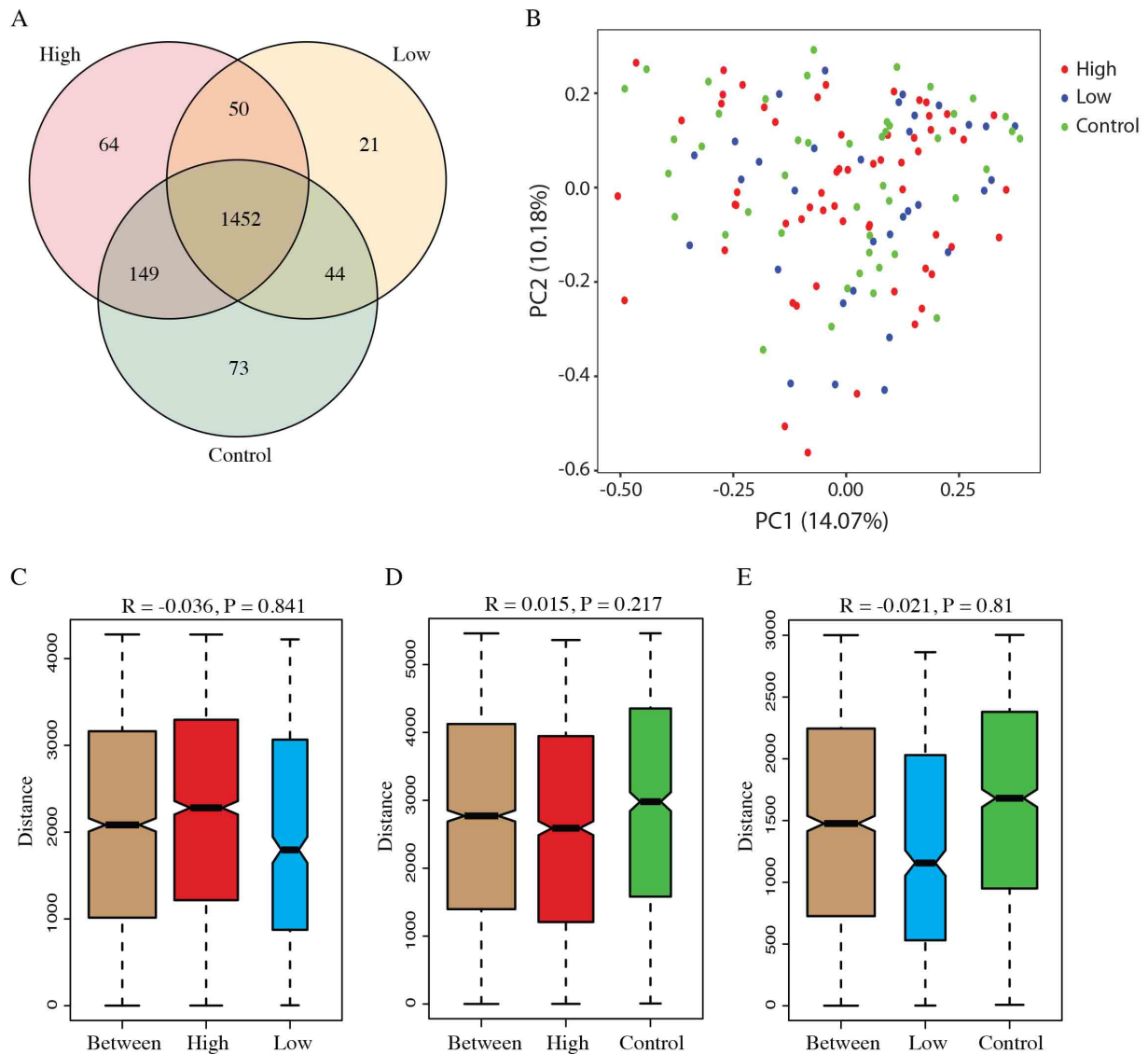


Figure S1. Analysis of Operational Taxonomic Unit (OTU) composition of study samples. **A.** Venn diagram showing the common and unique OTUs among the High intensity, Low intensity and Control groups. **B.** Plot of the Principal components (PC1 Vs PC2) of the sample OTUs. Analysis of Similarity (ANISOM) between the infection intensities and control groups, **C.** High vs Low **D.** High vs Control, **E.** Low vs control.

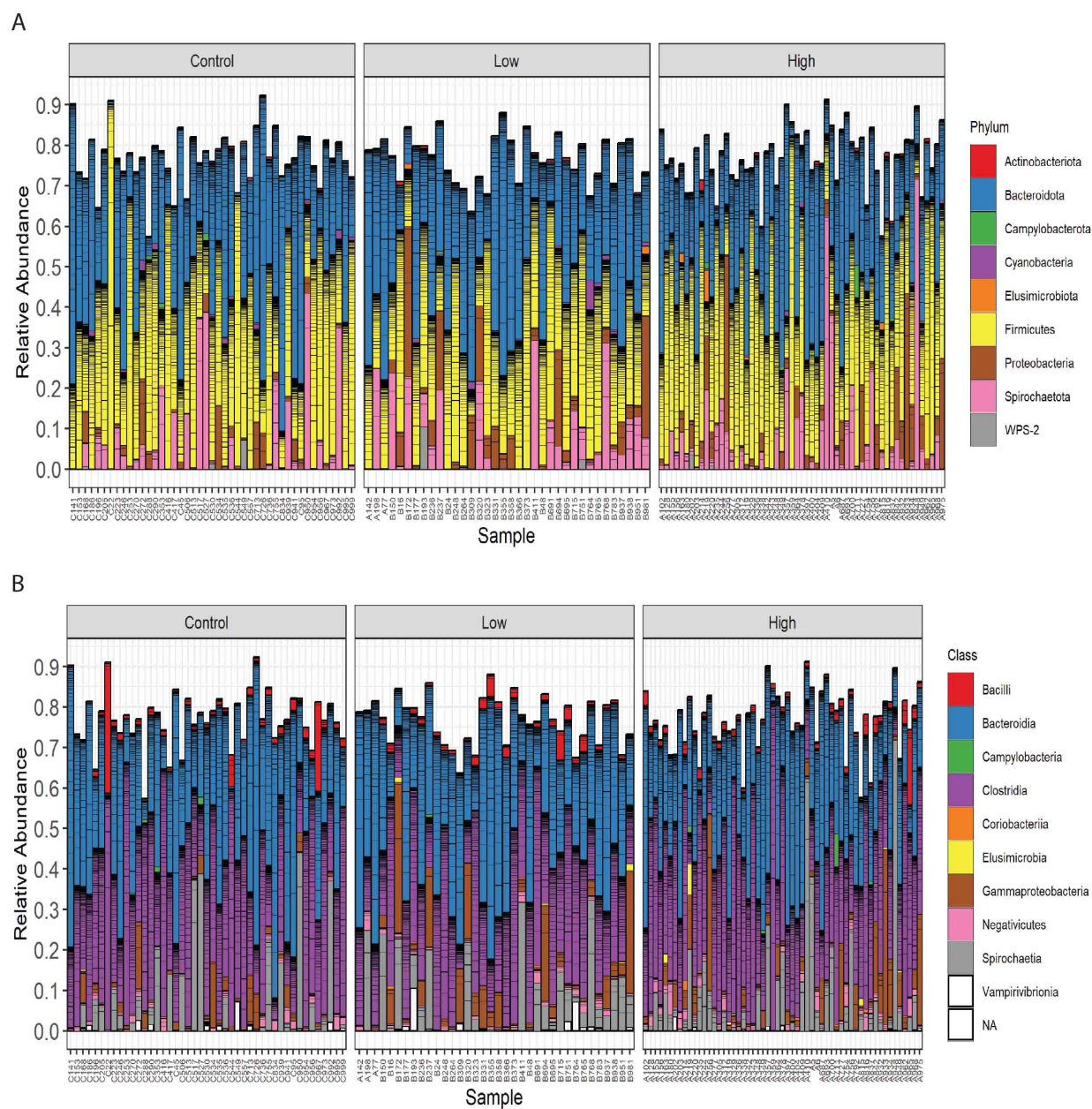


Figure S2. The relative frequency of the top bacterial taxonomic Phyla (A) and Class (B) in the study samples

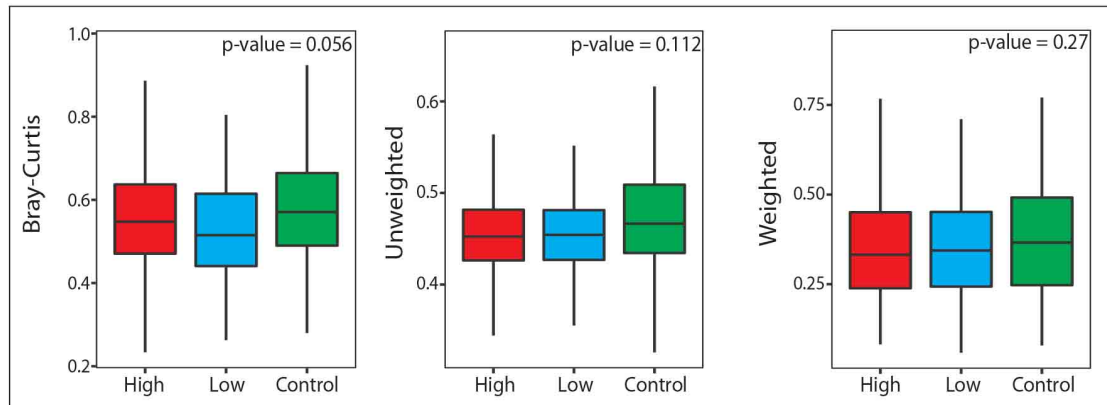
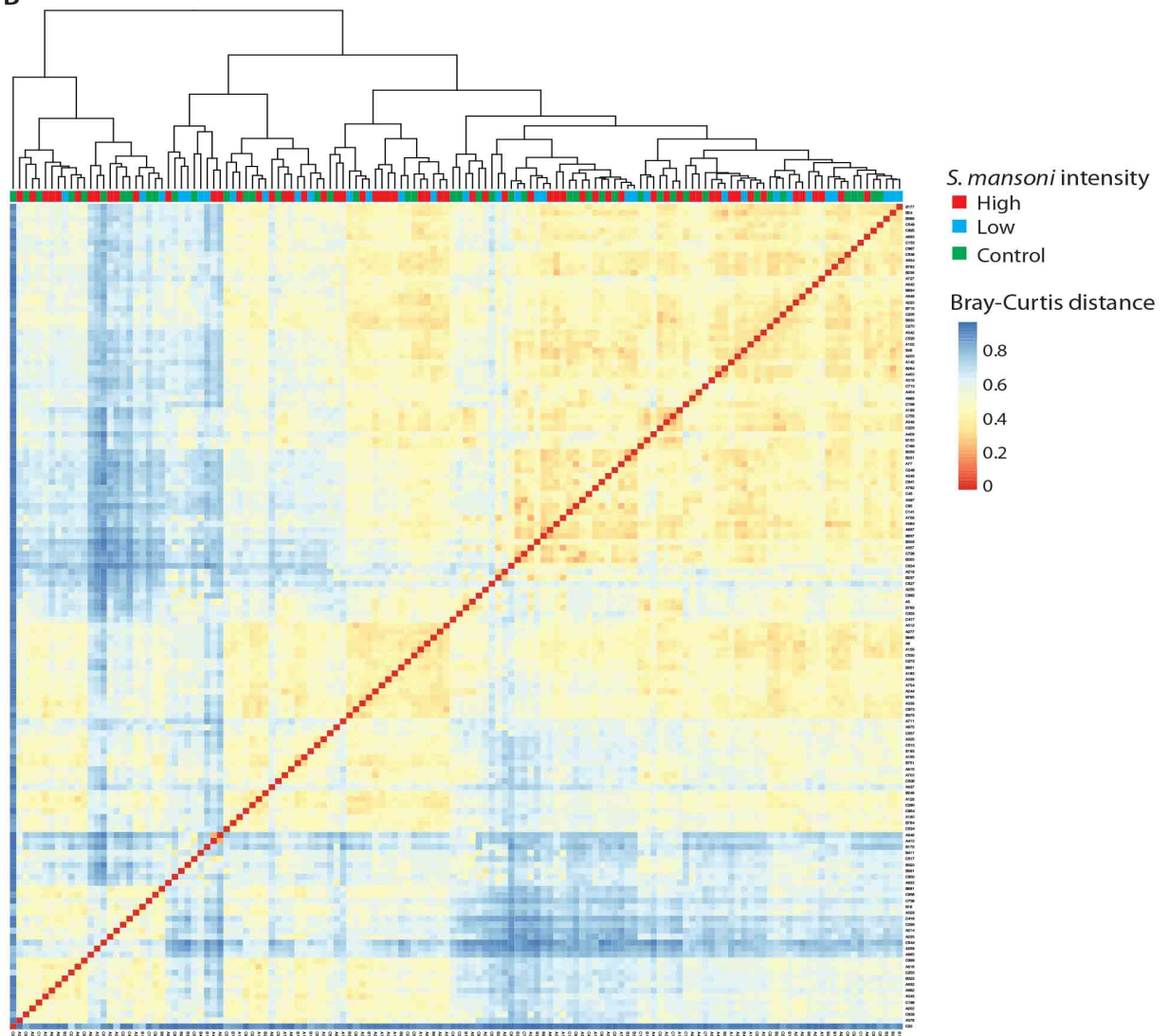
A**B**

Figure S3. A. Beta diversity analysis metrics of the samples using the Bray-Curtis, Unweighted and Weighted indices. **B.** Phylo-heatmap of the Beta diversity based of the Bray-Curtis distance clustering of the study samples

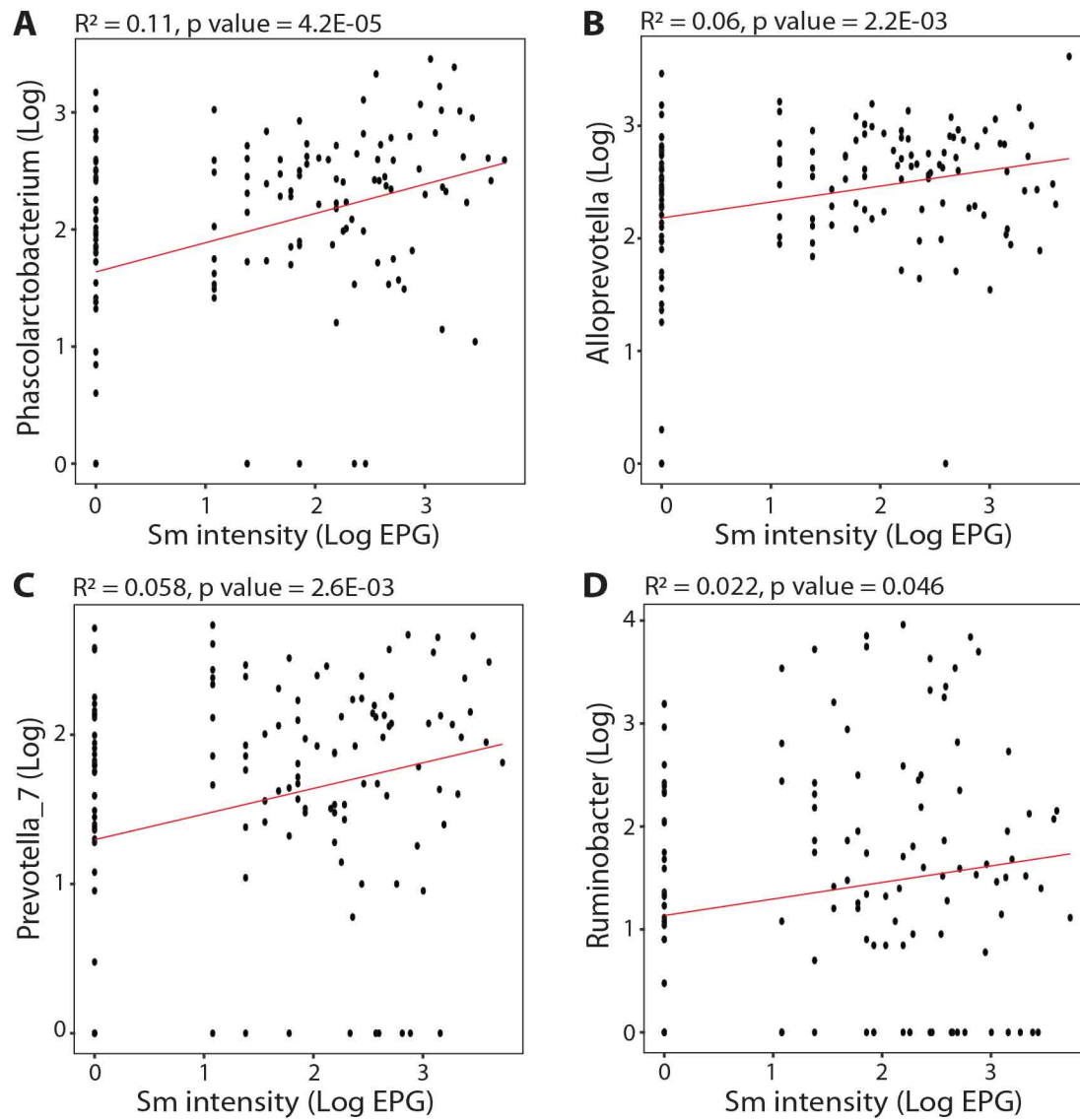


Figure S4. Linear regression association analysis between *S. mansoni* Infection intensity measured by Log KataKatz Eggs per Gram and genus **A.** *Phascolarctobacterium*, **B.** *Alloprevotella*, **C.** *Prevotella_7* and **D.** *Ruminobacter*.

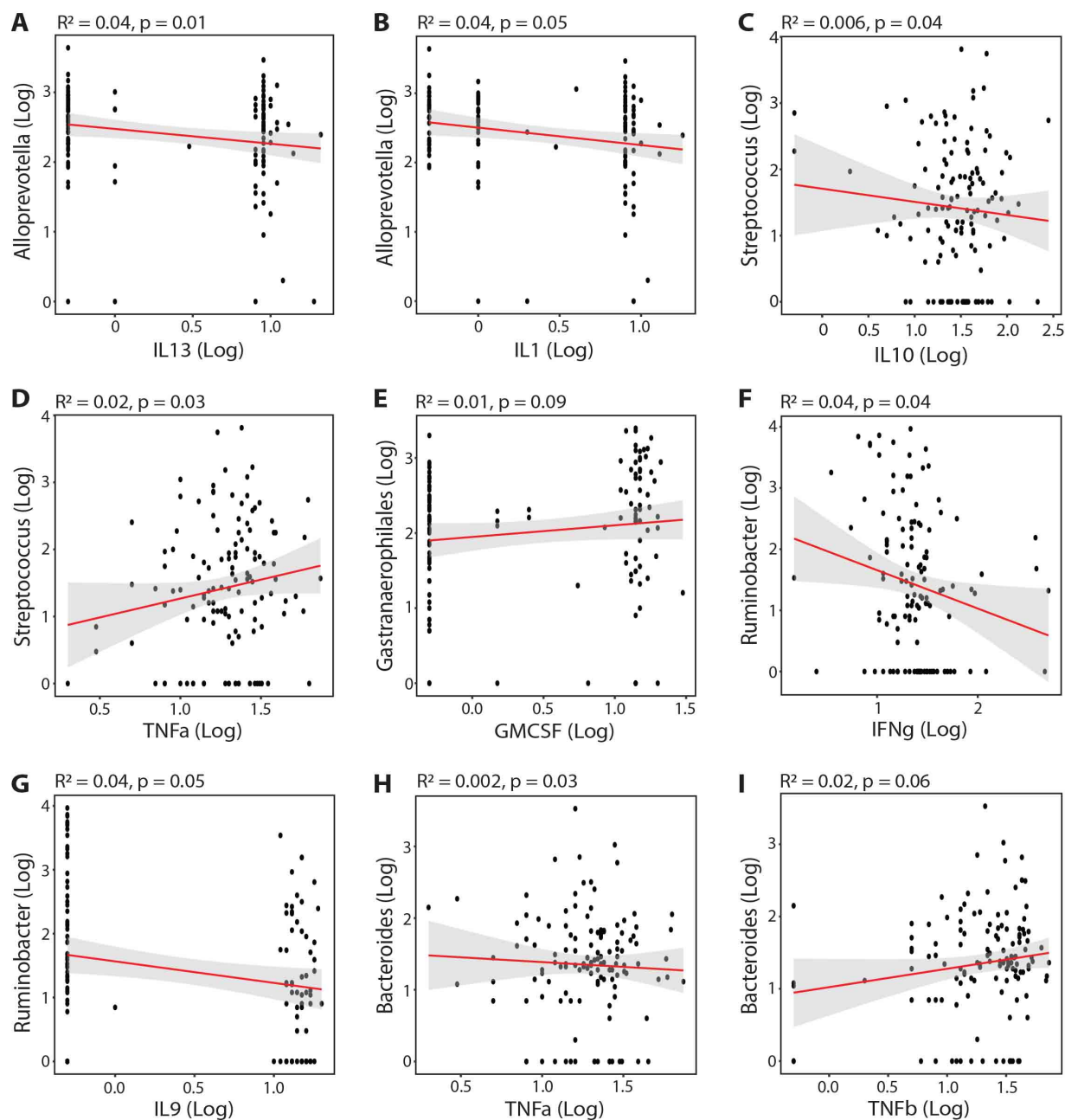


Figure S5. Linear regression analysis between the selected abundant genera that a highly associated with plasma cytokine levels.