

Supplementary Figures

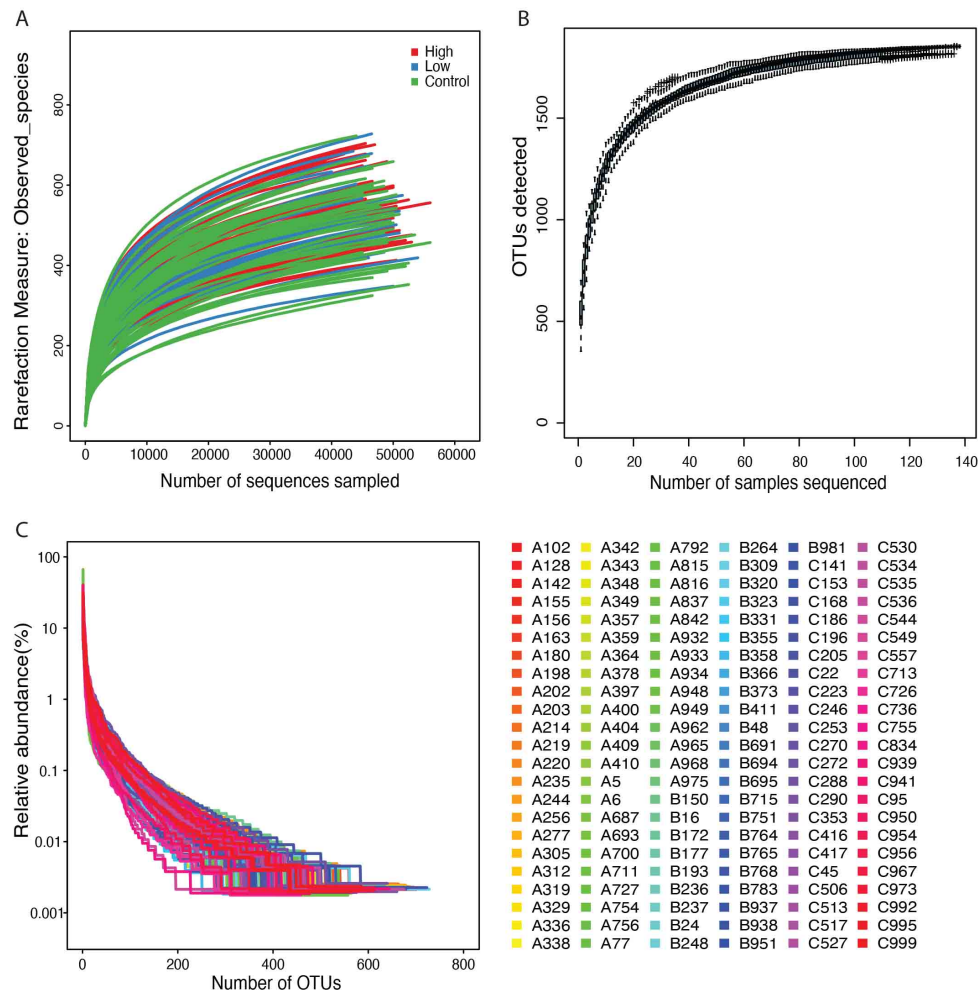


Figure S1. Analysis of the read sequences from the study samples. **A.** Rarefaction curves to assess species richness and sampling depth. Each curve represents a sample categorised by infection intensity (High, Low, Control). **B.** Species accumulation curves plot showing the effects of sample number on species diversity. **C.** OTU Rank curve showing the diversity of species (species richness and species evenness) in the samples. The relative abundance of each OUT in each sample was calculated and the species were ranked by their abundance in descending manner.

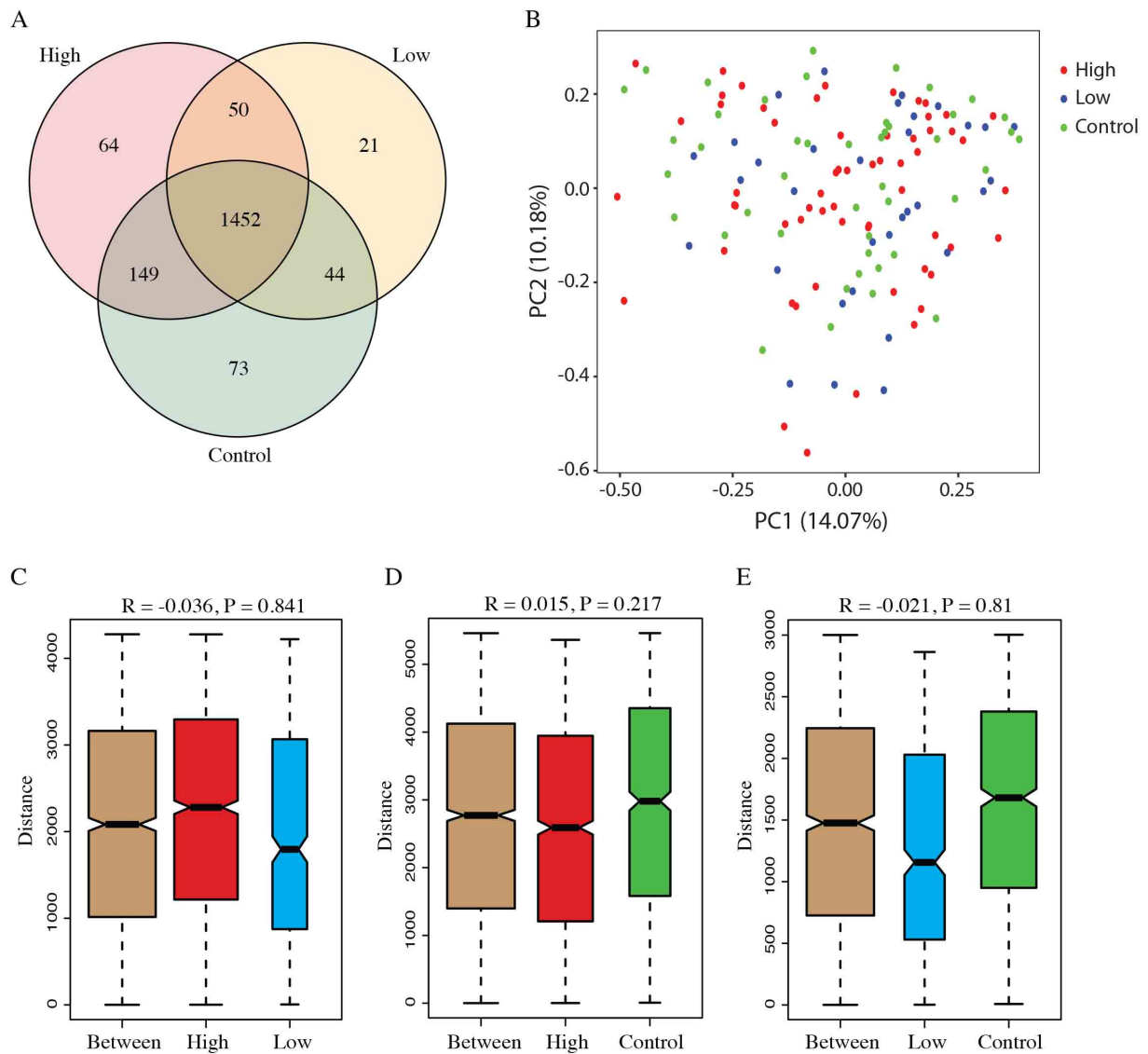


Figure S2. Analysis of Operational Taxonomic Unit (OTU) composition of study samples. **A.** Venn diagram showing the common and unique OTUs among the High intensity, Low intensity and Control groups. **B.** Plot of the Principal components (PC1 Vs PC2) of the sample OTUs. Analysis of Similarity (ANISOM) between the infection intensities and control groups, **C.** High vs Low **D.** High vs Control, **E.** Low vs control.

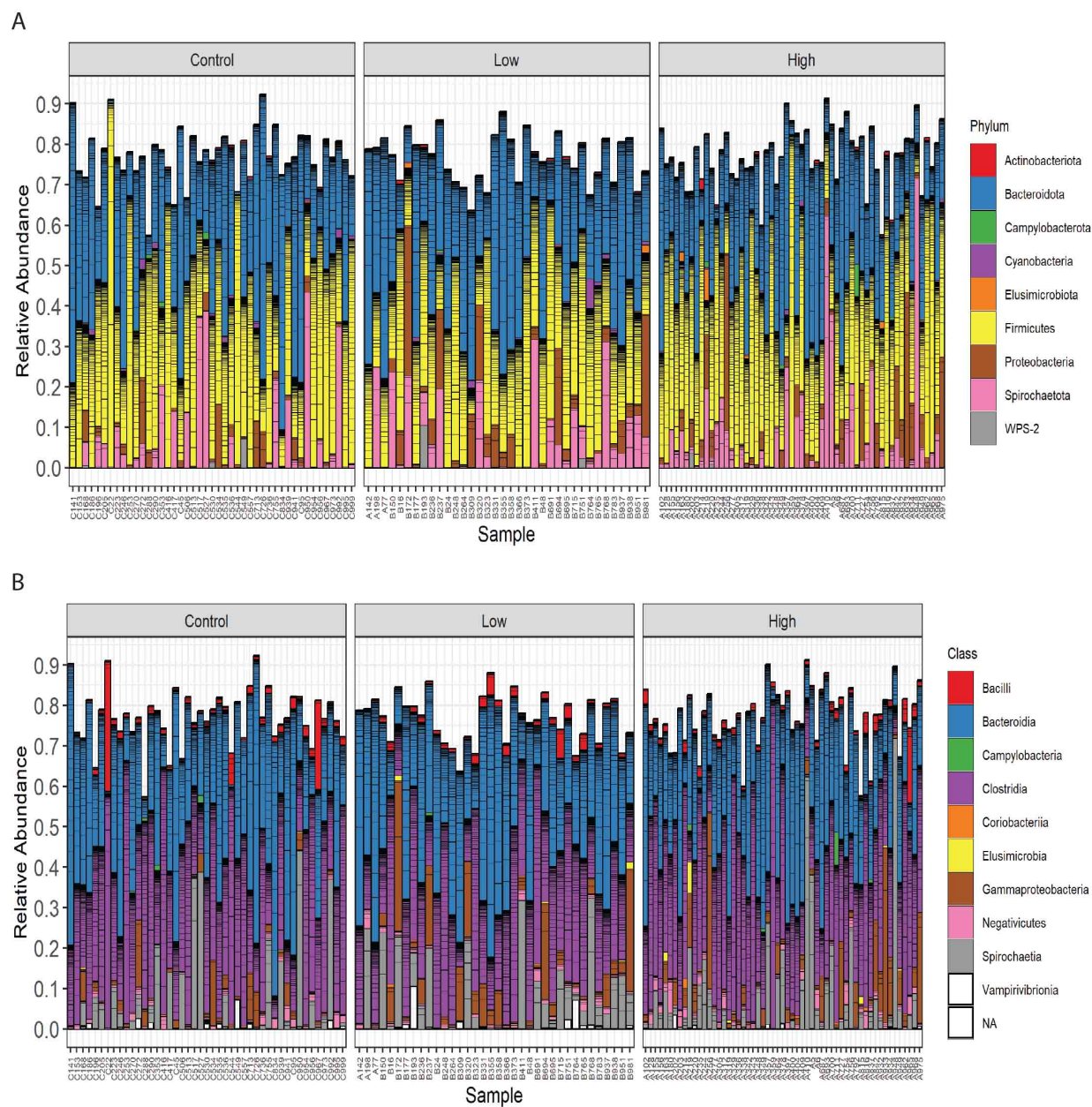


Figure S3. The relative frequency of the top bacterial taxonomic Phyla (A) and Class (B) in the study samples

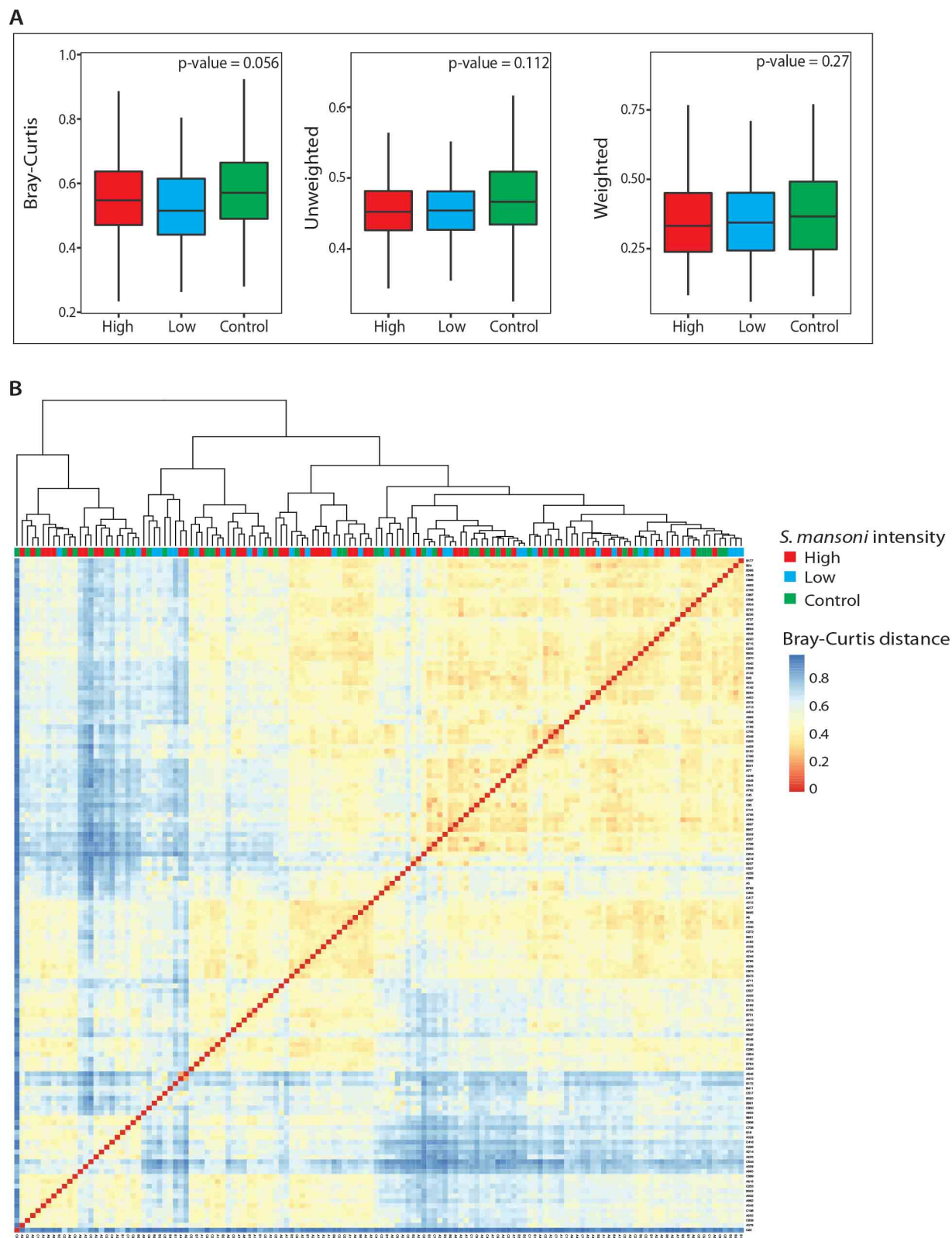


Figure S4. A. Beta diversity analysis metrics of the samples using the Bray-Curtis, Unweighted and Weighted indices. **B.** Phylo-heatmap of the Beta diversity based of the Bray-Curtis distance clustering of the study samples

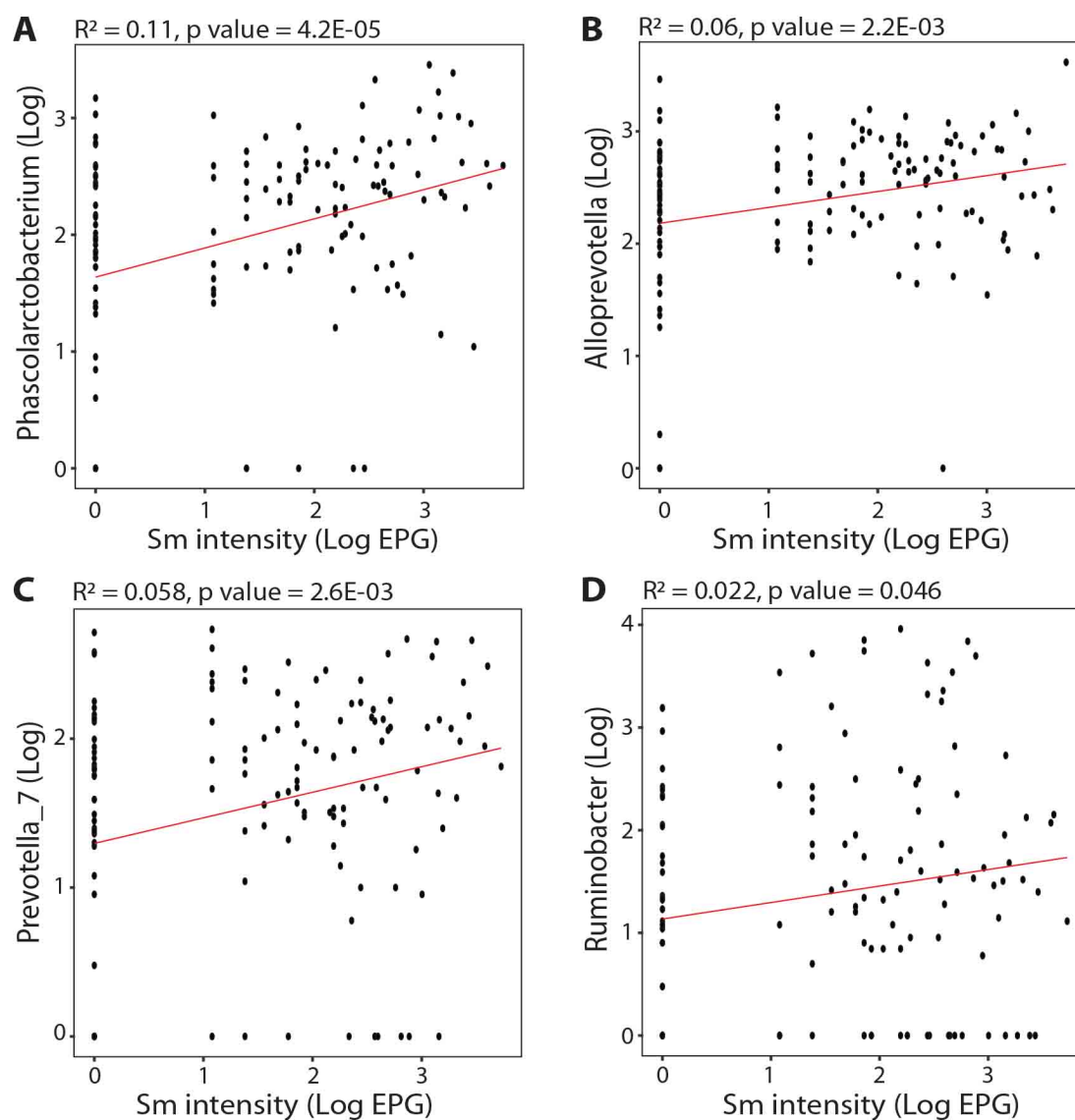


Figure S5. Linear regression association analysis between *S. mansoni* Infection intensity measured by Log KataKatz Eggs per Gram and genus **A.** *Phascolarctobacterium*, **B.** *Alloprevotella*, **C.** *Prevotella_7* and **D.** *Ruminobacter*.

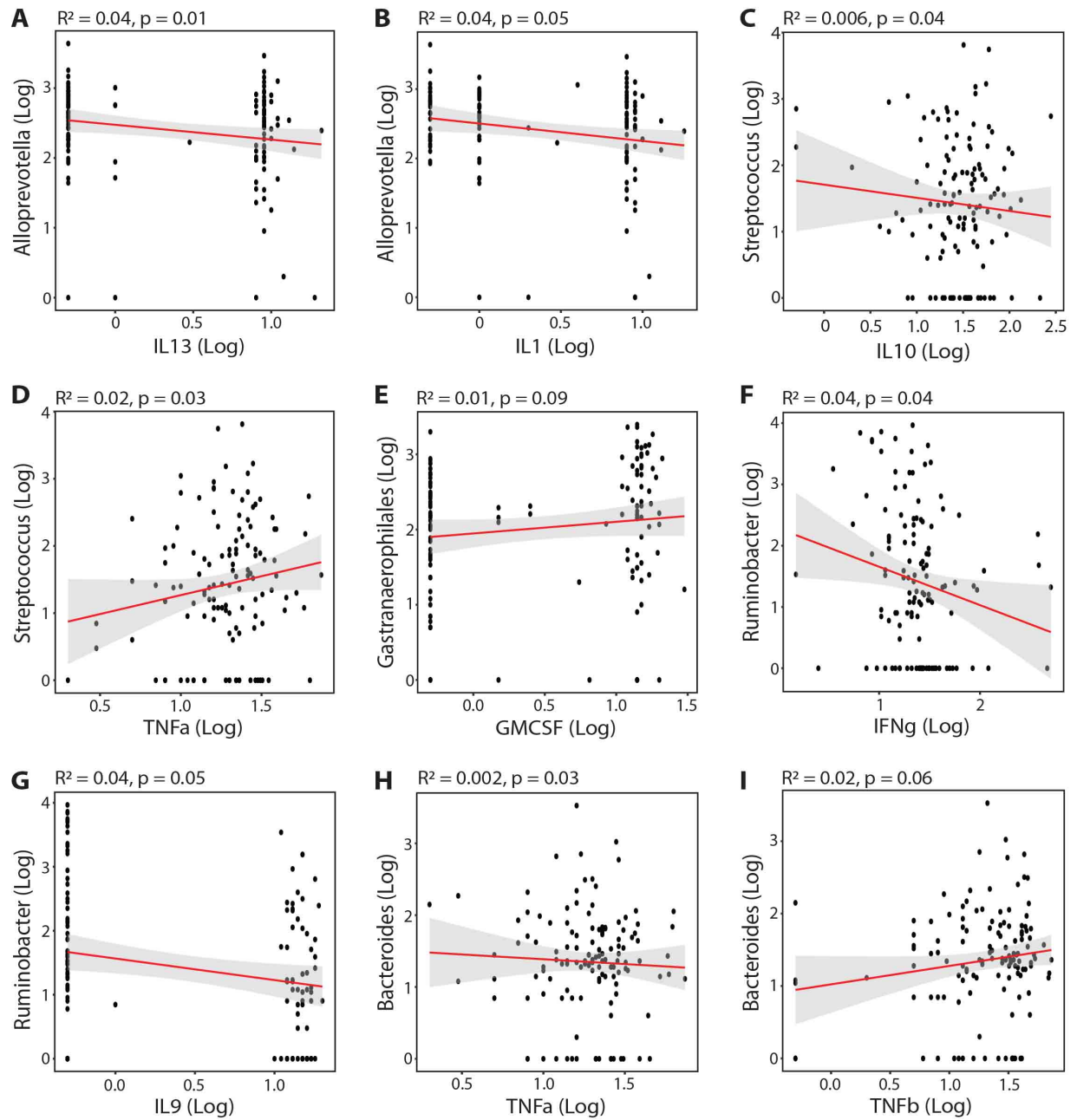


Figure S6. Linear regression analysis between the selected abundant genera that a highly associated with plasma cytokine levels.