

Supplementary Tables

Table S1. Metadata data on the samples used for this study.

Table S2. Summary of the Amplicon Sequence Variants (ASVs) read counts per sample.

Table S3. differential genus abundance output statistics from Lefse, DESeq2 and EdgeR algorithms.

Table S4. Summary statistics from the Linear regression analysis between *S. mansoni* infection intensity (EPG) and the genus-level abundance across the 138 samples are presented. Fisher test pvalues and multiple testing correction was performed using the Benjamini-Hochberg model and the corresponding false discovery rates (FDR) reported.

Table S5. RNASeq read counts of the cytokines genes in the 44 samples that are part of this study and extracted from Namulondo et al., 2023.

Table S6. Summary statistics from the Linear regression analysis between the cytokine levels and the genus-level abundance. Fisher test pvalues and multiple testing correction was performed using the Benjamini-Hochberg model and the corresponding false discovery rates (FDR) reported.