MAKERERE UNIVERSITY

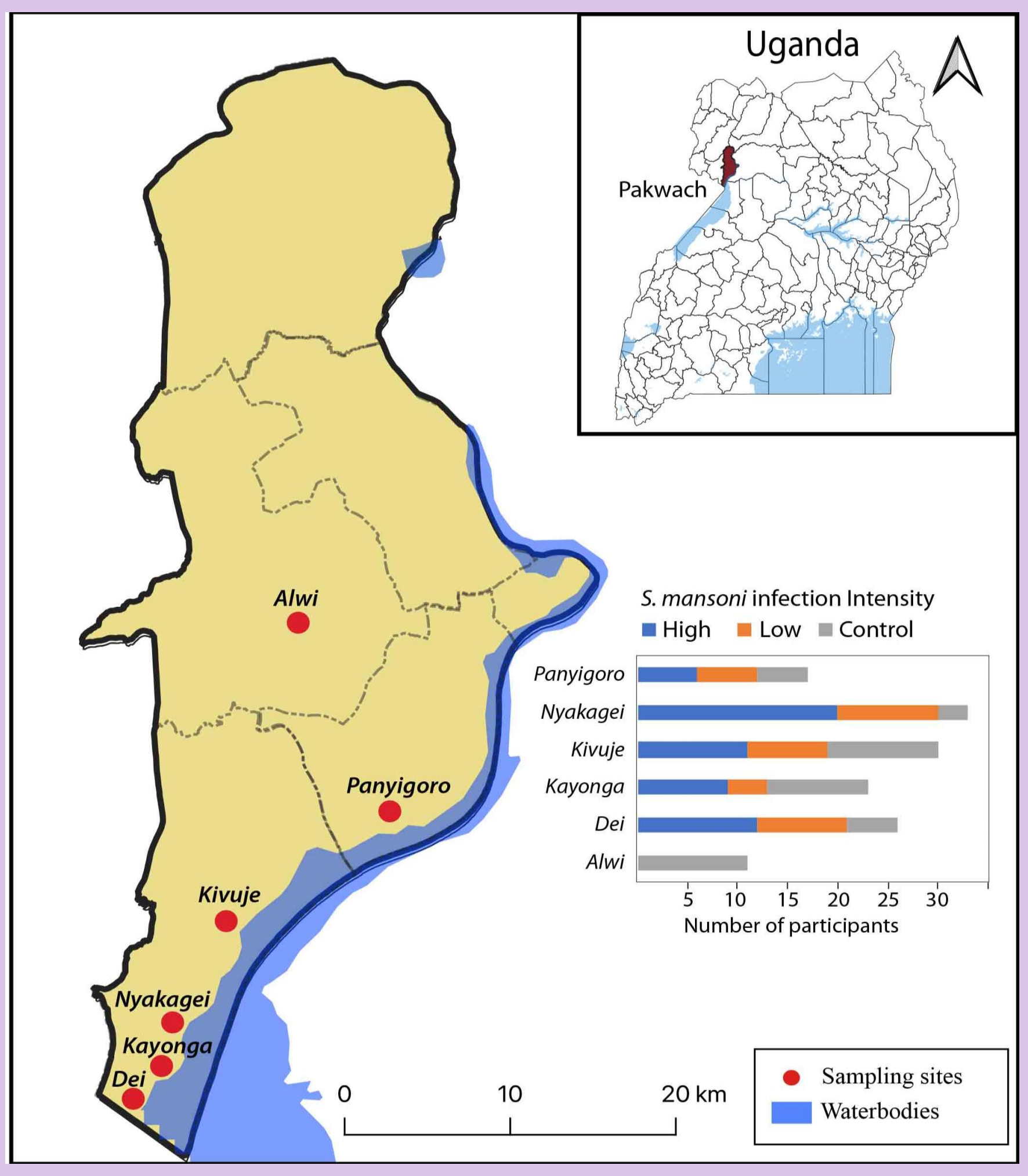
# Investigating gut microbiome diversity among children infected with schistosomiasis in the endemic region of Albert Nile, Pakwach district

Caroline Jackline Musiime

## Introduction

- Schistosomiasis (bilharzia) is a NTD in sub-Saharan Africa caused by the schistosome species (blood flukes) mostly in 10-20 yr-olds
- >4m people estimated to be infected (73/112 Ugandan districts) & ~55% of the population at risk
- >290 million infections worldwide & ~280,000 annual deaths
- Intestinal helminth parasites live in proximity with gut bacteria
- The gut microbiome impact on the disease burden has not been extensively studied within Uganda
- High prevalence of schistosomiasis among the young age group shows the imperative to focus on infection control & disease prevention in affected communities
- By investigating the gut microbiome diversity effects on the health status of schistosomiasis co-infected individuals

## Sample Population



**10-15 yr old children**

**Infection Intensity: Kato-Katz (Eggs/Gram, EPG)**

**Microscopic detection of *S. mansoni* eggs in feacal samples**

**Control (EPG = 0 ), Low (EPG = 1-100), High (EPG >100)**

**n = 138 archived fecal samples**

## Methodology

**DNA extraction**

**16SrRNA Library preparation (V3-V4 region)**

**DNB sequencing platform (BGI)**

**16S rRNA data analysis [QIIME2, FLASH (v1.2.11)]**

**OTU Clustering**

**Taxonomic composition of gut microbiome with *S. mansoni* infection**

**[UCHIME (v4.2.40), USEARCH (v7.0.1090), RDP classifier (v2.2), ANOSIM, Silva NR99 v138.1 16S/18S ribosomal RNA database, DECIPHER, phangorn R]**

**Phylogenetic Tree Heatmap [iTOL]**

**Alpha and Beta diversity analyses**

**Composition and diversity of gut microbiome with *S. mansoni* infection intensity phenotypes**

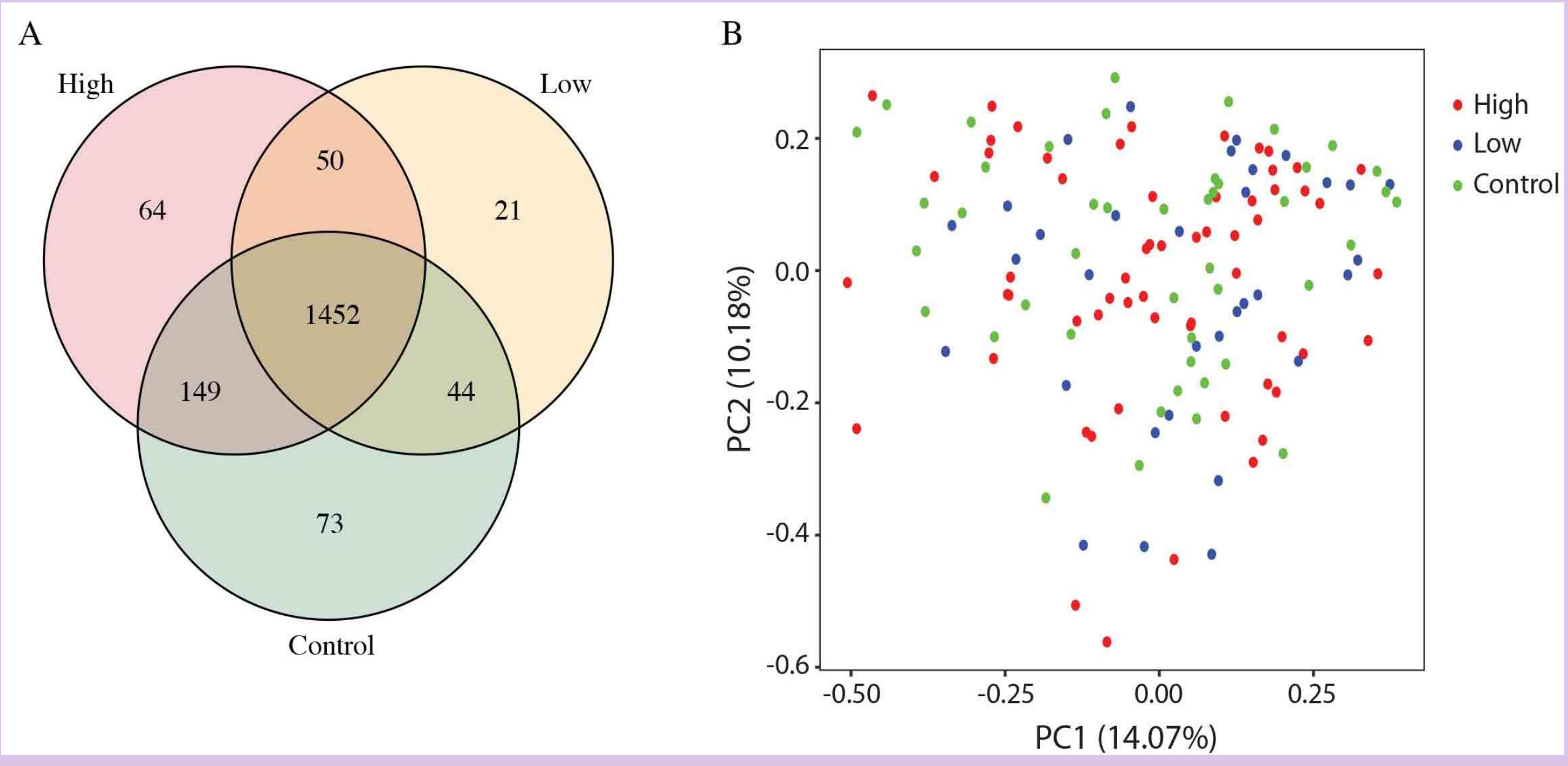
**Relative abundance comparisons**

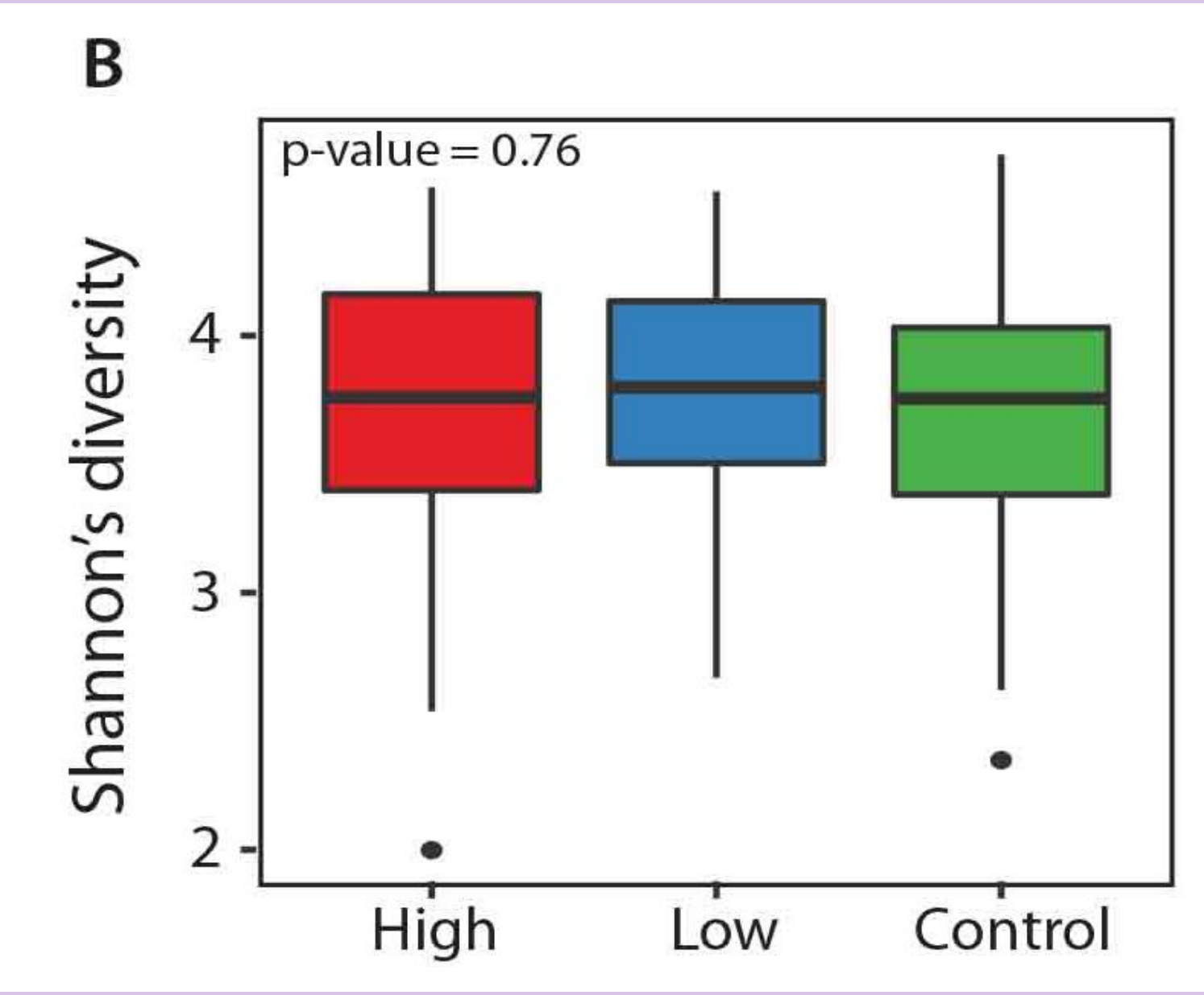
**Abundance enrichment analysis [DESeq2, *LEfSe*, edgeR]**

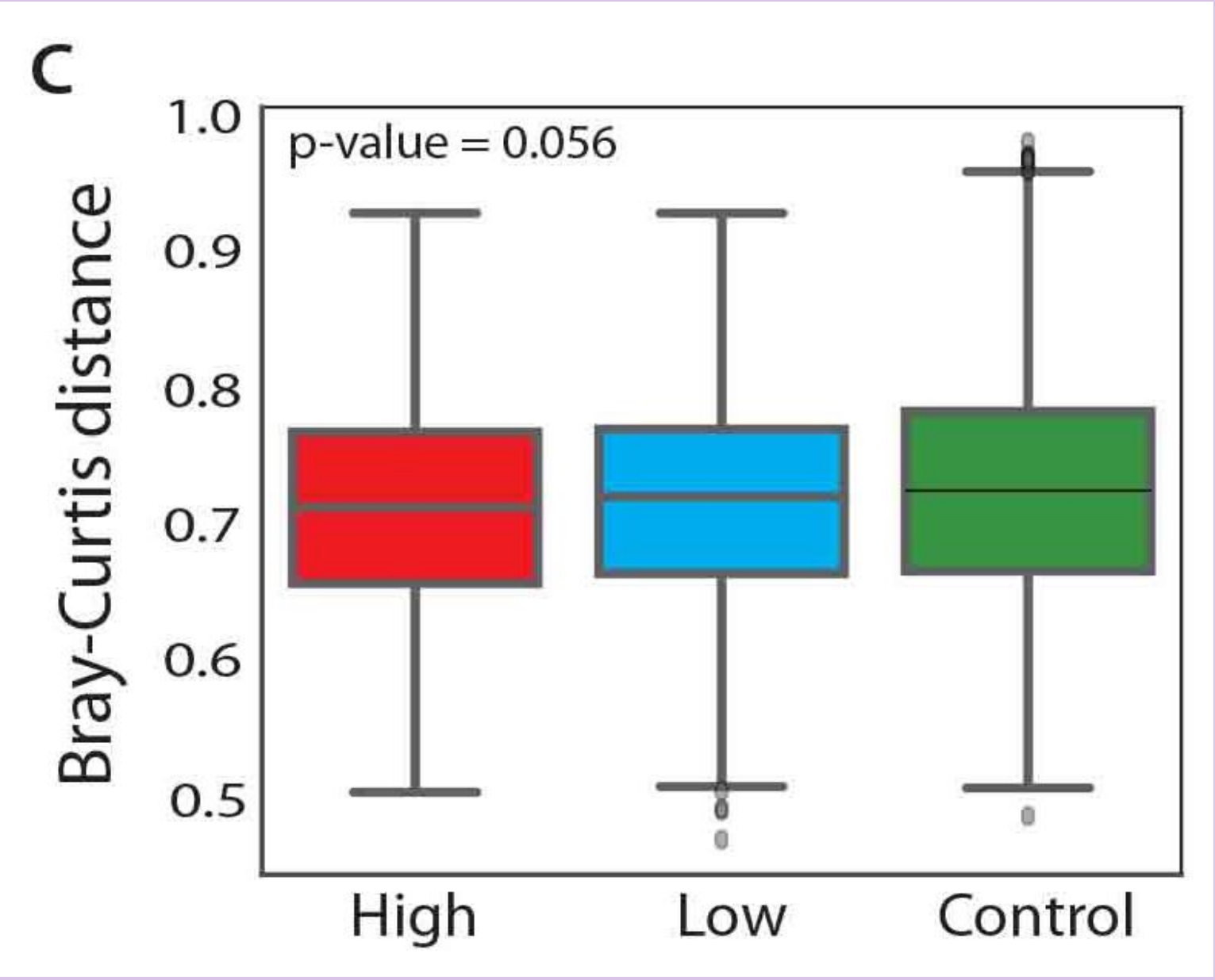
**Differential gut microbiome abundance with *S. mansoni* infection intensity**

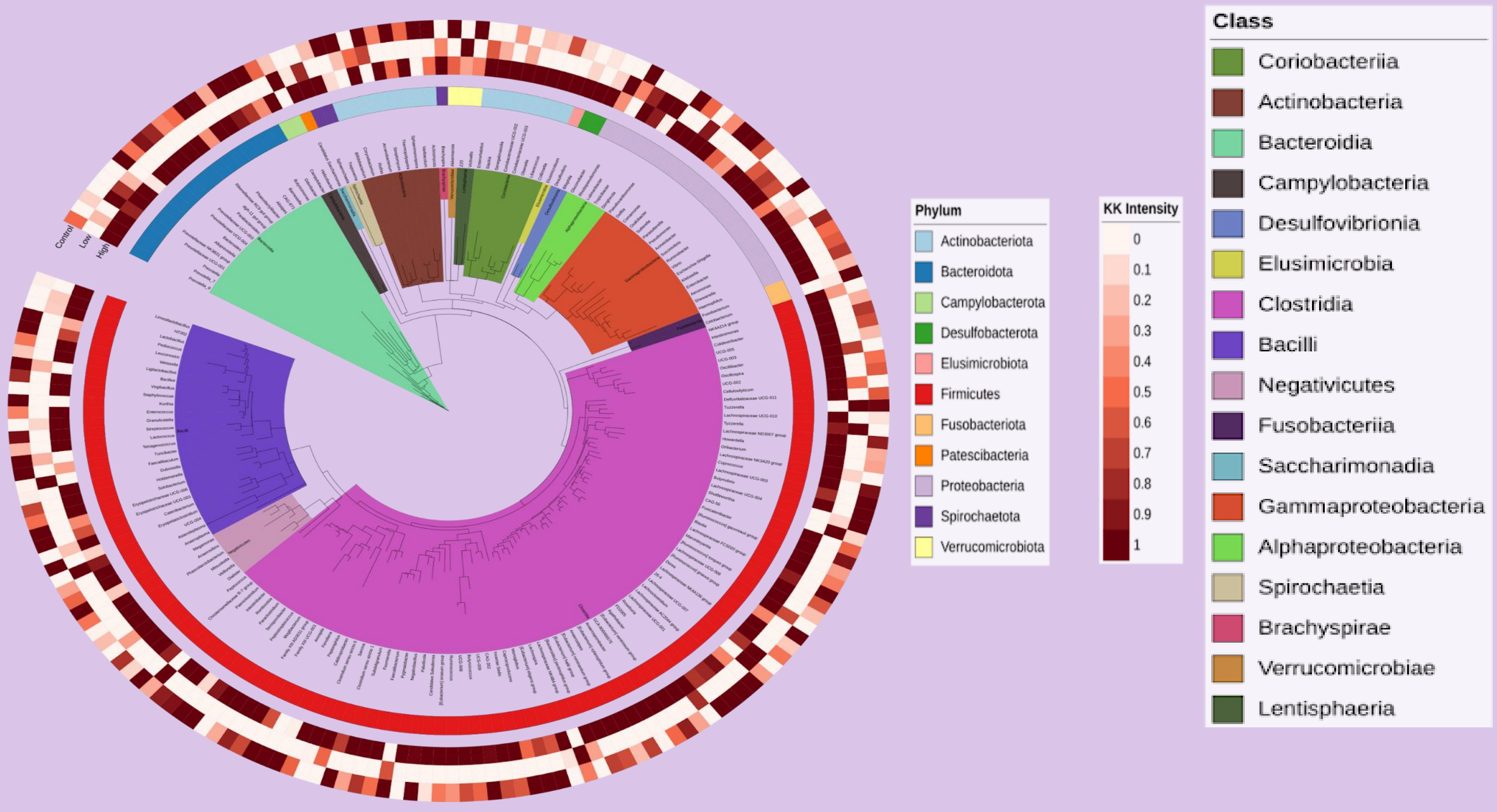
**Functional predictions [PICRUSt2 , ggpicrust2 R package]**

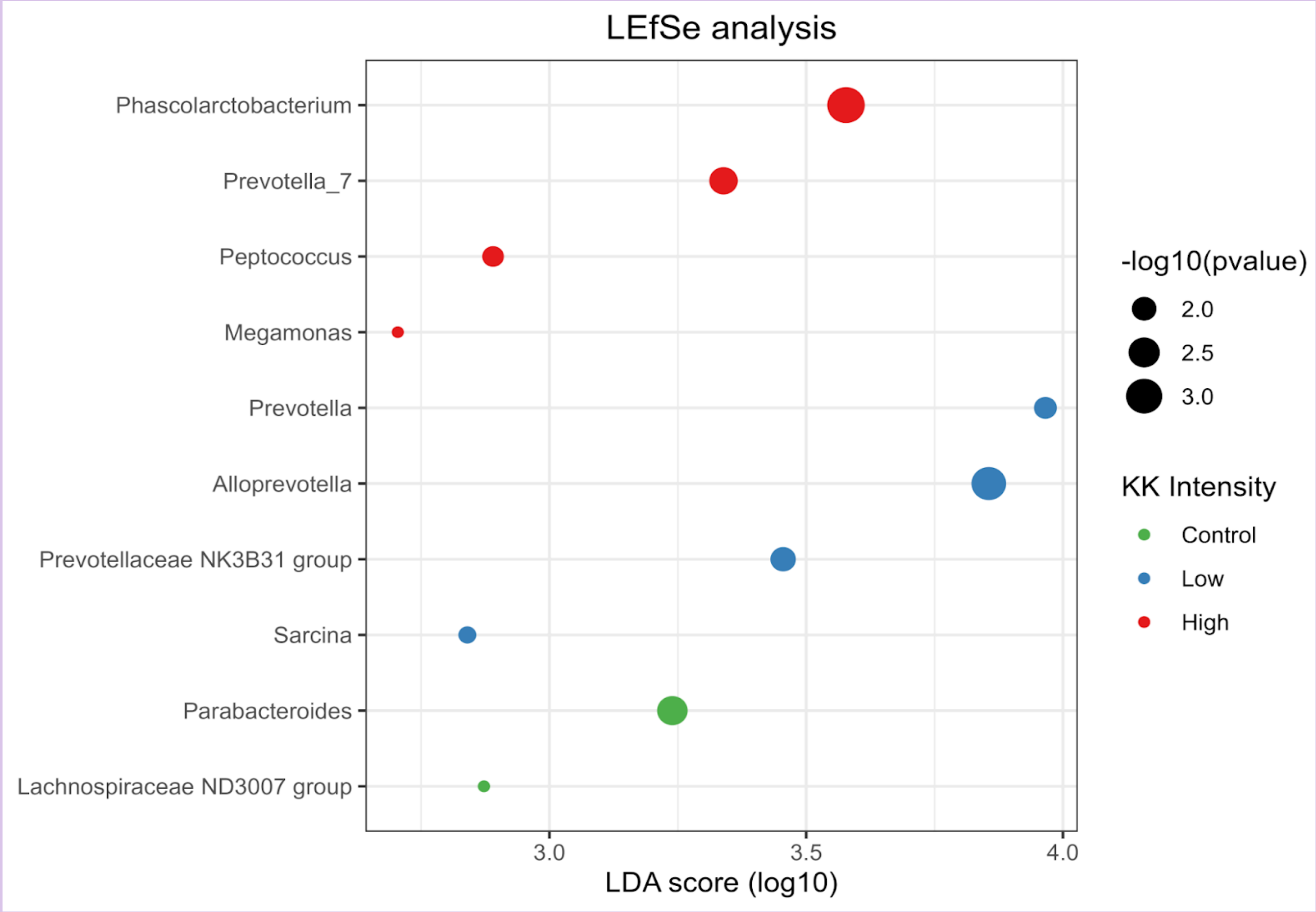
## Results











## Conclusion

- Dysbiosis observed with different infection intensities
- The diversity indices offered a comprehensive understanding of the microbial species' richness and evenness in the samples
- Differential abundance analysis highlighted key bacterial genera involved in gut microbiome shifts in metabolic and immune functions due to infection status, therefore might have biological implications
- This data suggests that the gut microbiome might be an important variable in schistosomiasis disease progression in children

## Acknowledgements

- Dr. Julius Mulindwa (PhD)
- Dr. Daudi Jjingo (PhD)
- Makerere Research Innovation Fund (MakRIF)
- African Center of Excellence in Bioinformatics & Data Intensive Science, Makerere University