A close-up of a graph

Description automatically generated

Figure\_Desq2\_heatmaps: Bi-cluster heatmap of differentially abundant ASVs in pairwise treatment comparisons. Columns indicate different samples, rows indicate different ASVs. Both rows and columns are clustered according to similarity in the abundance of differentially abundant ASVs. A) Bulk soil Bacteria, B) rhizosphere Bateria, C) Bulk soil Fungi, D) Rhizosphere Fungi.

Bi-cluster heatmaps of differentially abundant ASVs (defined with deseq2 at minimum log fold change of 2 and minimum fdr-adjsuted p value < 1-10 for Bacteria and 1-6 for Fungi) could cluster treatment sample groups very clearly in bacteria, but not in fungi (Figure\_Desq2\_heatmaps). This analysis indicated 430 differentially abundant ASVs in Bulk soil Bacteria, 286 ASVs in rhizosphere Bacteria, 39 ASVs in Bulk soil Fungi, and 29 ASVs in Rhizosphere Fungi samples. In Bacteria, order Bacillales dominated the ASV clusters that could more easily separate the sample groups. In Fungi, ASVs from order Hypocreales could best discriminate between samples, but this effect is far less clear than it is for Bacillales and Bacteria.