

Figure 1. Principal Coordinate Analysis (PCoA) of Weighted and Unweighted UniFrac distances. Principal coordinates analysis (PCoA) of gut microbiota composition among wild mammals from Kruger National Park based on weighted (A, C) and unweighted (B, D) UniFrac distances. Points represent individual samples coloured by dietary group: carnivores (orange), non-ruminants (purple), and ruminants (green). Percentages indicate variance explained by each axis. Outlier samples ($n = 6$) are shown in panels A and B for visualization but excluded in panels C and D and all downstream analyses. Outliers were consistently identified across both distance metrics and viewing angles (Fig. S2, S3).

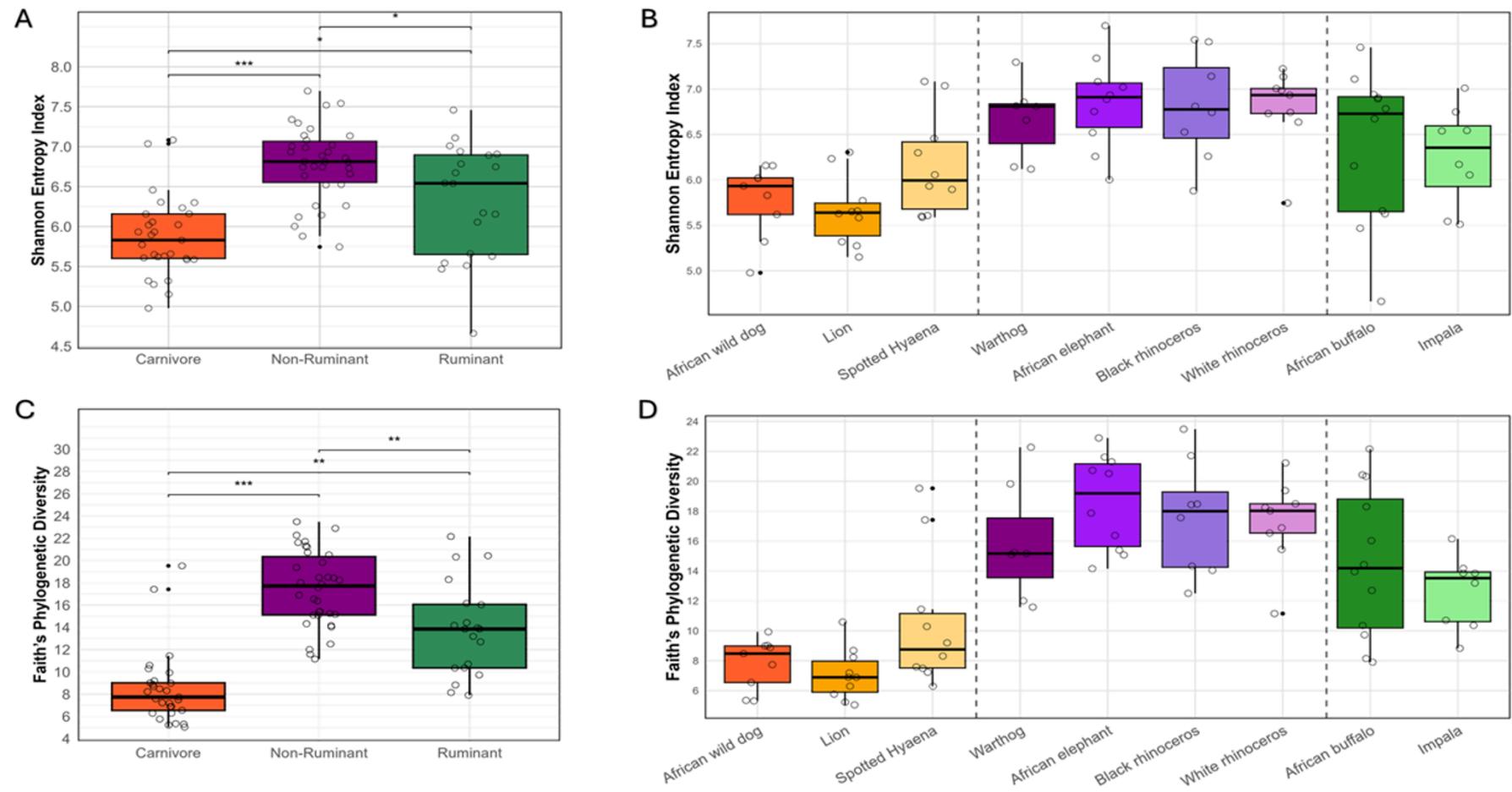


Figure 2. Alpha diversity of gut microbiota across dietary groups and host species. Boxplots display two measures of alpha diversity—Shannon entropy (A, B) and Faith's phylogenetic diversity (C, D)—among wild mammalian hosts from Kruger National Park. Panels A and C compare diversity across the three main dietary groups: carnivores, non-ruminants, and ruminants. Panels B and D show corresponding diversity metrics at the host species level within each dietary group. Individual data points represent samples per host, with horizontal lines indicating significance. These results highlight both dietary and species-level variation in gut microbial diversity.

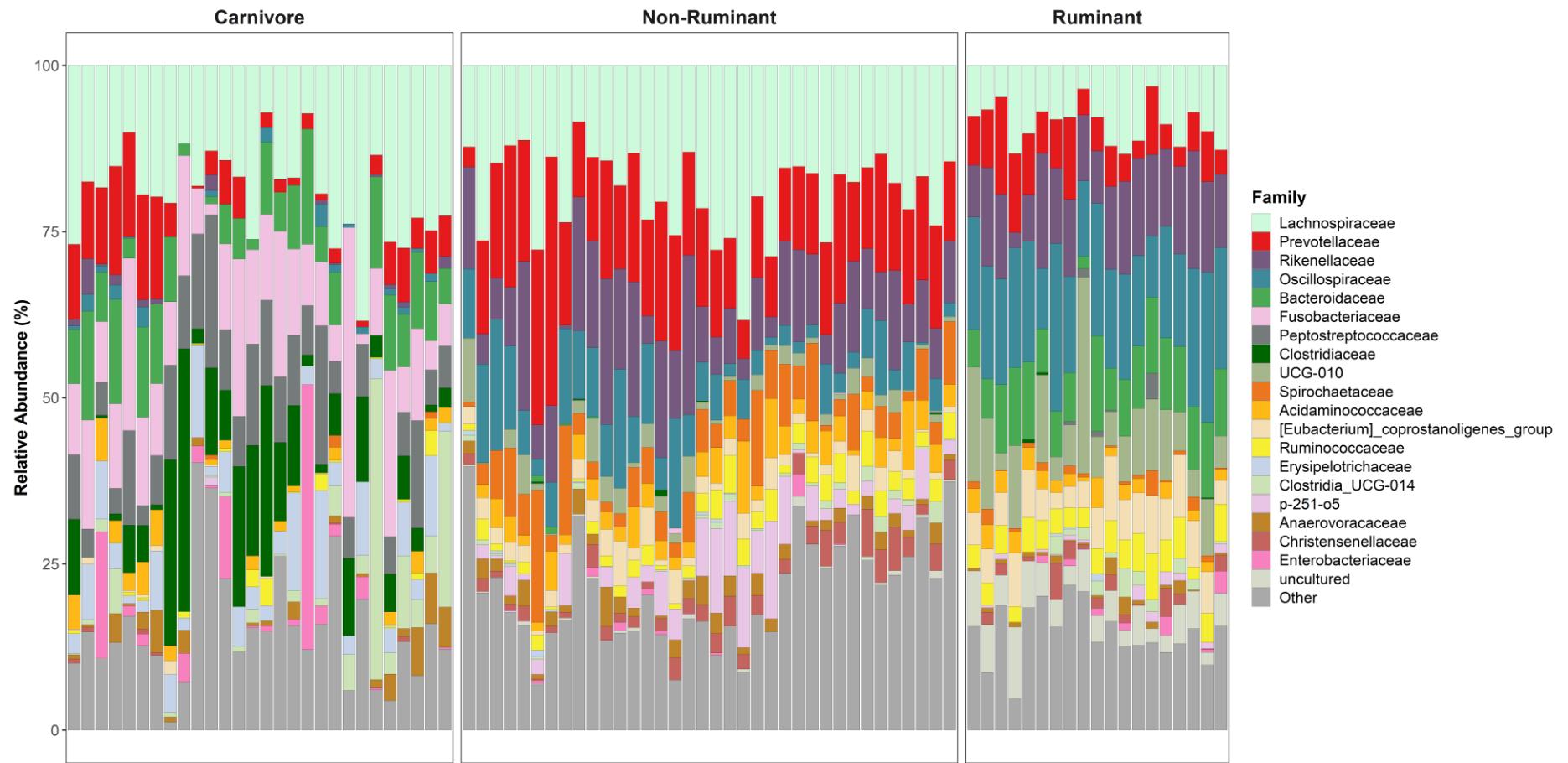


Figure 3. Taxonomic composition of gut microbiota across mammalian dietary groups on a family-level. Stacked bar plots show the relative abundance of the top 20 most prevalent bacterial families in individual gut microbiome samples from carnivores, non-ruminants, and ruminants. Samples are grouped by dietary category, with each bar representing an individual sample. Families comprising less than the top 20 are grouped under “Other.”

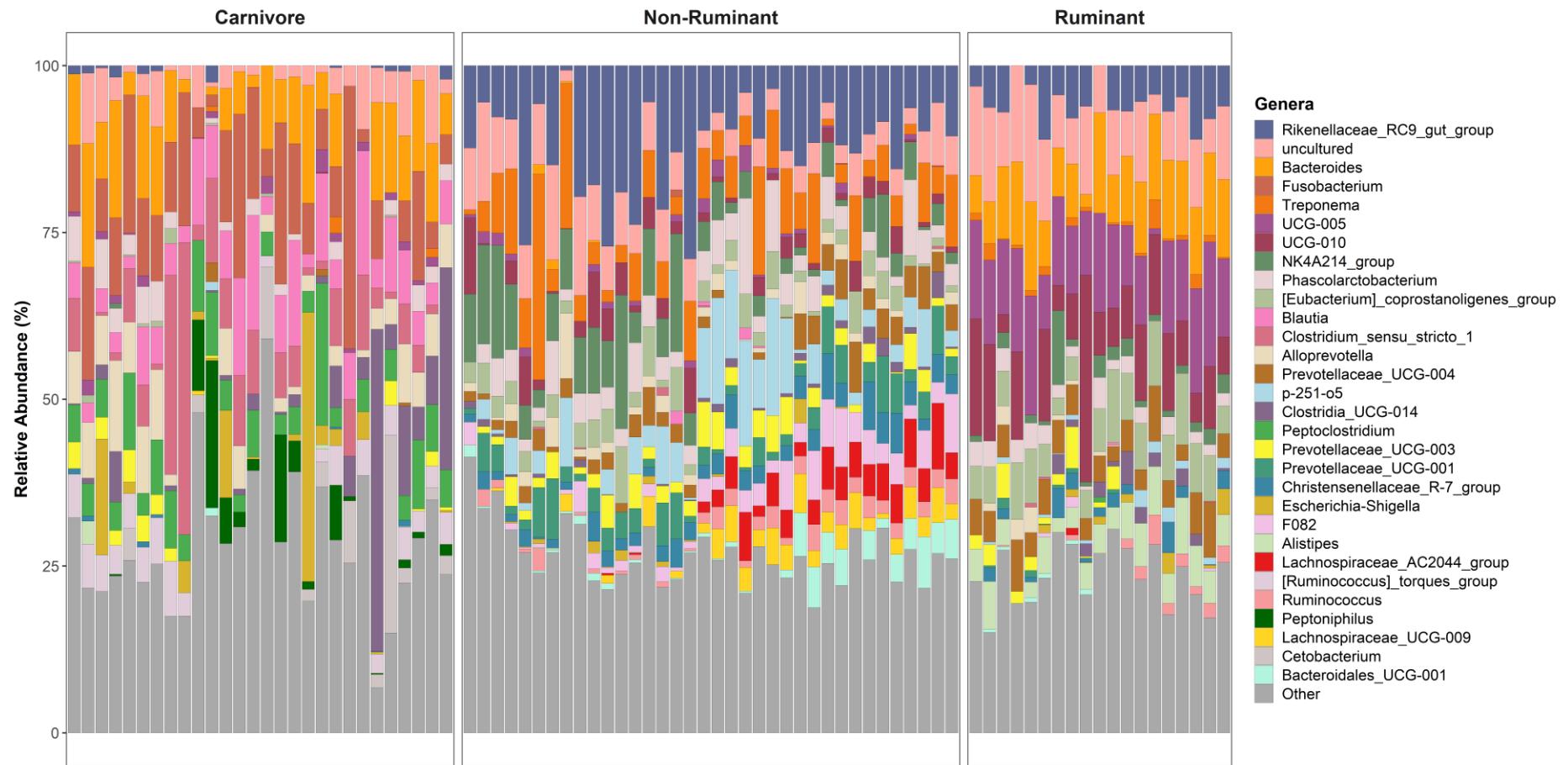


Figure 4. Taxonomic composition of gut microbiota across mammalian dietary groups on a genus-level. Stacked bar plots show the relative abundance of the top 30 most prevalent bacterial families in individual gut microbiome samples from carnivores, non-ruminants, and ruminants. Samples are grouped by dietary category, with each bar representing an individual sample. Genera comprising less than the top 30 are grouped under "Other."

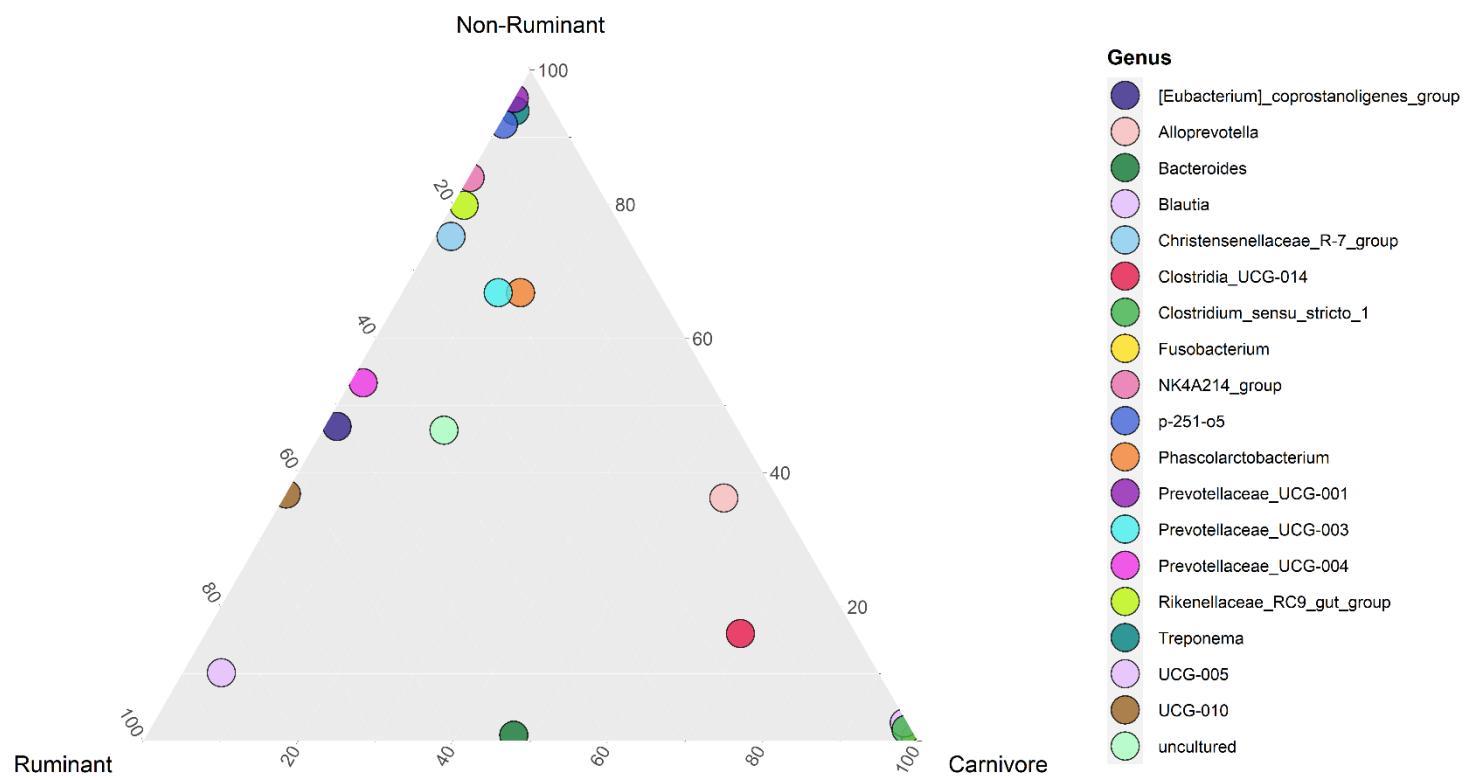


Figure 5. Ternary plot of genus-level taxonomic distribution across dietary groups. Each point represents a bacterial genus positioned according to its relative abundance across carnivore, non-ruminants, and ruminant hosts. Axes correspond to percentage contributions to each dietary group, with corners representing 100% contribution.

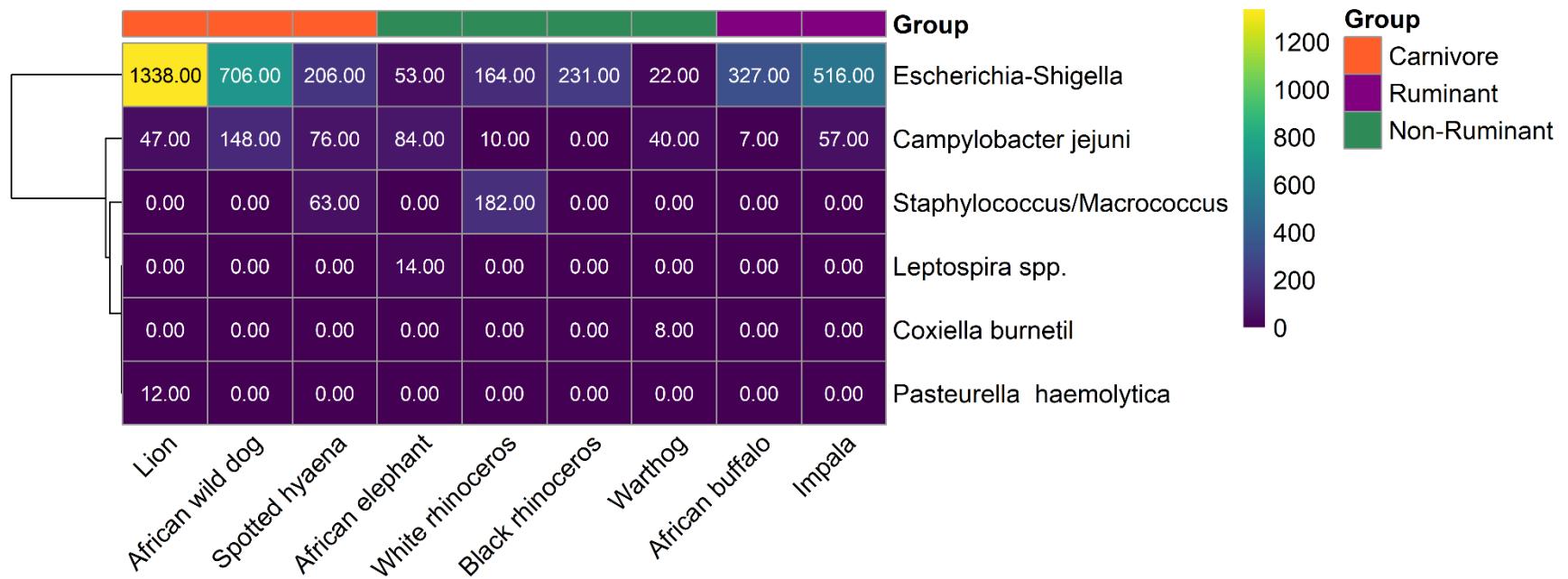


Figure 6. Heatmap of potential pathogenic genera across host species. Heatmap displays absolute read counts for genera with known or potential pathogenic roles (rows) across individual host species (columns). The top annotation panel indicates each species' dietary group.

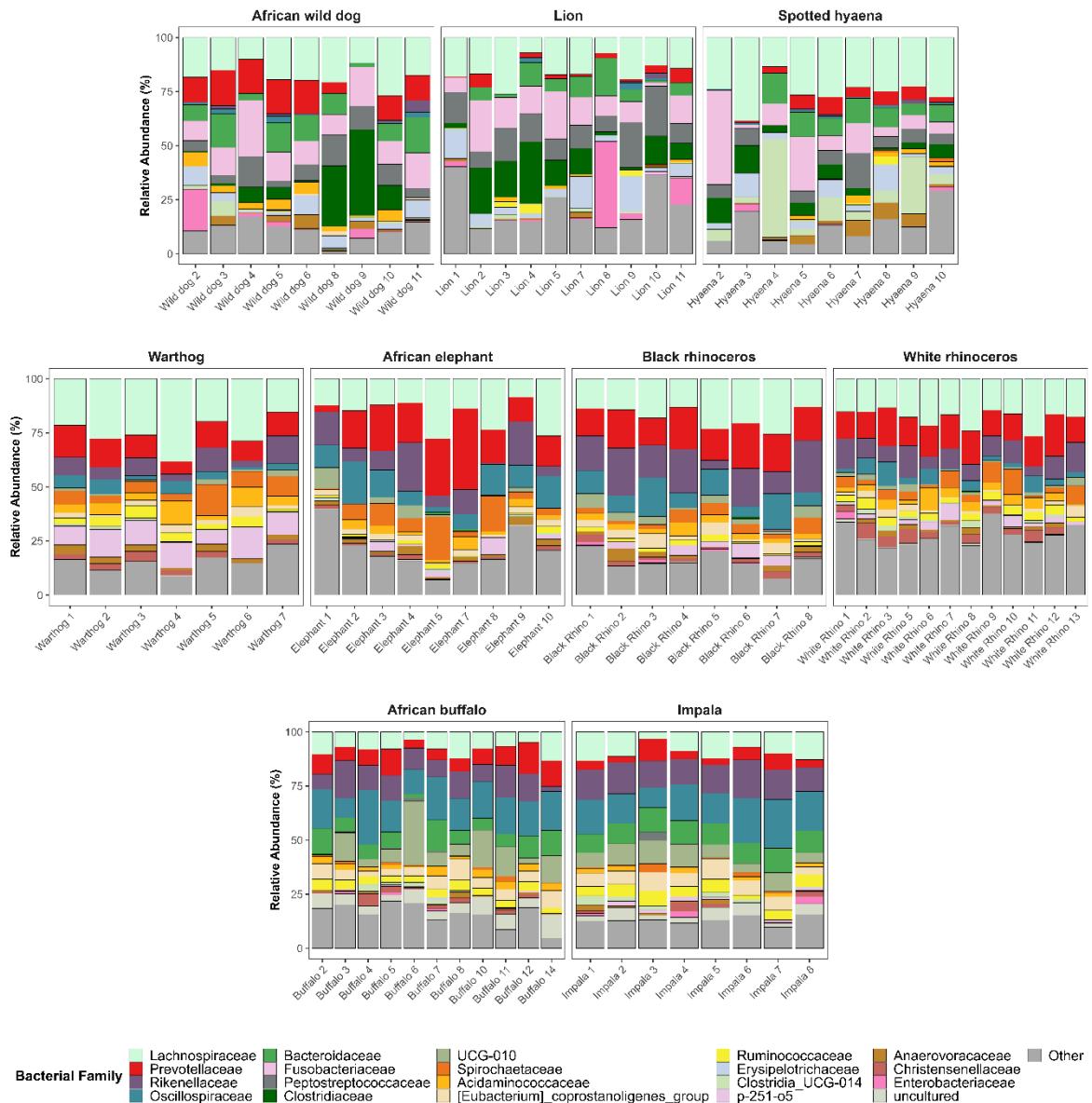


Figure 7. Family-level taxonomic composition of gut microbiota across host species. Family-level taxonomic composition of gut microbiota across host species within each dietary group. Stacked bar plots display relative abundances of the 20 most prevalent bacterial families in individual samples; families outside the top 20 are grouped as "Other." Samples are organised by host species within carnivores (row 1), non-ruminant (row 2), and ruminants (row 3).

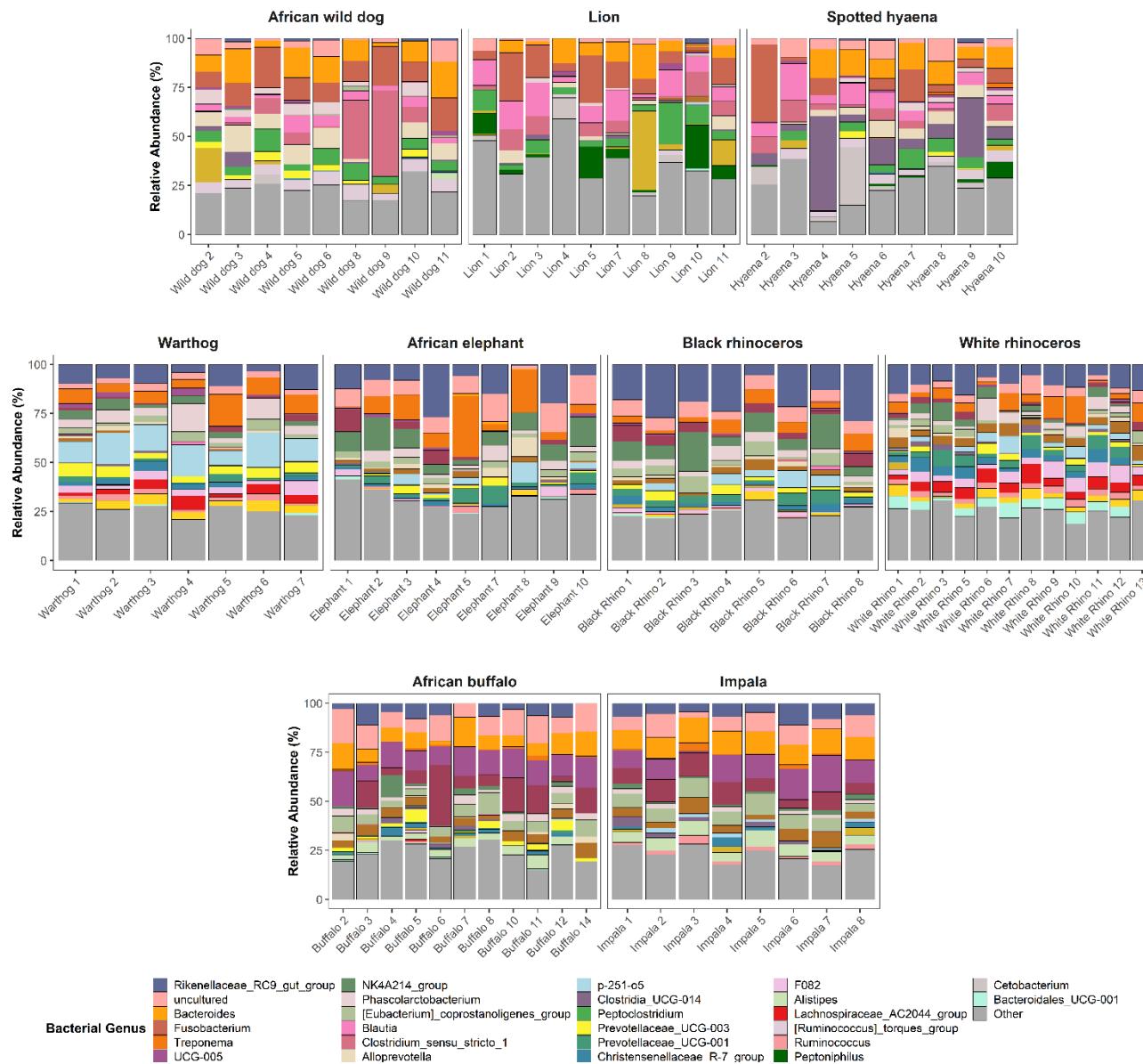


Figure 8. Genus-level taxonomic composition of gut microbiota across host species. Genus-level taxonomic composition of gut microbiota across host species within each dietary group. Stacked bar plots display relative abundances of the 30 most prevalent bacterial genera in individual samples; genera outside the top 30 are grouped as "Other." Samples are organised by host species within carnivores (row 1), non-ruminant (row 2), and ruminants (row 3).

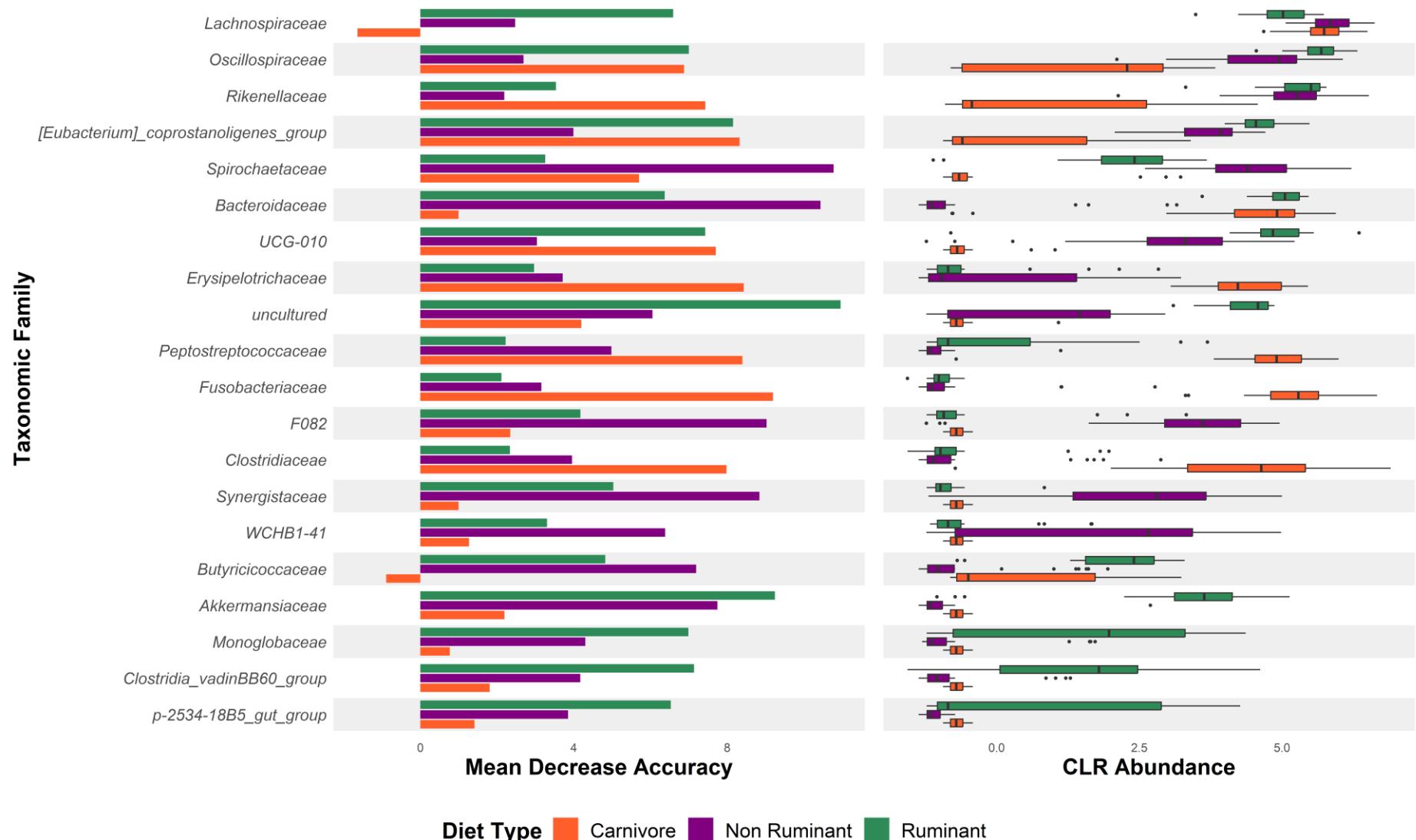


Figure 9. Random forest classification based on family-level abundances. Left panel: Random Forest variable importance (Mean Decrease in Accuracy) for the top 20 discriminating bacterial families. Right panel: CLR-transformed abundances for the same families across carnivores (orange), non-ruminants (green), and ruminants (purple).

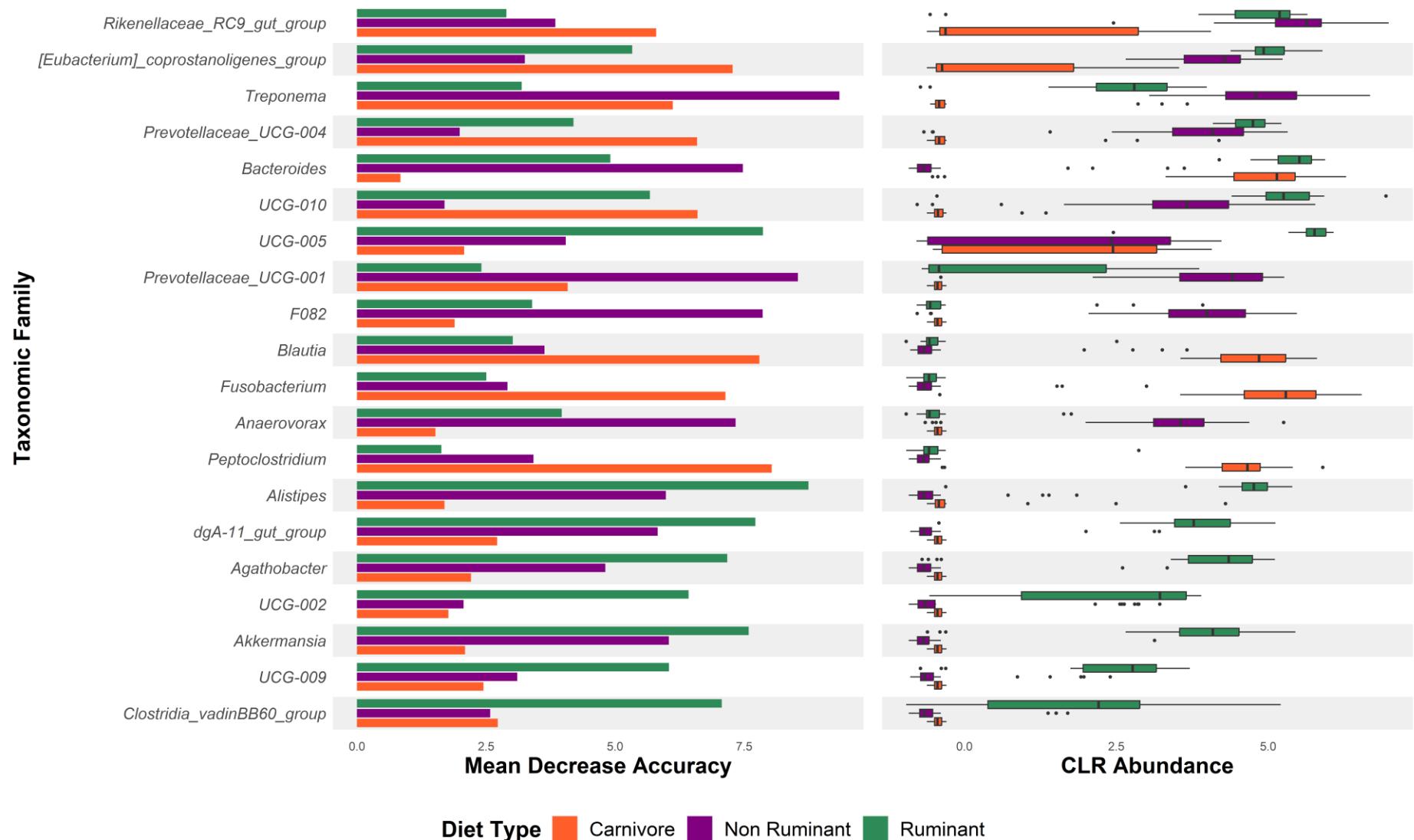


Figure 10. Random forest classification based on genus-level abundances. Random Forest variable importance (Mean Decrease in Accuracy) for the top 20 discriminating bacterial genera. Right panel: CLR-transformed abundances for the same genera across carnivores (orange), non-ruminants (green), and ruminants (purple).