

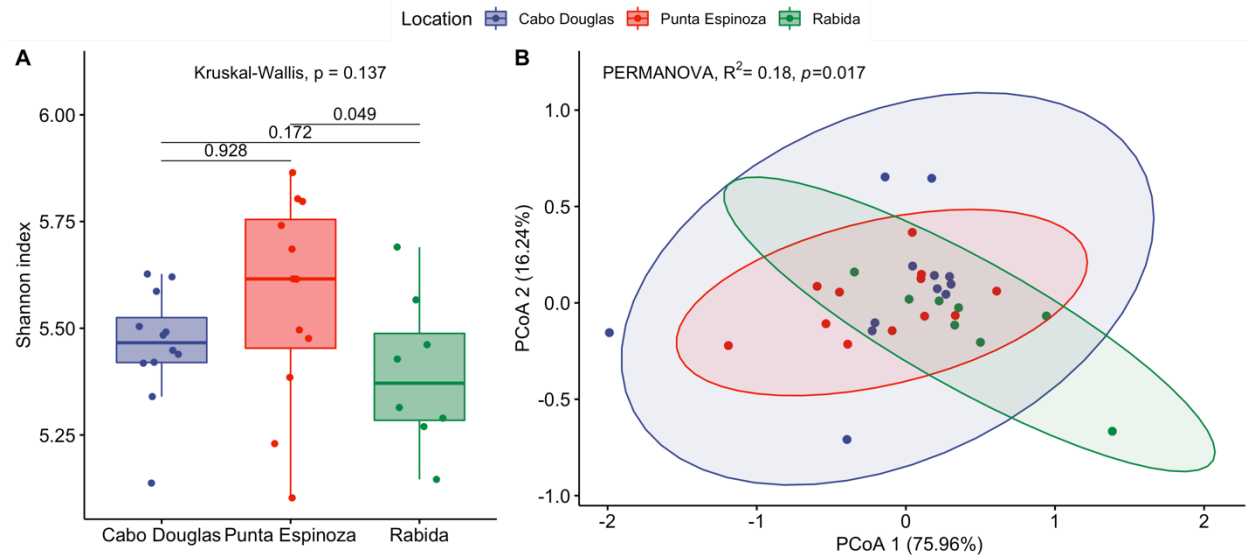


Figure S1. Diversity of marine iguana's gut metagenomes analyzed with Kraken2. A)

Shannon Index. B) PCoA of the Bray-Curtis dissimilarity.

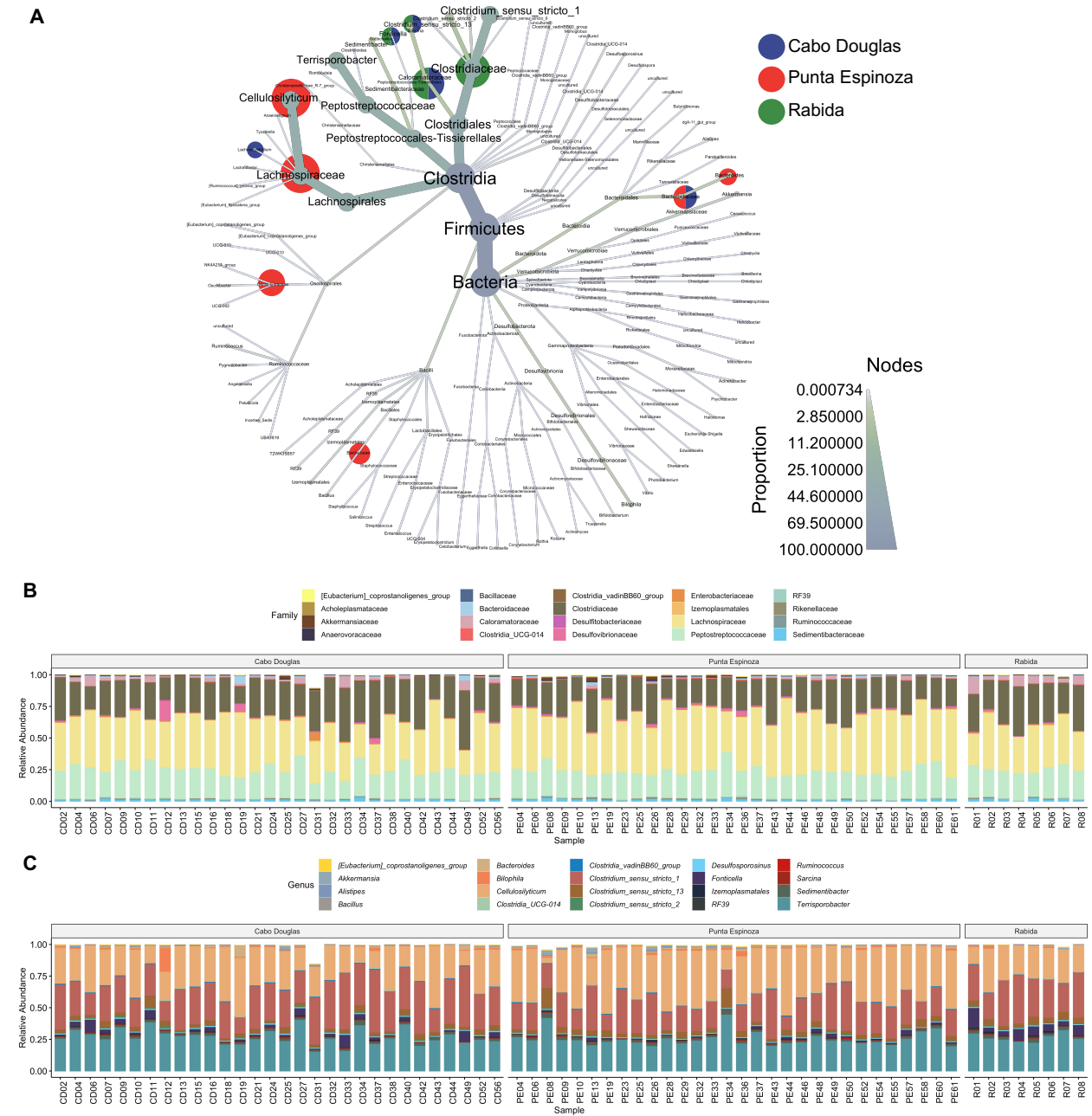


Figure S2. Gut microbiome composition (16S *r*RNA sequencing) of marine iguanas from Fernandina and Rabida Islands. A) Heat-tree showing the proportion of taxa from phylum to genus, taxa significantly higher is highlighted for each location/s. B) Relative abundance of the top 20 most abundant families per sample. C) Relative abundance of the top 20 bacterial genera.

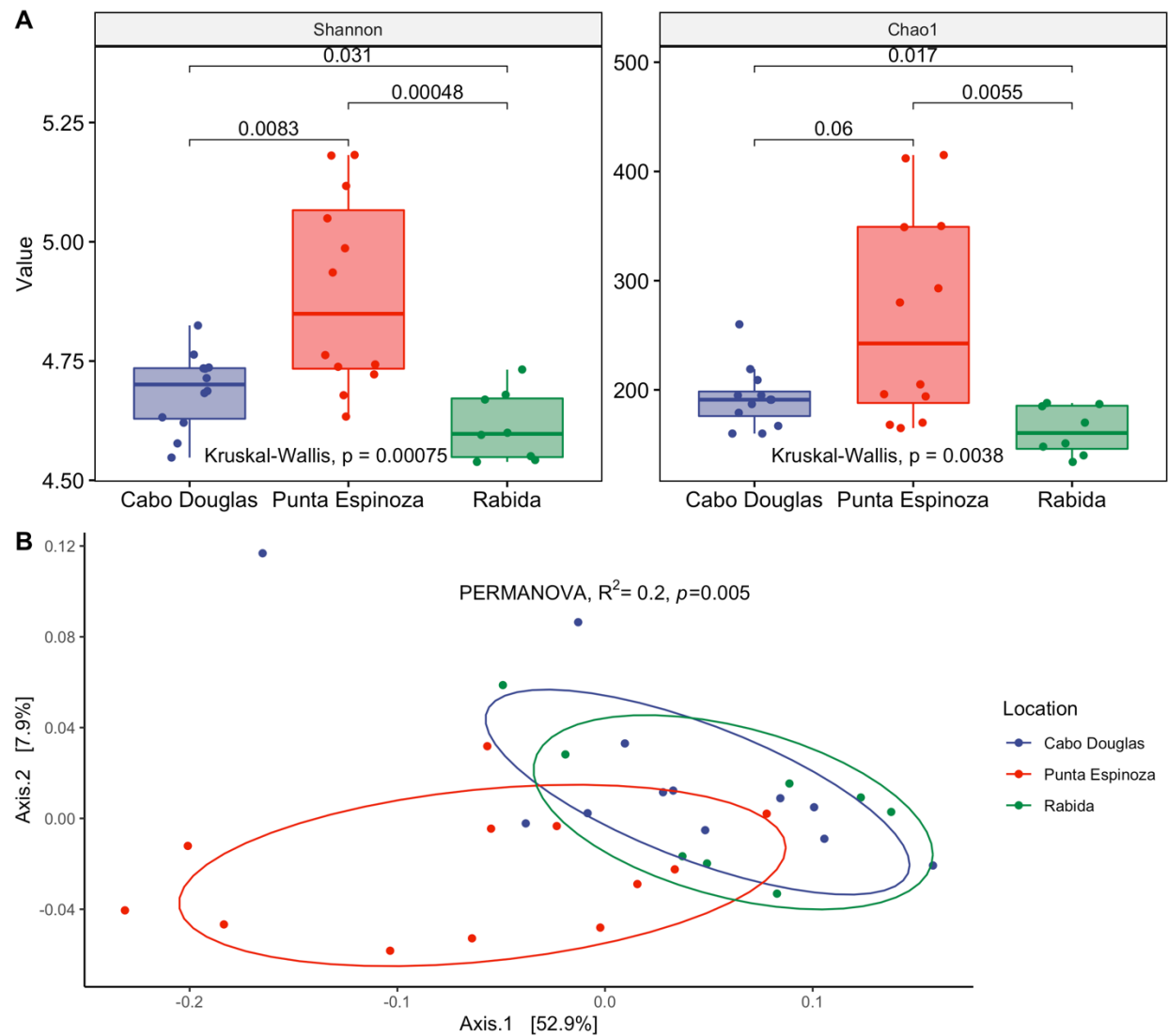


Figure S3. Microbial-associated metabolic pathway's diversity. A) Alpha diversity calculated with the indices Shannon and Chao1. B) Beta-diversity analyzed in a PCoA of a Bray-Curtis dissimilarity matrix.

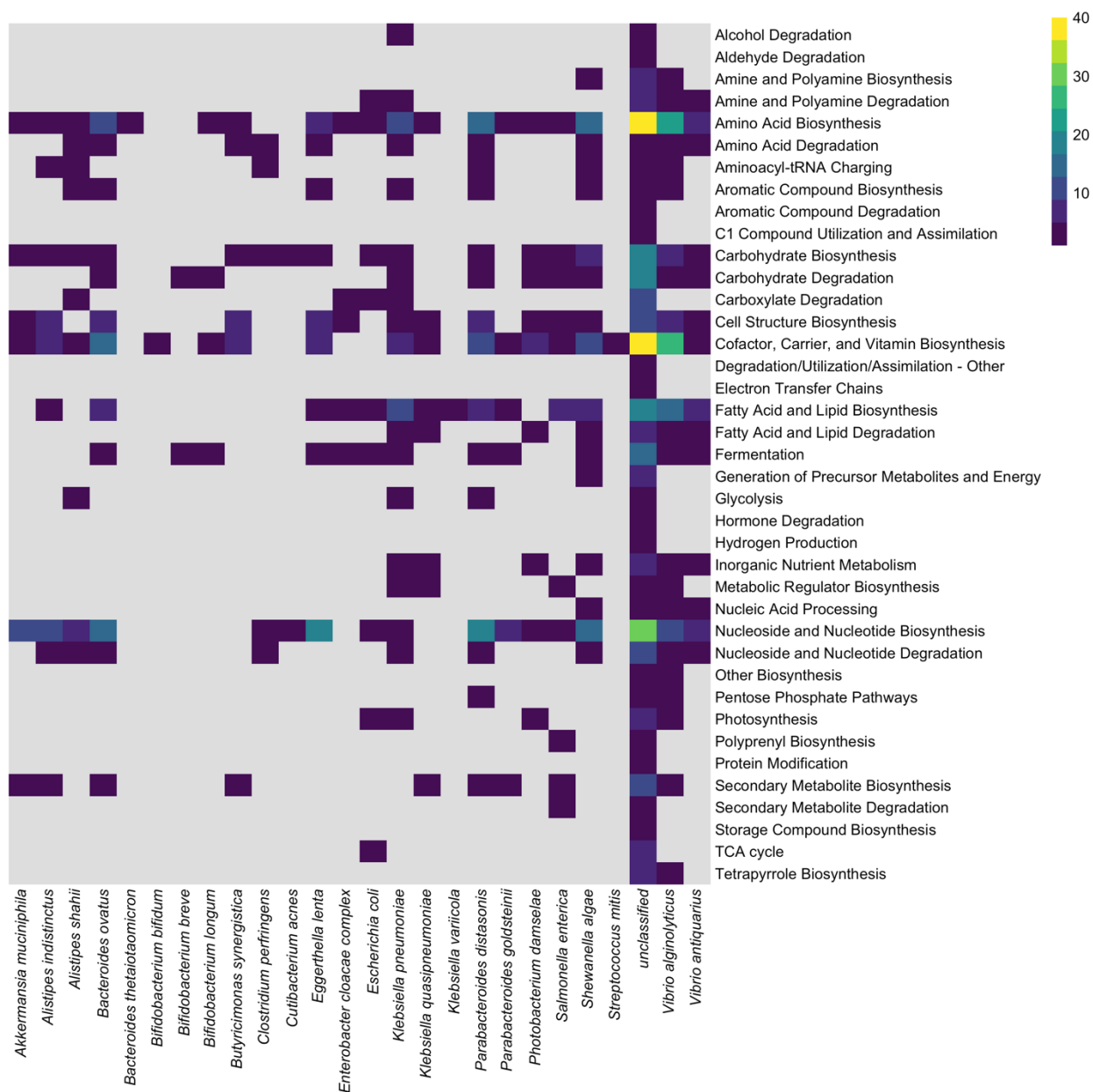


Figure S4. Heatmap showing the number of microbial-metabolic pathways per bacterial species.

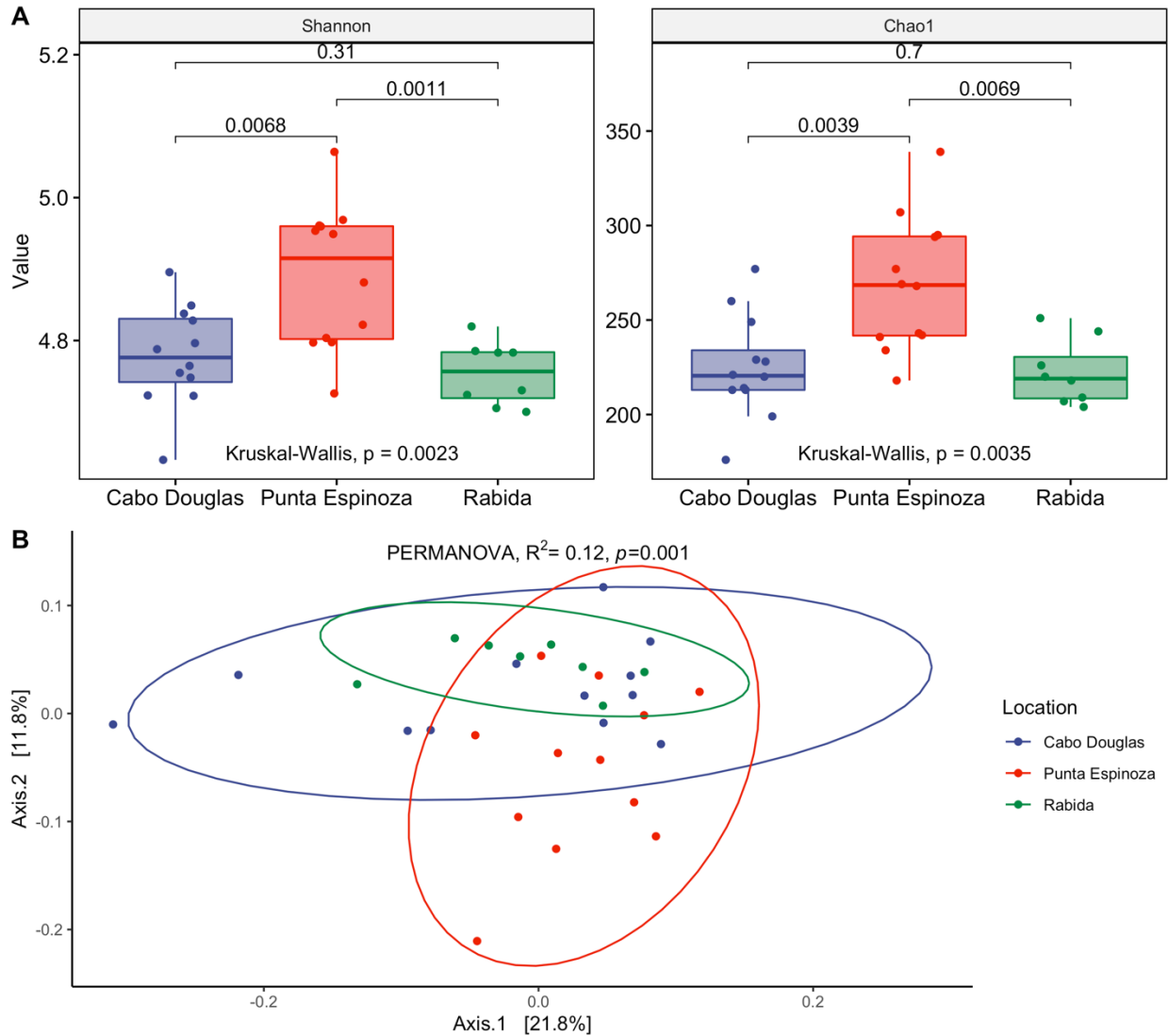


Figure S5. Resistome alpha and beta diversity. A) Alpha diversity calculated with the indices Shannon and Chao1. B) Beta-diversity analyzed in a PCoA of a Bray-Curtis dissimilarity matrix.

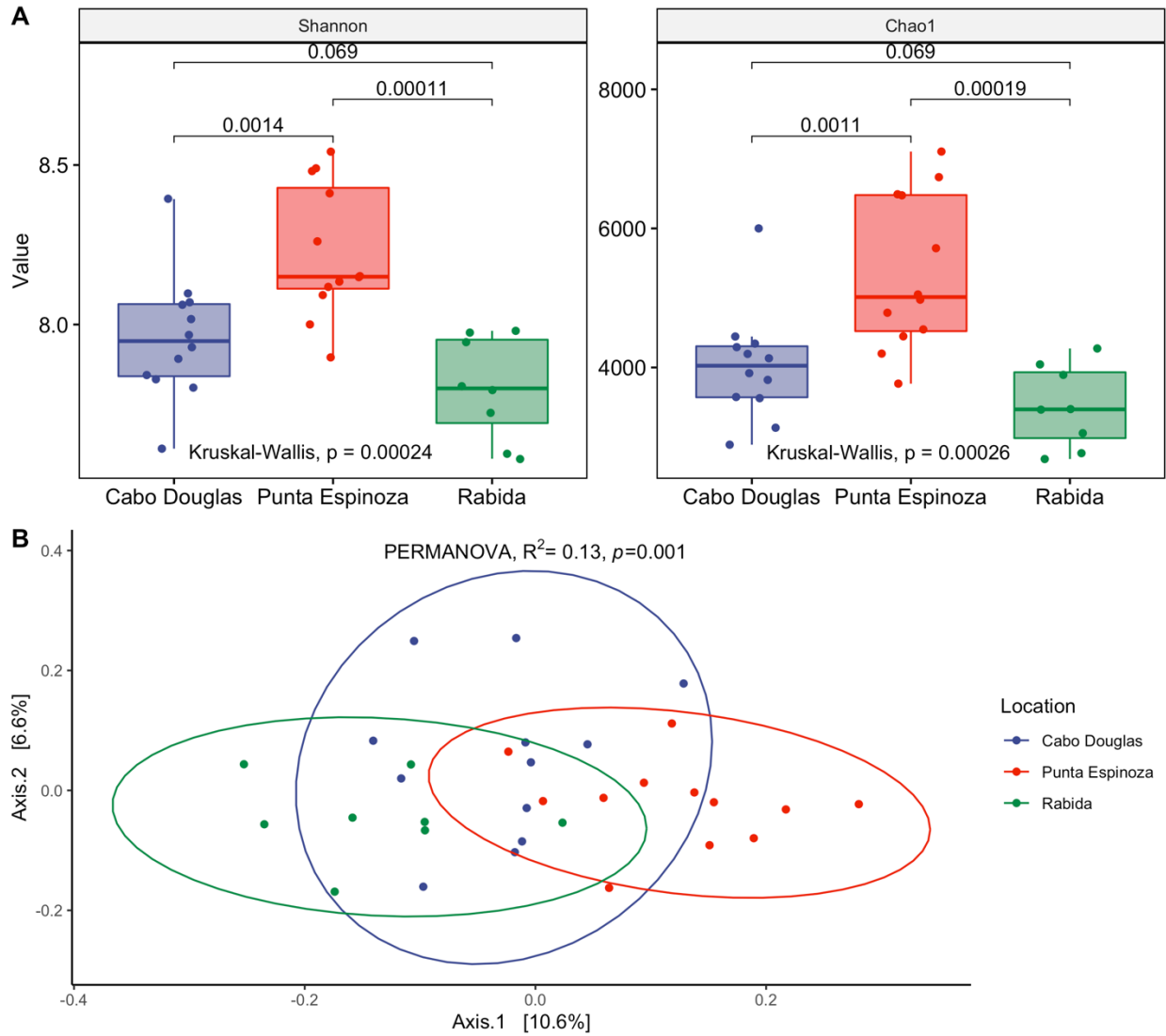


Figure S6. Mobilome alpha and beta diversity. A) Alpha diversity calculated with the indices Shannon and Chao1. B) Beta-diversity analyzed in a PCoA of a Bray-Curtis dissimilarity matrix.

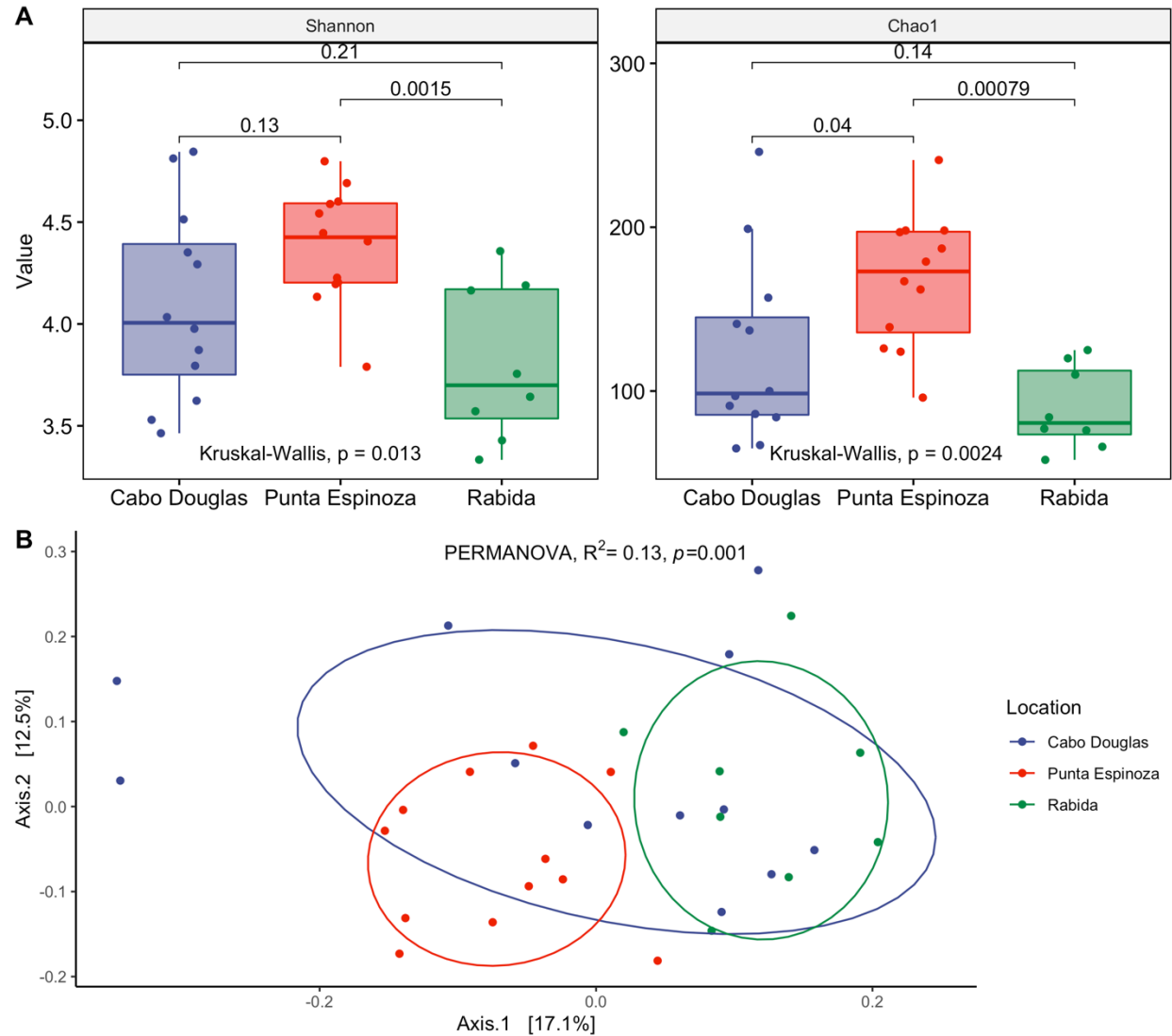


Figure S7. Virulome alpha and beta diversity. A) Alpha diversity calculated with the indices Shannon and Chao1. B) Beta-diversity analyzed in a PCoA of a Bray-Curtis dissimilarity matrix.

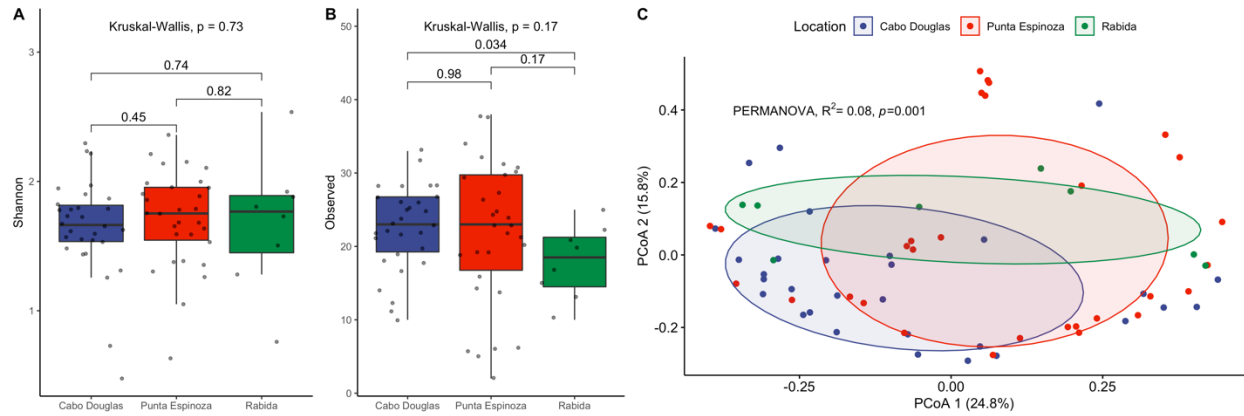


Figure S8. Alpha and beta diversity of the resistome/mobilome detected with SmartChip RT-PCR. (A) Shannon index; (B) Observed number of genes; and (C) Bray-Curtis dissimilarity PCoA.

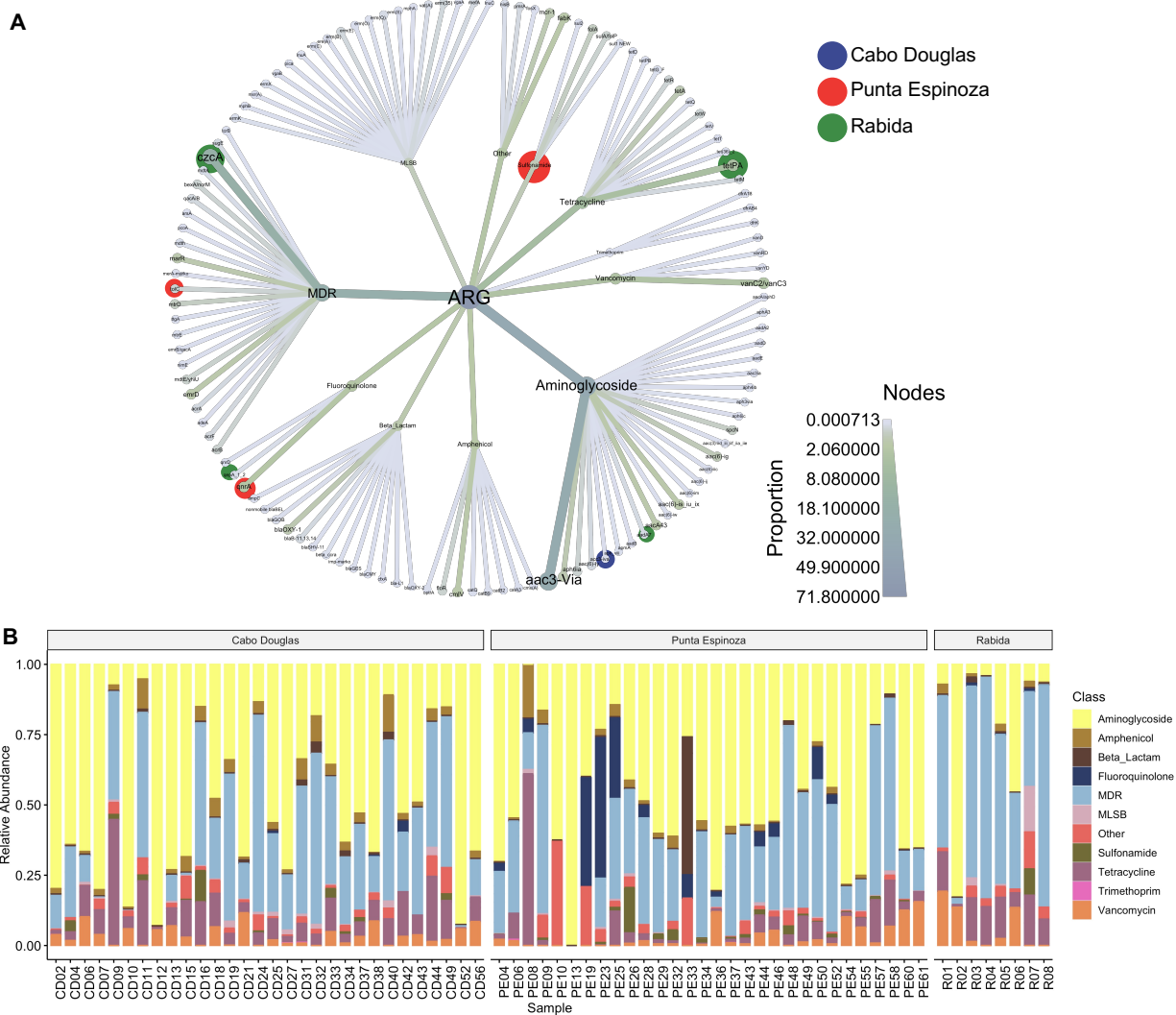


Figure S9. Gut resistome composition identified with SmartChip RT-PCR. A) Heat-tree showing the proportion of ARGs and differentially abundant ARGs among locations. **B)** Relative abundance of ARGs classes per sample and clustered by location.

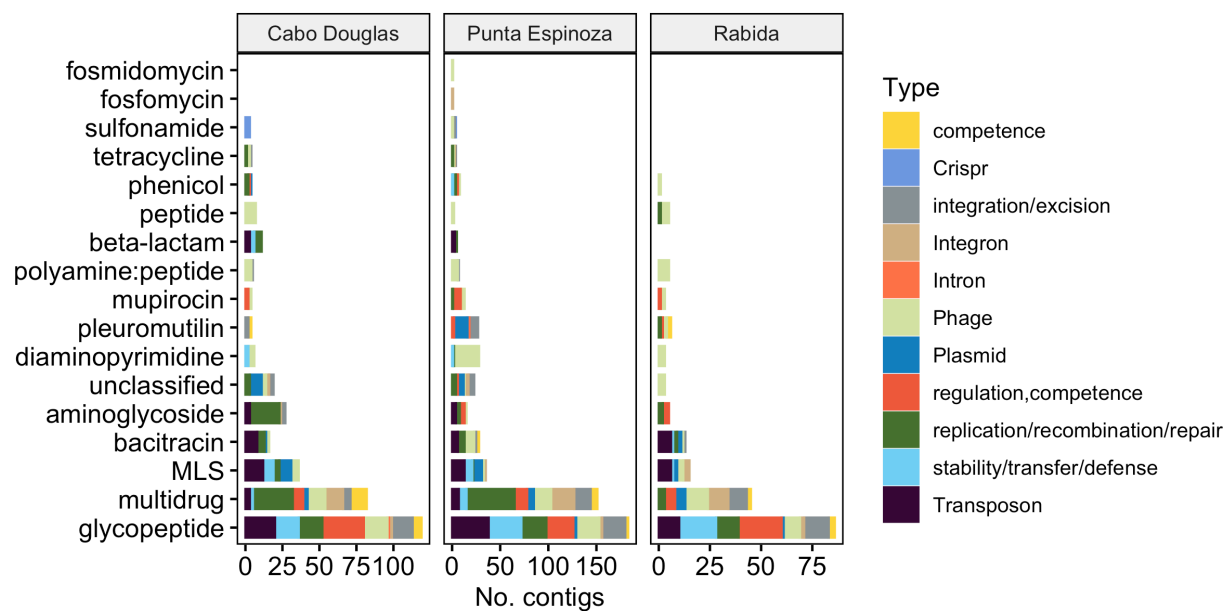


Figure S10. Number of ACC harboring genes involved in HGT by ARG class and location.

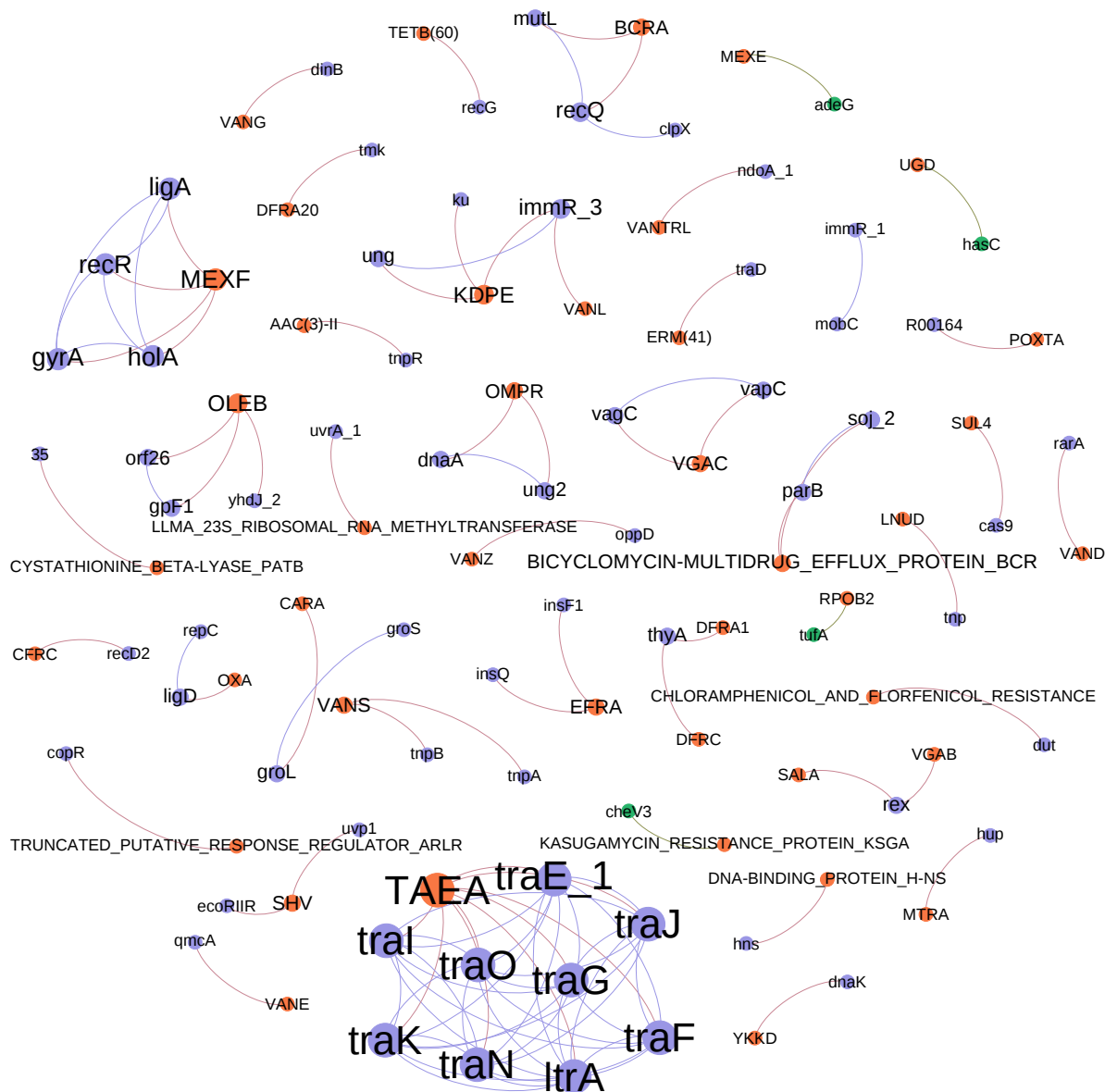


Figure S11. Co-occurrence network of ACCs between ARG, MGE, and virulence genes. Edges represent a correlation $\geq$ to 0.5 and a p-value < 0.01 . Correlations were calculated based on a presence/absence matrix per contig. ARG = orange, MGE = purple, Virulence = Green.