Exploring the Bacteriome and Resistome of Humans and Food-Producing Animals in Brazil

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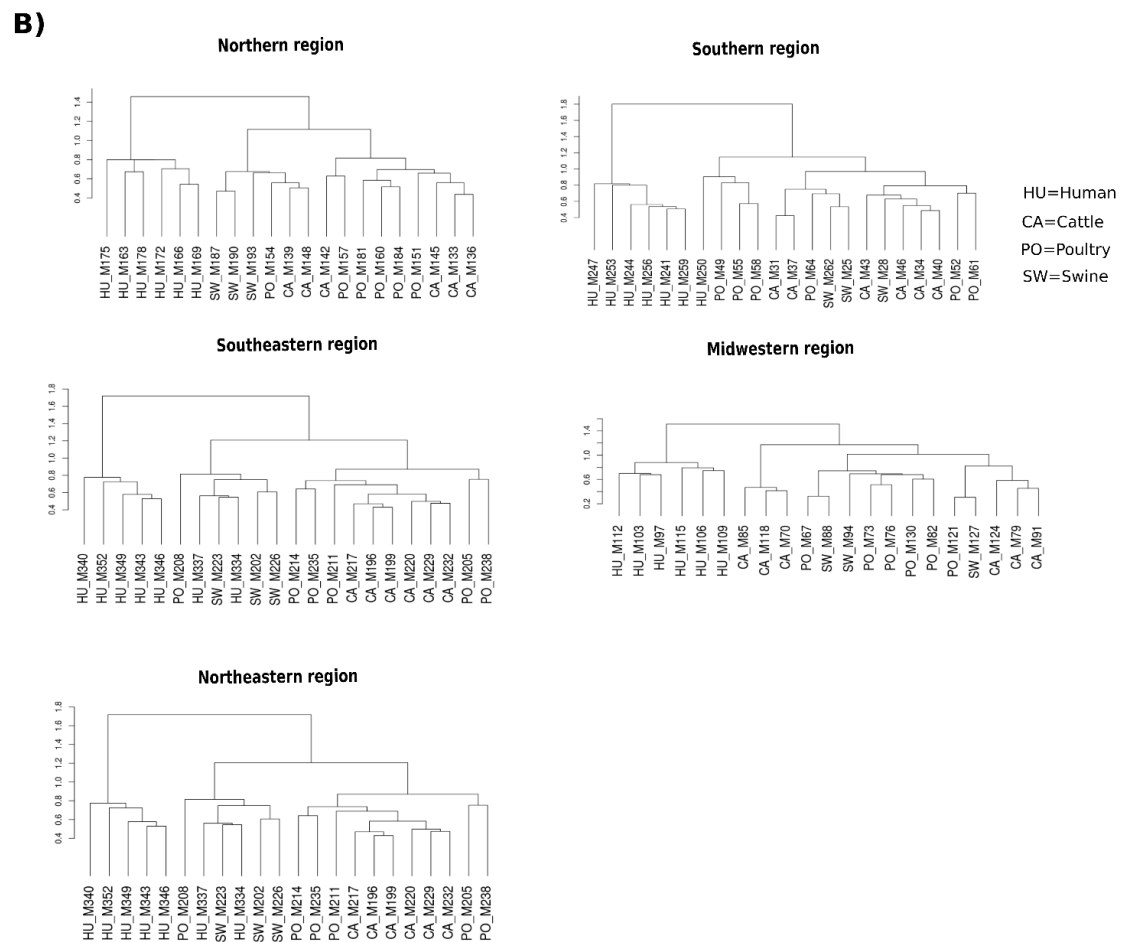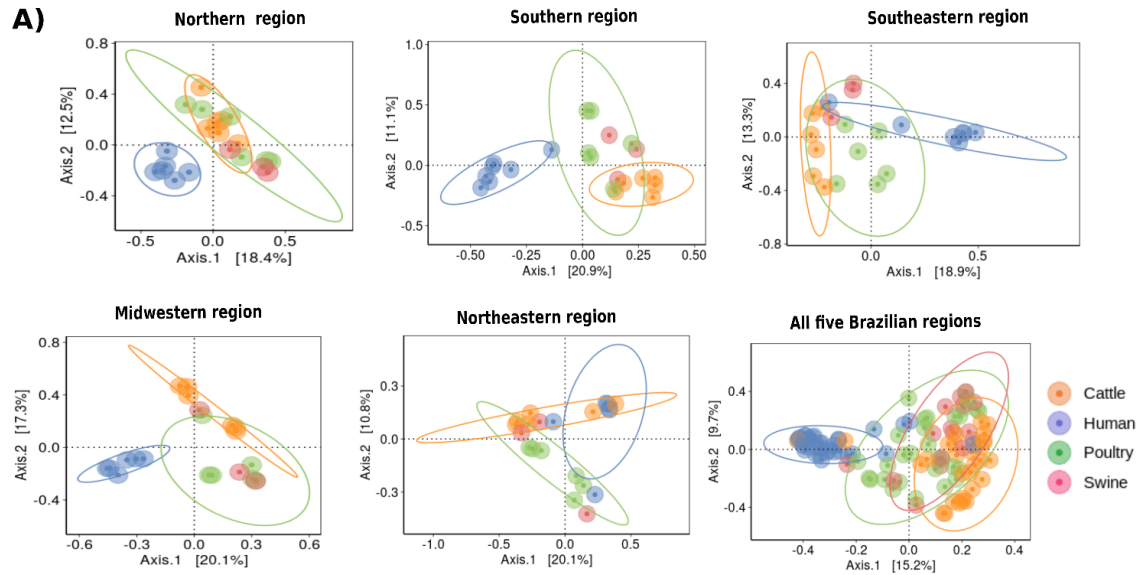

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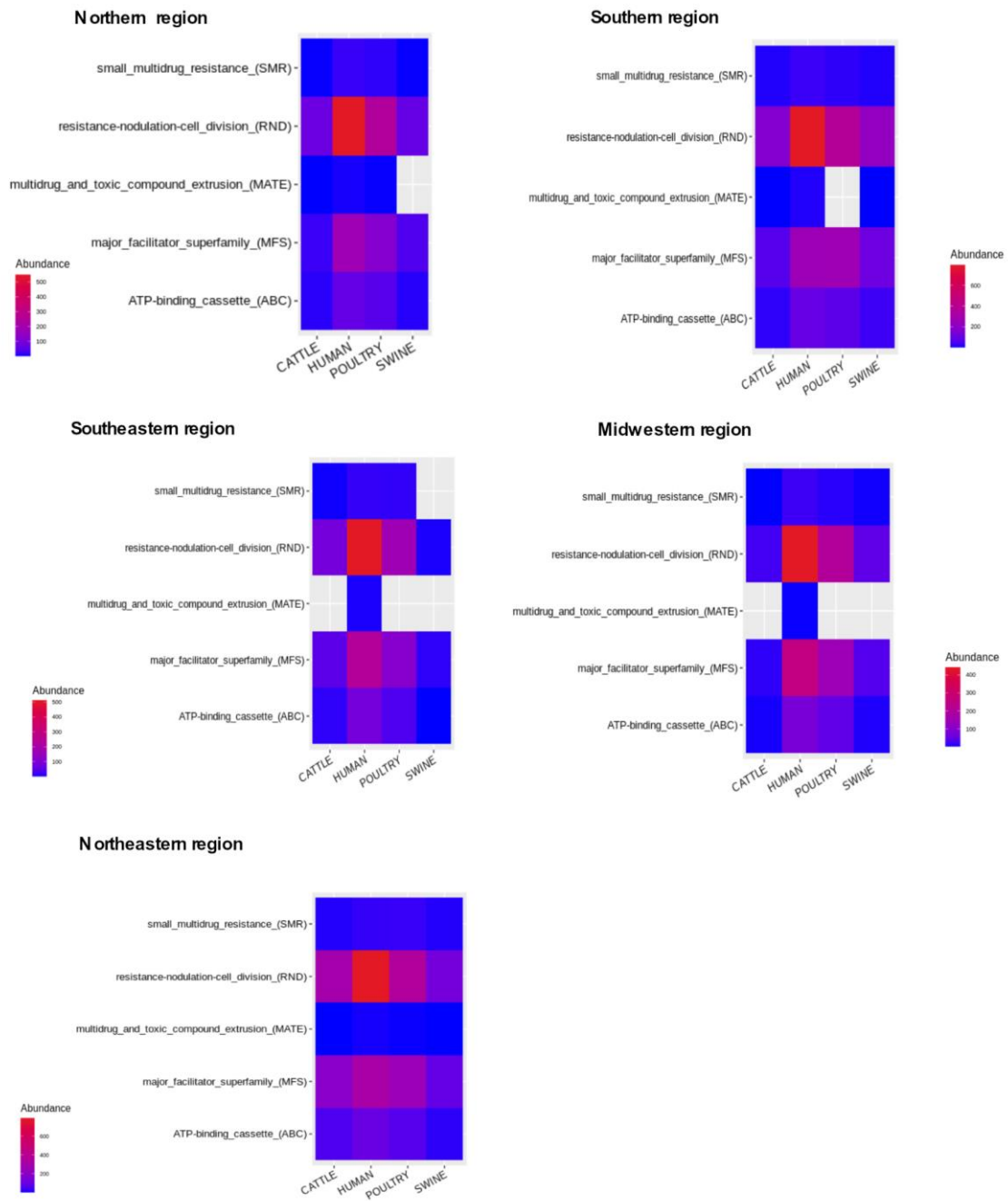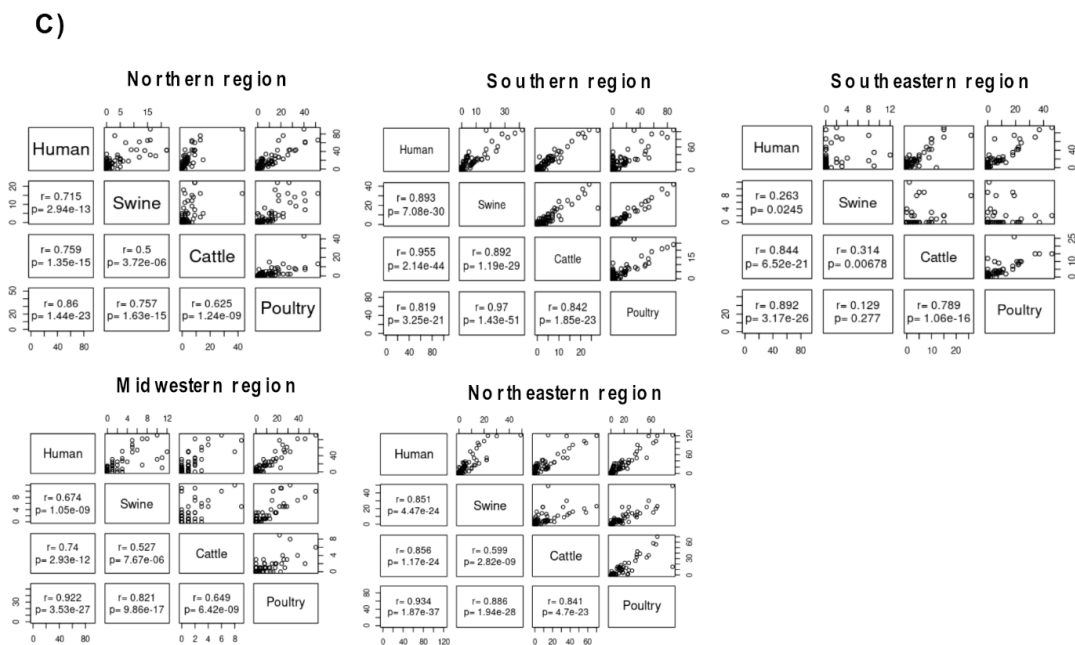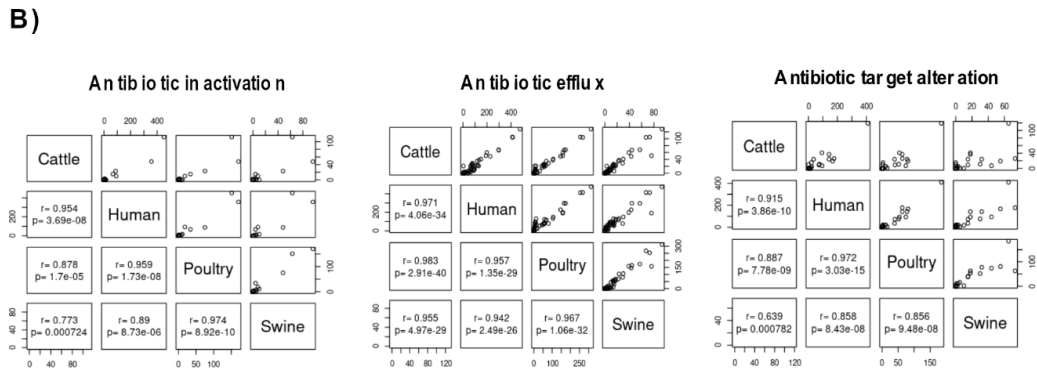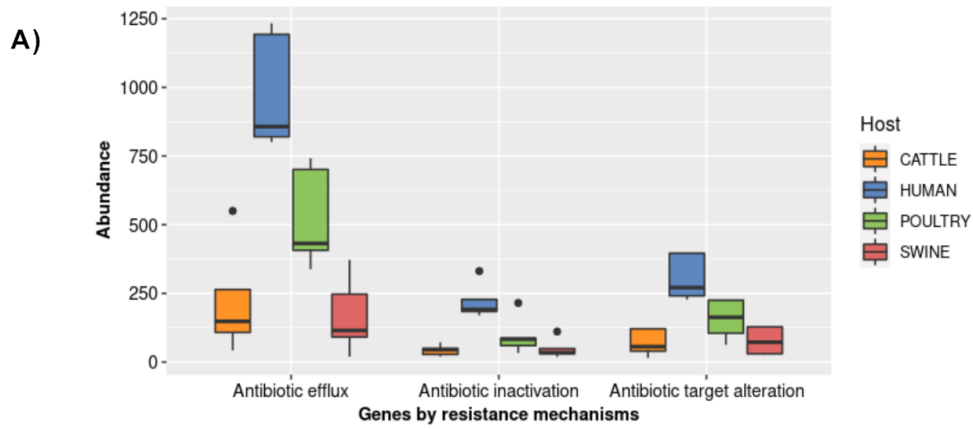
Supplementary Figures

Supplementary Figure 1. Dissimilarity of the bacterial   community composition indicated by principal coordinate analysis (PCoA) (A) and hierarchical clustering method (B). Samples from the five Brazilian regions are represented. (A) Each point represents a host, and the proximity or distance between points represents how different the samples are from one another. Circles represent ellipses at 95% confidence interval. The points and ellipses are colored according to the host. (B) For each region, the x-axis shows the hosts represented by HU (for human), CA (for cattle), PO (for poultry), and SW (for swine), followed by the ID sample. The y-axis shows the distance values between clusters. A clear difference in the bacterial   community composition is observed for the majority of humans sampled, which was not observed in other animals.
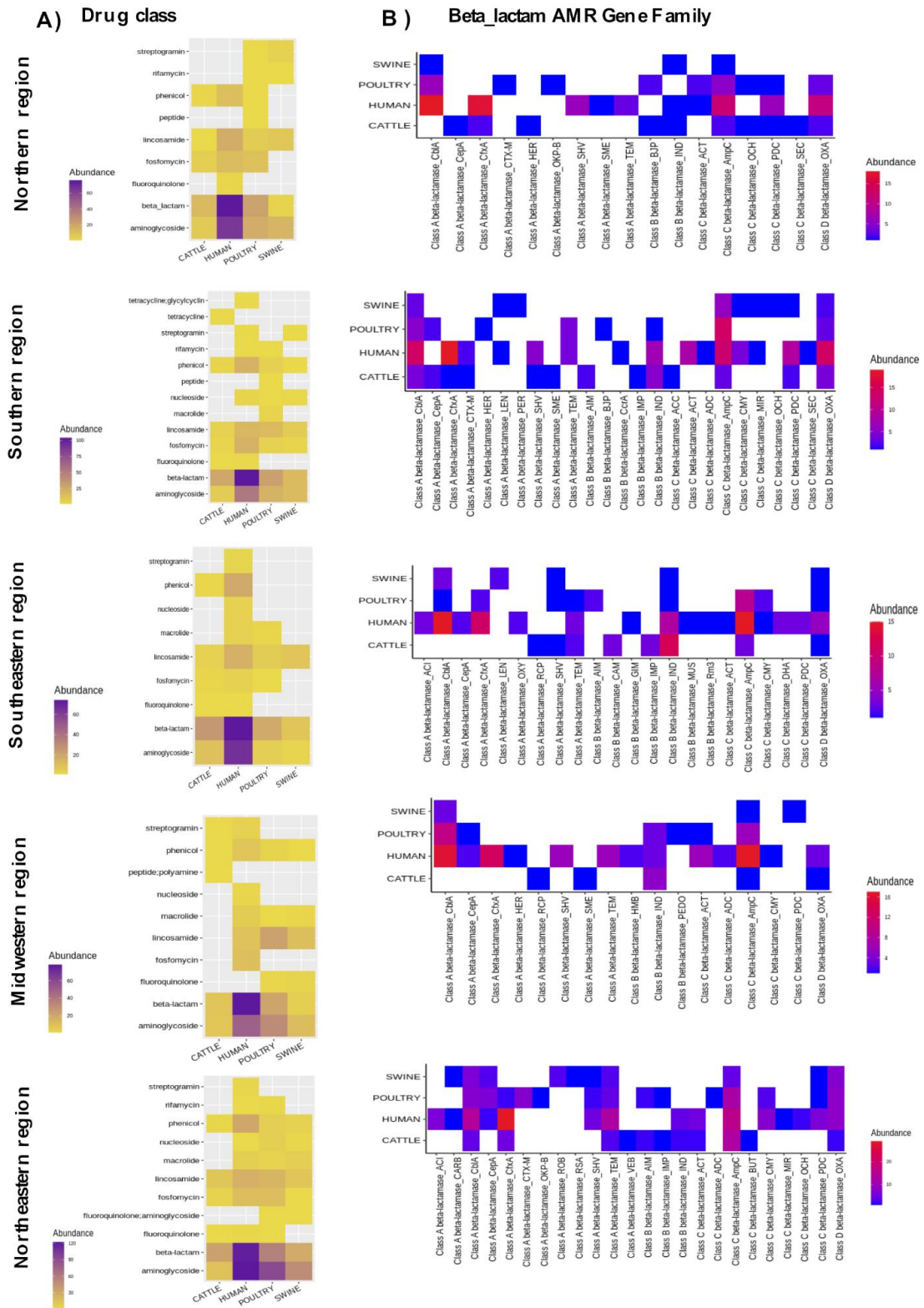
Supplementary Figure 2. Presence and abundance of antibiotic-modifying genes (A) and β-lactamase types (B) according to the host and the geographic region.

Supplementary Figure 3. Presence and abundance of the five efflux pump families according to the host and the geographic region

A)

B)

Antibiotic inactivation   Antibiotic efflux   Antibiotic target alteration

C)

Northern region   Southern region   Southeastern region

Midwestern region   Northeastern region

Supplementary Figure 4. (A) The AMR genes distribution by host obtained for the resistance mechanisms: antibiotic inactivation, antibiotic efflux, and antibiotic target alteration. Boxes represent the interquartile ranges between the first and third quartiles (25th and 75th percentiles, respectively), and the line inside denotes the median. Whiskers indicate the lowest and highest values within a range of 1.5-fold and the interquartile range (IQR) from the first and third quartiles, respectively. Dots represent outliers. Scatter matrices plots showing a pairwise correlation among poultry, cattle, swine, and humans by resistance mechanisms (B) and sampled regions (C). Dots represent drug classes identified for each resistance mechanism.