A screenshot of a graph

Description automatically generated

**Figure S1.** Genome quality of isolates and their classification status for vancomycin, doxycycline or erythromycin resistance prediction models with pangenome features (i.e., Prokka, RASTtk or Bakta). The y-axis represents the quality metric values of the 647 genomes. The x-axis represents how often the isolates were misclassified, with 0 always being correctly predicted and 3 being incorrectly predicted by all 3 pangenome prediction models.