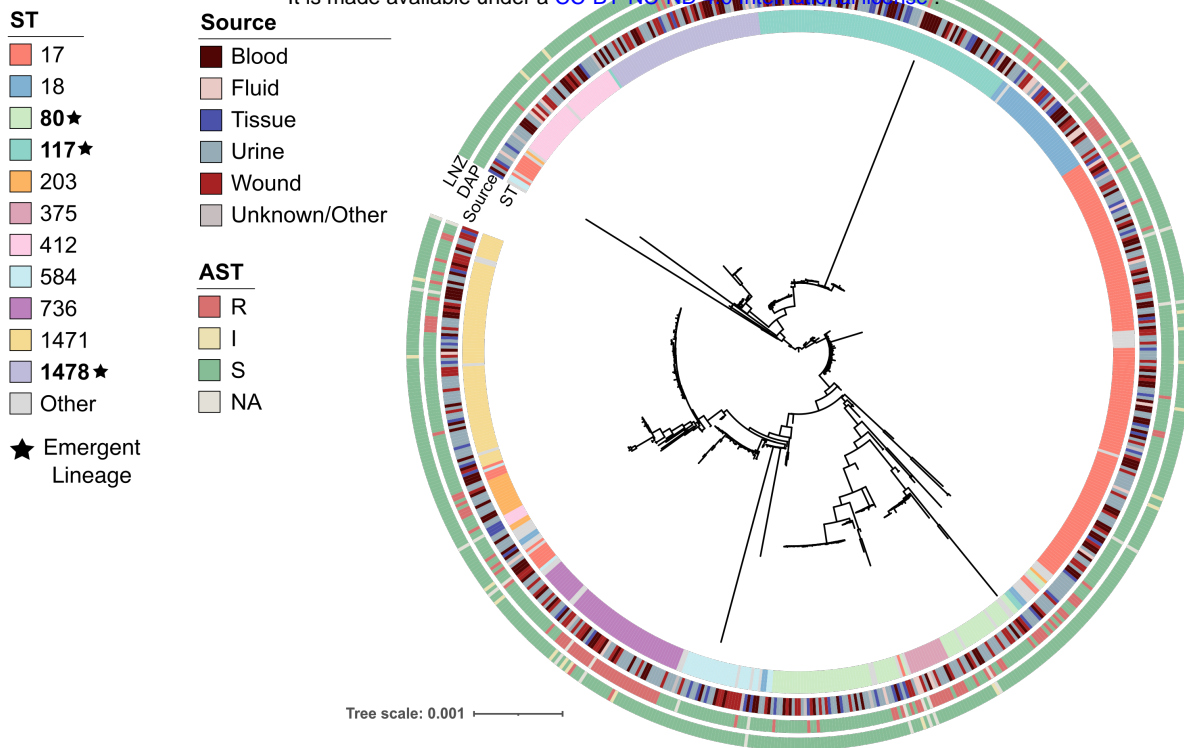
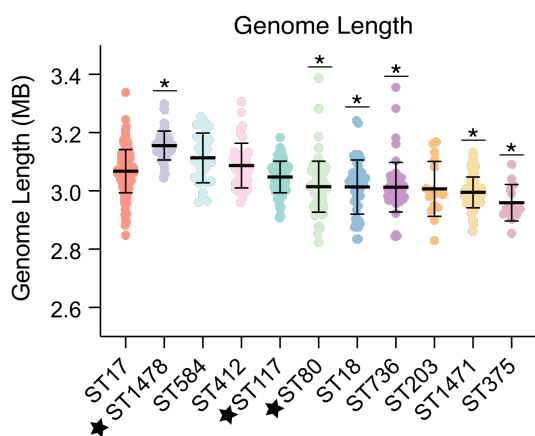


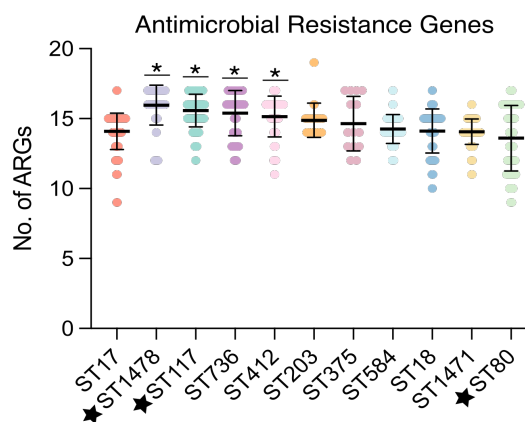
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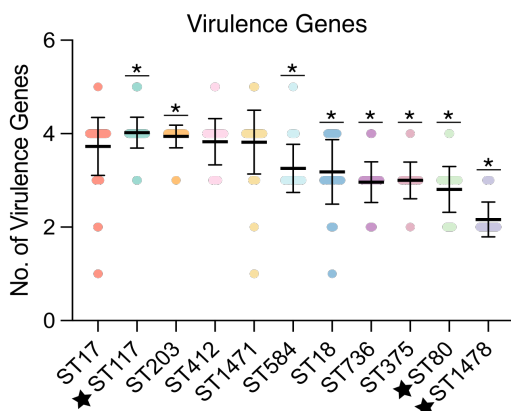
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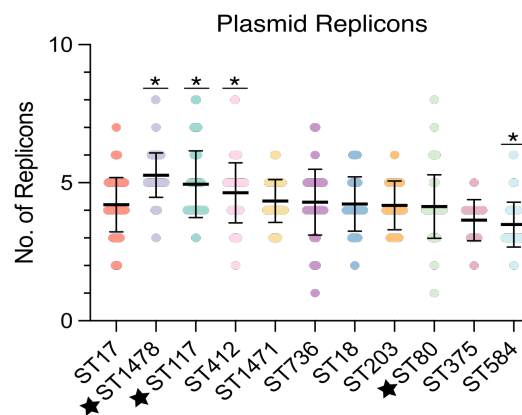
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D

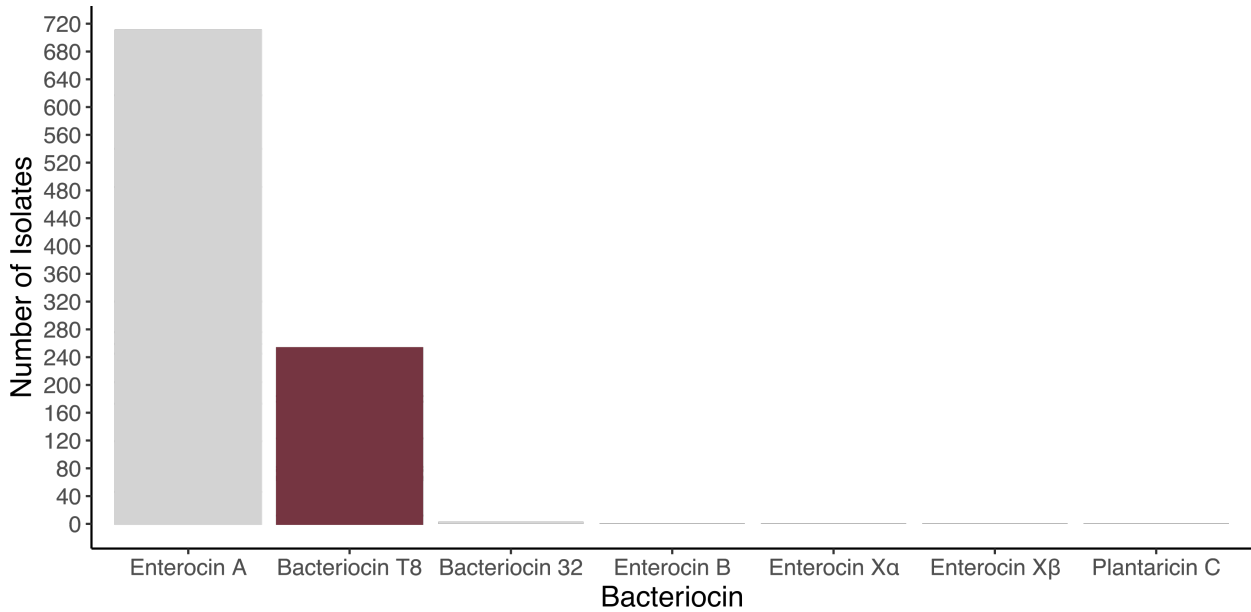


E

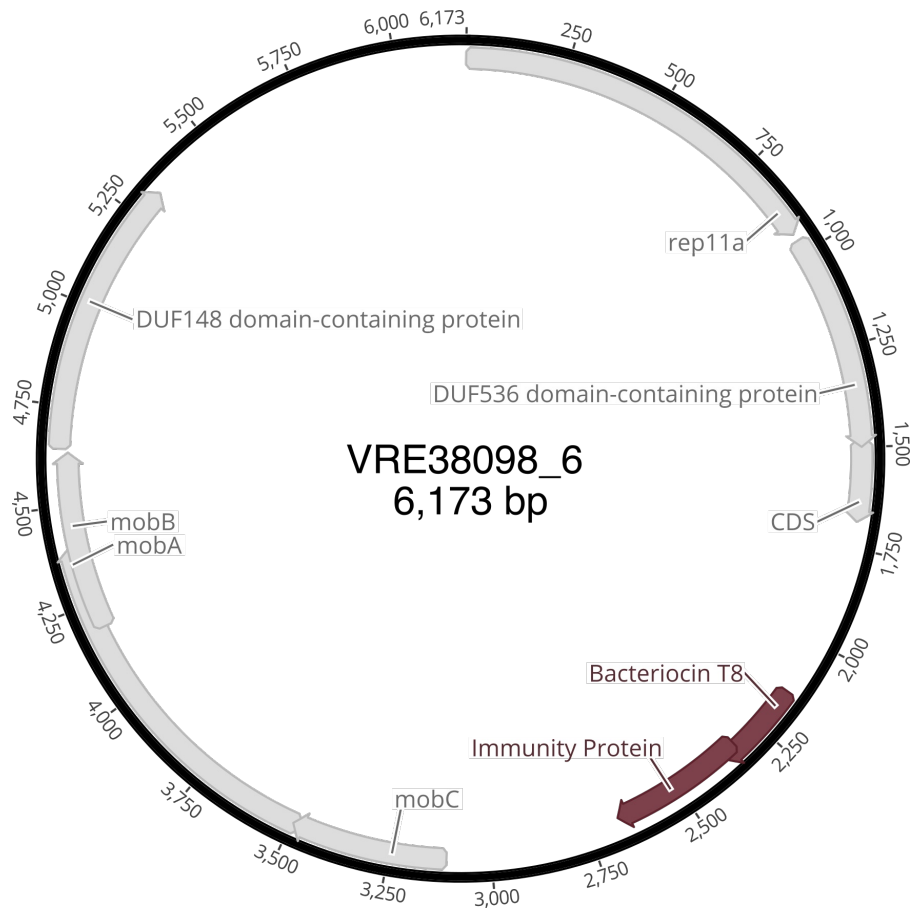


**Figure S1: Genetic relatedness and genomic features of 710 VREfm isolates from UPMC.** (A) The midpoint-rooted phylogenetic tree was constructed from a core genome alignment. Sequence types (ST) and isolation source are colored as indicated. Emergent lineages are noted by a black star. Antimicrobial susceptibility testing (AST) results for daptomycin (DAP) and linezolid (LNZ) were interpreted as resistant (R), intermediate (I), and susceptible (S). (B) Genome length, (C) presence of antimicrobial resistance genes, (D) presence of virulence genes, and (E) presence of plasmid replicons by main VREfm lineages. Averages of genomic features within each ST were compared to the average seen in the previously dominant ST17 lineage using a one-sided t-test. Asterisks indicate p-values < 0.0045. Horizontal lines represent the average and error bars show the standard deviation for each group.

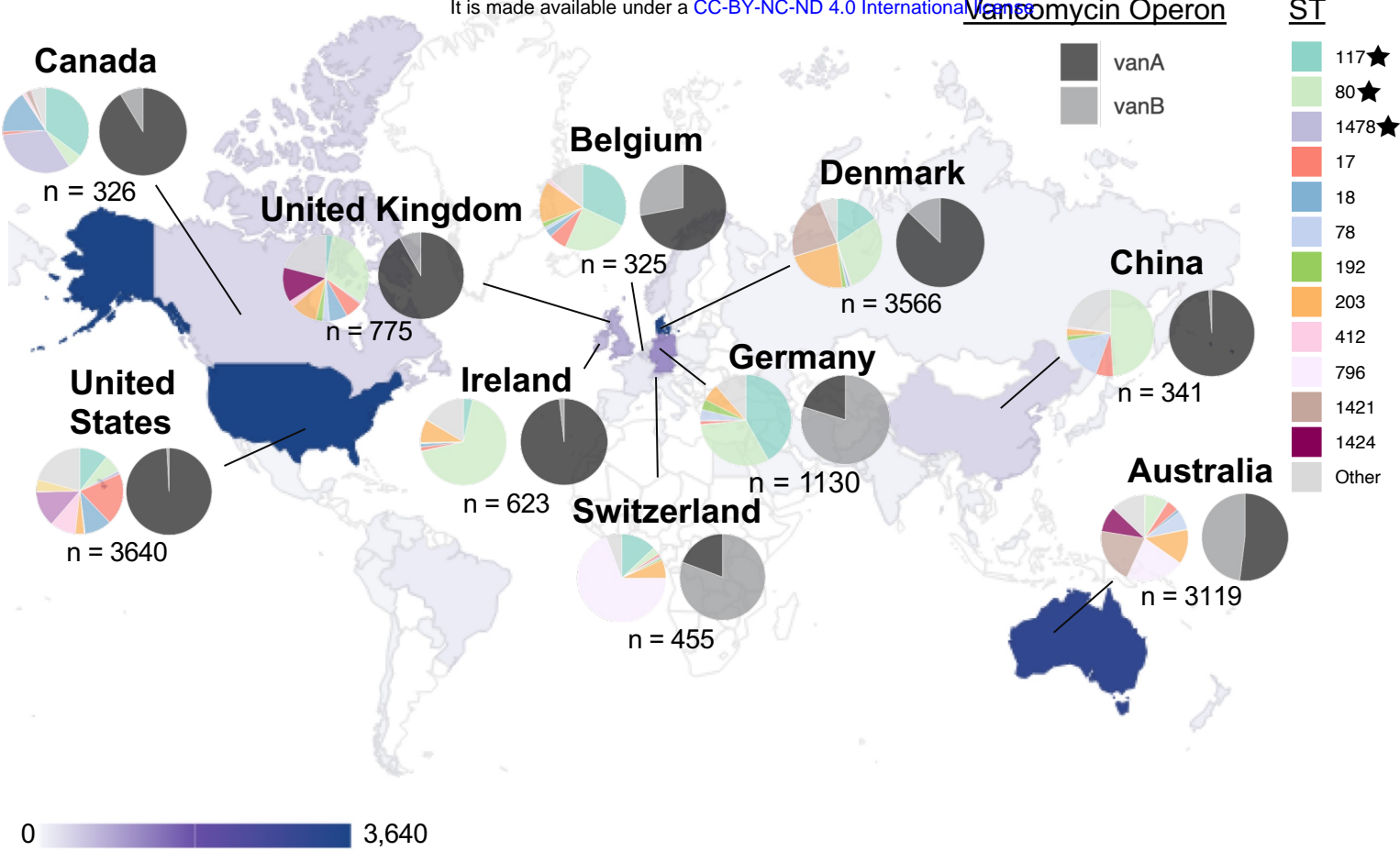
A



B



**Figure S2: Bacteriocin prevalence and genomic context of bacteriocin T8.** (A) Distribution of bacteriocins within 710 VREfm isolates from UPMC. Bacteriocins were identified using BAGEL4 with sequence identity and coverage thresholds of  $\geq 95\%$ . (B) Bacteriocin T8-encoding rep11a plasmid from the ST117 isolate VRE38098. Bacteriocin T8 and immunity factor are highlighted in burgundy.



**Figure S3. Global population structure of 15,631 VREfm genomes from human sources.** Geographical distribution of VREfm genomes pulled from NCBI. The number of genomes from each country is shown from lowest (light grey) to highest (purple). Countries with >300 genomes are highlighted with the distribution of STs and vancomycin resistance operons.