

Tree scale: 0.1

Strain isolated from

- Carriage
- Infection

Dataset

- Train
- Test

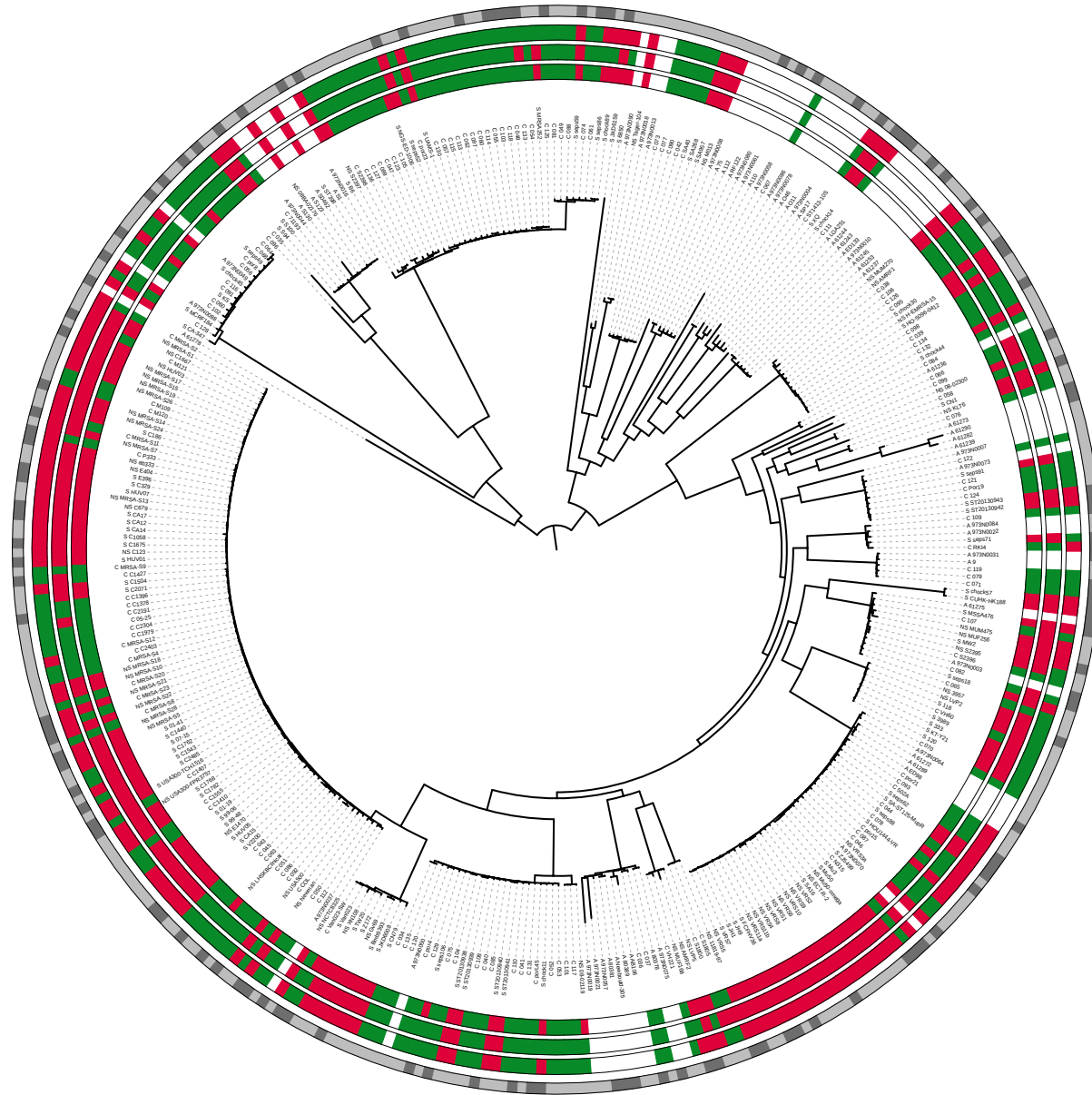


Figure S11: Predictions obtained using random forest to discriminate colonization and infection outcomes plotted on phylogenetic reconstruction of multiclonal *Staphylococcus aureus*. The first outer circle represents the actual phenotype. The second and third outer circle indicates prediction using CDS or IGRs, respectively. The fourth outer circle refer to strains used for the training or test sets, respectively.