

S2. Additional phylogenetics results

Figure 1. Solu's phylogram of the *S. aureus* dataset vs. reported sequence types (outer ring)

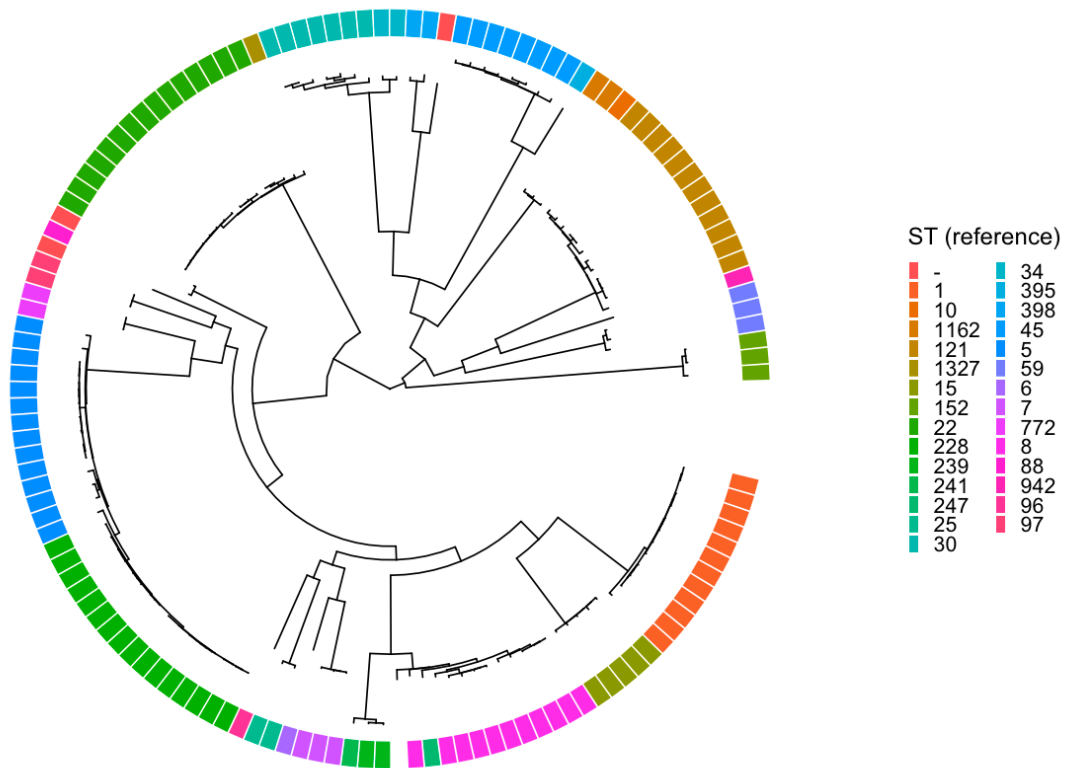


Figure 2. Solu’s phylogram of the *Candida auris* dataset vs. reported clade (outer ring)

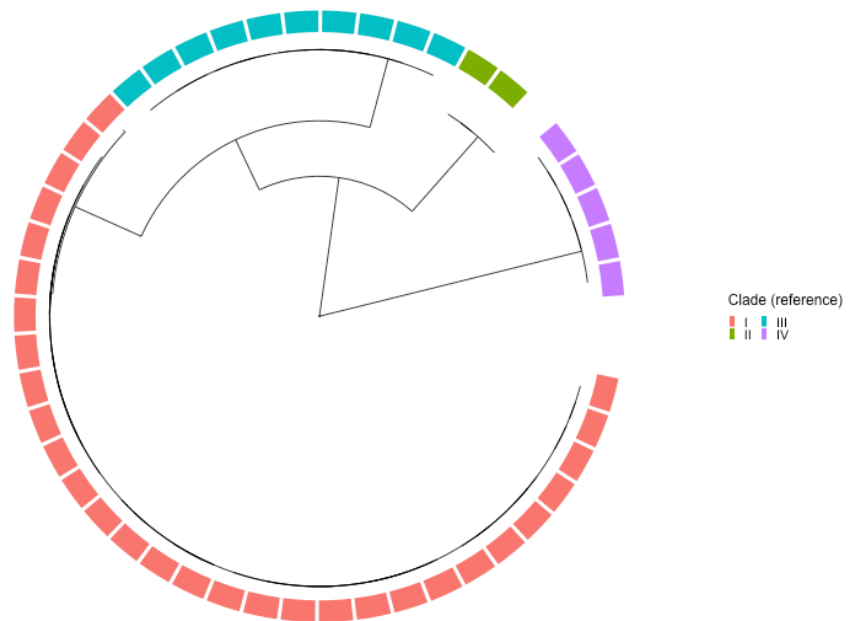


Table 1. Validation of Solu’s reference-based vs. reference-free phylogenetics

Dataset	Robinson-Foulds distance of Solu’s reference-based tree vs. Solu’s reference-free tree
<i>S. aureus</i>	0.08093671
<i>E. faecium</i>	0.2694115

<i>S. enterica</i>	0.4644507
<i>C. auris</i>	0.2362036

The tree distances were calculated with TreeDist 2.9.1 (1).

Figure 3. Tanglegram of *Staphylococcus aureus* reference-free (left) vs. reference-based (right) phylogenetic trees



Figure 4. Tanglegram of *Salmonella enterica* reference-free (left) vs. reference-based (right) phylogenetic trees

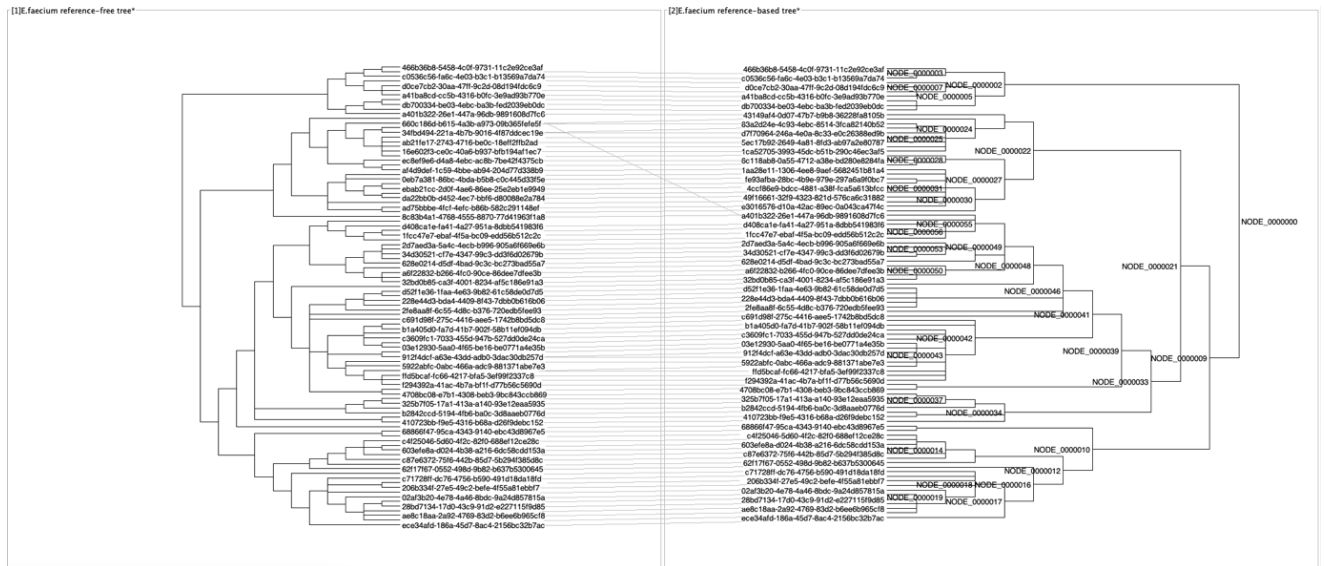


Figure 5. Tanglegram of *Candida auris* reference-free (left) vs. reference-based (right) phylogenetic trees

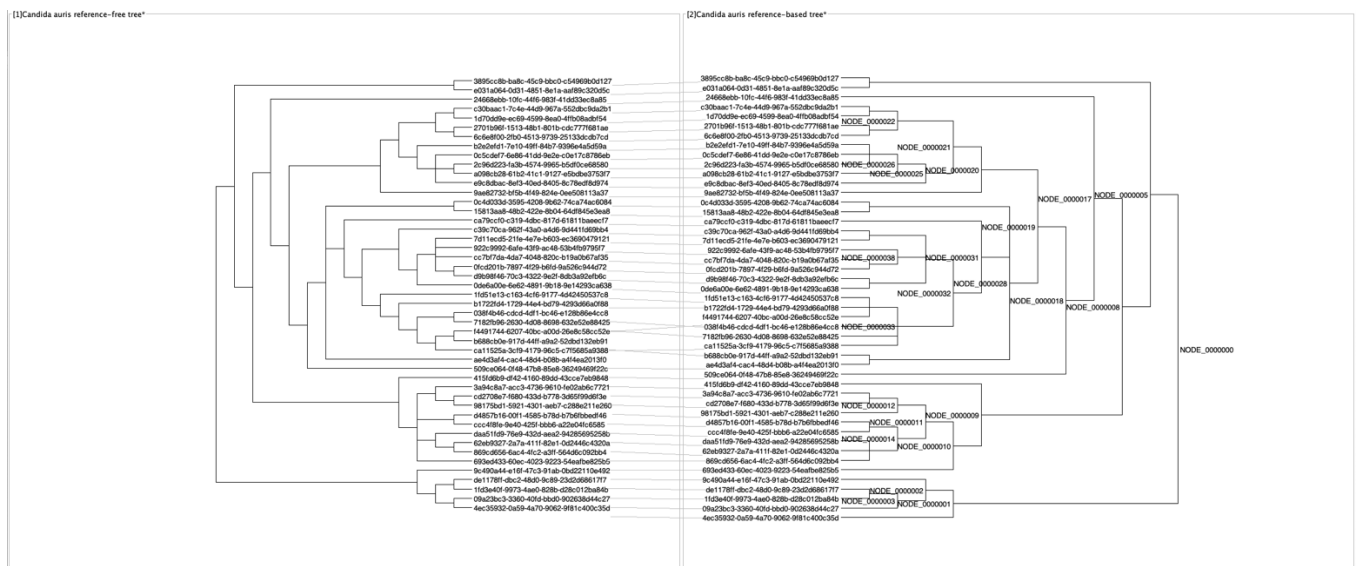
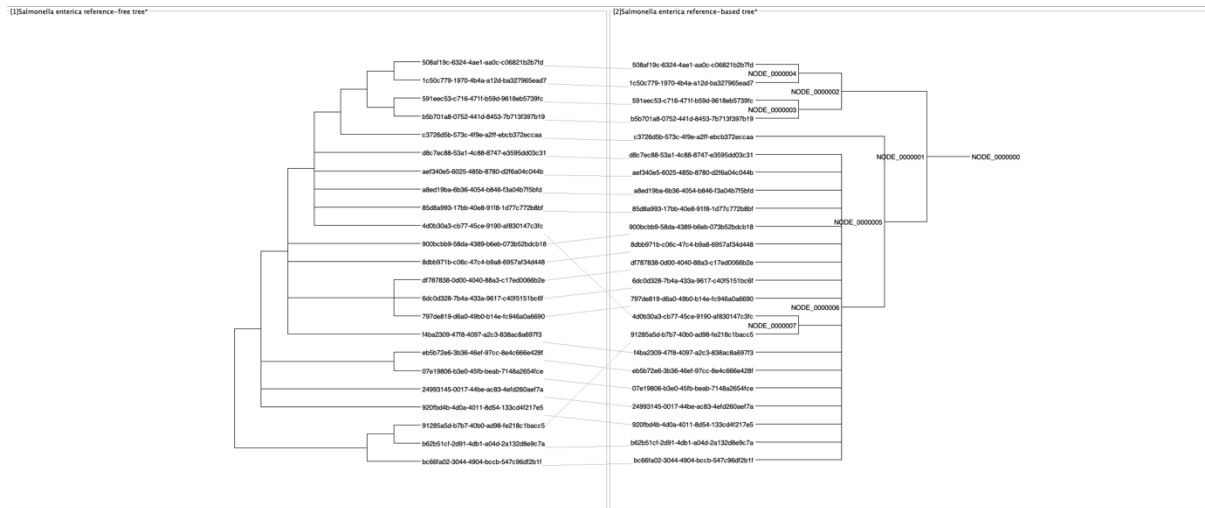


Figure 6. Tanglegram of *Salmonella enterica* reference-free (left) vs. reference-based (right) phylogenetic trees



All tanglegrams were created with Dendroscope v 3.8.10 (2).

References

1. Smith MR. Information theoretic generalized Robinson–Foulds metrics for comparing phylogenetic trees. 2020;36(20):5007–13.
2. Huson DH, Scornavacca C. Dendroscope 3: An Interactive Tool for Rooted Phylogenetic Trees and Networks. *Syst Biol.* 2012 Dec 1;61(6):1061–7.