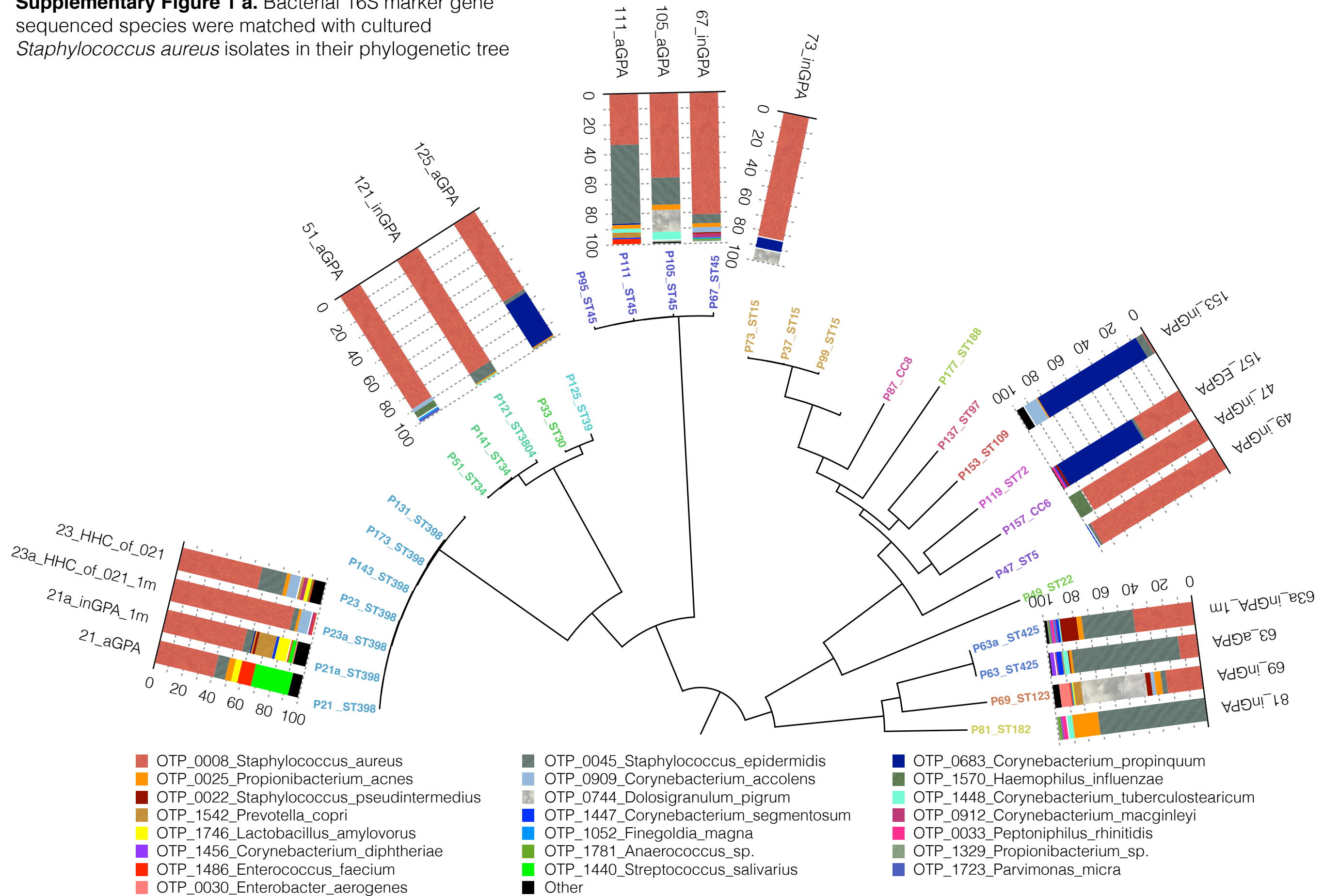
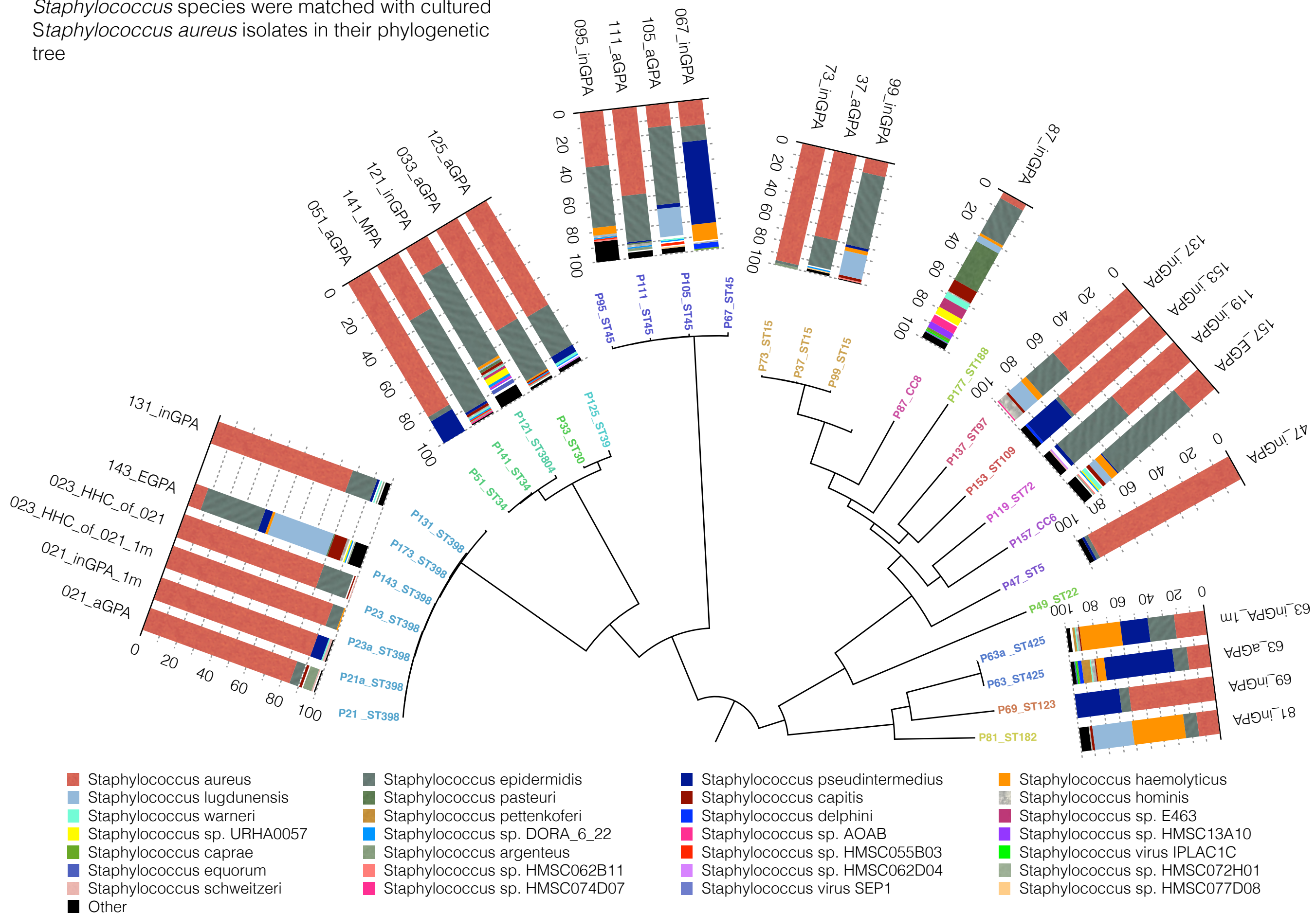


Supplementary Figure 1 a. Bacterial 16S marker gene sequenced species were matched with cultured *Staphylococcus aureus* isolates in their phylogenetic tree



Supplementary Figure 1 b. Shotgun sequenced *Staphylococcus* species were matched with cultured *Staphylococcus aureus* isolates in their phylogenetic tree



Supplementary Figure 1

31 cultured *Staphylococcus* isolates were sequenced and their assembled genomes were used for phylogenetic tree construction.

Supplementary Figure 1 a

Bacterial 16S marker gene sequenced species were matched with cultured *Staphylococcus aureus* isolates in their phylogenetic tree. The top 22 species with a minimum abundance of 0.1% were used for the stack bar chart presentation. The top 22 species represented 98.91% of all reads. Please note: a bacterial 16S profile was not available from all samples from which an isolate was sequenced.

Supplementary Figure 1 b

Shotgun sequenced *Staphylococcus* species were matched with cultured *Staphylococcus aureus* isolates in their phylogenetic tree

The top 28 taxa with a minimum abundance of 0.1% were used for the stack bar chart presentation. The top 28 taxa represented 97.25% of all reads. Please note: a *Staphylococcus* profile was not available from all samples from which an isolate was sequenced.