

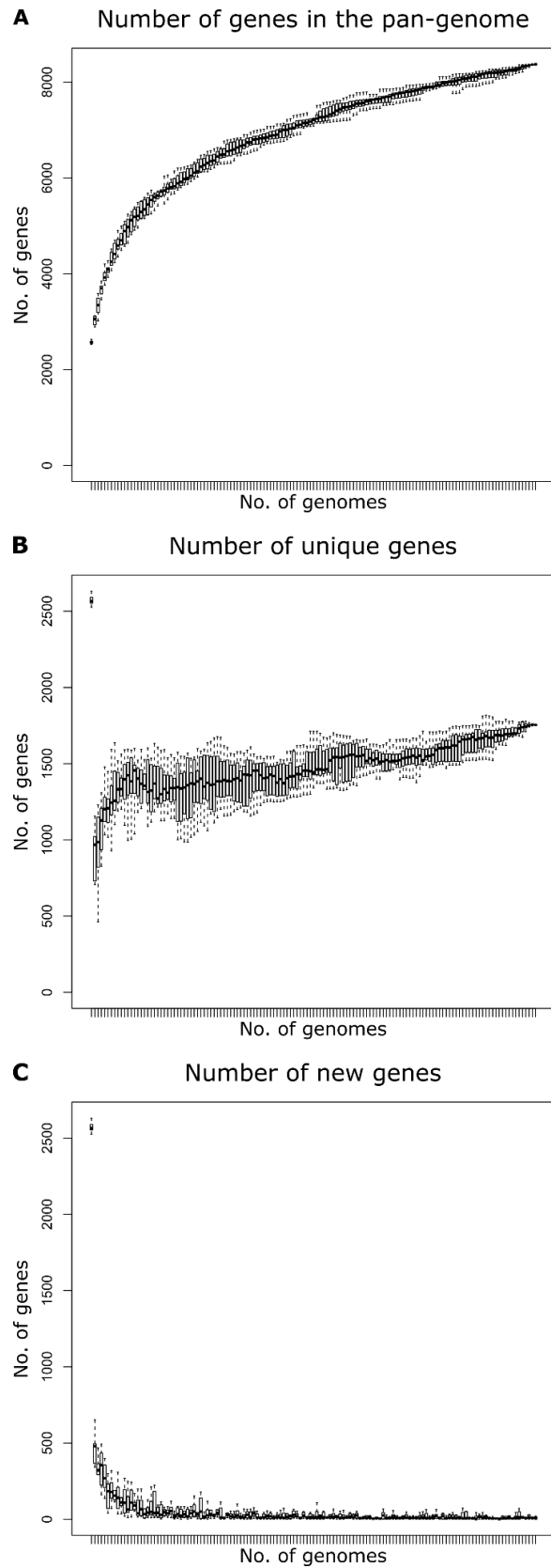


Fig S1. Pangenome analysis statistics. The Roary-computed Pangenome of the cohort consists of 8,373 genes (A), displaying a relatively high variability with a large proportion of unique genes (1,754) (B). However, the number of newly added genes per genome quickly drops to very small number (C).

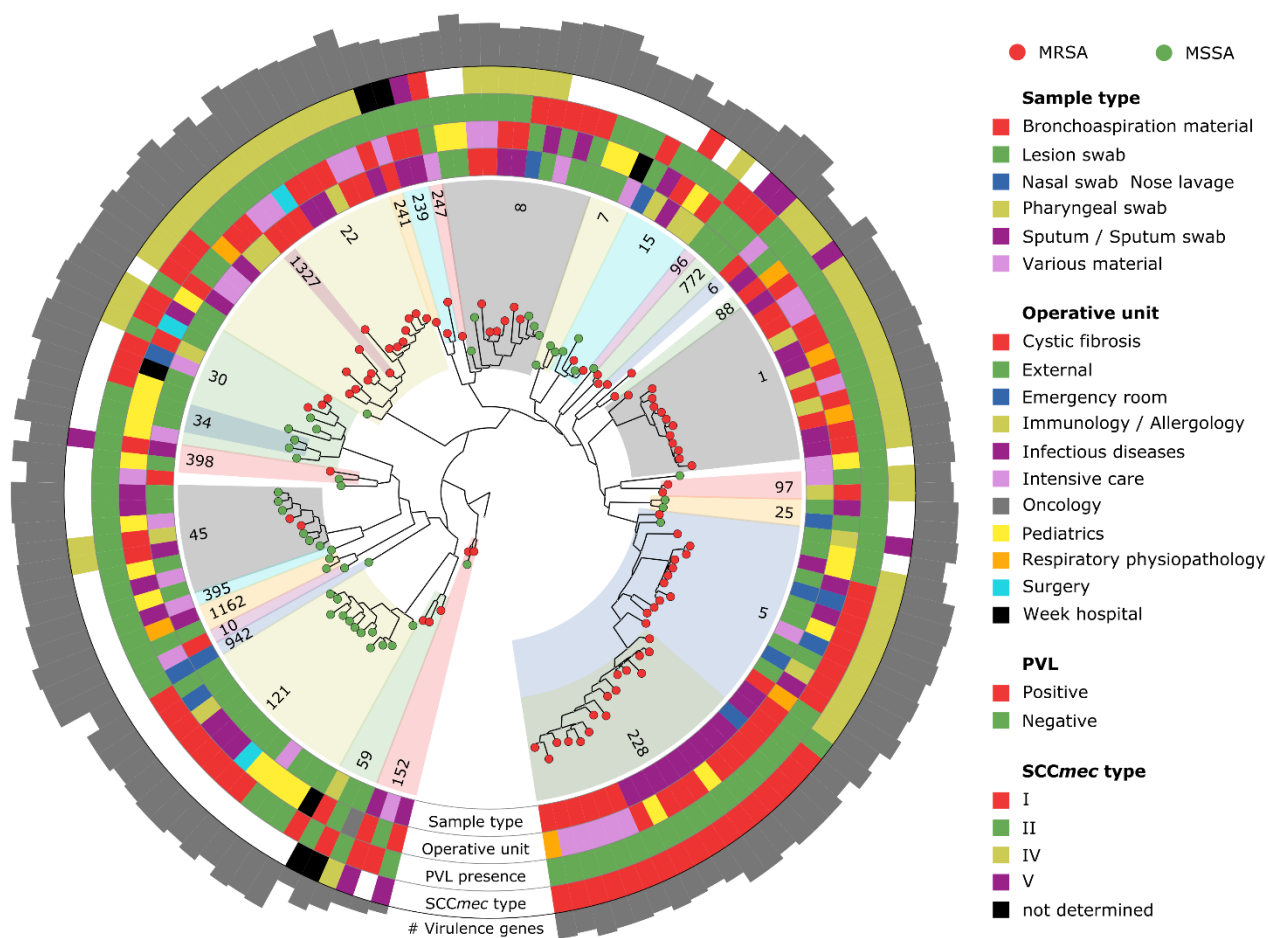


Fig S2. Phylogenetic model based on gene presence/absence (1,464 core and 6,909 accessory genes in total) in the 135 single-patient *S. aureus* isolates. STs are distinguished by means of numbers and background colours in the inner ring. Sample type, operative unit, PVL presence, and SCCmec type are colour-coded in the following rings. On the outermost ring, the number of virulence genes is reported as bar plot (total considered = 79).