Supplement

Supplemental file 1 (Excel spreadsheet) contains

Table S1: Overview of all isolates including metadata, accession number and, if existing, the publication that first described the respective isolate. Sequences that were taken from public databases but do not have a publication assigned are labelled "unpublished", while isolates that have neither been sequenced nor described before are labelled "this study". Accession numbers for isolates sequenced for this study are highlighted in bold font.

Supplemental file 2 (PDF) contains

Figure S1: Comparison of Maximum likelihood trees of multiple sequence alignments including (A) and without (B) recombinant sites. Both trees were calculated from concatenated cgMLST sequences present in all 451 ST45 isolates. For tree B, all genes containing possible recombination sites were purged from the alignment.

Supplemental file 3 (PDF) contains

Figure S2: Distribution of group-specific SNPs over the genome. Positions (with regards to the *S. aureus* COL reference genome) of SNPs specific for the AFR/AUS group across the genome are marked. Blue lines represent synonymous, red lines stand for non-synonymous SNPs.

and

Table S2: List of exact SNP positions.

Supplemental file 4 (Excel spreadsheet) contains

Dataset S1: Overview of genetic features of all isolates. Presence (1) / partial presence (-1) / absence (0) or type of different genes/ gene clusters associated with regulation, resistance or virulence are given.

Supplemental file 5 (PDF) contains

Figure S3: BEAST mcc tree including posterior probabilities for all nodes. 95%HPD is illustrated by blue bars on each node.