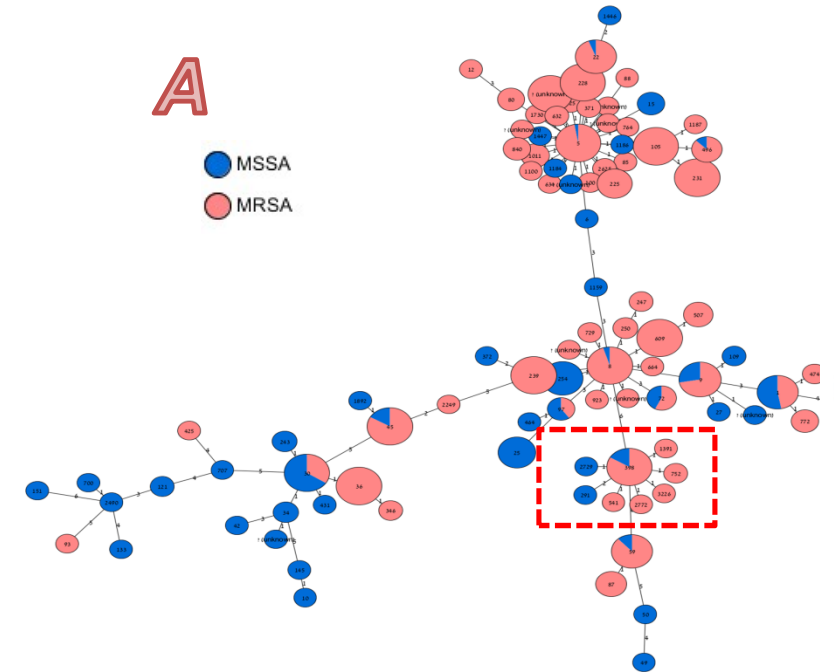


# Methods

- *S. aureus* genome assemblies were downloaded from NCBI and a local database was created
- Genomes were checked for quality using QUAST, and subsequently analyzed using an in house *S. aureus* pipeline (**Fig. 1**).
- Typing was performed by extracting the *spa* locus as well as the 7 MLST gene loci and querying against the respective databases
- cgMLST analysis and construction of minimum spanning trees was performed using SeqSphere v.3.0.1 (Ridom GmbH, Munster, Germany).
- The Simpson's diversity index (DI) was calculated for each method to compare performance.

# Phylogenetic analysis



# Results

## *S. aureus* bioinformatics pipeline

