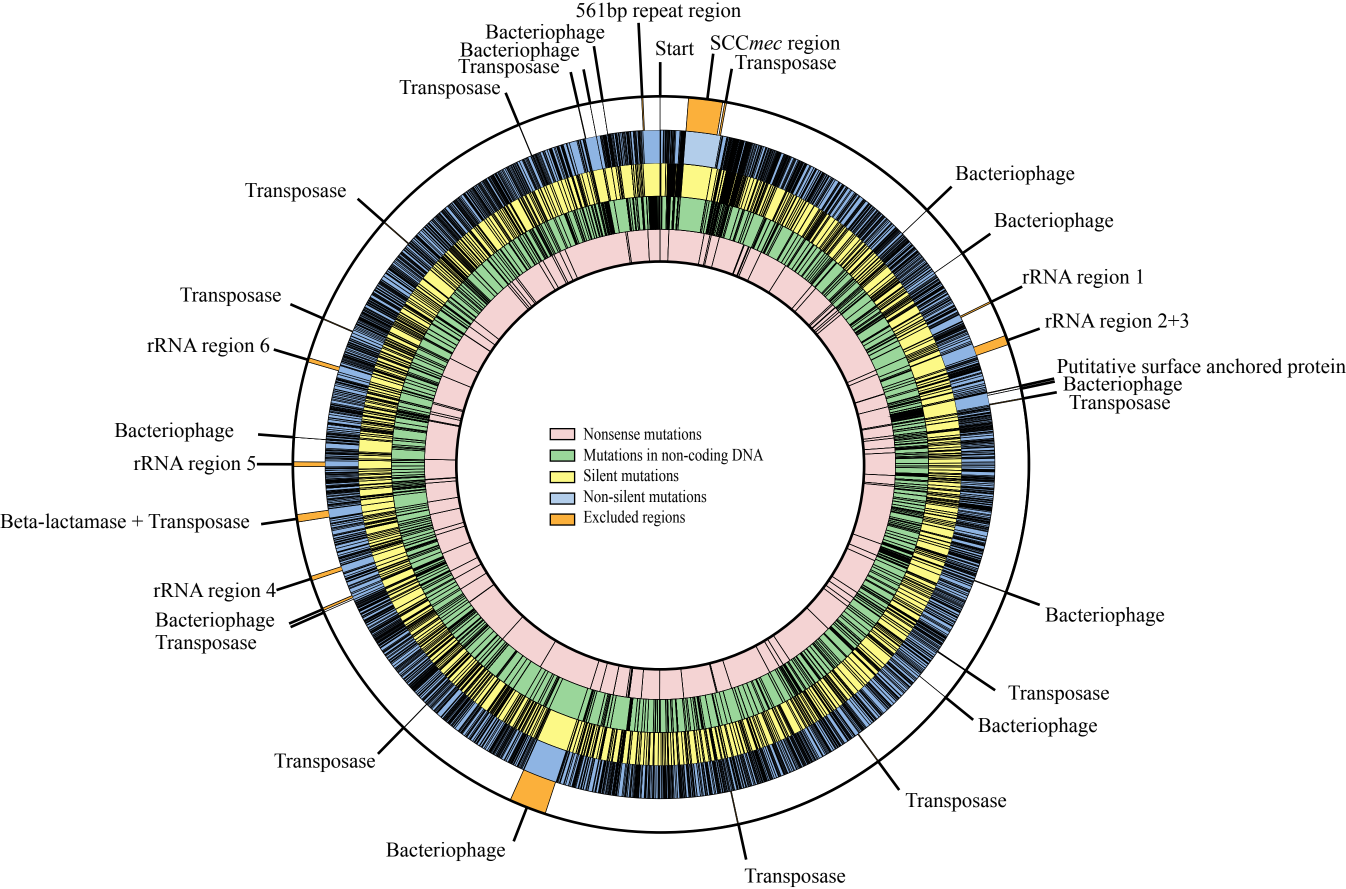
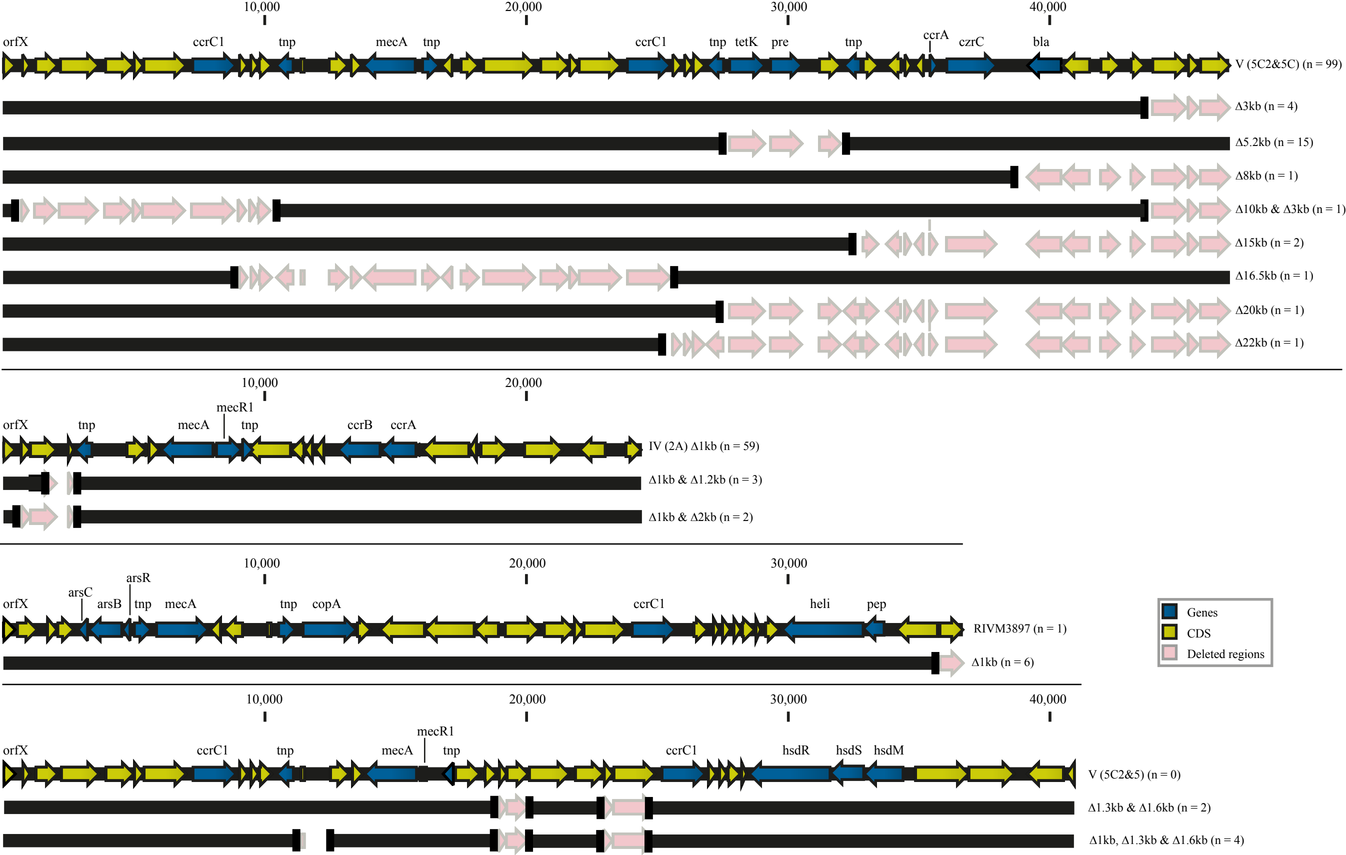
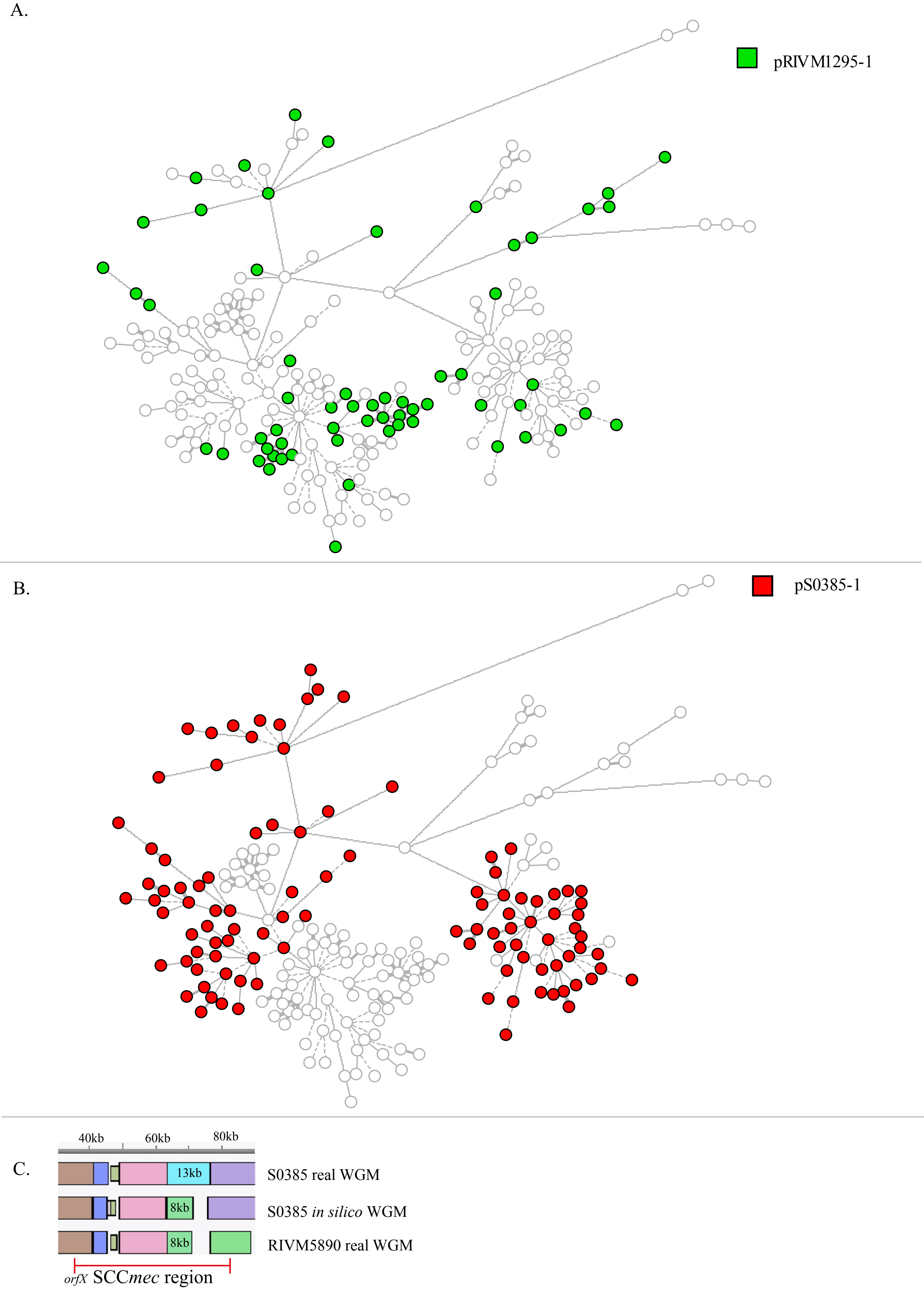
Supplemental Figure 1: SNVs mapped on the core genome of LA-MRSA strain RIVM1295. The lines in the colored rings show the distribution of the SNVs identified in the 206 LA-MRSA isolates relative to the core genome of strain RIVM1295. Each colored ring represents a different type of SNV as explained in the center of the circle. The outer ring displays the core genome of RIVM1295 used for SNV analysis and the distribution of the excluded variable regions that are depicted in orange. The complete genome of strain RIVM1295 is deposited in the NCBI database (accession number CP013616).

Supplemental Figure 2: Composition of the SCC*mec* region of 202 LA-MRSA isolates. The complete structures of the four SCC*mec* types identified in the collection are given. Blue arrows indicate genes, whereas yellow arrows indicate coding DNA sequences (CDS). The variants of each SCC*mec* type are given in black lines below the reference. The white space between the lines and the red arrows represent the deleted regions and genes and CDS in the SCC*mec* compared to the reference. The sizes of the deleted regions are indicated as Δxx kb on the right hand side of the figure. The complete genome of strain RIVM3897, including the SCC*mec* region, is deposited in the NCBI database (accession number CP013621).

Supplemental Figure 3: Distribution of plasmids among 206 LA-MRSA isolates. The trees were based on 6,461 SNV positions and clustering was done using a categorical coefficient. Each isolate in the trees is displayed as a circle. The distribution of plasmid pRIVM1295-1 over the SNV tree is shown in panel A. The spread of plasmid pS0385-1 among the LA-MRSA isolates is depicted in panel B. Panel C shows a detail of the whole genome maps of isolates S0385 and RIVM5890 and a detail of the *in silico* whole genome map based on the sequence of S0385 (accession number AM990992).


561bp repeat region
Start
SCC*mec* region
Transposase
Bacteriophage
Bacteriophage
Transposase
Transposase
Transposase
Transposase
rRNA region 6
Bacteriophage
rRNA region 5
Beta-lactamase + Transposase
rRNA region 4
Bacteriophage
Transposase
Transposase
Bacteriophage
Transposase
Transposase
Bacteriophage
Transposase
Bacteriophage
Bacteriophage
Bacteriophage
rRNA region 1
rRNA region 2+3
Pututative surface anchored protein
Bacteriophage
Transposase
Nonsense mutations
Mutations in non-coding DNA
Silent mutations
Non-silent mutations
Excluded regions


10,000
20,000
30,000
40,000
orfX
ccrC1
tnp
mecA
tnp
ccrC1
tnp
tetK
pre
tnp
ccrA
czrC
bla
V (5C2&5C) (n = 99)
Δ3kb (n = 4)
Δ5.2kb (n = 15)
Δ8kb (n = 1)
Δ10kb & Δ3kb (n = 1)
Δ15kb (n = 2)
Δ16.5kb (n = 1)
Δ20kb (n = 1)
Δ22kb (n = 1)
10,000
20,000
orfX
tnp
mecR1
mecA
tnp
ccrB
ccrA
IV (2A) Δ1kb (n = 59)
Δ1kb & Δ1.2kb (n = 3)
Δ1kb & Δ2kb (n = 2)
10,000
20,000
30,000
arsR
arsC
orfX
arsB
tnp
mecA
tnp
copA
ccrC1
heli
pep
RIVM3897 (n = 1)
Δ1kb (n = 6)
Genes
CDS
Deleted regions
10,000
20,000
30,000
40,000
mecR1
orfX
ccrC1
tnp
mecA
tnp
ccrC1
hsdR
hsdS
hsdM
V (5C2&5) (n = 0)
Δ1.3kb & Δ1.6kb (n = 2)
Δ1kb, Δ1.3kb & Δ1.6kb (n = 4)


A.
🟩 pRIVM1295-1
B.
🟥 pS0385-1
C.
40kb
60kb
80kb
13kb
S0385 real WGM
8kb
S0385 *in silico* WGM
8kb
RIVM5890 real WGM
orfX SCC*mec* region