

Supplementary Table S1. Phenotypic and genotypic resistance in the investigated strains (only antibiotics with detected resistance mechanisms are displayed)

strain	aminoglycoside		beta-lactams			fluoroquinolones			MLS				tetracyclin	
	phenotype ^a	genotype ^b	phenotype ^a		genotype ^b	phenotype ^a		genotype ^b	phenotype ^a			genotype ^b	phenotype ^a	genotype ^b
	gentamycin		cefoxitin-screen	oxacillin		ciprofloxacin	moxifloxacin		clindamycin IR ^c	Erythromycin	cindamycin		teracyclin	
MRSA ST5/t010	≤ 0.5 (S)	aadD, bleO	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	-	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≥ 16 R	tet(M)
MRSA ST8/t024	≤ 0.5 (S)	-	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	-	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≤ 1 (S)	-
MRSA ST22/t223	≤ 0.5 (S)	-	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	-	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≥ 16 R	tet(K)
MRSA ST45/t015	4 (R)	aac(6')-aph(2'')	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	grlA p.I45M	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≤ 1 (S)	-
MRSA ST30/t300	≤ 0.5 (S)	-	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	-	positive	≥ 8 (R)	≤ 0.25 (R) ^c	erm(C)	≥ 16 R R	tet(K)
MRSA ST59/t216	≤ 0.5 (S)	-	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	-	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≤ 1 (S)	-
MRSA ST1/t127	≤ 0.5 (S)	aph(3')-III, ant(6)-Ia	positive	≥ 4 (R)	blaZ, mecA	≤ 0.5 (I)	≤ 0.25 (S)	-	positive	≥ 8 (R)	≤ 0.25 (R) ^c	erm(C)	≥ 16 R	tet(K)
MRSA ST398/t034	≤ 0.5 (S)	ant(9)-Ia, str	positive	≥ 4 (R)	blaZ, mecA	1 (I)	≤ 0.25 (S)	-	negative	≥ 8 (R)	≥ 8 (R)	erm(A)	≥ 16 R	tet(M)
MSSA ST45	≤ 0.5 (S)	-	negative	≤ 0.25 (S)	-	≤ 0.5 (I)	≤ 0.25 (S)	-	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≤ 1 (S)	-
MSSA ATCC 6538	≤ 0.5 (S)	-	negative	≤ 0.25 (S)	-	≤ 0.5 (I)	≤ 0.25 (S)	grlA p.I45M	negative	≤ 0.25 (S)	≤ 0.25 (S)	-	≤ 1 (S)	-

^aValues represent minimal inhibitory concentrations (mg/L) as detected by VITEK AST as well as the S-I-R classification (in parenthesis) according to EUCAST; Results of screening reactions are presented as positive or negative

^bGenes or mutations (fluoroquinolones) detected in the genome of sequenced isolates are indicated if present

^cInducible resistance (IR) against clindamycin resulting in the classification as resistant (R) despite MIC values ≤ 0.25 mg/L