

Table S1. Rates of nonsusceptibility to antimicrobial agents of *S. aureus* blood isolates

Antimicrobial agent	AST method	Total (n = 567, 100%)			MRSA (n = 303, 53.4%)			MSSA (n = 264, 46.6%)			P value ^a
		Nonsusceptibility rate, Number (%)	MIC ₅₀ (µg/mL)	MIC ₉₀ (µg/mL)	Nonsusceptibility rate, Number (%)	MIC ₅₀ (µg/mL)	MIC ₉₀ (µg/mL)	Nonsusceptibility rate, Number (%)	MIC ₅₀ (µg/mL)	MIC ₉₀ (µg/mL)	
Oxacillin	BMD	303 (53.4)	32	>128	303 (100)	>128	>128	0 (0)	0.5	1	-
Erythromycin	DD	252 (44.4)	NA	NA	197 (65.0)	NA	NA	55 (20.8)	NA	NA	<0.001
Clindamycin	DD	180 (31.7)	NA	NA	168 (55.4)	NA	NA	12 (4.6)	NA	NA	<0.001
Quinupristin-dalfopristin	DD	9 (1.6)	NA	NA	5 (1.7)	NA	NA	4 (1.5)	NA	NA	0.357
Trimethoprim-sulfamethoxazole	DD	7 (1.2)	NA	NA	6 (2.0)	NA	NA	1 (0.4)	NA	NA	0.111
Linezolid	BMD	2 (0.4)	2	2	1 (0.3)	2	4	1 (0.4)	2	2	0.999
Tigecycline	BMD	6 (1.1)	0.06	0.25	6 (2.0)	0.06	0.25	0 (0)	0.06	0.06	0.071
Vancomycin	BMD	0 (0)	1	1	0 (0)	1	2	0 (0)	1	1	-
Teicoplanin	BMD	0 (0)	1	4	0 (0)	2	4	0 (0)	0.5	1	-
Daptomycin	BMD	0 (0)	0.25	0.5	0 (0)	0.5	0.5	0 (0)	0.25	0.5	-

^aThe difference of nonsusceptibility rates to each antimicrobial agent between MRSA and MSSA isolates was evaluated by Fisher's exact tests.

Abbreviations: AST, antimicrobial susceptibility testing; BMD, broth microdilution; DD, disk diffusion; MIC, minimum inhibitory concentration; MRSA, methicillin-resistant *S. aureus*; MSSA, methicillin-susceptible *S. aureus*; NA, not applicable.

Table S2. Oligonucleotide sequences of the primers used in this study

Target gene	Primer name	Primer sequence	Amplicon size (bp)
<i>mecA</i>	mecA_P4	TCCAGATTACAACCTTCACCAGG	162
	mecA_P7	CCACTTCATATCTTGTAACG	
<i>mecC</i>	mecC_F	GAAAAAAAGGCTTAGAACGCCTC	138
	mecC_R	GAAGATCTTTTCCGTTTTTCAGC	
<i>ccr1-3</i>	ccrAB-β2	ATTGCCTTGATAATAGCCITCT	Multi-F ^a
	ccrAB-2	AACCTATATCATCAATCAGTACGT	695
	ccrAB-3	TAAAGGCATCAATGCACAAACACT	937
	ccrAB-4	AGCTCAAAGCAAGCAATAGAAT	1791
<i>ccrC</i>	γR	CCTTTATAGACTGGATTATTCAAAATAT	518
	γF	CGTCTATTACAAGATGTTAAGGATAAT	
<i>ccr4</i>	α4.2	GTATCAATGCACCAGAACTT	1287
	β4.2	TTGCGACTCTCTTGCGGTTT	
<i>mec gene complex</i>	mA7	ATATACCAAACCCGACAACTACA	Multi-F ^a
	mI6	CATAACTTCCCATTTCTGCAGATG	1963
	IS7	ATGCTTAATGATAGCATCCGAATG	2827
	IS2(iS-2)	TGAGGTTATTGAGATATTTTCGATGT	804
<i>agr</i>	PanF	ATGCACATGGTGCACATGC	Multi-F ^a
	agr1	GTCACAAGTACTATAAGCTGCGAT	439
	agr2	TATTACTAATTGAAAAGTGGCCATAGC	574
	agr3	GTAATGTAATAGCTTGTATAATAATACCCAG	321
	agr4	CGATAATGCCGTAATACCCG	657
<i>pvl</i>	luk-PV-1	ATCATTAGGTAAAATGTCTGGACATGATCCA	433
	luk-PV-2	GCATCAASTGTATTGGATAGCAAAGC	
<i>tst-1</i>	TSST-F	ATGGCAGCATCAGCTTGATA	350
	TSST-R	TTTCCAATAACCACCCGTTT	
<i>sea</i>	sea-F	CCTTTGGAAACGGTTAAAACG	127
	sea-R	TCTGAACCTTCCCATCAAAAAC	
<i>seb</i>	seb-F	TCGCATCAAACCTGACAAACG	477
	seb-R	GCAGGTAATCTATAAGTGCCTGC	
<i>sec</i>	sec-F	CTCAAGAACTAGACATAAAAGCTAGG	271
	sec-R	TCAAATCGGATTAACATTATCC	
<i>sed</i>	sed-F	CTAGTTTGGTAATATCTCCTTTAAACG	319
	sed-R	TTAATGCTATATCTTATAGGGTAAACATC	
<i>see</i>	see-F	CAGTACCTATAGATAAAGTTAAAACAAGC	178
	see-R	TAACCTACCGTGGACCCTTC	
<i>seg</i>	seg-F	CGTCTCCACCTGTTGAAGG	327
	seg-R	CCAAGTGATTGTCTATTGTCG	
<i>seh</i>	seh-F	CAACTGCTGATTTAGCTCAG	360
	seh-R	GTCGAATGAGTAATCTCTAGG	
<i>sei</i>	sei-F	CAACTCGAATTTTCAACAGGTAC	465
	sei-R	CAGGCAGTCCATCTCCTG	
<i>sej</i>	sej-F	CATCAGAACTGTTGTTCCGCTAG	142
	sej-R	CTGAATTTTACCATCAAAGGTAC	

^aThe primers described as “Multi-F” indicate the forward primers in each set of multiplex PCRs.

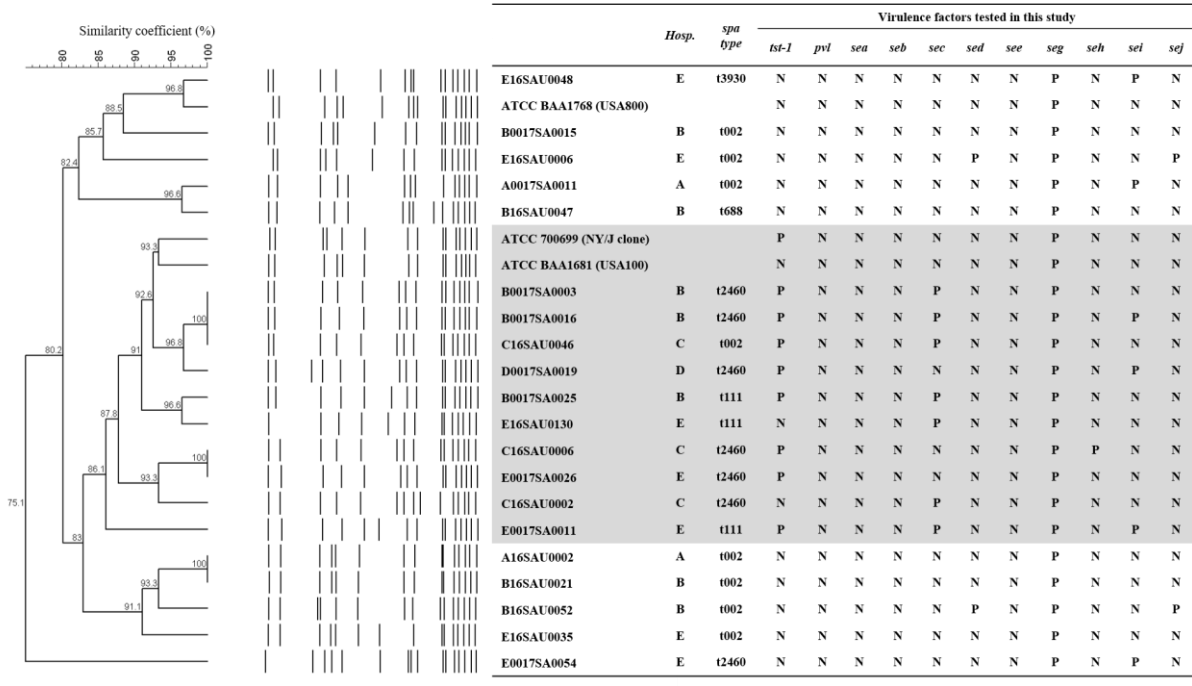


Figure S1. *SmaI*-macrorestriction banding patterns of CC5 MRSA isolates by PFGE.

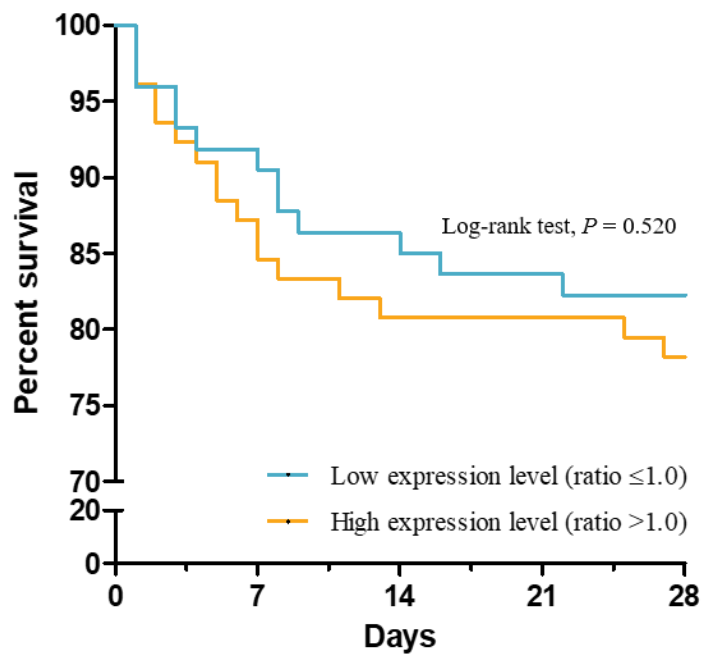


Figure S2. Kaplan-Meier curves stratified according to the expression level of TSST-1 in patients with *S. aureus* bloodstream infections.