Table S1: MICs of antibiotics (μg/ml) against WT and LT mutants of *S. aureus* MR23 cultured in BHIG broth.

Antibiotic	WT	Δ*isaA*	Δ*sceD*	Δ*isaA*Δ*sceD*	WT_ EV	WT_ pCNisaA	WT_ pCNsceD	Δ*isaA* _EV	Δ*isaA* _ pCNisaA	Δ*isaA* _ pCNsceD	Δ*sceD* _EV	Δ*sceD* _ pCNsceD
β-lactam												
Oxacillin	16	2	16	1	16	16	16	4	16	4	16	16
Ampicillin	4	0.5	4	0.5	4	4	4	0.5	4	4	4	4
Cefazolin	2	1	2	1	4	8	16	1	1	4	2	16
Cefmetazole	8	4	8	2	8	16	8	4	8	4	8	8
Flomoxef	4	1	4	1	4	2	4	1	4	2	8	16
Cefoxitin	>16	8	>16	8	>16	16	>16	8	16	16	>16	>16
Imipenem	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25	<0.25
Glycopeptide												
Vancomycin	2	2	2	2	2	4	2	2	2	2	2	2
Teicoplanin	2	2	2	2	2	2	2	2	2	2	2	2
Oxazolidinone												
Linezolid	2	1	1	1	2	2	2	2	2	2	2	2
Lincomycin												
Clindamycin	0.25	0.12	0.25	0.12	0.25	0.25	0.25	0.12	0.25	0.12	0.25	0.5

WT: wild type; Δ*isaA*: *isaA*-deleted strain; Δ*sceD*: *sceD*-deleted strain; Δ*isaA*Δ*sceD*: *isaA* and *sceD*-deleted strain; EV: pCN51Cm (empty vector); pCNisaA: pCN51Cm containing *isaA*; pCNsceD: pCN51Cm containing *sceD.*

Table S2: Primers used in this study.

Primer	Sequence (5' to 3')	Description
sceD_F	AAGGAGATATACATAATGAGTGAAGCGGACTTAAATAAAGCA	For construction of pETsceD
sceD_R	GGTGGTGGTGCTCGAGTGCAGTAACCCAATGTCCAG	
pCN51_iv_F	GTCGGCTTAAACCAGTTTTCC	For construction of pCN51Cm
pCN51_iv_R	GTAGCATGTCTCATTCAATTCCTAGG	
pKOR1_CAT_F	AATGAGACATGCTACCGTCTTCTTAATATGCGTAATTGCA	For construction of pCN51Cm
pKOR1_CAT_R	CTGGTTTAAGCCGACGATATCCCCGTATAGTGAGTCGTATTAC	
attB1_isaA_up_F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCTAAGATTGTCATATCAATTATTATTGCATC	For *isaA* deletion using pKOR1
isaA_up_SOE_R	GGAGGATTTTTTACTTTCCTTCATAATAAATAAAAGTAATGTTTAGACATTA	
SOE_isaA_down_F	TTTATTATGAAGGAAAGTAAAAAATCCTCCAGTAATAATTGTAAGTTTAT	
isaA_down_attB2_R	GGGGACCACTTTGTACAAGAAAGCTGGGTGATTCTGCTTGGTTGAGTGTCTTAC	
attB1_sceD_up_F	GGGACAAGTTTGTACAAAAAAGCAGGCTGGCGTAATGCGTCAGCTC	For *sceD* deletion using pKOR1
SceD_up_SOE_R	GAGGATTTTAAGATTGCCATTGCCATTTATGCATAGCTAATTAATAGTTATATAAGTAAC	
SOE_sceD_down_F	CTATGCATAAATGGCAATCTTAAAATCCTCCTACAAGTAATTTGTT	
sceD_down_attB2_R	GGGGACCACTTTGTACAAGAAAGCTGGGTTGAAACAATAAAATTATGTCCCCTAA	
attB1_mecA_up_F	GGGGACAAGTTTGTACAAAAAAGCAGGCTCGTGGAGACGAGCACTAATAACC	For *mecA* deletion using pKOR1
mecA_up_SOE_R	TGCTTCACTGTTTTGTTTATATTGAGCATCTACTCGTTTTTTATTTTTA	
SOE_mecA_down_F	GATGCTCAATATAAACAAAACAGTGAAGCAATCCGTAAC	
mecA_down_attbB2_R	GGGGACCACTTTGTACAAGAAAGCTGGGTTGACGGTAGACTTACCTTTAACATGTTACA	
isaA_fusion_pCN51_F	CGACTCTAGAGGATCAAGGGTTGATTGGATTCTAAAGG	For construction of pCNisaA
isaA_fusion_pCN51_R	AGGCGCGCCTGAATTTTAGAATCCCCAAGCACCTAAA	
sceD_fusion_pCN51_F	CGACTCTAGAGGATCAGACATAGATTGCAAAACGATTACA	For construction of pCNsceD
sceD_fusion_pCN51_R	AGGCGCGCCTGAATTTTATGCAGTAACCCAATGTCCA	
mecA_fusion_pCN51_F	CGACTCTAGAGGATCATATAAGGAGGATATTGATGAAAAAGATAAAA	For construction of pCNmecA
mecA_fusion_pCN51_R	AGGCGCGCCTGAATTTTATTCATCTATATCGTATTTTTTATTACCGTT	

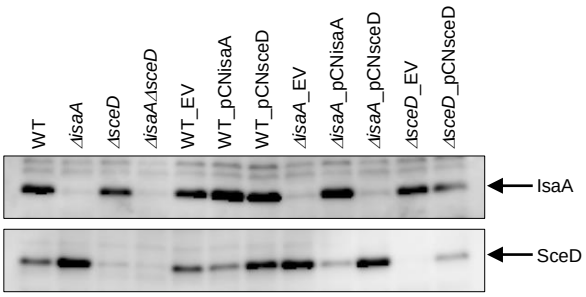

FIG S1 Western blot showing levels of IsaA and SceD in whole-cell fractions of *S. aureus* MR23 and LT mutants. WT, wild-type; EV, pCN51Cm (empty vector); pCNisaA, pCN51Cm containing *isaA*; pCNsceD, pCN51Cm containing *sceD*.

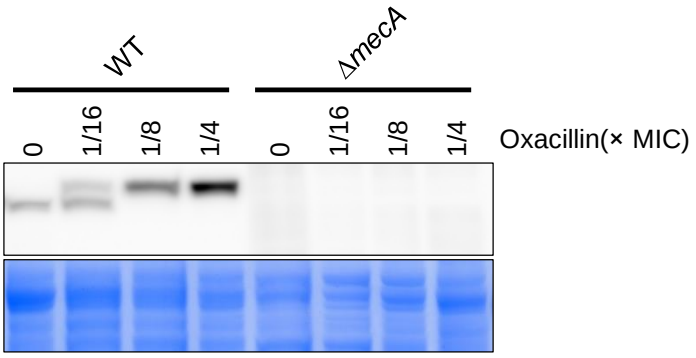

FIG S2 Western blot showing levels of PBP2a in wild-type (WT) and *mecA*-deletion mutant (Δ*mecA*) of *S. aureus* MR23. Concentrations of oxacillin used for induction are indicated above the panels. As a loading controls, a CBB-stained image gel of the same area was is shown below the panel.

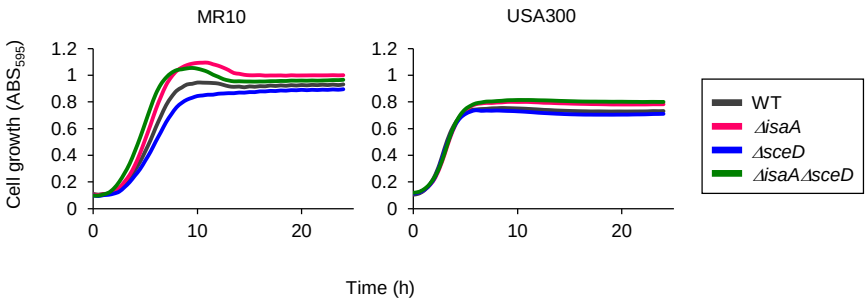

FIG S3 Effect of LT gene deletion on cell of *S. aureus* MR10 and USA300. The average of three independent cultures is shown.