

S3 Table. Antimicrobial resistance patterns in 195 ST59 *S. aureus* strains.

Antimicrobial resistance patterns ^a	No. (%) of strains			Antibiotic resistance elements (n)
	SCCmec IV (n=91)	SCCmec V (5C2&5) (n=74)	MSSA (n=30)	
E, K, G, C	39 (42.9)	0 (0)	1 (3.3)	MES ₆₂₇₂₋₂ (50), MES ₄₅₇₈ (9)
E, K, G	18 (19.8)	0 (0)	1 (3.3)	
E, K, S, C	12 (13.2)	42 (56)	15 (50)	MES _{PM1} (107)
E, K, S	7 (7.7)	22 (29.7)	9 (30)	
E, C	4 (4.4)	0 (0)	0 (0)	MES ₂₂₅₀ (6)
E	2 (2.2)	0 (0)	0 (0)	
E, K, G, S, C	1 (1.1)	2 (2.7)	0 (0)	For gentamicin resistance: Tn4001 (2), unknown (2); and for other antibiotic resistances: MES _{PM1} (4)
E, K, G, S	0 (0)	0 (0)	1 (3.3)	
E, K, C	2 (2.2)	0 (0)	0 (0)	MES ₆₂₇₂₋₂ (2) ^b , untypable (1) ^c
E, K	1 (1.1)	0 (0)	0 (0)	
C	3 (3.3)	2 (2.7)	0 (0)	IS1216V (12), cat-related
Susceptible to the above antimicrobials	3 (3.3)	6 (8)	3 (10)	segregants (5)

^a Antimicrobials: E, erythromycin; K, kanamycin; G, gentamicin; S, streptomycin; C, chloramphenicol.

^b A frame-shift mutation was found in the *aacA-aphD* gene (responsible for gentamicin resistance).

^c The *aacA-aphD* gene is intact.