

Table S1 Primers used in this study

Primers name	Primer sequences	Primer uses
1(forward)	GATTGAATCAGAACCTATTACGCT	Closing gap
1(reverse)	CCAATAATCGTAGCCATTGTATAG	Closing gap
2(forward)	CAGACGATGAGGCATTAGATGAAG	Closing gap
2(reverse)	GTACGGTTGTAATGGCTTTGAGGC	Closing gap
3(forward)	GGCCTCAAAGCCATTACAACCGTA	Closing gap
3(reverse)	CATTCGCTCACTTTTGTACTAA	Closing gap
4(forward)	CATGCATCCCCTTAATTCGAAAGC	Closing gap
4(reverse)	CTCTTCTGGTTGGAATGTGTGGTT	Closing gap
5(forward)	CGTCAGCACTTACAAAATCGGTTG	Closing gap
5(reverse)	GGAGTTAATCTACGTCTCATCTCA	Closing gap
6(forward)	CAGTTCATTGCTCACGATATGTGT	Closing gap
6(reverse)	CTCTTTGTCTCACTTTTGACCAAG	Closing gap
7(forward)	CTTGGTCAAAGTGAGACAAAGAG	Closing gap
7(reverse)	CATTACACTCTTGAGTCTCTCCCA	Closing gap
8(forward)	GACCAATACGTGGAAGTACACCAT	Closing gap
8(reverse)	GTAGCCAGTTAATTTCTACTAACCT	Closing gap
9(forward)	CATCACATGCAAAGCATTAGAGC	Closing gap
9(reverse)	CCATCCTAAATCGACCCAATACTT	Closing gap
10(forward)	GTATTGGGTCGATTTAGGATGGAA	Closing gap
10(reverse)	GATTTCCCGTACAATATGAGCTTC	Closing gap
11(forward)	GGACTTAAAGCAATCACGACAATT	Closing gap
11(reverse)	GCTTAGCGTCATTATAATGACCTC	Closing gap
12(forward)	CACACATGAACAAGAACAACCCGC	Closing gap
12(reverse)	GTGGTTCTGTTGCAAAGTTGAATT	Closing gap
13(forward)	CTTGTAGCCATGGCTATCCTTATT	Closing gap
13(reverse)	CAATGTGTTTAATCGCGTCTGTTC	Closing gap
14(forward)	CGCCAGTCGATTTAACGGACTTAA	Closing gap
14(reverse)	GGACAAATTCCAAGTTGCCCACTC	Closing gap
15(forward)	GCAGCTATTGTGGCGTAGAATTTA	Closing gap
15(reverse)	CACCCTCATTAGTCGATGTCATAT	Closing gap
16(forward)	GGATGACAGGAAATGAACTGAAAG	Closing gap
16(reverse)	GAATGCTGGCCACTCTCTACCAT	Closing gap
17(forward)	GCAACAAATAAGCTGCGTACCTTA	Closing gap
17(reverse)	CTTA ACTCTAACTCTGAGTAAGCT	Closing gap
18(forward)	GCAATTGGTGCAGGCACAGATGTT	Closing gap
18(reverse)	GACTCTGCAACTTCAGGAAATATT	Closing gap
19(forward)	CACTGTCATATACTTGAGCATGAAG	Closing gap
19(reverse)	CTTTGAGCGTCTCAATATCATTGG	Closing gap
20(forward)	GTCTCACGCTTACTATCTTCAACA	Closing gap
20(reverse)	GTTCTTTTTACATCTTCTGACACC	Closing gap
21(forward)	GCCAAGCCTCTAACATTAGAAGAA	Closing gap
21(reverse)	AAGGGACACCTATCGCCTTACATA	Closing gap
1R	CATACCTTACAACCTTTTACCGTCGA	Detecting SCC excision
1F	GCTGGTATTTTAGCATTATATCGG	Detecting SCC excision
2R	TGTGCCAATTTTCGCTTCATTC	Detecting SCC excision
2F	TTCGTTGATTTTCCATTAGTTG	Detecting SCC excision
3R	TGTAGATTTTGGCTTATTCACCTC	Detecting SCC excision
3F	TCGTTATCGCCATTTTAGTTGTAGC	Detecting SCC excision

Table S2 Predicted ORFs in the SCC elements of *S. haemolyticus* NW19A

Locus	Position	Genes	Description	Comments*
orf 1	101-580	<i>orfX</i>	rRNA large subunit methyltransferase	orfX
orf 2	826-1131		hypothetical protein	
orf 3	1330-2193		hypothetical protein	
orf 4	2277-3776		hypothetical protein	
orf 5	4002-5102		putative DNA polymorease	
orf 6	5095-5466		hypothetical protein	
orf 7	5463-7106		primase	
orf 8	7332-9008	<i>ccrCI</i>	cassette chromosome recombinase C1	RR
orf 9	9114-9452		hypothetical protein	
orf 10	9548-9859		hypothetical protein	
orf 11	9875-10381		hypothetical protein	
orf 12	10530-11204	<i>IS431-1</i>	transposase	IS
orf 13	11462-11629	<i>ΔmvaS</i>	truncated HMG-CoA synthase	
orf 14	12546-13289	<i>ugpQ</i>	glycerophosphoryl diester phosphodiesterase	
orf 15	13386-13814	<i>maoC</i>	acyl dehydratase	
orf 16	13860-15869	<i>mecA</i>	penicillin-binding protein 2	AR
orf 17	15984-16076	<i>ΔmecR1</i>	truncated mecR1	
orf 18	16114-16788	<i>ΔIS431-2</i>	truncated transposase	IS
orf 19	16848-17276	<i>phnB</i>	3-demethylubiquinone-9 3-methyltransferase	
orf 20	17588-18286		putative transcriptional regulator	
orf 21	18448-20436		hypothetical protein	
orf 22	20631-21740		putative DNA polymorease	
orf 23	21733-22101		hypothetical protein	
orf 24	22101-23717		primase	
orf 25	23942-25621	<i>ccrCI</i>	cassette chromosome recombinase C1	RR
orf 26	25674-26048		hypothetical protein	
orf 27	26127-26441		hypothetical protein	
orf 28	26482-27156	<i>IS431-3</i>	transposase	IS
orf 29	27353-28732	<i>tetK</i>	tetracycline resistance protein	AR
orf 30	28918-30159	<i>pre</i>	plasmid recombination enzyme	RR
orf 31	30786-31640	<i>ΔrepC</i>	truncated replication initiation protein	
orf 32	31728-32402	<i>IS431-4</i>	transposase	IS
orf 33	32461-33075		putative topoisomerase III	RR
orf 34	33352-33933		cassette chromosome helicase	RR
orf 35	34053-34328	<i>ΔccrA</i>	truncated cassette chromosome recombinase A	RR
orf 36	34440-34799		putative zinc/iron permease	HMR
orf 37	35006-35332	<i>yoza</i>	ArsR family transcriptional regulator	HMR
orf 38	35653-37587	<i>czrC</i>	cadmium and zinc resistance protein C	HMR
orf 39	38733-40061		metallo-beta-lactamase family protein	AR
orf 40	40080-41147		dihydroneopterin aldolase	
orf 41	41543-42301		putative membrane protein	
orf 42	42698-43243	<i>ydhK</i>	putative lipoprotein	
orf 43	43524-45314		hypothetical protein	
orf 44	44889-45314		hypothetical protein	
orf 45	45355-46053		hypothetical protein	
orf 46	46037-47209	<i>IS256</i>	transposase	IS
orf 47	47272-47844		hypothetical protein	
orf 48	48120-48896		putative HNH endonuclease	
orf 49	49075-50694	<i>ΔIS1272</i>	truncated transposase	IS
orf 50	51758-52192		acetyltransferase	
orf 51	52688-53035		merR family transcriptional regulator	HMR
orf 52	53113-53796		ThiJ/Pfpl family protein	
orf 53	53818-54483		putative oxidoreductase	
orf 54	54487-55491	<i>yfmJ</i>	alcohol dehydrogenase	
orf 55	55500-55865		putative membrane protein	
orf 56	56403-57020	<i>cadD</i>	cadmium resistance transporter family protein	HMR
orf 57	57039-57380	<i>cadX</i>	cadmium resistance transcriptional regulatory protein CadX	HMR
orf 58	57400-57801	<i>arsC</i>	thioredoxin-coupled arsenate reductase	HMR
orf 59	57819-59108	<i>arsB</i>	arsenical pump membrane protein	HMR
orf 60	59108-59425	<i>arsR</i>	arsenical resistance operon repressor	HMR
orf 61	59678-61741	<i>copB</i>	copper-transporting P-type ATPase B	HMR
orf 62	61756-63189	<i>cueO</i>	multicopper oxidase	HMR
orf 63	63209-63691	<i>ydhK</i>	putative lipoprotein	
orf 64	63897-64292	<i>arsC</i>	arsenate reductase	HMR

orf 65	64311-65603	<i>arsB</i>	arsenical pump membrane protein	HMR
orf 66	65603-65917	<i>arsR</i>	arsenic resistance operon repressor	HMR
orf 67	66057-67787	<i>arsA</i>	arsenite-activated ATPase	HMR
orf 68	67768-68115	<i>arsD</i>	arsenical resistance operon trans-acting repressor	HMR
orf 69	68397-68591	<i>yedL</i>	putative N-acetyltransferase	
orf 70	68637-68957		ArsR family transcriptional regulator	HMR
orf 71	69045-69929		Permease	
orf 72	69943-70071		hypothetical protein	
orf 73	70394-71380		ADP-ribosylglycohydrolase	

*HMR represents heavy metal resistance associated genes. AR represents antibiotic resistance genes. IS represents

Insertion Sequences. RR represents recombination related genes.

Table S3 Presence of defensive systems and origin of strains investigated in this study

Strain name	Origin	Defensive system*	Accession no.
NW19A	<i>S. haemolyticus</i>	No	KM369884
P126	<i>S. aureus</i>	No	KF593809
JCSC6994	<i>S. aureus</i>	No	AB505629
CR01	<i>S. capitis</i>	Cas system	KF049201
S0385	<i>S. aureus</i>	Type I R-M system	AM990992
JCSC1435	<i>S. haemolyticus</i>	Type I R-M system	AP006716
06-3288	<i>S. pseudintermedius</i>	No	FJ544922
P211	<i>S. aureus</i>	No	KF593810
JCSC5952	<i>S. aureus</i>	Type I R-M system	AB478780
JCSC4610	<i>S. aureus</i>	No	AB773816
WAMRSA40	<i>S. aureus</i>	Type I R-M system	JQ746621
JCSC6943	<i>S. aureus</i>	No	AB505628
08BA02176	<i>S. aureus</i>	Type I R-M system; Cas system	CP003808
SR 141	<i>S. aureus</i>	Type I R-M system	AB665980
ZH47	<i>S. aureus</i>	Type I R-M system	AM292304
JCSC3624(WIS)	<i>S. aureus</i>	Type I R-M system	AB121219
UMCG-M4	<i>S. aureus</i>	Type I R-M system	GQ902038
PM1	<i>S. aureus</i>	Type I R-M system	AB462393
TSGH17(JCSC7190)	<i>S. aureus</i>	Type I R-M system	AB512767
M013	<i>S. aureus</i>	Type I R-M system	CP003166
SA957	<i>S. aureus</i>	Type I R-M system	CP003603
JCSC7481	<i>S. aureus</i>	Type I R-M system	AB774378
GR1	<i>S. aureus</i>	Type I R-M system	AB781448
3957	<i>S. aureus</i>	Type I R-M system	AB781446
120	<i>S. aureus</i>	Type I R-M system	AB781444
JCSC6838	<i>S. aureus</i>	Type I R-M system	AB774373
118	<i>S. aureus</i>	Type I R-M system	AB777516
3989	<i>S. aureus</i>	Type I R-M system	AB781447
LVP2	<i>S. aureus</i>	Type I R-M system	AB781449
333	<i>S. aureus</i>	Type I R-M system	AB781445
CMFT1723	<i>S. aureus</i>	Type I R-M system	HF569096
CMFT3119	<i>S. aureus</i>	No	HF569105
SH621	<i>S. haemolyticus</i>	No	AB478934
JCSC6082	<i>S. aureus</i>	Type I R-M system	AB373032
85/2082	<i>S. aureus</i>	No	AB037671
T0131	<i>S. aureus</i>	Type I R-M system	CP002643
BK16691	<i>S. aureus</i>	Type I R-M system	GU235985
16K	<i>S. aureus</i>	Type I R-M system	AB666466
HU25	<i>S. aureus</i>	No	AF422696
Z172	<i>S. aureus</i>	Type I R-M system	CP006838
Bmb9393	<i>S. aureus</i>	Type I R-M system	CP005288
TW20	<i>S. aureus</i>	Type I R-M system	FN433596
XN108	<i>S. aureus</i>	Type I R-M system	CP007447
85/3907	<i>S. aureus</i>	No	AB047089
SH32	<i>S. haemolyticus</i>	Type III R-M system	KF006347
WCH1	<i>S. haemolyticus</i>	No	JQ764731
SH480	<i>S. haemolyticus</i>	No	AB477967
VH60	<i>S. aureus</i>	Type I R-M system	AB781450
ATCC 12228	<i>S. epidermidis</i>	Type I R-M system	AE015929
RP62A	<i>S. epidermidis</i>	Type I R-M system	CP000029
JCSC6945	<i>S. aureus</i>	Type I R-M system	AB505630

* R-M system is the abbreviation of the Restriction-Modification system.

Table S4 Comparative analysis of SCCs in NW19A with other related-bacteria

Genus*	Bacteria name	Fragments***										
		1	2-11	12-18	19-27	28-31	32-47	48-50	51-72	73-75	76-79	
SH	NW19A	1	2-11	12-18	19-27	28-31	32-47	48-50	51-72	73-75	76-79	
SA	P126 **	1	2-27(gain a gene behind orf27)(C2Δ)				28-47(lost orf46)					
SA	P211	1	2-27(gain a gene behind orf27, but lost orf8-24)				28-47(lost orf46)					
SA	S0385	1	2-27(C2Δ)				32-47(orf46 was replaced by 17 ORFs)					
SC	CR01	1	2-27(C2Δ)						51-63(lost orf62)			
SP	06-3228	1	2-27(C2Δ)									
SA	UMCG-M4	1	2-27(lost orf13) (C2Δ)									
SA	JCSC5952 **	1	2-27(gain ISSag7 in orf21) (C2Δ)									
SA	JCSC4610	1	2-21(gain ISSag7 in orf21) (C2Δ)									
SA	SR141	1	2-18(C2Δ)									
SA	08BA02176 **	1	12-27(C2Δ)								73-75	
SA	GR1 **	1	2-11	12-18(C2)	19-27							
SA	JCSC7481 **	1		12-18(C2)	19-27							
SA	JCSC6838	1			19-27							
SA	JCSC6082	1	2-11	12-18(C2)								
SA	JCSC6943	1		12-18(C2)					51-72			
SH	JCSC1435	1		12-18(C2)	19-27				51-72		76-79	
SH	SH32	1		C1		34-38		51-60	61-72	73-75		
SH	WCH1	1		C1				51-60	61-63	73-75		
SH	SH621	1		ND		34-38		51-63(lost orf62)			76-79	
SA	JCSC6945	1		C1				51-57	58-63			
SH	NCTC11042	1							58-63			
SE	ATCC12228	1					39-41		61-63	64-72		
SE	RP62A	1		A			39-41		61	64-72		
SH	SH480	1		12-18(C2)						65-72		
SA	ZH47	1	2-17(B2)									
SA	Z172 **	1	2-11	A		28-31						
SA	T0131 **	1	2-11	A								
SA	CMFT3119	1	2-11	B								
SA	BK16691 **	1	2-11									

* The abbreviation of *Staphylococcus* genus. SH, SA, SC, SP and SE represent *S. haemolyticus*, *S. aureus*, *S. capitis*, *S. pseudintermedius* and *S. epidermidis*, respectively.

** These strains contain same fragments as other strains not listed in this table. P126=JCSC6944; JCSC5952=WAMRSA40=PM1=JCSC7190=M013=SA957; 08BA02176=CMFT1723; GR1=3957; JCSC7481=120=118=3989=LVP2=333; Z172=85/2082=TW20; T0131=Bmb9393=XN108=85/3907; BK16691=16K=HU25.

*** The fragment regions displayed by ORFs. The letters A, B, B2, C1, C2, C2Δ represent different *mec* gene complexes; C2Δ represents class C2 *mec* gene complex with truncated IS431-2. ND: Not-Determined.