Supplemental Table S1. PCR primers used to characterize the novel composite pseudo SCC*mec*-SCC-SCC$_{CRISPR}$ element in ST779/t878 MRSA isolates and for confirmation of ambiguous DNA microarray results

Primer application	Primer pair	Nucleotide sequence (5'-3')	Nucleotide coordinates	Expected amplimer size (bp)	Reference
Confirmation of the genetic organization of the pseudo SCC*mec*-SCC-SCC$_{CRISPR}$ element in M06/0171	276F	GAATCAACGCATGACCCAAGG	276-296[a]	2295	This study
	dru 5'	GTTAGCATATTACCTCTCCTTGC	2548-2570[a]		(1)
	dru 3'	GCCGATTGTGCTTGATGAG	1766-1784[a]	3075	(1)
	mA1	TGCTATCCACCCTCAAACAGG	4840-4820[a]		(2)
	mA2	AACGTTGTAACCACCCCAAGA	4555-4575[a]	6074	(2)
	far476R	GATTATTTATATCATCTAGG	10628-10609[a]		(3)
	far476F	AGTAAAGCAGTTAGTATATC	10051-10070[a]	6936	(3)
	169R	TTCTAAATATTTCATCTTGGCTA	16986-16964[a]		This study
	154F	TGATTGCTCAAGGAGATCAAATTAA	15416-15440[a]	11624	This study
	270R	ATTGGTATGTTAAACTATTTTAAA	27039-27016[a]		This study

Primer application	Primer pair	Nucleotide sequence (5'-3')	Nucleotide coordinates	Expected amplimer size (bp)	Reference
	β4U	ATCGCTCCAGTGTCTATACTTCGC	30547-30570[a]	10405	(2)
	γR	CCTTTATAGACTGGATTATTCAAAATAT	40951-40924[a]		(2)
	407F	ATATTGTACGTGAAATTTTCGATT	40795-40818[a]	5310	This study
	461R	ATTATAGGCATATTTCACACTACG	46104-46081[a]		This study
	452F	ATCTCGTCAACTTGTTGGCGAGAT	45279-45302[a]	6332	This study
	516R	ATGATACGCCTCTCCCTATCAGTG	51610-51633[a]		This study
Amplification and sequencing of the CRISPR region of the pseudo SCC*mec*-SCC-SCC$_{CRISPR}$ element	CRISPR_F	ACCTGTTCCGGTCATTGTTCTAAC	50374-50397[a]	1560	This study
	CRISPR_R	ATCTATTTTCAATCTCAAACATTA	51910-51933[a]		This study
Amplification of the *mec* complex of the pseudo SCC*mec*-SCC-SCC$_{CRISPR}$ element	C2F	TATTAAAATAAGTGGAACAAT	5848-5868[a]	17911	This study
	C70R	TAAAGTTTCTTGCCCATACCTTGT	7003-7026[a]		This study

Primer application	Primer pair	Nucleotide sequence (5'-3')	Nucleotide coordinates	Expected amplimer size (bp)	Reference
Amplification of genes yielding ambiguous results by DNA microarray profiling	*seb-1*	TCGCATCAAACTGACAAACG	N/A	477	(4)
	seb-4	GCAGGTACTCTATAAGTGCCTGC	N/A		(4)
	sdrD-F	ACTGCTAACATTCAATATCC	1261-1280[b]	1289	This study
	sdrD-R	ATGTAACTGTTACGCCT	2566-2550[b]		
	clfB-F	AGTTCTTACCTGTATTGTC	1344-1362[b]	598	This study
	clfB-R	AAGCAACATATGATATC	1958-1942[b]		

[a] Nucleotide coordinates based on the nucleotide sequence of the composite pseudo SCC*mec*-SCC-SCC$_{\mathrm{CRISPR}}$ element of MRSA isolate M06/0171 (GenBank accession number HE980450).

[b] Nucleotide coordinates based on the nucleotide sequence of the *S. aureus* strain COL (GenBank accession number CP000046).

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Supplemental Table S2. Location of open reading frames (ORFs), predicted gene products and comparison with similar ORFs in GenBank for the pseudo SCC*mec*-SCC-SCC$_{\text{CRISPR}}$ element of MRSA isolate M06/0171

ORF/DR	Nucleotide coordinates	Comparative ORF (GenBank accession number)	Protein accession number	% amino acid identity	Gene product/DR nucleotide sequence
ORF_100 (*orfX*)	1-480	MRSA strain Mu50 (NC_002758.2)	NP_370548.1	99%	23S rRNA methyltransferase (formerly known as open reading frame *orfX*)
DR1	462-478	n/a	n/a	n/a	AGAAGCTTATCATAAAT
ORF_101 (*tnp*)	659-1333 (complement)	*Staphylococcus aureus* strain 45394F, SCC45394F/SCC*mec* IVk, (GU122149)	ADC40007.1	99%	Transposase for IS431
ORF_102 (*mvas* truncated)	1406-1758	*Staphylococcus epidermidis* BCM-HMP0060 (NZ_ACHE01000054)	ZP_04825712	100%	Hydroxymethylglutaryl-CoA synthase N-domain
***dru* region**	2004-2361	n/a	n/a	n/a	Direct repeat unit (*dru*)
ORF_103 (*ugpQ*)	2563-3306	*S. aureus* strain MU50 (NC_002758.2)	NP_370563.1	100%	Glycerophosphory diester phosphodiesterase
ORF_104	3403-3831	*S. aureus* strain MU50 (NC_002758.2)	NP_370564.1	100%	MaoC-like domain protein
ORF_105 (*mecA*)	3877-5883 (complement)	*S. aureus* SCC*mec* X (AB505630)	BAK53145.1	100%	Penicillin-binding protein 2a
ORF_106 (Δ*mecR1*)	5983-5999 (complement)	*S. aureus* SCC*mec* X (AB505630)	BAK53145.1	100%	Methicillin resistance regulatory sensor-transducer MecR1
ORF_107 (*tnp*)	6076-6750 (complement)	*S. aureus* strain 71193 (CP003045.1)	AFH70044	99%	Transposase for IS431
ORF_108	6928-8868	*S. epidermidis* strain VCU120 (AHLC01000034.1)	EHR82817.1	99%	DEAD/DEAH box helicase domain protein
ORF_109	9125-9433	MSSA*476* (NC_002953.3)	YP_042172	98%	Hypothetical protein (SAS0040)

ORF/DR	Nucleotide coordinates	Comparative ORF (GenBank accession number)	Protein accession number	% amino acid identity	Gene product/DR nucleotide sequence
ORF_110	9543-9701	*S. aureus* strain 45394F, (GU122149.1)	ADC40000.1	100%	Hypothetical protein (ORF022)
ORF_111 (*fusC*)	10019-10657	*S. aureus* strain MSSA*476* (NC_002953.3)	YP_042173	100%	Fusidic acid resistance protein
ORF_112 (*copB*)	10962-12921 (complement)	*S. epidermidis* VCU120 (AHLC01000034.1)	EHR82803	99%	Putative copper exporting ATPase
ORF_113 (*tnp*)	12978-13652	*S. aureus* strain Mu50 (NC_002758.2)	NP_370551	100%	Transposase for IS431
ORF_114 (*copC*)	13915-15975	*S. aureus* strain, JCSC6945 (AB505630)	BAK53188	100%	P-ATPase superfamily P-type ATPase copper (Cu2+) transporter
ORF_115	15993-16538	*S. aureus* strain USA300_FPR3757 (NC_007793.1)	YP_492797	99%	Putative lipoprotein
DR2	16743-16759	n/a	n/a	n/a	AGAAGCGTACCACAAAT
ORF_116	17439-18344	*S. epidermidis* strain VCU129 (AHLJ01000021.1)	EHS01958.1	93%	*ApbE* family protein
ORF_117	18427-21444	*S. epidermidis* strain RP62A (NC_002976.3)	YP_189929.1	96%	Putative NADH-dependent flavin oxidoreductase
ORF_118	21473-22849	*S. epidermidis* strain BCM-HMP0060 (NZ_ACHE01000077)	ZP_04826005	94%	Putative drug transporter Quinolone resistance protein NorB
ORF_119 (*speG*)	23471-23968 (complement)	*S. epidermidis* strain ATCC 12228	NP_763601	99%	Spermidine acetyltransferase
ORF_120	24376-24843 (complement)	*Staphylococcus haemolyticus* strain	YP_251974.1	98%	Hypothetical protein

ORF/DR	Nucleotide coordinates	Comparative ORF (GenBank accession number)	Protein accession number	% amino acid identity	Gene product/DR nucleotide sequence
		JCSC1435 (NC_007168)			
ORF_121	24858-25196 (complement)	*S. aureus* strain 45394F , SCC45394F and SCC*mec*IVk (GU122149.1)	ADC39991	93%	Hypothetical protein
ORF_122	25256..25646 (complement)	*S. aureus* strain USA300_FPR3757 (NC_007793.1)	YP_492778.1	91%	Hypothetical protein
ORF_123 (*nupC2)*	26167-27348 (complement)	*Staphylococcus lugdunensis* strain HKU09-01 (NC_013893)	YP_003470547	83%	Nucleoside transporter
ORF_124 (*indA*)	27359-28270 (complement)	*S. lugdunensis* strain M23590 (NZ_AEQA01000015.1)	ZP_07912579.1	79%	Indigoidine synthase A (indA) family protein
ORF_125	28254-29363 (complement)	*S. lugdunensis* M23590 (NZ_AEQA01000015.1)	ZP_07912578.1	67%	PfkB family carbohydrate kinase
ORF_126 (*ccrB4*)	29593-31281 (complement)	*S. haemolyticus* strain MCS13 (AB587081.1)	BAJ53095	98%	Cassette chromosome recombinase B4
ORF_127 (*ccrA4*)	31278-32639 (complement)	*S. aureus* strain CHE482 (EF126185)	ABL75417.1	93%	Cassette chromosome recombinase A4, has a premature stop codon at position 32310-32312 (complement)
ORF_128	32894-34186	*Staphylococcus hominis* VCU122 (AHLD01000058)	EHR87795.1	94%	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase family
DR3	34208-34231	n/a	n/a	n/a	AGAAGCTTATCACAAAT
ORF_129	34320-34949	*S. epidermidis* strain ATCC 12228 (AE015929)	AAO03695.1	95%	Conserved hypothetical protein
ORF_130	35215-36690	*S. saprophyticus* strain ATCC 15305 (NC_007350.1)	YP_300132	92%	Hypothetical protein (SSP0042)

ORF/DR	Nucleotide coordinates	Comparative ORF (GenBank accession number)	Protein accession number	% amino acid identity	Gene product/DR nucleotide sequence
ORF_131	36916-38016	*S. saprophyticus* strain ATCC 15305 (NC_007350.1)	YP_300133.1	90%	Hypothetical protein (SSP0043)
ORF_132 (*ccrAA*)	38377-40020	*S. aureus* strains M013 (NC_016928.1), T0131 (NC_017347) and ATCC BAA-39 (NZ_AEEK01000037)	YP_005296507.1, YP_005753915.1 and ZP_07362708.1 respectively	89%	Hypothetical protein located adjacent to *ccrC*
ORF_133 (*ccrC1*)	40245-41924	*S. aureus* strain UMCG-M4 (GQ902038)	ADC79473	95%	Cassette chromosome recombinase C1
ORF_134	42013-42351	*S. haemolyticus* strain JCSC1435 (NC_007168)	YP_251972.1	96%	Hypothetical protein
ORF_135	42445-42756	*S. pseudintermedius* strain 06-3228 (FJ544922)	ACL99846	99%	Hypothetical protein
ORF_136	42771-43274	*S. pseudintermedius* strain 06-3228 (FJ544922.1)	ACL99847.1	99%	Hypothetical protein
ORF_137	43731-44543	*S. epidermidis* strain VCU117 (AHLA01000056)	EHR83751	96%	Hypothetical protein
ORF_138	44760-45015	*S. aureus* strain T0131 (YP_005753900)	YP_005753900.1	64%	Type I site-specific restriction-modification system, R (restriction) subunit and related helicases [Defense mechanisms]
ORF_139 (*cas9/csn1*)	45349-48510	*S. lugdunensis* strain M23590 (NZ_AEQA01000016)	ZP_07912707	63%	CRISPR-associated protein Cas9/Csn1
ORF_140 (*cas 1*)	48518-49423	*S. lugdunensis* strain M23590 (NZ_AEQA01000016)	ZP_07912706	68%	CRISPR-associated protein Cas 1
ORF_141 (*cas2*)	49435-49743	*S. lugdunensis* strain M23590 (NZ_AEQA01000016)	ZP_07912705.1	70%	CRISPR-associated protein Cas 2

ORF/DR	Nucleotide coordinates	Comparative ORF (GenBank accession number)	Protein accession number	% amino acid identity	Gene product/DR nucleotide sequence
ORF_142	49754-50743	*S. lugdunensis* strain M23590 (NZ_AEQA01000016)	ZP_07912704.1	44%	CRISPR-associated conserved hypothetical protein
CRISPR	50774-51601	n/a	n/a	n/a	Clustered Regularly Interspaced Short Palindromic Repeats (CRISPR)
DR4	51614-51637	n/a	n/a	n/a	AGAGGCGTATCATAAGT

Abbreviations: ORF, open reading frame; DR, direct repeat; n/a, not applicable.