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UCS          TATTTCCGAAGAAATATTTACTATAAAAATTTTATAGCCATTAATTATAGTATTATAARAGATTTAGATAGCAGGAATCTTAATCAAGTTACGGTTAGTGTGAAGGGAGCTGTGAA
Chromosomal  TATTTCCTAGGAAATACGACTATAAACATTTATAGCCCTTATTCTGTGATTATAAAGATTTAGATAGCAGGAATCTTAATCAAGTTACGGTTAGTGTGAAGGGAGCTGTGAA
orf51         TATTTCCTAGGAAATACGACTATAAACATTTATAGCCCTTATTCTGTGATTATAAAGATTTAGATAGCAGGAATCTTAATCAAGTTACGGTTAGTGTGAAGGGAGCTGTGAA
orf46         TATTTCCTAGGAAATACGACTATAAACATTTATAGCCCTTATTCTGTGATTATAAAGATTTAGATAGCAGGAATCTTAATCAAGTTACGGTTAGTGTGAAGGGAGCTGTGAA

UCS          CATGGATTAGGCACTAATTAGTATTTACAGAAAGKAAYATTTTCTCACGAGGATTAGCAGAAAGGATTTTTGTGTTCAAGTGCAGCATATCGAATTTGGGAGAATGAAGAG
Chromosomal  CATGGATTAGGCACTAATTAGTATTTACAGAAAGKAAYATTTTCTCACGAGGATTAGCAGAAAGGATTTTTGTGTTCAAGTGCAGCATATCGAATTTGGGAGAATGAAGAG
orf51         CATGGATTAGGCACTAATTAGTATTTACAGAAAGKAAYATTTTCTCACGAGGATTAGCAGAAAGGATTTTTGTGTTCAAGTGCAGCATATCGAATTTGGGAGAATGAAGAG
orf46         CATGGATTAGGCACTAATTAGTATTTACAGAAAGKAAYATTTTCTCACGAGGATTAGCAGAAAGGATTTTTGTGTTCAAGTGCAGCATATCGAATTTGGGAGAATGAAGAG

UCS          TTATYCCCGATTACATAAATTGATTGAGCTTGCTTTCTTGTGTTAACGTTCTTAGACCAACTTGTAAAGGAGATGTTAAGTGTGAGAATGCAGTGGATACAGTAAATGGATAA
Chromosomal  TTATYCCCGATTACATAAATTGATTGAGCTTGCTTTCTTGTGTTAACGTTCTTAGACCAACTTGTAAAGGAGATGTTAAGTGTGAGAATGCAGTGGATACAGTAAATGGATAA
orf51         TTATYCCCGATTACATAAATTGATTGAGCTTGCTTTCTTGTGTTAACGTTCTTAGACCAACTTGTAAAGGAGATGTTAAGTGTGAGAATGCAGTGGATACAGTAAATGGATAA
orf46         TTATYCCCGATTACATAAATTGATTGAGCTTGCTTTCTTGTGTTAACGTTCTTAGACCAACTTGTAAAGGAGATGTTAAGTGTGAGAATGCAGTGGATACAGTAAATGGATAA

UCS          GTATAGTAAGATGATGTTTTTTGCTKCTTTATTCTTGGTGCGTTGATGAGGTTTGTGATGTGTTGTGCCCTTCTTTATCTATGGATGATTTGTGAT
Chromosomal  GTATAGTAAGATGATGTTTTTTGCTKCTTTATTCTTGGTGCGTTGATGAGGTTTGTGATGTGTTGTGCCCTTCTTTATCTATGGATGATTTGTGAT
orf51         GTATAGTAAGATGATGTTTTTTGCTKCTTTATTCTTGGTGCGTTGATGAGGTTTGTGATGTGTTGTGCCCTTCTTTATCTATGGATGATTTGTGAT
orf46         GTATAGTAAGATGATGTTTTTTGCTKCTTTATTCTTGGTGCGTTGATGAGGTTTGTGATGTGTTGTGCCCTTCTTTATCTATGGATGATTTGTGAT

UCS          GTATATGCATTTAAAGTAGATCAATTAAAGGAAACATGAYGGTMAAAACGTATAAAGAATTATTGATTATGTTGGAAATGGCATTAAAACCCAGAATTAAAGAA
Chromosomal  GTATATGCATTTAAAGTAGATCAATTAAAGGAAACATGAYGGTMAAAACGTATAAAGAATTATTGATTATGTTGGAAATGGCATTAAAACCCAGAATTAAAGAA
orf51         GTATATGCATTTAAAGTAGATCAATTAAAGGAAACATGAYGGTMAAAACGTATAAAGAATTATTGATTATGTTGGAAATGGCATTAAAACCCAGAATTAAAGAA
orf46         GTATATGCATTTAAAGTAGATCAATTAAAGGAAACATGAYGGTMAAAACGTATAAAGAATTATTGATTATGTTGGAAATGGCATTAAAACCCAGAATTAAAGAA

UCS          TTTATYTWTGGAAAGAGTATTTACAGTTTTAGGTTTCTTTAATTGCTGTGTAATCTTAGTACTTTAGTATGTTCTATTTGGGACTACTATAAAATAAGAATGTGTTAAAGACCCGTTTATA
Chromosomal  TTTATYTWTGGAAAGAGTATTTACAGTTTTAGGTTTCTTTAATTGCTGTGTAATCTTAGTACTTTAGTATGTTCTATTTGGGACTACTATAAAATAAGAATGTGTTAAAGACCCGTTTATA
orf51         TTTATYTWTGGAAAGAGTATTTACAGTTTTAGGTTTCTTTAATTGCTGTGTAATCTTAGTACTTTAGTATGTTCTATTTGGGACTACTATAAAATAAGAATGTGTTAAAGACCCGTTTATA
orf46         TTTATYTWTGGAAAGAGTATTTACAGTTTTAGGTTTCTTTAATTGCTGTGTAATCTTAGTACTTTAGTATGTTCTATTTGGGACTACTATAAAATAAGAATGTGTTAAAGACCCGTTTATA

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**Figure S1.** Nucleotide sequence comparison of *orf46* (bright purple), *orf51* (pale purple), and both recombined *orfs* after excision of the UCS in KM45013 (*orf* located in the UCS and the one on the chromosomal DNA). Their 120-bp upstream- and 84/86-bp downstream regions are also depicted and colored in blue or green, respectively. The start and stop codons of *orf46*, *orf51* and both recombined *orfs* are boxed. The expected sites (5'-TTACAG-3') involved in *orf46* and *orf51* recombination are shown in black. The nucleotide positions with double peaks in the sequence chromatograms (Sanger sequencing) of both recombined CDS are indicated as K (T or G), Y (T or C), R (G or A), W (A or T) or M (A or C) and colored in yellow. Divergent nucleotides in *orf46* and *orf51* with respect to those of the recombined *orfs* are underlined.

**Table S1.** Oligonucleotide primers used in this study and description of regions amplified.

Description	Gene/region amplified	Primer designation	Sequence (5'→3) <sup>a</sup>	Amplicon size (bp)
<i>ccrAm2/Bm2</i> of <i>SCCmec<sub>KM45013</sub></i>	<i>ccrAm2</i>	ccrAm2-fw ccrAm2-rv	TTCKTCCAGAACCGATATCA GGCAGCGTTCATTTAAWCSY	797 <sup>b</sup>
	<i>ccrBm2</i>	ccrBm2-fw ccrBm2-rv	GACGGCAAGCATACTCCAAT GCAGTGCTTCCTCTGGTTSK	808 <sup>b</sup>
<i>mec</i> complex of <i>SCCmec<sub>KM45013</sub></i>	<i>mecB</i>	mecB-fw mecB-rv	TGTTCGGCATTCCGACGAA TCTCCCTGGCCATATCCTGA	469 <sup>b</sup>
	<i>mecIm</i>	mecIm-fw mecIm-rv	TGAGGCATTGAGTGCTAAACA TTCGGTCAATTCTTCAGGTG	265 <sup>b</sup>
	<i>mecRIm</i>	mecRm-fw mecRm-rv	CAGCTGTGACATGGAAGTGA TACCAAGTTTCCCCACAKC	861 <sup>b</sup>
	<i>blaZm</i>	blaZm-fw blaZm-rv	AAGTACAATATTCAAGCGGGTGT AATTAGCTCCCTGCCCACTT	586 <sup>b</sup>
<i>orfX</i> of strain KM45013	<i>orfX</i>	orfX_KM-fw orfX_KM-rv	GAAGCGGAGCGCATACTATC GCATAGTTTGAGCGGTCCAT	197 <sup>b</sup>
Transposase gene of Tn6045	<i>tnp</i>	tnp-rv_096 tnp-fw_096	CGCCACAGGCCTTAAATAAT GCTCCGAAAATTGCGTAAAG	906 <sup>b</sup>
MCCL_0033	MCCL_0033	MCCL_0033_096-fw MCCL_0033_096-rv	GCTGGAAACGAAAGAAGCTG ACCCATAGCTCGCACAAAT	413 <sup>b</sup>
MCCL_0034	MCCL_0034	MCCL_0034_096-fw MCCL_0034_096-rv	AAAATGGATGCTGAGGGTGA TCCACCAATTCTTGTGCTG	339 <sup>b</sup>
Restriction analysis of <i>SCCmec<sub>KM45013</sub></i>	Joining region 3 (J3)	orfX_KM-fw ccrAm2-fw	GAAGCGGAGCGCATACTATC TTCKTCCAGAACCGATATCA	10,740 <sup>c</sup>
	5' end J2	ccrAm2-rv C16_ISP2	GGCAGCGTTCATTTAAWCSY ACAGGTACGCCGTCTCTGT	11,777 <sup>c</sup>
	3' end J2 + <i>mec</i> operon	C16_ISP3 blaZm-rv	AGCAGGCGTACCTGTTGAGT AATTAGCTCCCTGCCCACTT	17,074 <sup>c</sup>
<i>SCCmec<sub>KM45013</sub></i> CIs and UCS	<i>SCCmec<sub>KM45013</sub></i>	<i>SCCmec5'_inv</i> (1) <i>SCCmec3'_inv</i> (4, C)	TCCC ACTGATTCTGCCCTTT GGTGATAAAAGTGGCAAGG	688 <sup>c</sup>
	<i>SCC<sub>KM45013</sub></i>	<i>SCCmec5'_inv</i> (1) ISS2-up (2)	TCCC ACTGATTCTGCCCTTT CCCACTAGAAAAAGCGGATG	989 <sup>c</sup>
	<i>ψSCCmec<sub>KM45013</sub></i>	ISS2-dn (3) <i>SCCmec3'_inv</i> (4, C)	AACCAAATTCAACCATATGATAA GGTGATAAAAGTGGCAAGG	547 <sup>c</sup>
	UCS	mecIm-fw (B) <i>SCCmec3'_inv</i> (4, C)	TGAGGCATTGAGTGCTAAACA GGTGATAAAAGTGGCAAGG	1,702 <sup>c</sup>
	<i>SCCmec<sub>KM45013</sub></i>	orfX-fw2 (0) orf52_inv (5, D)	CGCTCAAACATATGCCCTCTC GTTTGGCCTTATGGGCTTT	1,744 <sup>c</sup> / 40,405 <sup>c</sup>
Detection of chromosomal regions after excision	<i>SCC<sub>KM45013</sub></i>	orfX-fw2 (0) ISS2-dn (3)	CGCTCAAACATATGCCCTCTC AACCAAATTCAACCATATGATAA	369 <sup>c</sup> / 27,245 <sup>c</sup>
	<i>ψSCCmec<sub>KM45013</sub></i>	ISS2-up (2) orf52_inv (5, D)	CCCACTAGAAAAAGCGGATG GTTTGGCCTTATGGGCTTT	2,029 <sup>c</sup> / 14,087 <sup>c</sup>
	UCS	orf45_inv (A) orf52_inv (5, D)	CACTGAATCAGCATGATGTCCT GTTTGGCCTTATGGGCTTT	1,535 <sup>d</sup> / 7,814 <sup>c</sup>

<sup>a</sup> Specifications for degenerate primer: K (T or G), Y (T or C), R (G or A), W (A or T), S (G or C), or M (A or C).<sup>b</sup> Taq DNA polymerase was used following the manufacturer's recommendations (Solis BioDyne).<sup>c</sup> GoTaq DNA polymerase was used following the manufacturer's recommendations (Promega).<sup>d</sup> HOT FIREPol DNA polymerase was used following the manufacturer's recommendations (Solis BioDyne).