

Supplementary Information

Table S1. Primers of target genes. The sets of forward and reverse primers for the candidate housekeeping genes are presented in 5' to 3' orientation, with their respective lengths, T_m, and amplicon sizes.

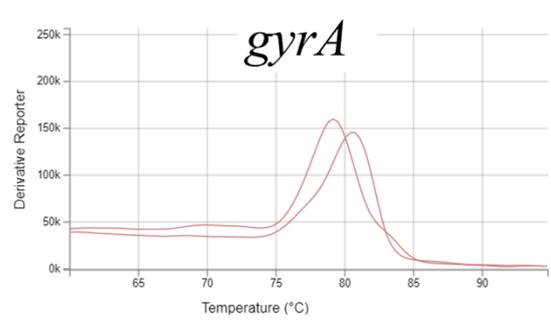
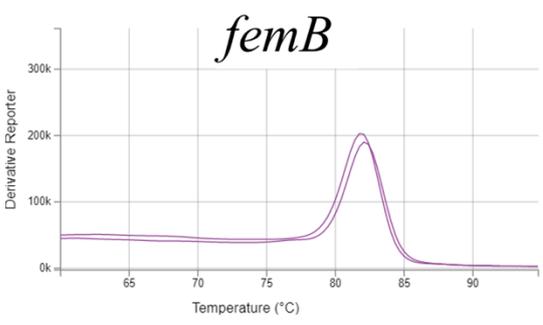
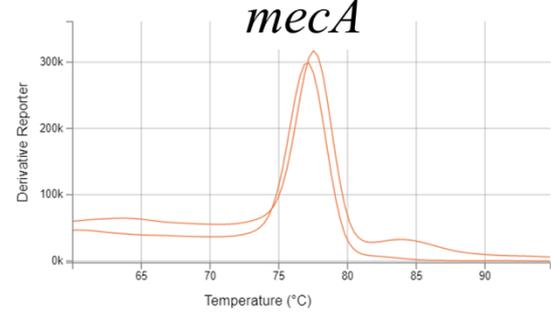
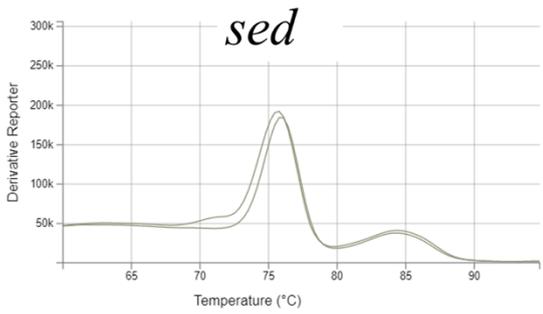
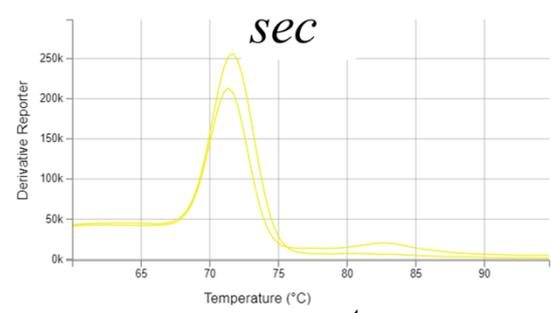
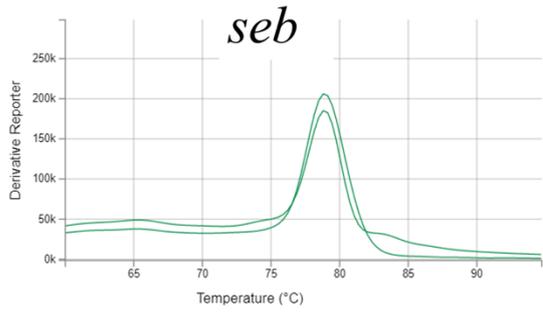
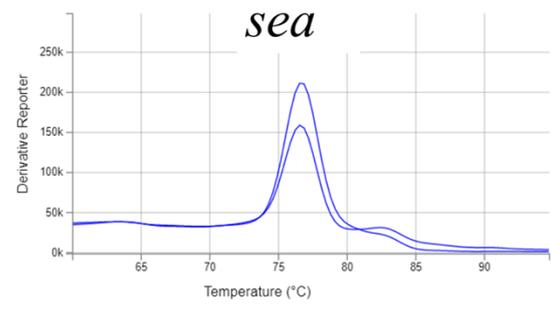
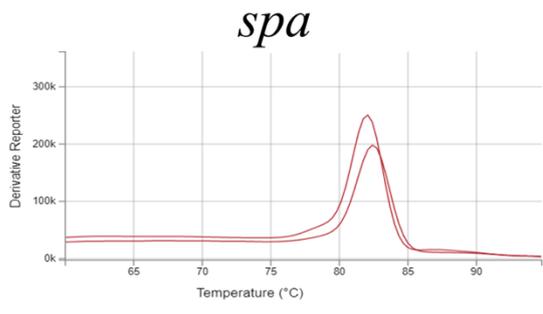
Primer name	Sequence (5'–3')	Length (bp)	T _m (°C)	Expected amplicon size (bp)
<i>SpAF</i>	ACGATCCAAGCCAAAGCACTAACG	24	50.0	149
<i>SpAR</i>	GCGTTGTTCTTCGTTCAAGTTAGGC	25	48.0	
<i>SEAF</i>	AAAATACAGTACCTTTGGAAACGGTT	26	54.1	92
<i>SEAR</i>	TTTCCTGTAAATAACGTCTTGCTTGA	26	53.9	
<i>SEBF</i>	ACACCCAACGTTTTAGCAGAGAG	23	57.3	81
<i>SEBR</i>	CCATCAAACCAGTGAATTTACTCG	24	53.7	
<i>SECIF</i>	AATAAAACGGTTGATTCTAAAAGTGTGAA	29	52.4	80
<i>SECIR</i>	ATCAAAATCGGATTAACATTATCCATTC	28	50.8	
<i>SEDF</i>	TGATTCTTCTGATGGGTCTAAAGTCTC	27	55.6	115
<i>SEDR</i>	GAAGGTGCTCTGTGGATAATGTTTT	25	55.0	
<i>mecAF</i>	GCTTTGGTCTTTCTGCATTCCT	22	55.6	91
<i>mecAR</i>	ACGTTCAATTTAATTTTGTTAAAGAAGATG	30	50.1	
<i>femBF</i>	AATTAACGAAATGGGCAGAAACA	23	52.3	93
<i>femBR</i>	TGCGCAACACCCTGAACTT	19	57.9	
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<i>SEBR</i>	CCATCAAACCAGTGAATTTACTCG	24	53.7	
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<i>SECIR</i>	ATCAAAATCGGATTAACATTATCCATTC	28	50.8	
<i>SEDF</i>	TGATTCTTCTGATGGGTCTAAAGTCTC	27	55.6	115
<i>SEDR</i>	GAAGGTGCTCTGTGGATAATGTTTT	25	55.0	
<i>mecAF</i>	GCTTTGGTCTTTCTGCATTCCT	22	55.6	91
<i>mecAR</i>	ACGTTCAATTTAATTTTGTAAAGAAGATG	30	50.1	
<i>femBF</i>	AATTAACGAAATGGGCAGAAACA	23	52.3	93
<i>femBR</i>	TGCGCAACACCCTGAACTT	19	57.9	

Table S2. Primers of bacterial housekeeping genes. The sets of forward and reverse primers for the candidate housekeeping genes are presented in 5' to 3' orientation,

Primer name	Sequence (5'–3')	Length (bp)	Tm (°C)	Expected amplicon size (bp)
<i>gyrAF</i>	CTACAAAGGGTCGTGGTGGTAAAGG	25	59.8	82
<i>gyrAR</i>	ATCGTCACTAAGCGTGCTAATGGC	24	59.7	
<i>gyrBF</i>	CGCAAGGACCTGAAAGACAC	20	56.6	114
<i>gyrBR</i>	GACCAGGAAGATCTCGGTCTC	21	57.1	
<i>eraF</i>	AACCACTCGCAACGCTTACAG	22	60.6	110
<i>eraR</i>	CCAGCACCCCTTCCCAACTCATG	22	61.3	
<i>SECAF</i>	TTCCGCCTCCCGCATTAGTCC	21	62.8	80
<i>SECAR</i>	ACGAAGAAGTCGCAAAGCTATG	24	59.7	
<i>dnaGF</i>	TTTCGGCTCATCGTTTCCCAAGG	23	60.2	128
<i>dnaGR</i>	TTAAGGCTCGTCAATCTGGTACTGG	25	58.5	

with their respective lengths, Tm, and amplicon sizes.



(i)

(ii)

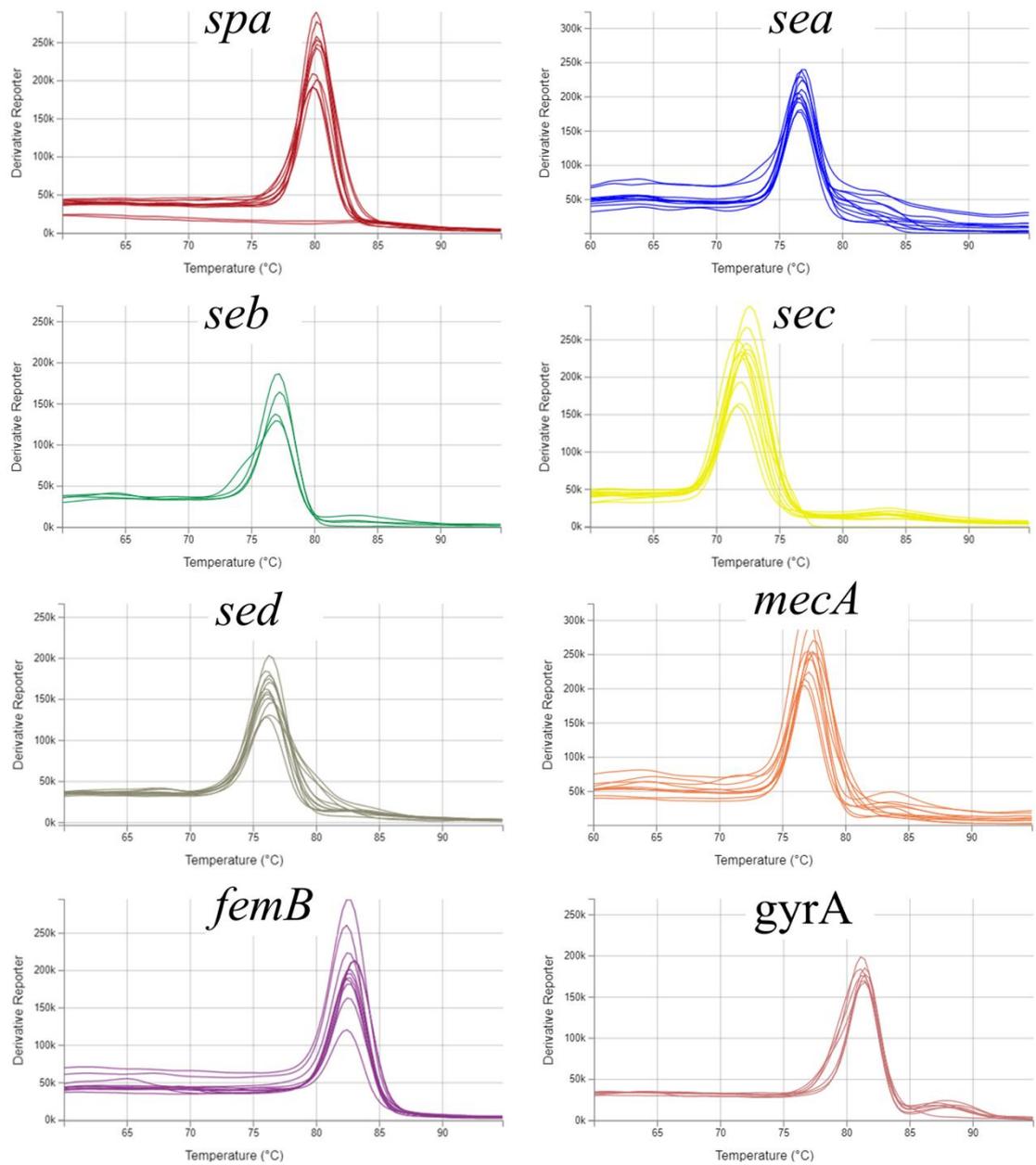


Figure S1. qPCR melt curve analysis for superantigen and MRSA gene primers. (i) Melt curves for reference *S. aureus* strains BNCC 139843 and BNCC 358401, demonstrating a single peak for each target gene (*SpA*, *SEA*, *SEB*, *SEC*, *SED*, *mecA*, *femB*, *gyrA*). (ii) Melt curves for ear swab DNA samples from Patient 1 and Participants 1–11, also showing single peaks for each primer set, confirming specific amplification in participant samples.