

Supplementary Data

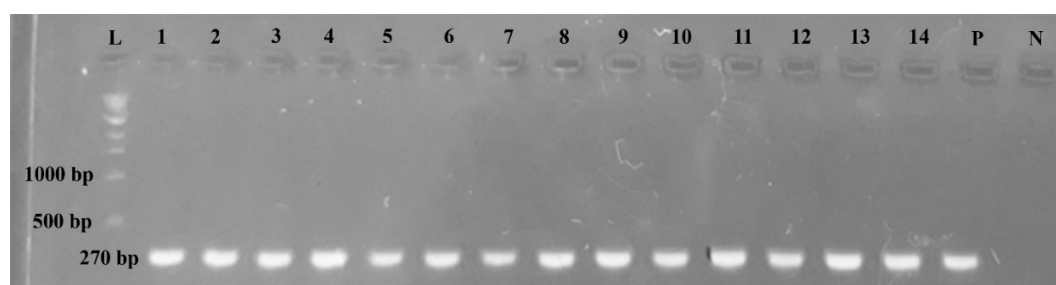


Figure S1. Amplification of *nuc* gene fragment (270 bp) through PCR from *Staphylococcus aureus* isolated phenotypically from clinical samples. Lanes 1-14 indicate representative *S. aureus* isolates (MR-1, MR-2, MR-3, MR-4, MR-5, MR-6, MR-7, MR-8, MR-9, MR-10, MR-13, MR-14, MR-15, and MR-33). Lane P, positive control; N, negative control; L, DNA marker.

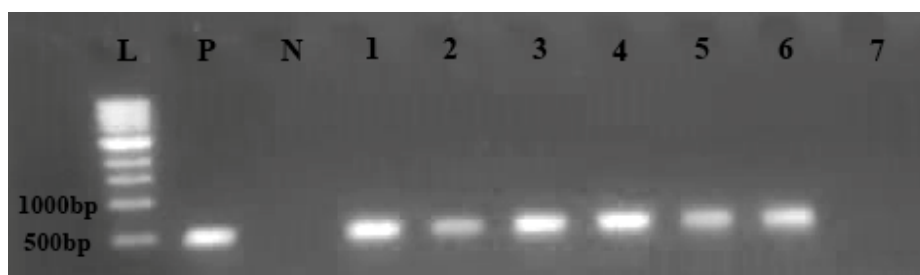


Figure S2. Amplification of *mecA* gene fragment (533 bp) through PCR from MRSA isolates. Lanes 1-6 indicate representative MRSA isolates (MR-1, MR-2, MR-5, MR-13, MR-14, and MR-33). MR-15 (lane 7) is *mecA*-negative. Lane P, positive control; N, negative control; L, DNA marker.

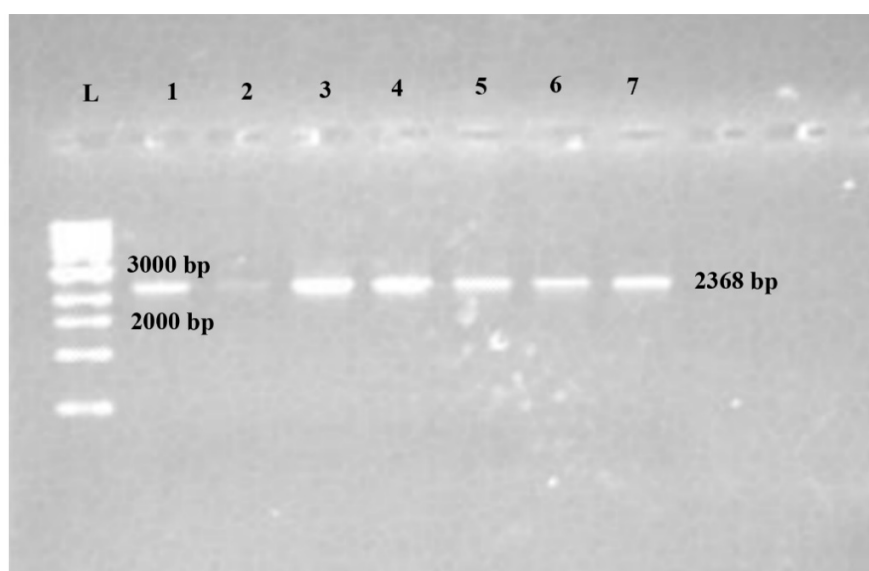


Figure S3. Amplification of the entire *mecA* gene region (2368 bp) through PCR from MRSA isolates. Lanes 1-7 indicate representative MRSA isolates (MR-1, MR-2, MR-5, MR-10, MR-13, MR-14, and MR-33). Lane P, positive control; N, negative control; L, DNA marker.