

## Supplementary

**Table S1. The sequence of the used primers, product size and PCR protocol of *mecA* and *mecC* genes.**

SCCmec type	Nucleotide sequence (5'-3')	PCR product Size (bp)	Ref	PCR protocol
<i>mecA</i>	F: GTAGAAATGACTGAACGTCCGATAA R: CCAATTCCACATTGTTTCGGTCTAA	310	[87]	Initial denaturation: 95°C for 1 min Amplification (30 cycles of): - Denaturation: 95°C for 30 s - Annealing: 50°C for 30 s - Extension: 72°C for 60 s Final extension: 72°C for 4 min The amplified product was identified by electrophoresis on 1.5% agarose gels using 100 bp DNA ladder.
<i>mecC</i>	F: GCTCCTAATGCTAATGCA R: TAAGCAATAATGACTACC	304	[15]	Initial denaturation: 95°C for 2 min Amplification (30 cycles of): - Denaturation: 94°C for 30 s - Annealing: 50°C for 30 s - Extension: 72°C for 30 s Final extension: 72°C for 4 min The amplified product was identified by electrophoresis on 1.5% agarose gels using 100 bp DNA ladder.

F, forward; R, reverse; bp, base pair; Ref, reference

**Table S2. Different bacterial and fungal isolates distribution in the collected clinical samples**

Isolated organism	Number	Sample
<b>Gram positive isolates</b>	210	
<i>Staphylococcus aureus</i>	118	Blood- urine-sputum-wound
CoNS	43	Blood- urine-CSF
<i>Enterococcus</i> spp	30	Blood- urine-wound
<i>Streptococcus</i> spp	19	Sputum-CSF
<b>Gram negative isolates</b>	307	
<i>E.coli</i>	82	Blood- urine-wound
<i>Klebsiella</i> spp	73	Blood- urine-sputum-wound-CSF
<i>Acinetobacter</i> spp	49	Blood- urine-sputum-wound-CSF
<i>Pseudomonas</i> spp	87	Blood- urine-sputum-wound
<i>Enterobacter</i> spp	4	Sputum-wound
<i>Stenotrophomonas</i> spp	12	Urine-sputum-wound
<b>Fungi</b>		
<i>Candida</i> spp	36	Urine-sputum-wound
<b>Total isolates</b>	553	

CoNS: coagulase-negative Staphylococci; CSF, cerebrospinal fluid; spp: species; *E.coli* : *Escherichia coli*