**Supplementary Materials and Methods**

**Multiplex MRSA-PCR and identification of MRSA from positive enrichment broths**

A 200 µL aliquot of each individual enrichment broth was DNA extracted using the BUGS´n BEADSTM STI/STI fast kit in a Bullet automated nucleic acid extractor (Nordiag A/S, Norway, now acquired by Diasorin S.p.a., Saluggia, Italy). A tri-plex real-time PCR assay with 400 nM of each primer and 150 nM of each probe (supplementary table) was used to identify *S. aureus* in 5 µL of the DNA extracts using 12.5 µL TaqMan® Fast Universal PCR Master Mix (2x), No AmpErase® UNG (Applied Biosystems, Stockholm, Sweden) in a 7500 Fast real time PCR system (Applied Biosystems) in a thermal cycling profile consisting of a pre PCR step for 10 min at 95oC followed by 38 cycles at 95oC for 15 s and 60oC for 30 s. Enrichment broths, positive for *mecA*, *nuc* Sa442 or both were inoculated onto CHROMagarTM Staph aureus (CHROMagarTM, Paris, France) and Columbia blood agar (Oxoid A/S, Roskilde, Denmark) biplates using a 10 µL loop per half. A 30 µg cefoxitin disk was placed in the primary streak on the CHROMagar half. *S. aureus* with zone diameters <25 mm were tested for *mecA* with PCR.

Supplementary table. Primers and probes for *S. aureus* quantification during the whole study period.

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| Name | Sequence and probe labelsa |
| Sa442 forward primer | CGTTGCATCGGAAACATTGTG |
| Sa442 reverse primer | GTATGACCAGCTTCGGTACTAC |
| Sa442 probe | Cy5-TCTGTATGTAAAAGCCGTCTTGAT-NFQb |
| nuc forward primer | CTGATAAATATGGACGTGGCTTAG |
| nuc reverse primer | GCAACTTTWGCYAARCCTTGAC |
| nuc probe | FAM-TGCTGATGGWAARATGGT-MGBc/NFQb |
| mecA forward primer | GATTATGGCTCAGGTACTGCTATCC |
| mecA reverse primer | ATGAAGGTGTGCTTACAAGTGCT |
| mecA probe | NED-CCTCAAACAGGTGAATT- MGBc/NFQb |

a All sequences in 5´to 3´direction. Ambiguities are according to IUPAC codes.

b Non fluorescent quencher

c Minor grove-binder modification