



Figure A2: Alignment of the microarray's probe and primer binding regions (1) in reverse complemented *icaC* alleles from *S. aureus* of different multilocus sequence types (ST) (created with MEGA v5.0 [2]). The microarray primer is used for linear amplification of the genomic region of interest, which subsequently binds to the oligonucleotide probe (binding regions highlighted by black squares). Yellow squares highlight the mismatches to the microarray probe and primer sequences within the binding sequences. Our results indicate that the single mismatch in the primer binding region of ST22's allele does not affect primer binding efficiency in the microarray, whereas the five mismatches in the probe binding region of the *icaC* allele of ST152 cannot be compensated and lead to a false negative typing result of the microarray.

References

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2. Tamura K, Peterson D, Peterson N, Stecher G, Nei M, and Kumar S. 2011. MEGA5: Molecular Evolutionary Genetics Analysis using Maximum Likelihood, Evolutionary Distance, and Maximum Parsimony Methods. Mol Biol Evol **28**:2731-2739.