

Figure S1. The *agr* system.

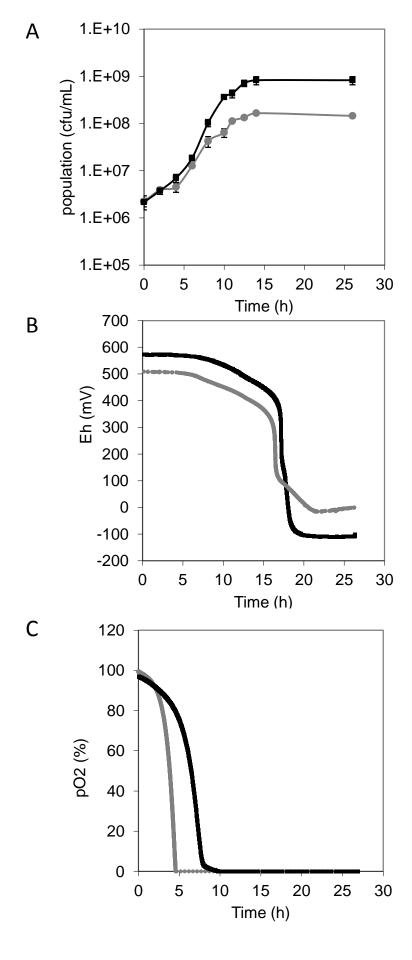


Figure S2. Kinetics of *S*. *aureus* growth (A), redox potential (Eh) (B) and partial oxygen pressure (pO₂) (C) during cultures of *S*. *aureus* MW2 alone (black squares) or in mixed cultures with *L*. *lactis* LD61 (grey circles), under the reference conditions with the addition of potassium ferricyanide.

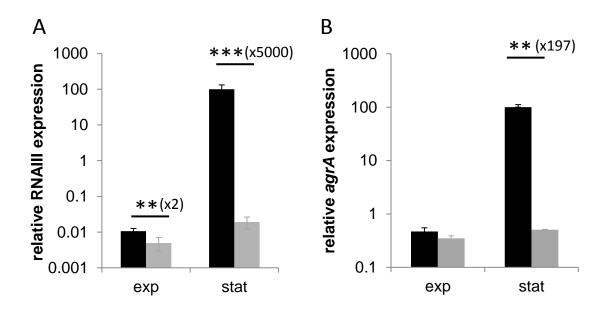


Figure S3. Expressions of RNAIII and *agrA* in *S. aureus* MW2 *srrA* in pure culture (black) and mixed culture with *L. lactis* LD61 (grey) under the reference conditions. The expressions of RNAIII (A) and *agrA* (B) were determined by qRT-PCR during exponential (exp), and stationary (stat) phases of growth and were expressed relative to those of RNAIII and *agrA* in the stationary phase in pure culture (100%), respectively. Significant changes of expression in pure vs. mixed cultures were determined for each time point using one-way analysis of variance, and are indicated by asterisks. **: P<0.01; ****: P<0.001.

 Table S1. List of primers used in the study

Primer name	Sequence (5'->3') ^a	Comments
BoxA2-srrAB-F-	GGA <u>GGATCC</u> GAAGTGAAAGCCCTAG	Amplification of
BamH1	AAAAAGGT	BoxA2 in S. aureus
		MW2
BoxA2-srrAB-R-	ATCAGCAAGTACGCGATGTG <u>CTCGAG</u>	Amplification of
XhoI	CTATTGGCCATTACTTGCTTCATGG	BoxA2 in S. aureus
		MW2
BoxB2-srrAB-F-	CCATGAAGCAAGTAATGGCCAA TAG	Amplification of
XhoI	<u>CTCGAG</u> CACATCGCGTACTTGCTGAT	BoxB2 in S. aureus
		MW2
BoxB2-srrAB-R-	AGA <u>AGATCT</u> TCATCAACCCACCAGGA	Amplification of
BglII	TTT	BoxB2 in S. aureus
		MW2
srrAB-up	AGACGATGAAGAAATGGATGCT	Validation of srrA
		deletion
srrAB-down	GTACCTTGTTTACCTCGCGTTC	Validation of srrA
a		deletion

^a restriction sites are underlined. Position of the stop codon inserted in the *srrA* sequence is indicated in bold.