

Table S2. Relative expression levels of stress response-associated genes in *S. aureus* mutant strains compared to SH1000.

Gene name	H ₂ O ₂ /stressless conditions expression ratio		<i>cymR</i> mutant/SH1000 expression ratio						
	SH1000	<i>cymR</i>	<i>cymR</i>	<i>perR</i>	<i>cymRperR</i>	<i>perRfur</i>	<i>cymRperRfur</i>	<i>fur</i>	<i>cymRfur</i>
<i>ahpF</i>	7.8	0.97	12.01	28.03	15.06	26.87	6.62	17.41	13.15
<i>dps</i>	22.8	9.29	4.40	82.71	13.14	92.52	4.85	2.67	6.89
<i>sodA</i>	0.98	0.54	5.05	1.08	5.89	1.36	3.64	1.44	5.05
<i>sodM</i>	0.59	0.81	2.86	1.15	3.53	1.78	2.08	1.74	4.44
<i>copA</i>	0.72	0.86	11.83	1.09	26.14	0.97	10.29	1.26	13.11

For qRT-PCR analysis, total RNA was extracted from *S. aureus* strains grown in TSB medium supplemented with 2 mM cystine. For H₂O₂ stress induction the bacteria were incubated with 20 mM H₂O₂ for 10 minutes. After reverse transcription, specific cDNAs were quantified by qRT-PCR using 16S rRNA gene for normalization. In bold are indicated the expression ratios > 2 of regulated genes.