

Table S1. Additional stress-regulated genes differentially expressed in the *S. aureus* $\Delta cymR$ mutant strain compared with strain SH1000

Gene name ^a (synonym)	Function/similarity	Transcriptome analysis ^b		Differential expression under stress conditions ^c
		$\Delta cymR$ / SH1000 expression ratio	P value	
SA1315	ferredoxin, putative	5.38	0.0129	Nitrite
SA1316	conserved hypothetical protein	2.09	<1.0E-16	H ₂ O ₂ , nitrite
SA0938	cytochrome d ubiquinol oxidase, subunit II	2.40	<1.0E-16	H ₂ O ₂ , nitrosative, nitrite
SA0937	cytochrome d ubiquinol oxidase, subunit I	2.36	<1.0E-16	H ₂ O ₂ , nitrosative, nitrite
SA1175	hypothetical protein	2.25	<1.0E-16	H ₂ O ₂
SA0509	conserved hypothetical protein	2.19	<1.0E-16	General (sigma B), nitrite
SA1589 <i>ribD</i>	riboflavin biosynthesis RibD hydrolase, haloacid dehalogenase-like family	2.01	0.0129	H ₂ O ₂ Nitrite
SA0517	transglycosylase domain protein	1.91	2.22E-16	Nitrite
SA1691	FMN oxidoreductase	1.83	1.18E-12	H ₂ O ₂ , nitrite
SA0817	conserved hypothetical protein	1.76	7.92E-06	H ₂ O ₂
SA0800	M23/M37 peptidase domain protein	1.72	1.00E-07	H ₂ O ₂ , nitrite
SA0205	riboflavin synthase, alpha subunit	1.67	3.81E-09	H ₂ O ₂
SA1588 <i>ribE</i>	alcohol dehydrogenase, zinc-containing	1.64	0.0129	Nitrite
SA1989*	putative DNA binding protein	1.64	1.71E-06	Nitrite
SA1235	conserved hypothetical protein	1.63	1.54E-08	Nitrite
SA2328	LexA repressor	1.60	0.00018	General (sigma B), H ₂ O ₂
SA1174 <i>lexA</i>	ABC transporter, ATP-binding protein	1.57	1.70E-07	H ₂ O ₂ General (sigma B)
SA0774	exonuclease	1.54	6.46E-07	H ₂ O ₂ , nitrosative, nitrite
SA1710	conserved hypothetical protein membrane protein, putative, authentic frameshift	1.52	1.30E-06	Nitrite
SA0526	negative regulator of competence	1.51	8.32E-05	H ₂ O ₂
SA2328	N-acetyltransferase family protein	1.50	3.33E-09	Nitrite
SA0857 <i>mecA</i> *	glutamine synthetase repressor	1.50	3.37E-06	H ₂ O ₂ , nitrite
SA2490	conserved hypothetical protein	1.49	4.29E-06	Nitrite
SA1149 <i>glnR</i>	TIGR00294	1.49	0.05	H ₂ O ₂ , nitrosative Nitrite
SA0524	site-specific recombinase XerD	1.47	7.29E-07	Nitrite
SA1328 <i>xerD</i> *	FemC protein, glutamine synthetase	1.46	1.07E-05	H ₂ O ₂ , nitrosative
SA1150 <i>glnA</i> *	RecA protein	1.45	0.0129	H ₂ O ₂ , nitrite
SA1128*	drug resistance transporter, EmrB/QacA subfamily	1.44	2.23E-05	H ₂ O ₂ , nitrite
SA2142*	conserved hypothetical protein	1.40	0.001	H ₂ O ₂ , nitrite
SA0412	conserved hypothetical protein	1.35	6.14E-07	H ₂ O ₂
SA2322	conserved hypothetical protein	0.71	0.00013	H ₂ O ₂
SA0747 <i>cspC</i>	cold-shock protein CspC	0.71	0.0089	Nitrite
SA1548	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative	0.71	0.0032	H ₂ O ₂
SA2485*	hypothetical protein	0.70	8.92E-05	General (sigma B)
SA1140 <i>glpF</i> *	glycerol uptake facilitator protein	0.70	8.78E-05	H ₂ O ₂
SA2197	conserved hypothetical protein	0.68	2.46E-06	H ₂ O ₂
SA0873*	conserved hypothetical protein	0.67	6.85E-06	Nitrite

SA2374	conserved hypothetical protein	0.66	5.02E-06	General (sigma B), H ₂ O ₂
SA1547*	PTS system, N-acetylglucosamine-specific component	0.65	6.25E-06	H ₂ O ₂ , nitrite
SA0617*	transporter, putative	0.63	0.01	H ₂ O ₂
SA0479		0.61	4.29E-08	H ₂ O ₂
SA0360*	conserved hypothetical protein	0.60	9.96E-06	General (sigma B), H ₂ O ₂
SA0341*	hypothetical protein	0.60	0.00018	H ₂ O ₂ , nitrite
SA2098	D-isomer specific 2-hydroxyacid dehydrogenase family protein	0.57	4.22E-10	Nitrite
SA0359	conserved hypothetical protein	0.57	0.005	H ₂ O ₂ , nitrite
SA2102*	formate dehydrogenase, alpha subunit, putative	0.55	4.26E-11	General (sigma B)
SA0996 <i>sdhB</i> *	succinate dehydrogenase, iron-sulfur protein	0.53	4.41E-09	Nitrosative, nitrite
SA0995 <i>sdhA</i> *	succinate dehydrogenase, flavoprotein subunit	0.51	3.46E-14	Nitrosative, nitrite
SA0682*	proton-dependent oligopeptide transporter family protein	0.51	1.23E-13	H ₂ O ₂
SA0131 <i>deoD</i> *	purine nucleoside phosphorylase	0.29	0.0052	H ₂ O ₂

a. The SA numbers (N315 strain) for *S. aureus* genes correspond to those of AureoList (<http://genolist.pasteur.fr/AureoList/>).

“*” indicates genes differentially expressed upon internalization of *S. aureus* in human epithelial cells [1].

b. The results obtained are representative of 8 hybridizations from 4 independent cultures in TSB medium with 2 mM cystine. The data sets generated were loaded into the GenoScript Database (<http://genoscript.pasteur.fr>)[2].

c. Differential expression of corresponding genes under indicated stress conditions including hydrogen peroxide (H₂O₂) [3], nitrite [4], nitrosative [5] and general (sigma B) [6] stresses.

References:

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4. Schlag S, Nerz C, Birkenstock TA, Altenberend F, Gotz F (2007) Inhibition of staphylococcal biofilm formation by nitrite. J Bacteriol 189: 7911-7919.
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