

**Table S4.** Virulence or host-interaction associated genes differentially expressed in the *S. aureus*  $\Delta cymR$  mutant strain compared to SH1000

Gene name <sup>a</sup> (synonym)	Function/similarity	Transcriptome analysis <sup>b</sup>		qRT-PCR <sup>c</sup>	Differential expression in strains mutant for virulence regulators <sup>d</sup>
		$\Delta cymR$ / SH1000 expression ratio	<i>P</i> value	$\Delta cymR$ / SH1000 expression ratio	
SA0363*	conserved hypothetical protein	0.18	0.00025		SarA
SA2353*	ssaA homolog	0.47	<1.0E-16	0.44	WalKR
SA0271	conserved hypothetical protein	0.50	1.71E-09		SarA, Rot, AgrA
SA1898	SceD protein, putative	0.51	2.97E-13	0.41	WalKR
SA0650	drug transporter	0.51	1.04E-13		MgrA
SA2343	hypothetical protein	0.51	1.87E-12		AgrA, SarA, MgrA
SA0675	ABC transporter, ATP-binding protein	0.51	0.025		Rot
SA2378*	glyoxalase family protein	0.54	1.01E-11	0.48	AgrA, SarA, MgrA, Rot
SA2082 <i>ureA</i>	urease, gamma subunit	0.54	1.03E-11		Rot, ArlR, MgrA
SA1747*	ABC transporter, ATP-binding protein	0.55	1.42E-06		SarA
SA2239	amino acid permease	0.57	5.50E-09		AgrA, MgrA
SA0443	conserved hypothetical protein	0.58	1.89E-09		MgrA
SA0432*	PTS system component	0.58	2.65E-09		AgrA
SA1965 <i>femD</i> *	phosphoglucosamine mutase	0.60	8.24E-09		
SA0672*	conserved hypothetical protein TIGR00370	0.60	9.69E-08		SarA, SaeSR
SA0244 <i>tagF</i>	teichoic acid biosynthesis protein F	0.63	3.09E-07	0.52	SarA
SA0523	glycosyl transferase, group 1	0.64	1.45E-06		SarA, Rot
SA0423	LysM domain protein	0.64	0.033		SarA
SA1985*	hypothetical protein	0.64	0.0019		SarA
SA0796 <i>dltD</i> *	extramembranal protein	0.65	1.08E-08	0.47	
SA2261	transporter, putative	0.65	2.58E-06		Rot
SA1956*	lytic regulatory protein	0.65	1.57E-05		MgrA, SarA
SA2171	hypothetical protein	0.66	3.66E-07		Rot
SA2088 <i>ureD</i> *	urease accessory protein UreD	0.66	3.75E-06		ArlSR, MgrA, Rot
SA2086 <i>ureF</i>	urease accessory protein UreF	0.67	9.48E-06		ArlSR, MgrA, Rot
SA2084 <i>ureC</i>	urease, alpha subunit	0.67	1.05E-05		ArlSR, MgrA, Rot
SA2331	hypothetical protein	0.67	1.29E-05		SarA
SA0905 <i>atl</i> *	bifunctional autolysin precursor D-alanine-D-alanyl carrier protein	0.67	9.78E-06		WalKR
SA0793 <i>dltA</i> *	ligase	0.68	0.044	0.51	
SA2441	glycosyl transferase, group 1	0.68	1.99E-05		
SA0794 <i>dltB</i> *	DltB protein	0.69	0.0028		
SA0651*	hypothetical protein	0.70	0.00016		Rot
SA1684*	conserved hypothetical protein	1.41	5.25E-05		AgrA, SarA
SA1194 <i>msrA</i>	methionine sulfoxide reductase	1.41	0.0011		Rot
SA2007	alpha-acetolactate decarboxylase, putative	1.44	1.28E-05		AgrA, ArlSR, MgrA, Rot
SA2006*	Map protein, putative	1.54	6.37E-09		AgrA, SarA, ArlR
SA1041 <i>pyrR</i>	pyrimidine operon regulatory protein	1.56	0.012		SarA, AgrA, MgrA
SACOL0673	hypothetical protein	1.62	2.17E-08		AgrA, SarA

SACOL1186	antibacterial protein	1.64	<1.0E-16		AgrA, SarA
SA1811	phospholipase C precursor	1.69	1.35E-05		SaeR
SA1131*	pyruvate ferredoxin oxidoreductase, alpha subunit, putative	1.77	1.40E-12		Rot
SACOL1187	antibacterial protein, phenol soluble modulins	2.07	8.88E-16	2.23	SarA
SA0914	chitinase-related protein	2.15	<1.0E-16		SarA, Rot
SA0395	conserved hypothetical protein	2.15	<1.0E-16		SarA, SaeSR
SA1490	YhjN protein; toxin production and resistance	2.21	<1.0E-16	3.77	SarA
SA0395	hypothetical protein, pathogen island	2.63	<1.0E-16	5.26	ArlSR, SarA, SaeSR
SAS016*	hypothetical protein	3.87	<1.0E-16		SarA

**a.** The gene numbers SACOL and SA correspond to *S. aureus* COL and N315 strain genomic sequence, respectively (<http://cmr.tigr.org/tigr-scripts/CMR/GenomePage.cgi?database=gsa>).

“\*” 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. The data sets generated were loaded into the GenoScript Database (<http://genoscript.pasteur.fr>)[2].

**c.** For qRT-PCR analysis, total RNA was extracted from *S. aureus* strains grown in TSB medium supplemented with 2 mM cystine.

**d.** Differential expression of corresponding genes in strains deficient for the indicated virulence regulators, including SarA [3-5], AgrA [3,4], ArlSR [6], SaeSR [7], Rot [8], MgrA [9] and WalKR [10].

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