Table S1: Differentially expressed genes in the Δ*rpoZ* mutant strain

Gene name/designation	Fold Change in $\Delta rpoZ$	Function
Hypothetical proteins		
SAUSA300_0431	+∞	Hypothetical protein
SAUSA300_1205	7.54	Hypothetical protein
SAUSA300_2493	7.32	Hypothetical protein
SAUSA300_2132	5.81	Hypothetical protein
SAUSA300_1606	5.42	Hypothetical protein
SAUSA300_0575	3.88	Hypothetical protein
SAUSA300_1739	3.83	Hypothetical protein
SAUSA300_0465	3.29	Hypothetical protein
SAUSA300_1335	3.22	Hypothetical protein
SAUSA300_1742	3.11	Hypothetical protein
SAUSA300_1746	2.92	Hypothetical protein
SAUSA300_0392	2.88	Hypothetical protein
SAUSA300_1740	2.84	Hypothetical protein
SAUSA300_1180	2.73	Hypothetical protein
SAUSA300_2131	2.58	Hypothetical protein
SAUSA300_1857	2.41	Hypothetical protein
SAUSA300_0779	2.4	Hypothetical protein
SAUSA300_1743	2.34	Hypothetical protein
SAUSA300_1759	2.31	Hypothetical protein
SAUSA300_1247	2.23	Hypothetical protein
SAUSA300_1915	2.21	Hypothetical protein
SAUSA300_0814	2.2	Hypothetical protein
SAUSA300_1701	2.12	Hypothetical protein
SAUSA300_0642	2.08	Hypothetical protein
SAUSA300_1582	2.07	Hypothetical protein
SAUSA300_2527	2.06	Hypothetical protein
SAUSA300_2236	-2.04	Hypothetical protein
SAUSA300_0824	-2.08	Hypothetical protein
SAUSA300_0177	-2.09	Hypothetical protein
SAUSA300_1863	-2.18	Hypothetical protein
SAUSA300_1748	-2.21	Transposase, frameshift
SAUSA300_1230	-2.39	Hypothetical protein
SAUSA300_1380	-2.62	Hypothetical protein
SAUSA300_0048	-2.9	Hypothetical protein
SAUSA300_0174	-3.02	Hypothetical protein
SAUSA300_0192	2.19	Hypothetical protein
SAUSA300_0805	-2.19	Hypothetical protein

Transport		
glpF	8.74	Glycerol uptake facilitator
SAUSA300_0208	4.17	Putative maltose ABC transporter, ATP-binding protein
ptsG	3.76	Glucose transporter subunit IIABC
SAUSA300_2466	3.67	ABC transporter permease protein
SAUSA300_0209	3.65	Putative maltose ABC transporter, maltose-binding protein
SAUSA300_2408	3.37	Oligopeptide permease, ATP-binding protein
SAUSA300_0941	3.07	Putative ferrichrome ABC transporter
SAUSA300_0210	2.98	Maltose ABC transporter, permease protein
4.5S RNA	2.74	Signal recognition particle
SAUSA300_2407	2.6	Peptide ABC transporter, ATP-binding protein
fhuA	2.4	Ferrichrome transport ATP-binding protein
opuD	2.39	Glycine betaine transporter
gntP	2.35	Gluconate permease
SAUSA300_2409	2.25	Oligopeptide permease
SAUSA300_0211	2.21	Maltose ABC transporter, permease protein
SAUSA300_0068	2.02	Cadmium-exporting ATPase, truncation
SAUSA300_2454	-2.05	ABC Transporter
tatC	-2.07	Sec-independent protein translocase
SAUSA300_2453	-2.1	ABC Transporter
SAUSA300_0176	-2.27	ABC transporter, permease protein
SAUSA300_0173	-2.33	Dipeptide/oligopeptide/nickel ABC transporter permease
SAUSA300_2557	-2.49	ABC transporter protein
SAUSA300_0613	-2.57	Putative Na^+/H^+ antiporter, MnhD component
SAUSA300_0175	-2.58	Putative lipoprotein/ transporter
SAUSA300_0614	-2.6	Putative Na^+/H^+ antiporter, MnhE component
Other		
SAUSA300_0045	7.99	HNH nucleases
SAUSA300_0471	4	Veg protein
sbrB	3.87	Small peptide encoding gene
comK	3.83	Competence transcription factor
SAUSA300_0538	3.7	Uncharacterized epimerase/dehydratase
SAUSA300_0328	2.74	Lipoate-protein ligase
SAUSA300_1198	2.53	Putative GTP-binding protein
cap5E	2.29	Capsular polysaccharide biosynthesis protein
SAUSA300_0821	2.23	SUF system FeS assembly protein
SAUSA300_2503	2.23	Secretory antigen SsaA
pknB	2.19	Serine/threonine kinase
typA	2.19	GTP-binding protein
SAUSA300_0474	2.1	Putative endoribonuclease, L-PSP
SAUSA300_0464	2.06	Predicted O-methyltransferase
scpB	2.04	Chromosome segregation and condensation protein B

SAUSA300_2512	2.01	Glyoxalase family protein
SAUSA300_0135	-2.04	Superoxide dismutase
SAUSA300_0534	-2.04	Putative amidohydrolases
SAUSA300_0795	-2.25	Thioredoxin like protein
SAUSA300_0985	-2.26	Hypothetical protein
SAUSA300_0234	-2.51	Putative flavohemoprotein
pcp	-3.52	CDD-2,6-dichloro-p-hydroquinone 1,2-dioxygenase
SAUSA300_0043	-9.73	Metallo-beta-lactamase/Zn-dependent hydrolase
Metabolism general		
gap	4.65	Glyceraldehyde-3-phosphate dehydrogenase 2
SAUSA300_0170	4.56	Aldehyde dehydrogenase
SAUSA300_0229	3.45	Acyl-CoA transferase
SAUSA300_0662	2.73	Acetyltransferase, GNAT family
sdhC	2.67	Succinate dehydrogenase, cytochrome b-558 subunit
acsA	2.45	Acetyl-coenzyme A synthetase
SAUSA300_0425	2.44	NADH dehydrogenase I, F subunit
SAUSA300_2484	2.38	3-hydroxy-3-methylglutaryl CoA synthase
gltA	2.37	Citrate synthase II
SAUSA300_0945	2.34	Isochorismate synthase family protein
SAUSA300_0424	2.32	Putative Cobalamin protein
sucB	2.21	Dihydrolipoyllysine-residue succinyltransferase
icd	2.14	Isocitrate dehydrogenase
sdhB	2.12	Succinate dehydrogenase, iron-sulfur subunit
SAUSA300_1986	2.05	Nitroreductase family protein
sucA	2.03	2-oxoglutarate dehydrogenase, E1 component
SAUSA300_1894	-2	Nicotinate phosphoribosyltransferase
SAUSA300_2316	-2.15	Acetyltransferase
SAUSA300_2475	-2.27	Acyl-CoA thioester hydrolase
budA 2736735..2737440)	-2.32	Alpha-acetolactate decarboxylase
folP	-2.53	Dihydropteroate synthase
panB	-2.83	3-methyl-2-oxobutanoate hydroxymethyltransferase
SAUSA300_0343	-2.84	Acetyltransferase
Regulation		
gntR	5.78	Transcriptional regulator, GntR family
malR	4.94	Transcriptional regulator, maltose operon repressor
scrR	3.3	Sucrose operon repressor
SAUSA300_0621	2.92	MntR Mn Repressor
treR	2.78	Trehalose operon Repressor
SAUSA300_2310	2.77	Putative transcriptional regulator
nsaS	2.74	NsaS Histidine Kinase
sarA	2.66	Staphylococcal accessory regulator A

SAUSA300_0954	2.61	Transcriptional regulator, MarR family
SAUSA300_0095	2.26	LysR Regulator, LysR family
SAUSA300_0023	2.2	YycI protein
SAUSA300_2530	2.08	Transcriptional regulator, TetR family
SAUSA300_0090	2.05	Hypothetical protein
SAUSA300_1583	-2	Cystine metabolism regulator
SAUSA300_2509	-2.07	Transcriptional regulatory, TetR family
nirR	-2.12	Nitrite reductase transcriptional regulator
argR	-2.19	Arginine repressor homolog
SAUSA300_0110	-2.41	Transcriptional Regulator, GntR family
Translation		
rpsO	5.08	30S ribosomal protein S15
rpmB	3.5	50S ribosomal protein L28
rumA	3.41	RNA methyltransferase
SAUSA300_2037	3.31	ATP-dependent RNA helicase
rpsB	2.91	30S ribosomal protein S2
infC	2.91	Translation initiation factor IF-3
rplA	2.67	Ribosomal protein L1
rplM	2.48	50S ribosomal protein L13
rpsI	2.37	30S ribosomal protein S9
rluB	2.3	Pseudouridine synthase B
rplT	2.28	50S ribosomal protein L20
rpmJ	2.27	50S ribosomal protein L36
rpsT	2.19	30S ribosomal protein S20
SAUSA300_0531	2.13	30S ribosomal protein S7
rpsD	2	30S ribosomal protein S4
SAUSA300_1823	-2.38	tRNA-Ser
SAUSA300_1827	-2.42	tRNA-Met
Phage proteins		
SAUSA300_1981	4.03	Phage terminase family protein
SAUSA300_1959	3.48	PhiPVL ORF044-like protein
SAUSA300_1943	2.94	Phi77 ORF040-like protein
SAUSA300_1966	2.82	Phi77 ORF014-like protein, phage anti-repressor protein
SAUSA300_1933	2.67	Hypothetical phage protein
SAUSA300_1962	2.63	PhiPVL ORF39-like protein
SAUSA300_1968	2.05	Putative phage transcriptional regulator
SAUSA300_1926	-2.02	Phi77 ORF044-like protein
SAUSA300_1954	-2.13	PhiPVL ORF050-like protein
SAUSA300_1948	-2.21	Phi77 ORF069-like protein
SAUSA300_1412	-2.49	PhiSLT ORF 50-like protein
SAUSA300_1953	-2.68	PhiPVL ORF051-like protein

SAUSA300_1951	-3.06	PhiPVL ORF052-like protein
SAUSA300_1952	-3.81	Phi083 ORF027-like protein
SAUSA300_1945	-7.94	Phi77 ORF071-like protein
Virulence determinats		
mecA	2.78	Penicillin-binding protein 2a
SAUSA300_1059	2.64	Staphylococcal superantigen like protein 12
hlgA	2.53	Gamma-hemolysin, component A
SAUSA300_1058	2.42	Alpha-hemolysin
SAUSA300_0033	2.21	Methicillin resistance regulator protein
splE	-2.02	Serine protease
sak	-2.11	Staphylokinase
nuc	-2.13	Nuclease
splB	-2.44	Serine protease
SAUSA300_0883	-2.54	Eap/Map protein
SAUSA300_2087	-2.73	Putative peptidase
lukF-PV	-3.13	Panton-Valentine leukocidin, LukF-PV
lukS-PV	-3.4	Panton-Valentine leukocidin, LukS-PV
aur	-3.74	Zinc metalloproteinase aureolysin
Purine and pyrimidne metabolism		
deoD	3.79	Purine nucleoside phosphorylase
purD	2.76	Phosphoribosylamine--glycine ligase
purS	2.67	Phosphoribosylformylglycinamidine synthase
purN	2.55	Phosphoribosylglycinamide formyltransferase
purH	2.5	Bifunctional purine biosynthesis protein
xseB	2.44	Exodeoxyribonuclease VII, small subunit
purM	2.11	Phosphoribosylformylglycinamidine cyclo-ligase
purB	2.08	Adenylosuccinate lyase
SAUSA300_2234	-2.32	Purine nucleosidase
Membrane/lipoproteins		
SAUSA300_0724	2.49	Putative lipoprotein
SAUSA300_2448	2.35	Putative membrane protein
SAUSA300_1685	2.23	Putativ membrane protein
SAUSA300_0922	2.1	Membrane protein
SAUSA300_2355	-2.23	Putative lipoprotein
pfoR	-2.47	Perfringolysin O regulator protein
SAUSA300_0443	-2.49	Putative Membrane protein
SAUSA300_0233	-2.64	Putative Membrane protein
SAUSA300_0410	-3.18	Staphylococcal tandem lipoprotein

Sugar metabolism		
pfkA	-2.79	6-phosphofructokinase
gpmA	-2.04	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
sdaAB	2.24	L-serine dehydratase, beta subunit
gntK	3.14	Gluconate kinase
murQ	3.4	N-acetylmuramic acid-6-phosphate etherase
SAUSA300_2455	3.54	Fructose-1,6-bisphosphatase
treC	3.69	Alpha-phosphotrehalase
pckA	3.87	Phosphoenolpyruvate carboxykinase
SAUSA300_1456	5.52	Alpha-amylase
Stress response/repair		
SAUSA300_0777	4.01	Cold shock protein C
SAUSA300_0816	3.44	CsbD-like protein
lexA	2.89	LexA repressor
SAUSA300_2639	2.88	Cold shock protein D
asp23	2.39	Alkaline shock protein 23
SAUSA300_1549	2.37	ComE operon protein I
clpB	2.31	Chaperone
recA	2.14	Recombinase A
Amino acid metabolism		
putA	6.78	Proline dehydrogenase
ald	2.08	Alanine dehydrogenase
leuD	2.06	3-isopropylmalate dehydratase, small subunit
SAUSA300_0119	-2.05	Ornithine cyclodeaminase
SAUSA300_0952	-2.75	Aminotransferase, class I
PTS system components		
treP	3.89	PTS system, trehalose-specific IIBC component
SAUSA300_2324	3.72	PTS system, sucrose-specific IIBC component
SAUSA300_0332	3.45	PTS system, IIA component
SAUSA300_0331	2.74	PTS IIB - ascorbate, lactose or cellobiose
ptsG	2.17	PTS system, glucose-specific IIABC component
Cell wall		
SAUSA300_1702	4.86	Cell wall surface anchor family protein
SAUSA300_0703	2.84	Lipoteichoic acid synthase
lytN	2.31	Cell wall hydrolase
SAUSA300_2435	2.01	Cell wall surface anchor family protein

Replication		
SAUSA300_1344	2.95	Putative DNA-replication protein, DnaD
SAUSA300_1042	2.15	DNA polymerase IV (family X)
nrdG	-3.48	Anaerobic ribonucleotide reductase, small subunit
nrdD	-4.59	Anaerobic ribonucleotide reductase, large subunit
Lipid Metabolism		
lip	3.67	Triacyglycerol lipase
acpP	3.25	Acyl carrier protein
plsX	2.11	Phosphate acyltrasferase
estA	-2.33	Tributyrin esterase
Transcription		
rpoC	2.6	RNAP Beta' subunit
nusA	2.11	Transcription elongation factor
rpoZ	-10.03	RNAP omega subunit

Table S2: List comparing the 20 most downregulated genes in a *S. aureus* SH1000 σ^B mutant strain (which have homologues in USA300) to the alterations in transcript abundance of the homologue genes in a USA300 Δ*rpoZ* strain.

Feature ID SH1000	Fold-Change (*sigB::tet*)	Feature ID USA300	Gene name	Fold Change (Δ*rpoZ*)
SAOUHSC_00624	-∞	SAUSA300_0609		-1.61
SAOUHSC_02442	-∞	SAUSA300_2143		-1.10
SAOUHSC_02882	-∞	SAUSA300_2502		1.41
SAOUHSC_02443	-15,213.97	SAUSA300_2144		1.31
SAOUHSC_00845	-4,178.80	SAUSA300_0816		3.44
SAOUHSC_02441	-3,188.61	SAUSA300_2142	*asp23*	2.39
SAOUHSC_02444	-1,540.56	SAUSA300_2145		-1.16
SAOUHSC_00356	-667.21	SAUSA300_0372		1.11
SAOUHSC_01729	-546.86	SAUSA300_1581		1.45
SAOUHSC_00358	-321.83	SAUSA300_0374		1.86
SAOUHSC_02466	-142.55	SAUSA300_2164		1.52
SAOUHSC_02387	-139.11	SAUSA300_2097		-1.39
SAOUHSC_03032	-97.75	SAUSA300_2629		-1.13
SAOUHSC_02774	-95.56	SAUSA300_2418		-1.08
SAOUHSC_01730	-89.95	SAUSA300_1582		2.07
SAOUHSC_02772	-77.38	SAUSA300_2416		1.13
SAOUHSC_00831	-75.12	SAUSA300_0786		1.19
SAOUHSC_02880	-70.09	SAUSA300_2500		1.64
SAOUHSC_02881	-62.08	SAUSA300_2501		1.44
SAOUHSC_02812	-54.8	SAUSA300_2447		1.90

Table S3: List comparing the 20 most upregulated genes in a *S. aureus* SH1000 σ^B mutant strain (which have homologues in USA300) to the alterations in transcript abundance of the homologue genes in a USA300 Δ*rpoZ* strain.

Feature ID SH1000	Fold-Change (*sigB::tet*)	Feature ID USA300	Gene name	Fold Change (Δ*rpoZ*)
SAOUHSC_00260	∞	SAUSA300_0281		-1.45
SAOUHSC_01315	∞	SAUSA300_1221		1.20
SAOUHSC_00069	80.09	SAUSA300_0113	*spa*	-1.54
SAOUHSC_02821	75.93	SAUSA300_2454		-2.05
SAOUHSC_00818	29.22	SAUSA300_0776	*nuc*	-2.13
SAOUHSC_03002	21.68	SAUSA300_2600	*icaA*	-1.06
SAOUHSC_02820	16.26	SAUSA300_2453		-2.10
SAOUHSC_00674	13.42	SAUSA300_0654	*sarX*	-1.50
SAOUHSC_00259	11.98	SAUSA300_0280		1.01
SAOUHSC_00913	11.1	SAUSA300_0878		-1.68
SAOUHSC_00072	10.88	SAUSA300_0116	*sirB*	1.19
SAOUHSC_02461	10.74	SAUSA300_2160		1.19
SAOUHSC_00244	9.97	SAUSA300_0266		-1.77
SAOUHSC_03004	9.64	SAUSA300_2601	*icaB*	-1.41
SAOUHSC_00492	9.19	SAUSA300_0495		1.01
SAOUHSC_02639	7.73	SAUSA300_2305		-1.21
SAOUHSC_00250	7.03	SAUSA300_0272		1.07
SAOUHSC_03036	6.24	SAUSA300_2633		1.00
SAOUHSC_01488	6.23	SAUSA300_1361		-1.12
SAOUHSC_01941	6.02	SAUSA300_1757	*splB*	-2.44