

Supplementary Material

Table S1. Primers used for quantitative real-time PCR.

SEQUENCE (5'-3')	PRIMER
ACGGTATCAACGTTTGCCGGTGA	Sa-Ehp-For
GCTCTTTGTGCTTTACGGTGTGTTGC	Sa-Ehp-Rev
AACAGCAGATGCGAGCGAAGG	Sa-Efb-For
TGCATCAGTTTTCGCTGCTGGT	Sa-Efb-Rev
AGCCCCATCACTCGGTGGTAA	Sa-HlgC-For
TGAATTCGCTTTGACGCCCA	Sa-HlgC-Rev
AAGCAATCGCTGACGCTGGT	Sa-FabH-For
AGGCAACTTTGCCCGTCCCTA	Sa-FabH-Rev
AGGTACCGAGCCAGCTAAAGGT	Sa-PlsX-For
CGCCATCCATTAATGTCTTCGCTTCA	Sa-PlsX-Rev
GCCGATGTGGATGGAGCGCA	Sa-GyrB-For
AAAGAGCGCGGTGCTCAGGG	Sa-GyrB-Rev
CCATCTGGAGTAGGTAAAGG	Sa-Gmk-For
CTACGCCATCAACTTCAC	Sa-Gmk-Rev

Table S2. Gene expression changes following AFN-1252 treatment.

S. aureus genes with significantly ($p < 0.05$) different expression levels (± 1.4 fold) following a 15 minute treatment with 50 ng/ml AFN-1252. The data was abstracted from the complete dataset deposited in NCBI's Gene Expression Omnibus(10) and are accessible through GEO Series accession number GSE19400 (<http://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE19400>).

Locus Tag	Gene	AFN/DMSO ^a	p-value	Function
SA0165		-2.05	0.000	similar to α -helical coiled-coil protein SrpF
SA0166		-1.80	0.005	ABC transporter
SA0167		-1.70	0.007	similar to membrane lipoprotein SrpL
SA0168		-2.08	0.008	similar to ABC transporter
SA0169		-2.20	0.000	acyl-CoA dehydrogenase
SA0198	<i>oppF</i>	-1.71	0.008	putative peptide ABC transporter protein ATP-binding
SA0199	<i>oppB</i>	-1.84	0.008	putative peptide ABC transporter integral membrane protein
SA0200		-2.46	0.000	putative peptide ABS transporter permease
SA0201	<i>rlp</i>	-2.00	0.003	RGD-containing lipoprotein
SA0202		-2.25	0.000	γ -glutamyltranspeptidase precursor
SA0213		-1.87	0.020	putative integral membrane protein
SA0219	<i>pflA</i>	-1.52	0.035	pyruvate formate-lyase 2 activating enzyme
SA0309	<i>geh</i>	-2.00	0.002	lipase precursor
SA0368		-2.31	0.000	putative excitatory amino acid transporter
SA0395		-2.86	0.000	hypothetical protein [Pathogenicity island SaPln2]
SA0397	<i>lpl2</i>	-1.54	0.040	hypothetical protein [Pathogenicity island SaPln2]
SA0411	<i>ndhF</i>	-1.97	0.000	NADH dehydrogenase subunit 5
SA0412		-2.24	0.001	hypothetical protein
SA0418	<i>cysM</i>	-2.13	0.000	cysteine synthase
SA0419	<i>metB</i>	-2.38	0.019	cystathionine γ -synthase
SA0420		-1.78	0.001	putative amino acid ABC transporter
SA0421		-1.56	0.002	putative amino acid ABC transporter
SA0422		-1.75	0.001	putative D-methionine-binding lipoprotein metQ precursor
SA0427		1.41	0.011	uncharacterized membrane protein
SA0471	<i>cysK</i>	-1.55	0.002	cysteine synthase
SA0660	<i>saeS</i>	-1.77	0.009	two-component sensor kinase
SA0661	<i>saeR</i>	-2.45	0.003	two-component response regulator
SA0662	<i>saeQ</i>	-4.94	0.000	hypothetical protein
SA0663	<i>saeP</i>	-4.40	0.000	hypothetical protein
SA0746		-2.36	0.000	thermonuclease precursor
SA0792		1.44	0.001	hypothetical protein
SA0793	<i>dltA</i>	1.62	0.006	D-alanine--poly(phosphoribitol)ligase subunit 1
SA0822	<i>argG</i>	-1.60	0.020	argininosuccinate synthase
SA0842	<i>fabH</i>	2.86	0.000	3-oxoacyl-[acyl-carrier-protein] synthase III
SA0843	<i>fabF</i>	1.79	0.005	3-oxoacyl-[acyl-carrier-protein] synthase II
SA0879	<i>htrA</i>	1.44	0.027	periplasmic serine protease
SA0891		-1.50	0.012	iron(III) ABC transporter, periplasmic protein
SA1000	<i>ehp</i>	-3.63	0.001	fibrinogen-binding protein precursor
SA1003	<i>efb</i>	-3.49	0.000	fibrinogen-binding protein precursor
SA1007		-1.70	0.009	α -hemolysin precursor (α -toxin)
SA1071	<i>fapR</i>	2.08	0.000	transcriptional regulator of fatty acid biosynthesis
SA1072	<i>plsX</i>	1.97	0.000	acyl-phosphate synthase
SA1073	<i>fabD</i>	1.73	0.000	malonyl coenzyme A-acyl carrier protein transacylase
SA1074	<i>fabG</i>	1.50	0.001	3-oxoacyl-[acyl-carrier protein] reductase
SA1140	<i>glpF</i>	1.58	0.001	glycerol uptake facilitator protein

SA1141	<i>glpK</i>	1.43	0.021	glycerol kinase
SA1142	<i>glpD</i>	1.86	0.000	anaerobic glycerol-3-phosphate dehydrogenase subunit A
SA1160	<i>nuc</i>	1.45	0.044	thermonuclease precursor
SA1175		-1.50	0.012	hypothetical protein
SA1188	<i>parE</i>	1.46	0.003	DNA gyrase B subunit
SA1224		1.50	0.002	probable ATP-binding component of ABC transporter
SA1270		-1.53	0.002	solute carrier family 7
SA1271		-1.65	0.005	threonine dehydratase
SA1272		-1.55	0.009	nicotinamide nucleotide transhydrogenase subunit α 1
SA1319		-1.71	0.026	hypothetical protein
SA1432		-2.06	0.000	branched-chain amino acid transport system II carrier protein
SA1433		-1.94	0.001	Lamb
SA1434		-2.02	0.002	similar to acetyl-CoA carboxylase α chain
SA1435		-2.13	0.000	similar to biotin carboxyl carrier subunit
SA1436		-1.80	0.000	putative urea carboxylase
SA1437		-1.65	0.000	urea carboxylase
SA1547	<i>ptaA</i>	1.45	0.034	PTS system, IIBC component
SA1550	<i>tyrS</i>	1.43	0.015	tyrosyl-tRNA synthetase
SA1586	<i>ribH</i>	1.46	0.026	6,7-dimethyl-8-ribityllumazine synthase
SA1587	<i>ribA</i>	1.41	0.008	riboflavin biosynthesis
SA1675		-1.60	0.008	amino acid ABC transporter
SA1746		-1.62	0.023	hypothetical protein
SA1747		-1.54	0.007	ATP-binding transport protein natA
SA1748		-1.62	0.018	transcriptional repressor
SA1750		-2.05	0.002	truncated cell surface protein map-w
SA1752		-8.18	0.000	truncated β -hemolysin
SA1811	<i>hly</i>	-3.63	0.000	phospholipase C precursor (β -hemolysin)
SA1812		-2.72	0.005	γ -hemolysin component B precursor
SA1820		-1.59	0.012	hypothetical protein [Pathogenicity island SaPI _{n1}]
SA1849		-2.21	0.002	hypothetical protein
SA1850		-2.06	0.001	putative transport permease
SA2080		-1.49	0.013	similar to butyryl-CoA dehydrogenase
SA2094		-1.58	0.002	sodium:proton antiporter
SA2121	<i>hutI</i>	-1.52	0.003	imidazolonepropionase
SA2169		1.48	0.007	hypothetical transcription regulatory protein
SA2206	<i>sbi</i>	-3.72	0.001	immunoglobulin G binding protein A precursor
SA2207	<i>hlyA</i>	-4.21	0.000	γ -hemolysin component A precursor
SA2208	<i>hlyC</i>	-4.99	0.000	γ -hemolysin component C precursor
SA2209	<i>hlyB</i>	-4.78	0.001	γ -hemolysin component B precursor
SA2264		-1.70	0.014	hypothetical protein
SA2405	<i>betA</i>	-2.71	0.002	betaine aldehydedehydrogenas
SA2406	<i>gbsA</i>	-2.47	0.000	betaine aldehydedehydrogenas
SA2408	<i>cutT</i>	-2.01	0.001	choline-glycine betaine transporter
SA2428	<i>arcA</i>	1.59	0.002	arginine deiminase
SA2434		1.40	0.004	PTS system, fructose-specific IIA:FPr component
SA2460	<i>icaD</i>	-1.54	0.007	intercellular adhesion protein D
SA2462	<i>icaC</i>	-1.61	0.003	intercellular adhesion protein C

^aRatio of expression levels in cells treated with AFN-1252 to DMSO control.