

TABLE A2. Genes with significantly decreased expression of at least 2.5-fold in this study¹

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
Adaption to atypical conditions					
SA0747	<i>cspC</i>	cold-shock protein C	0.65	0.84	0.40
SA1984	<i>asp23</i>	alkaline shock protein 23, ASP23	0.64	2.24	0.32
Cell division					
SA0905	<i>atl</i>	autolysin	0.42	0.49	0.18
SA2499	<i>gidB</i>	glucose inhibited division protein B	0.57	0.36	0.56
SA2500	<i>gidA</i>	glucose inhibited division protein A	0.55	0.34	0.51
Cell wall related genes					
SA0423		hypothetical protein, similar to autolysin	0.58	0.20	0.20
SA0793	<i>dltA</i>	D-alanine-D-alanyl carrier protein ligase	0.63	0.22	0.24
SA2100		hypothetical protein, similar to autolysin E	0.46	0.32	0.30
SA2354		hypothetical protein, similar to acyltransferase	0.73	0.37	0.47
Membrane bioenergetics (electron transport chain and ATP synthase)					
SA0910		hypothetical protein, similar to quinol oxidase polypeptide IV QoxD	0.41	0.20	0.12
SA0911	<i>qoxC</i>	Quinol oxidase polypeptide III QoxC	0.34	0.19	0.14
SA0912	<i>qoxB</i>	Quinol oxidase polypeptide I QoxB	0.37	0.21	0.11
SA0913		hypothetical protein, similar to quinol oxidase polypeptide II QoxA	0.40	0.24	0.19
SA0965	<i>ctaB</i>	cytochrome <i>caa3</i> oxidase (assembly factor) homologue	0.57	0.40	0.35
SA1909	<i>atpF</i>	ATP synthase B chain	0.72	0.38	0.49
SA1910	<i>atpE</i>	ATP synthase C chain	0.79	0.43	0.38
SA1911	<i>atpB</i>	ATP synthase A chain	0.66	0.43	0.39
Metabolism of amino acids					
SA0180		hypothetical protein, similar to branched-chain amino acid transport system carrier protein	0.54	0.34	0.33
SA2095		hypothetical protein, similar to D-octopine dehydrogenase	0.45	0.49	0.33
Metabolism of carbohydrates					
SA0562	<i>adh1</i>	alcohol dehydrogenase I	2.23	1.59	0.30
SA0994	<i>sdhC</i>	succinate dehydrogenase cytochrome b-558	0.58	0.62	0.35
SA0996	<i>sdhB</i>	succinate dehydrogenase iron-sulfur protein subunit	0.62	0.58	0.32
SA2008	<i>alsS</i>	alpha-acetolactate synthase	0.73	0.39	0.29
SA2102		formate dehydrogenase homologue	0.47	0.86	0.23
Metabolism of coenzymes and prosthetic groups					
SA0665		coenzyme PQQ synthesis homologue	0.73	0.38	0.54
SA0666		hypothetical protein 6-pyruvoyl tetrahydropterin synthase homologue	0.61	0.34	0.38
SA1494	<i>hemC</i>	porphobilinogen deaminase	0.65	0.33	0.42
SA1495	<i>hemX</i>	HemA concentration negative effector HemX	0.68	0.37	0.37
SA1537		hypothetical protein, similar to thiamine biosynthesis protein ThiI	0.65	0.35	0.43
SA1538		hypothetical protein, similar to iron-sulfur cofactor synthesis protein NifZ	0.52	0.31	0.48
SA1919		hypothetical protein, similar to protoporphyrinogen oxidase (HemK)	0.44	0.39	0.39
Metabolism of lipids					
SA0820	<i>glpQ</i>	glycerophosphoryl diester phosphodiesterase	1.11	0.47	0.29
Metabolism of nucleotides and nucleic acids					
SA0373	<i>xprT</i>	xanthine phosphoribosyltransferase	0.41	0.13	0.43
SA0511		hypothetical protein, similar to UDP-glucose 4-epimerase related protein	0.57	0.52	0.33
SA0927		conserved hypothetical protein	0.75	0.69	0.22
SA1043	<i>pyrB</i>	aspartate transcarbamoylase chain A	0.92	2.22	0.05
SA1044	<i>pyrC</i>	dihydroorotase	0.98	2.06	0.03
SA1045	<i>pyrAA</i>	carbamoyl-phosphate synthase small chain	1.05	1.58	0.07
SA1046	<i>pyrAB</i>	carbamoyl-phosphate synthase large chain	0.87	1.58	0.08
SA1047	<i>pyrF</i>	orotidine-5-phosphate decarboxylase	0.81	1.65	0.05
SA1048	<i>pyrE</i>	orotate phosphoribosyltransferase	0.87	1.43	0.07
SA1461	<i>apt</i>	adenine phosphoribosyl transferase	0.71	0.62	0.39
SA1921	<i>tdk</i>	thymidine kinase	0.61	0.50	0.39

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TABLE A2 - Continued

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
SA2027	<i>adk</i>	adenylate kinase	0.53	0.31	0.33
Pathogenic factors (toxins and colonization factors)					
SA0270		hypothetical protein, similar to secretory antigen precursor SsaA	0.67	0.51	0.13
SA0276		conserved hypothetical protein, similar to diarrheal toxin	0.84	0.34	0.99
SA0519	<i>sdrC</i>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	0.53	0.27	0.08
SA0521	<i>sdrE</i>	Ser-Asp rich fibrinogen-binding, bone sialoprotein-binding protein	1.74	1.40	0.32
SA0587		lipoprotein, streptococcal adhesin PsaA homologue	0.76	1.21	0.25
SA0742	<i>clfA</i>	fibrinogen-binding protein A, clumping factor	0.80	1.21	0.22
SA0746		staphylococcal nuclease	0.99	0.26	0.65
SA1645	<i>yentI</i>	enterotoxin YentI [Pathogenicity island SaPI _n 3]	1.28	1.30	0.39
SA1647	<i>sem</i>	enterotoxin SEM [Pathogenicity island SaPI _n 3]	1.47	1.31	0.36
SA2093	<i>ssaA</i>	secretory antigen precursor SsaA homologue	0.57	0.23	0.34
SA2206	<i>sbi</i>	IgG-binding protein SBI	0.87	0.33	1.30
SA2290	<i>fnbB</i>	fibronectin-binding protein homologue	0.49	0.27	1.29
SA2291	<i>fnb</i>	fibronectin-binding protein homologue	0.51	0.32	1.15
SA2353		hypothetical protein, similar to secretory antigen precursor SsaA	0.69	0.38	0.78
SA2356	<i>isaA</i>	immunodominant antigen A	0.73	0.51	0.36
SA2423	<i>clfB</i>	clumping factor B	0.81	0.90	0.17
Phage-related functions					
SA1798		hypothetical protein [Bacteriophage phiN315]	0.57	0.38	0.36
Protein modification, folding and secretion					
SA2028	<i>secY</i>	preprotein translocase SecY subunit	0.58	0.32	0.34
SA2446		hypothetical protein, similar to preprotein translocase SecY	0.87	0.39	1.08
Protein synthesis - initiation and termination					
SA1504	<i>infC</i>	translation initiation factor IF-3 InfC	0.72	0.40	0.53
SA1920	<i>prfA</i>	peptide chain release factor 1	0.47	0.37	0.41
Protein synthesis - ribosomal proteins and aminoacyl-tRNA synthetases					
SA0354	<i>rpsR</i>	30S ribosomal protein S18	0.73	0.48	0.29
SA0486	<i>gltX</i>	glutamyl-tRNA synthetase	0.57	0.35	0.53
SA0497	<i>rplJ</i>	50S ribosomal protein L10 (BL5)	0.48	0.28	0.32
SA0498	<i>rplL</i>	50S ribosomal protein L7/L12	0.51	0.37	0.30
SA0503	<i>rpsL</i>	30S ribosomal protein S12	0.48	0.28	0.40
SA0504	<i>rpsG</i>	30S ribosomal protein S7	0.42	0.28	0.44
SA1081	<i>rpsP</i>	30S ribosomal protein S16	0.55	0.52	0.31
SA1471	<i>rpmA</i>	50S ribosomal protein L27	0.46	0.37	0.59
SA1922	<i>rpmE</i>	50S ribosomal protein L31	0.61	0.48	0.38
SA2022	<i>rplQ</i>	50S ribosomal protein L17	0.45	0.22	0.26
SA2024	<i>rpsK</i>	30S ribosomal protein S11	0.44	0.31	0.30
SA2029	<i>rplO</i>	50S ribosomal protein L15	0.50	0.29	0.31
SA2030	<i>rpmD</i>	50S ribosomal protein L30	0.53	0.25	0.32
SA2031	<i>rpsE</i>	30S ribosomal protein S5	0.66	0.29	0.39
SA2032	<i>rplR</i>	50S ribosomal protein L18	0.49	0.25	0.29
SA2033	<i>rplF</i>	50S ribosomal protein L6	0.43	0.26	0.28
SA2034	<i>rpsH</i>	30S ribosomal protein S8	0.50	0.26	0.35
SA2035	<i>rplE</i>	50S ribosomal protein L5	0.47	0.24	0.26
SA2036	<i>rplX</i>	50S ribosomal protein L24	0.41	0.25	0.26
SA2037	<i>rplN</i>	50S ribosomal protein L14	0.43	0.22	0.28
SA2038	<i>rpsQ</i>	30S ribosomal protein S17	0.42	0.24	0.25
SA2039	<i>rpmC</i>	50S ribosomal protein L29	0.41	0.22	0.25
SA2040	<i>rplP</i>	50S ribosomal protein L16	0.53	0.24	0.31
SA2041	<i>rpsC</i>	30S ribosomal protein S3	0.43	0.25	0.24
SA2042	<i>rplV</i>	50S ribosomal protein L22	0.58	0.31	0.31
SA2043	<i>rpsS</i>	30S ribosomal protein S19	0.54	0.28	0.29

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TABLE A2 - Continued

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
SA2045	<i>rplW</i>	50S ribosomal protein L23	0.46	0.26	0.36
SA2046	<i>rplD</i>	50S ribosomal protein L4	0.46	0.27	0.36
SA2048	<i>rpsJ</i>	30S ribosomal protein S10	0.43	0.31	0.48
SAS052	<i>rpsD</i>	30S ribosomal protein S4	0.71	0.47	0.38
SAS079	<i>rpsN</i>	30S ribosomal protein S14	0.51	0.27	0.27
Protein transport and binding					
SA0183	<i>glcA</i>	PTS enzyme II, glucose-specific, factor IIA homologue	0.34	0.21	0.09
SA0272		hypothetical protein, similar to transmembrane protein Tmp7	0.47	0.33	0.97
SA0295		hypothetical protein, similar to outer membrane protein precursor	0.65	0.31	0.26
SA0374	<i>pbuX</i>	xanthine permease	0.52	0.11	0.50
SA0479	<i>nupC</i>	pyrimidine nucleoside transport protein	0.33	0.24	0.10
SA0616	<i>vraF</i>	ABC transporter ATP-binding protein	0.64	0.36	1.46
SA0617	<i>vraG</i>	ABC transporter permease	0.92	0.38	1.49
SA0688		hypothetical protein, similar to ferrichrome ABC transporter permease	1.26	0.75	0.32
SA0689		hypothetical protein, similar to ferrichrome ABC transporter permease	0.88	0.69	0.26
SA0690		hypothetical protein, similar to ferrichrome ABC transporter ATP-binding protein	0.44	0.52	0.37
SA0794	<i>dltB</i>	DltB membrane protein	0.79	0.26	0.31
SA0796	<i>dltD</i>	poly D-alanine transfer protein	0.75	0.24	0.30
SA0928		hypothetical protein, similar to cation ABC transporter	0.90	0.90	0.23
SA0950	<i>potA</i>	spermidine/putrescine ABC transporter, ATP-binding protein homologue	0.62	0.31	0.30
SA0951	<i>potB</i>		0.58	0.44	0.28
SA0952	<i>potC</i>	spermidine/putrescine ABC transporter homologue	0.51	0.23	0.28
SA1042	<i>pyrP</i>	uracil permease	1.16	2.02	0.07
SA1224		ABC transporter (ATP-binding protein) homologue	0.48	0.35	0.36
SA1979		hypothetical protein, similar to ferrichrome ABC transporter (binding protein)	0.46	0.55	0.32
SA2094		hypothetical protein, similar to Na ⁺ /H ⁺ antiporter	0.46	0.33	0.81
SA2117		hypothetical protein, similar to Na ⁺ /H ⁺ antiporter	0.82	0.36	0.76
SA2132		hypothetical protein, similar to ABC transporter (ATP-binding protein)	0.34	0.22	0.21
SA2135		hypothetical protein, similar to sodium/glutamate symporter	0.71	0.65	0.23
SA2142		hypothetical protein, similar to multidrug resistance protein	0.40	0.42	0.23
SA2191		hypothetical protein, similar to NirC	0.54	0.31	0.67
SA2300		hypothetical protein, similar to glucarate transporter	0.81	0.83	0.22
SA2302		hypothetical protein, similar to ABC transporter	1.12	0.83	0.27
SA2303		hypothetical protein, similar to membrane spanning protein	1.15	0.65	0.18
SA2326	<i>ptsG</i>	PTS system, glucose-specific IIABC component	0.64	0.42	0.32
RNA synthesis - regulation, elongation and modification					
SA0501	<i>rpoC</i>	RNA polymerase beta-prime chain	0.81	0.39	0.54
SA1041	<i>pyrR</i>	pyrimidine operon repressor chain A	0.72	1.28	0.13
SA1082	<i>rimM</i>	probable 16S rRNA processing protein	0.40	0.31	0.32
SA1083	<i>trmD</i>	tRNA-(guanine-N1)-methyltransferase	0.44	0.32	0.38
SA1583	<i>rot</i>	repressor of toxins Rot	0.55	0.64	0.23
SA1844	<i>agrA</i>	accessory gene regulator A	0.33	0.22	0.53
SA2023	<i>rpoA</i>	DNA-directed RNA polymerase alpha chain	0.43	0.23	0.25
SA2089	<i>sarR</i>	staphylococcal accessory regulator A homologue	0.53	0.36	0.31
Sensors (signal transduction)					
SA1843	<i>agrC</i>	accessory gene regulator C	0.51	0.27	0.70
Hypothetical proteins					
SA0121		hypothetical protein	0.64	X	0.34
SA0213		conserved hypothetical protein	0.33	0.39	0.37
SA0231		hypothetical protein, similar to flavohemoprotein	0.90	0.90	0.36
SA0262		hypothetical protein	0.51	0.47	0.20

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TABLE A2 - *Continued*

N315 ORF	Gene	Gene product	Fold change ²		
			SA137/93A (0.5xMIC)	SA137/93G (0.5xMIC)	SG511 (1xMIC)
SA0266		conserved hypothetical protein	1.47	1.03	0.34
SA0267		hypothetical protein	1.13	0.78	0.35
SA0268		hypothetical protein	1.05	0.90	0.39
SA0269		hypothetical protein	1.10	1.18	0.03
SA0291		hypothetical protein	0.31	0.36	0.11
SA0292		hypothetical protein	0.26	0.23	0.07
SA0406		hypothetical protein	0.70	0.98	0.35
SA0499		conserved hypothetical protein	0.54	0.28	0.53
SA0555		conserved hypothetical protein	0.74	0.53	0.27
SA0588		conserved hypothetical protein	0.63	1.26	0.30
SA0667		conserved hypothetical protein	0.79	0.21	0.40
SA0739		conserved hypothetical protein	0.27	0.29	0.04
SA0890		conserved hypothetical protein	0.42	0.20	0.58
SA0929		conserved hypothetical protein	0.73	0.94	0.34
SA0949		conserved hypothetical protein	0.73	0.31	0.52
SA1002		hypothetical protein	1.01	0.55	0.20
SA1049		hypothetical protein	1.11	1.44	0.13
SA1056		hypothetical protein	0.62	0.53	0.35
SA1265		conserved hypothetical protein	0.49	0.19	0.36
SA1275		conserved hypothetical protein	0.64	0.57	0.39
SA1536		conserved hypothetical protein	0.55	0.35	0.53
SA1693		conserved hypothetical protein	0.73	0.60	0.35
SA1840		conserved hypothetical protein	0.62	0.39	0.57
SA1912		hypothetical protein	0.55	0.45	0.33
SA1985		hypothetical protein	0.53	1.74	0.20
SA1986		hypothetical protein	0.49	1.56	0.19
SA2050		conserved hypothetical protein	0.59	0.29	0.44
SA2133		conserved hypothetical protein	0.51	0.31	0.21
SA2143		conserved hypothetical protein	0.46	0.53	0.30
SA2328		conserved hypothetical protein	0.90	1.38	0.37
SA2329		conserved hypothetical protein	0.26	0.22	0.21
SA2355		conserved hypothetical protein	0.80	0.39	0.72
SA2371		conserved hypothetical protein	0.69	0.80	0.29
SA2372		hypothetical protein	0.58	0.74	0.34
SA2443		hypothetical protein	0.84	0.37	1.00

¹ Significant changes of gene expression were determined by implementing SAM (significance analysis of microarrays; <http://www-stat.stanford.edu/~tibs/SAM/>).

² Fold change in transcript level indicated as mean of the “median of ratios” compared to control cells. Fold change in bold = classified as “significantly” regulated in this strain by SAM. “X” indicates the deletion of this ORF in the respective strain according to Reipert et al. (2003).