

**Table S1.**

Number of sequence reads for each sample

	Control	2H	4H
rRNA reads	199,382	3,319,783	196,865
(%)	0.65	10.85	0.61
mRNA reads	24,701,434	22,681,496	26,442,084
(%)	80.19	74.16	82.44
Intergenic reads	3,854,652	2,779,801	3,735,109
(%)	12.51	9.09	11.65
Unmapped reads	838,262	772,340	746,249
(%)	2.72	2.53	2.33
QC dropped reads	164,029	112,670	86,151
(%)	0.53	0.37	0.27
Total reads	29,757,759	29,666,090	31,206,458
(%)	96.6	97.0	97.3

**Table S3.**

Comparison of normalization methods for RNA-Seq data.

Coefficients of variation (CV)	Normalization method		
	RPKM	RLE	TMM
	0.3932	0.3693	0.3685

**Table S4.**

Primers for quantitative real-time PCR.

Gene	Gene locus	Oligonucleotide		Size (bp)	Reference
		Forward (5'→3')	Reverse (5'→3')		
16S rRNA	AWC34_RS01040	ACT CCT ACG GGA GGC AGC AGT	TAT TAC CGC GGC TGC TGG C	198	Clifford et al. 2012
<i>gbsB</i>	AWC34_RS11515	GAG CAT GTG GTG CTT TCG TAC	GGT GCA GCA GCA TCT AAC CAC	133	This study
<i>gbsA</i>	AWC34_RS11520	CTG GAC CCA TTT CGG TTT CTG	CCA AGT ATG TTC TGC TGG CGC	134	This study
<i>opuCA</i>	AWC34_RS10330	GTA TCT CTC GTA ATC GGG TC	CTC AAT TAT CTG GGG GAC AGC	118	This study
<i>opuCB</i>	AWC34_RS10325	GCT GGC ACA AGT ATG GGA ATG	CAT AAC TTG CTA GCG TCG CCC	136	This study
<i>opuCC</i>	AWC34_RS10320	GTA CCC CTC AAT ACG TCC ATC	GGT TAC ATC GTG AAG GTG ACG	134	This study
<i>opuCD</i>	AWC34_RS10315	GTC ACC TAA AGT TGG TGC TCC	GGG TAT GAC ACG AAA CCA AG	145	This study
<i>opuD1</i>	AWC34_RS05465	GGT GCG GCT GAA CCA ATG GC	GCG CTA ATG CTA CTA CGC C	145	This study
<i>opuD2</i>	AWC34_RS09135	GCC CCA ACT GAC TTT GAC	CGG AAA CAG CGA CCT TTG C	182	This study
<i>opuD3</i>	AWC34_RS10865	GGA CTC CAG CTC ATC CAC CAG	GAC AAG TGG CAC AGG AGA C	135	This study
<i>opuD4</i>	AWC34_RS10935	CAG CAG GCT TAG GTG TAG GG	GCC CAT TGC GAC TCT TGC AG	125	This study
<i>opuD5</i>	AWC34_RS11530	CTG TGC TGG TAT TGC TTC AG	CGC TGG CAG TAC GAA TGT TGC	175	This study
<i>abgT</i>	AWC34_RS10400	CAT CCG GGC ACA GGC GAT ACG	GCT ACC CCA ATA CCA AGC ATG	146	This study
<i>putP</i>	AWC34_RS10580	GAT TAT GGG ACT ACC TGG GG	GGT AGC GTA ATG GCA TCC CC	153	This study

**Table S5.**

Differential gene expression related to salt stress.

Gene locus	Gene	E.C. No.	Log2(Fold change)		COG	Product
			2H/CON	4H/CON		
UP regulated						
C: Energy production and conversion						
AWC34_RS05470	-	4.2.1.3	0.59	2.26	C	Aconitate hydratase AcnA
AWC34_RS07130	-	2.3.3.1	0.33	2.18	C	Citrate synthase
AWC34_RS09600	-	1.1.1.290	-0.3	2.06	C	2-hydroxyacid dehydrogenase
AWC34_RS10110	-	1.7.99.4	2.24	-3.98	C	Nitrate reductase subunit alpha
AWC34_RS11520	-	1.2.1.3	4.21	2.34	C	Betaine-aldehyde dehydrogenase
E: Amino acid transport and metabolism						
AWC34_RS00290	-	4.4.1.8	3.37	0.01	E	PLP-dependent transferase
AWC34_RS00295	-	2.5.1.48	3.52	-0.62	E	Cystathionine gamma-synthase
AWC34_RS00495	-	3.5.1.32	-0.93	2.06	E	Amidohydrolase
AWC34_RS01390	-	2.3.1.30	2.11	2.31	E	Serine O-acetyltransferase
AWC34_RS01730	-	3.5.3.11	1.91	2.21	E	Agmatinase
AWC34_RS02825	-	-	2.12	0.97	E	ABC transporter ATP-binding protein
AWC34_RS03630	-	2.6.1.17	1.93	2.11	E	Ornithine--oxo-acid transaminase
AWC34_RS03660	-	4.3.2.1	0.45	2.56	E	Argininosuccinate lyase
AWC34_RS03665	-	6.3.4.5	0.63	2.57	E	Argininosuccinate synthase
AWC34_RS05600	-	4.1.3.27	1.68	2.08	E	Anthranilate synthase component I
AWC34_RS05610	-	2.4.2.18	1.71	2.07	E	Anthranilate phosphoribosyltransferase
AWC34_RS05615	-	4.1.1.48	1.61	2.42	E	Indole-3-glycerol phosphate synthase TrpC
AWC34_RS06225	-	1.5.1.2	0.43	2.24	E	Pyrroline-5-carboxylate reductase
AWC34_RS07515	-	-	0.13	2.32	E	Osmoprotectant ABC transporter substrate-binding protein
AWC34_RS08450	-	4.2.1.9	2.1	0	E	Dihydroxy-acid dehydratase
AWC34_RS08455	-	2.2.1.6	2.2	0.15	E	Acetolactate synthase, large subunit, biosynthetic type
AWC34_RS08835	-	-	2.22	-0.04	E	Amidohydrolase
AWC34_RS10580	-	-	1.48	4.61	E	Sodium/proline symporter PutP
AWC34_RS11425	-	2.7.2.8	1.23	9.08	E	Acetylglutamate kinase
AWC34_RS11430	-	2.3.1.35	1.04	8.94	E	Bifunctional glutamate N-acetyltransferase/amino-acid acetyltransferase ArgJ
AWC34_RS11435	-	1.2.1.38	0.82	8.64	E	N-acetyl-gamma-glutamyl-phosphate reductase
AWC34_RS11440	-	2.6.1.13	0.52	7.91	E	Ornithine--oxo-acid transaminase
AWC34_RS11515	-	1.1.99.1	4.41	1.3	E	Choline dehydrogenase
AWC34_RS12770	-	4.3.1.3	0.84	3.01	E	Histidine ammonia-lyase
AWC34_RS10530	-	-	3.23	0.34	EG	Gluconate permease
AWC34_RS03780	-	-	2.74	1.84	EP	ABC transporter ATP-binding protein
AWC34_RS03785	-	-	2.34	1.27	EP	ABC transporter ATP-binding protein
F: Nucleotide transport and metabolism						
AWC34_RS00805	-	-	0.72	2.33	F	Purine permease
AWC34_RS04125	-	6.3.4.18	3.14	1.69	F	5-(carboxyamino)imidazole ribonucleotide synthase
AWC34_RS04130	-	6.3.2.6	3.86	2.19	F	Phosphoribosylaminoimidazolesuccinocarboxamidesynthase
AWC34_RS04135	-	6.3.5.3	4.15	2.06	F	Phosphoribosylformylglycinamidine synthase subunit PurS
AWC34_RS04140	-	6.3.5.3	3.76	2.07	F	Phosphoribosylformylglycinamidine synthase I
AWC34_RS04145	-	6.3.5.3	2.89	2.02	F	Phosphoribosylformylglycinamidine synthase subunit PurL

AWC34_RS04150	-	2.4.2.14	2.3	1.84	F	Amidophosphoribosyltransferase
AWC34_RS09220	-	2.7.4.3	0.76	2.16	F	Adenylate kinase
AWC34_RS10405	-	3.6.1.40	2.19	-0.14	FP	Exopolyphosphatase
G: Carbohydrate transport and metabolism						
AWC34_RS10535	-	2.7.1.12	3.93	1.2	G	Gluconokinase
AWC34_RS10925	-	-	0.67	4.04	G	Intercellular adhesion protein C
AWC34_RS11470	-	-	1.03	4.94	G	MFS transporter
AWC34_RS11630	-	2.7.1.31	2.62	0.71	G	Glycerate kinase
H: Coenzyme transport and metabolism						
AWC34_RS10130	-	4.99.1.4	2.43	-3.35	H	Bifunctional precorrin-2 dehydrogenase/sirohydrochlorin ferrochelataase
AWC34_RS10135	-	4.99.1.3	2.02	-3.4	H	Hypothetical protein
I: Lipid transport and metabolism						
AWC34_RS00235	-	2.8.3.1	2.74	2.42	I	Acyl CoA:acetate/3-ketoacid CoA transferase
AWC34_RS00240	-	-	2.93	3.08	I	Long-chain fatty acid--CoA ligase
AWC34_RS00245	-	1.3.8.6	2.86	1.9	I	Glutaryl-CoA dehydrogenase
AWC34_RS00250	-	1.1.1.35	2.03	1.52	I	3-hydroxyacyl-CoA dehydrogenase
AWC34_RS03260	-	-	2.06	0.89	I	Alpha/beta hydrolase
AWC34_RS00135	-	-	1.04	2.43	IQ	3-oxoacyl-ACP reductase
AWC34_RS00550	-	-	-0.01	4.22	IQ	KR domain-containing protein
J: Translation, ribosomal structure and biogenesis						
AWC34_RS04435	-	6.1.1.20	2.49	0.88	J	Phenylalanine--tRNA ligase subunit alpha
AWC34_RS06585	-	-	-0.41	2.38	J	30S ribosomal protein S21
AWC34_RS06840	-	6.1.1.21	1.62	2.19	J	Histidine--tRNA ligase
AWC34_RS09205	-	-	1.17	2.06	J	30S ribosomal protein S13
AWC34_RS09210	-	-	2.08	1.55	J	50S ribosomal protein L36
AWC34_RS09215	-	-	0.86	2.16	J	Translation initiation factor IF-1
AWC34_RS09235	-	-	0.67	2.14	J	50S ribosomal protein L30
AWC34_RS09240	-	-	1.01	2	J	30S ribosomal protein S5
AWC34_RS09255	-	-	1.08	2.13	J	30S ribosomal protein S8
AWC34_RS09260	<i>rpsN</i>	-	1.17	2.09	J	30S ribosomal protein S14 type Z
K: Transcription, regulators						
AWC34_RS09195	-	2.7.7.6	0.73	2	K	DNA-directed RNA polymerase subunit alpha
AWC34_RS10540	-	-	4.47	1.58	K	GntR family transcriptional regulator
L: Replication, recombination and repair						
AWC34_RS01955	-	4.1.99.3	2.07	1.39	L	Deoxyribodipyrimidine photo-lyase
M: Cell wall/membrane/envelope biogenesis						
AWC34_RS00605	-	-	-0.44	2.82	M	Lysozyme
AWC34_RS02505	-	-	2.51	0.31	M	NAD(P)-dependent oxidoreductase
AWC34_RS08790	-	2.5.1.7	2.05	1.17	M	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
AWC34_RS13385	-	2.7.8.12	-0.06	2.46	M	CDP-glycerol:glycerophosphateglycerophosphotransferase
O: Post-translational modification, protein turnover, chaperones						
AWC34_RS04970	-	3.4.25.2	2.29	0.68	O	ATP-dependent protease subunit HsIV
AWC34_RS10390	-	-	-0.41	2.62	O	Hypothetical protein
AWC34_RS11070	-	3.4.21.19	0.56	2.29	O	Serine protease
P: Inorganic ion transport and metabolism						
AWC34_RS03770	-	-	2.16	1.04	P	ABC transporter permease
AWC34_RS03775	-	-	2.67	1.99	P	ABC transporter permease
AWC34_RS05465	-	-	1.88	2.31	P	BCCT family transporter

AWC34_RS09135	-	-	2.21	2.02	P	BCCT family transporter	
AWC34_RS10865	-	-	0.85	3.72	P	BCCT family transporter	
AWC34_RS11530	-	-	3.22	2.6	P	BCCT family transporter	
AWC34_RS11635	-	-	2.52	0.8	P	2-keto-3-deoxygluconate permease	
R: General function prediction only							
AWC34_RS00305	-	-	0.67	3.92	R	Amidohydrolase	
AWC34_RS06690	-	-	2.06	0.88	R	YqeG family HAD IIIA-type phosphatase	
AWC34_RS11495	-	-	2.2	1.37	R	N-acetyltransferase	
S: Function unknown							
AWC34_RS00385	-	-	2.38	1.61	S	Hypothetical protein	
AWC34_RS02490	-	-	-0.68	2.59	S	Membrane protein	
AWC34_RS04240	-	-	2.01	0.19	S	Hypothetical protein	
AWC34_RS08650	-	-	0.57	2.22	S	Transglycosylase	
AWC34_RS09765	-	-	-0.33	2.1	S	Histidine transporter	
AWC34_RS10220	-	-	2.15	1.51	S	Hypothetical protein	
AWC34_RS10550	-	-	2.09	1.06	S	DUF2188 domain-containing protein	
AWC34_RS11275	-	-	2.6	-0.67	S	Tripartite tricarboxylate transporter substrate binding protein	
AWC34_RS11460	-	-	-0.04	2.29	S	ABC transporter permease	
AWC34_RS11465	-	-	2.08	3.95	S	Hypothetical protein	
AWC34_RS11640	-	-	2.13	0.33	S	DUF2088 domain-containing protein	
AWC34_RS12070	-	-	3.04	1.94	S	Transglycosylase	
AWC34_RS12080	-	-	2.59	2.52	S	Transglycosylase	
AWC34_RS12440	-	-	-1.03	2.26	S	DUF805 domain-containing protein	
U: Intracellular trafficking, secretion, and vesicular transport							
AWC34_RS09225	-	-	1.15	2.04	U	Preprotein translocase subunit SecY	
V: Defense mechanisms							
AWC34_RS09895	-	-	2.21	-0.06	V	ABC transporter ATP-binding protein	
AWC34_RS09900	-	-	2.32	-0.24	V	ABC transporter permease	
AWC34_RS11450	-	-	0.28	2.73	V	ABC transporter ATP-binding protein	
AWC34_RS12575	-	3.1.21.3	2.05	0.76	V	Type I restriction endonuclease subunit R	
Others							
AWC34_RS00115	-	-	0.49	2.34		Hypothetical protein	
AWC34_RS00285	-	2.1.1.10	2.37	-0.1		Bifunctional homocysteine methyltransferase/methylenetetrahydrofolate reductase	S-
AWC34_RS00545	-	-	-0.89	2.97		Peptide synthetase	
AWC34_RS00830	-	-	3.27	0.05		Hypothetical protein	
AWC34_RS01015	<i>ffs</i>	-	-1.8	4.33		Signal recognition particle sRNA large type	
AWC34_RS02925	-	-	2.01	0.15		EMYY motif lipoprotein	
AWC34_RS03155	<i>ssrA</i>	-	-0.61	3.19		Transfer-messenger RNA	
AWC34_RS04120	-	5.4.99.18	2.23	0.99		5-(carboxyamino)imidazole ribonucleotide mutase	
AWC34_RS06830	<i>ssrS</i>	-	0.54	3.14		6S RNA	
AWC34_RS07765	-	-	-0.74	2.61		Hypothetical protein	
AWC34_RS09050	-	-	-0.11	2.11		Multidrug resistance protein SepA	
AWC34_RS11455	-	-	0.2	2.29		ABC transporter	
AWC34_RS11665	-	-	0.94	2.11		Hypothetical protein	
AWC34_RS11750	-	3.4.24.75	2.63	0.48		M23 family peptidase	
AWC34_RS13095	-	-	-	2.55		Butanediol dehydrogenase	
AWC34_RS13320	-	-	0.39	3.6		D-alanine--poly(phosphoribitol) ligase subunit DltA	
AWC34_RS13375	-	-	-0.95	2.46		Hypothetical protein	

AWC34_RS13380	-	-	2.34	4.82		Putative holin-like toxin
AWC34_RS13440	-	-	-2.6	5.61		Type I toxin-antitoxin system Fst family toxin
AWC34_RS13455	-	-	-2.6	5.61		Type I toxin-antitoxin system Fst family toxin
Down regulated						
C: Energy production and conversion						
AWC34_RS10095	-	1.7.99.4	0.27	-2.63	C	Respiratory nitrate reductase subunit gamma
AWC34_RS10100	-	-	0.5	-4.36	C	Nitrate reductase molybdenum cofactor assembly chaperone
AWC34_RS10105	-	1.7.99.4	1.15	-4.62	C	Nitrate reductase subunit beta
AWC34_RS10110	-	1.7.99.4	2.24	-3.98	C	Nitrate reductase subunit alpha
AWC34_RS10120	-	1.7.1.15	0.99	-4.12	C	Nitrite reductase (NAD(P)H) small subunit
AWC34_RS10125	-	1.7.1.15	1.75	-3.85	C	Nitrite reductase large subunit
E: Amino acid transport and metabolism						
AWC34_RS08230	-	4.2.1.51	1.15	-2.32	E	Prephenate dehydratase
AWC34_RS12105	-	3.5.1.18	-2.28	-0.74	E	Hypothetical protein
AWC34_RS13170	-	4.1.3.16	-1.81	-2.24	E	4-hydroxy-tetrahydrodipicolinate synthase
G: Carbohydrate transport and metabolism						
AWC34_RS00650	<i>celC</i>	2.7.1.69	-0.32	-2.9	G	PTS lactose/cellobiose transporter subunit IIA
AWC34_RS05240	-	-	0.23	-2.27	G	Aquaporin family protein
AWC34_RS10510	-	3.2.1.31	-0.06	-2.6	G	Beta-glucuronidase
AWC34_RS10515	-	-	0.74	-2.57	G	MFS transporter
AWC34_RS11310	-	-	-0.25	-2.43	G	MFS transporter
AWC34_RS11355	-	-	0.63	-2.12	G	PTS sugar transporter subunit IIC
AWC34_RS11395	-	-	0.12	-2.01	G	MFS transporter
AWC34_RS12000	-	-	-1.96	-2.47	G	Sugar porter family MFS transporter
AWC34_RS12365	-	-	0.04	-2.28	G	Melibiose:sodium transporter MelB
H: Coenzyme transport and metabolism						
AWC34_RS10115	-	2.1.1.107	0.41	-4.3	H	Uroporphyrinogen-III C-methyltransferase
AWC34_RS10130	-	4.99.1.4	2.43	-3.35	H	Bifunctional precorrin-2 dehydrogenase/sirohydrochlorin ferrochelataase
AWC34_RS10135	-	4.99.1.3	2.02	-3.4	H	Hypothetical protein
I: Lipid transport and metabolism						
AWC34_RS03515	-	6.1.1.13	-2.19	-2.88	I	D-alanine--poly(phosphoribitol) ligase subunit 2
AWC34_RS03730	-	-	-0.27	-4.4	I	Acetyltransferase Putative O-acetyltransferase SACOL0978
J: Translation, ribosomal structure and biogenesis						
AWC34_RS04915	-	-	-2.28	0.55	J	50S ribosomal protein L19
AWC34_RS05275	-	2.5.1.75	-1.38	-2.12	J	TRNA (adenosine(37)-N6)-dimethylallyltransferase MiaA
K: Transcription, regulators						
AWC34_RS01665	-	-	-0.52	-2.36	K	LacI family DNA-binding transcriptional regulator
AWC34_RS03960	-	-	-1.82	-2.02	K	Competence protein ComK
AWC34_RS04045	-	-	-2.51	-4.3	K	MarR family transcriptional regulator
AWC34_RS05505	-	-	-0.79	-2.25	K	Transcription antiterminator
AWC34_RS06615	-	-	-2.3	-1.27	K	Heat-inducible transcription repressor HrcA
AWC34_RS10770	-	-	-0.83	-2.16	K	N-acetyltransferase
AWC34_RS12400	-	-	-1.71	-2.05	K	MerR family DNA-binding transcriptional regulator
AWC34_RS12945	-	-	-2.72	-1.51	K	ArsR family transcriptional regulator
AWC34_RS13310	-	-	-2.38	0.19	K	FCD domain-containing protein
L: Replication, recombination and repair						
AWC34_RS05330	-	3.1.31.1	-2.18	-0.79	L	Thermonuclease
AWC34_RS11485	-	-	-0.97	-2.66	L	Hypothetical protein

AWC34_RS13220	-	-	-2.05	-0.9	L	Recombinase family protein
AWC34_RS13295	-	-	-1.58	-2.13	L	Protein rep
AWC34_RS13445	-	-	-0.61	-2	L	Replication protein
M: Cell wall/membrane/envelope biogenesis						
AWC34_RS03510	-	-	-1.78	-2.63	M	D-alanyl-lipoteichoic acid biosynthesis protein DltB
AWC34_RS03520	-	-	-2.53	-3.21	M	D-alanyl-lipoteichoic acid biosynthesis protein DltD
AWC34_RS04425	-	-	1.54	-2.28	M	M23 family peptidase
AWC34_RS07615	-	2.7.8.12	-0.37	-3.54	M	Glycosyltransferase family 2 protein
AWC34_RS12225	-	2.4.1.83	-0.47	-2.97	M	Glycosyltransferase
O: Post-translational modification, protein turnover, chaperones						
AWC34_RS03075	-	3.4.21.92	-2.82	-1.02	O	ATP-dependent Clp protease proteolytic subunit
AWC34_RS03740	-	-	-2.71	-1.44	O	ATP-dependent chaperone ClpB
AWC34_RS06605	-	-	-2.04	-0.41	O	Molecular chaperone DnaK
AWC34_RS06610	-	-	-2.12	-0.97	O	Nucleotide exchange factor GrpE
AWC34_RS08340	-	-	-2.52	-1	O	Chaperonin GroEL
AWC34_RS08345	-	-	-2.02	-1.79	O	Co-chaperone GroES
AWC34_RS10070	-	-	-2.81	-0.46	O	Hsp20/alpha crystallin family protein
AWC34_RS11770	-	-	-1.3	-2.88	O	Hypothetical protein
P: Inorganic ion transport and metabolism						
AWC34_RS00225	-	-	-1.09	-2.94	P	Ferrichrome ABC transporter substrate-binding protein
AWC34_RS00695	-	-	-1.38	-5.78	P	QacE family quaternary ammonium compound efflux SMR transporter
AWC34_RS02900	-	-	-2.77	-1.38	P	Iron ABC transporter substrate-binding protein
AWC34_RS03405	-	-	-2.15	-0.12	P	HlyC/CorC family transporter
AWC34_RS09510	-	-	-3.55	-2.1	P	Ferrichrome ABC transporter substrate-binding protein
AWC34_RS10075	-	-	-0.49	-3.38	P	NarK/NasA family nitrate transporter
AWC34_RS12090	-	-	0.38	-3.08	P	Membrane protein
AWC34_RS12315	-	-	-2.58	-2.44	P	Iron-siderophore ABC transporter substrate-binding protein
AWC34_RS12320	-	-	-2.02	-1.26	P	Iron ABC transporter permease
AWC34_RS12325	-	-	-2.9	-1.53	P	Iron ABC transporter permease
AWC34_RS12950	-	-	-2.09	-1.86	P	Arsenical efflux pump membrane protein ArsB
Q: Secondary metabolites biosynthesis, transport and catabolism						
AWC34_RS03505	-	6.1.1.13	-0.74	-2.88	Q	D-alanine--poly(phosphoribitol) ligase subunit 1
R: General function prediction only						
AWC34_RS03560	-	-	-2.47	-0.53	R	Sodium:proton antiporter
AWC34_RS05565	-	5.3.2.6	-1.35	-2.78	R	4-oxalocrotonate tautomerase
AWC34_RS08815	-	-	0.32	-2.28	R	VOC family protein
AWC34_RS09940	-	-	0.35	-2.18	R	N-acetyltransferase
AWC34_RS10205	-	-	-0.47	-2.92	R	Lantibiotic ABC transporter ATP-binding protein
AWC34_RS11200	-	-	-0.94	-2.53	R	Thioesterase
AWC34_RS12060	-	-	-0.64	-2.64	R	HAD family hydrolase
AWC34_RS12250	-	-	-0.27	-2.05	R	Serine/threonine protein phosphatase
S: Function unknown						
AWC34_RS00460	-	-	-0.82	-2.42	S	Hypothetical protein
AWC34_RS00465	-	-	-1.11	-3.28	S	Hypothetical protein
AWC34_RS00580	-	-	0.91	-2.27	S	DUF2309 domain-containing protein
AWC34_RS00690	-	-	-1.25	-3.59	S	Multidrug resistance protein SMR
AWC34_RS01885	-	-	-0.7	-2.11	S	Metal-sensitive transcriptional regulator
AWC34_RS02310	-	-	-0.51	-2.16	S	HlyD family secretion protein



AWC34_RS02965	-	3.4.13.9	-1.06	-2.12	S	YigZ family protein
AWC34_RS03170	-	-	-2.29	-0.51	S	DUF418 domain-containing protein
AWC34_RS04105	-	3.4.24.28	-0.2	-2.41	S	DUF5011 domain-containing protein
AWC34_RS04450	-	-	0.9	-2.07	S	Cell division protein ZapA
AWC34_RS05480	-	-	-2.46	-0.57	S	Hypothetical protein
AWC34_RS06450	-	-	-3.02	0.49	S	DUF910 domain-containing protein
AWC34_RS07395	-	-	-2.35	-0.39	S	Hypothetical protein
AWC34_RS07695	-	-	-2.01	1.09	S	Signal transduction protein TRAP
AWC34_RS08290	-	-	-2	-0.1	S	Thioredoxin family protein
AWC34_RS09075	-	-	-2.11	-1.39	S	Hypothetical protein
AWC34_RS10090	-	-	0.13	-2.13	S	GAF domain-containing protein
AWC34_RS11080	-	-	-2.1	-1.15	S	DUF896 family protein
AWC34_RS12220	-	-	-0.99	-3.25	S	Hypothetical protein
AWC34_RS12620	-	-	-1.15	-4.06	S	Hypothetical protein
AWC34_RS12670	-	2.1.1.177	0.67	-2.22	S	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase RlmH
AWC34_RS12825	-	-	-2.59	-0.84	S	Sulfite exporter TauE/SafE family protein
AWC34_RS12900	-	-	-0.43	-2.87	S	Replication initiator protein
AWC34_RS13005	-	-	-2.59	-0.84	S	Sulfite exporter TauE/SafE family protein
AWC34_RS13010	-	-	-2.23	-1.03	S	Metal-sensitive transcriptional regulator
AWC34_RS13140	-	-	0.36	-2	S	Replication protein
AWC34_RS13270	-	-	0.36	-2	S	Replication protein
AWC34_RS13305	-	-	-2.86	-2.16	S	FeoB-associated Cys-rich membrane protein
T: Signal transduction mechanisms						
AWC34_RS03985	-	1.20.4.1	-2.38	-1.54	T	Arsenate reductase (thioredoxin)
AWC34_RS05280	-	-	-2.71	-1.95	T	RNA chaperone Hfq
AWC34_RS07180	-	-	-2.19	-1.32	T	Universal stress protein
AWC34_RS08370	-	-	-3.39	-1.57	T	Accessory gene regulator B
AWC34_RS08380	-	-	-2.1	-0.76	T	GHKL domain-containing protein
AWC34_RS12955	-	1.20.4.1	-2.79	-1.67	T	Protein ArsC 2
Others						
AWC34_RS00055	-	2.7.8.12	-3	-2.38		Hypothetical protein
AWC34_RS00060	-	-	-1.76	-2.15		Ferrous iron transport protein B
AWC34_RS00065	-	-	-1.69	-2.48		Ferrous iron transporter A
AWC34_RS00835	-	-	0.2	-2.04		Hypothetical protein
AWC34_RS02755	-	-	-2.03	0.1		Hypothetical protein
AWC34_RS03165	-	-	-3.08	-1.33		Hypothetical protein
AWC34_RS03205	-	-	-2.4	0.4		Hypothetical protein
AWC34_RS03225	-	-	-1	-2.66		Hypothetical protein
AWC34_RS03240	-	-	-0.78	-2.65		Hypothetical protein
AWC34_RS03295	-	-	-2.6	-2.98		Hypothetical protein
AWC34_RS03500	-	-	-1.36	-3.82		Teichoic acid D-Ala incorporation-associated protein DltX
AWC34_RS04245	-	-	-2.13	-0.83		Hypothetical protein
AWC34_RS04325	-	-	-2.2	-1.1		Hypothetical protein
AWC34_RS04540	-	-	-8.5	-1.63		Beta-class phenol-soluble modulins
AWC34_RS04545	-	-	-6.1	-1.98		Beta-class phenol-soluble modulins
AWC34_RS04550	-	-	-5.37	-1.95		Beta-class phenol-soluble modulins
AWC34_RS05325	-	-	-2.23	-0.75		Hypothetical protein
AWC34_RS05375	-	-	-0.28	-2.39		Hypothetical protein

AWC34_RS05800	-	-	-2.3	-0.72	Mid2-like cell wall stress sensor domain protein
AWC34_RS05980	<i>rnpB</i>	-	-2.38	0.01	RNase P RNA component class B
AWC34_RS06410	-	-	-1.78	-2.66	Hypothetical protein
AWC34_RS06640	-	-	-0.96	-2.04	DNA internalization-related competence protein ComEC/Rec2
AWC34_RS06935	-	-	-1.86	-2.24	DUF4930 domain-containing protein
AWC34_RS07620	-	-	-0.36	-2.56	Hypothetical protein
AWC34_RS08375	-	-	-2.6	-1.46	Cyclic lactone autoinducer peptide
AWC34_RS09405	-	-	-1.78	-3.49	MarR family transcriptional regulator
AWC34_RS09615	-	-	-1.41	-2.29	Hypothetical protein
AWC34_RS10080	-	-	-0.52	-2.02	DNA-binding response regulator
AWC34_RS10905	-	-	0.51	-2.21	Hypothetical protein
AWC34_RS10970	-	-	-0.82	-2.18	Lactococcin 972 family bacteriocin
AWC34_RS11995	-	-	-3.77	-2.64	Beta-class phenol-soluble modulins
AWC34_RS12065	-	-	-0.54	-3.11	Hypothetical protein
AWC34_RS12330	-	-	-2.82	-2.03	Hypothetical protein
AWC34_RS12345	-	-	-1.16	-2.51	Hypothetical protein
AWC34_RS12590	-	-	-3.27	-3.02	Hypothetical protein
AWC34_RS12625	-	-	-0.15	-2.02	Hypothetical protein
AWC34_RS12840	-	3.1.2.6	-3.37	-1.33	MBL fold metallo-hydrolase
AWC34_RS12860	-	-	-2.01	0.11	Hypothetical protein
AWC34_RS13015	-	-	-2.69	-1.37	Sulfurtransferase
AWC34_RS13020	-	3.1.2.6	-3.37	-1.33	MBL fold metallo-hydrolase
AWC34_RS13040	-	-	-2.01	0.11	Hypothetical protein
AWC34_RS13165	-	1.2.1.88	-2.4	-2.92	Betaine-aldehyde dehydrogenase
AWC34_RS13360	-	-	-1.78	-3.24	Putative holin-like toxin
AWC34_RS13365	-	-	-0.33	-2.74	Hypothetical protein
AWC34_RS13390	-	-	-0.22	-3.15	Hypothetical protein
AWC34_RS13415	-	-	-2.78	0.15	Hypothetical protein
AWC34_RS13435	-	-	-3.64	-1.14	Hypothetical protein
AWC34_RS13440	-	-	-2.6	5.61	Type I toxin-antitoxin system Fst family toxin
AWC34_RS13455	-	-	-2.6	5.61	Type I toxin-antitoxin system Fst family toxin

**Table S6.**

DEGs on exposure to 7% NaCl for both 2 and 4 h.

Gene locus	E.C. No.	Log2(Fold change)		COG	Product
		2H/CON	4H/CON		
AWC34_RS00235	2.8.3.1	2.74	2.42	I	Acyl CoA:acetate/3-ketoacid CoA transferase
AWC34_RS00240	-	2.93	3.08	I	Long-chain fatty acid--CoA ligase
AWC34_RS01390	2.3.1.30	2.11	2.31	E	Serine O-acetyltransferase
AWC34_RS04130	6.3.2.6	3.86	2.19	F	Phosphoribosylaminoimidazole succino carboxamide esynthase
AWC34_RS04135	6.3.5.3	4.15	2.06	F	Phosphoribosylformylglycinamide synthase subunit PurS
AWC34_RS04140	6.3.5.3	3.76	2.07	F	Phosphoribosylformylglycinamide synthase I
AWC34_RS04145	6.3.5.3	2.89	2.02	F	Phosphoribosylformylglycinamide synthase subunit PurL
AWC34_RS09135	-	2.21	2.02	P	BCCT family transporter
AWC34_RS11465	-	2.08	3.95	S	Hypothetical protein
AWC34_RS11520	1.2.1.3	4.21	2.34	C	Betaine-aldehyde dehydrogenase
AWC34_RS11530	-	3.22	2.6	P	BCCT family transporter
AWC34_RS12080	-	2.59	2.52	S	Transglycosylase
AWC34_RS13380	-	2.34	4.82		Putative holin-like toxin
AWC34_RS00055	2.7.8.12	-3	-2.38		Hypothetical protein
AWC34_RS03295	-	-2.6	-2.98		Hypothetical protein
AWC34_RS03515	6.1.1.13	-2.19	-2.88	I	D-alanine--poly(phosphoribitol) ligase subunit 2
AWC34_RS03520	-	-2.53	-3.21	M	D-alanyl-lipoteichoic acid biosynthesis protein DltD
AWC34_RS04045	-	-2.51	-4.3	K	MarR family transcriptional regulator
AWC34_RS09510	-	-3.55	-2.1	P	Ferrichrome ABC transporter substrate-binding protein
AWC34_RS11995	-	-3.77	-2.64		Beta-class phenol-soluble modulins
AWC34_RS12315	-	-2.58	-2.44	P	Iron-siderophore ABC transporter substrate-binding protein
AWC34_RS12330	-	-2.82	-2.03		Hypothetical protein
AWC34_RS12590	-	-3.27	-3.02		Hypothetical protein
AWC34_RS13165	1.2.1.88	-2.4	-2.92		Betaine-aldehyde dehydrogenase
AWC34_RS13305	-	-2.86	-2.16	S	FeoB-associated Cys-rich membrane protein