

Supplemental Data Summary

Fig. S1 Changes in gene expression profiling of *D. vulgaris* by functional category in response to salt adaptation.

Fig. S2 Expression changes of representative genes involved in energy metabolism under salt adaptation in comparison with salt shock (120 min).

Fig. S3 Expression changes of representative genes involved in transcription regulatory processes under salt adaptation in comparison with salt shock (120 min).

Fig. S4 Correlation of microarray data and RT-PCR data for 25 selected genes of *D. vulgaris*.

Fig. S5 A comparison of expression of representative genes of *D. vulgaris* involved in efflux systems, the ATP synthase, sulfate reduction, and cell motility under salt adaptation and salt shock (120 min).

Table S1 ORFs, used primers, and their product sizes for reverse transcription real time PCR assay.

Table S2 Up-regulated ORFs under salt adaptation but no significant changes under salt shock.

Table S3 Down-regulated ORFs under salt adaptation but no significant changes under salt shock.

Table S4 Up-regulated ORFs under salt shock but no significant changes under salt adaptation.

Table S5 Down-regulated ORFs under salt shock but no significant changes under salt adaptation.

Table S6 Up-regulated ORFs under both salt shock and salt adaptation conditions.

Table S7 Down-regulated ORFs under both salt shock and salt adaptation conditions.

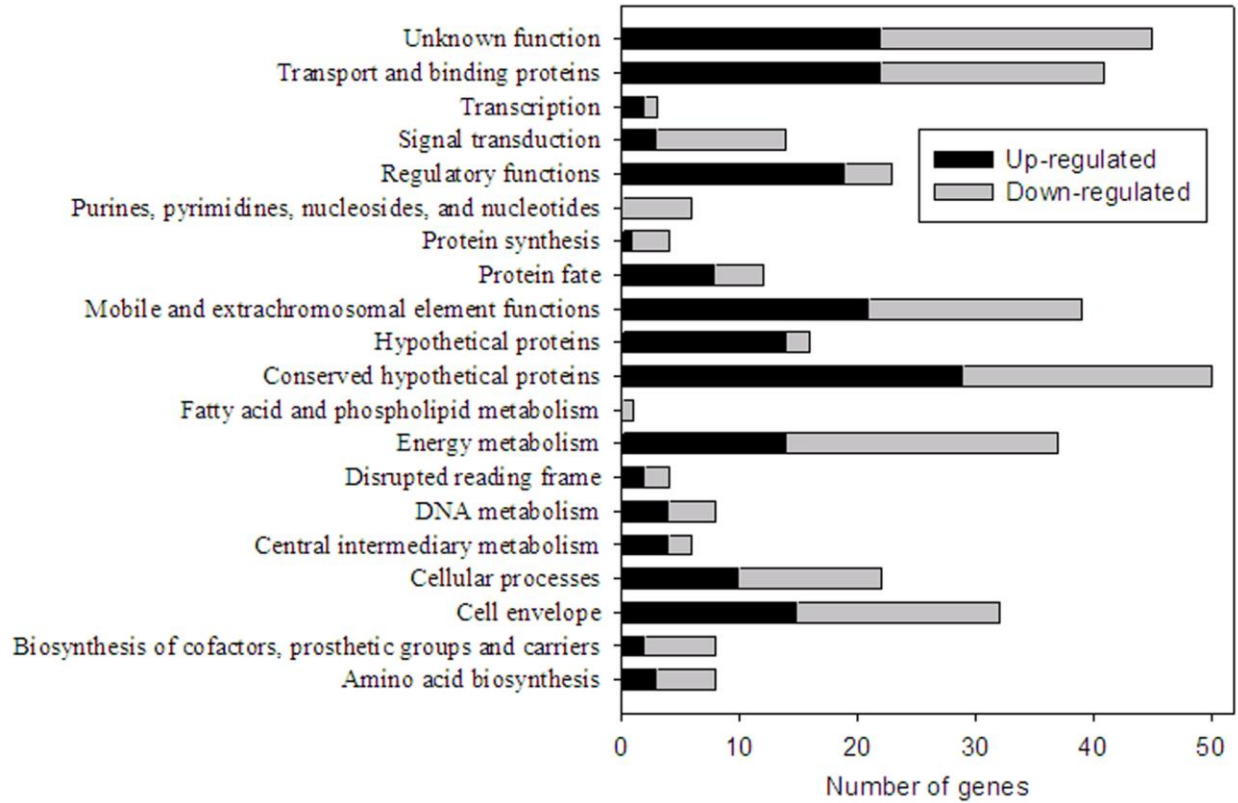


Fig. S1 Changes in gene expression profiling of *D. vulgaris* by functional category in response to salt adaptation. Inoculation of overnight activated *D. vulgaris* cells into the LS4D medium for the control, and LS4D + 250 mM NaCl for the treatment. Samples were taken at the mid-log phase (OD600 = ~0.25), and RNA and DNA were extracted, labeled, and co-hybridized with the *D. vulgaris* whole-genome microarray. Totally, 2647 ORFs were assigned to 20 functional categories based on the TIGR roles with 195 up-regulated and 184 down-regulated.

Locus (gene, predicted function)

DVU0531 (*hmcF*, HmcF, 52.7 kd protein in hmc operon)
DVU0532 (*hmcE*, HmcE, 25.3 kd protein in hmc operon)
DVU0533 (*hmcD*, HmcD, 5.8 kd protein in hmc operon)
DVU0534 (*hmcC*, HmcC, 43.2 kd protein in hmc operon)
DVU0535 (*hmcB*, HmcB, 40.1 kd protein in hmc operon)
DVU0536 (*hmcA*, HmcA, high-molecular-weight cytochrome c)
DVU0587 (*fdnG-I*, Formate dehydrogenase, α subunit)
DVU0588 (*hybA*, Formate dehydrogenase, beta subunit, putative)
DVU1769 (*hydA*, Periplasmic [Fe] hydrogenase, large subunit)
DVU1770 (*hydB*, Periplasmic [Fe] hydrogenase, small subunit)
DVU1919 (Hydrogenase expression/formation protein, putative)
DVU2680 (*fld*, Flavodoxin, iron-repressed)
DVU1568 (*ftn*, Ferritin)
DVU1569 (*porA*, Pyruvate ferredoxin oxidoreductase, α subunit)
DVU1570 (*porB*, Pyruvate ferredoxin oxidoreductase, β subunit)
DVU1946 (*oorB*, Pyruvate ferredoxin oxidoreductase, β subunit)
DVU0596 (*lytR*, DNA-binding response regulator LytR)
DVU0597 (*lytS*, Regulatory protein LytS)
DVU0598 (Carbon starvation protein A, putative)
DVU0599 (Carbon starvation protein A, putative)
DVU2025 (*por*, pyruvate-ferredoxin oxidoreductase)
DVU3026 (L-lactate permease family protein)
DVU3027 (*glcD*, Glycolate oxidase, subunit GlcD)
DVU3028 (Iron-sulfur cluster-binding protein)
DVU3029 (*pta*, Phosphate acetyltransferase)
DVU3030 (*ackA*, Acetate kinase)
DVU3133 (*glpF*, Glycerol uptake facilitator protein)
DVU3134 (*glpK*, Glycerol kinase)
DVU3349 (Pyruvate flavodoxin/ferredoxin oxidoreductase)

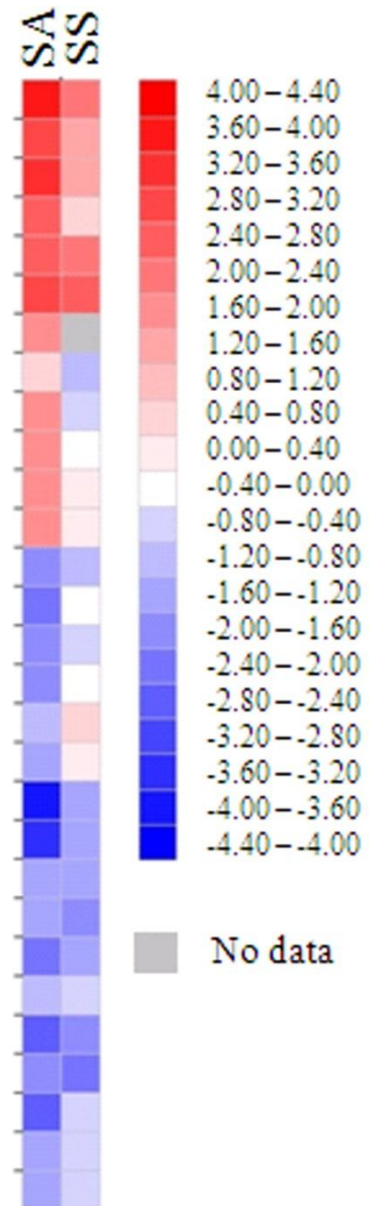


Fig. S2 Expression changes of representative genes involved in energy metabolism under salt adaptation in comparison with salt shock (120 min). Normalized gene expression data presented as the log₂-ratio of the NaCl treatment to control and visualized with JColorGrid software (Joachimiak, M.P., J.L. Weisman, and B.C.H. May. 2006. BMC Bioinformatics 7: 225). SA: salt adaptation; SS: salt shock at 120 min. Missing data are presented in the cells with a light gray color.

Locus (gene, predicted function)

A. Transcriptional regulators

DVU0030 (Transcriptional regulator, GntR family protein)
DVU0529 (*rrf2*, Transcriptional regulator, Rrf2 protein, putative)
DVU0813 (*hrcA*, Heat-inducible transcription repressor HrcA)
DVU1645 (Transcriptional regulator, ArsR family)
DVU1760 (Transcriptional regulator, TetR family)
DVU2106 (*flrC*, Sigma-54 dependent transcriptional regulator)
DVU2423 (Transcriptional regulator, putative)
DVU2567 (*lysX*, putative transcriptional regulator of lysine biosynthesis)
DVU2819 (Transcriptional regulator, TetR family)
DVU2956 (*flrA*, Sigma-54 dependent transcriptional regulator)
DVU2989 (*pspF*, *psp* operon transcriptional activator)
DVU3313 (Transcriptional regulator, LysR family)
DVU1881 (*phoH*, PhoH family protein)
DVU3131 (Transcriptional regulator, putative)

B. Sensory box histidine kinases/response regulators

DVU0530 (*rrf1*, Response regulator, *rrf1* protein)
DVU2129 (*cckA*, Sensory box histidine kinase/response regulator)
DVU2577 (DNA-binding response regulator, LuxR family)
DVU2578 (Response regulator)
DVU0258 (Sensory box histidine kinase/response regulator)
DVU0653 (*atoC*, putative sigma-54 dependent transcriptional regulator)
DVU0680 (Sensory box histidine kinase)
DVU0722 (Response regulator)
DVU0743 (Sensory box histidine kinase)
DVU2677 (Sensor histidine kinase/response regulator)
DVU2931 (Sensory box histidine kinase)
DVU3045 (*fexB*, Sensory box histidine kinase/response regulator)
DVU3221 (Sensor histidine kinase)

C. Chemotaxis proteins

DVU1593 (*cheY-1*, Chemotaxis protein CheY)
DVU2073 (*cheY-2*, Chemotaxis protein CheY)

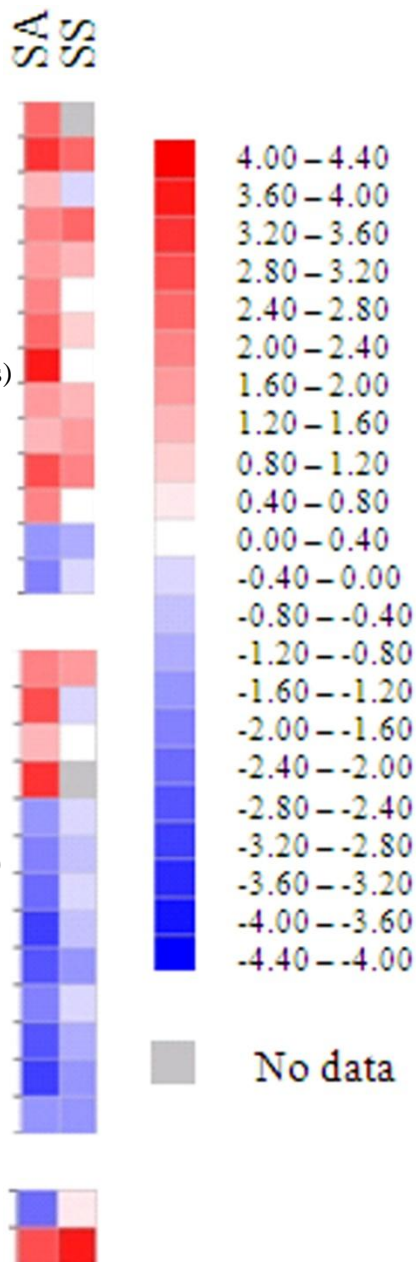


Fig. S3 Expression changes of representative genes involved in transcription regulatory processes under salt adaptation in comparison with salt shock (120 min). Details for data presentation are the same as described in Fig. S2.

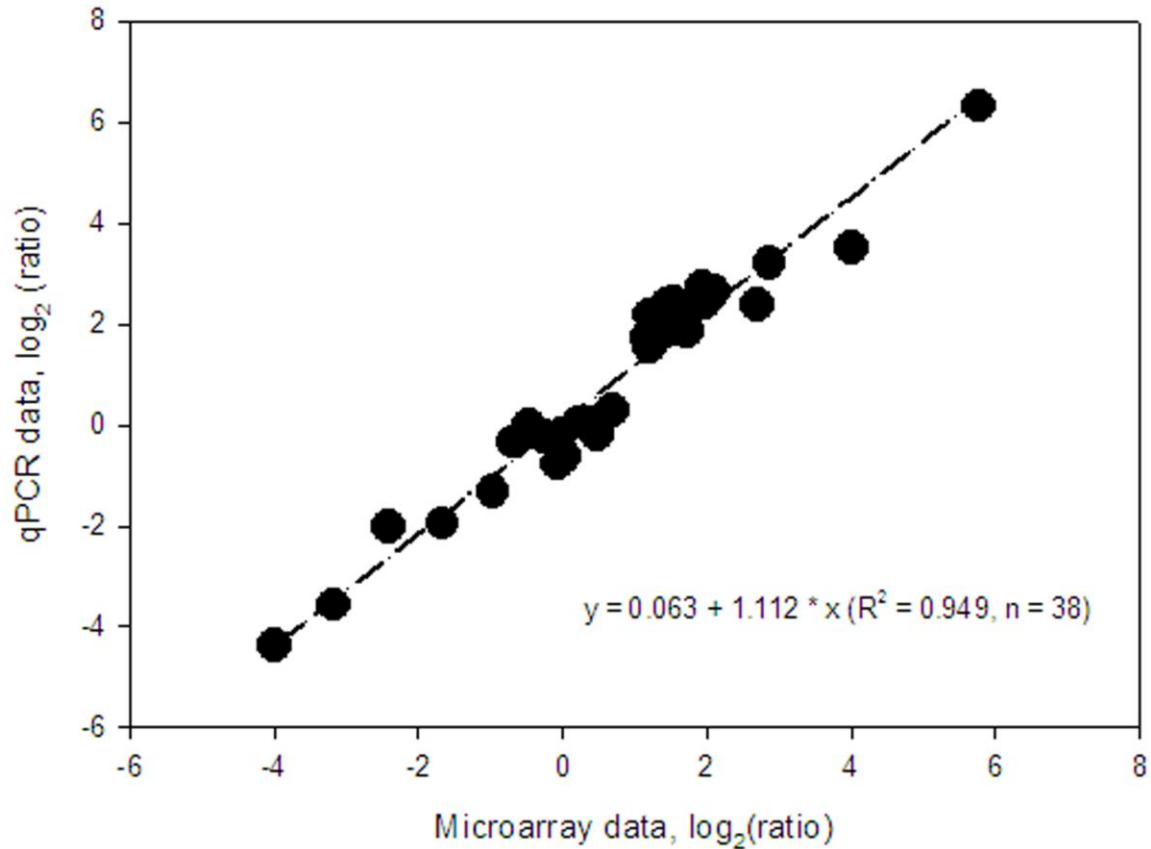


Fig. S4 Correlation of microarray data and RT-PCR data for 25 selected genes of *D. vulgaris*. 12 genes with a range of expression levels were randomly selected from salt adaptation, and 13 genes in three predicted operons were selected from both salt adaptation and salt shock experiments for RT-PCR to quantitatively verify the microarray data using specific primers (Table S1). A significant correlation ($R^2 = 0.949$) was observed for 38 data points.

Locus (gene, predicted function)

A. Efflux systems and ATPase

DVU0058 (Efflux transporter, RND family, MFP subunit)
DVU0059 (AcrB/AcrD/AcrF family protein)
DVU0060 (Efflux transporter, RND family, MFP subunit)
DVU0061 (Multidrug resistance protein, putative)
DVU0062 (RND efflux system, outer membrane protein)
DVU0063 (Transcriptional regulator, MarR family)
DVU0434 (*mnhA*, putative Ech hydrogenase, subunit EchA)
DVU2815 (Outer membrane efflux protein)
DVU2816 (Multidrug resistance protein)
DVU2817 (*acrA*, Multidrug resistance protein)
DVU3326 (Multidrug resistance protein, Smr family)
DVU3327 (Multidrug resistance protein, Smr family)
DVU0774 (*aptC*, ATP synthase, F1 epsilon subunit)
DVU0775 (*aptD*, ATP synthase, F1 beta subunit)
DVU0776 (*aptG*, ATP synthase, F1 gamma subunit)
DVU0777 (*aptA*, ATP synthase, F1 alpha subunit)
DVU0778 (*atpH*, ATP synthase, F1 delta subunit)
DVU0779 (*atpF2*, ATP synthase FO, B subunit, putative)
DVU0780 (*aptF1*, ATP synthase FO, B subunit, putative)

B. Sulfate reduction

DVU0846 (*apsB*, Adenylylsulphate reductase, beta subunit)
DVU0847 (*apsA*, Adenylyl-sulphate reductase, alpha subunit)
DVU0848 (*qmoA*, Heterodisulfide reductase, putative)
DVU0849 (*qmoB*, putative heterodisulfide reductase)
DVU0850 (*qmoC*, putative heterodisulfide reductase)

C. Cell motility and chemotaxis

DVU0048 (Chemotaxis protein MotB)
DVU0170 (Methyl-accepting chemotaxis protein)
DVU0591 (*mcpD*, Methyl-accepting chemotaxis protein)
DVU0608 (Methyl-accepting chemotaxis protein)
DVU0992 (*cheV-3*, Chemotaxis protein CheV)
DVU1458 (Chemotaxis protein CheZ, putative)
DVU1884 (Methyl-accepting chemotaxis protein)
DVU2585 (Methyl-accepting chemotaxis protein)
DVU3230 (Flagellar synthesis regulator FlhN)
DVU3231 (Flagellar biosynthesis protein FlhF, putative)

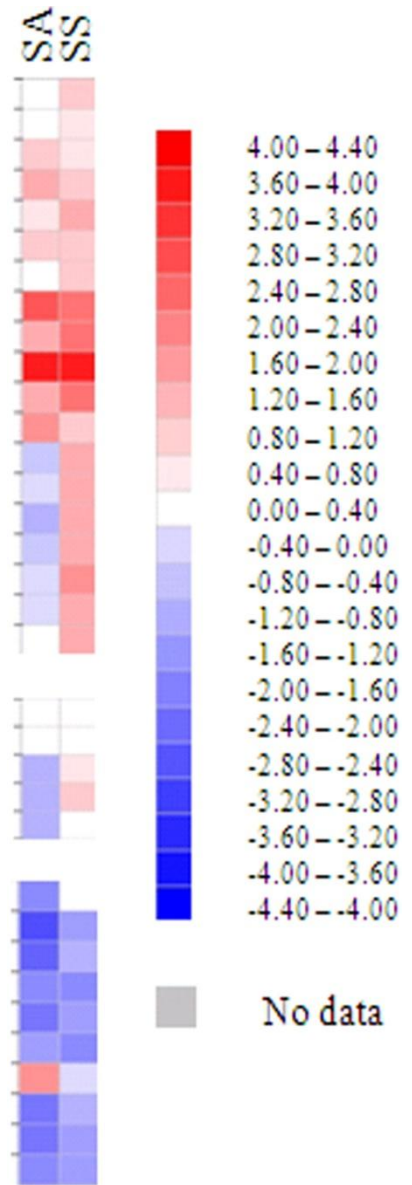


Fig. S5 A comparison of expression of representative genes of *D. vulgaris* involved in efflux systems, the ATP synthase, sulfate reduction, and cell motility under salt adaptation and salt shock (120 min). Details for data presentation are the same as described in Fig. S2.

Supplemental Data - Table S1

Table 1 ORFs, used primers, and their product sizes for reverse transcription real time PCR assay

Locus tag	Forward primer	Reverse primer	Predicted function	Size (bp)
DVU2867	GACTACGTGCTGGGCTTTGT	GCGGCGAAGTAGAAGAGGAA	Holin	98
DVU0722	TCGAGCGTATCATCCATTCA	CGCTGAGTGACGAAGTGAGT	Response regulator	99
DVU3133	GCCATCGTCTTTCTCGACTT	ATGTGGTTATGGCAGGGAAG	Glycerol uptake facilitator protein	100
DVU2093	CTCCATTTGCAAGACCATCC	ATCTCCATGCGCTTGTCTTC	ThiH protein	99
DVU2529	TCTCGACAACCTGTCACACC	TAGAGGGACTTGCCCACTT	Phosphoglycerate kinase	102
DVU1085	ACGCAAGGCCATAGACAGTT	CGCGTCTCACGCTCTATCTC	Phosphate transport system protein PhoU	99
DVU2526	ACTTCTTCGACCCTGAGACG	TATCTGTTCCGGGTTACCTT	Periplasmic [NiFe] hydrogenase, large subunit	101
DVU2574	TCGGAGATAGAGGTCTGTTTCG	GCACAGCACAGTGCAAGC	Ferrous ion transport protein, putative	99
DVU0724	ATGACCACGCTTCAGCTTTT	GGCGGATGGTAAGGTAGATG	Sodium/alanine symporter family protein	100
DVU0375	GAAGAACGACGTGCTCAACC	ACGTCTTGATCTCGCAGAC	Glu/Leu/Phe/Val dehydrogenase family protein	102
DVU2441	GCGTAACCCCTGAAGACATC	GCTCCTGCCTGAACATCCT	Heat shock protein, Hsp20 family	99
DVU2818	CAAGGATGTTGTGCTGCCTA	CACGGGAAAGTGTGGTGAAC	Hypothetical protein	99
DVU0774	CTCAGCGAGCAGGTTGATTA	TGGCCTTGTAGTAGAGGCTACC	AtpC, ATP synthase, F1 epsilon subunit	118
DVU0775	CTTGACGGTACGCTCGTTCT	GTTCAACACCCACCACGTT	AtpD, ATP synthase, F1 beta subunit	115
DVU0776	CAGATGGGTTTCGTTCTCGACTT	CTCACGAACTCGCCGTACA	AptG, ATP synthase, F1 gamma subunit	113
DVU0777	GCGATGGAATACACCACCAT	GCTTGCCGTTGTTACGGTAG	AptA, ATP synthase, F1 alpha subunit	115
DVU0778	TGAGAAGCGCAACGTCATT	ATATCCTGGATGAAGGCAAGG	atpH, ATP synthase, F1 delta subunit	114
DVU0779	AAATCAAGGCTGCCATCG	TTGTCGATGAGCTTTTTCGTG	atpF2, ATP synthase F0, B subunit, putative	118
DVU0780	AACTTTCTTGTACGCTGGTC	GGAAAACGCTCGGACTCTC	AptF1, ATP synthase F0, B subunit, putative	117
DVU1769	CTGCATCGCAAAGAAGTACG	CGATACCGCCTTCTTGAT	Periplasmic [Fe] hydrogenase, large subunit	119
DVU1770	TACATGCTTGACCGCATCA	CCGAGAGGCTTCTCAAGGTA	Periplasmic [Fe] hydrogenase, small subunit	119
DVU2571	ATCGGACGCACACTCGAAC	GTACCAAGCGTGGAGACGAT	Ferrous iron transport protein B	113
DVU2572	TGAACTTGGCAGGCGTGT	AGAGGGTGAACCCCTTGAGT	Ferrous iron transport protein A, putative	116
DVU2573	GACGTGGGATACAATGGTCGT	TACCCGTGCCGCCGCTTC	Hypothetical protein	119
DVU2574	CCGGTTCCGGAGATAGAGGTC	ACAGGTTCCGCACAGCACAGT	Ferrous ion transport protein, putative	112

Supplemental Table S2-7

Table S2 Up-regulated ORFs under salt adaptation but no significant changes under salt shock

Locus tag	Salt shock		Salt adaptation		Annotation
	Ratio	Zscore	Ratio	Zscore	
DVU0016	0.39	0.78	2.11	2.75	hypothetical protein
DVU0024	0.93	1.68	2.38	3.45	conserved hypothetical protein
DVU0086	0.21	0.40	1.06	2.00	hypothetical protein
DVU0103	0.98	1.69	1.94	3.19	cation ABC transporter, ATP-binding protein, putative
DVU0115	0.74	1.19	1.58	2.01	shikimate 5-dehydrogenase
DVU0122	-1.30	-1.96	2.07	3.78	hypothetical protein
DVU0124	0.73	1.06	1.38	2.33	hypothetical protein
DVU0163	0.24	0.44	1.35	2.48	lipoprotein, putative
DVU0186	-0.32	-0.51	1.65	2.96	conserved hypothetical protein
DVU0196	0.66	1.25	1.53	2.35	hypothetical protein
DVU0225	0.02	0.04	1.59	3.05	hypothetical protein
DVU0236	1.00	1.76	1.92	3.24	site-specific recombinase, phage integrase family
DVU0297	-0.17	-0.31	1.32	2.44	hypothetical protein
DVU0303	1.01	1.65	3.28	4.55	hypothetical protein
DVU0361	0.12	0.20	1.69	2.35	acetolactate synthase III, small subunit, putative
DVU0365	0.70	1.34	2.92	4.18	conserved hypothetical protein
DVU0375	0.70	1.12	2.70	3.69	Glu/Leu/Phe/Val dehydrogenase family protein
DVU0411	0.52	0.96	1.76	3.05	heptosyltransferase family protein
DVU0419	-0.14	-0.24	1.63	3.01	carboxynorspermidine decarboxylase
DVU0420	0.19	0.33	1.69	2.58	hypothetical protein
DVU0444	0.79	1.37	2.18	2.48	CBS domain protein
DVU0473	0.18	0.33	1.45	2.63	hypothetical protein
DVU0497	0.02	0.03	2.98	4.71	hypothetical protein
DVU0532	1.13	1.83	2.76	2.25	hmc operon protein 5
DVU0534	0.38	0.67	2.42	3.83	hmc operon protein 3
DVU0559	-0.11	-0.20	1.90	2.75	lipoprotein, putative
DVU0572	0.46	0.89	1.90	3.41	hypothetical protein
DVU0586	-0.56	-1.09	2.13	3.29	hypothetical protein
DVU0593	0.87	1.68	2.74	3.54	L-lysine exporter, putative
DVU0620	-0.22	-0.43	1.37	2.17	endoribonuclease, L-PSP family
DVU0724	0.53	1.04	1.42	2.69	sodium/alanine symporter family protein
DVU0753	0.27	0.51	1.17	2.09	amino acid ABC transporter, ATP-binding protein
DVU0758	0.11	0.21	1.66	3.08	hypothetical protein
DVU0772	-0.85	-1.58	2.25	2.40	hypothetical protein
DVU0781	0.43	0.84	1.56	2.57	hypothetical protein
DVU0782	0.51	0.85	1.15	2.04	hypothetical protein
DVU0813	-0.06	-0.12	1.35	2.16	heat-inducible transcription repressor HrcA
DVU0948	0.85	1.46	1.75	2.51	conserved hypothetical protein
DVU0949	-0.12	-0.14	3.01	3.10	conserved domain protein
DVU0999	0.46	0.89	1.46	2.08	thio:disulfide interchange protein, putative
DVU1068	0.42	0.78	2.70	4.57	branched-chain amino acid ABC transporter, permease protein
DVU1072	0.65	1.25	1.62	2.61	conserved hypothetical protein
DVU1091	-0.01	-0.01	1.26	2.15	conserved hypothetical protein
DVU1105	0.22	0.33	1.34	2.03	hypothetical protein
DVU1106	0.45	0.81	2.18	2.70	hypothetical protein
DVU1114	0.18	0.24	1.97	2.47	virion morphogenesis protein
DVU1115	0.46	0.83	2.95	3.96	conserved hypothetical protein
DVU1118	-0.36	-0.58	2.51	2.91	conserved hypothetical protein
DVU1121	0.67	1.23	2.26	3.33	hypothetical protein
DVU1122	0.39	0.57	3.12	3.60	portal protein, putative

DVU1123	0.32	0.58	3.03	3.73	conserved domain protein
DVU1124	0.92	1.34	3.47	5.12	hypothetical protein
DVU1130	0.43	0.82	1.72	2.48	DNA-binding protein
DVU1132	0.62	1.13	1.90	3.15	conserved hypothetical protein
DVU1140	0.51	0.97	1.95	3.12	bacteriophage transposase A protein, putative
DVU1143	0.20	0.33	2.57	3.01	hypothetical protein
DVU1154	0.94	1.81	4.12	5.32	hypothetical protein
DVU1166	-0.36	-0.69	2.05	3.24	hypothetical protein
DVU1173	0.04	0.08	1.64	2.60	integral membrane protein MviN
DVU1177	-0.09	-0.14	3.28	2.99	hypothetical protein
DVU1178	-0.44	-0.83	2.00	2.56	hypothetical protein
DVU1179	-0.05	-0.09	2.45	4.44	aldehyde:ferredoxin oxidoreductase, tungsten-containing
DVU1212	1.07	1.26	1.40	2.43	fxsA protein
DVU1256	0.18	0.35	1.49	2.62	heptosyltransferase family protein
DVU1410	0.20	0.40	1.11	2.03	conserved domain protein
DVU1473	0.81	1.22	1.15	2.15	hypothetical protein
DVU1475	0.28	0.54	1.79	2.47	PhoU family protein
DVU1479	0.33	0.53	1.21	2.29	conserved hypothetical protein
DVU1489	-0.12	-0.20	1.22	2.26	hypothetical protein
DVU1490	0.33	0.59	2.59	2.76	tail tape measure protein, putative
DVU1499	0.87	1.61	1.31	2.09	hypothetical protein
DVU1513	0.79	1.12	1.76	2.21	conserved hypothetical protein
DVU1514	0.76	1.31	1.81	2.65	hypothetical protein
DVU1515	0.24	0.35	1.54	2.03	type II DNA modification methyltransferase, putative
DVU1517	0.42	0.70	1.62	2.59	transcriptional regulator cII, putative
DVU1525	0.76	1.10	1.50	2.67	conserved domain protein
DVU1637	0.91	1.47	1.78	3.20	hypothetical protein
DVU1638	0.51	0.92	1.62	2.76	conserved domain protein
DVU1639	0.98	1.91	1.29	2.29	conserved domain protein
DVU1654	-0.15	-0.27	2.46	3.32	site-specific recombinase, phage integrase family
DVU1661	0.53	1.02	1.16	2.21	hypothetical protein
DVU1699	1.00	1.85	2.20	3.05	hypothetical protein
DVU1700	0.68	1.19	2.82	4.11	metallo-beta-lactamase family protein
DVU1712	0.53	0.47	2.92	4.46	hypothetical protein
DVU1713	0.35	0.33	1.45	2.47	hypothetical protein
DVU1716	0.73	1.12	1.93	2.42	hypothetical protein
DVU1717	0.20	0.34	1.58	2.72	hypothetical protein
DVU1719	1.42	1.83	1.83	2.66	conserved domain protein
DVU1720	0.49	0.70	1.85	3.38	hypothetical protein
DVU1723	0.24	0.34	2.34	3.21	hypothetical protein
DVU1740	0.48	0.81	2.54	3.81	hypothetical protein
DVU1741	0.01	0.02	2.52	4.36	hypothetical protein
DVU1750	0.24	0.47	1.53	2.75	hypothetical protein
DVU1757	0.12	0.17	2.76	3.00	site-specific recombinase, phage integrase family
DVU1763	0.88	1.67	2.69	2.73	hypothetical protein
DVU1767	0.67	1.07	1.78	2.90	radical SAM domain protein
DVU1769	-0.69	-1.30	1.57	2.07	periplasmic [Fe] hydrogenase, large subunit
DVU1770	-0.07	-0.12	1.62	2.19	periplasmic [Fe] hydrogenase, small subunit
DVU1884	0.39	0.57	1.91	2.35	methyl-accepting chemotaxis protein
DVU1905	0.39	0.72	1.56	2.40	hypothetical protein
DVU1919	0.08	0.13	1.66	2.98	hydrogenase expression/formation protein, putative
DVU1965	0.62	1.05	1.76	3.25	hypothetical protein
DVU1968	0.75	1.41	1.83	2.27	oxidoreductase, putative
DVU2003	0.58	1.13	2.69	4.17	transposase, IS5 family, truncation
DVU2007	0.11	0.21	2.04	3.67	nuclease, putative

DVU2017	-0.13	-0.22	1.56	2.83	ISDvu5, transposase
DVU2067	1.02	1.78	1.68	2.80	GGDEF domain protein
DVU2070	0.81	1.33	3.39	4.73	TPR domain protein
DVU2080	0.07	0.12	1.44	2.52	hypothetical protein
DVU2101	1.06	1.95	3.87	3.75	conserved hypothetical protein
DVU2106	0.32	0.50	2.09	3.61	sigma-54 dependent transcriptional regulator
DVU2107	0.46	0.87	2.32	2.20	hypothetical protein
DVU2122	-0.09	-0.14	2.44	2.66	type II/IV secretion system protein
DVU2125	-0.22	-0.31	2.04	3.22	TPR domain protein
DVU2127	0.14	0.23	2.43	2.94	von Willebrand factor type A domain protein
DVU2129	-0.21	-0.36	2.88	3.04	sensory box histidine kinase/response regulator
DVU2145	0.87	1.62	1.71	3.00	chloramphenicol acetyltransferase, putative
DVU2146	-0.39	-0.73	2.45	4.06	hypothetical protein
DVU2154	0.73	1.13	2.40	4.25	tail assembly protein, putative
DVU2155	0.08	0.14	1.64	2.07	hypothetical protein
DVU2156	0.69	0.78	2.52	3.79	hypothetical protein
DVU2158	0.73	1.23	3.11	3.12	hypothetical protein
DVU2159	0.55	0.92	2.85	4.95	hypothetical protein
DVU2160	0.58	0.99	2.15	2.79	hypothetical protein
DVU2161	0.41	0.55	2.77	3.48	hypothetical protein
DVU2163	-0.15	-0.23	1.79	2.10	hypothetical protein
DVU2164	0.18	0.32	2.07	3.19	lipoprotein, putative
DVU2165	-0.58	-1.02	2.37	3.39	lysozyme, putative
DVU2167	-0.09	-0.17	2.45	3.13	hypothetical protein
DVU2172	-0.19	-0.29	2.07	2.37	hypothetical protein
DVU2181	0.46	0.78	1.49	2.02	antirepressor, putative
DVU2182	0.99	1.41	4.18	3.54	hypothetical protein
DVU2183	0.82	1.13	5.05	3.43	hypothetical protein
DVU2189	0.16	0.28	1.36	2.18	transcriptional regulator cII, putative
DVU2204	0.27	0.47	1.81	3.22	tryptophanase
DVU2218	0.33	0.61	2.17	2.93	GTP-binding protein, putative
DVU2247	0.18	0.31	2.77	4.76	antioxidant, AhpC/Tsa family
DVU2249	0.46	0.76	2.75	3.51	hypothetical protein
DVU2266	0.00	0.00	3.04	3.79	hypothetical protein
DVU2278	0.70	1.03	2.82	4.94	membrane protein, putative
DVU2283	0.99	1.80	1.38	2.14	hypothetical protein
DVU2327	0.12	0.24	2.39	3.81	hypothetical protein
DVU2341	0.78	1.18	1.56	2.76	amino acid ABC transproter, permease protein, His/Glu/Gln/Arg/opine family
DVU2344	0.23	0.37	2.85	3.31	hypothetical protein
DVU2358	1.02	1.67	1.75	2.68	hypothetical protein
DVU2372	0.45	0.84	1.21	2.29	hypothetical protein
DVU2423	0.90	1.66	2.41	3.60	transcriptional regulator, putative
DVU2426	0.16	0.29	2.23	2.83	hypothetical protein
DVU2441	0.94	1.67	4.01	7.42	heat shock protein, Hsp20 family
DVU2442	0.72	1.40	3.64	6.72	heat shock protein, Hsp20 family
DVU2450	0.32	0.61	1.21	2.19	conserved hypothetical protein
DVU2480	-0.08	-0.15	2.75	4.20	hypothetical protein
DVU2494	0.17	0.31	1.70	3.07	peptidase, M48 family
DVU2542	0.28	0.45	1.88	3.30	hypothetical protein
DVU2556	-0.09	-0.17	1.45	2.25	hypothetical protein
DVU2559	0.35	0.52	2.47	4.14	adenosylmethionine--8-amino-7-oxononanoate aminotransferase
DVU2560	1.22	1.94	3.29	2.03	conserved domain protein
DVU2567	0.20	0.33	3.48	3.32	conserved hypothetical protein
DVU2573	1.18	1.90	1.94	3.43	hypothetical protein

DVU2577	0.02	0.04	1.48	2.53	DNA-binding response regulator, LuxR family
DVU2595	0.36	0.63	1.83	3.04	hypothetical protein
DVU2602	0.27	0.38	2.62	3.65	conserved domain protein
DVU2611	0.62	1.22	3.44	5.59	conserved hypothetical protein
DVU2637	0.10	0.19	2.95	4.02	HAMP domain protein
DVU2671	0.80	1.54	1.32	2.28	HDIG/HD/KH domain protein
DVU2680	0.18	0.29	1.90	3.31	flavodoxin
DVU2681	0.79	1.34	2.50	2.71	hypothetical protein
DVU2688	0.38	0.70	1.59	2.35	bacteriophage transposase A protein
DVU2690	0.59	1.08	1.92	2.42	hypothetical protein
DVU2692	0.31	0.53	1.71	2.09	conserved domain protein
DVU2695	0.33	0.50	2.83	4.38	conserved hypothetical protein
DVU2697	0.92	1.25	1.15	2.01	hypothetical protein
DVU2700	0.35	0.63	1.44	2.24	hypothetical protein
DVU2701	0.35	0.62	2.10	2.40	hypothetical protein
DVU2704	0.06	0.11	2.24	2.72	conserved hypothetical protein
DVU2706	0.24	0.31	2.21	2.75	conserved hypothetical protein
DVU2720	0.57	1.10	1.78	2.09	hypothetical protein
DVU2724	0.36	0.65	2.09	2.92	phage baseplate assembly protein V, putative
DVU2725	0.97	1.48	1.87	3.27	membrane protein, putative
DVU2726	-0.16	-0.31	1.30	2.36	hypothetical protein
DVU2727	0.24	0.46	2.40	3.14	conserved hypothetical protein
DVU2740	0.61	0.96	3.18	5.34	high-affinity branched-chain amino acid ABC transporter, ATP-binding protein
DVU2742	0.93	1.76	1.79	2.08	high-affinity branched chain amino acid ABC transporter, permease protein
DVU2755	0.60	1.12	1.49	2.66	conserved hypothetical protein
DVU2769	0.30	0.56	1.42	2.49	conserved hypothetical protein
DVU2775	1.07	1.94	1.32	2.10	hypothetical protein
DVU2786	0.17	0.23	2.48	3.86	hypothetical protein
DVU2789	0.13	0.22	2.21	3.49	Gpr1/Fun34/YaaH family protein
DVU2808	-0.04	-0.08	2.61	3.79	TonB domain protein
DVU2827	0.35	0.61	1.41	2.06	sigma-54 dependent transcriptional regulator
DVU2828	0.11	0.21	2.18	2.30	site-specific recombinase, phage integrase family
DVU2856	0.09	0.17	2.05	2.91	conserved domain protein
DVU2874	0.69	1.16	1.70	2.90	hypothetical protein
DVU2917	0.34	0.60	1.33	2.42	UDP-3-0-acyl N-acetylglucosamine deacetylase
DVU2919	0.11	0.20	1.38	2.50	hypothetical protein
DVU2986	0.96	1.87	2.47	4.48	phage shock protein C
DVU3021	0.90	1.75	1.77	2.53	HDIG domain protein
DVU3081	0.20	0.34	1.45	2.19	membrane protein, putative
DVU3083	0.24	0.47	1.31	2.16	hypothetical protein
DVU3093	0.48	0.90	1.14	2.05	rubredoxin-like protein
DVU3095	0.69	1.25	2.07	2.87	transcriptional regulator, Fur family
DVU3105	-0.37	-0.69	1.22	2.32	hypothetical protein
DVU3110	0.87	1.69	1.84	2.33	L-aspartate oxidase, putative
DVU3115	0.48	0.94	2.03	3.66	hypothetical protein
DVU3124	0.64	0.86	2.16	4.08	hypothetical protein
DVU3129	0.14	0.26	2.50	3.69	hypothetical protein
DVU3138	0.56	1.05	2.18	3.92	hypothetical protein
DVU3143	-0.48	-0.84	2.15	2.73	iron-sulfur cluster-binding protein
DVU3194	0.74	1.10	1.45	2.32	GTP-binding protein EngA
DVU3251	0.17	0.29	2.64	4.37	membrane protein, HPP family
DVU3285	0.88	1.38	2.17	2.40	hypothetical protein
DVU3297	0.35	0.65	1.34	2.48	tryptophan-specific transport protein

DVU3311	0.41	0.77	1.35	2.20	hypothetical protein
DVU3313	0.08	0.14	2.32	4.07	transcriptional regulator, LysR family
DVU3325	0.78	1.49	1.62	2.74	hypothetical protein
DVU3328	0.67	1.25	1.44	2.65	hypothetical protein
DVU3332	0.90	1.67	1.62	2.54	heavy metal translocating P-type ATPase
DVU3333	0.72	0.91	2.63	2.23	hypothetical protein
DVU3354	0.27	0.50	2.21	2.30	hypothetical protein
DVUA0003	1.56	1.53	1.40	2.16	hypothetical protein
DVUA0018	-0.23	-0.40	2.14	3.84	hypothetical protein
DVUA0026	-0.74	-0.80	2.15	2.72	hypothetical protein
DVUA0028	0.54	0.79	1.99	3.09	hypothetical protein
DVUA0085	0.32	0.38	2.08	3.08	conserved hypothetical protein
DVUA0103	0.16	0.29	1.38	2.44	type III secretion protein, HrpO family
DVUA0132	-0.80	-0.93	1.21	2.01	CRISPR-associated protein, TM1801 family
DVUA0140	0.44	0.49	4.14	3.56	hypothetical protein
DVUA0141	0.06	0.09	1.32	2.23	hypothetical protein

Table S3 Down-regulated ORFs under salt adaptation but no significant changes under salt shock

Locus tag	Salt shock		Salt adaptation		Annotation
	Ratio	Zscore	Ratio	Zscore	
DVU0818	1.20	2.03	-1.53	-2.36	conserved domain protein
DVU0027	-1.10	-1.95	-1.63	-2.22	membrane protein, putative
DVU0048	0.41	0.79	-1.33	-2.17	chemotaxis protein MotB
DVU0053	-0.25	-0.47	-1.26	-2.10	sulfate permease, putative
DVU0075	-0.47	-0.90	-2.26	-2.91	aminotransferase, DegT/DnrJ/EryC1/StrS family
DVU0077	-0.27	-0.54	-1.39	-2.26	conserved hypothetical protein
DVU0116	0.15	0.29	-1.65	-2.58	polysaccharide deacetylase family protein
DVU0127	-0.51	-0.99	-1.96	-3.52	membrane protein, putative
DVU0134	-0.06	-0.11	-1.61	-2.35	glycosyl transferase, group 2 family protein
DVU0150	0.19	0.32	-1.74	-2.27	membrane protein, putative
DVU0170	-1.00	-1.58	-2.44	-3.55	methyl-accepting chemotaxis protein
DVU0189	-0.27	-0.51	-2.72	-3.56	phage/plasmid primase, P4 family
DVU0192	0.22	0.42	-1.69	-2.88	adenine specific DNA methyltransferase, putative
DVU0194	-0.34	-0.59	-2.47	-3.82	terminase, large subunit, putative
DVU0195	-0.11	-0.21	-1.43	-2.37	hypothetical protein
DVU0201	-1.02	-1.85	-2.85	-3.58	hypothetical protein
DVU0202	-1.07	-1.96	-2.71	-3.29	holin
DVU0214	-0.63	-1.23	-2.06	-3.38	tail/DNA circulation protein, putative
DVU0216	-0.79	-1.43	-2.45	-3.24	phage baseplate assembly protein V, putative
DVU0217	-0.84	-1.62	-2.26	-3.94	tail protein, putative
DVU0218	-0.77	-1.46	-1.35	-2.32	tail protein, putative
DVU0221	-0.55	-0.96	-1.91	-2.87	tail fiber assembly protein, putative
DVU0233	0.51	0.97	-2.18	-2.45	hypothetical protein
DVU0235	1.00	1.92	-1.33	-2.11	hypothetical protein
DVU0254	-0.35	-0.63	-1.32	-2.01	hypothetical protein
DVU0258	-0.02	-0.03	-1.43	-2.23	sensory box histidine kinase/response regulator
DVU0277	-0.17	-0.33	-1.40	-2.29	transcriptional regulator, AraC family
DVU0293	-0.55	-1.02	-1.73	-2.87	prokaryotic dksA/traR C4-type zinc finger family protein
DVU0298	-0.25	-0.45	-1.49	-2.09	hypothetical protein
DVU0305	-1.01	-1.87	-1.30	-2.01	ferredoxin II
DVU0339	-0.40	-0.74	-1.70	-2.25	D-isomer specific 2-hydroxyacid dehydrogenase family protein
DVU0340	-0.72	-1.12	-1.26	-2.01	acetyltransferase, CysE/LacA/LpxA/NodL family
DVU0341	-0.98	-1.88	-2.29	-2.93	3-deoxy-D-manno-octulosonate cytidyltransferase
DVU0348	-0.48	-0.84	-2.12	-3.31	hypothetical protein

DVU0350	-0.33	-0.63	-1.76	-2.25	spore coat polysaccharide biosynthesis protein spsF
DVU0372	0.33	0.50	-2.31	-2.08	membrane protein, putative
DVU0424	-0.04	-0.07	-1.24	-2.08	cardiolipin synthetase
DVU0425	-0.11	-0.20	-2.09	-3.79	hypothetical protein
DVU0446	-0.11	-0.19	-2.55	-3.33	sodium/solute symporter family protein
DVU0591	-0.53	-1.04	-2.02	-2.87	methyl-accepting chemotaxis protein
DVU0650	-1.11	-1.43	-2.39	-4.11	chelataase, putative
DVU0653	-0.45	-0.74	-2.00	-2.19	sigma-54 dependent transcriptional regulator, putative/response regulator
DVU0676	-0.74	-1.45	-1.83	-2.81	amino acid ABC transporter, permease protein, His/Glu/Gln/Arg/opine family
DVU0680	-0.11	-0.19	-2.04	-3.92	sensory box histidine kinase
DVU0707	-0.13	-0.23	-1.14	-2.00	TRAP dicarboxylate family transporter
DVU0722	-0.69	-1.07	-3.17	-5.43	response regulator
DVU0729	-0.65	-1.27	-1.49	-2.17	hypothetical protein
DVU0731	-0.10	-0.17	-1.97	-2.62	hypothetical protein
DVU0747	0.40	0.48	-1.78	-2.54	ABC transporter, ATP-binding protein
DVU0769	-0.28	-0.56	-1.67	-2.08	pyridoxal kinase, putative
DVU0786	-0.44	-0.62	-1.36	-2.20	penicillin-binding protein
DVU0807	-0.06	-0.09	-1.40	-2.20	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase
DVU0836	0.86	1.62	-1.23	-2.04	tRNA (guanine-N1)-methyltransferase
DVU0867	-0.14	-0.24	-1.97	-2.49	aromatic amino acid decarboxylase, putative
DVU0884	0.03	0.06	-1.62	-2.28	conserved hypothetical protein
DVU0897	0.02	0.03	-1.61	-2.52	RNA modification enzyme, MiaB-family
DVU0899	-0.31	-0.61	-1.20	-2.16	conserved hypothetical protein
DVU0934	0.09	0.15	-1.40	-2.10	hypothetical protein
DVU0961	-0.74	-1.38	-1.79	-2.61	conserved hypothetical protein
DVU0962	-0.46	-0.85	-2.18	-3.07	hypothetical protein
DVU0965	-0.57	-0.91	-1.38	-2.19	hypothetical protein
DVU0978	-0.49	-0.90	-1.99	-2.64	ABC transporter, periplasmic substrate-binding protein, putative
DVU0980	-0.52	-1.02	-2.92	-3.90	DAK2 domain protein
DVU0981	-0.89	-1.65	-1.77	-2.76	multiphosphoryl transfer protein, putative
DVU0990	-0.04	-0.08	-1.79	-2.09	endonuclease III, putative
DVU0991	-0.41	-0.63	-2.02	-2.33	conserved hypothetical protein
DVU0992	-1.10	-1.98	-1.81	-3.10	chemotaxis protein CheV
DVU1004	-0.48	-0.91	-2.19	-3.41	membrane protein, putative
DVU1025	-0.23	-0.45	-1.49	-2.63	uracil phosphoribosyltransferase
DVU1272	0.58	0.89	-1.93	-2.74	general secretion pathway protein E, putative
DVU1284	0.00	0.01	-1.50	-2.11	primosomal protein n
DVU1390	-0.85	-1.07	-1.44	-2.43	hypothetical protein
DVU1447	-0.64	-1.20	-1.63	-2.15	CgeB family protein
DVU1555	0.10	0.15	-2.29	-2.83	hypothetical protein
DVU1559	-0.12	-0.21	-1.48	-2.18	aldehyde oxidoreductase
DVU1568	-1.00	-1.87	-1.90	-3.19	ferritin
DVU1570	-0.46	-0.89	-1.96	-2.39	pyruvate ferredoxin oxidoreductase, beta subunit
DVU1588	0.10	0.17	-1.52	-2.51	hypoxanthine phosphoribosyltransferase
DVU1593	0.73	1.42	-2.12	-2.44	chemotaxis protein CheY
DVU1608	-0.52	-0.96	-1.85	-2.20	DNA ligase, NAD-dependent
DVU1687	-0.81	-1.36	-1.40	-2.01	glycosyl transferase, group 2 family protein
DVU1772	-0.13	-0.24	-2.05	-2.07	pyridine nucleotide-disulfide oxidoreductase
DVU1811	-1.32	-1.87	-1.50	-2.26	protoheme IX farnesyltransferase, putative
DVU1812	-1.09	-1.89	-1.66	-2.31	cytochrome c oxidase, subunit II, putative
DVU1878	0.09	0.16	-1.87	-2.11	threonine aldolase, low-specificity
DVU1879	0.24	0.44	-1.47	-2.40	glycosyl transferase, group 1 family protein
DVU1881	-1.08	-1.99	-1.45	-2.46	phoH family protein

DVU1912	-0.06	-0.12	-1.17	-2.03	conserved hypothetical protein TIGR00150
DVU1913	-0.39	-0.77	-2.36	-2.72	aspartate kinase, monofunctional class
DVU1946	-0.35	-0.69	-1.73	-2.08	pyruvate ferredoxin oxidoreductase, beta subunit, putative
DVU1991	-0.66	-1.08	-1.42	-2.49	hypothetical protein
DVU2012	-0.37	-0.65	-2.72	-4.47	hypothetical protein
DVU2037	-0.97	-1.90	-2.02	-3.32	cobS protein, putative
DVU2047	-0.25	-0.46	-1.66	-2.25	hypothetical protein
DVU2093	0.08	0.13	-1.66	-2.73	thiH protein
DVU2117	-0.50	-0.94	-1.45	-2.35	membrane protein, putative
DVU2119	-0.80	-1.31	-2.14	-3.70	type II/III secretion system protein
DVU2124	-0.18	-0.32	-2.47	-2.89	conserved hypothetical protein
DVU2251	0.42	0.84	-1.51	-2.67	DNA-binding protein
DVU2306	-1.02	-1.99	-1.55	-2.89	phosphate transporter family protein
DVU2345	-0.68	-1.31	-2.26	-2.22	hypothetical protein
DVU2364	-0.82	-1.48	-2.58	-3.89	aminotransferase, classes I and II
DVU2388	-0.64	-1.23	-1.98	-2.74	tolQ protein
DVU2431	-0.01	-0.02	-1.22	-2.01	hypothetical protein
DVU2449	-0.54	-0.82	-1.77	-2.49	S-adenosylmethionine synthetase
DVU2472	-0.84	-1.55	-1.24	-2.26	conserved hypothetical protein
DVU2478	-0.80	-1.42	-1.97	-2.65	phosphate ABC transporter, permease protein, putative
DVU2483	-0.56	-1.05	-1.97	-2.23	cytochrome c family protein
DVU2503	-1.02	-1.98	-1.45	-2.53	UDP-N-acetylmuramate--alanine ligase
DVU2544	0.01	0.02	-1.99	-2.96	iron-sulfur cluster-binding protein
DVU2568	-0.20	-0.31	-2.03	-2.67	peptidase, M20/M25/M40 family
DVU2585	-0.72	-1.38	-1.95	-2.98	methyl-accepting chemotaxis protein
DVU2620	-0.47	-0.88	-1.40	-2.40	conserved hypothetical protein
DVU2658	-0.09	-0.17	-1.75	-2.71	conserved hypothetical protein
DVU2673	-0.82	-1.64	-1.72	-2.15	anaerobic glycerol-3-phosphate dehydrogenase, subunit A, truncation
DVU2676	-0.95	-1.52	-3.30	-3.09	hypothetical protein
DVU2677	-0.02	-0.03	-1.72	-2.12	sensor histidine kinase/response regulator
DVU2699	-0.03	-0.06	-2.85	-4.07	transglycosylase SLT domain protein
DVU2735	-0.61	-1.01	-1.73	-2.10	phenylacetate-coenzyme A ligase
DVU2763	-0.18	-0.35	-1.87	-2.50	TPR/GGDEF domain protein
DVU2806	-0.98	-1.65	-1.51	-2.05	MotA/TolQ/ExbB proton channel family protein
DVU2807	-0.29	-0.56	-2.20	-2.45	biopolymer transport protein, ExbD/TolR family
DVU2851	-0.95	-1.73	-2.67	-4.42	tail protein, putative
DVU2853	-0.46	-0.89	-2.93	-4.24	phage baseplate assembly protein V, putative
DVU2857	-0.92	-1.79	-2.47	-3.63	conserved hypothetical protein
DVU2863	-1.11	-2.00	-4.14	-7.26	hypothetical protein
DVU2866	-1.09	-1.98	-2.79	-3.44	conserved hypothetical protein
DVU2897	-0.56	-0.97	-2.02	-2.18	conserved hypothetical protein
DVU2898	0.12	0.14	-1.86	-2.84	conserved hypothetical protein
DVU2901	0.10	0.19	-1.42	-2.14	aspartate carbamoyltransferase
DVU2970	-0.71	-1.02	-1.55	-2.04	acetyltransferase, GNAT family
DVU2983	1.01	1.86	-2.37	-2.23	3-isopropylmalate dehydratase, small subunit
DVU2984	0.98	1.87	-3.14	-3.46	conserved hypothetical protein
DVU2985	0.68	1.35	-1.54	-2.55	3-isopropylmalate dehydrogenase
DVU2996	-0.45	-0.72	-1.93	-3.09	NAD-dependent epimerase/dehydratase family protein
DVU2997	-0.31	-0.60	-2.04	-3.05	hypothetical protein
DVU3010	-0.80	-1.36	-1.53	-2.47	aminotransferase, DegT/DnrJ/EryC1/StrS family
DVU3018	-0.70	-1.25	-1.40	-2.11	radical SAM domain protein
DVU3055	-0.17	-0.30	-2.16	-2.12	ribonuclease, Rne/Rng family
DVU3068	-0.06	-0.12	-1.48	-2.09	GAF domain/sensory box/EAL domain protein
DVU3074	0.24	0.46	-1.66	-2.12	membrane protein, putative

DVU3099	-0.71	-1.40	-1.61	-2.13	tolQ protein
DVU3104	-0.27	-0.52	-1.70	-2.58	peptidoglycan-associated lipoprotein, putative
DVU3112	-0.18	-0.35	-1.60	-2.11	TPR domain protein
DVU3126	-0.67	-1.19	-1.54	-2.23	paraquat-inducible protein A, degenerate
DVU3131	-0.23	-0.45	-1.94	-3.12	transcriptional regulator, putative
DVU3133	-0.47	-0.91	-2.41	-2.40	glycerol uptake facilitator protein
DVU3134	-0.53	-0.93	-1.44	-2.21	glycerol kinase
DVU3196	0.08	0.15	-1.74	-2.89	twin-arginine translocation pathway signal sequence domain protein
DVU3230	-0.93	-1.72	-1.85	-2.37	flagellar synthesis regulator FleN
DVU3235	-1.06	-2.00	-1.18	-2.08	IMP cyclohydrolase, putative
DVU3294	-0.68	-1.32	-2.27	-2.45	aldehyde dehydrogenase (NADP) family protein
DVU3321	-0.43	-0.80	-2.25	-3.69	hypothetical protein
DVU3324	0.49	0.91	-1.83	-2.13	ABC transporter, ATP-binding protein
DVU3342	-0.10	-0.15	-1.21	-2.32	hypothetical protein
DVU3349	-0.80	-1.47	-1.43	-2.02	pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-binding domain protein
DVU3371	-0.95	-1.46	-3.06	-3.71	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase
DVUA0023	-0.79	-1.25	-2.29	-2.77	ABC transporter, permease protein, putative
DVUA0025	-1.74	-1.40	-2.02	-2.28	response regulator receiver domain protein
DVUA0061	-0.01	-0.02	-1.45	-2.42	membrane protein, putative
DVUA0138	-0.09	-0.14	-2.42	-2.67	sensor histidine kinase

Table S4 Up-regulated ORFs under salt shock but no significant changes under salt adaptation

Locus tag	Salt shock		Salt adaptation		Annotation
	Ratio	Zscore	Ratio	Zscore	
DVU0051	1.20	2.35	0.16	0.15	conserved hypothetical protein TIGR00044
DVU0052	1.09	2.06	0.68	1.11	GTP-binding protein Era
DVU0058	1.05	2.01	0.45	0.47	efflux transporter, RND family, MFP subunit
DVU0062	1.63	3.14	0.88	1.72	RND efflux system, outer membrane protein, NodT family
DVU0063	1.25	2.21	1.04	1.83	transcriptional regulator, MarR family
DVU0066	2.13	3.21	0.84	0.80	cytidine/deoxycytidylate deaminase domain protein
DVU0087	1.35	2.60	0.78	1.52	conserved domain protein
DVU0094	1.41	2.64	-0.06	-0.04	methyl-accepting chemotaxis protein
DVU0153	1.35	2.59	0.39	0.70	hypothetical protein
DVU0230	2.03	3.77	1.36	1.54	transcriptional regulator cII, putative
DVU0285	1.22	2.28	0.33	0.46	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit
DVU0368	1.77	2.57	-0.01	-0.01	hypothetical protein
DVU0371	1.74	3.43	0.72	1.14	conserved hypothetical protein
DVU0434	1.13	2.12	0.55	0.94	Ech hydrogenase, subunit EchA, putative
DVU0452	1.40	2.66	0.00	0.01	hypothetical protein
DVU0460	1.93	3.76	0.21	0.41	predicted phospho-2-dehydro-3-deoxyheptonate aldolase
DVU0461	2.08	3.95	0.06	0.10	predicted 3-dehydroquinase synthase
DVU0462	2.00	3.77	-0.54	-0.99	chorismate mutase/prephenate dehydratase
DVU0463	2.03	3.78	-0.24	-0.43	3-phosphoshikimate 1-carboxyvinyltransferase
DVU0464	1.29	2.52	-0.52	-0.66	prephenate dehydrogenase
DVU0465	1.80	3.46	-0.34	-0.27	anthranilate synthase, component I
DVU0466	1.53	2.99	0.85	1.37	anthranilate synthase, glutamine amidotransferase component
DVU0467	1.86	3.59	-0.10	-0.16	anthranilate phosphoribosyltransferase
DVU0468	1.64	3.23	0.40	0.66	indole-3-glycerol phosphate synthase
DVU0469	1.79	3.50	-0.16	-0.25	N-(5-phosphoribosyl)anthranilate isomerase
DVU0470	1.16	2.17	-0.01	-0.01	tryptophan synthase, beta subunit
DVU0471	1.41	2.73	0.09	0.15	tryptophan synthase, alpha subunit

DVU0477	1.99	3.22	1.07	1.83	isocitrate dehydrogenase, NADP-dependent
DVU0485	1.25	2.15	-1.24	-1.23	membrane protein, putative
DVU0503	1.35	2.60	-0.07	-0.09	polyribonucleotide nucleotidyltransferase
DVU0506	2.27	4.29	0.99	1.74	DHH family protein
DVU0507	1.61	2.85	0.34	0.47	conserved hypothetical protein
DVU0508	1.60	3.03	0.01	0.03	translation initiation factor IF-2
DVU0510	1.49	2.74	-0.17	-0.28	N utilization substance protein A
DVU0523	1.11	2.01	-0.18	-0.31	negative regulator of flagellin synthesis FlgM
DVU0530	1.93	3.07	2.20	1.77	response regulator, rrf1 protein
DVU0602	2.08	4.07	1.24	0.02	hypothetical protein
DVU0605	1.91	3.64	1.03	1.09	hypothetical protein
DVU0637	1.27	2.43	1.15	1.97	conserved hypothetical protein
DVU0745	1.49	2.76	0.08	0.15	ABC transporter, periplasmic substrate-binding protein
DVU0774	1.73	3.25	-0.02	-0.03	ATP synthase, F1 epsilon subunit
DVU0775	1.52	2.72	0.22	0.33	ATP synthase, F1 beta subunit
DVU0776	1.46	2.66	-0.46	-0.61	ATP synthase, F1 gamma subunit
DVU0777	1.72	2.94	-0.25	-0.33	ATP synthase, F1 alpha subunit
DVU0778	1.98	3.63	0.35	0.45	ATP synthase, F1 delta subunit
DVU0779	1.63	2.98	0.00	0.00	ATP synthase F0, B subunit, putative
DVU0780	1.55	3.05	0.48	0.84	ATP synthase F0, B subunit, putative
DVU0798	1.14	2.01	0.94	1.39	hypothetical protein
DVU0818	1.20	2.03	-1.53	-2.36	conserved domain protein
DVU0834	2.72	5.30	0.78	1.32	ribonuclease HII
DVU0845	1.26	2.42	0.26	0.36	hypothetical protein
DVU0849	1.20	2.12	-0.48	-0.60	heterodisulfide reductase, iron-sulfur-binding subunit, putative
DVU0871	1.56	2.76	0.64	1.11	uridylyate kinase
DVU0872	1.47	2.69	0.57	1.00	glycosyl transferase, group 2 family protein
DVU0877	2.51	4.79	0.02	0.02	hypothetical protein
DVU0879	1.27	2.46	1.22	1.91	hypothetical protein
DVU0929	1.22	2.35	0.10	0.18	GTP-binding protein, GTP1/OBG family
DVU0930	1.49	2.74	0.46	0.71	glutamate 5-kinase
DVU0931	1.99	3.89	0.50	0.91	phosphomethylpyrimidine kinase
DVU0933	1.53	2.95	-0.19	-0.13	response regulator
DVU1009	1.67	2.79	0.85	1.55	hypothetical protein
DVU1030	1.29	2.55	1.17	1.90	universal stress protein family
DVU1079	2.47	4.70	1.62	1.39	tRNA modification GTPase TrmE
DVU1080	1.77	3.40	1.35	1.32	iron-sulfur cluster-binding protein
DVU1138	1.09	2.13	1.33	1.67	hypothetical protein
DVU1207	1.33	2.39	-0.23	-0.32	3-oxoacyl-(acyl-carrier-protein) synthase III
DVU1231	1.08	2.07	0.27	0.38	ammonium transporter
DVU1248	1.05	2.02	0.39	0.73	arginyl-tRNA synthetase
DVU1274	1.71	3.14	-1.00	-1.69	hypothetical protein
DVU1300	1.26	2.20	0.73	1.14	translation elongation factor G
DVU1301	1.16	2.03	-0.22	-0.39	hypothetical protein
DVU1306	1.34	2.49	-0.41	-0.53	ribosomal protein L2
DVU1307	1.54	2.62	-0.64	-0.96	ribosomal protein S19
DVU1310	1.19	2.25	-0.69	-1.05	ribosomal protein L16
DVU1311	1.21	2.27	-0.71	-1.01	ribosomal protein L29
DVU1313	1.33	2.60	-0.66	-1.04	ribosomal protein L14
DVU1315	1.46	2.70	-0.58	-0.90	ribosomal protein L5
DVU1316	1.31	2.49	-0.66	-1.02	ribosomal protein S14
DVU1317	1.12	2.17	-0.36	-0.49	ribosomal protein S8
DVU1318	1.10	2.14	-0.09	-0.14	ribosomal protein L6
DVU1319	1.19	2.18	-0.55	-0.91	ribosomal protein L18
DVU1320	1.53	2.68	-0.54	-0.95	ribosomal protein S5

DVU1321	1.56	2.93	-0.40	-0.75	ribosomal protein L30
DVU1322	1.57	2.94	-0.47	-0.88	ribosomal protein L15
DVU1323	2.10	3.74	-0.29	-0.54	preprotein translocase, SecY subunit
DVU1330	1.09	2.14	0.58	1.08	ribosomal protein L17
DVU1331	1.10	2.00	0.12	0.23	transcriptional regulator, LysR family
DVU1333	1.78	2.92	-0.04	-0.08	hypothetical protein
DVU1480	1.58	2.75	0.75	1.24	conserved domain protein
DVU1491	2.05	4.01	1.36	1.79	conserved hypothetical protein
DVU1494	1.22	2.26	0.44	0.72	hypothetical protein
DVU1506	2.14	3.95	1.03	1.29	hypothetical protein
DVU1507	2.03	3.75	-0.53	-0.52	hypothetical protein
DVU1573	1.48	2.60	1.10	1.74	peptidyl-tRNA hydrolase
DVU1619	1.08	2.05	0.48	0.75	phosphoglycerate mutase, 2,3-bisphosphoglycerate-independent
DVU1621	1.31	2.50	-1.14	-1.31	hypothetical protein
DVU1636	1.46	2.60	0.37	0.71	inorganic pyrophosphatase, manganese-dependent
DVU1641	1.91	3.70	1.75	1.84	conserved hypothetical protein
DVU1644	1.76	2.96	1.19	1.89	permease, putative
DVU1659	1.05	2.09	0.59	0.62	hypothetical protein
DVU1664	1.13	2.18	0.96	1.80	GTP-binding protein
DVU1665	1.07	2.10	0.50	0.89	3-dehydroquinate dehydratase, type II
DVU1666	1.08	2.05	-0.47	-0.81	translation elongation factor P
DVU1675	1.23	2.26	0.99	1.72	hypothetical protein
DVU1694	2.71	4.76	1.51	1.33	C4-type zinc finger protein, DksA/TraR family
DVU1695	1.44	2.84	0.05	0.06	tail fiber assembly protein, putative
DVU1697	1.54	2.92	0.84	0.79	hypothetical protein
DVU1698	1.41	2.60	1.54	1.87	hypothetical protein
DVU1726	1.83	3.42	-0.41	-0.39	hypothetical protein
DVU1728	2.05	4.04	1.45	1.51	conserved hypothetical protein
DVU1755	1.12	2.19	1.52	1.91	hypothetical protein
DVU1764	1.12	2.22	1.01	1.93	conserved hypothetical protein
DVU1791	1.09	2.10	0.35	0.63	GatB/Yqey family protein
DVU1821	1.20	2.20	0.22	0.17	conserved hypothetical protein
DVU1823	1.35	2.37	0.20	0.16	glutamate synthase, iron-sulfur cluster-binding subunit, putative
DVU1952	1.23	2.32	0.76	1.39	hypothetical protein
DVU1969	1.18	2.28	0.95	0.99	hypothetical protein
DVU1970	2.15	3.61	1.74	1.13	response regulator
DVU2184	1.14	2.10	0.96	0.73	DNA-binding domain, excisionase family
DVU2197	1.75	3.19	0.77	0.80	site-specific recombinase, phage integrase family
DVU2206	1.53	2.83	0.33	0.54	conserved hypothetical protein
DVU2275	1.49	2.55	1.02	1.90	sigma-54 dependent transcriptional regulator
DVU2298	1.43	2.74	0.82	1.42	glycine/betaine/L-proline ABC transporter, permease protein
DVU2299	1.48	2.56	0.87	1.49	glycine/betaine/L-proline ABC transporter, ATP binding protein
DVU2343	1.63	2.74	1.37	1.32	amino acid ABC transporter, ATP-binding protein
DVU2433	1.89	3.55	0.74	0.55	hypothetical protein
DVU2434	1.84	3.19	0.52	0.79	hypothetical protein
DVU2591	1.05	2.01	-0.65	-0.72	tail fiber assembly protein, putative
DVU2649	1.13	2.02	1.77	1.86	hypothetical protein
DVU2672	1.48	2.93	0.99	1.72	membrane protein, putative
DVU2816	2.44	3.60	1.81	1.39	multidrug resistance protein
DVU2914	1.20	2.18	-0.04	-0.08	peptide chain release factor 1
DVU2915	1.83	3.52	1.29	1.33	hypothetical protein
DVU2922	1.18	2.05	0.06	0.11	preprotein translocase, SecE subunit
DVU2928	1.10	2.02	-0.46	-0.77	DNA-directed RNA polymerase, beta subunit
DVU2954	1.23	2.18	0.36	0.61	GGDEF domain protein
DVU2981	1.36	2.51	-0.18	-0.18	2-isopropylmalate synthase

DVU3090	1.46	2.86	0.08	0.13	outer membrane protein, OMPP1/FadL/TodX family
DVU3092	1.37	2.57	0.30	0.30	hypothetical protein
DVU3149	1.15	2.23	0.52	0.94	signal peptide peptidase SppA, 36K type
DVU3188	1.08	2.09	0.60	1.02	NLP/P60 family protein
DVU3203	1.11	2.15	0.29	0.44	DNA polymerase III, delta prime subunit, putative
DVU3212	1.21	2.27	1.14	1.68	pyridine nucleotide-disulfide oxidoreductase
DVU3245	1.44	2.66	0.61	1.19	transcription elongation factor GreA
DVU3290	1.48	2.62	1.11	1.05	conserved domain protein
DVU3291	1.54	2.31	0.30	0.48	glutamate synthase, iron-sulfur cluster-binding subunit, putative
DVU3292	2.09	3.92	-0.85	-1.17	pyridine nucleotide-disulfide oxidoreductase
DVU3300	1.45	2.78	0.39	0.49	hypothetical protein
DVU3308	1.28	2.45	-0.12	-0.20	metallo-beta-lactamase family protein
DVU3310	1.64	3.18	0.11	0.14	ATP-dependent RNA helicase, DEAD/DEAH family
DVU3326	2.41	4.55	1.67	1.42	multidrug resistance protein, Smr family
DVU3385	2.34	4.28	1.59	1.30	hypothetical protein
DVU3394	1.32	2.35	1.25	1.40	hypothetical protein
DVUA0089	1.78	2.88	-1.10	-1.14	hypothetical protein

Table S5 Down-regulated ORFs under salt shock but no significant changes under salt adaptation

Locus tag	Salt shock		Salt adaptation		Annotation
	Ratio	Zscore	Ratio	Zscore	
DVU0006	-1.33	-2.34	-0.67	-0.99	universal stress protein family
DVU0019	-1.12	-2.23	-0.49	-0.83	nigerythrin
DVU0041	-1.12	-2.16	-0.98	-1.31	transglycosylase, SLT family
DVU0080	-1.44	-2.79	-2.19	-1.75	fumarate hydratase, class II
DVU0118	-1.30	-2.17	-1.08	-1.19	sigma-54 dependent transcriptional regulator/response regulator
DVU0123	-2.34	-3.85	-0.87	-0.49	membrane protein, putative
DVU0138	-1.25	-2.27	-0.86	-1.48	response regulator
DVU0200	-1.27	-2.30	-1.78	-1.74	major head protein
DVU0211	-1.61	-2.15	-0.98	-1.80	tail tube protein, putative
DVU0259	-1.87	-3.65	-1.11	-1.97	DNA-binding response regulator
DVU0280	-1.44	-2.53	-0.94	-1.69	glycosyl transferase, group 1 family protein
DVU0337	-1.18	-2.18	-1.62	-1.91	hypothetical protein
DVU0344	-1.25	-2.43	0.95	1.36	methyl-accepting chemotaxis protein
DVU0428	-1.16	-2.07	-0.44	-0.64	conserved hypothetical protein
DVU0521	-1.09	-2.05	-0.42	-0.70	carbon storage regulator
DVU0522	-1.32	-2.39	-0.07	-0.09	conserved hypothetical protein
DVU0624	-1.43	-2.82	-0.45	-0.76	NapC/NirT cytochrome c family protein
DVU0630	-1.20	-2.23	-0.05	-0.09	hypothetical protein
DVU0699	-1.32	-2.38	-2.29	-1.83	sensory box sensor histidine kinase/response regulator, authentic frameshift
DVU0817	-1.45	-2.81	-0.91	-1.59	hypothetical protein
DVU0881	-1.83	-3.24	-0.28	-0.49	translation elongation factor G, putative
DVU0964	-1.23	-2.33	-0.25	0.00	Glu/Leu/Phe/Val dehydrogenase family protein
DVU0987	-1.45	-2.81	-1.02	-1.86	heavy metal-binding domain protein
DVU1021	-1.13	-2.08	-0.11	-0.17	conserved hypothetical protein
DVU1049	-1.09	-2.09	-0.33	-0.59	ABC transporter, ATP-binding protein
DVU1093	-1.31	-2.52	-0.78	-1.23	HAD-superfamily hydrolase, subfamily IA, variant 3
DVU1238	-1.54	-2.92	-0.90	-1.55	amino acid ABC transporter, periplasmic amino acid-binding protein
DVU1375	-1.16	-2.05	-0.57	-1.00	hypothetical protein
DVU1458	-1.21	-2.37	-0.99	-1.64	chemotaxis protein CheZ, putative
DVU1541	-1.12	-2.17	0.28	0.35	hypothetical protein
DVU1544	-1.21	-2.36	-0.05	-0.08	mechanosensitive ion channel family protein
DVU1548	-1.33	-2.44	0.07	0.09	outer membrane transport protein, OmpP1/FadL/TodX family

DVU1837	-1.17	-2.24	-0.43	-0.80	competence protein, putative
DVU1838	-1.25	-2.31	-0.75	-1.40	thioredoxin reductase
DVU1882	-1.74	-2.90	-1.48	-1.56	HDIG domain protein
DVU1922	-1.24	-2.31	-0.63	-0.80	periplasmic [NiFe] hydrogenase, large subunit, isozyme 1
DVU1935	-1.35	-2.54	-1.65	-1.43	phosphonate ABC transporter, permease protein
DVU1948	-1.13	-2.18	-0.25	-0.38	conserved hypothetical protein
DVU2016	-1.11	-2.03	-0.01	-0.01	GGDEF domain protein
DVU2019	-1.27	-2.36	-0.65	-0.87	conserved hypothetical protein
DVU2108	-1.83	-3.42	-1.22	-1.79	MTH1175-like domain family protein
DVU2109	-1.81	-2.77	-0.84	-1.42	MTH1175-like domain family protein
DVU2162	-1.78	-2.83	-1.72	-1.44	hypothetical protein
DVU2312	-1.23	-2.38	-0.71	-0.90	hypothetical protein
DVU2313	-1.25	-2.44	-1.47	-1.52	6-phosphogluconolactonase
DVU2386	-1.49	-2.72	0.18	0.18	ABC transporter, permease protein
DVU2398	-1.20	-2.20	-0.60	-0.98	conserved hypothetical protein
DVU2399	-2.03	-3.70	-0.91	-1.39	hydrogenase, putative
DVU2400	-1.81	-3.14	-0.92	-1.39	hydrogenase, putative
DVU2401	-1.56	-2.82	-0.36	-0.63	hydrogenase, iron-sulfur cluster-binding subunit, putative
DVU2402	-1.80	-3.40	-1.00	-1.62	heterodisulfide reductase, A subunit
DVU2403	-1.35	-2.56	-0.85	-1.25	heterodisulfide reductase, B subunit
DVU2404	-1.13	-2.12	-0.60	-0.96	heterodisulfide reductase, C subunit
DVU2445	-1.25	-2.01	-1.07	-1.85	hypothetical protein
DVU2451	-1.36	-2.54	0.06	0.12	L-lactate permease family protein
DVU2452	-1.89	-3.71	0.20	0.29	hypothetical protein
DVU2502	-1.20	-2.34	-0.23	-0.28	UDP-N-acetylenolpyruvoylglucosamine reductase
DVU2579	-1.45	-2.83	-1.24	-0.02	TPR domain protein
DVU2609	-1.36	-2.65	-0.55	-0.96	chemotaxis MotB protein, putative
DVU2615	-1.50	-2.87	-2.02	-1.93	bacterial extracellular solute-binding protein, family 3
DVU2626	-1.24	-2.28	-1.46	-1.61	hypothetical protein
DVU2778	-1.25	-2.14	-1.48	-1.64	hypothetical protein
DVU2782	-1.41	-2.42	-0.55	-0.77	hypothetical protein
DVU2791	-1.31	-2.51	-0.62	-1.18	cytochrome c family protein
DVU2794	-1.34	-2.48	-1.41	-1.28	electron transport complex protein RnfG, putative
DVU2860	-1.18	-2.15	1.33	1.13	conserved hypothetical protein
DVU2861	-1.24	-2.40	-0.20	-0.30	hypothetical protein
DVU2935	-1.19	-2.25	-0.68	-1.27	phosphoglycerate mutase
DVU3009	-1.21	-2.36	-0.67	-1.21	radical SAM domain protein
DVU3012	-1.17	-2.24	-0.79	-1.15	membrane protein, putative
DVU3015	-1.59	-2.91	-1.15	-1.23	conserved domain protein
DVU3024	-1.35	-2.62	-1.50	-1.89	hypothetical protein
DVU3025	-1.34	-2.47	-1.50	-1.53	pyruvate-ferredoxin oxidoreductase
DVU3026	-1.93	-3.72	-1.41	-1.99	L-lactate permease family protein
DVU3033	-1.33	-2.26	-1.88	-1.95	iron-sulfur cluster-binding protein
DVU3187	-1.97	-3.75	-1.10	-1.90	DNA-binding protein HU
DVU3220	-1.31	-2.54	-1.04	-1.90	sigma-54 dependent transcriptional regulator/response regulator
DVU3231	-1.06	-2.06	-1.43	-1.69	flagellar biosynthesis protein FlhF, putative
DVU3263	-1.22	-2.34	-1.49	-1.55	fumarate reductase, iron-sulfur protein
DVU3271	-1.28	-2.46	0.10	0.14	cytochrome d ubiquinol oxidase, subunit I
DVU3293	-1.12	-2.21	-1.55	-1.88	thiamine pyrophosphate-requiring enzyme
DVU3319	-1.13	-2.06	-1.37	-1.26	proline dehydrogenase/delta-1-pyrroline-5-carboxylate dehydrogenase
DVU3350	-1.16	-2.17	-1.03	-1.88	iron-sulfur cluster-binding protein
DVU3355	-1.46	-2.65	-1.02	-1.12	SPFH domain/Band 7 family protein
DVU3356	-1.66	-3.15	-0.49	-0.90	NAD-dependent epimerase/dehydratase family protein
DVUA0070	-1.72	-2.13	0.17	0.28	conserved domain protein

DVUA0098	-2.02	-3.05	0.36	0.55	dehydrogenase, putative
DVUA0099	-2.09	-3.14	-0.93	-1.12	HAMP domain protein
DVUA0100	-1.98	-3.66	-0.44	-0.62	sigma-54 dependent transcriptional regulator
DVUA0104	-1.83	-3.25	0.72	0.73	type III secretion inner membrane protein, HrcV family
DVUA0114	-2.35	-2.44	-1.03	-1.32	hypothetical protein
DVUA0115	-2.35	-3.22	-1.26	-0.99	type III secretion system protein, YscF family
DVUA0116	-2.90	-3.27	-1.32	-1.47	conserved hypothetical protein
DVUA0119	-1.77	-2.78	-1.71	-1.95	type III secretion system ATPase
DVUA0121	-1.84	-2.16	-0.72	-0.66	type III secretion system protein, YopQ family
DVUA0123	-1.69	-2.50	-1.83	-1.53	anti-anti-sigma factor
DVUA0124	-2.51	-4.17	-1.36	-1.18	sigma factor serine-protein kinase
DVUA0125	-1.15	-2.02	1.02	0.84	transglycosylase, SLT family
DVUA0135	-1.70	-2.18	0.73	1.32	CRISPR-associated protein Cas2

Table S6 Up-regulated ORFs under both salt shock and salt adaptation conditions

Locus tag	Salt shock		Salt adaptation		Annotation
	Ratio	Zscore	Ratio	Zscore	
DVU0061	1.38	2.44	1.80	3.24	multidrug resistance protein, putative
DVU0065	3.29	6.39	3.31	5.06	hypothetical protein
DVU0085	1.44	2.74	2.48	3.72	tryptophan synthase, beta subunit
DVU0223	2.88	5.32	2.83	4.68	conserved hypothetical protein
DVU0224	2.50	4.36	1.78	2.92	conserved hypothetical protein
DVU0273	1.25	2.20	1.69	2.93	conserved hypothetical protein
DVU0308	2.68	4.43	2.84	4.07	membrane protein, putative
DVU0367	1.38	2.69	2.02	2.87	Ser/Thr protein phosphatase family protein
DVU0369	2.52	4.41	2.30	2.35	hypothetical protein
DVU0458	1.42	2.74	1.93	3.27	hypothetical protein
DVU0504	1.36	2.55	1.20	2.16	ribosomal protein S15
DVU0525	1.24	2.30	2.99	2.76	transcriptional regulator, MarR family
DVU0526	1.81	3.39	3.01	5.05	drug resistance transporter, putative
DVU0529	2.59	3.67	3.51	2.98	transcriptional regulator, rrf2 protein, putative
DVU0531	2.17	3.71	3.75	2.62	hmc operon protein 6
DVU0533	1.52	2.55	3.45	2.75	hmc operon protein 4
DVU0535	2.04	2.98	2.64	2.92	hmc operon protein 2
DVU0536	2.37	4.23	3.00	2.75	high-molecular-weight cytochrome C
DVU0603	2.50	4.67	1.57	2.92	hypothetical protein
DVU0604	1.48	2.80	2.49	4.10	hypothetical protein
DVU0878	3.01	5.77	1.74	2.59	dnaK suppressor protein, putative
DVU1277	1.24	2.29	2.21	3.91	hypothetical protein
DVU1294	1.48	2.11	1.34	2.54	conserved hypothetical protein
DVU1334	1.33	2.57	1.11	2.01	trigger factor
DVU1505	2.44	4.71	1.47	2.04	holin, putative
DVU1508	1.97	3.92	2.47	3.66	conserved hypothetical protein
DVU1645	2.46	4.70	1.98	3.20	transcriptional regulator, ArsR family
DVU1689	1.82	3.44	1.76	2.41	hypothetical protein
DVU1696	1.72	3.14	2.38	3.61	hypothetical protein
DVU1729	2.75	4.76	2.14	2.13	killer protein, putative
DVU1730	2.28	3.91	2.46	3.36	DNA-binding protein
DVU1760	1.33	2.49	1.67	2.32	transcriptional regulator, TetR family
DVU1855	1.53	2.98	2.89	2.79	integrase, truncation
DVU1872	1.83	3.50	1.62	2.12	hypothetical protein
DVU1971	3.65	6.16	3.25	5.53	conserved domain protein
DVU2002	1.15	2.01	2.22	3.99	hypothetical protein
DVU2073	3.66	6.11	3.08	4.28	chemotaxis protein CheY

DVU2176	1.16	2.28	1.71	2.69	hypothetical protein
DVU2274	1.48	2.56	1.40	2.03	hypothetical protein
DVU2279	1.64	2.37	1.80	2.97	hypothetical protein
DVU2280	1.90	3.72	2.34	3.04	amino acid permease family protein
DVU2284	1.33	2.44	1.36	2.46	hypothetical protein
DVU2294	2.45	4.65	2.43	3.19	femAB family protein
DVU2297	1.62	3.13	1.59	3.11	glycine/betaine/L-proline ABC transporter, periplasmic-binding protein
DVU2527	1.40	2.33	1.15	2.08	transcriptional regulator, putative
DVU2571	1.88	3.54	2.87	5.09	ferrous iron transport protein B
DVU2572	1.98	3.60	2.11	3.21	ferrous iron transport protein A, putative
DVU2574	1.46	2.31	1.21	2.13	ferrous ion transport protein, putative
DVU2634	1.49	2.64	2.32	3.67	hypothetical protein
DVU2647	1.70	3.16	1.49	2.37	endoribonuclease, L-PSP family
DVU2651	1.33	2.50	2.51	3.74	hypothetical protein
DVU2652	3.22	6.23	2.13	3.91	hypothetical protein
DVU2653	1.18	2.13	3.11	5.66	hypothetical protein
DVU2744	1.78	3.20	2.40	4.48	high-affinity branched-chain amino acid ABC transporter, periplasmic amino acid binding protein
DVU2815	2.46	4.75	2.89	2.53	outer membrane efflux protein
DVU2817	3.71	7.00	3.69	3.39	multidrug resistance protein
DVU2818	4.40	8.00	5.77	7.61	hypothetical protein
DVU2819	1.47	2.86	1.61	2.24	transcriptional regulator, TetR family
DVU2822	1.29	2.38	2.87	3.43	TRAP dicarboxylate family transporter
DVU2918	1.73	3.27	2.31	2.39	hypothetical protein
DVU2941	1.95	3.10	1.21	2.13	conserved hypothetical protein
DVU2956	1.55	2.74	1.39	2.40	sigma-54 dependent transcriptional regulator
DVU2987	1.15	2.22	2.90	5.42	hypothetical protein
DVU2988	1.33	2.21	3.51	6.67	phage shock protein A
DVU2989	2.17	3.94	2.96	2.87	psp operon transcriptional activator
DVU3302	1.56	2.42	5.42	3.82	hypothetical protein
DVU3327	1.29	2.42	2.21	3.94	multidrug resistance protein, Smr family
DVU3330	1.09	2.02	1.74	3.00	conserved hypothetical protein
DVU3331	1.23	2.21	2.65	3.78	hypothetical protein
DVUA0002	2.03	2.68	2.23	2.34	ParA family protein
DVUA0082	2.22	3.41	1.97	2.55	site-specific recombinase, phage integrase family
DVUA0084	1.82	2.01	3.48	3.48	transcriptional regulator, AbrB family

Table S7 Down-regulated ORFs under both salt shock and salt adaptation conditions

Locus tag	Salt shock		Salt adaptation		Annotation
	Ratio	Zscore	Ratio	Zscore	
DVU0131	-1.13	-2.22	-2.93	-3.20	hypothetical protein
DVU0132	-1.03	-2.03	-2.16	-4.02	membrane protein, putative
DVU0197	-1.42	-2.41	-1.26	-2.01	phage portal protein, lambda family
DVU0198	-1.36	-2.33	-2.30	-3.07	minor capsid protein C, degenerate
DVU0199	-1.66	-2.98	-3.13	-4.22	conserved hypothetical protein
DVU0203	-1.20	-2.27	-2.64	-2.40	conserved hypothetical protein
DVU0204	-1.38	-2.45	-2.15	-2.43	lipoprotein, putative
DVU0205	-1.49	-2.61	-2.35	-3.32	hypothetical protein
DVU0206	-1.04	-2.06	-1.98	-3.04	hypothetical protein
DVU0207	-1.33	-2.55	-1.60	-2.36	hypothetical protein
DVU0208	-1.48	-2.65	-2.21	-2.23	hypothetical protein
DVU0209	-1.50	-2.82	-1.79	-3.18	conserved hypothetical protein
DVU0210	-1.24	-2.30	-2.20	-4.12	tail sheath protein, putative
DVU0219	-1.43	-2.76	-2.38	-4.36	tail protein, putative

DVU0253	-1.21	-2.00	-1.82	-3.02	oxidoreductase, FAD/iron-sulfur cluster-binding domain protein
DVU0299	-2.70	-5.14	-2.73	-3.95	anaerobic ribonucleoside-triphosphate reductase, putative
DVU0300	-2.39	-4.60	-2.68	-4.62	radical SAM domain protein
DVU0598	-1.52	-2.78	-3.90	-4.99	carbon starvation protein A, putative
DVU0599	-1.27	-2.24	-3.46	-6.39	carbon starvation protein A, putative
DVU0608	-1.52	-2.80	-1.47	-2.32	methyl-accepting chemotaxis protein
DVU0646	-1.08	-2.10	-1.92	-2.51	precorrin-2 C20-methyltransferase
DVU0743	-1.40	-2.10	-2.43	-3.43	sensory box histidine kinase
DVU1378	-1.19	-2.21	-1.58	-2.55	ketol-acid reductoisomerase
DVU1411	-1.50	-2.79	-1.39	-2.58	thiamine biosynthesis protein ThiC
DVU1778	-2.00	-3.89	-1.53	-2.68	cation efflux family protein
DVU2034	-1.11	-2.01	-1.46	-2.12	hypothetical protein
DVU2036	-1.24	-2.28	-2.37	-2.91	helix-turn-helix protein, CopG family
DVU2305	-1.07	-2.06	-2.38	-2.68	conserved hypothetical protein
DVU2349	-1.41	-2.60	-1.89	-2.80	carbohydrate phosphorylase family protein
DVU2514	-1.43	-2.72	-2.65	-3.08	pyruvate kinase
DVU2515	-1.31	-2.51	-1.93	-2.32	HD domain protein
DVU2543	-1.51	-2.96	-1.86	-2.29	hybrid cluster protein
DVU2569	-1.15	-2.21	-1.41	-2.05	peptidyl-prolyl cis-trans isomerase, FKBP-type
DVU2798	-1.71	-3.24	-1.84	-2.56	ApbE family protein
DVU2858	-1.27	-2.04	-2.43	-4.36	tail tube protein, putative
DVU2859	-1.21	-2.08	-1.30	-2.10	tail sheath protein, putative
DVU2862	-1.79	-3.43	-3.19	-5.07	hypothetical protein
DVU2864	-1.17	-2.15	-1.25	-2.16	hypothetical protein
DVU2867	-1.39	-2.41	-3.98	-6.18	holin
DVU2869	-1.36	-2.60	-2.64	-4.43	major head protein
DVU2870	-1.65	-2.77	-2.40	-4.24	conserved hypothetical protein
DVU2931	-1.11	-2.13	-2.53	-3.86	sensory box histidine kinase
DVU3027	-1.41	-2.51	-2.10	-2.29	glycolate oxidase, subunit GlcD
DVU3029	-1.77	-3.33	-2.47	-2.56	phosphate acetyltransferase
DVU3030	-2.30	-4.11	-1.89	-2.32	acetate kinase
DVU3031	-2.08	-3.96	-2.28	-3.64	conserved hypothetical protein
DVU3032	-1.86	-3.24	-2.07	-2.40	conserved hypothetical protein
DVU3045	-1.27	-2.26	-2.84	-3.86	sensory box histidine kinase/response regulator
DVU3107	-1.33	-2.33	-1.99	-3.51	cytochrome c family protein
DVU3113	-1.24	-2.41	-1.69	-3.07	carbamoyl-phosphate synthase, small subunit
DVU3183	-1.33	-2.15	-1.28	-2.35	desulfoferrodoxin
DVU3184	-1.84	-2.95	-1.13	-2.15	rubredoxin
DVU3221	-1.40	-2.71	-1.45	-2.07	sensor histidine kinase