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Global transcriptional, physiological and metabolite analyses of *Desulfovibrio vulgaris*

Hildenborough responses to salt adaptation

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Running title: Salt adaptation in *Desulfovibrio vulgaris* Hildenborough

ABSTRACT

The response of *Desulfovibrio vulgaris* Hildenborough to salt adaptation (long-term NaCl exposure) was examined by physiological, global transcriptional, and metabolite analyses. The growth of *D. vulgaris* was inhibited by high levels of NaCl, and the growth inhibition could be relieved by the addition of exogenous amino acids (e.g., glutamate, alanine, tryptophan) or yeast extract. Salt adaptation induced the expression of genes involved in amino acid biosynthesis and transport, electron transfer, hydrogen oxidation, and general stress responses (e.g., heat shock proteins, phage shock proteins, and oxidative stress response proteins). Genes involved in carbon metabolism, cell motility, and phage structures were repressed. Comparison of transcriptomic profiles of *D. vulgaris* responses to salt adaptation with those of salt shock (short-term NaCl exposure) showed some similarity as well as a significant difference. Metabolite assays showed that glutamate and alanine were accumulated under salt adaptation, suggesting that they may be used as osmoprotectants in *D. vulgaris*. A conceptual model is proposed to link the observed results to currently available knowledge for further understanding the mechanisms of *D. vulgaris* adaptation to elevated NaCl.

INTRODUCTION

Desulfovibrio vulgaris Hildenborough is a sulfate-reducing bacterium (SRB) (Postgate, 1984) that can be found ubiquitously in anaerobic environments with sulfate (Ouattara and Jacq, 1992), such as gas pipelines, subsurface metal tanks, sediments, and off-shore oil production facilities (Blessing et al., 2001; Ye et al, 2004). These niches can also contain high concentrations of salt (e.g. NaCl). The potential of *D. vulgaris* for bioremediation because of its capacity to immobilize soluble forms of toxic metals as well as its deleterious role in metal corrosion have been widely recognized (Lovley and Phillips, 1994; Valls and Lorenzo 2002). Therefore, an understanding of mechanisms that *D. vulgaris* uses to survive and adapt to environments with high concentrations of salt (e.g. NaCl) may contribute to the development of successful bioremediation strategies and to the prediction of biocorrosion for petroleum energy-related industries.

The response of a microorganism to high salinity can be divided into two phases. The initial reaction to a sudden increase in salt concentration is termed “salt shock”, while the subsequent survival and adaptation to a high salinity environment termed “salt adaptation”. In both cases, an exposure of *D. vulgaris* to high salinity may present two different, but related environmental stimuli: one is osmotic stress, and the other is ionic stress (Han et al., 2005). Hyper-osmotic stress triggers water efflux from the cell that results in a reduction of turgor pressure and dehydration of the cytoplasm thereby increasing the ion concentration in the cytosol. Whereas ionic stress causes ions (e.g. Na⁺) to enter the cytoplasm, leading to a further increase in the ion concentration, and subsequently damaging the membrane systems and deactivating key enzymes (Sleator and Hill, 2002).

Bacteria use a range of mechanisms to respond to high salinity. The most common is an accumulation of compatible solutes, such as glutamate (McLaggan et al., 1994; Botsford et al., 1994), trehalose (Strom and Kaasen, 1993), proline (Whatmore et al., 1990), glycine betaine (Ko et al., 1994), and ectoine (Jebbar et al., 2005). These solutes increase the internal osmotic pressure without interfering with vital cellular protein functions (Csonka and Hanson, 1996) and are accumulated either by biosynthesis or import. Another strategy used by bacteria is the exclusion of harmful ions (e.g. Na^+) via a variety of transport systems, such as Na^+/H^+ antiporters, $\text{Ca}^{2+}/\text{Na}^+$ exchangers, and Na^+ /solute symporters (Ma et al., 1995; Padan and Krulwick, 2000; Liu et al., 2005), which may be present constitutively or induced in the presence of high salinity. Na^+/H^+ antiporters also play key roles for salt tolerance in *Cyanobacteria* (Waditee et al., 2002) and *Arabidopsis* (Shi et al., 2003). Bacterial responses to salt stress also include the induction of chaperons, chaperon-like proteins, and peptidases to correct errors caused by high salinity during DNA and protein synthesis (Hecker and Völker, 2001).

Genome-wide transcriptional analyses of salt and/or osmotic stress responses have been performed in many different bacteria and archaea, including *E. coli* (Weber and Koide, 2002), *B. subtilis* (Steil et al., 2003), *Shewanella oneidensis* MR-1 (Liu et al., 2005), *Yersinia pestis* (Han et al., 2005), *Pseudomonas aeruginosa* (Aspedon et al., 2006), *Sinorhizobium meliloti* (Dominguez-Ferreras et al., 2006), and *Methanosarcina mazei* (Pflüger et al., 2007). A wide set of differentially expressed genes were observed in all studies. Since the annotated *D. vulgaris* genome is available (Heidelberg et al., 2004), a series of transcriptional studies of *D. vulgaris* responses to different environmental stresses have been conducted (He et al., 2006; Clark et al., 2006; Chhabra et al., 2006; Bender et al., 2007; Mukhopadhyay et al., 2007). In particular, a study of the response of *D. vulgaris* to salt shock (Mukhopadhyay et al., 2006) demonstrated that

import of osmoprotectants (e.g. glycine betaine, ectoine) was the primary mechanism to counter hyperionic stress (Mukhopadhyay et al., 2006). This study also showed that several efflux systems, ATP synthesis pathways, and chemotaxis genes were highly up-regulated while flagellar biosynthesis and lactate uptake and transport systems were down-regulated (Mukhopadhyay et al., 2006). In other organisms such as *B. subtilis*, both salt shock and salt adaptation have been studied. Only a small number of genes were found to be differentially expressed in both treatments (Steil et al., 2003). This may be true for most mesophilic bacteria including *D. vulgaris*.

In this study, possible mechanisms of *D. vulgaris* adaptation to high salinity were explored via transcriptomic profiling combined with cell growth, physiological, and metabolite analyses. Here, salt adaptation is defined as that they have survived an initial salt stress and grown until the mid-lag phase even with a slow growth rate since an inoculation of *D. vulgaris* cells into a NaCl-added medium, while salt shock as that the mid-log growing *D. vulgaris* cells are exposed to NaCl for a short time (30-480 min). Based on this work definition, our objectives of this study were to: (i) examine transcript changes in amino acid metabolism and transport and energy metabolism in *D. vulgaris* in response to salt adaptation, (ii) identify potential osmoprotectants in *D. vulgaris* during salt adaptation, (iii) compare the global transcriptomic profiling of *D. vulgaris* in response to salt adaptation and salt shock, and (iv) elucidation of physiological states for initial and prolonged responses to stress. A conceptual model is proposed for adaptation to high salinity in *D. vulgaris*.

METHODS AND MATERIALS

Oligonucleotide probe design and microarray construction

The 70mer oligonucleotide microarray for *D. vulgaris* was constructed as described previously (He et al., 2006). All designed oligonucleotides were commercially synthesized without modification by MWG Biotech Inc. (High Point, NC). The concentration of oligonucleotides was adjusted to 100 pmol/ μ l. Oligonucleotide probes prepared in 50% DMSO (Sigma Chemical Co., MO) were spotted onto UltraGAPS glass slides (Corning Life Science, NY) using a Microgrid II Arrayer (Genomic Solutions Inc., MI). Each oligonucleotide probe had two replicates on a single slide. Additionally, 6 different concentrations (5 to 300 ng/ μ l) of genomic DNA were also spotted (4 replicates on a single slide) as general positive controls. In total, there were 7284 spots on the array. After printing, the oligonucleotide probes were fixed onto the slides by UV cross-linking (600 mJ of energy) according to the protocol of the manufacturer (Corning Life Science, NY).

Cell growth

D. vulgaris cultures were routinely grown in a defined lactate sulfate medium (LS4D). LS4D consisted of 60 mM sodium lactate, 50 mM Na₂SO₄, 8.0 mM MgCl₂, 20 mM NH₄Cl, 2.2 mM K₂HPO₄, 0.6 mM CaCl₂, 30 mM PIPES [piperazine-N,N-bis(2-ethanesulfonic acid)], 12.5 ml trace mineral solution per liter (Brandis and Thauer, 1981), NaOH to a pH of 7.2, and 1.0 ml of a 10 x vitamin solution per liter (Brandis and Thauer, 1981) added after autoclaving. As the reductant for the LS4D medium, 5 ml per liter of an anaerobic titanium citrate solution was used. This solution contained 20% (wt/vol) titanium(III) chloride, 0.2 M sodium citrate, and 8.0% (wt/vol) sodium carbonate. Cell growth was monitored at an optical density (OD) of 600 nm. For transcript analysis, the control and NaCl treatment samples were harvested at the mid-log phase (OD₆₀₀ ~ 0.25), approximately 15 and 100 hrs after inoculation, respectively in triplicates at room temperature under anaerobic conditions, snap frozen in liquid nitrogen, and then stored at -

80°C. To determine the effects of amino acids on *D. vulgaris* growth, 100µl of 200 mM (the final concentration of 2 mM) amino acids that were prepared and filter-sterilized under anaerobic conditions were added into the LS4D medium with or without 250 mM NaCl. Cultures of 10 ml were incubated at 37°C in 30 ml anaerobic culture tubes and closed with butyl rubber stoppers and aluminum seals. For metabolite analysis, the biomass of *D. vulgaris* was cultured at 37°C in the LS4D minimal medium with or without 250 mM NaCl, and cells were collected at the mid-log phase ($OD_{600} \sim 0.25$), approximately 15 and 100 hrs after inoculation, respectively in triplicates at room temperature under anaerobic conditions, snap frozen in liquid nitrogen, and then stored at -80°C.

RNA extraction, purification and labeling

Total cellular RNA was isolated using TRIzolTM Reagent (Invitrogen Life Technologies, Carlsbad, CA). RNA samples were treated with RNase-free DNase I (Ambion, Austin, TX) and purified using the Mini RNeasy Kit (Qiagen, Chatsworth, CA). 10 µg of total cellular RNA was incubated at 70°C for 10 min in the presence of 10 µg of random primers (Invitrogen Life Technologies). The labeling reaction was catalyzed by 200 U of SuperscriptTM II RNase H⁻ reverse transcriptase (Invitrogen Life Technologies) in the presence of 500 µM dATP, dGTP, and dCTP, 25 µM dTTP, and 25 µM of the fluorophor Cy5-dUTP (Amersham BioSciences, UK). The reverse transcription reaction was allowed to proceed for 2 h at 42°C, followed by RNA hydrolysis in 1 N NaOH at 37°C for 10 min. The labeled cDNA probes were purified immediately using a QIAquick PCR purification column and concentrated in a Savant Speedvac centrifuge (Savant Instruments Inc., Holbrook, NY). For each biological sample, three slides were used. In addition to the duplicates of arrays on the same slide, three biological cell samples produced a total of 18 possible spots for each gene.

Genomic DNA extraction, purification and labeling

Genomic DNA was isolated and purified from *D. vulgaris* as described (Zhou et al., 1995). The purified genomic DNA was fluorescently labeled by random priming using Klenow fragment of DNA polymerase as described previously (He et al., 2005). The labeled genomic DNA was purified immediately using a QIAquick PCR purification column and concentrated in a Savant speedvac centrifuge (Savant Instruments Inc., Holbrook, NY).

Microarray hybridization, washing and scanning

Labeled genomic DNA (Cy3) was used as a common reference to co-hybridize with labeled RNA (Cy5) samples for each slide. Hybridization was performed by a TECAN HS4800Pro Hybridization Station (TECAN U.S., Durham, NC) based on the protocol of the manufacturer. This fully automated system allows hybridization, washing, and drying of up to 12 arrays for each extension (with a total of 4 extensions) at one time and provides more sensitive and consistent hybridization results. After hybridization, slides were scanned using a ProScanArrayTM microarray analysis system (Perkin Elmer®, Boston, MA).

Microarray data analysis

To determine fluorescent signal intensities for each spot, 16-bit TIFF scanned images were analyzed by using the software ImaGene version 6.0 (Biodiscovery Inc., Los Angeles, CA) to quantify spot signal, spot quality, and background fluorescent intensities. Any flagged spots (e.g. empty spots and bad spots) were removed before normalization. Details of microarray data analysis were previously described in Mukhopadhyay et al. (2006).

Real-time PCR quantification

In order to validate microarray hybridization results, twelve genes were selected for further analysis with real-time PCR. A specific primer pair for each gene was designed with a product of

approximately 100 bp, and detailed information about the selected genes and their primers is listed in Table S1. Real-time PCR (50 μ l) was performed using Thermo-fast 96 PCR plates (BioRad Laboratories, Hercules, CA), which were sealed with iCycler IQ optical quality tapes (BioRad Laboratories) on an iCycler IQ thermocycler (Bio-Rad, Laboratories). Each measurement was performed in three replicates. A dilution series of positive control DNA was used in the same plates as calibration standards. Positive control DNA was generated by standard PCR amplifications, and the amplicons were purified using the QIAquick PCR Purification Kit (QIAGEN Inc., Valencia, CA) according to the protocol of the manufacturer. The purified PCR fragments were visualized and the size was confirmed by agarose gel electrophoresis, quantified using the PicoGreen dsDNA Assay Kit (Invitrogen, Carlsbad, CA), and then serially diluted to generate calibration standards. Data analysis was carried out with iCycler software (BioRad Laboratories). Based on the standard curve, a cycle threshold (CT) value was converted to the copy number of the gene in a sample. A ratio of the copy number for the treatment to the control was calculated and compared with the ratio of gene expression for each gene.

Metabolite extraction

D. vulgaris cells were grown in LS4D medium with (NaCl-stressed) or without (control) 250 mM NaCl. Both control and NaCl-stressed *D. vulgaris* cells were collected in triplicate at the mid-log phase and then pooled. A final volume of 400 ml was drawn from each pool of biomass. The cells were then harvested by centrifugation at 11,000 x *g* for 10 min at 4 °C. Metabolites were extracted via a methanol/water/chloroform extraction procedure, after which solid phase extraction (Oasis HLB, Waters, MA, USA) was used for the removal of salts from the sample (Baidoo et al., 2008). All amino acids, with the exception of betaine, glutamate and serine, were quantified via isotopically labeled amino acid standards, which were purchased from Sigma-

Aldrich (MO, USA) and C/D/N Isotopes (Quebec, Canada). Betaine, glutamate and serine were quantified based on their percent recoveries from the solid phase extraction cartridge.

Capillary electrophoresis (CE) conditions

CE separation conditions were used as previously described in Baidoo et al. (2008). However, for the detection of betaine, glutamate and serine, the sample was introduced to the capillary at 50 mbar for 250 seconds.

Mass spectrometry (MS)

MS analysis was conducted on an Agilent 6210 TOF LC/MS (Agilent Technologies, Santa Clara, CA, USA) and an Agilent 1100 series isocratic HPLC pump for sheath liquid delivery. CE and electrospray ionization (ESI) MS coupling was achieved using an orthogonal coaxial sheath-flow interface, and the Agilent CE system was interfaced to the Agilent 6210 TOF LC/MS via a G1603A Agilent CE-MS adapter kit and a G1607A Agilent CE-ESI-MS sprayer kit (Agilent Technologies, Santa Clara, CA, USA). Both the Agilent CE system and Agilent 6210 TOF LC/MS were controlled by the Chemstation software package (Agilent Technologies, Santa Clara, CA, USA). A contact closure between both instrument set-ups was established in order to trigger the MS into operation upon the initiation of a run cycle from Chemstation. The Agilent 6210 TOF LC/MS was initially calibrated using the ES tune mix (Agilent Technologies, Santa Clara, CA, USA) and internally calibrated, during runs, via reference masses from tetrabutylammonium acetate (Sigma-Aldrich, St. Louis, MO, USA) and tetraethylammonium acetate (Fluka, Seelze, Germany). Data acquisition and processing were carried out by the Agilent MassHunter Work Station Console software package. Grounding of the CE-ESI-MS sprayer ensured that a full 30 kV potential difference was applied across the length of the capillary for more efficient separation. An electrical contact at the outlet end was provided by the

sheath liquid (methanol and water, 50:50, v/v) at a flow rate of 8 μ l/min. Nitrogen gas was used as both the nebulizing (8 psi) and drying (8 liter/min) gases to facilitate the production of gas-phase ions. A drying gas temperature of 200°C was used throughout.

RESULTS

Growth of *D. vulgaris* during salt adaptation

D. vulgaris cells were grown in the LS4D medium with NaCl at different concentrations (0 to 500 mM). Low NaCl concentrations up to 100 mM did not significantly affect cell growth monitored by OD₆₀₀. The maximal OD₆₀₀ were adversely affected at 250 mM NaCl (Fig. 1A), under which the final OD₆₀₀ of *D. vulgaris* cells was decreased by 50% (Fig. 1A). *D. vulgaris* could not grow in the LS4D medium with 500 mM NaCl (Fig. 1A). To determine the effects of yeast extract (YE) on the growth of *D. vulgaris* with high salt, cells were grown in the LS4D medium with or without 0.5% (wt/vol) YE. With 250 mM NaCl supplementation, the culture with YE had an OD₆₀₀ of approximately 0.9 versus 0.60 for the culture without YE, and grew more rapidly, though the final OD₆₀₀ was still notably lower than the control (Fig. 1B). The results indicated that YE was beneficial for *D. vulgaris* growth and that some of its components (e.g., amino acids) could mitigate growth defects during a long-term exposure of *D. vulgaris* to NaCl. Experiments were conducted to examine transcriptional, metabolic, and physiological responses of *D. vulgaris* to 250 mM NaCl.

Transcriptional analysis of *D. vulgaris* responses to salt adaptation

For assessing transcript changes, the Z score cutoff for significant change was set to |2.0|. With this criterion, among 2647 ORFs that were assigned to 20 functional categories based on the TIGR roles, 195 and 184 ORFs were significantly up-regulated or down-regulated, respectively,

in cultures of *D. vulgaris* grown for an extended time in medium supplemented with 250 mM NaCl (Fig. S1). More than one third (111 ORFs or 15.2%) of the genes altered in expression encode hypothetical, conserved hypothetical, and function-unknown proteins. The other most significantly changed (up- or down-regulated) gene categories included amino acid metabolism with 8 (10.3%) ORFs, protein synthesis and fate with 16 (6.3%) ORFs, DNA metabolism with 8 (9.6%) ORFs, cell envelope with 32 (13.0%) ORFs, cellular process with 22 (13.8%) ORFs, energy metabolism with 37 (14.2%) ORFs, mobile and extrachromosomal element functions with 39 (30.5%) ORFs, signal transduction and regulatory functions with 37 (14.2%) ORFs, and transport and binding proteins with 41 (16.5%) ORFs (Fig. S1). In this study, our analysis was focused on the genes involved in amino acid metabolism and transport, energy metabolism, and regulatory functions, and general stress responses.

(A) *Amino acid metabolism and transport.* *DVU0375* encoding a putative Glu/Leu/Phe/Val dehydrogenase family protein was highly expressed when *D. vulgaris* was adapted to 250 mM NaCl (Table 1). This increase might reasonably be expected to result in an increase in biosynthesis of glutamate, leucine, phenylalanine, and/or valine. The gene *aroE* for shikimate 5-hydrogenase that produces shikimate, a precursor of aromatic amino acids, was also up-regulated (Table 1), as were *trpB-1* encoding the beta subunit of a tryptophan synthase and *tnaA* encoding a tryptophanase (Table 1). The *D. vulgaris* genome has a predicted five-gene operon (*DVU2981-2985*) for leucine biosynthesis, of which three genes, *DVU2983* (*leuD*), *DVU2984*, and *DVU2985* (*leuB*) were significantly down-regulated under salt adaptation (Table 1). Two operons involved in amino acid transport had a trend of up-regulation under salt adaptation although all genes in the operon were not significantly increased in expression. One was glycine/betaine/L-proline ABC transporter system of three genes (*DVU2297-2299*) and the other

was a high-affinity branched-chain amino acid ABC transporter system with five genes (DVU2740-2744) (Table 1). In addition, two genes, DVU0724 for a sodium/Ala symporter family protein and DVU3297 (*mtr*) for a tryptophan-specific transport protein were over-expressed under salt adaptation (Table 1). The results were interpreted to suggest that some amino acids, such as glutamate, tryptophan, and leucine might play a role in *D. vulgaris* responses to a salt challenge and that the import of glycine-betaine into the cell from the environment could be one of the mechanisms for *D. vulgaris* osmoregulation.

(B) *Energy metabolism.* The transcript levels for all genes (DVU0531 to DVU0536) in the *hmc* operon encoding the high-molecular-weight cytochrome (HMC) increased under salt adaptation (Fig. 2). Consistent with the up-regulation of the *hmc* operon, the genes encoding a formate dehydrogenase (DVU0587-0588), periplasmic [Fe] hydrogenase (DVU1769-1770), hydrogenase expression/formation protein (DVU1919), and iron-repressed flavodoxin (DVU2680) were also over-expressed (Fig. 2). In contrast, the transcript levels for genes encoding ferritin (DVU1568), pyruvate ferredoxin oxidoreductase (DVU1569-1570, and DVU1946), pyruvate kinase (DVU2514), and two putative carbon starvation proteins (DVU0598 and DVU0599) decreased under salt adaptation (Fig. 2). In addition, three genes (*glcD*, *pta*, and *ackA*) in the same predicted operon, and two genes (*glpF* and *glpK*) in another operon were down-regulated under salt adaptation (Fig. 2). The results suggest that electron transport in NaCl-stressed cells was much more active than the control cells, and that the utilization of carbon intermediates, such as pyruvate, glycolate, and glycerol was slower under salt adaptation.

(C) *Sensory and regulatory genes.* Two-component signal (TCS) transduction systems are a mechanism that bacteria use to sense and respond to dynamic environments (Stock et al., 2000). In the *D. vulgaris* genome, 63 putative sensory histidine kinases (HK) and 66 response regulators

(RR) are predicted (<http://microbesonline.org>). Fourteen putative transcriptionally related genes altered their expression under salt adaptation with twelve (DVU0030, *rrf2*, *hrcA*, DVU1643, DVU1760, *flrC*, DVU2423, *lysX*, DVU2819, *pspF*, *flrA*, and DVU3313) up-regulated and only two (*phoH* and DVU3131) down-regulated (Fig. 3). The *rrf2* was reported to regulate the expression of *hmc* operon with 6 genes (DVU0531-0536) (Keon et al., 1997), and indeed the transcript levels for all those genes increased under salt adaptation (Fig. 2). Similarly, *pspF* (Fig. 3) is predicted to activate the *psp* operon with 3 genes (DVU2986-2988), which were all over-expressed 5.5- to 11.4-fold under salt adaptation.

Among histidine kinases and regulators that are dual function, four (*rrf1*, *cckA*, DVU2577, and DVU2578) putative sensory/regulatory genes were up-regulated, and nine (DVU0258, *atoC*, DVU0680, DVU0722, DVU0743, DVU2677, DVU2931, *fexB*, and DVU3221) were down-regulated under salt adaptation (Fig. 3). Consistent with the expression of *rrf2* and the *hmc* operon, *rrf1* was also increased (Fig. 2, Fig. 3). It has been reported that the expression of DVU0258 and DVU0680 was significantly down-regulated at the stationary phase in formate-based medium (Zhang et al., 2006). The expression of these two genes was also decreased under salt adaptation (Fig. 3). In addition, the transcripts of *cheY-1* and *cheY-2* significantly changed under salt adaptation with *cheY-1* down-regulated and *cheY-2* up-regulated. The results indicate that the expression of regulatory genes significantly changed during *D. vulgaris* adaptation to NaCl, suggesting that as-yet unknown regulatory networks are involved in cell survival during exposure to saline conditions.

(D) *Ion transport and general stress response.* The predicted iron uptake and transport regulon has two putative operons predicted to be regulated by Fur (Rodionov et al., 2004). One contains two genes, *feoB* (DVU2571) and *feoA* (DVU2572), and the other contains another *feoA*

(DVU2574). All three genes were up-regulated under salt adaptation and shock conditions (Table 2). With either NaCl treatment, the transcript levels of two genes predicted to be a MarR family gene (DVU0525), and a drug resistance transporter gene (DVU0526) in the same operon also increased while the expression of another two-gene (DVU2305-2306) operon related to phosphate transport decreased (Table 2).

Most genes involved in protein synthesis (e.g. ribosomal proteins) were repressed in NaCl-stressed cells (GEO Number), consistent with slower growth for salt-stressed cultures. The expression of a two-gene operon related to heat shock (DVU2441-2442) was highly increased, and the expression of peptidase-related genes (DVU2568-2569) was down-regulated (Table 2). *pspA* and *pspC* predicted to encode phage shock proteins were highly induced (Table 2). In addition, the expression of all seven genes (DVU0198-204) was induced in a seven-gene operon possibly encoding bacteriophage functions. In another operon of three genes, the transcript levels of two genes (*rhl* and *perR*) significantly increased although the transcript for gene *rbr* was not significantly up-regulated ($Z = 1.09$) (Table 2). The results indicate that *D. vulgaris* also uses general strategies for survival under salt adaptation conditions.

Validation of microarray data by real-time quantitative RT-PCR

To verify the microarray data, 12 ORFs (Table S1) with a range of expression levels were randomly selected for real-time quantitative reverse-transcription PCR using the same RNA prepared for microarray hybridization. The results showed that the microarray data were highly correlated with the RT-PCR measurements with $r^2 = 0.96$ ($n = 12$) (Fig. S2). This result is also consistent with other studies, such as nitrite stress (He et al., 2006) and growth transitions (Clark et al., 2006) using the same microarray platform.

Accumulation of amino acids in salt-stressed *D. vulgaris* cells

To determine if changes at the transcript level for amino acid biosynthesis genes were reflected at the metabolite level as well, metabolite assays of both control and treated cells were conducted. Compared to the control, in NaCl-stressed cells, the levels of eight amino acids, Glu, His, Ser, Lys, Gln, Ala, Leu, and Thr, and Glycine betaine increased between 1.5- to 8-fold with an accumulation of Glu at 10.25 nmoles/mg and Ala at 9.89 nmoles/mg. The levels of seven amino acids, Pro, Asp, Gly, Ile, Met, Arg, and Val changed in a range of 80-139% in comparison with the control. Curiously, the levels of the three aromatic amino acids, Phe, Tyr, and Trp, decreased to 62%, 57%, and 55%, respectively. Asparagine was not detected in the control (Table 3). Based upon both gene expression data and metabolite measurements, the most accumulated amino acids, such as Glu and Ala may be used as osmoprotectants in *D. vulgaris* adaptation to NaCl.

Relief of salt inhibition of *D. vulgaris* growth by an external addition of amino acids

To examine the effects of amino acids on salt adaptation of *D. vulgaris*, Glu, Ala, Lys, Trp and Leu were added individually to the LS4D medium and cell growth was monitored spectrophotometrically (OD₆₀₀). Significant growth effects (advantageous or deleterious) were not observed by the supplementation of the medium with amino acids for the control (Fig. 4A). However, when 250 mM NaCl was also added to the medium, the addition of Glu, Ala, Leu, and Trp significantly relieved the deficiencies in terms of growth rate, and the final OD₆₀₀ of *D. vulgaris* increased by approximately 35%. The order of growth stimulation was Glu > Ala > Leu=Trp, and no growth improvement was observed with the addition of Lys (Fig. 4B). To be consistent with this observation, some amino acid transporters (DVU0724, DVU2341, DVU2740-2744, and DVU3297) were up-regulated under salt adaptation (Table 1). We interpreted the results to mean that particular amino acids (e.g., Glu or Ala) could increase the

ability of *D. vulgaris* to grow at high salinity, which was consistent with the accumulation of Glu and Ala in *D. vulgaris* under salt adaptation conditions (Table 3).

Comparison of effects of salt shock and salt adaptation on *D. vulgaris* gene expression

Based on a Z-score cut-off of $|2.0|$, the changes in transcript levels of *D. vulgaris* genes in responses to salt shock (at 120 min) and salt adaptation showed significant differences and similarities as well (Fig. 5). For salt-shocked data, the 120-min time point was selected since the largest number of genes were differentially expressed at that time point (Mukhopadhyay et al., 2006). In salt-adapted cultures, 228 ORFs were up-regulated (Fig. 5-I, Table S2), and 161 ORFs (Fig. 5-II, Table S3) were down-regulated that did not change their gene expression significantly under salt shock. Similarly, 154 ORFs were up-regulated (Fig. 5-III, Table S4), and 99 ORFs were down-regulated (Fig. 5-IV, Table S5) under salt shock that did not change gene expression under salt adaptation. On the other hand, transcriptomic profiling between salt adaptation and salt shock showed some similarities with 72 ORFs increased (Fig. 5-V, Table S6), and 53 ORFs decreased in expression (Fig. 5-VI, Table S7) under both conditions. These genes differentially expressed under both treatments represented only 16.3% of the 767 genes detected in the two conditions combined.

A comparison of transcriptomic profiling for amino acid biosynthesis of *D. vulgaris* under salt adaptation and salt shock showed that the cell might develop complex response mechanisms. First, the genes predicted to be involved in the synthesis of Glu, Trp, and Leu were different in the two treatments. DVU0375, potentially encoding glutamate dehydrogenase, was up-regulated under salt adaptation, while *gltB-1* and DVU3291 were up-regulated under salt shock; *trpB-1*, *trpB-2* and *trpA* were all up-regulated under salt shock, but only *trpB-1* under salt adaptation; five genes in the predicted operon of Leu synthesis had a trend of up-regulation

under salt shock, but a trend of down-regulation under salt adaptation (Table 1). Similarly, amino acid transport genes differentially expressed under salt adaptation and salt shock. For example, DVU0724, DVU2341, and *mtr* were all induced under salt adaptation but not under salt shock (Table 1). The results indicate that *D. vulgaris* may use different strategies to accumulate osmoprotectants to cope with osmotic stress under salt adaptation and salt shock.

Second, efflux systems including Na⁺/H⁺ antiporters, and cation/multidrug resistance proteins may function to pump cations (e.g., Na⁺) out of the cell. Four genes (*acrB*, DVU2815, *acrA*, and DVU3327) were highly expressed under both salt adaptation and salt shock, but additional five genes (DVU0058, DVU0063, *mnhA*, DVU2816, and DVU3326) were only significantly up-regulated under salt shock (Fig. 6). To be consistent with more energy requirement for efflux processes, the F-type ATPase genes (DVU0774-0780) were observed to be up-regulated under salt shock but not under salt adaptation (Fig. 6). The results suggest that an exclusion of Na⁺ from the cell might be a more important mechanism for an initial salt shock than for long-term salt adaptation in *D. vulgaris*.

Third, most of genes involved in carbon metabolism were down-regulated under both salt shock and salt adaptation. For example, all genes in the operon (DVU3025-3030) were generally down-regulated, and two putative carbon starvation protein A genes (DVU0598-0599) were highly expressed in *D. vulgaris* under both salt shock and salt adaptation (Fig. 2). Additionally, more genes including *ftn*, *porA*, *porB*, *oorB*, *glpF*, *glpK* and DVU3349 were down-regulated under salt adaptation but did not significantly change their expression under salt shock (Fig. 2). The results suggest that the decreased carbon metabolism was consistent with slower growth during salt adaptation and possibly the re-direction of carbon flow to the production of osmoprotectants.

Fourth, two chemotaxis genes (*DVU0048* and *cheV-3*) were down-regulated under salt adaptation and one (*DVU1458*) for salt shock, and similarly, four methyl-accepting chemotaxis genes (*DVU0170*, *mcpD*, *DVU0608*, and *DVU2585*) were down-regulated under salt adaptation and one (*DVU0608*) for salt shock (Fig. 6). In addition, only one gene (*DVU1884*) was found to be up-regulated under salt adaptation and none for salt shock (Fig. 6). The results suggest that the cell trying to move away from stress conditions was not a major strategy under salt adaptation although it could be an initial response to salt shock. However, most genes involved in flagellar biosynthesis were not significantly changed under salt shock or salt adaptation with one gene (*DVU3230*) for salt adaptation and another gene (*DVU3231*) for salt shock down-regulated (Fig. 6), suggesting that the cell general motility may not be significantly changed under both salt adaptation and salt shock conditions.

Fifth, almost all significant changers of regulatory genes of *D. vulgaris* under salt shock could be also observed under salt adaptation, for example, *rrf2*, *DVU1645*, *pspF*, *flex*, and *cheY-2* (Fig. 3). However, more genes were only significantly down-regulated, or over-expressed under salt adaptation, and examples were *cckA*, *flrC*, *lysX*, *DVU3313*, and *cheY-1* (Fig. 3). The results indicate that *D. vulgaris* adaptation to elevated NaCl requires the coordination of more genes, and perhaps via a more complicated regulatory network as well.

Finally, *D. vulgaris* may also use common strategies to deal with salt adaptation and salt shock, which was reflected in the similar expression profiling of genes involved in amino acid synthesis and transport, such as *trpB-1*, the three-gene operon of glycine/betaine/L-proline ABC transporter, and the five-gene operon of high-affinity branched chain amino acid ABC transporter (Table 1), electron transfer, such as *hmcF-A* genes (Fig. 2), carbon metabolism, such as *DVU0598*, *DVU0599*, *por*, *glcD*, *pta*, and *ackA* (Fig. 2), inorganic ion transport, such as *feoA*,

feoB, and DVU2306 (Table 2), and general stress responses, such as DVU1729, DVU1730, *pspC*, *pspA*, *slyD*, and DVU0198-0200 (Table 2). The results suggest that those processes are critical for *D. vulgaris* to respond to both salt shock and salt adaptation.

DISCUSSION

In this study, we examined the adaptation of *D. vulgaris* to high salinity by transcriptomic, growth, and metabolite analyses. The global transcriptomic profiling identified groups of genes involved in amino acid biosynthesis and transport, energy metabolism, regulatory functions, and general stress responses that were important for salt adaptation. Metabolite measurements revealed that amino acids, such as glutamate might be used as osmoprotectants in *D. vulgaris*, and this notion was supported when an external addition of glutamate relieved salt inhibition. A comparison of transcriptomic profiling suggests that *D. vulgaris* may use different strategies to deal with the initial salt shock and salt adaptation. A conceptual model is constructed to provide an integrative understanding of the mechanisms of *D. vulgaris* adaptation to elevated NaCl.

One of the major strategies for bacteria to survive and grow under osmotic and salt stress conditions is to accumulate compatible solutes such as amino acids by import or synthesis. Our previous study (Mukhopadhyay et al., 2006) suggested that *D. vulgaris* might mainly import osmoprotectants (e.g., glycine betaine) to deal with salt shock, which may be an initial mechanism for salt adaptation. A few amino acid transport genes (e.g., *proW*, *livF*, *livM*, DVU2744) were highly up-regulated, and those high-affinity branched-chain amino acid ABC transporters are expected to import amino acids at low exogenous concentrations. An accumulation of glutamate has been found to be an important osmoregulatory mechanism in bacteria, such as *Rhizobium meliloti* (Botsford and Lewis, 1990), *Salmonella typhimurium* (Botsford et al., 1994), *Erwinia chrysanthemi* strain 3937 (Goude et al., 2004), and *Escherichia*

coli (Csonka et al., 1996; McLaggan et al., 1994; Nandineni et al., 2004) in response to osmotic and/or salt stresses. In this study, metabolite assays showed that Glu was increased approximately 8-fold under salt adaptation compared to the control, and consistently, it was observed that an external addition of 2 mM Glu could significantly relieve salt growth inhibition in *D. vulgaris*. Glutamate is a central player in global nitrogen metabolism (Reitzer, 2003; Yan et al., 2007). In bacteria, it is well known that two pathways are responsible for glutamate synthesis: one is the GS-GOGAT cycle through the combined action of glutamine synthetase (GS, encoded by *glnA*) and glutamate synthase (GOGAT, GOGAT, encoded by *gltBD*), and the other is the GDH pathway by the action of glutamate dehydrogenase (GDH, encoded by *gdhA*). It appears that both pathways for glutamate biosynthesis exist in the *D. vulgaris* genome (<http://www.microbesonline.org/>). Although no genes have not been specifically assigned as glutamate dehydrogenase (GDH), two genes (DVU0375 and DVU0964) are annotated as Glu/Leu/Phe/Val dehydrogenase family proteins, and indeed, DVU0375 was significantly up-regulated under salt adaptation. Although no significant changes in expression were observed under salt adaptation, one gene (DVU1258) predicted to be glutamine synthetase (GS) and five genes (DVU1821-23, DVU2476, and DVU3291) for glutamate synthase (GOGAT) are present in the genome, and in contrast, there was a trend of over-expression of DVU1821 and DVU1823 (although the DVU1822 data is missing) in the same operon, and DVU3291 in another operon with other two genes under salt shock (Mukhopadhyay et al., 2006). However, it is not known if *D. vulgaris* mainly uses the GS-GOGAT pathway under salt shock, and the GDH pathway under salt adaptation for glutamate synthesis.

Although the intracellular concentration of Ala also reached 9.89 nmoles/mg, and one gene (DVU0724) predicted to encode a sodium/alanine symporter family protein was also up-

expressed, there have been no reports in the literature for this or the other accumulated amino acids (e.g., Leu, Ser, Gln, Lys) to be identified as osmoprotectants in bacteria. In growth assays, the addition of 2 mM Ala did alleviate the inhibitory effect of NaCl, which confirmed that the accumulation of Ala was indeed a response to salt adaptation. Of all the amino acids tested, only Lys did not appear to have a mitigating effect on the growth. However, the present data do not provide insight into the mechanism by which the accumulation or addition of these amino acids can alleviate salt inhibition, and further investigations are required to understand such mechanisms. This study indicates that *D. vulgaris* may accumulate compatible solutes, such as glutamate as an important strategy for survival and then growth under salt adaptation.

The transcriptomic data suggest a decrease in carbon metabolism under salt adaptation, and this was mainly reflected in the slower growth rate and in the down-regulation of carbon utilization genes and putative carbon starvation genes. First, although the membrane-bound lactate dehydrogenase (DVU0600, $Z = -1.2$) and the primary pyruvate:ferredoxin oxidoreductase (DVU3025, $Z=-1.5$) were not significantly altered, several genes (*porA*, *porB*, *oorB*, and DVU3349) that encoded pyruvate ferredoxin oxidoreductase were significantly decreased in expression under salt adaptation. Second, the genes *pta* and *ackA* were also significantly down-expressed, which may result in a decreased substrate-level ATP synthesis coupled to the conversion of acetyl-CoA to CoASH and acetate. In addition, two genes encoding putative carbon starvation proteins were also significantly down-regulated, suggesting that *D. vulgaris* utilized less carbon sources under salt adaptation, which is consistent with slow cell growth.

However, electron transport processes appeared to be more active or unchanged, which is supported by the expression of genes involved in both hydrogen cycling (Odom and Peck, 1981) and formate cycling (Heidelberg et al., 2004). In the proposed hydrogen cycling, periplasmic and

cytoplasmic hydrogenases are required to form a proton gradient for ATP synthesis and transport processes. In this study, a periplasmic hydrogenase (DVU1769-70) was up-expressed under salt adaptation although the transcript levels of genes encoding two cytoplasmic hydrogenases (Ech and Coo) were not significantly increased. Similarly, formate cycling also generates a proton gradient and provides energy for transport processes and ATP synthesis (Heidelberg et al., 2004). Indeed, two genes (DVU0587-8) encoding a formate dehydrogenase (Fdh) were up-regulated under salt adaptation in this study. Therefore, energy supply for transport processes could be kept stable or more active even though carbon metabolism activity in *D. vulgaris* was decreased in response to salt adaptation. Interestingly, sulfate reduction occurred in the cytoplasm remained unchanged although hydrogenase activity occurred in the periplasm seems to be increased. One possibility could be that such electron transport processes are modulated by the complicated c-type cytochrome network in *D. vulgaris* (Heidelberg et al., 2004).

In heterotrophic bacteria, such as *E. coli* and *B. subtilis*, the expression of salt-inducible genes was regulated by the sigma factors RpoS and SigB, respectively (Boor, 2006; Hengge-Aronis, 1996; Hecker et al., 1996; Hecker et al., 2001). In the photoautotrophic bacterium *Synechocystis sp.* PCC 6803, a few HKs were identified as sensors for salt stress (Marin et al., 2003). However, *D. vulgaris* appears not to have an RpoS ortholog, and no similar sensors, or regulators responsible for salt adaptation have been identified thus far. Fur is considered a global regulator in the *D. vulgaris* genome (Hemme et al., 2004). It was observed that high salinity caused iron deficiency and led to derepression of *fur* in *B. subtilis* (Hoffmann et al., 2002). Although the expression of *fur* did not significantly change under salt stress conditions, some genes predicted to be regulated by Fur, such as DVU0273, DVU2574 (*feoA*), DVU2680, and DVU3330 (Rodionov et al., 2004) did show increases in expression under salt adaptation (GEO

number). Similar results were also observed in *D. vulgaris* under nitrite stress (He et al., 2006) and salt shock (Mukhopadhyay et al., 2006). Thus, Fur may also play an important role in *D. vulgaris* under salt adaptation. The homolog of *fur*, *perR* (DVU3095) was significantly up-regulated under salt stress conditions. PerR is predicted to regulate oxidative stress genes and also responds to iron concentrations (Bsat et al., 1998; Chen et al., 1995). *rdl* that encodes rubredoxin-like protein and is predicted to be regulated by PerR was over-expressed under salt adaptation. However, since the function of most regulatory genes is unknown, an identification of regulatory networks in *D. vulgaris* as well as in other organisms in response to salt adaptation remains a great challenge.

Responses of *D. vulgaris* to elevated NaCl may follow a temporal pattern from salt shock to salt adaptation. This was first reflected in the changes in the expression of specific genes involved the import of osmoprotectants, efflux of harmful ions, energy supply, and cell motility. At an initial stage, *D. vulgaris* may mainly import efficient osmoprotectants, exclude Na⁺ from the cell, and move away from the stressful environment. The dynamic change in the expression of chemotaxis genes was a good example. At early time points of salt shock, many chemotaxis-related genes were identified to be up-regulated; at later time points of salt shock, only a few such genes were over-expressed, and most of them remain unchanged (Mukhopadhyay et al., 2006). When *D. vulgaris* was in the process of adaptation to evaluated NaCl, only two chemotaxis genes were up-regulated, and most of them were down-regulated. Second, such a dynamic progress was seen in the accumulation of Glu. For example, the concentration of Glu was measured at a more than 8-fold increase under salt adaptation, but only about 2-fold increase under salt shock (Mukhopadhyay et al., 2006) in comparison with the control. In addition, the expression of regulatory genes also showed a similar trend, and more genes were observed to be

changed under salt adaptation than under salt shock. However, the mechanisms of dynamic adaptation to salt stress are unknown, which points to our on-going study on long-term evolution of *D. vulgaris* in response to elevated NaCl.

Considering all together, a simple conceptual model is proposed for *D. vulgaris* adaptation to elevated NaCl (Fig. 7). Salt stress signal may be sensed by unknown HKs and then transduced to regulators, which regulate cellular activities of *D. vulgaris* in response to high salinity. In this model, only three categories of cellular activities (energy metabolism, general stress response, and amino acid or solute metabolism and transport) are emphasized based on our experimental results from growth, physiological, transcriptomic, and metabolite analyses. First, the transport of iron, phosphate (P_i), and amino acids into the cell and the exclusion of Na^+ from the cell require ATP hydrolysis. Although the transcriptomic data suggest a reduction of the ATP generation from the oxidation of lactate and pyruvate under salt adaptation, the over-expression of hydrogen oxidation and electron transport genes suggests that ATP generated from proton gradient may be increased. Perhaps consequently, sulfate reduction of *D. vulgaris* remained unchanged under salt stress conditions (Fig. 7A). Second, the most significant responses of *D. vulgaris* to salt adaptation were the decreased cell growth, and the over-expression of genes related to heat shock, phage shock, and oxidation. The latter is important for *D. vulgaris* to maintain the integrity of protein and membrane structures, prevent oxidative stress, suppress viral infections, and then adapt to such salt stress conditions (Fig. 7B). Third, the accumulation of small molecules (e.g., amino acids) to counter osmotic stress is one of the most important mechanisms in *D. vulgaris*. Our data strongly suggests that biosynthesis or import of one or more particular amino acids is the primary mechanism for salt adaptation. Of these, glutamate may be the most effective amino acid for *D. vulgaris* adaptation to a high salinity environment (Fig. 7C).

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Table 1 Expression changes of genes in *D. vulgaris* involved in amino acid biosynthesis and transport.

| Locus | Gene | Predicted function | Salt adaptation | | Salt shock | |
|--------------------------|-----------------|---|---------------------------------|----------------|--------------------|-------------|
| | | | Log ₂ R ^a | Z ^b | Log ₂ R | Z |
| A. Amino acid metabolism | | | Log ₂ R ^a | Z ^b | Log ₂ R | Z |
| DVU0085 | <i>trpB-1</i> | Tryptophan synthase, beta subunit | 2.48 | 3.72 | 1.44 | 2.74 |
| DVU0470 | <i>trpB-2</i> | Tryptophan synthase, beta subunit | -0.01 | -0.01 | 1.16 | 2.17 |
| DVU0471 | <i>trpA</i> | Tryptophan synthase, alpha subunit | 0.09 | 0.15 | 1.41 | 2.73 |
| DVU2204 | <i>tnaA</i> | Tryptophanase | 1.81 | 3.22 | 0.27 | 0.47 |
| DVU0115 | <i>aroE</i> | Shikimate 5-dehydrogenase | 1.58 | 2.01 | 0.74 | 1.19 |
| DVU0375 | NA ^c | Glu/Leu/Phe/Val dehydrogenase family protein | 2.70 | 3.69 | 0.70 | 1.12 |
| DVU1823 | <i>gltB-1</i> | Glutamate synthase, iron-sulfur clustering-binding subunit, putative | 0.20 | 0.16 | 1.35 | 2.37 |
| DVU3291 | NA | Glutamate synthase, iron-sulfur clustering-binding subunit, putative | 0.30 | 0.48 | 1.54 | 2.31 |
| DVU2981 | <i>leuA</i> | 2-isopropylmalate synthase | -0.18 | -0.18 | 1.36 | 2.51 |
| DVU2982 | <i>leuC</i> | 3-isopropylmalate dehydratase, large subunit, putative | -1.62 | -1.67 | 1.23 | 1.94 |
| DVU2983 | <i>leuD</i> | 3-isopropylmalate dehydratase, small subunit | -2.37 | -2.23 | 1.01 | 1.86 |
| DVU2984 | NA | conserved hypothetical protein | -3.14 | -3.46 | 0.98 | 1.87 |
| DVU2985 | <i>leuB</i> | 3-isopropylmalate dehydrogenase | -1.54 | -2.25 | 0.68 | 1.35 |
| B. Amino acid transport | | | | | | |
| DVU0724 | NA | Sodium/Ala symporter family protein | 1.42 | 2.69 | 0.53 | 1.04 |
| DVU2297 | <i>proW</i> | Glycine/betaine/L-proline ABC transporter, periplasmic-binding protein | 1.59 | 3.11 | 1.62 | 3.13 |
| DVU2298 | <i>opuBB</i> | Glycine/betaine/L-proline ABC transporter, permease protein | 0.82 | 1.42 | 1.43 | 2.74 |
| DVU2299 | <i>proV</i> | Glycine/betaine/L-proline ABC transporter, ATP binding protein | 0.87 | 1.49 | 1.48 | 2.56 |
| DVU2341 | NA | Amino acid ABC transporter, permease protein, His/Glu/Gln/Arg/opine family | 1.56 | 2.76 | 0.78 | 1.18 |
| DVU2740 | <i>livF</i> | High-affinity branched-chain amino acid ABC transporter, ATP-binding protein | 3.18 | 5.34 | 0.61 | 0.96 |
| DVU2741 | <i>livG</i> | High-affinity branched chain amino acid ABC transporter, ATP-binding protein | 0.54 | 0.64 | 1.05 | 1.66 |
| DVU2742 | <i>livM</i> | High-affinity branched chain amino acid ABC transporter, permease protein | 1.79 | 2.08 | 0.93 | 1.76 |
| DVU2743 | <i>livH</i> | High-affinity branched-chain amino acid ABC transporter, permease protein | 0.29 | 0.32 | 0.15 | 0.22 |
| DVU2744 | NA | High-affinity branched-chain amino acid ABC transporter, periplasmic amino acid binding protein | 2.40 | 4.48 | 1.78 | 3.20 |
| DVU3297 | <i>mtr</i> | Tryptophan-specific transport protein | 1.34 | 2.48 | 0.35 | 0.65 |

a: log₂ (treatment/control); b: Z score; c: no gene name has been assigned to this locus yet.

Table 2 Expression changes of genes in representative operons of *D. vulgaris* under salt adaptation in comparison with salt shock.

| Locus | Gene | Predicted function | Salt adaptation | | Salt shock | |
|--|-----------------|--|---------------------------------|----------------|---------------------------------|----------------|
| | | | Log ₂ R ^a | Z ^b | Log ₂ R ^a | Z ^b |
| A. Inorganic ion transport and metabolism | | | | | | |
| DVU0525 | NA ^c | Transcriptional regulator, MarR family | 2.99 | 2.76 | 1.24 | 2.30 |
| DVU0526 | NA | Drug resistance transporter, putative | 3.01 | 5.05 | 1.81 | 3.39 |
| DVU2571 | <i>feoB</i> | Ferrous iron transport protein B | 2.87 | 5.09 | 1.88 | 3.54 |
| DVU2572 | <i>feoA</i> | Ferrous iron transport protein A, putative | 2.11 | 3.21 | 1.98 | 3.60 |
| DVU2574 | <i>feoA</i> | Ferrous iron transporter component <i>feoA</i> | 1.21 | 2.13 | 1.46 | 2.31 |
| DVU2305 | NA | Conserved hypothetical protein | -2.38 | -2.68 | -1.07 | -2.06 |
| DVU2306 | NA | Phosphate transporter family protein | -1.55 | -2.89 | -1.02 | -1.99 |
| B. General stress response | | | | | | |
| DVU1729 | NA | Killer protein, putative | 2.14 | 2.13 | 2.75 | 4.76 |
| DVU1730 | NA | DNA-binding protein | 2.46 | 3.36 | 2.28 | 3.91 |
| DVU2441 | <i>hspC</i> | Heat shock protein, Hsp20 family | 4.01 | 7.42 | 0.94 | 1.67 |
| DVU2442 | NA | Heat shock protein, Hsp20 family | 3.64 | 6.72 | 0.72 | 1.40 |
| DVU2986 | <i>pspC</i> | Phage shock protein C | 2.47 | 4.48 | 0.96 | 1.87 |
| DVU2987 | NA | Hypothetical protein | 2.90 | 5.42 | 1.15 | 2.22 |
| DVU2988 | <i>pspA</i> | Phage shock protein A | 3.51 | 6.67 | 1.33 | 2.21 |
| DVU3093 | <i>rdl</i> | Rubredoxin-like protein | 1.14 | 2.05 | 0.48 | 0.90 |
| DVU3094 | <i>rbr</i> | Rubrerythrin | 0.68 | 1.09 | 0.37 | 0.51 |
| DVU3095 | <i>perR</i> | Peroxide-responsive regulator PerR | 2.07 | 2.87 | 0.69 | 1.25 |
| DVU0198 | NA | Minor capsid protein C, degenerate | -2.30 | -3.07 | -1.36 | -2.33 |
| DVU0199 | NA | Conserved hypothetical protein | -3.13 | -4.22 | -1.66 | -2.98 |
| DVU0200 | NA | Major head protein | -1.78 | -1.74 | -1.27 | -2.30 |
| DVU0201 | NA | Hypothetical protein | -2.85 | -3.58 | -1.02 | -1.85 |
| DVU0202 | NA | Holin | -2.71 | -3.29 | -1.07 | -1.96 |
| DVU0203 | NA | Conserved hypothetical protein | -2.64 | -2.40 | -1.20 | -2.27 |
| DVU0204 | NA | Lipoprotein, putative | -2.15 | -2.43 | -1.38 | -2.45 |
| DVU2568 | <i>cpsA</i> | Peptidase, M20/M25/M40 family | -2.03 | -2.67 | -0.20 | -0.31 |
| DVU2569 | <i>slyD</i> | Peptidyl-prolyl cis-trans isomerase | -1.41 | -2.05 | -1.15 | -2.21 |

a: log₂ (treatment/control); b: Z score; c: no gene name has been assigned to this locus yet.

Table 3 Accumulation of amino acids in both control and NaCl treated *D. vulgaris* cells.

| Amino acid | Control (nMol/mg, \pm sd, n =5) | NaCl (nMol/mg, \pm sd, n =5) | NaCl/control |
|---------------|-----------------------------------|------------------------------------|--------------|
| Glutamate | 10.25 \pm 0.63 | 82.82 \pm 8.01 | 8.08 |
| Histidine | 0.07 \pm 0.00 | 0.20 \pm 0.04 | 2.74 |
| Serine | 1.30 \pm 0.12 | 2.54 \pm 0.26 | 1.95 |
| Betaine | 1.40 \pm 0.08 | 2.68 \pm 0.58 | 1.92 |
| Lysine | 0.15 \pm 0.01 | 0.28 \pm 0.06 | 1.85 |
| Glutamine | 3.63 \pm 0.38 | 6.48 \pm 0.51 | 1.79 |
| Alanine | 9.89 \pm 0.92 | 17.53 \pm 3.89 | 1.77 |
| Leucine | 0.50 \pm 0.01 | 0.79 \pm 0.05 | 1.57 |
| Threonine | 1.45 \pm 0.08 | 2.21 \pm 0.17 | 1.52 |
| Proline | 1.46 \pm 0.18 | 2.03 \pm 0.35 | 1.39 |
| Aspartate | 7.41 \pm 0.48 | 10.21 \pm 1.13 | 1.38 |
| Glycine | 8.86 \pm 1.70 | 10.32 \pm 3.16 | 1.16 |
| Isoleucine | 0.69 \pm 0.04 | 0.72 \pm 0.02 | 1.05 |
| Methionine | 0.05 \pm 0.00 | 0.05 \pm 0.01 | 1.02 |
| Arginine | 0.94 \pm 0.03 | 0.89 \pm 0.03 | 0.94 |
| Valine | 5.39 \pm 1.43 | 4.30 \pm 1.14 | 0.80 |
| Tyrosine | 0.21 \pm 0.00 | 0.13 \pm 0.00 | 0.62 |
| Phenylalanine | 0.01 \pm 0.00 | 0.01 \pm 0.00 | 0.57 |
| Tryptophan | 0.005 \pm 0.00 | 0.003 \pm 0.00 | 0.55 |
| Asparagine | ND | 1.87 \pm 0.41 | |

Where n and sd are abbreviations for the number of analytical measurements and the standard deviation, respectively.

Figure legends:

Fig. 1 Growth curves of *D. vulgaris* grown in the LS4D medium. The stock culture was activated overnight before inoculation. A. 1.0% of overnight activated culture was inoculated into the LS4D medium containing 0, 50, 100, 250, or 500 mM NaCl. B. 1.0% of overnight activated culture was inoculated into the LS4D medium containing 250 mM NaCl with or without 0.5% (wt/vol) yeast extract (YE) added, and the controls without NaCl or without YE were also included.

Fig. 2 Expression changes of representative genes of *D. vulgaris* involved in energy metabolism under salt adaptation in comparison with salt shock (120 min). Gene expression intensity data with the ratio of the NaCl treatment to the control converted to \log_2 values and visualized by JColorGrid software (Joachimiak et al., 2006). SA: salt adaptation; SS: salt shock at 120 min. No data are presented in the cells with gray color.

Fig. 3 Expression changes of representative genes of *D. vulgaris* involved in regulatory processes under salt adaptation in comparison with salt shock (120 min). Details for data presentation are the same as described in Fig. 2.

Fig. 4 Relief of salt inhibition of *D. vulgaris* by an external addition of amino acids, Glu, Ala, Leu, Trp and Lys in the LS4D medium under the control (A) and 250 mM NaCl stress (B) conditions. *D. vulgaris* cells were grown at 37°C and their growth was monitored at OD₆₀₀.

Fig. 5 A general comparison of global transcriptomic profiling of *D. vulgaris* under salt adaptation and salt shock. Z score was set to $|2.0|$. Totally, 3321 ORFs were detected for both stress conditions, and all their Z scores were shown. The x-axis presents data from salt adaptation, and the y-axis from salt shock. I. Up-regulated genes under salt adaptation; II. Down-regulated genes under salt adaptation; III. Up-regulated genes under salt shock; IV. Down-regulated genes under salt shock; V. Up-regulated genes under both conditions; VI. Down-regulated genes under both conditions; VII. Insignificantly changed genes are located in the central rectangle. The number in each pair of brackets is the gene number in each above defined category.

Fig. 6 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. 2.

Fig. 7 A conceptual model of *D. vulgaris* Hildenborough responses to a long-term NaCl exposure. Color codes: red, up-regulation or increase; blue, down-regulation or decrease; gray, no significant change. A. Energy metabolism; B. General stress response; C. Protein, amino acid, and solute metabolism and transport.

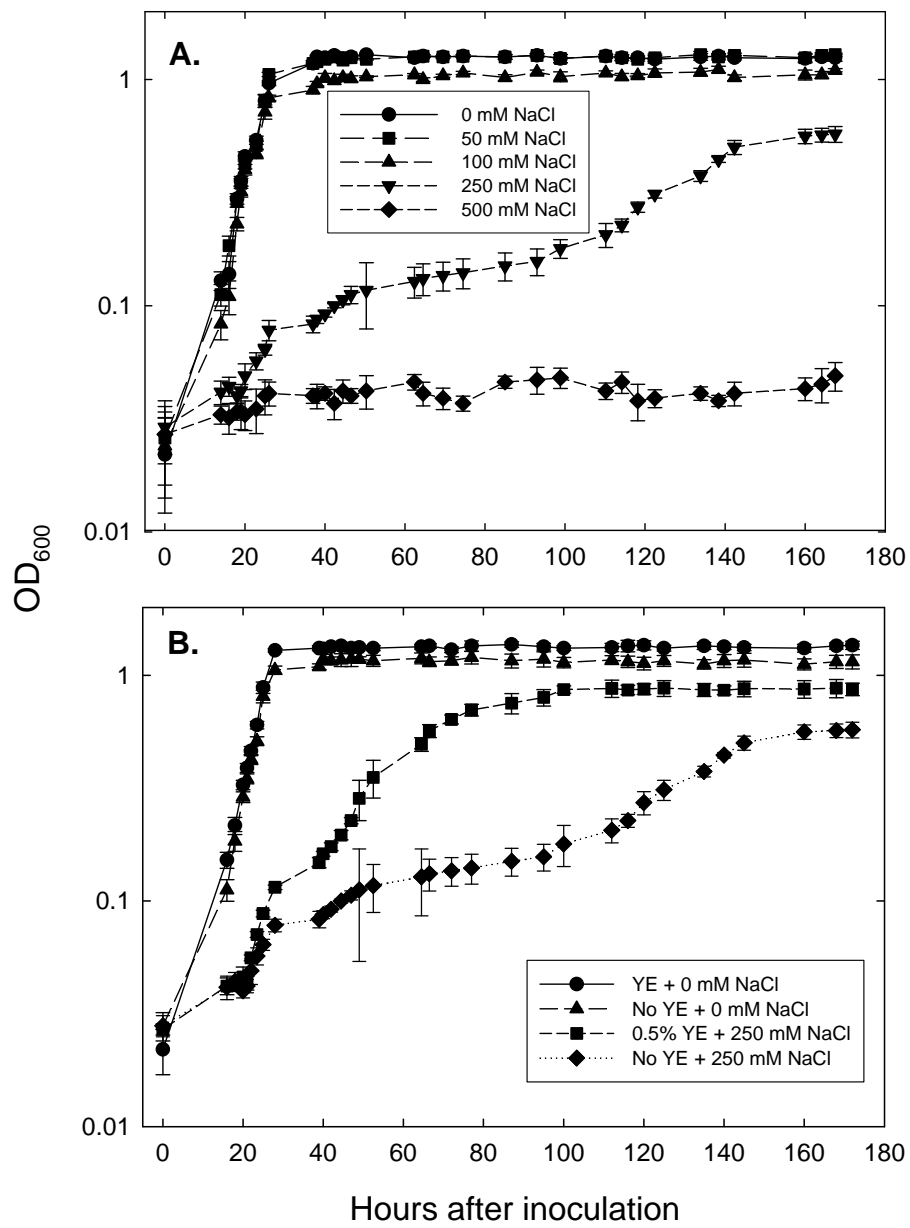


Fig. 1

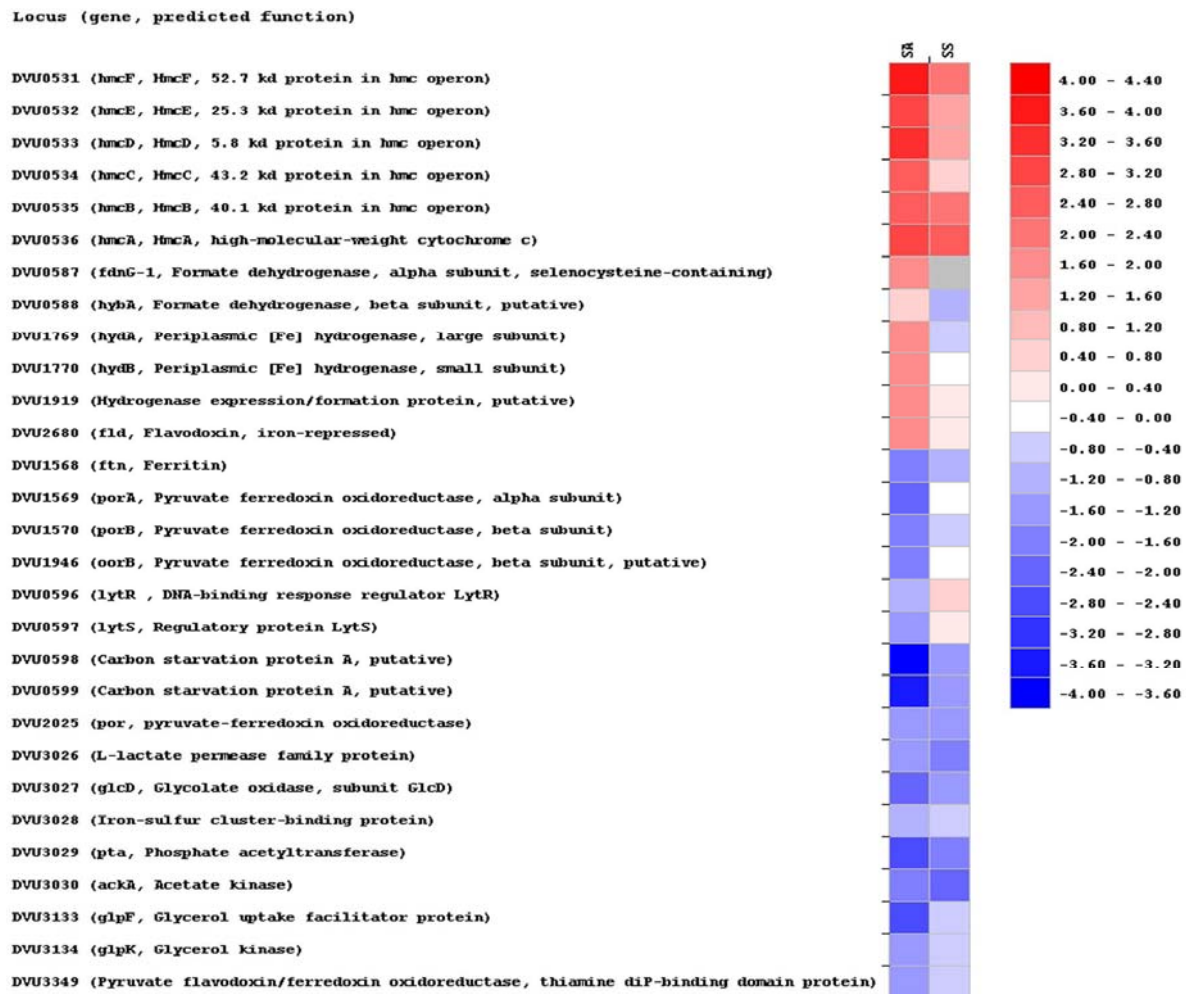


Fig. 2

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, Predicted transcriptional regulator for lysine biosynthesis and transcriptional regulator)
 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, Sigma-54 dependent transcriptional regulator, putative/response 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)

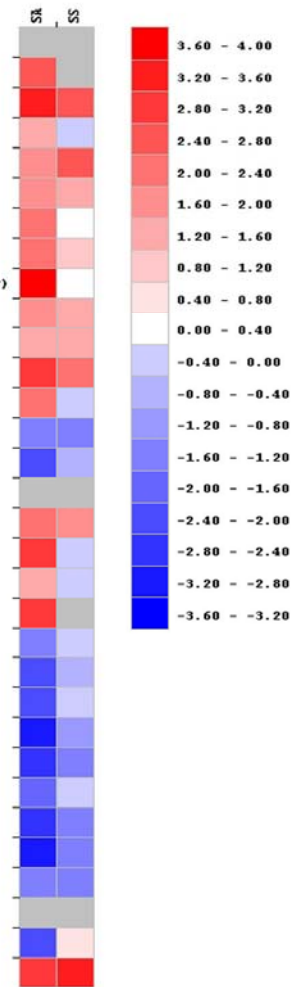


Fig. 3

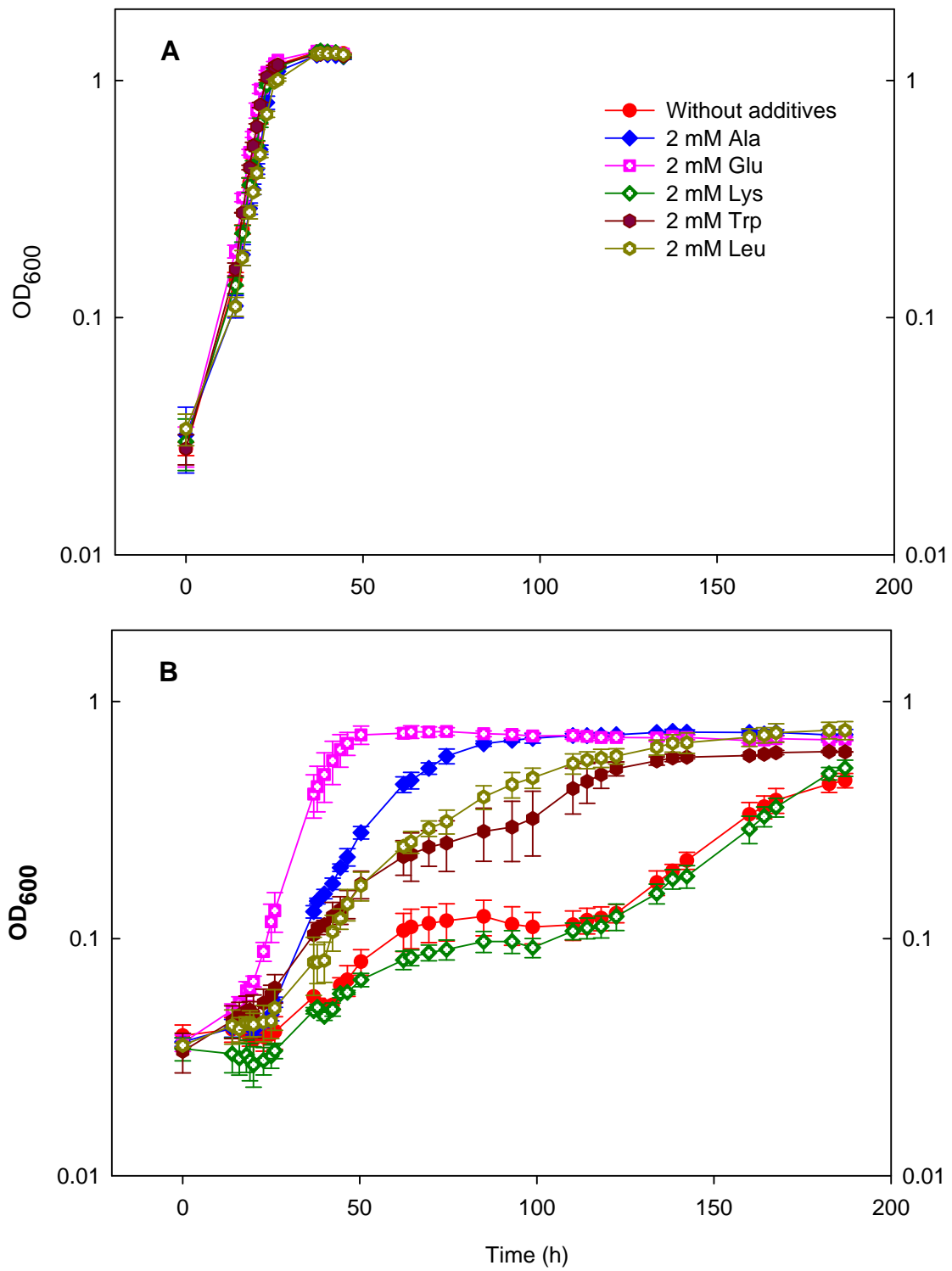


Fig. 4

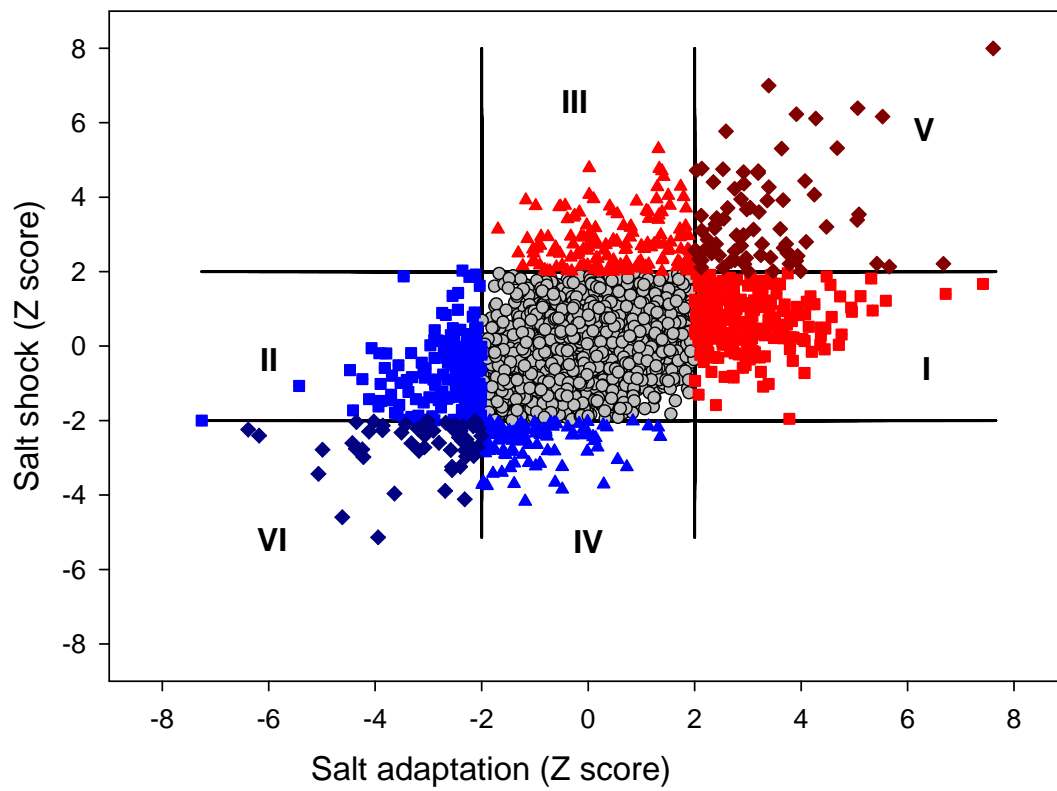


Fig. 5

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, NodT family)
 DVU0063 (Transcriptional regulator, MarR family)
 DVU0434 (mahA, Ech hydrogenase, subunit EchA, putative)
 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 F0, B subunit, putative)
 DVU0780 (atpF1, ATP synthase F0, B subunit, putative)

B. Sulfate reduction

DVU0846 (apsB, Adenylylsulphate reductase, beta subunit)
 DVU0847 (apsA, Adenylyl-sulphate reductase, alpha subunit)
 DVU0848 (gmoA, Heterodisulfide reductase, putative)
 DVU0849 (gmoB, Heterodisulfide reductase, iron-sulfur-binding subunit, putative)
 DVU0850 (gmoC, Heterodisulfide reductase, transmembrane subunit, putative)

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)

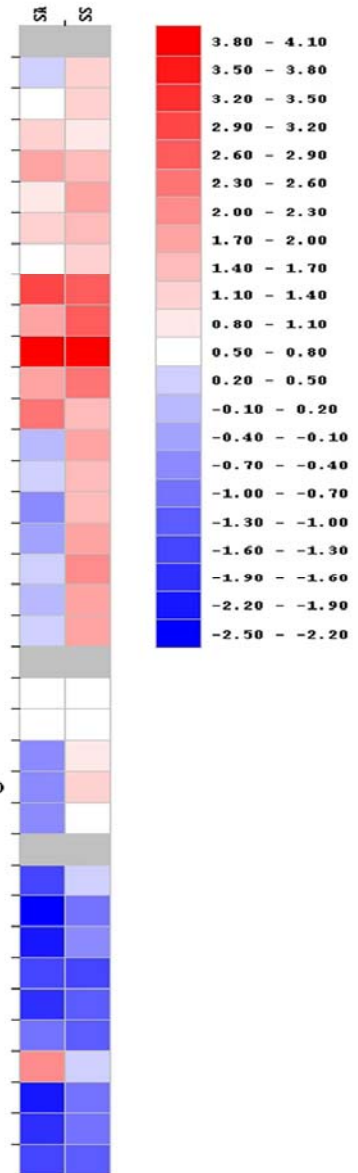


Fig. 6

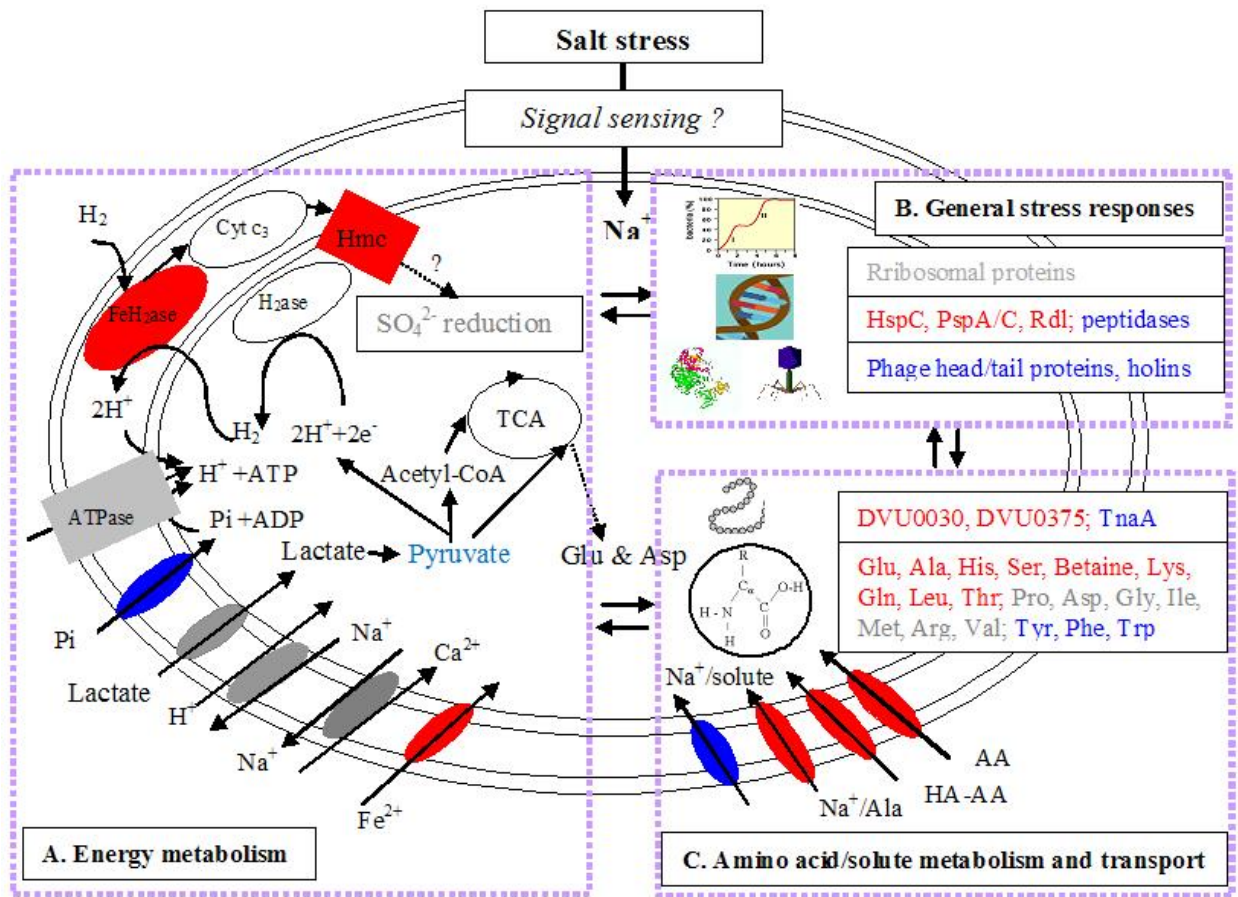


Fig. 7

Supplemental Data Summary

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

Fig. S2 Correlation of microarray data and RT-PCR data for 12 randomly selected genes of *D. vulgaris*.

Table S1 Table 1 ORFs, used primers, and their product sizes for reverse transcription real time PCR assay.

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

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

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

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

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

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

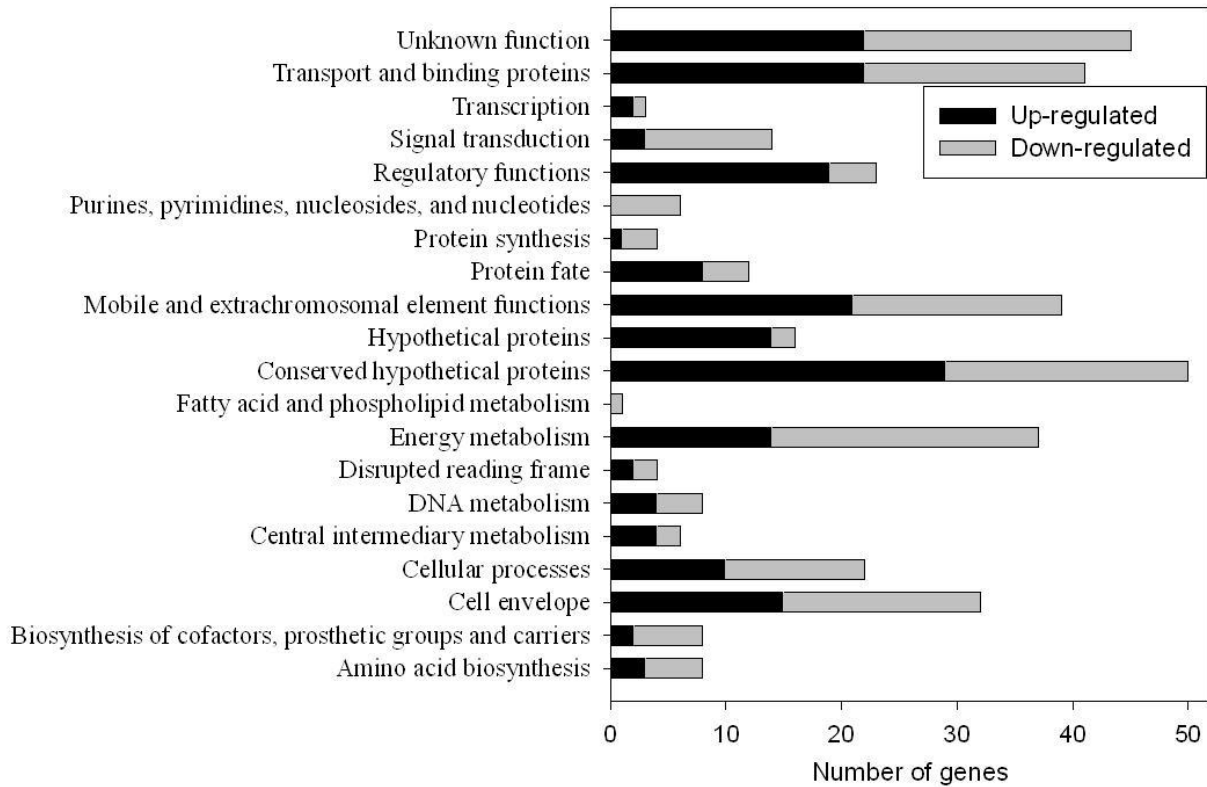


Fig. S1 Changes in gene expression profiling of *D. vulgaris* by functional category in response to salt adaptation. Inoculation of overnight activated *D. vulgaris* cells into the LS4D medium for the control, and LS4D + 250 mM NaCl for the treatment. Samples were taken at the mid-log phase (OD600 = ~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.

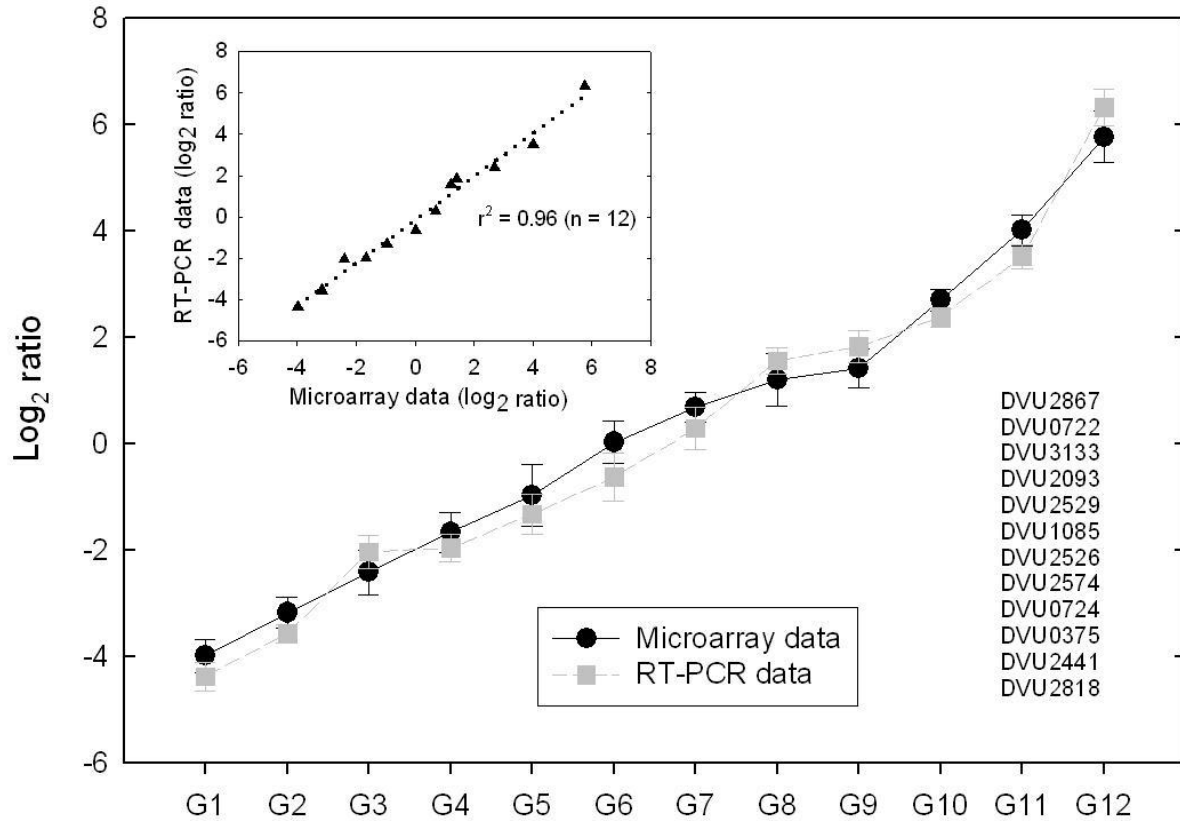


Fig. S2 Correlation of microarray data and RT-PCR data for 12 randomly selected genes of *D. vulgaris*. 12 genes (G1-12) with a range of expression levels were randomly selected for RT-PCR to quantitatively verify the microarray data using specific primers (Table S1). The same RNA prepared for microarray hybridization was used.

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 | TATCTGTTCCGGGTTACCT | 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 | ACGTCCTTGATCTCGCAGAC | Glu/Leu/Phe/Val dehydrogenase family protein | 102 |
| DVU2441 | GCGTAACCCCTGAAGACATC | GCTCCTGCCTGAACATCCT | Heat shock protein, Hsp20 family | 99 |
| DVU2818 | CAAGGATGTTGTGCTGCCTA | CACGGGAAAGTGTGGTGAAC | Hypothetical protein | 99 |

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 |

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|---------|-------|-------|------|------|--|
| 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 |

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|---------|-------|-------|------|------|--|
| 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 |

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|----------|-------|-------|------|------|--|
| 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 |

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|---------|-------|-------|-------|-------|--|
| 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 | uridylylase 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 |