DEVELOPMENT OF GENOME-WIDE GENETIC ASSAYS IN *DESULFOVIBRIO VULGARIS* HILDENBOROUGH

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By

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The undersigned, appointed by the dean of the Graduate School, have examined the dissertation entitled

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a candidate for the degree of doctor of philosophy,

and hereby certify that, in their opinion, it is worthy of acceptance.

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Thanks Mom and Dad

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Abstract

Illumina® sequencing and other massively-parallel, short read sequencing technologies have become prevalent methods for querying the genetic systems of organisms. This trend was initially driven by the demand for general *de novo* and resequencing applications in eukaryotes, but applications have recently grown in scope to also include more specific assays and methods intended for use in prokaryotic systems. This thesis seeks to develop two such assays for use in the sulfate reducing bacteria type species *Desulfovibrio vulgaris* Hildenborough. These novel assays continue advances made in other bacteria, and the use of this environmentally relevant obligate anaerobe will ensure their extension to other bacteria outside easily-manipulated groups studied previously. The first assay is a variation on existing transposon sequencing (Tn-seq) assays, which seek to determine gene fitness profiles and essential genes by simultaneous analyses of whether the absence of each gene product alters the growth kinetics of the bacterium. Here we modify the Tn-seq procedure with delivery of the transposon through conjugation and liquid culture enrichment of the mutant pool, creating transposon liquid enrichment sequencing (TnLE-seq). This simplifies and shortens the process, and also reduces barriers to application of the technique in microbes lacking a facile genetic system. The second assay provides a means of mapping consensus 3' end sites of RNA transcripts across a reference genome. This method is known as 3' RNA-seq and compliments an established technique for determining 5' start sites. Together these facilitate the application of current sequencing technology to a wider array of microbes and a new type of biologically relevant genetic data.

Chapter 1 – Introduction

1.1 History of *Desulfovibrio vulgaris* Hildenborough

The obligate anaerobe *Desulfovibrio vulgaris* Hildenborough (DvH) (*109*) (Figure 1, Figure 2) has long been considered the type strain for study of the sulfate reducing bacteria (SRB) as a group. DvH was originally isolated from a clay sample taken in Hildenborough, Kent, England in 1946 (*108*) and is motile, Gram-negative, and a member of the phylum Proteobacteria and the deltaproteobacteria class. Over time, SRB research has focused on variety of applications ranging from mitigation of oil souring that occurs from sulfide production by SRB in commercial oil wells (*38*) to a better understanding of corrosion of underground ferrous metal structures (*99*) and potential heavy metal bioremediation strategies in groundwater (*86*).

In general, genetic modification systems used in this species have advanced beyond those of related SRB but at a slower pace than more genetically tractable

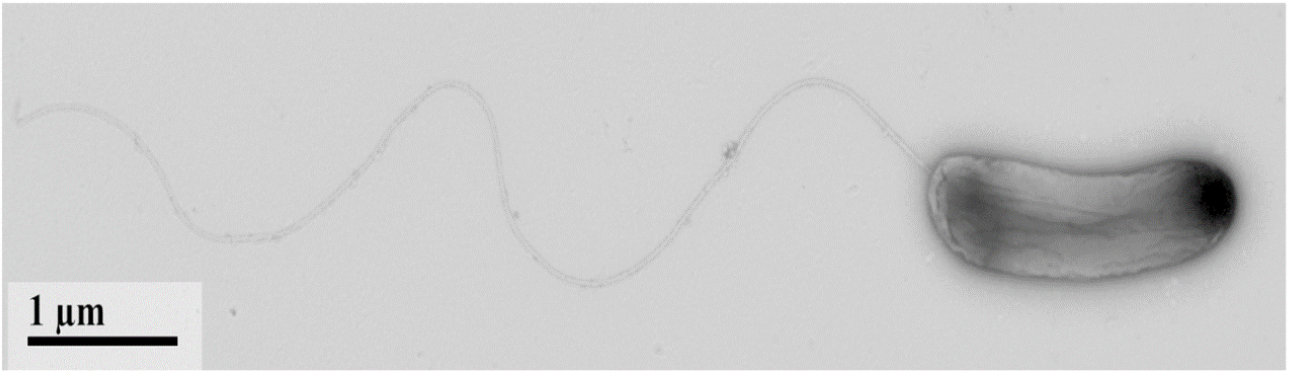


Figure 1. Transmission electron micrograph of a single Desulfovibrio vulgaris Hildenborough (DvH) bacterium.

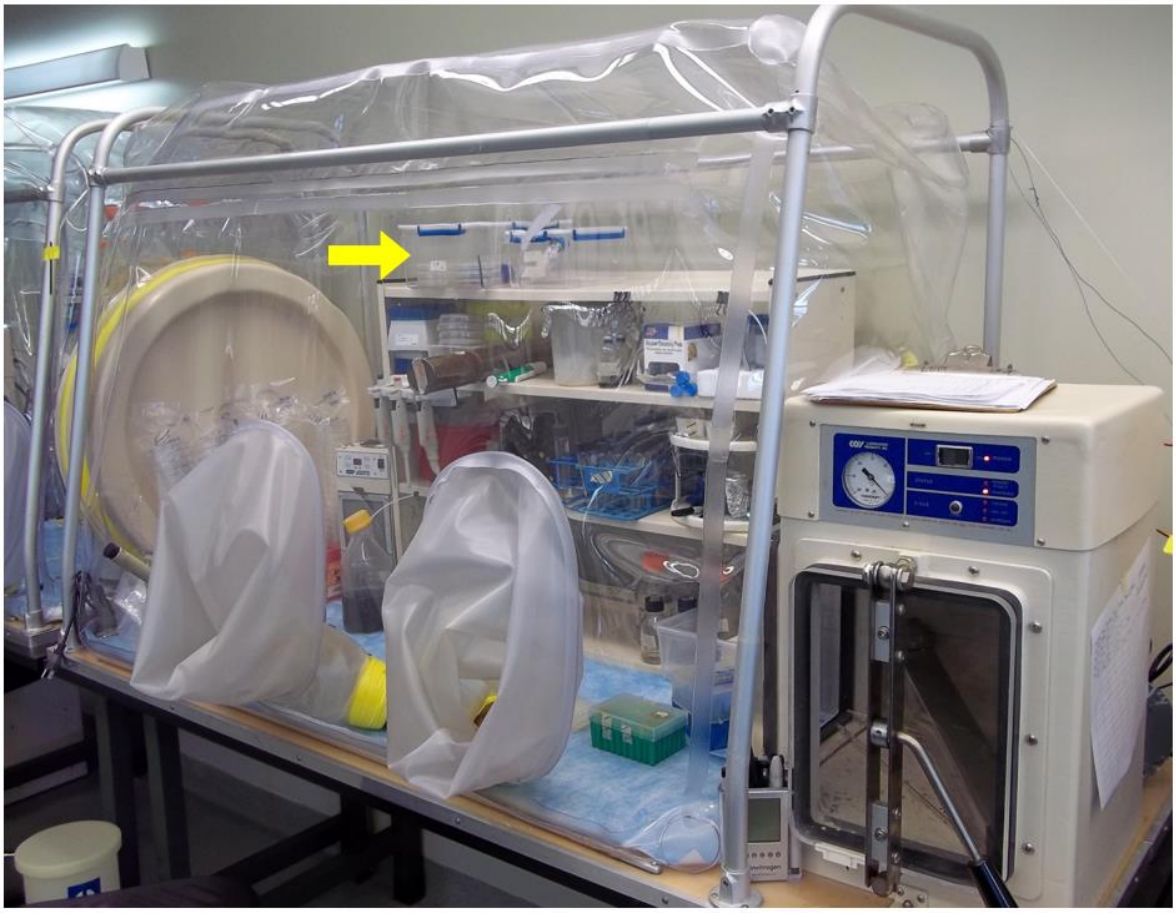


Figure 2. Anaerobic glove bag used for growth and manipulation of DvH. Smaller, sealed anaerobic boxes (arrow) are used for storage of plates containing growing colonies.

aerobic bacteria, particularly those of the gammaproteobacteria such as *E. coli*. The completed genome sequence of DvH was published in 2004 (*51*). A markerless deletion system was successfully developed for use in this species five years later (*15, 62-64*). Furthermore, transposon mutagenesis via conjugation with an *E. coli* host has produced cataloged transposon mutant libraries containing over $1x10^4$ mutants in both DvH (Wall lab, unpublished) (Figure 3) and the related strain *Desulfovibrio alaskensis* G20 (*73*). Together, this access to directed and random gene deletion mutants has allowed further elucidation of SRB metabolism.

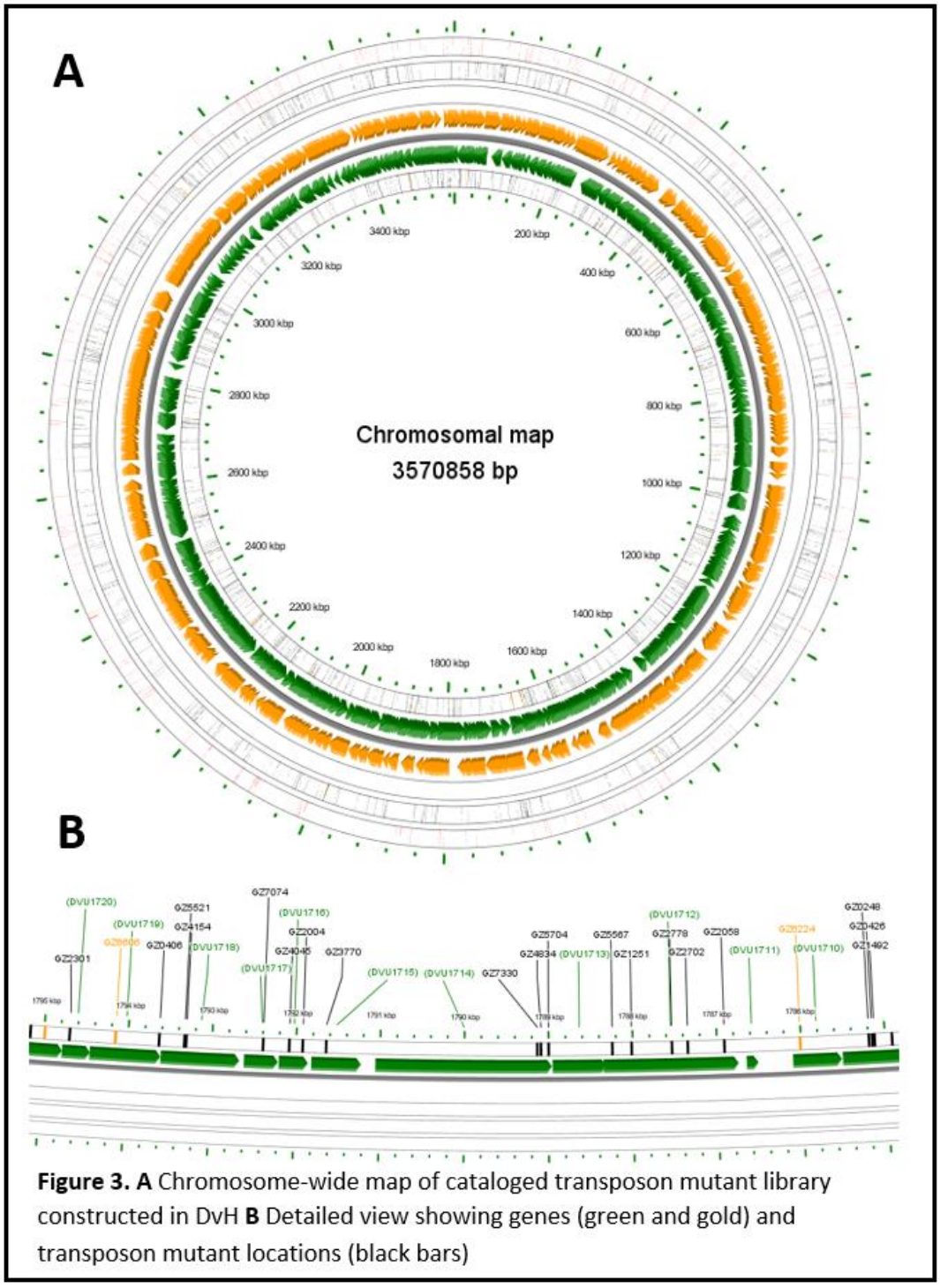


Figure 3. A Chromosome-wide map of cataloged transposon mutant library constructed in DvH **B** Detailed view showing genes (green and gold) and transposon mutant locations (black bars)

Accurate gene annotation data for DvH is being continually refined by both experimental (*110*) and computational methods (*60*) and is easily available online (*31*). High-density transcript microarray data is also readily available for expression changes

among a variety of conditions affecting SRB (*9, 93, 101, 135, 136*). Finally, affinity tagging of a large number of proteins across the DvH genome has allowed for interaction studies of key protein complexes (*16, 72*). Taken together, these technological advances have provided a framework for much progress regarding the understanding of the biology of DvH and SRB in general.

1.2 Motivation for this work

Despite much progress, the sophistication of SRB genetic systems has continually lagged behind those of the more easily grown enteric bacteria. This is particularly true regarding the application of rapidly developing high throughput sequencing assays over the past decade. While *de novo* sequencing and assembly of genomes of new isolates is relatively straightforward, adapting other assays to take advantage of this powerful technological development can be more challenging. This is reinforced by the fact that even recent studies involving SRB have employed outdated microarray techniques for the analysis of gene expression data (*111*), despite overwhelming evidence to support the superiority of sequence-based RNA-seq methods (*23, 24, 87, 118, 119*).

The continually falling per-sample costs associated with sequencing coupled with the wide availability of smaller and more flexible instrument systems presents many opportunities for diverse methods of genome analysis. These new methods are often pioneered in eukaryotic systems (*29, 66*) before being carefully adapted for use in the very well-studied prokaryotes such as *E. coli*. Depending on the requirements of the assay, it may then take another series of modifications before such a protocol can be used with less readily grown and/or genetically manipulated bacterial species. This

overcoming of obstacles to facilitate wider adoption of current sequencing techniques is a primary goal of this work, as are improvements to current techniques and the examination of biologically relevant processes.

The general Transposon sequencing (Tn-seq) protocol was one of the first high throughput genetic assays to be developed for use in bacteria (*44, 45, 52, 77, 125*). This technique seeks first to generate a pool of $1x10^4$-$1x10^6$ individual transposon mutants, then carry out a growth competition phase wherein each of these distinct mutants competes for resources, and finally to use mutant abundance data from deep sequencing reads to draw conclusions regarding the fitness contributions of every non-essential gene in the genome. At the start of the current work, these procedures were unavailable to any bacterial species not meeting the criteria of high genetic electrocompetency, aerobic growth, and robust growth on surface agar. The objective here has been the relaxing of these requirements. Of particular interest are 1) the development of all-liquid growth conditions to eliminate surface plating and allow analysis of anaerobic species, 2) the introduction of the transposon by conjugation rather than electroporation, and 3) an overall reduction in the time required to generate a given sequencing sample. The success of such a method would then allow comparison studies evaluating gene fitness changes under varied metabolic conditions such as presence/absence of yeast extract or inhibitory levels of sodium nitrate (*70*). The reduction of time constraints in particular would also make possible the study of gene fitness across background deletion mutants such as those lacking the uracil

phosphoribosyltransferase (Upp) component of the pyrimidine salvage pathway or a redox-sensing regulator (Rex) (*19*).

Another opportunity to advance genomic assays in DvH presented itself in a report on a new transcription start site (TSS) mapping technique known as 5' RNA-seq (*110*). This study identified consensus TSS with high precision across the DvH genome, and further applied this information to computationally predict consensus promoter sequences. However, it did not address transcript end sites (TES) with the same level of precision, instead relying on older transcript microarray technology to confer some computationally predicted intrinsic terminator locations (*67*). Price and colleagues found that "it is not clear how to identify the precise 3' ends of bacterial transcripts experimentally, but RNA-seq protocols are evolving rapidly" (*110*). The present work seeks to fulfill this need through the development of 3' RNA-seq. This approach is complementary to the established 5' RNA-seq and uses many of the same principles, but read sequencing is targeted to 3' transcript ends in order to fill in the other half of operon boundaries at single-nucleotide resolution.

This work seeks to separately address both of these needs. Protocols were developed specifically for use in DvH; however, much attention was given to the subsequent broad application of these genetic approaches in other organisms. In particular, newly isolated environmental bacteria which have similarly been recalcitrant to advanced sequencing methods will benefit from these approaches. Success in these pursuits will not only move the specific study of the DvH genome forward, but will stimulate the field of prokaryotic high-throughput genome analysis in general.

Chapter 2 – Optimizing transposon insertion in DvH to create saturation libraries of mutations in non-essential genes

2.1 Introduction

Various transposons exist for relatively high efficiency insertion of a selectable element into bacterial genomes, thus often creating a mutant deficient in the product of the interrupted gene. High throughput applications such as cataloged mutant libraries and Tn-seq applications most often rely on one of two general transposon types, the Mariner and Tn*5* based transposons. The Mariner family of transposons was originally derived from an unstable mutation in a eukaryotic genome (*57*). They can be modified to carry a variety of resistance markers to aid in selection, require a TA site for insertion into a genome, and are active in a wide variety of hosts (*30*). Tn*5*-derived transposons were isolated from bacteriophage DNA (*53*), usually encode a kanamycin resistance gene, and do not have a known sequence preference for insertion (*32*). I chose a Tn*5*-derived transposon with enhanced insertion efficiency, Tn*5*-RL27 (*78*), which is encoded on the plasmid pRL27 for stable replication in *E. coli*. This decision was based on the successful use of Tn*5*-RL27 for the generation of Tn mutants in DvH and related strains by members of our laboratory and collaborators at that time (*73*).

With the transposon and corresponding plasmid backbone selected (Figure 4), the next step was to determine whether simple electroporation of the plasmid into DvH cells would yield a sufficiently high number of mutants per reaction for pooling >$1x10^6$

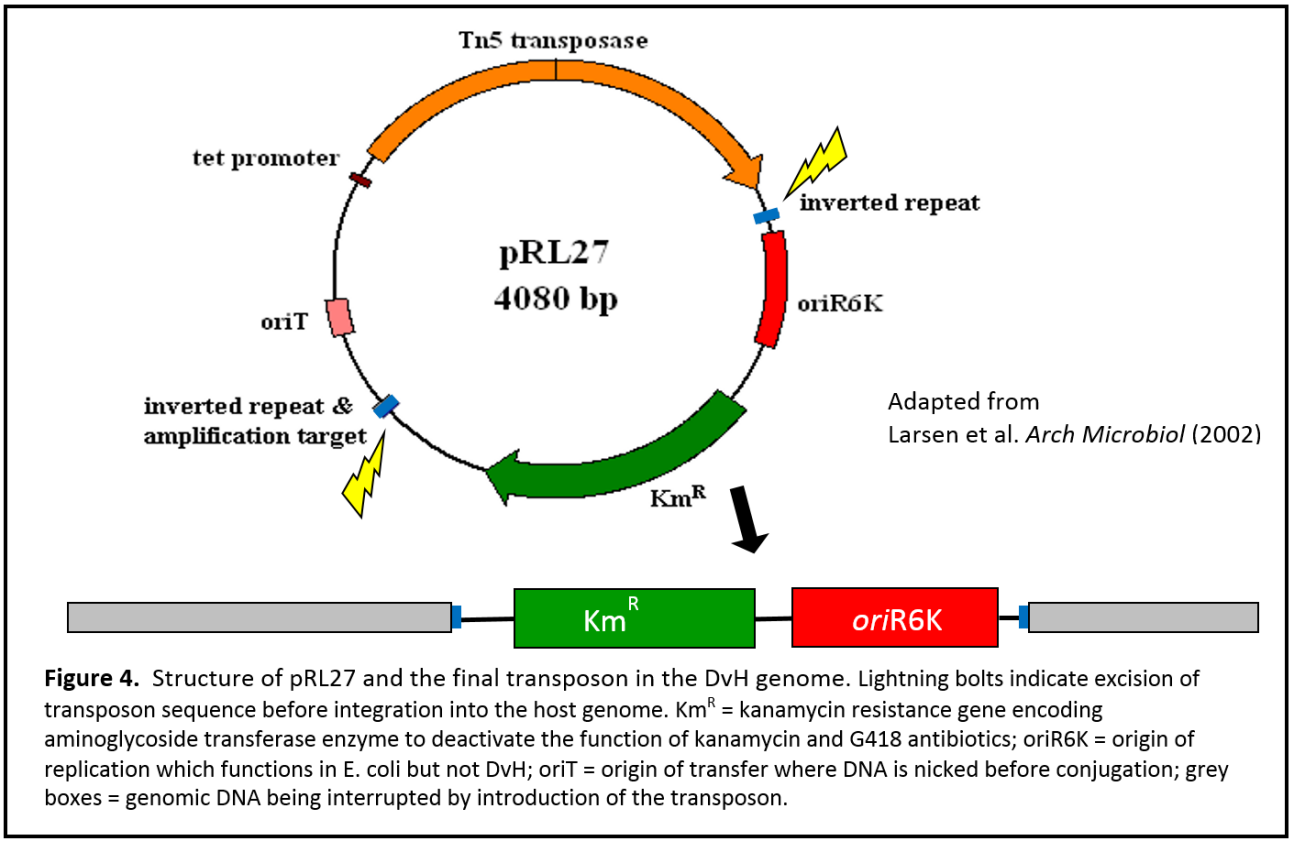


Figure 4. Structure of pRL27 and the final transposon in the DvH genome. Lightning bolts indicate excision of transposon sequence before integration into the host genome. Km^R = kanamycin resistance gene encoding aminoglycoside transferase enzyme to deactivate the function of kanamycin and G418 antibiotics; oriR6K = origin of replication which functions in E. coli but not DvH; oriT = origin of transfer where DNA is nicked before conjugation; grey boxes = genomic DNA being interrupted by introduction of the transposon.

mutants together in a single culture. This would be the simplest solution, but DvH is known to have a relatively low natural competence and possesses multiple restriction endonuclease systems for degrading foreign DNA. These include canonical Type I (*hsdRSM*) and Type II (DVUA0019-20) restriction systems (*31*) (www.MicrobesOnline.org), as well as a putative Type ISP (DVU2175) system (unpublished observation). Both the Type I and II systems have been individually knocked out in DvH by a markerless deletion approach (*62*) and derived strains were available for electroporation to assay a potential increase in transformation efficiency. The alternative to introduction of a whole, double-stranded plasmid via electroporation is conjugation of the plasmid from *E. coli* into the DvH cell. This system was well established in our laboratory, and largely circumvents restriction systems due to single-

stranded introduction of the plasmid. This method has the potential to carry over live *E. coli* cells and impact the growth competition phase of transposon mutagenesis, however.

2.2 Mutagenesis via electroporation

Electroporation is the process of passing an electric current through a suspension containing both cells and exogenous DNA in order to briefly open pores in the cell membrane and allow uptake of the DNA. It is a faster and simpler process than most other means of foreign DNA introduction but varies greatly in terms of efficiency depending on the recipient strain and/or type of DNA being introduced. In the case of pRL27 introduction for Tn-seq applications, whole, unmethylated double-stranded plasmid DNA is introduced. It is therefore susceptible to degradation by any of the three restriction-modification systems encoded in the DvH genome, and physiology of the cell itself may further impact the rate of successful plasmid uptake in comparison to more genetically tractable strains.

A baseline rate of transposon insertion was first established in DvH by plating serially diluted, triplicate samples of cultures before and after introduction of the plasmid via electroporation. These plates were counted after growth to determine CFU concentration (and thus the approximate number of cells per ml) of the cultures. It is important to follow specific plating methods developed here for DvH in order to obtain consistent results (Appendix A). For electroporation, an established protocol for DvH was used (*134*). Cultures were spun down in mid-logarithmic phase and washed as

described before a final suspension in electroporation buffer. This cell slurry contained approx. $1x10^9$ DvH cells per 100 µl electroporation cuvette and ~$3.6x10^3$ transformants per µg (transformants/µg) were obtained during electroporation of wild-type (WT) DvH. Because it can be difficult to load 1 µg of plasmid DNA into a small electroporation cuvette, typical results on a per-reaction basis were closer to ~$1\text{-}2x10^3$ transformants per cuvette, which is consistent with rates seen by other experiments undertaken in the Wall lab. Importantly, in repetitions of this procedure with strains JW7035 (*Δupp ΔhsdR*) and JW9050 (*Δupp ΔDVUA0020*), the rate of Tn mutagenesis per tube was unchanged from WT recipient experiments. Previous electroporation of the related, though stably replicating, plasmid pSC27 into JW7035 yielded a similar result of $2.4x10^3$ transformants/µg (*62*). Plasmid uptake into WT DvH was $2.1x10^0$ transformants/µg in the Keller et al. study, however, suggesting that the *ΔhsdR* deletion does have a beneficial impact on transformation rates in stable plasmids. Strain JW9050 was not previously assayed for competence, and results obtained here did not show a significant uptake difference in conjunction with a transposable element from a non-stable plasmid (pRL27).

In any case, transformation efficiency would need to be greatly enhanced for any relatively easy generation of a ~$1x10^6$ Tn mutant pool in DvH. At the most efficient rates achieved here ($3.6x10^3$ transformants/ug), and assuming efficiency increased linearly from 0.25 to 1 µg plasmid per cuvette, approximately 270 electroporations would be needed to provide a pool of $1x10^6$ Tn mutants. Although possible, the labor involved in generating the pool of transposon mutations would greatly hinder the repeatability of

the Tn-seq assay and limit subsequent investigations of gene fitness changes resulting from key mutations available as inframe deletion mutants. It is worth noting that the generation of a strain lacking all three known restriction endonucleases (hsdR, DVUA0020, and DVU2175) might greatly increase transformation efficiency in DvH. If loss of each system contributed synergistically to transformation competency, it might be possible to reduce the number of electroporation reactions needed to generate the pool of mutants to a manageable number. Yet further investigation of genetic interactions in mutant host strains would have to start from this hypothetical strain with improved competency, limiting the benefits of its use.

2.3 Mutagenesis via conjugation

Conjugation occurs when an *E. coli* strain with specialized DNA transfer machinery confers genetic material to recipient cells. When using members of the *Desulfovibrio* genus as a recipient, donor *E. coli* must contain a compatible broad host range system such as an integration of the RP4 plasmid (*7*). This genetic element is present in the *E. coli* strain used here, BW29427, and confers a Tra^+ phenotype whereby a plasmid containing an origin of transfer (*oriT*) sequence can be transferred to a broad range of recipient bacteria (*89*). During incubation, a sex pilus embedded in the outer membrane of the donor attaches to the Tra^- recipient cell and establishes contact between the plasma membranes of the two cells. Meanwhile, the DNA of the plasmid being transferred is enzymatically nicked within the *oriT* sequence, unwound as single-stranded DNA (ssDNA), and passed through a plasma membrane pore that now connects the donor and recipient cell (*47*). This introduction of single stranded DNA

circumvents the restriction systems of the recipient bacteria, which was confirmed by comparing conjugation efficiency of WT DvH vs JW7035 cultures (data not shown). In the case of a stable plasmid, the unwound ssDNA can hybridize to itself to provide a priming site for DNA replication machinery and be converted to a full dsDNA plasmid. This same process may take place for a suicide vector before the cell replicates and loses the original unstable plasmid due to a lack of compatible origin of replication. In the case of an unstable plasmid encoding a transposon, the recipient cell must have the transposon integrated into the genome if it is to produce daughter cells containing antibiotic markers encoded in the transposon.

Conjugation from an *E. coli* donor is well established in *Desulfovibrio* strains (*127*) and this approached was previously used in our lab to generate a cataloged library of transposon mutants in DvH (Grant Zane, data available at desulfovibriomaps.biochem.missouri.edu/mutants/). Conjugation was chosen to create the transposon mutant pool for Tn-seq both for the ability to compare this pool directly to cataloged mutant data and for the relative efficiency of transposon introduction.

2.4 Materials and Methods

Electroporation protocol – Performed as previously described (*134*).

Conjugation protocol – This method was modified from a protocol written by Grant Zane, which was modified from a protocol by Jennifer Kuehl at Lawrence Berkeley National Lab (*73*).

On Day 1, 1 µl of solution containing 50-100 ng/µl plasmid pRL27 was transformed into chemically competent WM3064 (*E. coli*) cells as described in the One Shot® TOP10 Competent Cells manual (Life Technologies cat. #C4040-10). The heat shock step was extended to 45 seconds due to use of a thick plastic tube. The final cell culture was plated by pipetting 200 µl on an LC + 50 µg/ml kanamycin + 100 µM DAP plate and incubating for 24 hours at 37°C. DvH (recipient strain) freezer stock was inoculated by adding 1 ml thawed stock into in 10 ml of MOYLS4, which consisted of MOY liquid media as previously described (*134*) plus 60 mM sodium lactate, 60 mM sodium sulfate, and 1.2 mM sodium thioglycolate. This was incubated at 34°C for 24 hours. All handling of DvH was done in an anaerobic glove bag. On Day 2, or when colonies were grown, 3-5 colonies of transformed *E. coli* cells were picked into 5 ml LC + 50 µg/ml kanamycin + 100 µM DAP liquid and shaken at 200 RPM overnight at 37°C. Importantly, only freshly transformed colonies were used in this step, within 3-4 days of introducing pRL27. The DvH culture was subcultured by adding 2 ml to 20 ml MOLS4 (defined) and incubated at 34°C overnight.

On Day 3, 400 µl of the *E. coli* culture were subcultured to 10 ml LC + 100 µM DAP liquid medium in a 125 ml flask and grown for 4 h at 37°C and 100 RPM shaking. This reduction in shaking speed was important for preservation of conjugative pili. The following optional plating step was added, for tracking CFUs of cultures to follow multiple populations through conjugation and enrichment. After 4 h incubation, 100 µl of both *E. coli* and DvH cultures were removed for separate serial dilutions into 900 µl aliquots of the respective growth media. Cultures were diluted in successive 10-fold

increments in 1.5 ml Eppendorf tubes until a total dilution of $1x10^9$-fold was obtained. Triplicates of each of the $1x10^7$- $1x10^8$- and $1x10^9$- fold dilutions were plated for later counting to determination of CFU concentration in these cultures. For *E. coli*, 3 ml LC top agar (0.75% wt/vol) was inoculated with the serially diluted culture then poured on top of LC agar (1.5% wt/vol) supplemented with 50 µg/ml kanamycin and 100 µM DAP as described above. (For DvH, see Appendix A for detailed plating instructions to obtain consistent CFU counts.)

The 10 ml *E. coli* culture was divided into five aliquots of 1.5 ml each, and centrifuged at $1.5x10^3$ x *g* for 5 min. in a tabletop centrifuge. The 20 ml DvH culture was divided into ten aliquots of 1.5 ml each, and centrifuged at $1.28x10^4$ x *g* for 1 min. in a tabletop centrifuge. All supernatant from the *E. coli* tubes was removed and all 15 tubes were brought into the anaerobic glove bag. All but 50 µl of supernatant was removed from the ten tubes with DvH pellets, and two DvH pellets per *E. coli* pellet were combined to create five mixed cell slurries (this step must be completed in an anaerobic glove bag). These five aliquots of 100µl cell slurry were pipetted onto five separate pieces of sterile nitrocellulose membranes which ware arranged on a solid MOYLS4 agar plate. Filters were circular with 47 mm diameter and 0.45 µm pore size (Pall life sciences cat. no. 60173), but cut in triangular quarters before autoclaving to sterilize them. MOYLS4 agar plates used for this step were first dried in the anaerobic glove bag for 1-2 weeks. After pipetting the slurry onto the filters, it was slowly absorbed into the filters and the plate was turned upside down. This plate was incubated in the glove bag at 34°C overnight.

On the fourth day, sterile forceps were used to pick all 5 membranes into 15 ml of MOYLS4 and this tube was tapped on a solid surface until cell spots were removed from the membranes and suspended in the medium. This culture was incubated in the anaerobic glove bag for 4 hours at 34°C. Another optional plating step was performed, where 100 µl from this recovery culture was removed and serial dilutions and plating were performed as described above and in Appendix A. Triplicates of each of $1x10^{7}$- $1x10^{8}$- and $1x10^{9}$- fold dilutions were plated on MOYLS4 plates for total CFU counts for DvH, and each of $1x10^{4}$- $1x10^{5}$- and $1x10^{6}$- fold dilutions were plated on MOYLS4 + 400 µg G418 per ml for DvH exconjugant CFU counts.

2.5 Results

Twelve successful conjugations of pRL27 from *E. coli* to DvH were performed, with transfer of the Tn-RL27 kanamycin resistance marker occurring at a rate of between 1.6x10-3 and 1.0x10-4 exconjugants per WT cell. The average rate for these experiments was 3.6x10-3 exconjugants per WT (Table 1). Additionally, two preliminary

Table 1. Population tracking by colony counts, performed before and after mutant generation

			Average CFU/ml[A] (N)	
Population	**Strain**	**Features**	**Pre-conjugation**	**Post-conjugation**
Recipients	DvH	WT, Km^S	$5.0x10^9$ (12)	$2.4x10^9$ (12)
Exconjugants	DvH::TnRL27	Km^R	0	$6.8x10^5$ (12)
Average. Km^S CFU per Km^R CFU			--	$3.6x10^{-3}$

[A] Colony counts were quantified by serial dilution, added to agar while molten and poured into plates so CFUs formed within the agar in triplicate. Plates were supplemented with 400µg G418/ml where necessary

trials were performed where *E. coli* and DvH pellets were resuspended in a total of 60 or 80 µl of medium instead of the established protocol volume of 100 µl. This was meant to

enhance contact between individual members of the two species, but transformation rates in both fell well within the range of rates seen in 100 µl resuspensions ($2.3x10^{-3}$ and $2.5x10^{-3}$ exconjugants per WT for 60 and 80 µl, respectively). A resuspension volume of 100 µl was used for all further conjugations. Since 5x conjugations could be carried out in a single Petri dish and the total recovery volume for these was 15 ml per experiment, total yield averaged $1.0x10^{7}$ Tn mutants per experiment. This number exceeds the number of base pairs in the 3.7 Mb DvH genome and is therefore more than enough to saturate the genome with transposon insertions when all mutants are pooled and insertion sites mapped to a single reference sequence. This high degree of coverage is important because it almost entirely eliminates the possibility that a gene of significant length would be excluded from this analysis by chance. This assertion is further supported by the final read alignment data outlined later in this work.

Chapter 3 – Development of liquid enrichment and library preparation procedures for Tn-seq

3.1 Introduction

All Tn-seq methods described in the literature thus far have selected for the growth of transposon mutants (exconjugants) over the parental strain by plating cultures on solid agar supplemented with an antibiotic. In this setup, colonies that grow to a visible size can be assumed to carry the antibiotic marker, and thus possess the transposon of interest integrated into their genome. Untransformed cells do not grow, and thus are efficiently eliminated during this step. Though an effective technique for most aerobic bacteria, plating presents multiple potential problems for anaerobic bacteria. One issue is the increased exposure to oxygen when plating. This procedure adds a significant selective pressure to the mutant population before the actual growth competition phase can be started. Another problem is the logistical challenge of handling large numbers of plates. This is not only made harder due to space limitations in an anaerobic system but also has general drawbacks for all Tn-seq applications. Surface plating for manual collection of thousands of colonies is labor- and time-intensive, necessitating freezer stock preparations of mutant libraries if further studies are needed. This practice both adds unnecessary cell stresses from the freeze/thaw process and hampers the ability to generate new libraries in genetically diverse background strains quickly.

Table 2. Impact of oxidation stress on DvH gene products

Study	Oxygen exposure	Analysis method	Protein encoding genes significantly impacted (of 3,404 total)
Fourier 2006	1 mM O_2 (1 h flushing)	2D protein gel	54
Mukhopadhyay 2007	0.1% O_2 (0-4 h)	Transcript microarray	12
Mukhopadhyay 2007	21% O_2 (0-4 h)	Transcript microarray	847
Pereira 2008	1 mM O_2 (1 h flushing)	Transcript microarray	307
Zhou 2010	1 mM H_2O_2	Transcript microarray	1012

One concern with exconjugant enrichment by surface plating anaerobes is the exposure of colonies to oxidation stress. Many studies (*41, 42, 93, 102, 137*) have been conducted concerning the impact of oxygen and hydrogen peroxide exposure in DvH. All experiments found that transcript and/or protein levels were significantly altered in a wide variety of genes. Proteomic studies examining the effect of oxygen flushing (*42*) on protein levels evaluated by two dimensional gel electrophoresis procedures found significant changes in 54 proteins (*41*). Transcript microarrays increased the sensitivity of genome-wide assays and found significant transcript changes in anywhere from 12 to 1012 genes, depending on the type of oxygen exposure (Table 2) (*93, 102, 137*). A primary objective of the enrichment phase of a Tn-seq experiment should be to eliminate stresses with potentially widespread effects. Sequencing is often not possible immediately after introduction of the transposon due to extremely high background levels of wild-type DNA compared to mutants. This necessitates the establishment of unbiased baseline fitness values via a control experiment. In fact, one of the most

interesting conditions for Tn-seq analysis might be an anaerobic vs. microaerophilic comparison. This analysis would compare to data obtained in the studies in Table 2. It would be difficult, likely omitting a very significant number of genes with high fitness values, if surface plating were used and a true anaerobically grown starting pool could not be established.

The time investment involved in surface plating and scraping colonies into a single culture is perhaps the biggest obstacle in accomplishing a Tn-seq assay as described in the literature from 2008-2011 (*5, 43-46, 77, 125*). Most of these descriptions did not include the specific number of plates scraped, but one that did puts the number in excess of 1,000 plates (*77*). Others do not achieve the same level of saturation, perhaps due to limitations in the number of enrichment plates used. These have "insertions per base pair" ratios of 1:182 (*45*), 1:120 (*48*), and 1:191 (*11*). The goal here was to replicate the saturation seen in the 1,000 plate study, which generated a ratio of 1:13 insertions:base-pair (*77*), but to achieve this while also eliminating plating. This change would not only save time and aerobic stress on growing mutants, but also eliminate the freezing and thawing of mutant library cultures. Achieving a reduction in handling of the Tn mutant pool would remove an obvious growth stress while also limiting the total number of doublings of the mutant pool before applying experimental conditions. These increases in efficiency of handling are important improvements when seeking to provide an opportunity for comparison of all transposon mutants in a pool where every mutant has a unique mutation.

In the procedure developed here, changes were also made to an established method of selectively isolating transposon junctions by polymerase chain reaction (PCR) and adding the adapters necessary to allow the final fragment library to amplify on an Illumina flowcell. DNA fragment library was based on a published technique known as transposon-directed insertion site sequencing (TraDIS) (*6, 77, 107*), which also describes the bacterial mutagenesis and enrichment stages modified for application here. Briefly, the library preparation described in the TraDIS technique calls for the isolation of genomic DNA (gDNA) followed by a sonication step to shear the DNA into fragments. These fragments are then end-repaired and have standard Illumina® paired-end adapters ligated randomly to both ends of all fragments using the NEBNext® DNA Library Prep Master Mix Set for Illumina® (New England Biolabs, Ipswitch, MA). A PCR reaction of 22 cycles is carried out such that one primer amplifies from one of the standard Illumina® adapters present on the end of most fragments and the other primer amplifies only from the transposon junctions present in a small subset of fragments. These primers contain additional sequences to extend beyond the original fragment on either side and promote binding to the Illumina® flowcell later in the process, so the overall effect is both to enrich for those fragments containing transposon-gDNA junctions and to make sure that only those fragments are sequenced. Finally, TraDIS sequencing occurs via a primer that sits 10 base pairs upstream of the exact transposon-gDNA junction. When sequence data are received from libraries with this setup, each read therefore contains the last 10 bases of the transposon followed by 26 bases of gDNA sequence that is used to map the transposon insertion location to a reference

genome (when 36 total cycles of sequencing are performed). This method nearly fit the library preparation and sequencing needs of the newly designed Tn-seq assay, but important changes were made and will be outlined in Chapter 3.3.

3.2 Development of a liquid enrichment protocol

Following the delivery of the transposon to DvH by conjugation (detailed in Chapter 2) and a recovery phase, in the final experimental design, the exconjugate mixture was grown in 500 ml of MOYLS4 medium (or other medium for later comparison trials) both to enrich transposon mutants that had acquired the gene encoding kanamycin resistance (also conferring G418 resistance) and to allow these mutants to compete with each other until reaching mid-exponential growth phase. This culture formed the parental strain transposon pool grown in rich medium and sequencing of insertion sites recovered revealed the cohort of essential genes as those without mutations. Briefly, to generate the transposon mutant pool, the five post-conjugation membranes for each condition were combined into a 15 ml culture of MOYLS4 lacking diaminopimelic acid and grown without antibiotic selection for four hours. This step allowed the aminoglycoside 3'-phosphotranferase (*65, 117*) gene encoded in the newly introduced TnRL-27 transposon (*78*) to be transcribed before any antibiotic was introduced, thereby preventing unintended inhibition of mutant cells. Next, the 15 ml culture was diluted 10-fold to 150 ml MOYLS4 without diaminopimelic acid and containing the G418 antibiotic (a kanamycin analog). This culture was grown to an optical density of 0.40 at 600 nm (OD_{600}) to allow DvH exconjugants resistant to G418 an opportunity to outcompete wild-type DvH. Such growth was completed in about 24 h

under these standard conditions, and cultures were still in the exponential-growth phase at that time.

After 3 trials with the 150 ml cultures, CFU counts showed that wild-type DvH cells had persisted at an average of approximately 23 for every one DvH exconjugant CFU (Table 3). This was not an unexpected result, as G418 is bacteriostatic binding the ribosome and preventing accurate translation of new proteins. A low representation of transformants was not ideal, however, because only one per 24 individual genomes would contain the transposon later to be selectively captured in the DNA fragment library preparation phase. Therefore this large amount of background DNA would make enrichment of useful fragments containing transposon junctions difficult.

Additionally, the *E. coli* donor cell density found in the first enrichment was $9.1x10^6$ CFU/ml. Although this strain is an auxotroph for diaminopimelic acid (DAP) and this nutrient was not supplied in the recovery or enrichment cultures, the relatively rapid nature of the assay means that this donor did not immediately die off. *E. coli* elimination is important to reduce any potential impact on DvH mutant competition, to limit sequencing of the transposon insertions in the *E. coli* DNA and to eliminate the transposon donor plasmid pRL27. This plasmid is present in relatively low copy numbers in *E. coli* (10-20 per cell) due to the Pir^+ phenotype of strain WM3064 used here (*89*).

To mitigate these problems, the 15 ml of the recovered culture was diluted into a larger volume. This dilution could potentially enhance selection for G418 resistant transposon mutants because there would be more total G418 per cell while leaving the

concentration of the antibiotic unchanged. It was possible that G418 sensitive (wild-type) DvH would no longer be able to benefit from any inactivation of the drug by the aminoglycoside 3'-phosphotranferase produced in the transposon mutants. This would lead to a higher ratio of mutants to wild-type DvH. Additionally, further dilution would almost certainly decrease the concentration of donor *E. coli* which cannot grow in the absence of DAP. DAP possibly released from dead cells would also be diluted with the greater volume.

The final step in the liquid enrichment technique was monitoring the culture until it reached mid-exponential phase and harvesting for later DNA isolation and preparation of an Illumina® fragment library. DvH cultures grown on lactate and sulfate as electron donor and recipient, respectively, have consistently been shown to reach final (stationary phase) optical densities of 0.8-1.0 when measured at a wavelength of 600 nm (*124, 134*). The cell harvesting technique should be sufficiently robust to accommodate gene deletion strains as hosts for gene fitness studies which may not reach the upper end of this range, so I chose a final OD_{600} of 0.4 as a balance between allowing enough cell growth/competition and avoiding genetic pressures that can occur in late exponential stage when bacteria are preparing for stationary phase (*22, 136*). After harvesting the 500 ml enriched culture (3,696 x *g*, 12 min), the pellets were washed by suspending in 250 ml sterile, anaerobic growth medium and centrifuging the culture twice. Finally, the cells were resuspended in one to two ml of this growth medium before continuing with the steps described below.

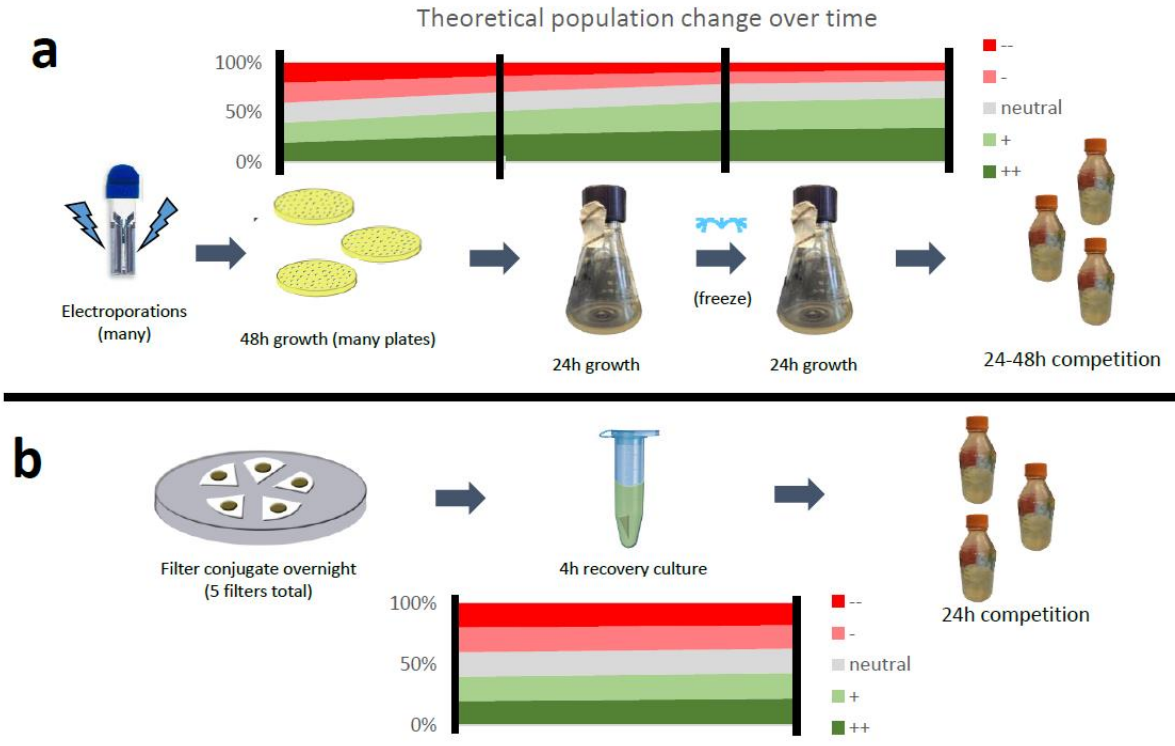


Figure 5. Comparison of mutagenesis and enrichment in two different Tn-seq experimental approaches. **a)** Method outlined in Langridge et al., and similar to many other Tn-seq experiments. The freezing and second 24 h growth steps are not performed in all methods **b)** TnLE-seq method as outlined in this work

3.3 Changes to an existing Illumina library preparation technique

Although the TraDIS library preparation method outlined in the Langridge et al. study was close to fitting the need for determining the transposon insertion sites, some important changes were required (Figure 5). Liquid enrichment has the potential to retain more DNA not associated with the transposon mutants. Therefore, steps were taken to reduce the quantity of *E. coli* and wild-type DvH gDNA, as well as donor plasmid. A size selection scheme was added to the Illumina® fragment library preparation to enhance selection for only those fragments that contained transposon-gDNA junctions, and the input mass of DNA for the final PCR step was increased. Finally,

the sequencing primer was designed to sit at the exact end of the transposon sequence, rather than 10 base pairs upstream of the transposon end. This change was made to avoid redundant base calls that would interfere with the function of the HiSeq® instrument, an issue that did not occur when previous experiments were conducted on older sequencing systems.

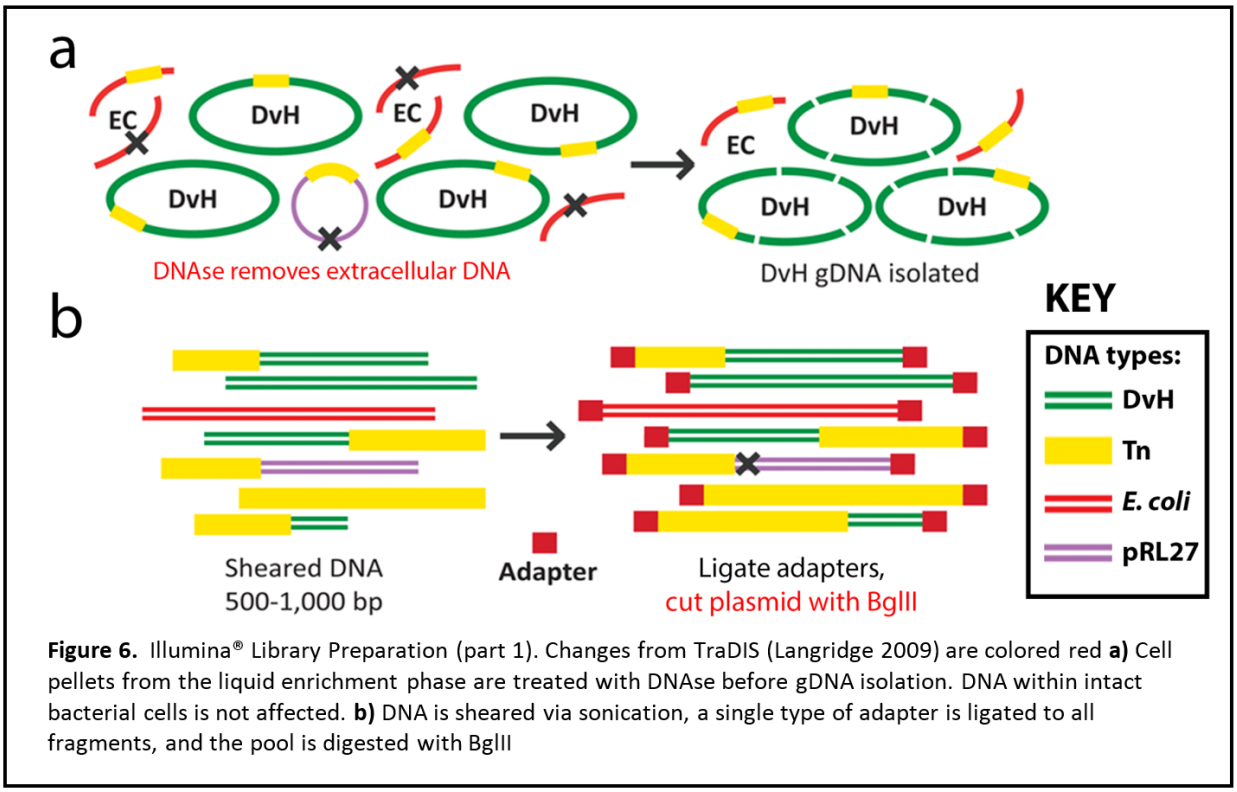


Figure 6. Illumina® Library Preparation (part 1). Changes from TraDIS (Langridge 2009) are colored red **a)** Cell pellets from the liquid enrichment phase are treated with DNAse before gDNA isolation. DNA within intact bacterial cells is not affected. **b)** DNA is sheared via sonication, a single type of adapter is ligated to all fragments, and the pool is digested with BglII

The liquid enrichment phase efficiently enriched DvH transposon mutants to 56% of the CFUs obtainable for the final pool (on average across 12 experiments with enrichment improved in later trials), but steps were taken to promote elimination of other DNA. The degradation of donor cell DNA obtained from lysis in the absence of DAP increased the proportion of DvH transposon junctions as a fraction of total DNA to make PCR enrichment more effective in fewer cycles. It also eliminated most donor plasmid

sequences from the final pool, thereby removing redundant and unwanted sequences to save sequencing capacity. Unwanted DNA was eliminated in two ways. First, the slurry of bacteria (harvested as described above) was incubated with DNase for one hour to degrade extracellular DNA (Figure 6A). Following this incubation, the cells were pelleted, the DNase-containing supernatant removed, and the pellets frozen at -20°C to await gDNA isolation as described in the Langride et al. (2009) library preparation technique. The second change made was the addition of a BglII restriction endonuclease digestion of DNA fragments following Illumina® adapter ligation. This digestion step removes pRL27 (donor plasmid) fragments from the pool by cutting plasmid DNA immediately downstream of the transposon end, thereby physically separating the transposon from the opposite adapter needed to amplify the fragment (Figure 6B). This enzyme cuts DvH genomic DNA as well, but effects only 134 sites in the entire genome. This effect is localized to a very small area surrounding each site and was computationally corrected for. This was accomplished by calculating an average drop in read coverage across all BglII recognition sites and adding back a proportionate number of reads to all genes containing such sites.

Further refinements to the TraDIS technique (*77*) were added to ensure a strong selection for sequences containing transposon junctions and to adapt the technique for use on the newer Illumina® HiSeq® 2000 sequencer compared to the Illumina® GA®-series instruments used in previous studies. The first innovation was the use of two gel purification steps (Figure 7A & 7B). The gel slice taken before PCR enrichment isolated fragments in the 500-1,000 base pair range and ensured that no free adapters were

included in the PCR reaction, as in other Illumina® library preparation protocols. After PCR, a second gel excision was added to isolate DNA in the 300-500 base pair range to ensure that only those fragments being shortened in PCR were sent for sequencing (Figure 7B). Amplification of full-length fragments occurred but did not produce DNA that will amplify on the flowcell to provide useful data, whereas amplification of shortened fragments provided the transposon junctions that will bind the sequencing

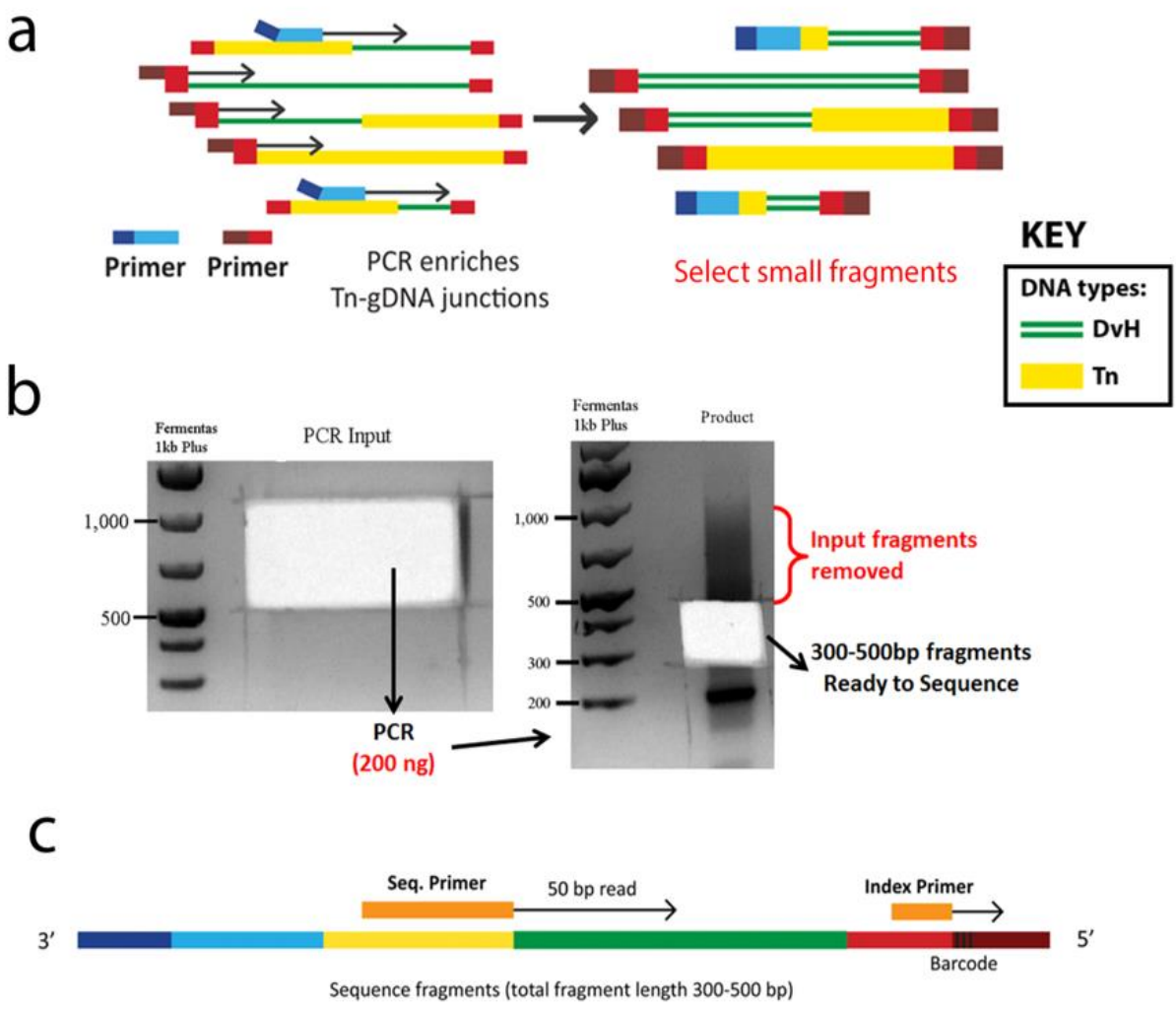


Figure 7. Illumina® Library Preparation (part 2). Changes from TraDIS method (Langridge 2009) denoted by red text **a & b)** 22 cycles of PCR amplifies all fragments and adds flowcell-specific end sequences. Gel purification of small fragments isolate only fragments containing transposon-gDNA junction sites. **c)** Single-stranded view of primer binding to a final fragment on the sequencing flowcell

primer. The second gel purification at lower size ranges ensured that only the second population of fragments were submitted. The second improvement was the use of 200 ng DNA as a PCR input. Langridge et al. compared 25, 65, and 100 ng DNA inputs and found that 100 ng gave them the highest number of unique insertions (and therefore the greatest genome coverage). They did not compare a larger input, however, which likely further increases genome coverage and helps to reduce over-amplification of sequences from fast-growing transposon mutants. This modification also ensured that enough DNA product was obtained for the additional gel purification step. The final modification made to the TraDIS protocol was to change the annealing position of the sequencing primer during sequencing (Figure 7C). Previous experiments had designed sequencing primers to sit 10 base pairs away from the end of the transposon, thereby sequencing the last 10 bases of the inserted sequence before reading into genomic DNA sequence that would provide the transposon location in the genome. This was meant to provide more confidence in the exact transposon position and ensure that no mis-priming took place while sequencing. The problem was that having an identical first 10 bases of every read is incompatible with the internal data processing of the new model of Illumina® sequencer, the HiSeq® 2000 (*71*). Eliminating this redundant transposon data was of little consequence to the overall accuracy of sequencing, given the stringency of primer binding in Illumina® systems at 65°C and would require an exceedingly rare DNA sequence present randomly in gDNA to cause mis-priming. The benefit of this change is the use of a platform that supports an approximately 10-fold higher number of reads per sample than the older Illumina® GA_{II}® system.

In addition to modifying the TraDIS technique as described here, attempts were made to develop an entirely new technique of enriching total gDNA for transposon junctions. This method would have relied on annealing a biotinylated DNA fragment to a sequence near the end of the transposon and pulling junction-containing fragments down with streptavidin-coated magnetic beads. Ultimately this method was unsuccessful, likely due to the extremely low ratio of transposon sequences to all other DNA sequences in a given gDNA sample. Problems with bead:supernatant ratios, incubation times and temperatures, or buffer conditions could also contribute to the failure of a bead-pulldown method for transposon enrichment.

3.4 Materials and methods

3.4.1 Mutant enrichment and collection of final bacterial pool.

This section describes a new method of mutant enrichment not found in other Tn-seq techniques

The 15 ml post-conjugation culture was diluted 1:33 to a final volume of 500 ml MOYLS4 with 400 µg G418 per ml, without DAP and with 0.38 mM titanium citrate added to lower the redox potential of the medium. This culture was grown at 34°C to an optical density at 600 nm (OD_{600}) of 0.40 to allow DvH exconjugants resistant to G418 an opportunity to outcompete wild-type DvH. Such growth was typically completed in about 24 h under these standard conditions, and cultures were still in the exponential-growth phase at that time. This culture was divided into 50 ml plastic conical tubes, the tubes removed from the anaerobic chamber, and cells harvested by centrifugation at 3,696 x *g* at 4°C for 12 min. Cells were resuspended and washed twice with 25 ml

anaerobic MOYLS4 medium. The final cell pellets were combined and resuspended in 1.5 ml of MOYLS4 medium. Ambion Turbo DNase (Life Technologies) (15 µl) and the enzyme buffer (170 µl) were added, and the mixture was incubated at 37°C for 30 min to digest extracellular DNA. After addition of 15 µl fresh Turbo DNase, the exconjugant cells were incubated a further 30 min. Cells were again collected by centrifugation, and the supernatant was discarded. The pellet was resuspended in 500 µl MOYLS4 medium, incubated at 75°C for 10 min to inactivate DNase, and then frozen in aliquots at 20°C for later genomic DNA (gDNA) extraction. All steps from conjugation through pellet freezing were accomplished in 5 days, with the exception of the time needed to quantify the DvH CFUs (Appendix A). CFUs of donor *E. coli*, wild-type DvH, and DvH resistant to G418 were recorded by serial dilution and plating immediately before harvesting the cells (Table 3). This served as the third time point for CFU analysis, in addition to those outlined in Chapter 2.

The procedure described above was expanded to produce multiple mutant pools in parallel by increasing the number of conjugation membranes and enrichment cultures. In order to eliminate the effect of possible variation in conjugation efficiency among membranes, it was important to combine all exconjugants into a proportionately larger culture before taking aliquots for individual pools. Each of these pools of mutants can be diluted into a different experimental medium as described above. The remainder of the protocol proceeded with DNA manipulation of individual pools in parallel, and each ultimately provided a separate fitness profile for the genome. Multiple pools were analyzed on the same Illumina lane though use of separate, barcoded Adapter 2.0

sequences (Appendix B) with an index sequencing cycle to identify these barcodes (Figure 7).

3.4.2 DNA isolation, fragmentation, and size selection.

This procedure was adapted from the TraDIS method described in Langridge et al., with my modifications to that method denoted in Figures 6 & 7

The final enriched cell pellet from a 500 ml DvH transposon mutant pool was frozen, ready for immediate DNA extraction, library construction, and sequencing. This pellet was thawed at room temperature and gDNA purified with the Gram Negative Bacteria protocol of a Wizard genomic DNA purification kit (Promega Corporation, Madison, WI). Cells were not spun before step 1 of the Wizard protocol; instead, 6 ml of nucleus lysis solution was added directly to the thawed pellet and mixed by pipetting. DNA was recovered according to the Promega Wizard protocol and then rehydrated in 1 ml elution buffer and left at room temperature overnight. DNA concentration was quantified by a NanoDrop (Thermo Fisher Scientific, Waltham, MA) assay. The DNA was diluted to 600 ng/µl, divided into 200 µl aliquots, and fragmented to 500 to 1,000 bp on a Bioruptor standard UCD- 200 sonication device (Diagenode, Inc., Denville, NJ). Multiple trials were performed with on-off interval shearing to establish sonication parameters, which varied with changes in DNA concentration and volume. A final DNA pool containing 500- to 1,000-bp fragments was verified by electrophoresis on an agarose gel. After verification, ~240 µg of fragmented DNA was subjected to electrophoresis on a 2% (wt/vol) agarose gel and the 500- to 1,000-bp band carefully excised. Clean equipment and buffers were used to avoid DNase contamination, and

bacterial gDNA to be sequenced was not exposed to UV light during gel excision. The DNA was extracted and purified from the gel slice by using a Wizard SV clean-up system (Promega; centrifugation protocol). The resulting products were purified by application of the standard protocol in a MinElute PCR purification kit (Qiagen, Valencia, CA) to concentrate fragments and eliminate residual ethanol. Purified DNA fragments were diluted such that 5 µg DNA was dissolved in 85 µl MinElute EB buffer (Qiagen). Illumina Adapter 2.0 was created by incubating a mixture of the two Adapter 2.0 oligonucleotides (10 µM each; see Appendix B) at 70°C for 1 min followed by 39.5°C for 5 min. This double-stranded adapter was attached to the 500- to 1,000-bp fragments by the use of a NEBNext DNA Sample Prep kit as described for the End Repair, dA-Tailing, and Adapter Ligation modules. The fragment pool was digested with BglII for elimination of residual pRL27 which would yield uninformative sequences. Free adaptors and small DNA fragments were eliminated by gel purification. The gel slice containing fragments of 500 to 1,000 bp was excised, and this DNA was isolated. PCR amplification was carried out to enrich Tn-gDNA junctions among DNA fragments (Figure 6) and to add Adapter 1.0 (Appendix B) for cluster generation for Illumina sequencing. PCR parameters (Appendix B) were designed to amplify the fragment pool from transposon ends preferentially. Products were purified with a final gel electrophoresis and excision procedure, retaining Tn-gDNA junctions in fragments in the 300- to 500-bp range. TOPO cloning by the standard procedure for the pCR4®Blunt-TOPO® blunt cloning vector (Thermo Fisher Scientific, Waltham, MA) was used to estimate the composition of the final pool before high-throughput sequencing. TOPO clones were sequenced at the MU

DNA Core on an Applied Biosystems 3730xl 96-capillary DNA Analyzer (Thermo Fisher Scientific, Waltham, MA). Completed libraries were sent to the Vincent J. Coates Genomics Sequencing Laboratory (Berkeley, CA), where they were quantified via the Qubit® High Sensitivity dsDNA protocol (Qubit Products, New York, NY) and sequenced with 7 pM initial loading concentration on one lane of an Illumina® HiSeq® 2000 instrument (San Diego, CA) with 50 base pair, single-end reads.

Table 3. CFU tracking, 1:10 vs 1:33 dilution

			Average CFU/ml[b] (N)			
Population	**Strain**	**Features[a]**	**Pre-conjugation**	**Post-conjugation**	**Final culture (1:10 dilution)**	**Final culture (1:33 dilution)[c]**
Recipients	DvH	WT, Km^S	$5.0x10^9$ (12)	$2.4x10^9$ (12)	$6.4x10^7$ (3)	$5.7x10^6$ (8)
Exconjugants	DvH::Tn*5*-RL27	Km^R	0	$6.8x10^5$ (12)	$2.7x10^6$ (3)	$9.1x10^6$ (8)
Donors	*E. coli* BW29427 (pRL27)[d]	DAP^-, Tra^+, Km^r	$4.3x10^8$ (12)	$4.4x10^7$ (9)	$9.1x10^6$ (2)	$1.5x10^6$ (7)
Average. Km^S CFU per Km^R CFU			--	$3.6x10^{-3}$	$2.3x10^1$	$6.0x10^{-1}$

[a] Dap^- mutants require diaminopimelic acid for growth. Tra^+, carries genes for plasmid mobilization by conjugation; Km^r or Km^s, resistance or sensitivity to kanamycin or G418. [b] Colony counts were quantified in triplicate by serial dilution and growth of organisms at 37°C on surfaces (*E. coli*) or by adding organisms to agar while the agar was molten and pouring the reaction mixture into plates so that CFU formed within the agar (DvH). Plates were supplemented with 400 µg G418/ml, 50 µg kanamycin/ml, and/or 90 µM DAP where necessary. [c] These cultures were first diluted from postconjugation cultures at the ratio indicated, and the enrichment-growth-phase analysis was performed with G418 and without DAP (to select for exconjugants and against donors, respectively). [d] *E. coli* strain with donor plasmid; genotype, *thrB1004 pro thi rpsL hsdS lacZ*_M15 *RP4-1360*_(*araBAD*)*567* _*dapA1341*::[*erm pir* (wt)].

3.5 Results

To solve the problem of low ratios of DvH exconjugants to wild-type DvH, as well to inhibit the persistence of donor *E. coli*, a larger volume of medium was used to dilute the 15 ml recovery culture. Whereas, the initial dilution was to a final volume of 150 ml (10-fold dilution ratio), the increase was to a 500 ml final volume (approximately 33-fold dilution). This served to greatly improve the final transposon mutant to wild-type DvH ratio, from 1:23 to 1.7:1. It also increased the number of times DvH transposon mutants were allowed to double, as that mutant population made up 56% of all cells in the 33-

fold dilution compared to only 4% for the 10-fold dilution (Table 3). This also meant an increase in the number of doublings for DvH cells. Too great an increase in the number of generations could cause some slow growers to be lost from the assay completely, but there was an average of 8 doublings from recovery culture to collection of DNA at the end of the hybrid enrichment/competition phase. This means that a transposon mutant with an average growth rate would expand from a single cell to 256 daughter cells in this time. A mutant with a growth rate of twice the average for the pool would undergo 16 doublings in the same time, resulting in 6.5×10^4 daughter cells. Such "super grower" mutants would have the potential to overtake the culture and decrease the chance of slower growing mutants having their transposon junctions sequenced for mapping. However it was expected that a loss-of-function transposon mutant conferring such a strong growth advantage would be very rare. Vastly more mutants would be expected to have growth rates near the population average, thereby mitigating the possible dominance of the "super growers". A very slow-growing mutant with a growth rate of one-eighth the genome average would double once under this setup, leading to only two daughter cells and a 128-fold lower representation than the average.

The modified Illumina® library preparation scheme was validated by TOPO cloning fragments from the final DNA pool into a plasmid vector and sequencing individual fragment regions by Sanger sequencing. This served as a low-cost way to assess the composition of the library, and to ensure that quality data would be generated when a similar fragment library was fully sequenced on an Illumina® HiSeq® 2000. Initial rounds of sequencing were performed while still refining the protocol.

Specifically, I had not yet started washing the pellets of the final bacteria pool and the BglII digestion step had not been added. At this point, 40 fragment clones were successfully sequenced. If run on a HiSeq® instrument these would have resulted in five of the desired transposon locations in DvH, six donor plasmid (pRL27) sequences, and two transposon locations in *E. coli*. The remaining 27 fragments contained only one type of binding adapter with random DvH genomic DNA, and would not have amplified on the flowcell. A second round of 11 clones were prepared for sequencing after refining the pellet washing steps, adding BglII digestion to remove pRL27 sequences (Figure 6), and adding a second gel purification step (Figure 7). Of these clones, four fragments successfully mapped insertions to DvH, five to *E. coli*, one returned plasmid sequence, and one would not have amplified on a flowcell.

The goal of this library preparation was to obtain ~$3x10^7$ reads per flowcell, thereby allowing high-resolution mapping of individual transposition events and transposon abundances in DvH. Even with a very high saturation level of $1x10^6$ unique mutants per pool, this number of reads would allow 30x average coverage of transposon insertion points. Such coverage would be sufficient for calculating relative fitness values for genes and ultimately fitting each gene to the essential or non-essential model (i.e. required for growth or dispensable under the current experimental conditions). If ratios of fragment types were expanded from either round of sequencing of TOPO clones to extrapolate possible data for a future high-throughput (Illumina® HiSeq®) run, the objective would likely have been met. With 5/13 and 4/11 sequenced fragments (38% and 36%, respectively) providing useful data, and even with a

conservative estimate of $1x10^8$ reads per flowcell, this leaves approximately $3.6\text{-}3.8x10^7$ reads providing transposon insertion locations in DvH. Although overall DvH mapping rate among Illumina®-compatible fragments changed little between the first and second round of validation sequencing, both pRL27 sequences and non-binding fragments were greatly reduced in the second round. These results were likely due to the addition of BglII digestion and a final small-fragment gel purification step, respectively.

Chapter 4 – Creation of an informatics pipeline and statistical analysis of TnLE-seq data

4.1 Introduction

Sequencing to determine transposon-gDNA junction locations within the final TnLE-seq fragment library returned a list of $1x10^7$-$1x10^8$ raw sequence reads. These were stored in the FASTQ file format (*25*), which also contains read quality data. The challenge was to process these raw data in such a way that they can both be visualized when mapped onto the reference genome and be converted to gene fitness values for all genes individually. This process generally involves removing low-quality reads, mapping read sequences to the reference genome, and finally obtaining a list of all unique insertion sites with the corresponding abundance of reads found at each site. From here, this list can be processed to visualize the insertion sites in various graphical programs and used to determine relative fitness values in all non-essential genes in the genome. When the TnLE-seq protocol was first refined in 2010-2011, various bioinformatic pipelines were available for this type of Tn-seq data processing. None of these data analysis packages met the specific requirements of the TnLE-seq library format, however. Many of these existing tools were based on outdated types of alignment software or output processed data only to expensive proprietary viewing software. The final pipeline needed to be fast, to rely only on free software that could be passed easily to other groups, and to meet the output parameters of software in use by collaborators for related DvH datasets. The computational pipeline was designed by

$$\text{Fitness} = \left(\frac{\#\text{ insertions in gene}^{a}}{\text{length of gene}}\right) \Big/ \left(\frac{\#\text{ insertions in all genes}}{\text{length of all genes}}\right)$$

Figure 8. Formula to obtain the gene fitness value for any gene [a] In all cases, "gene" here refers to a trimmed region of the coding sequence lacking the first 5% and last 15% of nucleotides

piecing together different open-source tools and writing custom Perl scripts as necessary. A custom Perl script, based on a similar script used previously, was written by Grant Zane to assign gene fitness values to all annotated genes simultaneously.

In order to simplify comparisons between studies in different bacteria, statistical analyses for determination of essential genes and comparisons of gene fitness values were modeled closely on established protocols. The use of a similar Tn5 transposon and a similarly high unique insertion rate of the Langridge et al. (2009) study made it ideal for comparison to the study described here. Essential gene determination by modeling two gamma distributions (an essential and non-essential model) was based on this study, as was the use of $\log_2$-corrected fold-change ratios to determine significant changes in the fitness of a gene (Figure 8) between conditions. A major departure from the Langridge et al. approach resulted from the liquid enrichment method. The time from mutant generation to the end of the enrichment phase was very short in the method developed here. The short interval conferred many advantages in terms of capturing a wide range of fitness values, eliminated problems with super-growers dominating enrichment, enhanced reproducibility in varying background strains, and additional benefits already outlined here. This short preparation time also meant a

“before and after” fitness comparison was not possible, because of the low cell counts available immediately following transposon introduction. Therefore, a “pool vs pool” comparison was employed. A parental strain grown in a standard medium serves to generate a baseline set of gene fitness values for comparison with mutant pools grown on different media. Wild type or parental mutant pools also served to provide comparison data for mutant pools constructed in genetically altered hosts. Any inconvenience in the deviation from standard methods was found to be overcome by the benefits listed, especially in difficult to manipulate microbes or anaerobic strains which are incompatible with previous techniques.

4.2 Development of a computational pipeline to assign gene fitness values from raw reads

For the purposes of Tn-seq, gene fitness can be described as the total number of insertions mapped to the gene divided by the length of the gene. This is normalized to the genome average and correlates to the degree to which that gene was dispensable for growth under the given condition. Thus the increase in fitness value is inversely proportional to the degree to which that gene is required, and fitness value is defined by the formula in Figure 8. All original Tn-seq approaches applied in other studies adhere to this basic organization (*43-45, 77, 125*). These approaches differ in the gene regions used for obtaining read counts. Reads in the entire coding sequence were used by Langridge et al. and van Opijnen and coworkers; whereas, others counted only those reads mapping to a central portion of the gene (*43-45*). The latter approach eliminates consideration of transposon mutants that may interrupt only the most proximal or distal

end of a gene and therefore not fully abrogate function of gene products. Therefore the overall negative correlation between insertions in the gene and contribution of the gene to growth fitness is refined by ignoring potential low-impact mutations occurring at the ends of even very important genes. There is disagreement among researchers as to the necessity of this modification when interpreting different datasets. One study shows an effect in only 4 genes upon removal of the distal 10% of reads (*125*), while another shows a "significant change" across the genome when removing the same portion (*45*). In any case, using only the middle 5-85% region does not appear to hamper the analysis and is likely beneficial for accurate calling of fitness in genes with very low numbers of reads overall.

The first step in the computational pipeline between raw sequence reads and fitness values (Appendix C) was the elimination of low-quality reads as determined by the CASAVA tool (Illumina®, San Diego CA). This quality scoring was performed based on a proprietary calculation within the sequencing system itself. It was therefore not open to modification, but a complete set of reads were provided and subsequently filtered by elimination of reads through removal of those with a "Y" (filtered) designation in a FASTQ line. Each step in the sequence processing pipeline is described in detail in section 4.6 and in Appendix C.

Alignment of reads to the reference genome comes next. This is a critical step in the process, with the speed, accuracy, features, and output format of various packages of alignment software playing a prominent part in the overall pipeline. Generally the three aligners used for Tn-seq experiments are MAQ (*81*), SOAP (Short Oligonucleotide

Alignment Program) (*83*), and Bowtie (*76*). Each of the four Tn-seq studies published prior to this work chose a different aligner, with Langridge et al. using MAQ (*77*), Gawronski et al. using SOAP (*44*), and van Opijnen et al. using Bowtie (*125*). Goodman et al. used a program of their own design, called MapSAM (*45*). Bowtie was chosen here primarily for its ability to align large datasets in a matter of minutes compared to days for MAQ and SOAP and for its comparable performance to these in terms of accuracy (*76*). SOAP often cannot be run on a desktop computer due to large memory requirements, whereas Bowtie and MAQ will run on any machine with at least two gigabytes of random access memory (RAM). Bowtie also has more complete documentation of its parameters than many other open-source programs. The decision to choose Bowtie was ultimately reinforced by the majority of later Tn-seq papers describing Bowtie as the aligner of choice (*11, 43, 46, 98*). Bowtie 2 was released (*75*) prior to the second round of sequencing described here, when the pipeline was updated with the new version. All data presented in this thesis are a result of alignment with Bowtie 2.

With non-mapping reads eliminated and successfully mapped reads assigned to a precise genome location, several processing steps were needed to arrive at the list of genome positions with read abundances that would be used to calculate gene fitness. Reads aligning in multiple locations were eliminated from the pool, the file format was altered to fit downstream tools, and reads were reduced from 50 base pair sequences to a single nucleotide representing the nucleotide in the genome immediately following the transposon insertion found in the original mutant (Appendix C). These were then

sorted in ascending order based on genome position. This is a very RAM-intensive step, requiring approximately 30 gigabytes of RAM for a full lane of HiSeq® data (proportionally less for multiplexed samples), and it may have to be carried out on a compute cluster such as the Lewis compute cluster operated by the University of Missouri Bioinformatics Consortium (http://umbc.rnet.missouri.edu/). All other steps in the process may be accomplished on an ordinary desktop computer, though processing times will be somewhat longer than when using a specialized compute cluster. The next step utilized the Vancouver Short Read Analysis Package (*39*) to collapse all reads at each insertion site to a single line with one read-count value, thereby greatly reducing the file size.

These data were then ready to be read into a specialized Perl script, written by Grant Zane, which calculates gene fitness values for all genes. It does this by also accessing a file containing the latest gene annotation data in Genbank format from MicrobesOnline (www.microbesonline.org) (*31*) and binning each insertion site into the gene in which it occurs. Read counts are added up across each gene, discarding those in the first 5% and last 15% of the coding sequence, and gene fitness values are calculated from these data by using the formula found in Figure 8. The text file output from this step contains a list of genes, gene names, and descriptions, as well as gene length values, total reads per gene and final fitness values for all genes. This file can easily be copied into a spreadsheet program for further manipulation.

4.3 Visualization of insertion points and corresponding read counts across a bacterial genome

Although most data analyses were carried out using the spreadsheet output method described in the previous section, it is also useful to have a graphical output that can be viewed alongside a wide range of other data. Some previous studies do not mention visualization of reads across the genome, and those that do (*11, 69, 125*) generally employ a proprietary program suite such as CLC Workbench (Qiagen, Venlo, Netherlands). For TnLE-seq, the genome visualization software of choice was Artemis Genome Browser (*13, 113*) because it is regularly used by SRB researchers in particular to visualize microarray, RNA-seq, transcription terminator and other datasets across the annotated DvH genome (*110*). These datasets can be viewed simultaneously and therefore it would be ideal to add TnLE-seq data alongside other data for close analysis of genes and operons. Artemis is also a free and open source program, where CLC Workbench and other commercial platforms generally charge substantial yearly fees for software licenses.

The input format for visualization in Artemis is difficult to generate, however, requiring the addition of two steps to convert the file type mentioned above to Artemis (.ART) format (*13*). I wrote two custom Perl files for this conversion, which took both insertion location and insertion abundance values from the complex spreadsheet-ready file listed above. These data were finally arranged such that the final file contained one line for every base of the DvH genome, with an insertion number for each base. This

leaves most lines with a value of zero, but numbers ranging from very few to many thousands on those locations where insertions mapped.

4.4 Statistical analysis to determine essential genes

One primary objective of TnLE-seq is to reproducibly call genes as “essential” (compared to “non-essential”) within a single growth competition experiment. The statistical model used for this purpose in the Langridge et al. (2009) study was replicated for this dataset. First a histogram of all fitness values is created by binning all genes into interval groups according to their fitness values. When a bar graph is created from these data, gene fitness value is shown on the x-axis, with the number of genes per fitness interval represented on the y-axis. This graph naturally displays a bimodal distribution, with non-essential genes distributed around a fitness value of one (interpreted to mean

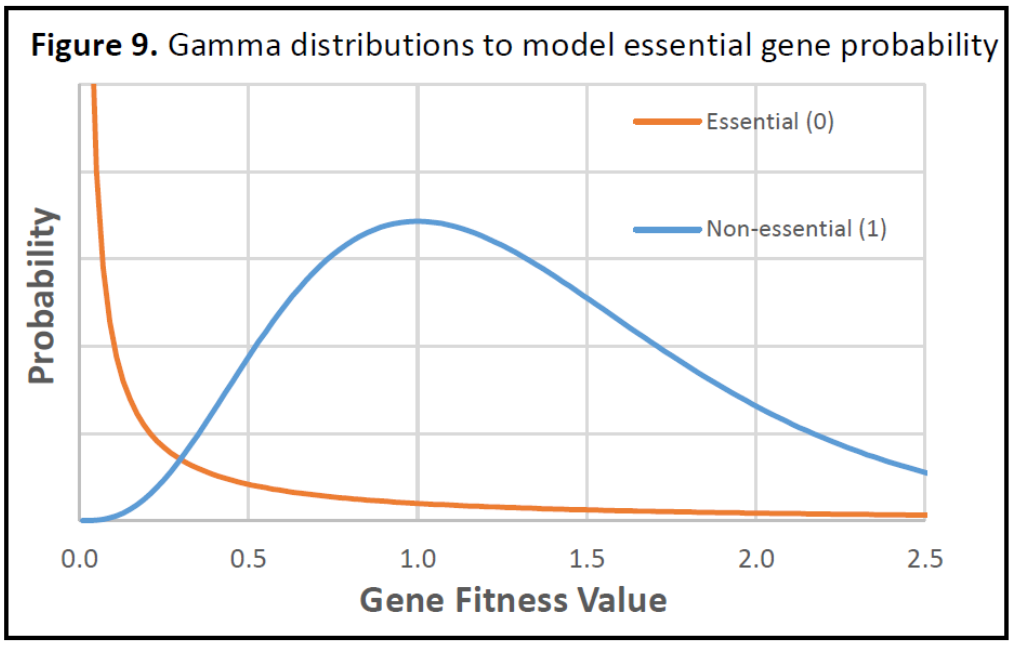
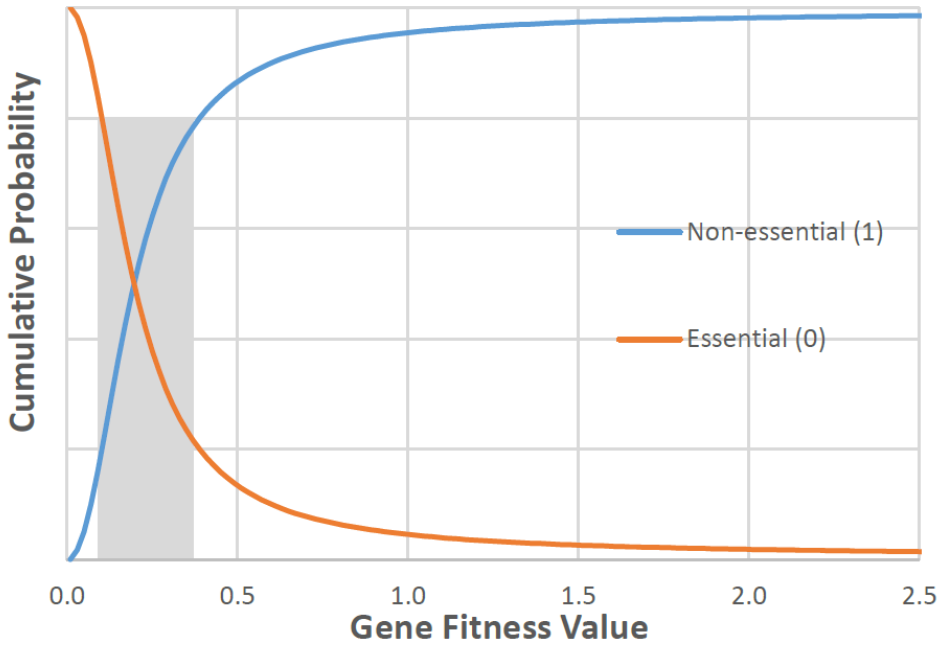


Figure 9. Gamma distributions to model essential gene probability

Figure 10. Cumulative probability to call essential vs non-essential



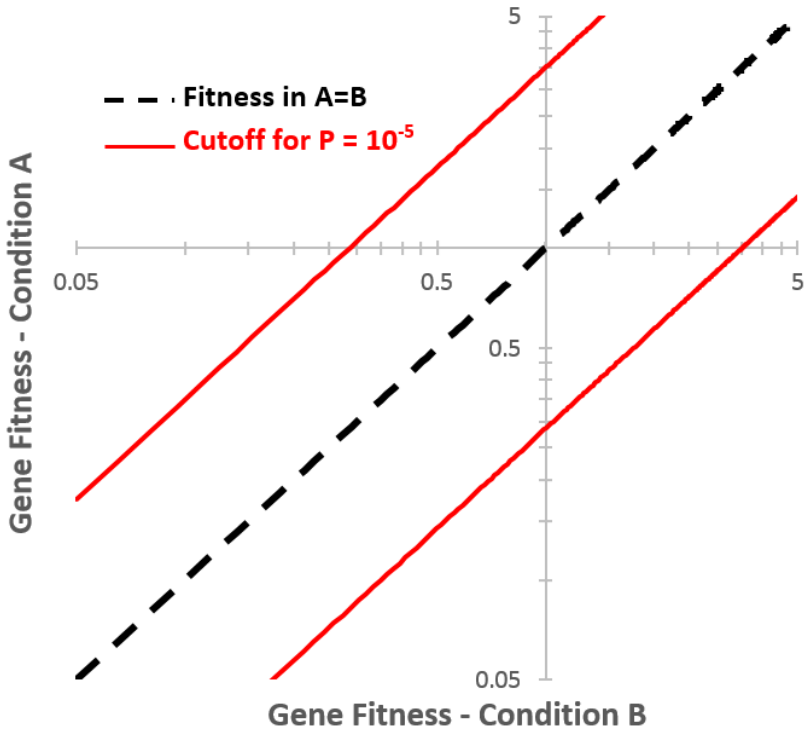
The shaded area represents the area of uncertainty for calling essential genes based on fitness. Genes to the left of this are essential, genes to the right are non-essential

no benefit or detriment occurred with inactivation of the gene) and essential genes approaching a fitness of zero. When a gamma function is estimated for each of these modes (Figure 9) by using a statistical fitting tool such as EasyFit (MathWave Technologies), it is possible to calculate cumulative probability of a gene belonging to either category (Figure 10). The requirement used by Langridge et al. to determine essential or non-essential genes was that a gene must be four times as likely to belong to one category as the other. The relatively small number of genes not meeting this requirement are not fit to either category.

4.5 Statistical analysis of changes in gene fitness between experiments

Another important statistical determination is the comparison of a set of gene fitness results from an experimental growth condition to those established in a prior "baseline" experiment. These experimental changes could include variation of media composition, application of a stress condition, and/or use of a host strain with a different genotype. To begin the comparison, 100 reads were added to each gene to smooth for underrepresented genes (*77*). Genes considered essential in the baseline condition were removed, because comparisons of very low fitness scores could easily return false positive results; however, it is important to compare essential gene lists created

Figure 11. Two-condition comparison of all gene fitness values



Fitness values of genes falling between the red lines are not significantly different between conditions. Genes falling outside the red lines are considered significantly different.

separately from the two assays to ensure genes have not lost essentiality in the experimental assay.

To accomplish this gene-by-gene analysis, Log_2 likelihood ratios of smoothed fitness values between pools were calculated for each remaining gene. These Log_2 ratios were fitted to a normal distribution. Genes exhibiting log_2 likelihood ratios with P-values below $1x10^{-5}$ were considered to have significantly altered fitness values as shown by comparisons between the pools. These data can be conveniently represented graphically (Figure 11) and R^2 value calculated to describe the correlation between total fitness values in the pools.

4.6 Materials & Methods

4.6.1 Sequencing and development of a computational pipeline for raw read processing

Sequencing was carried out under the supervision of Minyong Chung at the Vincent J. Coates Genomics Sequencing Laboratory (Berkeley, CA) in two batches of one flowcell each on the Illumina® HiSeq platform. The first batch consisted of a non-multiplexed pool from an assay performed with wild-type DvH in MOYLS4 (rich) medium. This DNA fragment library was loaded onto the sequencer at a final concentration of 12 pM and served as a proof-of-concept and to optimize subsequent experiments. The second batch was submitted approximately a year later and was a multiplexed sample, containing a mixture of five libraries from five different TnLE-seq

pools (Tables 4 & 5). This mixture was loaded at a total concentration of 7 pM, due to excessive cluster generation during the previous assay.

A detailed description of computational tools can be found in Appendix C. The

Table 4. Read quality summary

Index	Mutant	Growth Medium	Total Reads	Quality Reads	% passing filter	% of lane used
none	WT DvH	MOYLS4	2.4E+08	1.3E+08	53.7%	100%
Mulitplexed lane - 5 libraries			2.2E+08	1.8E+08	82.2%	100%
A (2)	WT DvH	MOYLS4	4.6E+07	3.8E+07	82.2%	21.4%
B (4)	WT DvH	MOLS4	5.1E+07	4.2E+07	83.0%	23.5%
C (5)	WT DvH	MOLS4 + 0.1 M NO_3	4.4E+07	3.6E+07	82.5%	20.3%
D (6)	JW710 (Δ*upp*)	MOLS4	2.9E+07	2.4E+07	82.3%	13.7%
E (12)	JW3319 (Δ*upp*, Δ*rex*)	MOLS4	4.5E+07	3.7E+07	81.1%	21.1%

Table 5. Alignment/coverage summary

Mutant	Growth Medium	DvH reads aligned	% of Library	Unique insertions	bp per insertions	Avg. insert height	5% cutoff[a]	1% cutoff[a]
WT DvH	MOYLS4	4.8E+07	37.2%	2.7E+05	13.7	175	41	63
Mulitplexed lane - 5 libraries		1.3E+08	71.5%					
WT DvH	MOYLS4	3.1E+07	80.6%	3.4E+05	11.0	89	33	51
WT DvH	MOLS4	1.4E+07	33.8%	1.9E+05	19.8	75	59	91
WT DvH	MOLS4 + 0.1 M NO_3	3.2E+07	87.8%	1.1E+05	34.8	292	104	160
JW710 (Δ*upp*)	MOLS4	2.0E+07	81.5%	5.2E+05	7.3	38	22	34
JW3319 (Δ*upp*, Δ*rex*)	MOLS4	3.0E+07	82.5%	5.4E+05	7.0	56	21	32

[a] P-value for X bases without an insertion site

first part of this pipeline takes raw sequence reads (and associated quality scores) in FASTQ format as the input and outputs a table of exact genome locations and the number of reads associated with each location. The second part of the pipeline converts these data to Artemis (.ART) format for visualization of mapped insertion abundance across the reference genome.

4.6.2 Fitness calculation for all genes

Fitness calculation was performed with the script TnSeqFitness.pl, written by Grant Zane. This script inputs a Genbank annotation file (www.microbesonline.org) containing gene names and locations along with a .PEAK file (Appendix C) containing insertion sites and read counts to calculate gene fitness values. Fitness values were calculated by dividing the total number of transposon insertions in the gene by the length (in base pairs) of the 5% to 85% region of the gene. This value was normalized to the genome average by dividing it by the average number of insertions per base pair in the 5% to 85% regions of all nonessential genes in the genome (Figure 12). This list can be copied to any spreadsheet for further manipulation or posted on a website for other researchers to access.

Figure 12. Generation of gene fitness values from aligned reads

Usage: `perl TnseqFitness.pl <INPUT 1> <INPUT 2> <OUTPUT>`

Genbank gene annotation data (INPUT 1):

locusId	str	stop	sysName	Id	start	type	desc name
209721	-	699	DVUA0001	1945	872	1	hypothetical protein (TIGR)
209720	+	1689	DVUA0002	1945	871	1	ParA family protein (TIGR) s
209719	+	5135	DVUA0003	1945	1740	1	hypothetical protein (TIGR)
209718	+	5843	DVUA0004	1945	5490	1	DNA-binding protein HU, puta
408368	-	6498	DVUA0005	1945	7433	1	universal stress protein fam
209717	-	7456	DVUA0006	1945	8451	1	magnesium transporter MgtE,
209716	-	8901	DVUA0007	1945	10445	1	nitrogenase cofactor biosynt
209715	-	10458	DVUA0008	1945	11972	1	nitrogenase molybdenum-iron
408369	-	11959	DVUA0009	1945	13665	1	nitrogenase MoFe cofactor bi
209713	-	14308	DVUA0010	1945	14610	1	ferredoxin, 2fe-2s (TIGR)

Transposon peaks (INPUT 2):

Line	Genome	Location	Abundance
0	882	6	44.0
1	882	8	56.0
2	882	18	34.0
3	882	45	5.0
4	882	50	269.0
5	882	59	12.0
6	882	60	43.0
7	882	62	51.0
8	882	63	23.0

Fitness formula (within Perl script):

$$\text{Fitness} = \left(\frac{\#\text{ insertions in gene}}{\text{length of gene}}\right) \Big/ \left(\frac{\#\text{ insertions in all genes}}{\text{length of all genes}}\right)$$

Gene fitness values (OUTPUT):

gene	fitness	fit/ave	adj-fit	adj-fit/ave
DVU0001	5.35008	0.77810	5.84206	0.85110
DVU0002	0.06234	0.00907	0.02167	0.00316
DVU0003	0.04965	0.00722	0.00000	0.00000
DVU0004	0.45508	0.06619	0.00973	0.00142
DVU0005	9.65776	1.40460	10.42357	1.51857
DVU0006	10.24301	1.48972	11.22642	1.63553
DVU0007	9.37157	1.36298	10.46841	1.52510
DVU0008	3.22222	0.46863	3.44000	0.50116
DVU0009	8.61749	1.25331	8.44141	1.22979
DVU0010	8.41446	1.22378	7.62914	1.11146

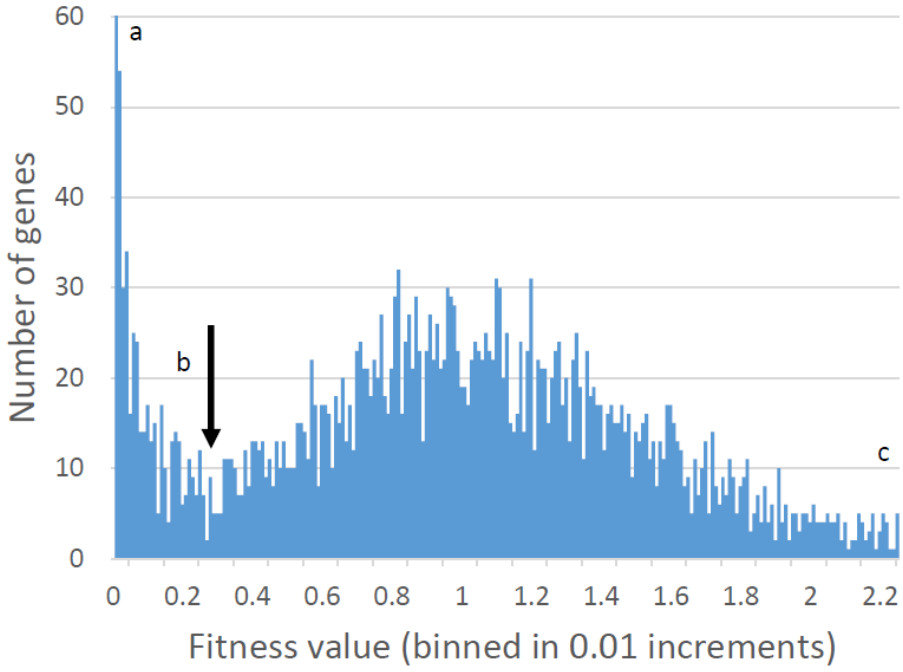
[a] Downloaded from www.microbesonline.org (3.4×10^3 genes total) [b] obtained from processing of reads (1×10^7-1×10^8 reads total, spread among 1×10^5-5×10^5 insertion points) [c] final fitness, normalized fitness, normalized adjusted (5-85% region) fitness, and adjusted fitness for all genes

4.6.3 Statistical determination of essential genes

This method was replicated from Langridge et al. (2009) (77), but different software was used

To call genes as "essential" or "non-essential" within a single experiment, first a detailed histogram was generated to group genes along a continuum of fitness values. Bin sizes for histogram data were kept at or below 0.02 on the scale of fitness values for precision. Next, a cutoff point was selected as the point nearest to the bin with the lowest number of genes, while still between the peaks at zero and one (Figure 13). All values below this point in the spreadsheet were then fitted to a gamma distribution

Figure 13. Sample histogram for fitting gamma distributions



[a] Bar for bin 0.00-0.01 extends beyond the figure [b] arrow denotes cutoff point for distribution fitting [c] Fitness values >2.25 not shown

within EasyFit version 5.5 (MathWave Technologies). This gave a formula for a gamma curve with a maximum approaching zero on the x-axis, which was used to calculate probabilities for all fitness values along the continuum. Similarly, values above this point were separately entered into the software to generate a gamma curve formula with a maximum near one.

These formulae represent curves similar to those shown in Figure 10, and were used in conjunction with the GAMMDIST function of Microsoft® Excel® 2010 to generate cumulative probabilities as shown in Figure 11. At any given point along the x-axis, the addition of the cumulative probability (y-axis) for one of these two models with the other equals one. Therefore, the requirement that a gene have a four-fold likelihood of fitting one model over the other was simplified to requiring a cumulative probability value of 0.8 (80%) or greater for one condition. This ultimately left a small range of genes with very low fitness values fitting confidently to the essential model. Next came another small range of genes that could not be fit to either model. Finally came a very large area along the x-axis where genes were called as non-essential.

4.6.4 Statistical determination of fitness value changes between experiments

This method was replicated from Langridge et al. (2009) (77), with the addition of a graphical format which includes p-value cutoff lines for interpretation

For every gene in the genome, smoothed fitness values were generated as described in section 4.5. Two conditions (control and experimental) were listed side by side for each comparison and a Log_2 likelihood ratio was generated for each pair of

fitness values with the formula *ratio = Log_2(experimental/control)*. Ratios above two (higher fitness in experimental pool) or below negative two (lower fitness in experimental pool) were considered significant with a p-value of $1x10^{-5}$ and a $2.5x10^{-4}$ false discovery rate according to the normal model (*77*). For better visualization of the data, each gene was plotted on a scatter plot with logarithmic axes and lines were added corresponding to p-value cutoffs (Figure 11).

4.7 Results

4.7.1 Data quality from Illumina® sequencing assays

Prior to evaluating the biological relevance of high throughput sequencing data, it is important to ensure the quality of sequence reads being produced. A key metric impacting Illumina® sequencing is the physical density at which DNA fragments from the library amplify to form clusters that can be read by cameras following the binding of each fluorescent nucleotide during the sequencing process. More clusters lead to more total reads; however, high cluster densities can interfere with read calling and lower the number of high-quality reads obtained (*68*). This problem is especially relevant when using an untested library preparation technique such as the one described here.

The first sequencing assay was meant as a proof-of-concept experiment to validate the novel TnLE-seq method. This consisted of a single (non-multiplexed) library derived from a wild-type DvH pool grown on standard rich medium, and was analyzed on a single Illumina® HiSeq® 2000 lane. The loading concentration of 12 pM proved to be higher than ideal, as $2.4x10^8$ clusters were generated but only $1.3x10^8$ were of high

enough quality to be analyzed (Table 4). This quality read rate of about 53% still provided ample reads to assay a single library. The second sequencing assay again utilized a single lane on an Illumina® HiSeq® instrument, but this time included five libraries from different experiments (Table 4). These five fragment pools generated a slightly lower number of total reads due to a loading concentration of only 7 pM, but this enabled better cluster separation and a larger number of quality reads. Total quality reads from this multiplexed assay were $1.8x10^8$ (82% quality rate) and these were spread reasonably well among the five libraries (Table 4).

Another consideration when sequencing is optimizing the proportion of high quality reads that map to the DvH genome (Figure 14). This topic is discussed in further detail in Chapter 3, as it relates to precautions for removing *E. coli* and pRL27 sequences

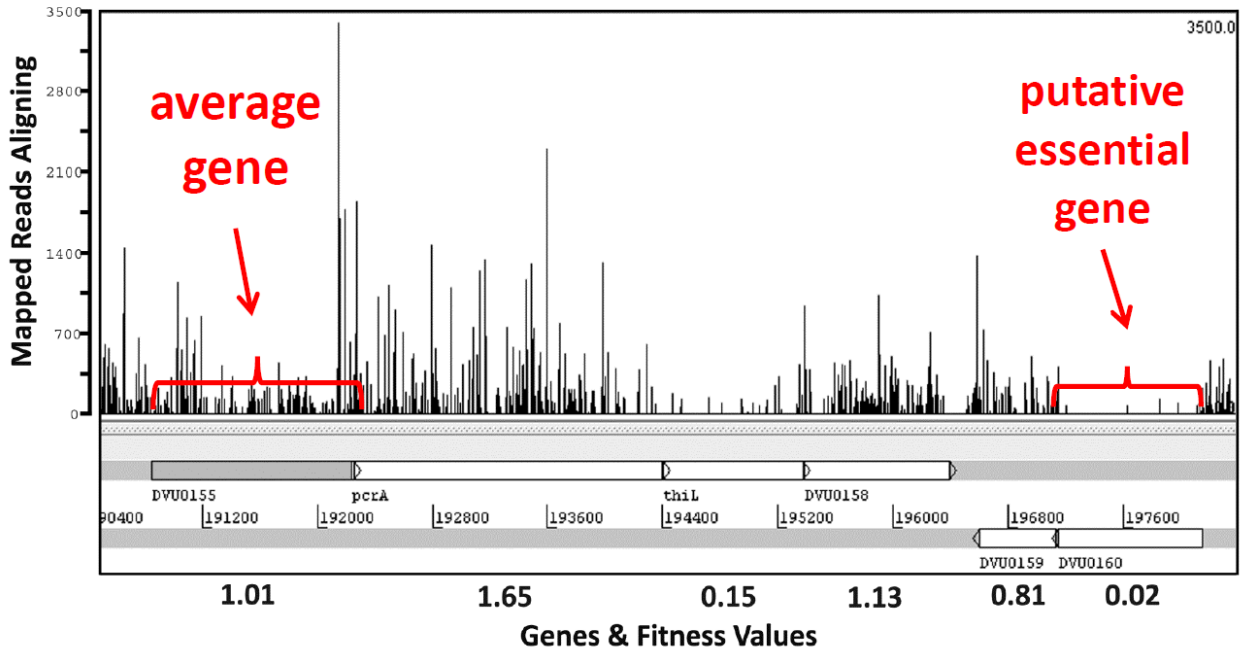


Figure 14. Example of read abundance mapping across the DvH genome (Artemis Genome Browser). Predicted genes are shown as gray or white boxes with arrows. Vertical black lines represent insertion points, with height corresponding to the number of reads mapped uniquely to that location by the Bowtie aligner. Numbers below the screenshot indicate relative fitness values calculated for the pictured genes.

during the enrichment and DNA library preparation phases. In the first sequencing run, only 37.2% of quality reads mapped to the reference DvH genome (Table 5). This was partly due to the occurrence of 25% *E. coli* reads and 6% pRL27 reads, but also to 33% un-aligned reads. The former two read groups can likely be attributed to evolving means of eliminating these non-DvH sequences (Chapter 3), while the unaligned reads may have simply resulted from sequencing errors caused by a flowcell somewhat overloaded with fragment clusters. All of these problems were significantly alleviated during the second sequencing run, wherein DvH reads made up 71.5% of all quality reads (Table 5) and E. coli, pRL27, and unaligned reads were reduced to 12%, 2%, and 15%, respectively.

4.7.2 Essential gene determination within each pool

Essential genes were determined for four growth competition experiments (Table 6). One of these was repeated a second time for confirmation, and a fifth was assayed but displayed an extremely atypical gene fitness distribution and was not included in this analysis (see section 4.7.6). The proportion of the genome found to be essential stayed remarkably constant across these conditions, with all pools exhibiting essential genes in the range of 16-20% of the genome. Interestingly, the defined

Table 6. Essential genes

Strain	Growth Medium	Genes (of 3402 total[a])		
		Essential	Not called	Non-essential
WT DvH (Nov. 2011)	MOYLS4	571	66	2758
WT DvH (Dec. 2012)	MOYLS4	590	52	2760
WT DvH	MOLS4	546	84	2772
JW710 (Δ*upp*)	MOLS4	675	35	2692
JW3319 (Δ*upp*, Δ*rex*)	MOLS4	680	44	2678

[a] Total gene number was reduced to 3,401 in JW710 and 3,400 in JW3319 by deletion

medium assay (WT-MO) showed the lowest proportion of essential genes with 546 of 3,402 called as essential. This is counterintuitive, as we would expect more genes to be essential for growth when yeast extract is absent. This assay did find significant fitness changes in genes related to amino acid synthesis, however, as would be expected when cultures lack amino acids provided by yeast extract in rich media (MOY) trials (see section 4.6.4). It is possible the relatively low percentage of DvH reads found in this sample skewed essential gene discovery, but $1.4x10^7$ DvH-aligning reads in this sample should be sufficient for fitness analysis. Also of interest is the increase in essential genes when moving to the Δ*upp* background strain in the latter experiments. It is possible the loss of the pyrimidine scavenging function normally provided by this gene has an effect on these approximately 80-130 genes. This difference is explored further below.

4.7.3 Comparison of replicate pools (WT-MOY vs WT-MOY)

These data were originally published in Fels et al. 2013, found as Appendix E

To provide a control for potential variability across TnLE-seq experiments, a replicate of the original assay (wild-type DvH grown in rich medium) was prepared. This replicate was grown approximately one year after the first pool, and was sequenced on one-fifth of a HiSeq® lane (Table 5). We also explored the possible loss of data from multiplexing samples when sequencing on the Illumina platform. A comparison was made between the original TnLE-seq pool from DvH cells grown in rich medium that was not sequenced on a multiplexed Illumina lane and the biological replicate of this condition that was multiplexed. The latter was sequenced with four additional samples

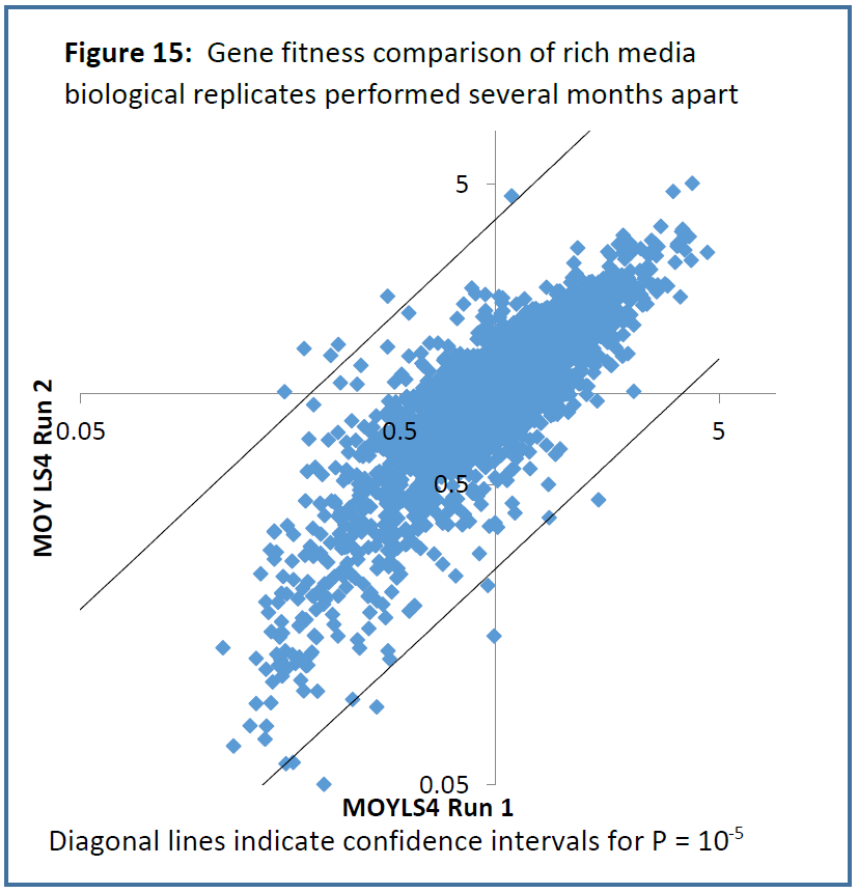


Figure 15: Gene fitness comparison of rich media biological replicates performed several months apart

Diagonal lines indicate confidence intervals for P = 10^{-5}

on one Illumina lane. Log_2 likelihood ratios of fitness values between the pools were calculated, essential genes were removed, and remaining fitness values were fitted to a normal distribution. The R^2 value of this comparison was 0.80. Genes exhibiting log_2 likelihood ratios with P-values below 10^{-5} were considered to have significantly altered fitness values as shown by comparisons between the pools (Figure 15). Significantly altered fitness was seen for only 13 genes in the comparison of biological replicate pools. Of these, one was a direct result of ambiguity involving the multiplex barcode (commonly referred to as barcode bleed (*68*) causing incorrect sequence binning for that gene, four were located within two nearly identical 30-kb phage insertion islands (*129*), and the remaining eight were small genes with an average length of 232 bp. In

the case of these small genes, small changes in transposon location or abundance may have affected the resulting fitness. Therefore, comparison of biological replicates revealed high reproducibility.

4.7.4 Gene fitness comparison of rich (with yeast extract) and minimal growth media

These data were originally published in Fels et al. 2013 (40), found as Appendix E

A comparison was also made for the rich medium pool and a defined medium pool sequenced on the same lane (Figure 16), which returned 25 genes with significant fitness differences. Of these, 24 are annotated to code for specific biosynthetic enzymes, as would be expected when switching to a minimal (yeast extract-free) growth medium. The remaining gene (DVU1039) is annotated as a putative lipoprotein. This low number of essential biosynthetic genes in the absence of yeast extract might have been influenced by crossfeeding of amino acids and other nutrients from lysed *E. coli* or WT DvH cells. No gene was found to exhibit significant fitness differences in both the control and rich- versus defined-medium analyses. These clear results displaying 96% of all significant gene fitness changes in well-understood amino acid synthesis genes provides an excellent proof-of-concept for further condition comparisons. They also lend support to the idea that our significance requirement is adequately stringent. Additional biosynthetic genes would be returned if this requirement were relaxed; however, this would come at the possible expense of false-positive identifications.

4.7.5 Gene fitness comparison of wild-type DvH and a Δ*upp* strain

Uracil phosphoribosyltransferase is encoded by the *upp* gene and plays a central role in the pyrimidine salvage pathway (*1*). This gene is very important to genetic work conducted in DvH because strains lacking it are resistant to the toxic nucleoside analog 5-fluorouracil (5-FU). In the markerless deletion strategy developed in our lab, the strain JW710 (Δ*upp*) is used as the parental strain to all further markerless deletion mutants (*62*). This is accomplished in JW710 by first cloning a cassette containing *upp* and a common antibiotic marker into the genome in place of the gene of interest by homologous recombination of upstream and downstream sequences. Successful mutants are then selected for by growth in the presence of the corresponding antibiotic.

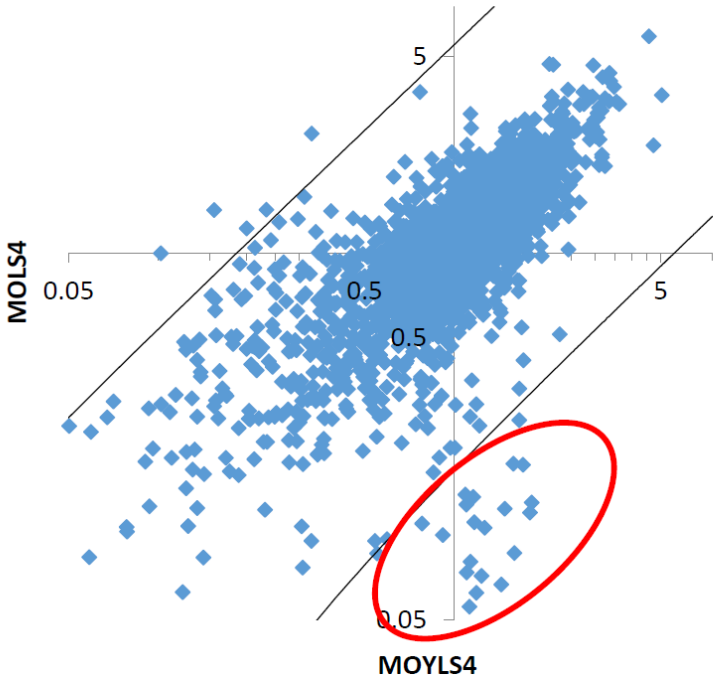


Figure 16: Gene fitness comparison of rich and minimal

Diagonal lines indicate confidence intervals for P = 10^{-5}. Red oval indicates amino acid biosynthetic genes which are essential in defined (MOLS4) but not rich (MOYLS4) medium.

A second homologous recombination step removes the cassette and these recombinants are selected for by growth with 5-fluorouracil. This final step selects for mutants that have lost the cassette, including the *upp* gene, because only mutants that have lost *upp* are deficient in 5-FU uptake and are therefore resistant to its toxic effects.

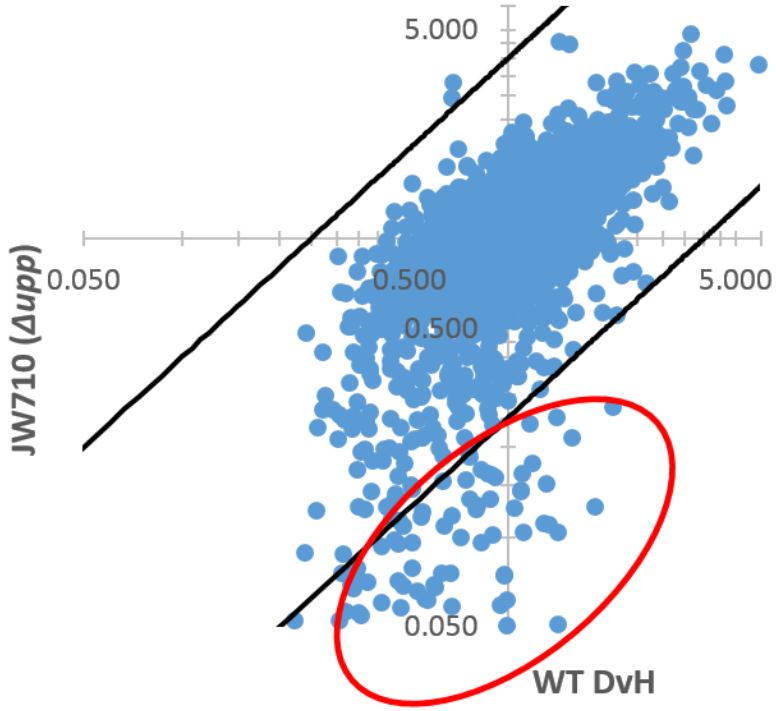
All new markerless deletion strains in DvH therefore have a Δ*upp* background, making TnLE-seq comparisons of these strains to JW710 more appropriate than to WT DvH. Comparison of WT DvH to JW710 (Δ*upp*), both gown in defined (MOLS4) medium, was conducted to assay any further gene fitness changes caused by the loss of the *upp* gene (Figure 17). Other members of the pyrimidine scavenging pathway, including *pyr*BCDEFK and *upp*S, were expected to be affected by this change; however, significant changes in 121 genes were found (Table 7). These include primarily genes that were non-essential in WT DvH but became essential in the JW710 background. Interestingly, these genes appear to be concentrated according to certain Clusters of Orthologous Groups (COG) functions (*122*). COG groups F, H, I, and M made up 45% of genes with significant fitness change from WT DvH to JW710, while these COG groups make up just 11% of total genes in the genome. Overall, this widespread impact of the loss of *upp* was

Table 7. Gene fitness changes between experiments

Comparison (Control vs. Exp)	Fitness compared to control (of 3402 genes[a]) lower	not changed	higher	R^2 value
Control (MOY vs. MOY)	7	3389	6	0.80
Yeast Extract (MOY vs. MO)	19	3378	5	0.71
upp deletion (WT vs. JW710)	119	3281	2	0.58
rex deletion (JW710 vs. JW3319)	1	3397	2	0.93

[a] Total gene number is reduced to 3,401 in JW710 and 3,400 in JW3319

Figure 17: Gene fitness comparison of WT DvH and JW710



Diagonal lines indicate confidence intervals for $p = 10^{-5}$. Red oval indicates genes which are essential in JW710 but not in WT DvH.

unexpected, but not entirely out of the question given the abundance of its protein and the importance of uracil retention in a defined medium.

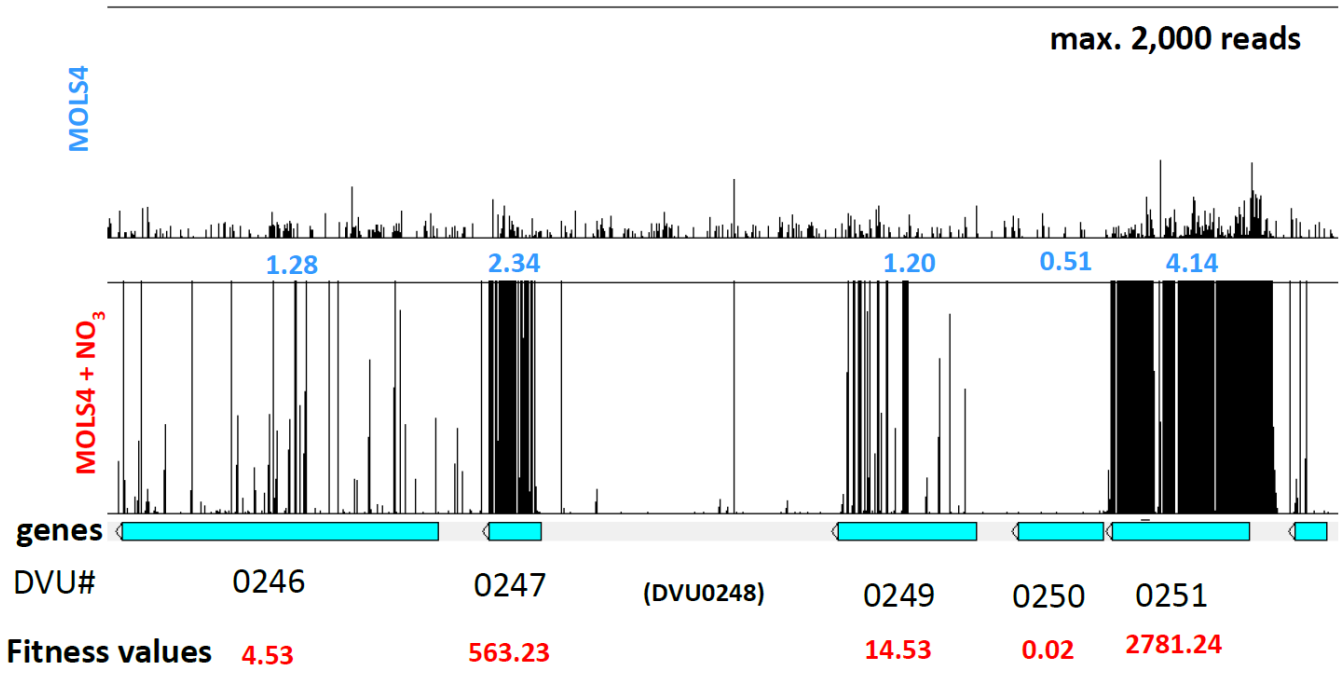
4.7.6 Gene fitness values in DvH JW710 grown in minimal medium with inhibitory nitrate

This topic is explored in detail in Korte et al. 2014 (70), which is attached as Appendix F

Another important fitness assay to aid other work being done in DvH was the analysis of a transposon mutant pool grown on high-nitrate medium. A key field site for the study of microbes in contaminated groundwater is located near an old uranium

enrichment site at Oak Ridge National Laboratory (Oak Ridge, TN). From a microbial community perspective, it would be interesting to determine the mechanisms allowing sulfate reducing bacteria (SRB) to grow in the presence of excess nitrate found there. Additionally, this strong growth stress has been used to prevent SRB growth in industrial applications such as in oil wells, but growth has been shown to resume after a lag time due to an unknown mechanism. A graduate student in the Wall lab, Hannah Korte, had performed growth curves, generated gene deletion mutants, and used other methods to determine the genetic basis for this long (~70 hours when grown from a 1/10 dilution) lag phase seen when WT DvH is grown on nitrate. She had routinely used 100 mM nitrate, which is consistent with contaminated groundwater samples, as an addition to normal MOLS4 defined medium used in the preceding comparisons.

Figure 18: Gene fitness comparison of JW710 with and without inhibitory nitrate



Black bars denote mapped transposon sites, with bar height corresponding to total reads per site. The scale of the y-axis is consistent between the two horizontal tracks. Gene fitness in the control MOLS4 is somewhat skewed in these genes, due to "barcode bleed" (Kircher 2012) from extremely over-represented reads in the nitrate pool

Table 8. Genes with highest fitness in the presence of 100 mM nitrate

Gene	Name	Description (TIGR)	Gene Fitness
DVU0251		membrane protein, putative	2781.24
DVU0247	*ntrX*	response regulator	563.23
DVUA0023	*atoC*	ABC transporter, permease protein, putative	68.39
DVU0249		conserved hypothetical protein	14.53
DVU0916		AT-rich DNA-binding protein	13.99
DVU0123		membrane protein, putative	8.03
DVU2515		HD domain protein	7.71
DVU0540		sensor histidine kinase	6.83
DVU1999		sulfate transporter family protein	4.59
DVU0246		pyruvate phosphate dikinase, PEP/pyruvate binding…	4.53
DVU1583		TPR domain protein	3.51
DVU1946	*oorB*	pyruvate ferredoxin oxidoreductase, beta subunit…	3.06
DVU0248		sensory box histidine kinase, authentic point mutation	2.69
DVU1455		conserved hypothetical protein	2.53
DVU0252		hypothetical protein	2.52

shaded cells denote genes located in the operon shown in Figure 18

When TnLE-seq was performed in parallel to compare WT DvH in MOLS4 and WT DvH in MOLS4 + 100 mM nitrate in parallel, the results were different than any other analysis presented here. There was an extremely strong “jackpot effect” wherein the only transposon mutants exhibiting strong growth during nitrate stress were those with insertions in a handful of co-localized genes (Figure 18). This lends support to the hypothesis that mutations disrupting the function of these genes (see Table 8 for a complete list) allow for growth in high-nitrate conditions. In the case of a Tn-seq assay, individual transposon mutants lacking functional copies of these genes were created at the beginning of the experiment. The lag seen in growth can therefore be attributed to the time needed for this small subset of the original mutant pool to double until these mutants made up the vast majority of the population. The operon shown in Figure 18

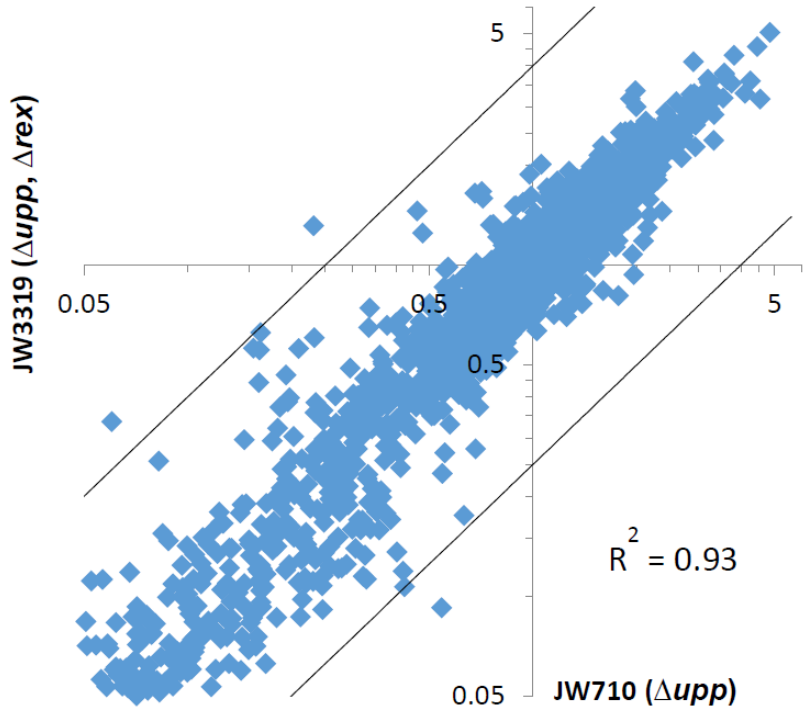
(also known as the “nitrate cluster”) had been hypothesized to be important for growth in the presence of nitrate (*70*) and in fact this was the case. According to the TnLE-seq assay, it contained six of the top 15 genes in terms of fitness values (Table 8), meaning interruption of these genes confers a very significant fitness advantage to an individual mutant. This effect was so strong, in fact, that a scatter plot or statistical analysis as presented in other comparisons would provide little benefit here.

4.7.7 Gene fitness comparison of JW710 and Δ*rex* strain

This topic is explored further in Christensen et al. (2015) (19)

Another TnLE-seq parallel pool comparison was performed to examine gene fitness changes in a mutant strain (JW3319) lacking the Rex redox-sensing transcriptional regulator protein. This regulator and the gene encoding it (*rex*) were studied by Geoff Christensen, also a graduate student in the Wall Lab, to assay regulatory effects it might have on transcription of key sulfate reduction genes in DvH. He prepared the markerless deletion mutant strain JW3319 (Δ*upp*, Δ*rex*) and began using real-time PCR and other methods to characterize the regulatory effects of the protein. I performed a TnLE-seq assay to directly compare gene fitness differences between JW3319 (Δ*upp*, Δ*rex*) and the parental strain JW710 (Δ*upp*), with the idea that additional genes may have significantly altered fitness contributions in the absence of this transcriptional regulator.

Figure 19: Gene fitness comparison of JW710 and JW3319



Diagonal lines indicate confidence intervals for P = 10^{-5}.

JW710 and JW3319 underwent conjugation separately, due to the difference in the background genotypes, and were grown and processed in parallel to provide a fitness comparison as described in sections 4.7.3 to 4.7.5. These pools achieved the highest number of unique insertions ($5.2x10^5$ and $5.4x10^5$, respectively) of any pools described here. In fact, each of these experiments displays a higher insertion density than any other reported Tn-seq assay, averaging 1/7.3 and 1/7.0 insertions/bp, respectively. It is worth noting that the overall similarity in gene fitness between JW3319 and the parental JW710 is actually higher than any other TnLE-seq comparison of pools, with an R^2 value of 0.93 (Figure 19). This is likely due to the fact that the

mutant pools were grown and processed in parallel, rather than approximately a year apart as in the control comparison outlined in section 4.7.3. These JW710 and JW3319 experiments also output a higher proportion of DvH-aligning reads and a higher insertion rate than the other pools, potentially contributing to the excellent agreement between fitness values of these pools.

Only three genes were found to have significantly changed fitness values when assayed in Δ*rex* background, however. These genes encode two hypothetical proteins (DVU3359 and DVU1672) and a predicted cytidylate kinase enzyme (DVU1028). None of these are predicted by RegPrecise 3.0 to be regulated by Rex (*96*) and may be simply a result of experimental noise. This result, though disappointing in terms of elucidating interaction data between *rex* and other gene, is not entirely unexpected given the function of the Rex regulator. Rex binds promoters to impact transcription levels of target operons, but TnLE-seq fitness data is largely independent of these expression changes. TnLE-seq instead concerns the interruption of protein coding sequences, and transcriptional read-through allowed by the Tn5-RL27 sequence ensures transcription past the transposon (*78*). This is why polar effects are not seen within operons for any of these TnLE-seq data, and it also helps to explain the lack of result for Δ*rex* analysis. Furthermore, this lack of significantly impacted genes is explained by a new understanding of the low correlation between expression and fitness in environmental bacteria (*111*). Observations such as these will help us to select appropriate TnLE-seq comparison subjects in the future.

Chapter 5 – Isolation of high quality RNA from mid-logarithmic phase DvH cultures

5.1 Introduction

To examine the impact of Rho factor and PNPase on mRNA transcript length in DvH, mutants deleted for the encoding genes were constructed and the RNA from each compared to that of the parental strain. These studies were proposed to be aided by the simultaneous development of a system for accurate, genome-wide determination of transcript end sites (TES) by Illumina library construction and sequence analysis. Such an approach depends on the isolation of very high quality RNA that has not undergone degradation via RNases or other means. High RNA integrity scores translate to a higher number of full-length transcripts at the start of Illumina library preparation (discussed further in Chapter 6) and this quality translates directly to preservation of 3' transcript ends. Therefore, spurious cleavage products that would appear as confounding signals are reduced and measurement of a strong consensus TES signal may be possible. These sites can then be compared to predicted locations of biologically relevant terminators or used to study transcription attenuation across mutant strains. Conversely, low RNA integrity will likely increase unwanted signal noise that naturally results from non-specific transcription attenuation near the end of a bacterial operon or from endonuclease cleavage for degradation of mRNAs. Several factors that impact the reliable isolation of quality RNA will be discussed in this chapter. These factors include the use of a widely-accepted total-RNA quality metric, development of a reliable

method for RNA isolation from DvH cultures, and consideration of how experiments in mutant strains lacking RNA-processing machinery may impact RNA isolation yield and quality.

5.2 Use of a standard RNA quality metric

An important aspect of RNA quality analysis is the establishment of a quick and reliable assay to score total RNA samples for physical integrity. When analysis of RNA via electrophoresis on gel slabs was the only means of sizing RNA, RNA quality often meant drawing subjective conclusions from the sharpness of ribosomal RNA (rRNA) bands in relationship to degraded rRNA or messenger RNA (mRNA) signals. These methods were proven to be unreliable for determining RNA quality when consistent reverse transcription PCR (RT-PCR) results were the standard (*90*). More recently, RNA samples were evaluated based on better-defined ratios of 18S to 28S rRNA (for eukayotes) along with a comparison of either of these peaks to "degradation" peaks (*3*). Within the last decade, however, the advent of modern and highly sensitive multi-sample gel capillary electrophoresis (CE) instruments has led to RNA quality scoring by sophisticated software suites (*26*). These suites employ precise algorithms, which are often known only to the manufacturer of the CE instrument, and take many aspects of an RNA-sizing trace into account when delivering a quality score. The algorithms were first available as application notes accompanying CE instruments, the most prominent of which being the Agilent 2100 Bioanalyzer (*10, 90*). Some details of the scoring process were later published in the peer-reviewed literature (*115*).

The fast, cheap, and unbiased digital results provided by the Agilent 2100 made its software the industry standard for comparison of RNA sample integrity before use in any RNA assay, most notably RT-PCR experiments and RNA microarrays, and later RNA sequencing (RNA-seq) applications. The scoring process considers eight regions of the electropherogram generated by the instrument. These include the “pre”, 5S, “fast”, 18S, “inter”, 28S, and “post” regions, in addition to a standard marker peak spiked into the sample. The algorithm can be switched to a prokaryotic mode that replaces the 18S and 28S measurements with 16S and 23S, respectively. After running a complex analysis involving all of these areas of the CE trace, the software returns a RNA Integrity Number (RIN) ranging from 0 (highly degraded RNA) to 10 (high-quality, degradation-free RNA) (*115*). Many labs have recently switched to a newer CE system produced by Advanced Analytical Technologies, which is capable of operating in a 96-well format. This system operates in a very similar manner to the Agilent 2100, but scores are determined by a metric called the RNA Quality Number (RQN). RQN, like RIN, uses a 0-10 scale, and was designed to be interchangeable with RIN scores despite using data derived from a different instrument. A direct comparison of over 100 samples run on each system found that RIN and RQN numbers correlated with an R^2 value of 0.96 (*132*). Therefore RQN and RIN analysis are essentially interchangeable, and represent the most reliable metrics available for total RNA quality analysis at this writing.

5.3 RNA isolation options

Many methods are available for the isolation of total RNA from cell cultures. Each provides advantages in terms of yield, cost, RNA quality and time investment. The

methods can roughly be divided into two groups: older, guanidinium thiocyanate-based phase separation protocols and more recently developed column-based centrifugation kits. The standard for RNA isolation has traditionally been acid guanidinium-phenol-chloroform extraction (*17*) and is still used widely for some applications (*18*). The TRI Reagent® protocol (Sigma-Aldrich, St. Louis, MO) is a variation of this type of purification and has been used in our lab to isolate RNA for qPCR applications (*19*). This method allows for relatively quick separation of large amounts of RNA from DNA and other cell material, but employs toxic compounds and can reduce the quality of RNA. Qiagen RNeasy™ Mini Plus Kits are a more recent development that utilize silica-membrane spin columns to bind RNA from cell samples. This system utilizes β-mercaptoethanol as a reductant to denature RNases during initial suspension of an isolated cell pellet and also provides a separate column to completely remove DNA that has the potential to interfere with downstream RNA processing. The Qiagen system is capable of isolating up to 100 µg of total RNA per column. It also requires RNA to be at room temperature for a shorter period than the TRI Reagent process and is generally capable of isolating higher quality RNA from sulfate-reducing bacteria (Jennifer Kuehl, personal communication). Other methods tested include Direct-zol™ on-column RNA binding from a guanidinium thiocyanate suspension and an alternate β-mercaptoethanol/silica membrane column kit both from Zymo Research (Irvine, CA).

5.4 Δ*rho* and Δ*pnp* deletions and potential impact on RNA quality

Marker replacement gene deletions to study the effect of individual loss of both Rho transcription termination factor and polynucleotide phosphorylase were created in

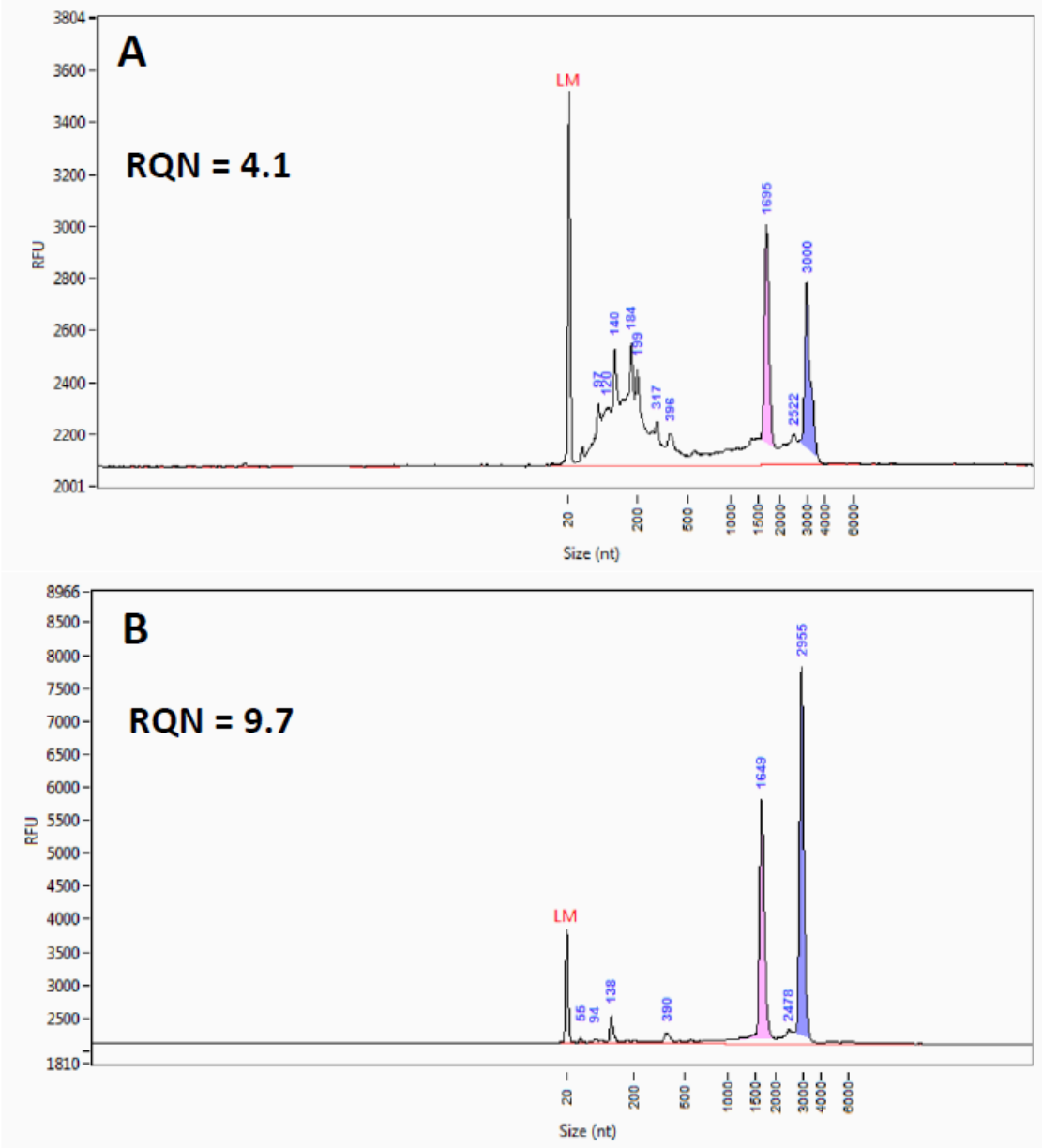


Figure 20. Representative Fragment Analyzer™ electrophoretograms used to calculate RQN **A:** Representative electrophoretogram of a low-quality (RQN = 4.1) total-RNA sample. Primary factors contributing to this low score include significant small RNA fragments in the 20-500 nt range and a larger 16S rRNA peak (pink) than 23S peak (purple). **B:** Representative electrophoretogram of a high-quality (RQN = 9.7) total-RNA sample. Absence of significant fragments in the 20-500 nt range and a higher 23S peak compared to 16S. Both samples are free of DNA, as indicated by a lack of peaks in the >6000 nt fraction. LM denotes a loading marker, which is present in all samples.

DvH by a previously described method (Keller 2009). These were constructed in the 5-fluorouracil resistant parental strain JW710 (*Desulfovibrio vulgaris* Hildenborough genotype Δ*upp*) and resulted in the deletion strains JW2099 (Δ*upp*, Δ*rho*::[*upp kan*]) and JW9005 (Δ*upp*, Δ*pnp*::[*kan*]). Both gene deletions are expected to alter observed 3' ends of mRNA. Generally, deletion of Rho is expected to accomplish this by reducing the attenuation of RNA polymerase (RNAP) in some operons; whereas, the Pnp deletion is expected to alter the processive degradation of 3' ends of transcripts across the genome.

The Rho transcription termination factor is well studied in the *E. coli* model (*4, 95, 106, 114*). It functions to modulate processivity of RNAP by acting as a helicase to impede the physical progress of transcription. Furthermore, Rho-mediated termination is enhanced by the cis-acting recruitment signal of C-rich tracts of nascent RNA (*20*) and the effect of Rho is down-regulated by the anti-termination effects of accessory proteins such as NusG (*14*). This sophisticated transcription regulation provides an intriguing area of study; however, Rho is an essential gene product in *E. coli* (*28*) and studies involving this model species must employ the inhibitor bicyclomycin (BCM) to examine only a short-term cessation of the associated transcriptional attenuation. Further studies have examined *in vitro* functions of Rho to elucidate mechanistic details (*14, 82*), or employed allelic variations of the encoding gene (*79*), however, the effect of a *rho* deletion in a bacterium has not been studied. An examination of the loss of Rho protein requires both a bacterial species in which *rho* is present but not essential to growth and a genetic system for gene deletion with a strong selection for recovery of the mutant strain. DvH

is a candidate to meet both of these criteria, as a streamlined system for gene deletion has been developed (*64*) and a homolog of *rho* with 91.1% amino acid identity in the related species *Desulfovibrio alaskensis* G20 has been found to be dispensable in transposon mutant pools (*73*). The ability to delete *rho* from DvH was confirmed when the gene was replaced with a cassette containing the *upp* and *kan* genes (Wall lab, unpublished data). This strain was viable, though slow-growing, and was verified via Southern blot and PCR to lack the *rho* (DVU1571) gene.

Although no studies of Rho have been specifically undertaken in DvH, an educated guess can be made regarding the total proportion of operons it affects. In the most detailed study involving operon structure in DvH (*110*), the authors submit multiple pieces of evidence to support the hypothesis that Rho is weakly active in this genome. These include the low amino acid sequence identity of 67% to Rho in *E. coli*, and the expendability of *rho* in the related *Desulfovibro alaskensis* G20. Furthermore, there is evidence of a fully transcribed antisense gene sequence (DVU1250) in DvH. This feature is present only in genomes where Rho is weakly active, such as the Gram-positive species *Bacillus subtilis (112).* The non-essential Rho activity of *B. subtilis* may offer a parallel model for insight into Rho function jiu89in DvH. *B. subtilis* has been found to produce a Rho termination factor that is 56% identical to and present at <5% the level of the Rho factor of *E. coli* (*56, 112*). Taken together, this evidence helps explain the expendability of Rho in DvH, but experimental evidence will be necessary to determine which (if any) operons are reliably affected by this type of transcription termination.

This degree of activity may be crucial to understanding the potential impact of Rho deletion on the quality of isolated mRNA. If relatively few operons are in fact affected, the change in RQN values may be negligible. If many operons are affected, increased variability in transcript length may create more noise in the high sensitivity electrophoresis traces during analysis and therefore negatively impact quality scores. Antisense transcription of genes, which is found to be directly increased by loss of Rho in E. coli (*104*), will also likely impact RNA quality scores. dsRNA hybrid complexes often serve to recruit RNA endonucleases such as RNase III (*12*), thus resulting in an increase of the short mRNA fragments that greatly decrease RQN scores for isolated RNA.

The other gene deleted in this study, *pnp*, encodes the protein polynucleotide phosphorylase (PNPase, also known as polynucleotide nucleotidyltransferase). This enzyme is a homolog to PNPase in the well-studied RNA degradation pathway of *E. coli*. It acts on 3' ends of free RNA fragments to processively convert them to mononucleotides (*33*), in a similar manner to RNases R and II. This makes it important for re-use of ribonucleotides after the endoribonucleases E, G, III, and P have cleaved long mRNA fragments to shorter ones. DvH possesses homologs to these four endoribonucleases as well as all three exoribonucleases mentioned above, therefore it is logical that PNPase would be expendable. Interestingly, PNPase enzyme in *E. coli* was found to degrade the transcript that encodes it through a temperature-dependent hairpin structure that forms in the transcript leader sequence and first recruits RNase III (*58*). This regulatory sophistication lends emphasis to the importance of controlling PNPase levels, which may cause excessive RNA damage if not kept in check.

The simplest phenotypic trait expected upon the elimination of PNPase activity would be less degradation of mRNA and therefore higher RQN scores for RNA isolated from JW9005 (Δ*upp*, Δ*pnp*::[*kan*]). This would also lead to a higher RNA yield, and it has in fact been shown that PNPase deletion in *E. coli* raises total mRNA levels by 17% (*91*). However, the majority of RNA in a cell is ribosomal RNA which PNPase degrades more efficiently than the other RNases (*33*). A compensatory mechanism may correct for this loss of rRNA degradation in order to maintain the ability to recycle valuable phosphate-rich nucleotides. This mutation or change in regulation would likely enhance the function of either exoribonuclease R (encoded by *rnr*, DVU2467) or exoribonuclease II (encoded by DVU3207), which share the general RNA regulatory and recycling roles of PNPase (*33*). Such overproduction of other processive 3' to 5' exoribonucleases may over-correct for the loss of PNPase, thereby hastening RNA degradation in general and possibly also negatively impacting the growth fitness of JW9005. Some insight into these changes will be provided by mutant growth rates, RQN results, and RNA yield, as well as possibly by expression and 3' RNA-seq data.

5.5 Materials and Methods

5.5.1 RNA isolation protocol

All cultures used for RNA isolation were grown in an anaerobic glove bag with an atmosphere of 95% nitrogen and 5% hydrogen. Replicates of each mutant strain were grown simultaneously by inoculating glass bottles with 10% vol/vol of fresh mid-logarithmic phase culture. These were carried out in five 40 ml aliquots for total RNA-

seq samples and individual 150 ml aliquots for 3' RNA-seq samples. All cultures were grown to an OD_{600} of 0.29-0.31 and transferred to 15 ml plastic tubes, then cells were immediately harvested by centrifugation at 3,696 x *g* at 4°C for 12 min. The supernatant was poured off, tubes were tapped upside down to remove excess moisture, and lids were replaced before immediately freezing the pellets at -80°C. For column-only RNA isolation protocols, pellets were resuspended in the same tubes by addition of the binding buffer provided in each column-based kit. For tri-phase isolation protocols, 3.5 ml of culture was added to 10.5 ml trizol on ice in the anaerobic glove bag, then inverted repeatedly to mix and immediately frozen at -80°C. Isolation of RNA by both types of procedures was then undertaken by the standard instructions of the respective product.

Several commercial protocols were used for the purification of RNA from DvH cultures before selecting a method that gave the best combination of yield and total RNA quality as measured by RQN analysis. 1) The standard TRI Reagent® phase-separation protocol (Sigma-Aldrich product #T9424, St. Louis, MO) was tried first. This was followed by 2) a scaled-up version of the TRI Reagent® LS standard protocol (Sigma-Aldrich product #T3934, St. Louis, MO) in order to transfer the bacterial sample directly from a growing culture to the TRI Reagent® and eliminate the initial centrifugation step. The Direct-zol™ RNA Miniprep protocol (Zymo Research product #R2050, Irvine, CA) was modified to use TRI Reagent® LS for pellet suspension, and the initial binding step was performed via vacuum instead of centrifugation to facilitate use of a larger initial volume. For all TRI Reagent®-based extraction procedures, digestion of DNA with TURBO

DNase™ (Life Technologies, Carlsbad, CA) and RNA electrophoresis were performed as previously described (*19*).

3) A separate column-only method for both eliminating DNA and binding/eluting RNA, the Qiagen RNeasy™ Mini Plus kit (Qiagen, Venlo, Netherlands), was also attempted. This employed the optional addition of 1% (vol/vol) β-mercaptoethanol to the suspension solution and a final elution of RNA into 30 µl of nuclease-free water. Finally, 4) the similar Quick-RNA™ MiniPrep standard protocol was attempted (Zymo Research product #R1054, Irvine, CA).

5.5.2 RNA quality scoring

All total RNA samples were submitted to the MU DNA Core (web.rnet.missouri.edu/biotech/dnacore) in 4 µl aliquots at 100 ng/µl for analysis on a Fragment Analyzer (Advanced Analytical Technologies, Ames, IA). RNA Quality Number (RQN) results were scored in prokaryotic mode on a 10-point scale and traces were visually examined to ensure no DNA carryover was present in the high molecular weight fraction.

5.6 Results

When attempting to quantify transcript ends simultaneously across a genome, the most important criterion for evaluating RNA extraction methods should be quality of the resulting total-RNA sample. The accepted method for RNA quality scoring is the RQN (described in chapter 5.2) and maximizing the quality of the initial RNA pool is critical to the base-pair-resolution measurement of transcript ends. RNA yield is another

important metric for evaluating RNA isolation methods, as is the related ability to concentrate RNA fragments into a very small volume. Yield and concentration criteria are secondary to quality, however, due to relatively low input requirements of the library preparation techniques (discussed further in Chapter 6). Finally, time and cost considerations must be taken into account, with cheaper and less time intensive methods favored over more expensive and cumbersome techniques. Also a factor is the speed of RNA isolation that allows parallel processing of cultures representing multiple background mutants and growth conditions. Process timing is critical when employing multiple analysis techniques on the same cultures such as total transcript expression analysis and transcript end sequencing.

The oldest and most readily available RNA isolation technique was the TRI Reagent™ cell pellet suspension and separation protocol. This was immediately found to be lacking in both RNA quality and yield, however, so the related TRI Reagent™ LS protocol was attempted. This variation on tri-phase separation allowed for a growing bacterial culture to be directly added to the guanidinium thiocyanate solution instead of first pelleting the cells by centrifugation. This quickly halted cell growth and possible RNA degradation; however, three parts TRI Reagent LS™ had to be used for one part cell culture and downstream processing was hampered by this large volume. To isolate RNA from 7 ml of cell culture, TRI Reagent LS™ had to be added to achieve a final volume of 28 ml. Standard phase separation and binding of RNA to a Zymo Direct-zol™ column by application of a vacuum were both attempted to improve the concentration of RNA. Out of 14 such preparations on parental strain cultures, all had an RQN between 2.1 and 7.7.

These scores would likely not be adequate for precise mapping of transcript ends by a newly developed procedure such as 3' RNA-seq, so all tri-phase based methods were abandoned in favor of column-only protocols.

The Qiagen RNeasy™ Mini kit (Qiagen, Venlo, Netherlands) had been used successfully by other researchers working with species of *Desulfovibrio* (*110, 111*) to isolate RNA with RQN numbers over 9. The more recent addition of column-based DNA binding and removal in the Qiagen RNeasy™ Mini Plus kit had also been tested and found to offer similar quality and DNA removal but without the additional time and sample heating associated with enzyme-based DNA removal (Jennifer Kuehl, personal communication). In fact, this kit-based system was found to be superior to phase-separation in RNA quality, speed of isolation, and cost. Yield was essentially unchanged, as both RNeasy™ Plus and TRI Reagent LS™ methods produced ~2-5 µg total RNA per

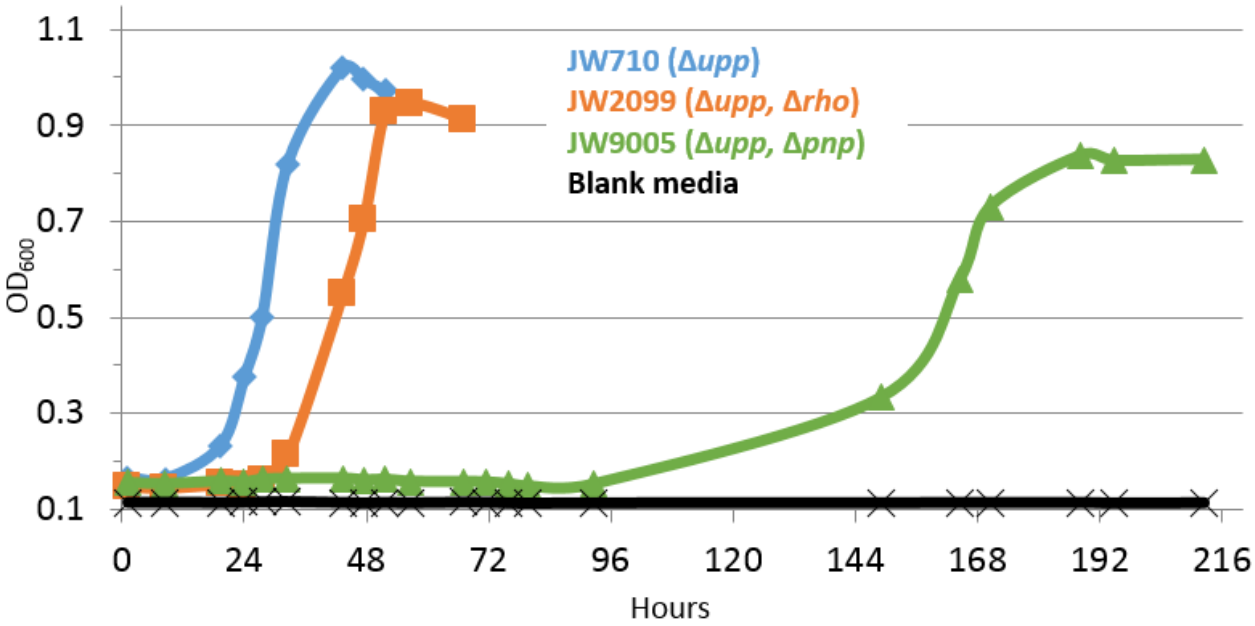


Figure 21. Growth comparison of deletion mutant strains. Each line represents an average of parallel biological triplicate cultures, each inoculated at 10% vol/vol in MOLS4 media (Zane 2010)

reaction. Column removal of DNA with this kit was found to be 80-90% effective, but failed to remove all DNA in the remaining samples as judged by PCR amplification and/or Fragment Analyzer analysis. An alternate protocol was designed to utilize two DNA removal columns per sample. Ultimately, however, it became more practical to grow extra culture replicates in parallel and also isolate multiple RNA samples from a given culture in order to choose those with the highest RQN and without DNA carryover for final library preparation. The RNeasy™ Plus kit with standard β-mercaptoethanol protocol and 30 µl elution was used for all libraries eventually sent for Illumina™ sequencing.

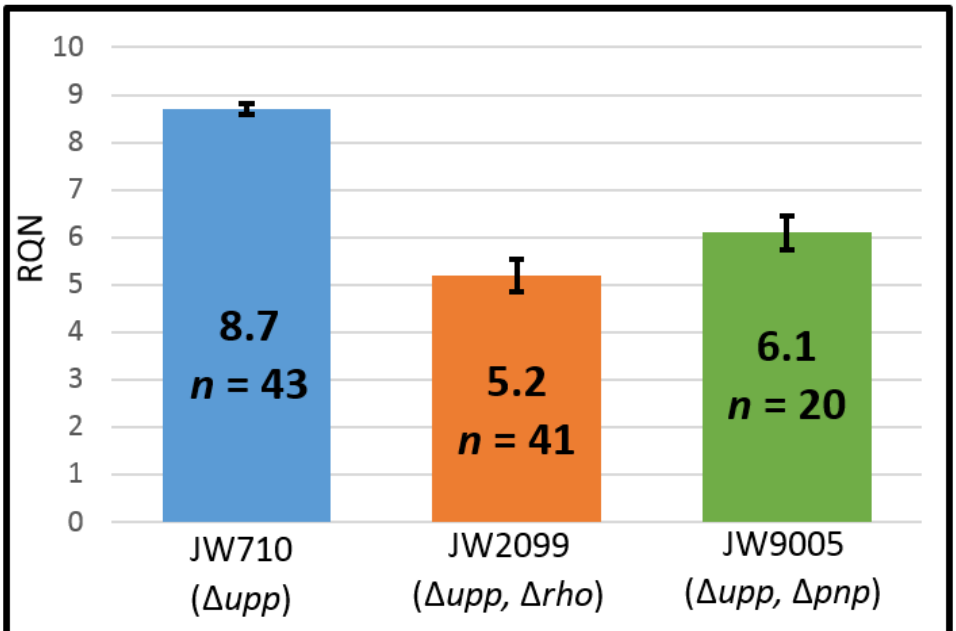


Figure 22. Average RQN scores by DvH strain. Average RQN for JW2099 and JW9005 are each significantly different from the parental strain JW710 ($p < 0.001$ using Student's t-test). Sample sizes represent only samples sent for RQN analysis and found to be free of DNA contamination. These were drawn from 75, 80, and 60 samples for JW710, JW2099, and JW9005, respectively.

Individual deletion of either the *rho* or *pnp* gene had a negative impact on growth rate (Figure 21). Compared to the parental strain JW710, the Δ*rho* (JW2099) deletion appeared to induce a short lag time while growing at the same rate. The Δ*pnp* (JW9005) conferred a more pronounced growth defect and appeared to have a longer lag, a slower growth rate and reached a lower OD when it did grow. These deficiencies were somewhat ameliorated by the addition of 1% wt/vol yeast extract. Most slow-growing bacteria are aided by the addition of these rich nutrients, but it is possible that nitrogen in yeast extract has an especially great impact on mutants deficient in the regulation or recycling of nitrogen-rich RNA.

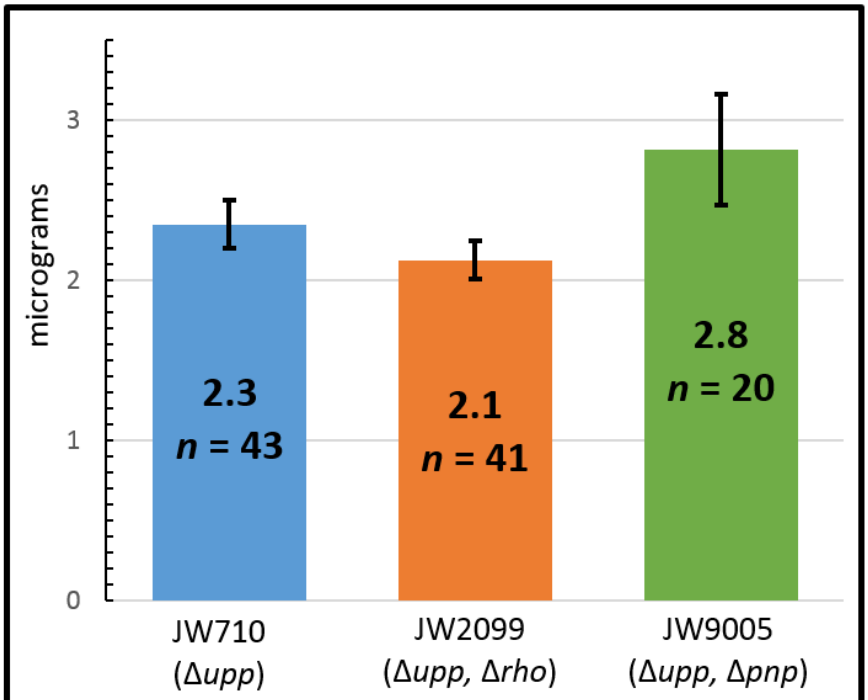


Figure 23. Average RNA Yield by DvH Strain (µg). Average yield for neither JW2099 nor JW9005 were significantly different from the parental strain JW710 (p = 0.15 for each comparison using Student's t-test). Sample sizes (*n*) represent only samples sent for RQN analysis and found to be free of DNA contamination. These were drawn from totals of 75, 80, and 60 samples for JW710, JW2099, and JW9005, respectively.

Deletion of both *rho* and *pnp* genes also significantly negatively impacted the quality of isolated RNA (Figure 21). A simple explanation for this quality decrease in the extracted RNA could be the slowed growth exhibited by these deletion mutants. In less-robust cultures, it is likely that some cells lyse early in the growth phase and therefore contribute to the accumulation of small RNA degradation products. Intracellular processes could also contribute to the poor quality scores. In the case of Rho deletion, antisense transcription allowed by the absence of this transcription termination factor likely contributed to some degree of RNA duplex formation and targeted RNA cleavage by RNase III and other processes. In mutants lacking PNPase, putative compensatory mechanisms for degrading and/or recycling RNA might overcorrect for the loss of this enzyme. All of these scenarios result in a decrease of the average length of mRNA and rRNA isolated from the cultures, which is the factor most directly responsible for lowering RQN scores.

Conversely, deletion of either *rho* or *pnp* genes did not significantly affect RNA yield (Figure 22) when the same RNEasy™ Plus isolation method was used. This was not unexpected for a strain lacking Rho because the essential and highly active Rho found in *E. coli* affects only 20% of operons (*105*). Furthermore, a mid-log phase culture would be expected to have ribosomes actively translating a large proportion of transcripts and blocking binding of Rho to C-rich Rho utilization (*rut*) sites (*106*). Loss of PNPase leading to similar RNA yields is harder to explain, given that some process must be compensating for the loss of this enzyme function given the lower isolation quality of RNA from that mutant. Yield does appear to be somewhat higher in the PNPase deletion

strain than in the parental strain, and it is possible this difference would become statistically significant if more samples were isolated (Figure 22). It is also conceivable that the small columns used here simply cannot bind all the RNA in a pellet harvested from 15 ml mid-log culture, and therefore any change in the raw RNA amount is lost from one isolation to the next. This is not likely, however, given the column binding capacity of 100 µg stated by the manufacturer (Qiagen, Venlo, Netherlands). Due to the large number of repetitions of the best-established RNA isolation method, the samples obtained here almost certainly represent the highest quality RNA samples possible for mutants lacking these RNA processing genes. The decrease in quality from the parental to these mutant strains may impact later analysis; however, the rapid isolation and

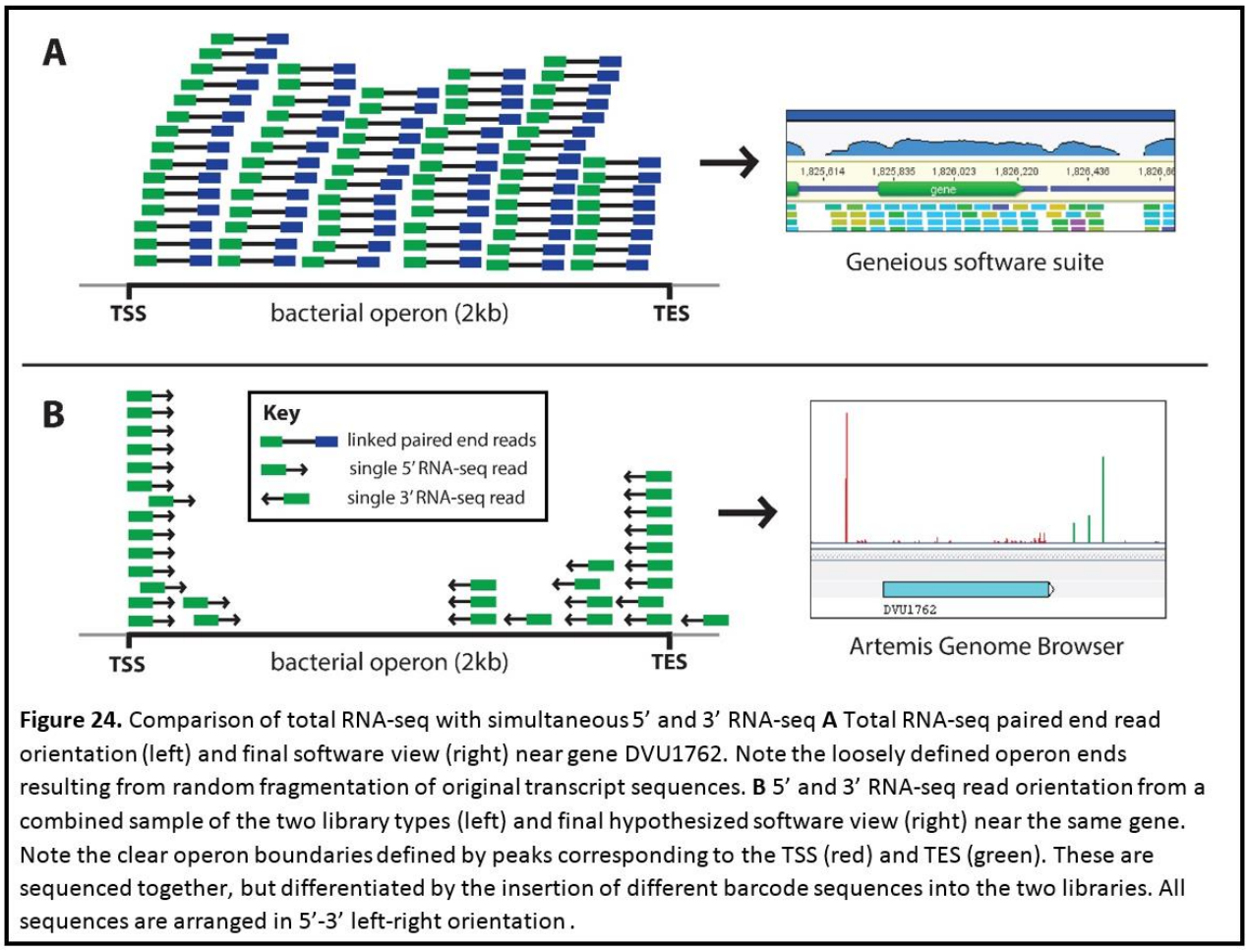


Figure 24. Comparison of total RNA-seq with simultaneous 5' and 3' RNA-seq **A** Total RNA-seq paired end read orientation (left) and final software view (right) near gene DVU1762. Note the loosely defined operon ends resulting from random fragmentation of original transcript sequences. **B** 5' and 3' RNA-seq read orientation from a combined sample of the two library types (left) and final hypothesized software view (right) near the same gene. Note the clear operon boundaries defined by peaks corresponding to the TSS (red) and TES (green). These are sequenced together, but differentiated by the insertion of different barcode sequences into the two libraries. All sequences are arranged in 5'-3' left-right orientation .

consistent RQN scores for these mutants suggests any impact will be a function of the altered RNA metabolism of these mutants.

Chapter 6 – Development of the 3’ RNA-seq method to determine transcript ends

6.1 Introduction

Transcription start sites (TSS) represent the point upstream of any bacterial operon where RNA polymerase (RNAP) recruitment occurs and transcription of that operon begins. They are important for discerning operon structure in newly sequenced genomes, gaining information about consensus promoter sequences, and evaluating transcript abundance or polarity. These TSS can currently be predicted to base-pair resolution across an entire genome with the 5’ RNA-seq protocol (*110*). This method takes advantage of ongoing advances in Illumina™ massively parallel sequencing and addition of a barcode multiplexing strategy could easily enable simultaneous assay of several strains or growth conditions. 5’ RNA-seq is a relatively simple and robust method for examining key elements of bacterial transcription, and the per-experiment cost associated with the method can decrease rapidly depending on the experimental design. It can be used to complement well established total RNA-seq techniques which sequence fragmented transcripts (Figure 24A). In comparison to the total RNA-seq method, 5’ RNA-seq provides a much more precise TSS signal and requires less sequencing coverage but does not provide significant transcript abundance information on its own.

The 5’ RNA-seq approach also does not attempt to quantify transcription end sites (TES). These features complement TSS information, thereby making up the other half of information regarding operon boundaries. Described here is a method for high throughput assay of 3’ end locations of bacterial transcripts. This method, designated 3’ end RNA sequencing (3’ RNA-seq), was designed using similar molecular biology principles and a comparable overall workflow to 5’ RNA-seq (Figure 25). It seeks to ligate a known adapter sequence to transcript ends early in the library construction process, thereby minimizing noise associated with RNA degradation products. Furthermore, with only small adjustments to both methods, 5’ RNA-seq and 3’ RNA-seq can be performed simultaneously on separate portions of the same initial mRNA pool (Figure 24B). With a barcoding strategy in place, these separate libraries can be combined with each other and with similar libraries made from other starting mRNA pools to evaluate genome-wide TSS and TES location information across parallel conditions and/or isolates. This combined strategy optimizes the biological information gained from Illumina™ sequencers because analyzing a single bacterial library on one Illumina™ flowcell almost always yields orders of magnitude more sequencing information than is statistically relevant. This scheme also greatly reduces costs associated with sequence analysis on this platform.

An appropriate input sample for 3’ RNA-seq library construction and sequence analysis is a pool of RNA fragments (Figure 26A) isolated from a single bacterial monoculture. This pool must contain at least two micrograms of RNA and be free of

DNA. It must also be concentrated to a volume of 25 µl or less of nuclease-free water and have been assigned a high RNA quality number (RQN), ideally an RQN of greater than 9. The output of this library preparation process will be a pool of blunt ended double stranded DNA (dsDNA) fragments containing adapters sufficient for cluster generation on an Illumina™ sequencer, a known region for binding of the sequencing adapter, and an insert sequence corresponding to directional TES of transcripts from the original pool (Figure 26B). High throughput sequencing of this final pool will allow a genome-wide map of consensus TES locations to be generated, and the process can be easily carried out in parallel to compare multiple bacterial strains and/or growth conditions.

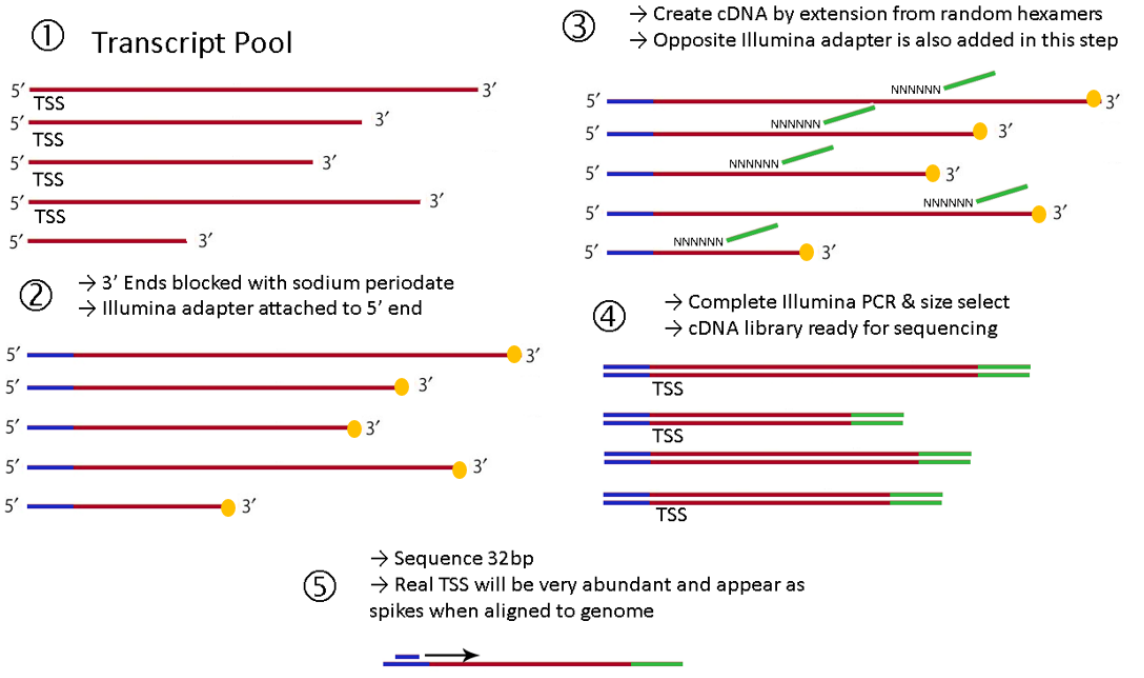


Figure 25. Summary of the 5′ RNA-seq library preparation protocol. Red lines represent transcript-derived sequences, blue lines represent Illumina™ adapter A, green lines represent Illumina™ adapter B. N sequences represent a random hexamer DNA strand.

The regulation of TES locations is somewhat more complex than that associated with TSS locations. This is partly because transcript attenuation is governed by multiple types of termination signals. The first of the two most commonly studied termination signals are intrinsic terminators, which consist of well conserved, short RNA hairpin structures that form from nascent transcript in the exit groove of RNA polymerase (RNAP) to stop forward transcription progress and cause dissociation from the DNA template (*106*). The second type of well-studied signal is that of Rho, a helicase enzyme which binds cytosine-rich tracts of nascent transcript in the absence of active ribosomes and is able to propel itself into RNAP, thus stopping transcription (*105*). Other reasons for the possible detection of multiple TES per operon include the natural propensity for

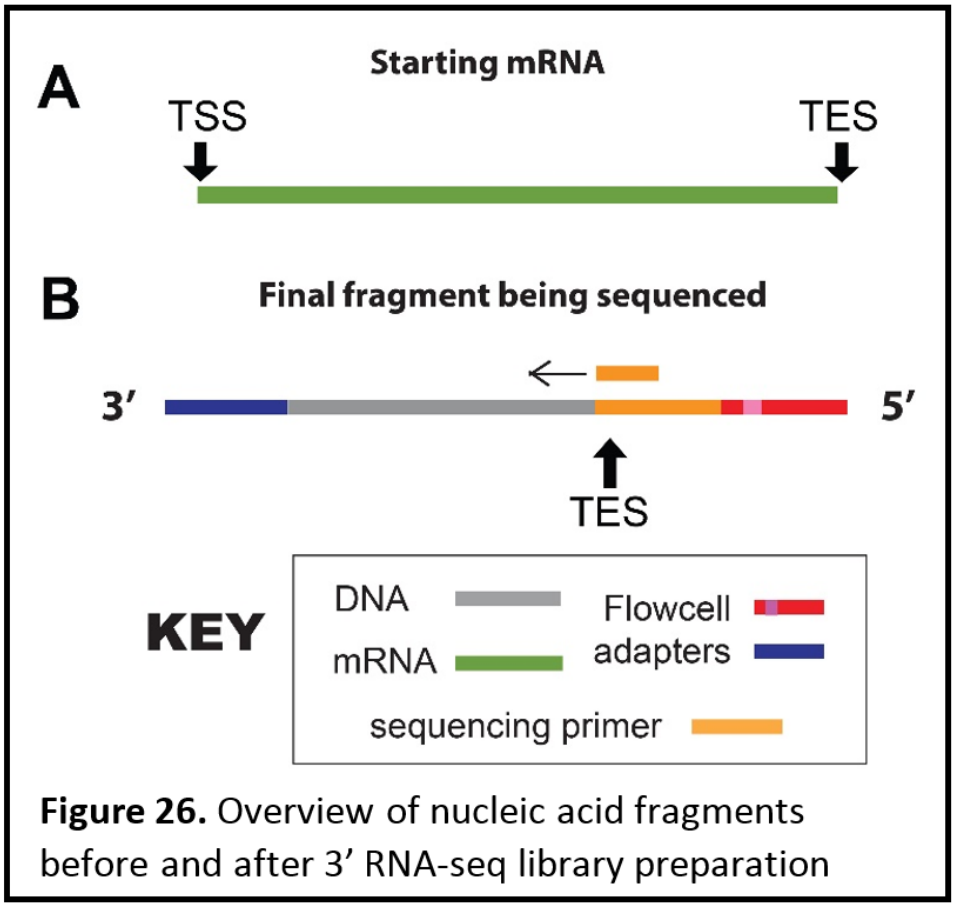


Figure 26. Overview of nucleic acid fragments before and after 3′ RNA-seq library preparation

RNAP to separate from the template strand during transcription and the fact that bacterial exoribonucleases tend to degrade transcripts in a 3' to 5' manner. These factors may lead to detection of multiple, spurious transcript ends in many operons and thereby render determination of consensus TES locations more difficult than those observed with TSS location discovery by 5' RNA-seq (*110*). However, the presence or extent of this signal noise will not be clear until a genome-wide map of 3' RNA-seq is actually obtained.

6.2 Ribosomal RNA depletion

When isolating total RNA in preparation for sequence analysis of messenger RNA (mRNA), it is desirable to first reduce the proportion of ribosomal RNA (rRNA) present in the sample. This is important because rRNA makes up well over 90% of the total RNA found in most bacteria and sequencing capacity can be used much more efficiently to assay mRNA if rRNA is first depleted from the RNA input pool. Eukaryotic samples are often enriched for mRNA using poly-T capture probes; however, this is not possible for bacterial samples that lack poly-A tails attached to transcripts (*8*). Methods must instead be employed to selectively remove rRNA molecules from bacterial total RNA samples before library construction. Success in removing a high proportion of rRNA from a starting pool ultimately limits the number of redundant rRNA fragments sequenced, thereby freeing read capacity for analysis of protein coding sequences.

Multiple approaches are now widely used to remove rRNA. The original method for elimination of rRNA was the simple removal of rRNA bands after agarose gel

electrophoresis of the sample (*88*), but this method is no longer in use because it also removes mRNA transcripts of similar size to rRNA. The three general categories of current commercially-available methods include bead-based pulldown methods to selectively remove rRNA bound to biotinylated probes, enzymatic methods to selectively degrade rRNA based on 5' phosphate modification, and RNA duplex methods using an endoribonuclease to selectively degrade probe-rRNA hybrid dsRNA. Studies conducted soon after introduction of the Ambion MICROBExpress™ bead-based pulldown kit found it to be superior to selective enzymatic ssRNA degradation methods both in terms of rRNA removed (*21, 50*) and in terms of reducing sequence bias of final libraries (*50*). This bead pulldown method was later enhanced by the use of computerized design of target probes based on bacterial species (*84*), but the results were often not dramatic as compared to the basic MICROBExpress™ kit. The duplex-specific nuclease (DSN) method is effective, but complicates development of new techniques because it is used after final libraries have been constructed and DNA molecules have been melted apart (*133*). It also requires a five hour incubation at 68°C, thereby adding significant time and risk of DNA damage.

The Ambion MICROBExpress™ method was chosen for rRNA depletion during the development of 3' RNA-seq. In addition to positive reports of this method's effectiveness (*21, 50*), it was the method used for 5' RNA-seq experiments (*110*) and therefore would provide 3' RNA-seq with a starting mRNA pool most closely resembling the 5' RNA-seq pools in the same organism. This variable is therefore eliminated in later comparisons of the two methods. It is worth noting, however, that other methods have

been developed and may increase effectiveness of rRNA removal before future replications of this same library preparation protocol (*8*). The Ribo-zero™ method (Epicenter, Madison, WI) in particular was shown to eliminate more rRNA than older methods with a new variation on probe hybridization and bead-based pulldown (*8*).

6.3 Selective ligation of a known DNA aptamer to 3' RNA ends

Perhaps the most crucial step in developing a successful method to sequence 3' ends of mRNA is to rapid and irreversible binding of a known oligonucleotide sequence to the distal end of all transcripts. This serves to both prevent enzymatic and/or heat damage to 3' ends and to provide a binding point of known sequence for later conversion of the mRNA to cDNA. This is another step where library preparation of bacterial transcripts differs from eukaryotic samples. Here, eukaryotic techniques again exploit the poly-A tails of mRNA to begin 3' end-specific preparations by annealing poly-T primers to the A-tailed mRNA (*49, 55*). These oligos are fused to Illumina-specific and/or barcode tagged adapters and prime the reverse transcriptase reaction that creates the first cDNA strand. It would be possible to first add poly-A tails to bacterial mRNA, but this poly-T based priming method is prone to mis-priming and unknown homopolymer lengths (*55*). These problems complicate or render impossible sequencing of the final library, which requires exact priming accuracy and often cannot tolerate homopolymer repeats near the start of a given read (*71*). This is especially true when moving to the less-flexible Illumina™ HiSeq family of instruments from the older and lower-throughput Illumina™ Genome Analyzer family. For this reason, direct ligation of an oligonucleotide with a known sequence to the 3' mRNA ends is preferable.

Ligation of nucleotides to the 3' ends of ssRNA is a well-understood enzymatic process. Since the discovery of T4 RNA Ligase 1 (*116*), this enzyme has been routinely used for the stepwise creation of custom RNA sequences (*37*) and for radiolabeling of RNA ends with ribonucleotides containing P^{32} (*35, 36*). T4 RNA Ligase 2 was discovered later as a distinct enzyme with similar properties (*54*). Deep sequencing library preparations for studying small RNAs (sRNA) and micro RNA (miRNA) now routinely use both enzymes sequentially to build an RNA-DNA hybrid molecule consisting of known DNA adapters flanking the original sRNA or miRNA molecules (*59*). This method is labor intensive because it requires two separate ligation reactions and at least three denaturing poly acrylamide gel electrophoresis (PAGE) purifications before PCR amplification to obtain the final library. The method also requires starting RNA

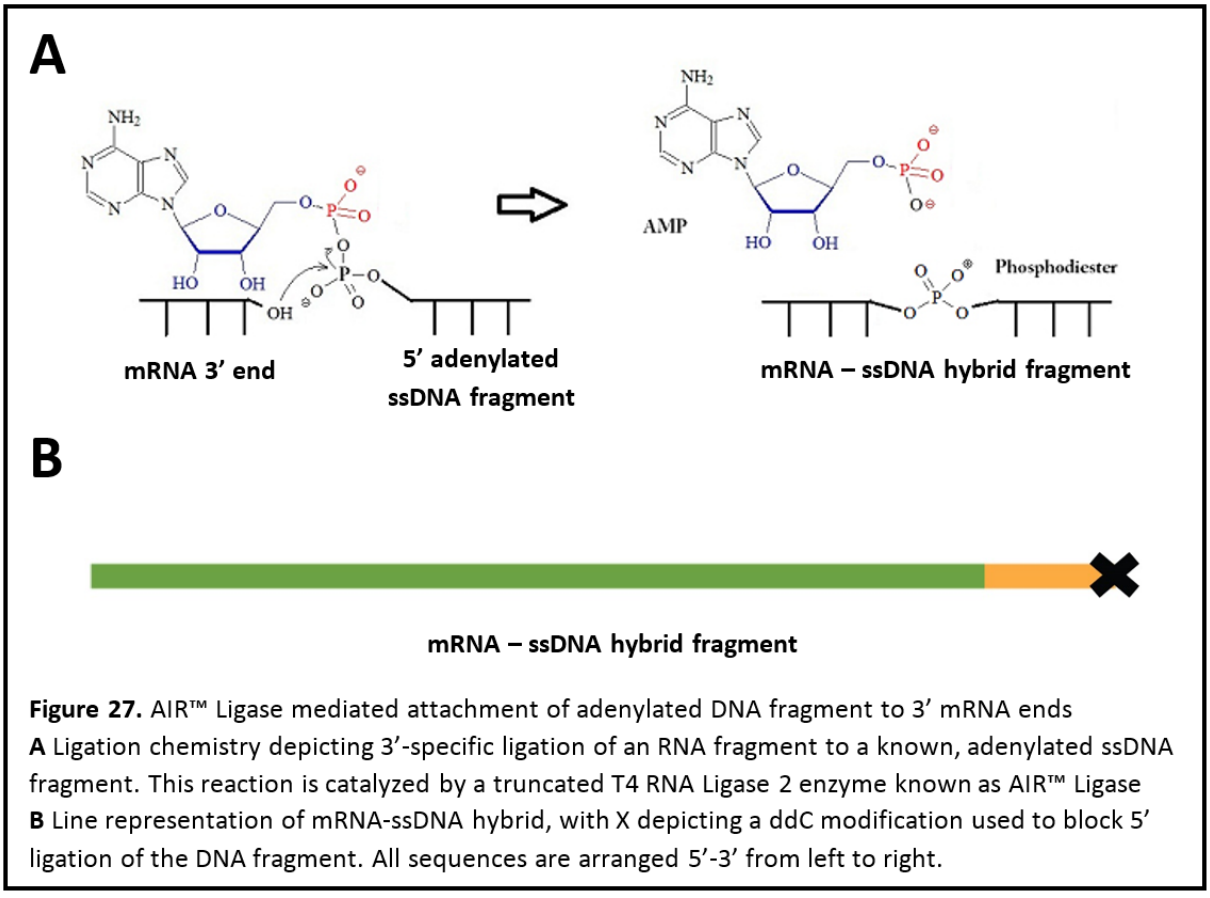


Figure 27. AIR™ Ligase mediated attachment of adenylated DNA fragment to 3' mRNA ends
A Ligation chemistry depicting 3'-specific ligation of an RNA fragment to a known, adenylated ssDNA fragment. This reaction is catalyzed by a truncated T4 RNA Ligase 2 enzyme known as AIR™ Ligase
B Line representation of mRNA-ssDNA hybrid, with X depicting a ddC modification used to block 5' ligation of the DNA fragment. All sequences are arranged 5'-3' from left to right.

molecules short enough (<500 nt) to be compatible with the Illumina™ platform, thus precluding its use in sequencing intact mRNA samples.

Though the entire sRNA/miRNA library construction procedure cannot be used to create 3' end-specific mRNA libraries, the first step of the process can be used. This step is catalyzed by the commercial enzyme AIR™ Ligase, which is a truncated form of T4 RNA Ligase 2 lacking the ability to adenylate 5'-PO_4 donor molecules (*126*). AIR™ Ligase therefore is unable to create dimers of mRNA molecules because it functions in the absence of free adenosine triphosphate (ATP) and requires the donor molecule (in this case the DNA adapter) to be pre-adenylated on the 5' end (Figure 27A). DNA dimers are prevented by a further addition of a dideoxycytosine (ddC) to block the 3' end of the adapter (Figure 27B). Other downstream methods must now be developed to complete a sequence-ready Illumina™ library of the appropriate length and adapter composition.

6.4 First and second strand cDNA synthesis

First strand synthesis of cDNA requires only a DNA primer complementary to the DNA adapter attached to the mRNA strand in the previous section, in combination with enzymes from a standard reverse transcriptase (RT) kit. For 3' RNA-seq, the ThermoScript™ kit is used because the RT included is thermostable. This allows cDNA synthesis to occur at a higher temperature (60°C) to overcome potential RNA hairpins which could otherwise prevent cDNA synthesis in some transcripts of DvH, a high GC content organism. Additionally, the use of the RNaseOUT™ enzyme supplied in the kit ensures mRNA stability during this critical step. This reaction results in a collection of

DNA molecules with a common 5’ end sequence followed by cDNA representing the complementary sequence to the original mRNA (Figure 28A). Because Thermoscript™ RT lacks full RNase H activity, the original ssRNA strands are still bound to these ssDNA molecules. This results in hybrid duplex molecules (Figure 28A). It would be possible to eliminate the RNA in this duplex with addition of an RNase H step, but here the 94C denaturing step in the next segment of the protocol was found to be sufficient for separation of the two strands before second strand cDNA synthesis and PCR.

Second strand cDNA synthesis essentially consists of a single PCR cycle with an Illumina adapter fused to a random DNA hexamer as a primer. Only the random hexamer binds to the existing first strand cDNA, and it can potentially do so at any point along the fragment (Figure 28B). Although this fragment could be multiple kilobases long

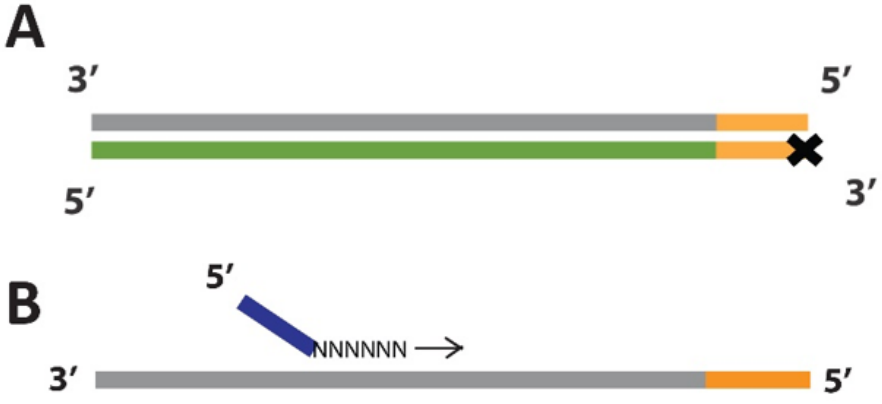


Figure 28. First- and second-strand cDNA synthesis **A** First strand cDNA (grey) is made from the mRNA template (green) starting from a primer (gold) binding a known sequence region. **B** Second strand cDNA is made by a random hexamer fusion primer (blue) replicating the first strand in the opposite direction

(depending on which input mRNA transcript served as the original template), PCR will naturally favor shorter dsDNA products. Products either too short or too long for amplification and sequencing on the Illumina™ platform will be removed with a later agarose gel sizing step. It should also be noted that imperfect binding of the random hexamer at this step could introduce changes in nucleotide sequence; however, this hexamer has been introduced on the opposite end of the fragment from the one being sequenced in the final pool (Figure 30C).

6.5 Exonuclease I treatment and PCR amplification of the final library

At this point in the library preparation the DNA fragments are partially dsDNA but with a potentially lengthy ssDNA overhang (Figure 29A) left over from the initial production of cDNA (Figure 28A). A gel purification at this stage would be ideal in order to eliminate very long or very short dsDNA fragments before PCR amplification of the library; however, long ssDNA overhangs on many fragments have the potential to cause these fragments to migrate inconsistently through agarose. Removal of this ssDNA overhang is therefore desirable, and can be accomplished by specific enzymatic degradation with exonuclease I (*80*). Exonuclease I acts to preferentially degrade ssDNA in a 3' to 5' manner (*74*), so it is ideal to eliminate this overhang (Figure 29B) and allow uniform migration of fragments through the agarose gel used for size selection.

Both ends of the dsDNA fragments now contain known sequences long enough to bind primers and undergo PCR for generation of enough DNA mass to load on a sequencer. One of these primers may simply contain the specified sequence for binding

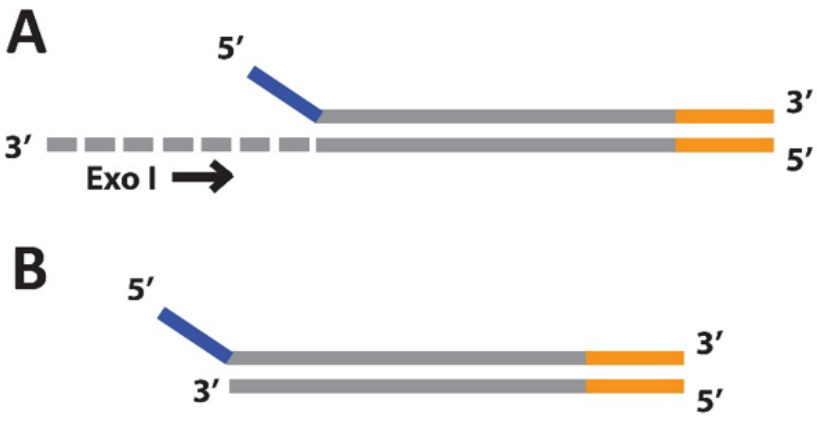


Figure 29. Exonuclease I treatment. **A** Exonuclease I acts in a processive 3′ to 5′ manner to digest a 3′ ssDNA overhang corresponding to the original 5′ end of mRNA. **B** Removal of this overhang, which could extend two or more kilobases depending on the original transcript length, allows for uniform migration of the DNA through an agarose gel

the Illumina™ flowcell (blue in Fig. 30). The other must be a longer fusion primer capable of hybridizing the original adenylated DNA oligo (Figure 27) and adding the opposite Illumina™ adapter for later amplification on the flowcell of the instrument. In multiplexing strategies, this primer may also contain a short barcode sequence unique to the individual mRNA pool. This facilitates later generation of an index read and therefore the analysis of many samples simultaneously in the same sequencing lane. Following a final gel purification to retain only fragments 200-500 base pairs (bp) in length, a completed library will consist of billions of blunt-ended duplex DNA fragments (Figure 30B). These will all share common Illumina™ flowcell-binding adapters on either end (red and blue in Figure 30B), as well as a known internal sequence for targeted

binding of a common sequencing primer (gold in Figure 30B). These final molecules will differ by cDNA inserts corresponding to different original transcript ends in a strand-specific manner. Fragments derived from different pools will also differ by six base pair barcodes located between an Illumina™ adapter and the sequence primer binding region (black in Figure 30B).

The two strands of these fragments are first melted apart when loaded onto the Illumina™ platform. Individual ssDNA strands are then free to bind to the flowcell by annealing of the short adapter end sequences to oligonucleotides bound to the glass

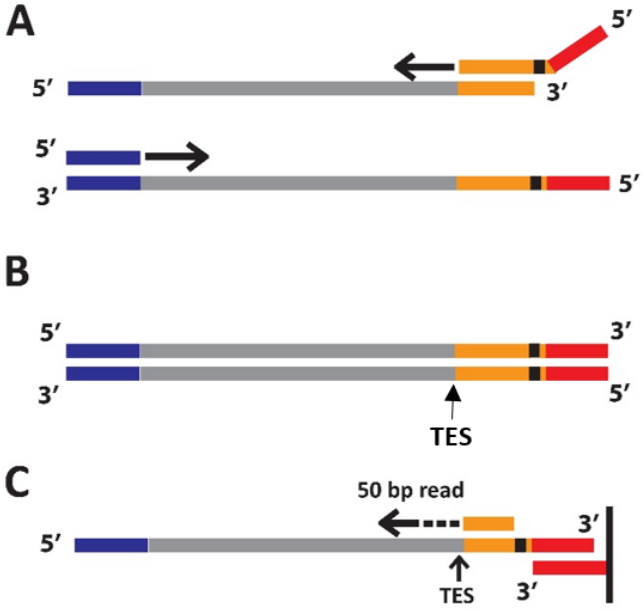


Figure 30. PCR and final sequence analysis **A** PCR is used to amplify the library and attach the final Illumina™ adapter sequence (blue) **B** The final fragment pool contains both adapters (red and blue) and a known sequence (orange) adjacent to the original TES **C** In the flowcell, one strand of the library remains bound to the flowcell (vertical black line) and the read (dotted black line) proceeds from the sequencing primer location

surface (Figure 30C). Cluster amplification via solid-state bridge PCR ensures that each bound fragment has been amplified to cover a large enough area of the flowcell that it can be optically detected when uniform fluorescent nucleotides are first incorporated into each strand in a cluster. This nucleotide incorporation occurs in a stepwise manner such that sequence reads of individual clusters, and therefore of individual fragments in the library, can be generated. Data are output to a text file format for later alignment to the reference genome.

6.6 Methods

For all RNA steps, strict efforts were made to eliminate environmental RNases and to keep RNA samples ice-cold in between incubations. RNA-free™ wipes were used to decontaminate all workplace surfaces and pipettes, paper filter masks were worn to prevent droplet exhalation, and steps were carried out quickly to reduce the chance of spontaneous RNA damage. These steps became less crucial after first-strand cDNA formation, as DNA is less prone to environmental nucleases and spontaneous damage. All oligonucleotide sequences are listed in Appendix D. All steps describe construction of a single library, though several libraries can be made in parallel if desired.

6.6.1 Ribosomal RNA depletion

The starting point for rRNA removal was a total RNA sample eluted into ~25 µl nuclease-free water and stored at -80°C. This sample was verified to have a high quality score (>9 RQN for the parental strain but the RQN was less for RNA-processing gene deletion mutants) and to be free of DNA contamination. It was put through the standard

MICROBExpress™ bacterial rRNA removal protocol (Ambion cat # AM1905, Austion, TX), with the exception that up to 25 µl total RNA was sometimes added to the initial binding mixture. This modification from the stated maximum of 15 µl was needed to process less-concentrated samples and did not have a noticeable effect on RNA removal rates. All samples going into a single replicate of the MICROBExpress™ system were kept in the recommended range of 2-10 µg total RNA input mass. After rRNA removal and ethanol precipitation, each RNA pellet was resuspended in 15 µl nuclease-free water for 15 minutes on ice. This rRNA-depleted sample was then quantified on a Qubit™ 2.0 fluorimeter (Thermo Fisher Scientific cat. # Q32866, Waltham, MA) with the high-sensitivity RNA protocol (cat. # Q32852). These samples were stored at -80°C for later library preparation.

6.6.2 Polynucleotide kinase treatment and 3' adapter ligation

To begin the RNA modification and library preparation part of the protocol, samples were thawed on ice. For each sample, a 20 µl mixture was made in a standard 200 µl PCR tube containing 1-2 µg of rRNA-depleted RNA diluted to 16 µl in nuclease-free water, 2 µl T4 polynucleotide kinase (PNK) 10X buffer, 1 µl 10 mM ATP, and 1 µl T4 PNK enzyme (New England Biolabs cat # MO201, Ipswich, MA) thoroughly mixed in by pipetting up and down. This mixture was incubated in a thermocycler for 30 minutes at 37°C. RNA samples were then purified through RNeasy™ MinElute™ columns (Qiagen cat # 74204, Venlo, Netherlands) and eluted by 12 µl nuclease-free water. Next, another 20 µl reaction was made in a PCR tube containing 10.2 µl PNK-treated RNA, 4.8 µl 50% PEG 8000, 1 µl of 50 µM adenylated Oligo 1.0 (Appendix D), 2 µl AIR™ Ligase 10X buffer,

and 2 µl AIR™ Ligase (Bioo Scientific cat # 512105, Austin, TX). These components were mixed well and incubated in a thermocycler for two hours at 25°C. This RNA-DNA hybrid product was then purified with RNeasy™ MinElute™ columns and eluted in 12 µl nuclease-free water.

6.6.3 First-strand cDNA synthesis

The mRNA ligated to the DNA-adapter (150-500 ng total mass in 10 µl) was then pipetted into a new PCR tube on ice, where 1 µl of 10 µM Oligo 2.0 and 2 µl of a 10 mM dNTP mixture were added. This combined sample was incubated in a thermocycler at 65°C for 5 min and placed back on ice. To this mix was added 4 µl 5X cDNA Synthesis Buffer, 1 µl RNaseOUT enzyme, 1 µl 0.1 M DTT, and 1 µl Thermoscript™ RT enzyme (all from Thermo Fisher Scientific cat # 11146-024). This mixture was incubated in a thermocycler with a program consisting of 60 minutes at 60°C followed by five minutes at 80°C and a final hold at 4°C. This product was purified on a Qiagen DNA MinElute™ column (Qiagen cat # 28004) and eluted in 25 µl nuclease-free water.

6.6.4 Second-strand cDNA synthesis

First-strand cDNA (typically at least 300 ng total mass) was diluted to 34.5 µl in a PCR tube on ice. To this was added 10 µl 5X Phusion™ buffer, 2.5 µl of 10 µM Oligo 3.0, 2 µl of a 10 mM dNTP mix, and 1 µl Phusion™ polymerase (New England Biolabs cat # MO530), then incubated in a thermocycler with the program “3RNAPCR1” (Appendix D). The product from this reaction was purified by repeating the ethanol purification steps found in the MICROBExpress™ protocol used in section 6.6.1.

6.6.5 Exonuclease I treatment and first gel purification

The second-strand cDNA pellet obtained from ethanol precipitation was resuspended in 10 µl nuclease-free water in a PCR tube. To this was added 1.3 µl Exonuclease I buffer and 1 µl Exonuclease I enzyme (New England Biolabs cat # MO293) for a total reaction volume of 12.3 µl. This mixture was incubated at 37°C for 30 minutes. The sample was then subjected to electrophoresis for 60 min at 120 V in a 2% (wt/vol) agarose gel. A gel slice containing the 200-500 base pair region of the sample lane was excised from the gel and purified first by the centrifugation protocol of a Wizard SV gel purification kit (Promega Corporation cat # A9281, Madison, WI). This fraction was then further concentrated with a DNA MinElute™ kit and eluted in a final volume of 10 µl. This sample was quantified on a Qubit 2.0 fluorimeter by the dsDNA high sensitivity protocol (Thermo Fisher Scientific cat # Q32851). Samples typically made up at least 100 ng total DNA mass at this step.

6.6.6 Illumina™ PCR and final gel purification

The second-strand cDNA template (approximately 100 ng) was diluted to 32 µl in a PCR tube and a 50 µl PCR reaction mixture was made by adding 10 µl 5X Phusion™ buffer, 2.5 µl of 10 µM Oligo 3.1, 2.5 µl of 10 µM Oligo 4.X, 2 µl of a 10 mM dNTP mix, and 1 µl Phusion™ polymerase. ("Oligo 4.X" differs between multiplexed samples according to the barcode strategy, see Appendix D). This preparation was mixed well and incubated in a thermocycler using the program "3RNAPCR2" (Appendix D). The blunt-end double stranded PCR product was then purified over a DNA MinElute™

column and eluted into 10 µl. This DNA sample was subjected to gel electrophoresis and purified from the 200-500 base pair gel section by two sequential column methods as described in section 6.6.5, with a final elution volume of 10 µl.

6.6.7 Library validation via TOPO® cloning and Sanger sequencing

The final library was quantified using the Qubit® 2.0 dsDNA High Sensitivity Assay kit (Life Technologies, Thermo Fisher Scientific). Replicates of the protocol were usually found to yield 5-15 ng/µl in 10 µl (50-150 ng DNA total). This is sufficient for Illumina sequencing submission; however, low-throughput cloning and Sanger sequencing was performed to validate library composition before incurring the cost associated with a full lane of Illumina™ sequence analysis. This confirmation was accomplished with the pCR®4Blunt-TOPO® blunt cloning vector (Thermo Fisher Scientific cat # K285). The standard protocol was used except for the fragment capture incubation step, which was extended from 5 to 20 min to account for a low concentration of fragments in the completed library. Complete plasmids were isolated from an *E. coli* host strain and insert sequences were analyzed by sequencing at the MU DNA Core on an Applied Biosystems 3730xl 96-capillary DNA Analyzer (Thermo Fisher Scientific). Transcript ends represented by cDNA segments within the cloned fragments were mapped to the DvH genome in a directional, strand-specific manner with the NCBI Basic Local Alignment Search Tool (BLAST).

6.6.8 Library distribution validation and submission for Illumina™ sequence analysis

The final Illumina™ fragment library was quantified using the Qubit® 2.0 dsDNA high sensitivity assay kit and diluted to a concentration of 10 nM in at least 20 µl. This unit conversion from mass per volume to molarity was performed assuming an average fragment length of 300 base pairs due to the observation that more fragments are closer to the lower limit of 200 base pairs than the upper limit of 500. Multiplexed samples were mixed to achieve equal concentrations of each library and a final overall fragment concentration of 10 nM. These samples and corresponding custom sequencing primers (Appendix D) were sent to the University of Missouri DNA Core for 50 base-pair single-read (SR) sequencing on the Illumina™ HiSeq 2500 platform (www.biotech.missouri.edu/dnacore/illuminaseqservices.html). The samples were sequenced in Rapid Run mode to allow for the use of a custom sequencing primer on only two lanes of the instrument. Sequencing in normal mode would also be possible, but all eight flowcells would then need to contain 3' RNA-seq libraries.

6.7 Results

The sequences of 14 fragments from an early 3' RNA-seq Illumina™ library were determined as described in section 6.6.7. Of these, 12 contained all sequence elements necessary for both amplification on the flowcell and sequencing of a directional transcript-derived insert (Figure 30A). This result indicates a successful proof-of-concept for the library construction method and lends confidence for successful sequencing of similar libraries on the latest Illumina™ HiSeq platform. Further information can be

tentatively inferred from this small sample size of TES-specific sequence reads. This includes information regarding the efficiency of rRNA removal and the proximity of discovered transcript ends to predicted terminator locations. Thus all steps were accomplished that would allow testing of the hypothesis that deep sequencing tools could provide the statistic power to identify complete transcript 3' ends among RNA degradation products and aberrant terminations during synthesis.

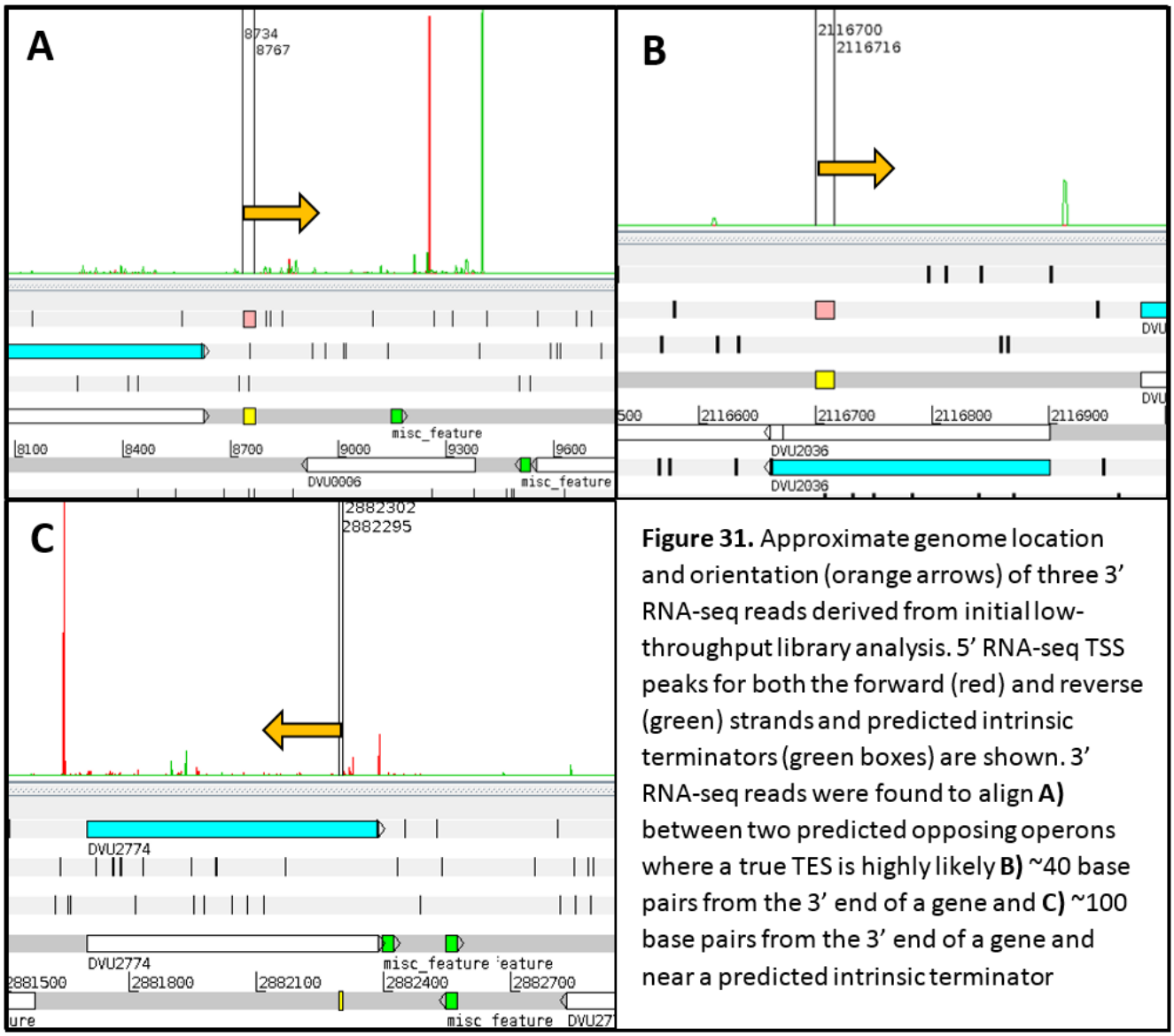


Figure 31. Approximate genome location and orientation (orange arrows) of three 3' RNA-seq reads derived from initial low-throughput library analysis. 5' RNA-seq TSS peaks for both the forward (red) and reverse (green) strands and predicted intrinsic terminators (green boxes) are shown. 3' RNA-seq reads were found to align **A)** between two predicted opposing operons where a true TES is highly likely **B)** ~40 base pairs from the 3' end of a gene and **C)** ~100 base pairs from the 3' end of a gene and near a predicted intrinsic terminator

A high proportion of these initial fragments (9 of 12, or 75%) were found to have transcript-derived insert sequences which map to 16S or 23S rRNA sequences. This prevalence of rRNA-derived fragments was understandable given the very high proportion of rRNA in bacterial cells and the known drop in efficiency of the MICROBExpress™ bead-based removal kit when used in bacteria other than E. coli (*21*). The efficiency of this removal step is likely to increase as the associated protocol becomes more routine in the laboratory. It is also important to note that high hybridization-dependent rRNA removal rates require high RNA quality (*50*), and the early pools analyzed via TOPO™ cloning were generated from lower-quality total RNA samples from tri-phase isolation (RQN 6-8) than those of later pools isolated with the RNeasy™ column-based approach (RQN 9+). Furthermore, the presence of rRNA-derived fragments (and therefore rRNA reads in the final data set) do not directly interfere with results from mRNA-derived fragments. Instead they reduce sequence capacity available for mRNA reads and should be taken into account when determining the number of 3' RNA-seq libraries to combine for sequencing on a single Illumina™ lane.

Of the three insert sequences mapping to predicted mRNA regions, all were oriented in the expected 3' to 5' direction leading away from the Oligo 1.0 junction point which corresponds to an original TES site in the starting mRNA pool (Figure 26). One of these aligned in an intergenic location between two inward-facing predicted operons (Figure 31A). This location is highly likely to represent a true TES location, because a transcription terminator would be needed to prevent excessive antisense transcription which could hybridize and interfere with the transcript of the opposing

operon (*104*). The two remaining TES prediction reads are located within genes, but are oriented in the 3' to 5' direction and are within close proximity to either a gene end (Figure 31B) or a predicted intrinsic terminator (Figure 31C). The locations of these TES within genes is likely a result of this analysis being conducted on a library made from a total RNA sample with an RQN of 7.2. This score corresponds to a sample that has undergone some degradation, and the later use of RNeasy™ columns has improved RNA quality scores for the parental DvH strain. With current isolations routinely providing samples of RQN 9+, it can be inferred that degradation will be lessened and fewer 3' RNA-seq reads will map to locations inside genes.

Given the previously described RNA quality and rRNA removal limitations of this early library preparation, these results were considered sufficient confirmation to proceed with Illumina™ sequencing of a newly prepared library. Even without improvement in these areas, the method was expected to return a very large number of mRNA-derived TES locations. It is quite probable that successful analysis of approximately $1x10^8$ reads will yield useful TES information, and the ease of interpreting these data would depend primarily on the degree of noise resulting from mapping of degraded mRNA ends. Additionally, the significantly improved quality scores of later RNA samples could lead to the ability to multiplex over a dozen 3' RNA-seq libraries on one Illumina™ flowcell, while still maintaining enough read depth to generate genome-wide and library-specific TES consensus sites.

Figure 32. Final library described here vs. an ideal library **A** Completed library fragment described here **B** Ideal final library fragment capable of sequencing on the Illumina™ platform. As shown here, the bottom strands of these fragments will be bound to the flowcell at the start of Read 1

Final 3' RNA-seq libraries were loaded on a total of four Illumina flowcells, with two different sequencing primer orientations in two separate assays (Appendix D). Neither of these approaches were able to generate any sequence data. Further examination of the inner workings of Illumina™ flowcells was carried out. This included determining which strand of DNA is left bound to the flowcell after cluster generation and what end remains bound to the surface, which is proprietary information not provided by the Illumina™ company itself. Ultimately it was determined that the Illumina™ flowcell-binding end adapters, while functional for amplification on the flowcell, were not oriented correctly compared to the primer binding sequence. Simply re-designing the oligonucleotide sequences used to add these sequences would allow them to be placed on the reverse ends of initial adapter-ligated mRNA molecules, thus

correcting this problem (Figure 32). Although such modifications could not be made in time for analysis within the current study, future 3' RNA-seq experiments are possible as long as this change is implemented.

Chapter 7 – Analysis of differential expression by total RNA-seq

7.1 Introduction

While generating a new type of data such as genome-wide location maps of transcript boundaries by simultaneous 5’ and 3’ RNA-seq, it is necessary to verify these data against an established protocol. This comparison was performed previously between 5’ RNA-seq and microarray methods (*110*); however, recent and continuing advances to the throughput of sequencing platforms have largely rendered expression analysis microarray studies obsolete (*119*). Therefore, the current state of the field demands that any new high-throughput transcript analysis technique be compared to the total RNA-seq standard. The three general phases of this technique include RNA isolation, cDNA library preparation, and sequence analysis on the Illumina™ platform. As both this approach and the novel 3’ RNA-seq method describe here rely on identical RNA isolation and sequencing techniques, these variables are eliminate from the comparison of methods. This greatly simplifies comparisons of the methods by isolating the library generation phase itself as the only variable to consider when comparing the new 3’ RNA-seq method to the established total RNA-seq protocol.

The method which later came to be generally known as RNA-seq first appeared in peer-reviewed journals in 2007. The first study, like all those derived from it, aimed to generate complementary DNA (cDNA) by reverse transcription of all transcripts in an isolated RNA sample simultaneously (*66*). This cDNA generation was followed by a library construction method which made transcript sequences available for analysis on a

massively parallel sequencing platform, in this case a polony sequence-by-ligation (SBL) approach (*66*). These sequences were then mapped back to a reference genome and counted on a per-gene basis to obtain relative transcript abundance data for all genes. When comparing RNA samples obtained from mice with different genetic backgrounds, this group was able to identify key transcript abundance changes in particular genes (also known as differential expression between experiments) caused by those genetic differences.

Variations of this early approach expanded on both the range of input RNA samples and the sequencing platform used. Human cell lines (*23, 24*), human tissue samples (*87, 118*) and yeast samples (*94, 131*) were quickly added as options for sequence-based differential expression analysis. Analysis of prokaryotic transcripts by this approach is not fundamentally different from most eukaryotic methods because fragmentation of RNA greatly reduces the impact of poly-A tails on library preparation. Studies analyzing gene expression in bacteria soon followed the early eukaryotic analyses (*27, 100, 103*) and even include analyses of transcript abundance within a single bacterial cell (*120, 121*). Multiple sequencing platforms were also employed, such as 454™ (*123*), SOLID™ (*23, 24*), and early Illumina™ instruments (*92, 94, 119, 131*). Fragment length biases (*123*) and other issues (*87*) with 454™ applications, coupled with the continued total read count deficiencies of the SOLID™ platform, has diminished the use of these sequencing methods over time. The continued rapid expansion of read capacity from Solexa™/Illumina™ 1G to GA platforms, and finally to the current HiSeq

series of instruments, led to widespread adoption of Illumina™ sequencing as the default choice for a variety of high-throughput applications, including total RNA-seq.

Total RNA-seq approaches were found to be generally superior to microarray studies in several ways. Illumina™-based RNA-seq was found to possess greater sensitivity to low-abundance transcripts (*119*) due to its digital counting approach. This allows detection of very low-abundance transcripts which would not be discovered in the analog fluorescent probe setup of microarray techniques. To illustrate this difference, one study detected transcripts from as many as 25% more genes in RNA-seq (*118*). Advantages are also reported in cross-lab portability (*119*), cost, and detection of additional truly differentially expressed genes (*87*). Most importantly in the context of the current comparison to precise transcript boundary mapping techniques, total RNA-seq also provides greater resolution of transcript locations than microarrays (*119*). For these reasons, Illumina™-based RNA-seq using a standard, commercially available library preparation kit was chosen as a means of validating transcript end sites (TES) detected by the novel 3' RNA-seq assay.

7.2 Potential impact of *pnp* deletion on transcript expression

In addition to serving as validation for any data gained from 3' RNA-seq, expression data from total RNA-seq would provide useful information when analyzed alone. Comparison of the DvH strain JW9005 (Δ*upp*, Δ*pnp*::[*kan*]) with the parental strain JW710 (Δ*upp*) allows insight into the role of polynucleotide phosphorylase (PNPase) in mRNA degradation. This enzyme has been previously studied in both *E. coli*

and *Bacillus subtilis* and found to be non-essential for growth in these species, though strains lacking PNPase grow somewhat more slowly than wild-type, particularly at lower temperatures (*34, 130*). PNPase was also found to be more critical for mRNA turnover in *B. subtilis*, likely do to the absence of an RNase II homolog in that species (*97*). The absence of this RNA processing enzyme is the cause for a number of phenotypes in *B. subtilis*, including competence deficiency, tetracycline sensitivity, filamentous growth, and dysregulation of *trp* operon expression (*97*).

A very recent study published by Liu and colleagues used RNA-seq to verify this slight increase in overall mRNA when PNPase is deleted from B. subtilis (*85*). Their RNA-seq method provides increased sensitivity and resolution over previous assays of PNPase function, and reveals a significant polarity effect across transcripts in a small subset (~10%) of mRNAs. They hypothesize that only these transcripts are dependent on PNPase for degradation and that other transcripts not displaying this polarity can be efficiently degraded by other 3' exonucleases, primarily RNase R (*85*). Similar studies have not been carried out in bacterial strains which contain RNase II homologs, such as E. coli and DvH. It is likely that polarity of mRNA decay would be less pronounced in these species compared to *B. subtilis*, because intact RNase II is more capable of compensating for PNPase loss than any other *B. subtilis* exoribonuclease (*130*).

7.3 Methods

7.3.1 RNA isolation and total RNA-seq library preparation with commercial kits

Bacterial culture growth, total RNA isolation, and quality scoring were all performed as described in Chapter 5 of this work. The MICROBExpress™ bacterial rRNA removal protocol (Ambion cat # AM1905, Austion, TX) was performed as described in Chapter 6. 250 ng of the resulting mRNA was used as the input sample for total RNA-seq library construction using the standard NEBNext® mRNA Library Prep Master Mix Set for Illumina® kit protocol (New England Biolabs cat. # E6110, Ipswich, MA). RNeasy™ MinElute™ columns (Qiagen cat # 74204, Venlo, Netherlands) and Axygen MagBeads™ (Axygen Biosciences, Union City, CA) were used for RNA and DNA concentration during this protocol, respectively. An NEBNext® Multiplex Oligos for Illumina® kit (New England Biolabs cat # E7335) was used to add index primers to separate fragment pools and Axygen MagBeads™ were used for the final size selection of sequence-ready fragments.

7.3.2 Sample submission and Illumina™ sequencing

Final Illumina® libraries were quantified using a Qubit™ 2.0 fluorimeter (Thermo Fisher Scientific cat. # Q32866, Waltham, MA) with the high-sensitivity dsDNA protocol (cat. # Q32851). Libraries were diluted to a final combined concentration of 10 nM and submitted to the University of Missouri DNA Core for 50 base-pair paired-end (PE) sequencing on the Illumina™ HiSeq 2500 platform (www.biotech.missouri.edu/dnacore/illuminaseqservices.html).

7.3.3 Alignment of paired end reads to the DvH reference genome

1) **Align reads with Bowtie**

   bowtie2 --threads 4 --no-unal -x <Bowtie 2 index of reference sequence> -1 <.FASTQ input (Read 1)> -2 <.FASTQ input (Read 2)> -S <output SAM file (.MAP)>

2) **Convert from SAM to BAM (binary SAM) format**
   samtools view -bS <input SAM file (.MAP)> <output BAM file (.BAM)>

3) **Sort the BAM file**
   samtools sort <input BAM file (.BAM)> <output sorted BAM file (.BAM)>

4) **Remove duplicate read pairs (PCR duplicates)**
   samtools rmdup <input sorted BAM file (.BAM)> <output sorted, duplicate-free BAM file (.BAM)>

5) **Convert from BAM back to SAM format for importing to Geneious suite:**
   samtools view <input sorted, duplicate-free BAM file (.BAM)> -o <output final SAM file (.MAP)>

Illumina sequence reads were uploaded to the Lewis compute cluster operated by the University of Missouri Bioinformatics Consortium (http://umbc.rnet.missouri.edu/). They were aligned to the reference DvH genome, sorted by genome location, and duplicates were removed as described in the box above.

7.3.4 Differential expression analysis with Geneious™ software

Final sorted, duplicate-free alignments in the SAM file format were input to Geneious (v8) software suite (Biomatters, Aukland, New Zealand) on a standard PC (*61*). These were mapped onto an annotated DvH reference genome (www.MicrobesOnline.org) within Geneious. Expression levels for individual coding sequences (CDS) within each replicate of the procedure were calculated through use of the "Calculate Expression Levels" command. Differential expression was calculated between pools using the "compare transcripts" option of the "Compare Expression Levels" command. This analysis allows output of spreadsheets containing transcript per

million (TPM) values, which are a normalized derivative of reads per kilobase per million (RPKM) (*92*) created to reduce statistical biases in RPKM comparisons (*128*), for all genes. Also output to spreadsheet form are gene descriptions, raw read counts, and p-values corresponding to the statistical significance of differential expression of each gene between the two input conditions.

7.4 Results

7.4.1 Sequencing results

Paired-end sequencing of seven libraries was successful, with greater than 97% of reads passing the on-instrument quality filter in each library. However, one of the JW9005 (Δ*upp*, Δ*pnp*::[*kan*]) replicates (JW9005-3) produced significantly fewer reads than the other libraries (Table 9). One of the libraries (JW710-1) did not belong to the two sets of biological triplicates. Expression data from this library was compared to the libraries grown in triplicate, and similar results were seen as with other parental libraries. However, this preparation was carried out before the others and also has a

Table 9. Library information

Sample name	RNA isolated MM/DD/YY	RNA Quality (RQN)	Quality reads (millions)	Unique reads aligned (millions)
JW710[A]-1	02/13/14	8.5	23	7.9
JW710-2	12/22/14	9.7	33	10.4
JW710-3	12/22/14	9.8	30	11.6
JW710-4	12/22/14	9.7	31	11.7
JW9005[B]-1	4/17/14	7.1	38	14.6
JW9005-2	4/17/14	7.0	40	16.2
JW9005-3	4/17/14	7.0	5.5	2.7

[A] genotype Δ*upp* [B] genotype Δ*upp*, Δ*pnp*::[*kan*]. JW710-1 was not used for comparisons

slightly lower quality score than other parental strains. For these reasons, and for simplicity of analysis, this library was excluded from further comparisons.

7.4.2 Control comparisons among biological triplicates

Biological triplicates corresponding to separate assays of parental and Δ*pnp* strains grown in parallel were compared amongst themselves to examine the degree of noise present in the current RNA-seq assay. Comparisons between replicate parental libraries returned 160 (4.7% of annotated genes) 184 (5.4%), and 208 (6.1%) significantly differentially expressed (DE) genes (Figure 33, Table 10), as measured by transcript per

Table 10. Control and Experimental comparisons

Pools compared	DE genes ($p<0.01$)	% genome DE
Control:		
JW710-2 vs JW710-3	184	5.4
JW710-2 vs JW710-4	208	6.1
JW710-3 vs JW710-4	160	4.7
JW9005-1 vs JW9005-2	62	1.8
JW9005-1 vs JW9005-3	219	6.4
JW9005-2 vs JW9005-3	244	7.1
Experimental:		
JW710-2 vs JW9005-1	1491	43.8
JW710-3 vs JW9005-1	1494	43.9
JW710-4 vs JW9005-1	1499	44.1
JW710-2 vs JW9005-2	1518	44.6
JW710-3 vs JW9005-2	1561	45.9
JW710-4 vs JW9005-2	1545	45.4
JW710-2 vs JW9005-3	822	24.2
JW710-3 vs JW9005-3	826	24.3
JW710-4 vs JW9005-3	826	24.3

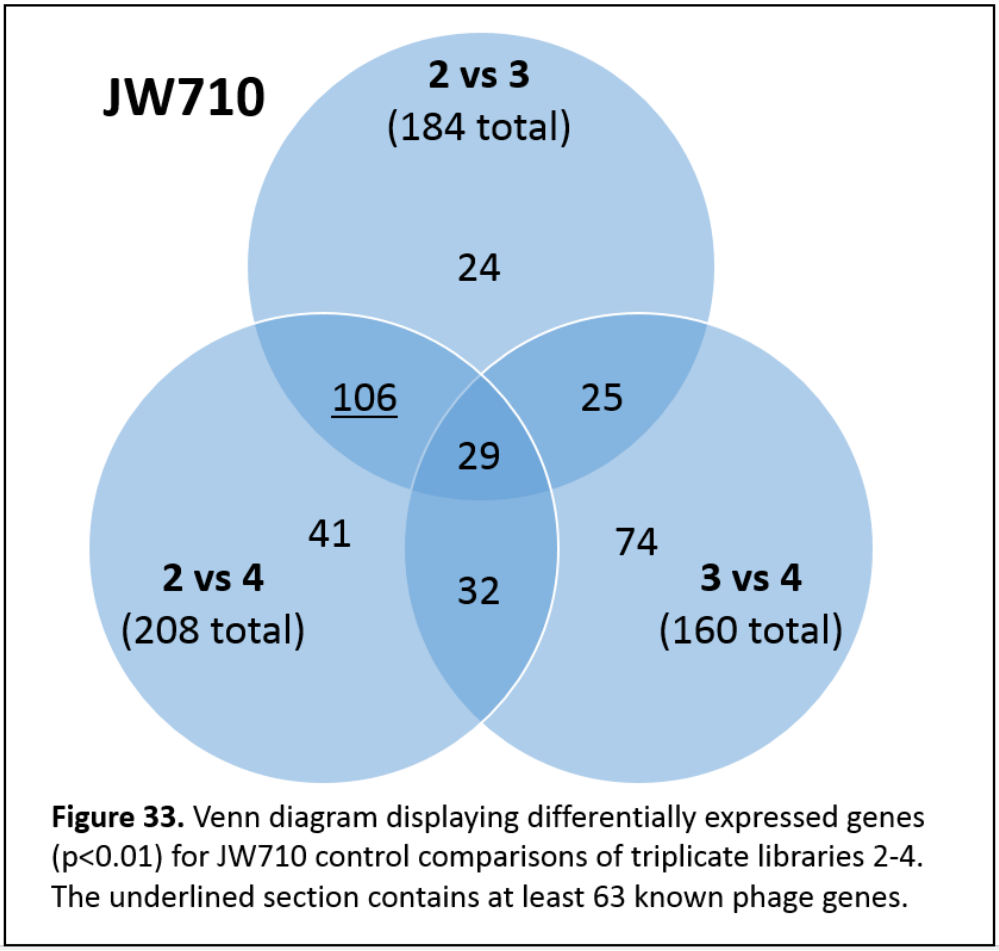


Figure 33. Venn diagram displaying differentially expressed genes (p<0.01) for JW710 control comparisons of triplicate libraries 2-4. The underlined section contains at least 63 known phage genes.

million (TPM) values normalized to the median of gene expression ratios. Significance cutoffs for this comparison required a p-value < 0.01. Using the same requirements, comparisons between Δ*pnp* libraries returned 62 (1.8%), 219 (6.4%), and 244 (7.1%) significantly DE genes (Figure 34, Table 10). Total unique genes appearing in these comparisons are 329 for parental libraries and 284 for Δ*pnp* libraries. These genes show surprisingly little overlap, with only 92 (17.7% of all genes found to be DE in either pool) genes in common between the two overall comparisons (Figure 35). Overall, variation among biological triplicates was observed to be low. This agrees with the general reproducibility of digital sequencing methods in general.

7.4.3 Experimental comparison of parental and Δ*pnp* strains

When parental transcript pools were compared to Δ*pnp* pools, a large portion of the genome was found to be differentially expressed (Table 10). This major expression change is seen in 24-45% of the genome, lending support for PNPase as an integral part of normal mRNA metabolism in DvH. Furthermore, DE rates appear to vary among Δ*pnp* pools. A possible explanation is the varying success of compensatory mutations or regulatory patterns in growing cultures as they overcome the fitness defect conferred by loss of PNPase. Nonetheless, other variables such as read depth cannot be entirely ruled out despite the precautions implemented, and may contribute to these differences. Safeguards against read depth bias include removal of probable PCR

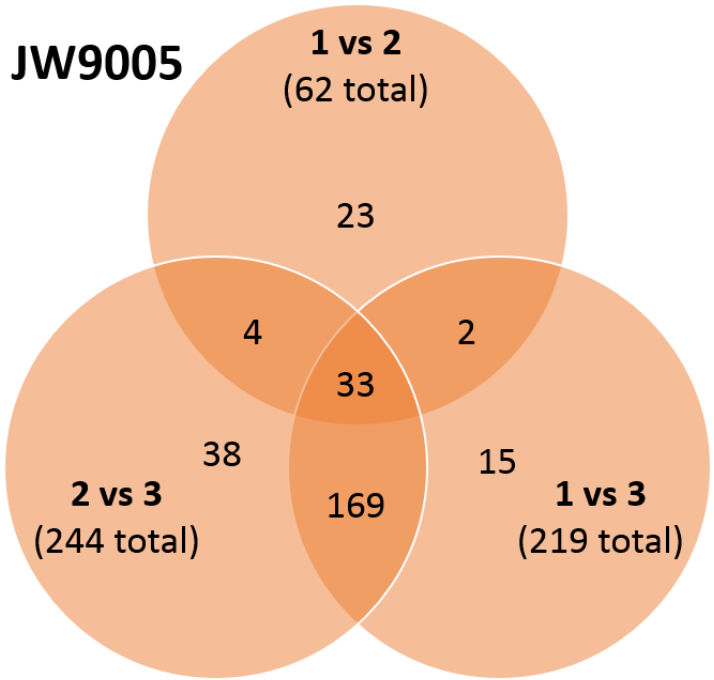


Figure 34. Venn diagram displaying differentially expressed genes (p<0.01) for JW9005 control comparisons of triplicate libraries 1-3. JW9005-3 pool returned significantly fewer sequence reads. No clear pattern in gene types can be determined.

duplicates (read pairs with identical start and stop positions) and use of normalized transcript per million (TPM) comparisons to correct for sequence read differences between samples.

Clear polarity effects across operons were not observed when examining read coverage on a per-gene basis (Figure 36). Gaps between short areas of transcripts are much less prevalent in parental vs PNPase mutant samples, however (Figure 36). This effect is likely related to the lower average quality scores obtained from PNPase mutant cultures, which are impacted by presence of short mRNA degradation products. This irregular transcript presence is possibly a direct result of increased action of the hydrolytic exoribonucleases RNase II and RNase R. This compensation has been observed in *E. coli* (*33*) and DvH contains homologs of genes encoding these enzymes. Endoribonuclease action may contribute to the gaps seen in mRNA, with the resulting

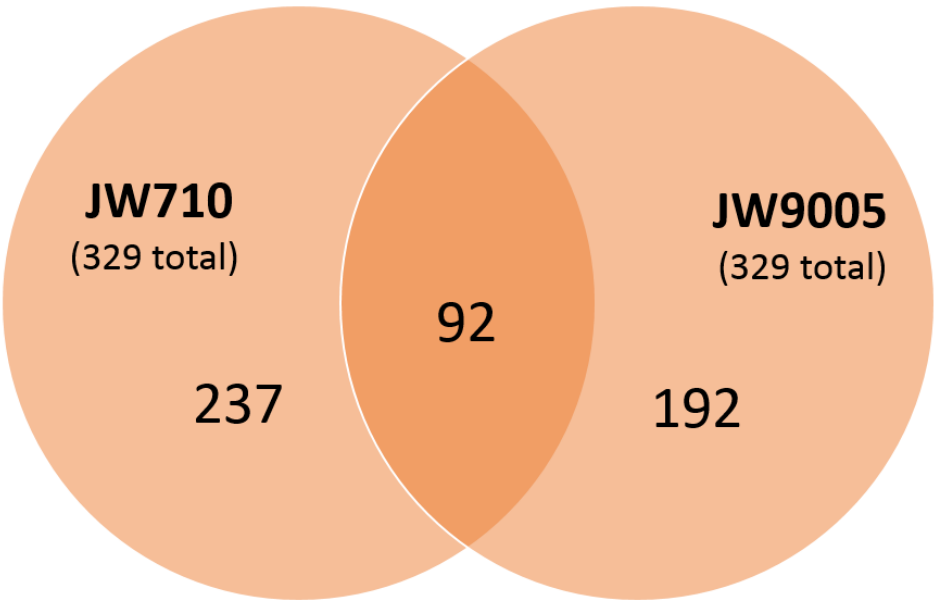


Figure 35. Venn diagram displaying unique differentially expressed genes ($p<0.01$) in common between JW710 and JW9005 analyses

small RNA molecules being degraded more slowly by RNases II and R. Overall, evidence has not been found for strong operon polarity effects in the DvH PNPase mutant, which instead exhibits a more fragmented collection of transcripts evenly spread across operons.

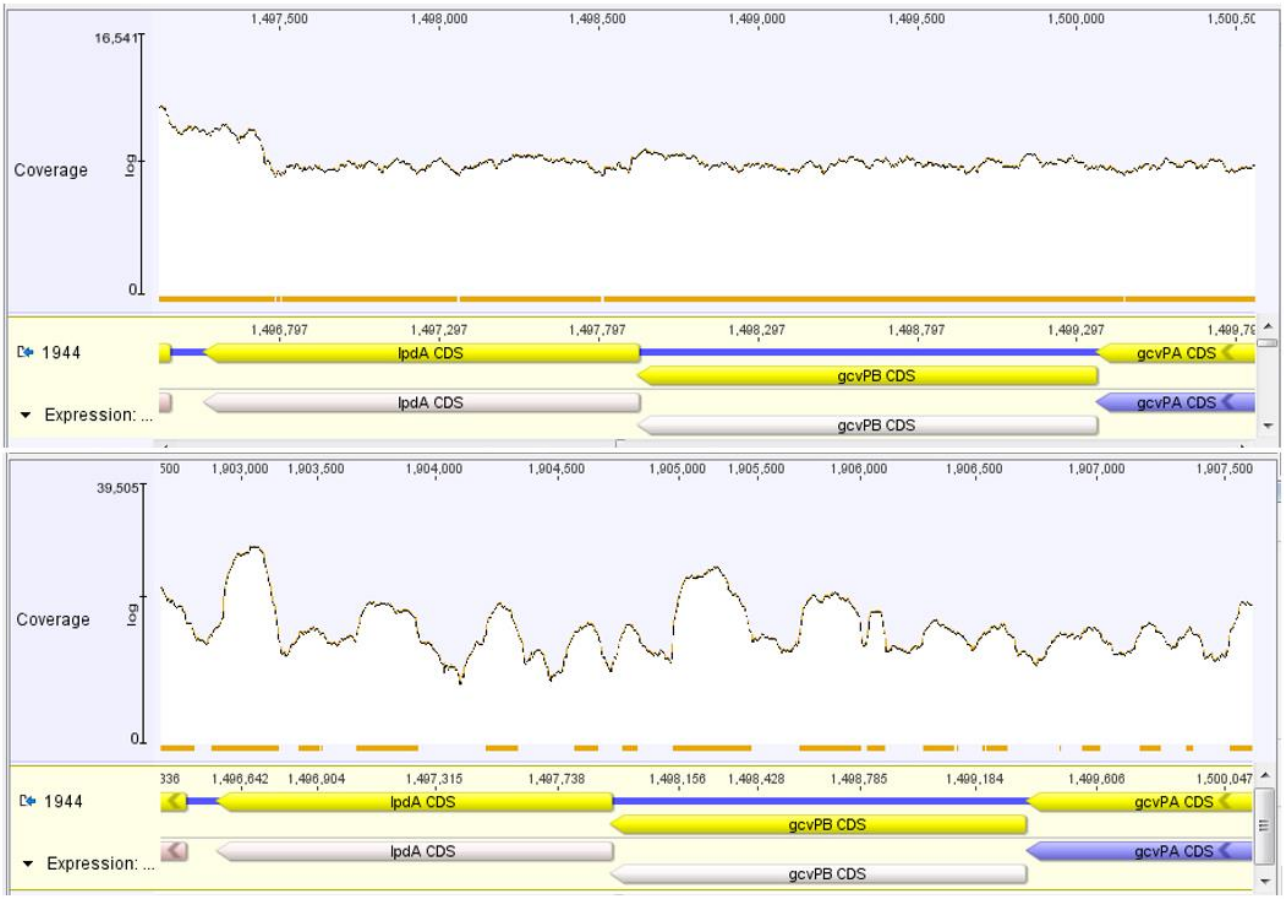


Figure 36. Representative high-resolution transcript abundance in parental and PNPase mutant. Unique read density (white area under the black line) was mapped in pools JW710-2 (top) and JW9005-1 (bottom) for the same segment of the genome.

Chaper 8 –Contributions to the field and future directions

8.1 Contributions to the field

The completed Transposon Liquid Enrichment sequencing (TnLE-seq) technique was the first reported application of the general Tn-seq assay to an anaerobic bacteria, and also the first to carry out all growth in liquid media (*40*) (Appendix E). TnLE-seq was successfully used to probe changes in gene fitness when mutant populations were exposed to nutrient-rich yeast extract and inhibitory concentrations of sodium nitrate (*70*) (Appendix F). It was also used to evaluate the impact of background mutations including the deletion of genes encoding uracil phosphoribosyltransferase (upp) and a redox-sensing regulator (Rex) (*19*). In the case of yeast extract and nitrate additions, TnLE-seq analysis confirmed existing hypotheses regarding these growth medium modifications. The procedure also uncovered new information regarding the Δ*upp* genotype of DvH, suggesting that deficiency in this nucleotide scavenging gene product has a more widespread impact than previously understood. Conversely, very little impact on genome-wide gene fitness was seen in the Δ*rex* redox-sensor deficient genotype as compared to the parental strain. This is likely due to a combination of a lack of overall transcriptional control in environmental bacteria (*111*) and difficulties assaying a transcriptional regulator via Tn-seq.

Much was accomplished to further the pursuit of rapid, high-throughput assay of transcript end site (TES) in bacteria via 3’ RNA-seq. The library preparation protocol was completed successfully as shown by low-throughput analysis, but difficulties concerning

the inner workings of the Illumina™ platform prevented generation of high-throughput sequence reads. Modifications concerning the composition of the final fragment pool were devised, though not implemented in this work. Finally, total RNA-seq data originally meant as a control analysis for 3' RNA-seq provided interesting data on its own. The absence of the PNPase exoribonuclease was found to greatly impact mRNA metabolism in DvH, and some insight into the significance of this enzyme relative to homologs in other bacteria was gained.

8.2 Future Directions

TnLE-seq has been established as a valid means of determining genome-wide gene fitness values in the sulfate reducing bacteria. Little change to the protocol is needed for use in organisms such as *Desulfovibrio alaskensis* G20 and *D. sulfuricans* ND132, and in fact this work is already underway. Modification of the protocol to fit other organisms is possible and dependent on the organism to a large degree. Changes in transposon system, selectable marker, and transposon delivery methods are of key concern when translating this technique to new bacterial species, especially those which lack procedures for many commonly established genetic tools. In particular, the altered physiology of Gram-positive bacteria make high frequency DNA introduction via conjugation challenging. Regardless of changes in transposon delivery system or composition, much information has been gained regarding the liquid enrichment phase established here. This innovation alone should allow wider application of the general Tn-seq approach, while also greatly decreasing time and effort associated with the creation of complex mutant pools.

The future of the 3' RNA-seq procedure is more difficult to determine. New libraries could likely be generated and successfully sequenced to gain some degree of information regarding TES, however the wide-spread appeal of this assay is less clear than for TnLE-seq. Transcript end locations can currently be inferred with varying degrees of accuracy by current techniques including total RNA-seq and microarray studies. Furthermore, new techniques are rapidly becoming available, such as the Isoform Sequencing (Iso-seq™) approach (*2*) developed by Pacific Biosciences for use on their Single Molecule, Real-Time (SMRT®) sequencing platforms. This assay uses full-length transcripts to generate a library of large molecules which are then sequenced to gain reads of 5+ kilobases. Thus TES are precisely determined along with TSS and all other transcript information. Evidence has not been published of Iso-seq™ use in prokaryotes, but the modification required to the protocol is minimal and involves addition of poly-A tails to the 3' end of prokaryotic mRNA.

Total RNA-seq continues to be a dominant approach for assaying differential expression of genes. Ribosomal RNA removal from bacterial samples has greatly improved recently. Experiments in *Salmonella enterica* have shown Ribo-zero™ bead-based removal kit to eliminate many times more rRNA than the MICROBExpress™ kit used here (*8*). This is not expected to directly affect the quality of mRNA assays, but worth noting. Further study of PNPase and related exoribonucleases in DvH is necessary in order to be able to classify the relative function of each, as has been accomplished in *B. subtilis* and *E. coli* (*33*).

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Appendix A – DvH plating technique for accurate CFU counts

This protocol is essential for obtaining accurate CFU counts in DvH. The objective is to allow each individual bacterial cell from the serial dilution of a culture to grow independently on a solid agar plate, ideally forming 10-200 colonies per plate for accurate counting to estimate the starting cell concentration of the diluted culture. Important variables to control throughout the procedure are temperature and redox potential of the agar. DvH cells being plated should never come into contact with medium above ~42°C and multiple different reductants should be present in the medium being used. Although failure to follow one or both of these guidelines may allow growth of some colonies, a percentage may also be rendered unable to grow and thus results will be inconsistent between experiments.

Molten MOYLS4 (containing 15 g agar per L and 1.2 mM sodium thioglycolate) (Zane 2010) was prepared at least 3 hours before plating. One bottle containing 300 ml agar was autoclaved for every three sets of plating triplicates. This allowed extra volume for plating 2-3 lawns of DvH for hydrogen sulfide generation to reduce the other plates. The tops of the bottles were sealed after autoclaving to prevent re-oxidation and placed in a 55°C water bath to cool for at least 1 hour. Bottles of molten MOYLS4 agar and appropriately sized air tight plate boxes (Mitsubishi Gas Chemical cat. #R685025) were cycled into a 34°C anaerobic glove bag and the medium was allowed to cool while preparing serial dilutions of cultures for CFU counts. Eppendorf tubes (1.5 ml) containing 900 ul MOYLS4 liquid medium were prepared for each step in the serial dilution. A culture sample of 100 ul was removed from each dilution tube and pipetted up and down into the first 900 ul of medium. This was repeated for each tube until

reaching the desired dilution ($1x10^{-9}$ was appropriate for the starting DvH culture before conjugation, dilutions for other cultures are listed in the main text).

Before plating, all media bottles were verified to have cooled to approximately 37-40°C and anaerobically prepared titanium citrate was added to the medium to a final concentration of 0.38 mM. Bottles of media were swirled to observe the resazurin indicator change from pink (oxidized) to clear (reduced). Titanium citrate was stored in an airtight bottle even when in a glove bag. Serially diluted culture samples in the amounts described above were pipetted directly into empty, sterile Petri dishes and molten MOYLS4 agar was added to cover the bottom of each dish. Dishes were swirled at least 30 times in a figure-eight motion and allowed to solidify, then all dishes were placed together in an air-tight box. Boxes were sealed and brought out of the glove bag.

Boxes were quickly opened under atmospheric conditions, and the appropriate number of AnaeroPack sachets were added (Mitsubishi Gas Chemical cat #R681001) to the box. An oxygen indicator strip (optional) was added, then the box containing the plates was quickly re-sealed. The DvH cells were suspended in solid agar, so they were able to withstand this brief oxygen exposure, and the AnaeroPack catalyst required oxygen to drive the conversion of oxygen to carbon dioxide. The box was incubated at 37°C for three days, then colonies were counted and CFU/ml calculated based on the degree of original dilution through three sets of triplicates.

Appendix B – TnLE-seq PCR and oligo information

PCR setup[A] for enrichment of Tn-gDNA junctions

Reagent:	**Volume:**
Phusion® HF Buffer (5x)	10 ul
Primer 1.0	5 ul
Primer 2.0 (*add after 2 cycles*)	5 ul
Template DNA	(200 ng)
10mM dNTP mixture	2 ul
Phusion® DNA polymerase	1 ul
dH2O	to 50 ul

[A] Adapted from New England Biolabs NEBNext® protocol (see **Fig S1b**)

Thermocycler program for PCR enrichment of Tn-gDNA junctions

Cycle Step	Temp.	Time (min:sec)
1. Initial Denaturation	*98*°C	00:30
2. Denaturation	98°C	00:10
3. Annealing	66°C	00:30
4. Extension	72°C	01:00
5. Final Extension	72°C	05:00
6. Hold	4°C	indefinite

[A] Steps 2-4 (gray) are repeated twice, then Primer 2.0 is added for an 20 additional cycles.

Primer and adapter sequences for Illumina™ library preparation[A]

Primer:	**Sequence:**
Adapter 2.0 (phos. oligo)	5’- p-GATCGGAAGAGCGGTTCAGCAGGAATGCCGAG[B] -3’
Adapter 2.0 (non-phos. oligo)	5’- ACACTCTTTCCCTACACGACGCTCTTCCGATCT -3’
Primer 1.0 (single oligo, **Adapter 1.0** + Tn-RL27)	5’- **AATGATACGGCGACCACCGAGATCTACAC** AGCCTCTCAAAGCAATTTTGAGTGACACAGGAACACTTAACGGCTGA -3’
Primer 2.0 (single oligo)	5’- **CAAGCAGAAGACGGCATACGAGATCGGT** CTCGGCATTCCTGCTGAACCGCTCTTCCGATCT -3’
Sequencing Primer	5'- CCGAGCTCGAATTCATCGATGATGGTTGAGATGTGTATAAGAGACAG -3'

[A] See Figure S2 for final fragment composition. [B] Colors of sequences correspond to **Fig. S1** and **S2**

Appendix C – TnLE-seq computational pipeline

1) Download resulting FastQ file with raw reads and remove filtered reads with CASAVA v1.8 (available at http://support.illumina.com/sequencing/sequencing_software/casava.ilmn) and standard settings. Output is all reads passing default Illumina quality parameters.
2) Create a Bowtie index of the reference genome using the `bowtie-build` indexer (Langmead et al. 2009).
3) Align filtered reads to this index by running Bowtie v0.12.7 (Langmead et al. 2009) on a compute node cluster. This outputs a `.map` file, in Bowtie format, containing aligned positions of all reads in the genome. Use default settings to allow 2 mismatches in the seed sequence (at the default length of 28 bp):
```
Bowtie <genome index basename> <fastq with reads passing filter> <MAP file (output)>
```
4) Execute `ConvertToBed.jar` from the Vancouver Short Read Analysis (VSRA) Package (Fejes et al. 2008) to convert alignments to BED format (unsorted):
```
java -jar ConvertToBed.jar -aligner bowtie -input <bowtie alignment file> -output
<directory for BED output> -name bed
```
5) Shorten reads to represent only the location of the read's first base by using the custom Perl script `FirstBase.pl` (available online). This provides sharp insertion points that correspond to the single base pair immediately following each transposon insertion in the mutant pool, rather than long 50bp spans that would overlap when visualized later.
```
perl FirstBase.pl <standard BED file> <modified BED file (output)>
```
6) Sort the insertions according to genome position using `SortFiles.jar` from the VSRA Package:
```
java –jar SortFiles.jar bed <directory for sorted output> <unsorted input file>
```
7) Create PEAKS and WIG files from the sorted BED file using FindPeaks.jar within the FindPeaks v4.0 module of the VSRA Package. These files display insertion counts for each transposon location.
```
java –jar FindPeaks.jar –aligner be –dist_type 3 –max_pet_size 100 –input <sorted
BED file> -output <directory for PEAKS and WIG files>
```
8) Execute `PeaksToTab.pl` (available online) to remove duplicate columns and output only peak locations and heights, separated by tabs rather than on separate lines.
```
perl PeaksToTab.pl <PEAKS file> <tab-separated file (output)>
```
9) Execute `ArtCreator.pl` (available online) to arrange the tab-separated file in ART format, which can be read by the Artemis genome browser. This file contains a separate line for every base pair of the reference genome, with values corresponding to the number of insertions mapping to that location. (Genome length is specified within the script)
```
perl ArtCreator.pl <tab-separated file> <ART file (output)>
```
10) Stacked insertions across the genome can now be viewed in Artemis[14], as shown in **Fig 2**, by first opening the reference genome with annotations then selecting "Graph → Add User Plot" from the menu and importing the ART file. Window size should be set to 1 to avoid rounding peaks, and y-axis Min/Max Values can be changed by right clicking in the plot area.
11) Obtain fitness values for all individual genes in list form by executing the following Perl script. This outputs both full-gene fitness values and those trimmed for 5%-85% of the coding sequences. (Again, genome length is specified within the script)
```
perl TnseqFitness.pl <Tab-delimited annotation list (Input 1)> <PEAKS file (Input
2)> <Processed fitness list (TXT)>
```

Appendix D – 3’ RNA-seq oligos and PCR programs

Custom oligonucleotide set for 3’ RNA-seq

Oligo 1.0	5’- /5rApp/AGATCGGAAGAGCGGTTCAGCAGGAATGCCGAGAGA*T/3ddC/ -3’
Oligo 2.0	5’- GATCTCTCGGCATTCCTGCTGAACCGCTCTTCCGATC*T -3’
Oligo 3.0	5’- AATGATACGGCGACCACCGAGATCTACACAGA*TNNNNNN -3’
Oligo 4.X (single oligo with variable barcode)	5’- CAAGCAGAAGACGGCATACGAGATXXXXXX GATCTCTCGGCATTCCTGCTGAACCGCTCTTCCGATC*T -3’
Seq. Primer, Read 1	5’- CTAGAGAGCCGTAAGGACGACTTGGCGAGAAGGCTAGA -3’
Index read primer	5’- GGAAGAGCGGTTCAGCAGGAATGCCGAG -3’
Seq. Primer, Read 1	5’- TCTAGCCTTCTCGCCAAGTCGTCCTTACGGCTCTCTAG -3’

Key

ORANGE – 3’ attachment adapter and complementary sequences

BLUE – Adapter A, for binding and amplification on Illumina flowcell

RED – Adapter B, for binding and amplification on Illumina flowcell

XXXXXX – Barcode, sequence specific to each original library

NNNNNN – Random hexamer

Thermocycler programs

Program “3RNAPCR1”:

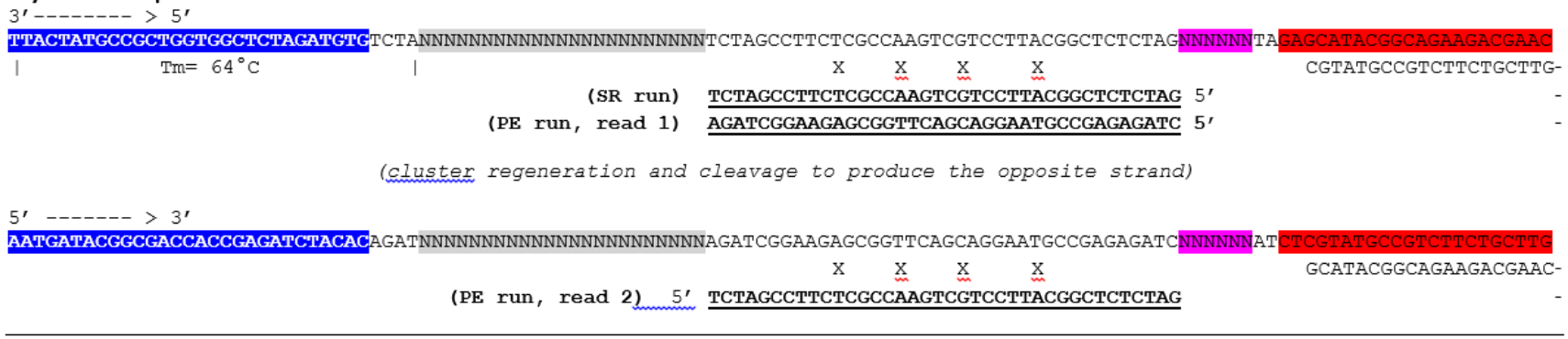
Cycle Step	Temp. (°C)	Time (min:sec)
1. Initial Denaturation	98°C	00:30
5. Final Extension	72°C	05:00
6. Hold	4°C	indefinite

Program “3RNAPCR2”:

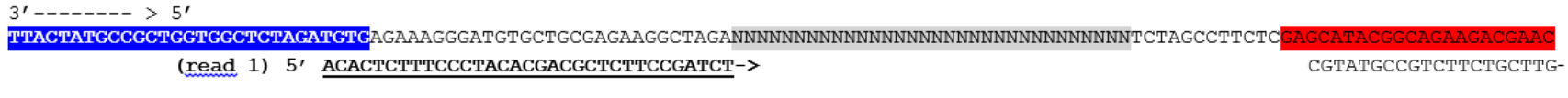
Cycle Step	Temp.	Time (min:sec)
1. Initial Denaturation	98	00:30
2. Denaturation	98	00:10
3. Annealing	66	00:30
4. Extension	72	01:00
5. Final Extension	72	05:00
6. Hold	4	indefinite

BLUE – Universal Adapter, for binding and amplification on Illumina flowcell
RED – Indexing Adapter, for binding and amplification on Illumina flowcell
PINK – Barcode, six nucleotides specific to each library mixed on a single flowcell
GREY – Insert sequence (derived from original transcript)
UNDERLINED – Sequencing Primer

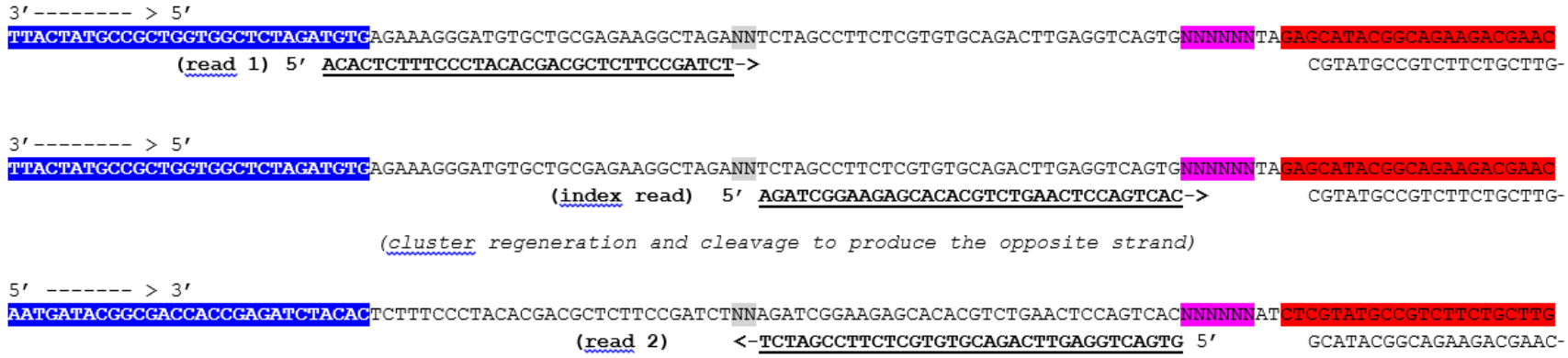
My 3' RNA-seq:



Established 5' RNA-seq (no multiplexing strategy):



Standard Illumina fragment:



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Rapid Transposon Liquid Enrichment Sequencing (TnLE-seq) for Gene Fitness Evaluation in Underdeveloped Bacterial Systems

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Whole-genome fitness analysis in microbes that uses saturating transposon mutagenesis combined with massively parallel sequencing (Tn-seq) is providing a measure of the contribution of each gene to a given growth condition. With this technique, gene fitness profiles and essential genes are discovered by simultaneous analyses of whether the absence of each gene product alters the growth kinetics of the bacterium. Here we modify the standard Tn-seq procedure to simplify and shorten the process by including delivery of the transposon through conjugation and liquid culture enrichment of the mutant pool, creating transposon liquid enrichment sequencing (TnLE-seq). To illustrate the success of these modifications and the robustness of the procedure, analyses of gene fitness of two cultures of the strictly anaerobic bacterium *Desulfovibrio vulgaris* Hildenborough were performed, with growth on lactate as the electron donor and sulfate as the electron acceptor. These data demonstrate reproducibility and provide a base condition for analysis of fitness changes in deletion mutants and in various growth conditions. The procedural modifications will facilitate the application of this powerful genetic analysis to microbes lacking a facile genetic system. Pilot studies produced 2.5×10^5 and 3.4×10^5 unique insertion mutants in the anaerobe *Desulfovibrio vulgaris* Hildenborough grown under typical laboratory conditions in rich medium. These analyses provided two similar high-resolution maps of gene fitness across the genome, and the method was also applied to growth in minimal medium. These results were also compared to the coverage obtained with a ca. 13,000-member cataloged transposon library constructed by sequencing transposon insertion sites in individual mutants.

The complement of enzymes expressed in cells is predicted to change in response to physical and chemical circumstances. The goal of much research is to understand which proteins change, why and how they change, and what the consequences of the changes are. Once understood, this information is expected to lead to an ability to manipulate enzyme levels for predicted outcomes. However, tools for quantification of global gene expression levels and transcriptomic or proteomic analyses have biological or technical limitations that prevent direct correlations between expression levels and survival and growth during environmental challenges (1). To obtain a more direct readout of the contribution of gene function, a massively parallel mutant analysis method, saturating transposon mutagenesis combined with massively parallel sequencing (Tn-seq), has been developed for assaying microbes (2–7). Random transposon mutants in a pool of sufficient size to ensure representative mutants of all nonessential genes are subjected *en masse* to a growth treatment. Mutants in which genes are inactivated that are essential or beneficial to the microbe under the chosen conditions are lost or recovered at lower-than-average frequency. The presence and number of mutants are determined by deep sequencing of the DNA regions flanking the transposons. Aliquots of a single pool can be used to compare gene fitness changes in response to multiple environmental conditions.

With sequencing costs decreasing, complete genomes are rapidly being assembled from a variety of natural and laboratory samples. However, the ability to assign a biological function to individual genes has been lagging behind their raw discovery (8). To bridge this gap, Tn-seq has become a powerful means of characterizing genes important to survival of pathogenic microbes under various host conditions (9). This approach has seen relatively limited use outside easily grown enteric species. Additionally, complex soil populations have shown preferential growth of a single species as a result of a chemical or physical stress (10). Tn-seq may be extended to characterize these ecologically responsive microbes by linking fitness value changes in specific genes to the stress condition.

Desulfovibrio vulgaris Hildenborough (DvH) is a Gram-negative, obligately anaerobic soil bacterium and a model organism for the sulfate-reducing bacteria (SRB). The electroporation yield of transformants in DvH is $<10^3$ per 3×10^{10} wild-type (WT) cells in a single cuvette. This low yield of transformants makes electroporation an arduous method of mutagenesis, as hundreds of transformations would be required to generate genome-saturating quantities of transposon mutants. Additionally, manipulation of DvH cultures must be carried out in an anaerobic chamber to avoid oxygen exposure and surface plating for transposon selection increases the risk of accidental exposure. The comparatively low growth rate of DvH is also an important factor when applying a technique developed in aerobic bacteria capable of robust growth.

Despite these culturing challenges, gene annotation in DvH is relatively advanced and genetic tools are available. These include

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TABLE 1 Population tracking by colony counts, performed throughout mutant generation and enrichment phases

Function	Strain	Feature(s)[a]	Colony count (CFU/ml)[b]		
			Preconjugation	Postconjugation	24-h culture[c]
Donors	BW29427 (pRL27)[d]	DAP^-, Tra^+, Km^r	7.3×10^8	8.8×10^6	1.5×10^5
Recipients	*D. vulgaris*	WT, Km^s	1.3×10^9	3.1×10^9	4.4×10^6
Exconjugates	*D. vulgaris*::TnRL27	Km^r	0	5.2×10^5	5.0×10^6

[a] Dap^- mutants require diaminopimelic acid for growth. Tra^+, carries genes for plasmid mobilization by conjugation; Km^r or Km^s, resistance or sensitivity to kanamycin or G418.
[b] Colony counts were quantified in triplicate by serial dilution and growth of organisms at 37°C on surfaces (*E. coli*) or by adding organisms to agar while the agar was molten and pouring the reaction mixture into plates so that CFU formed within the agar (*D. vulgaris*). Plates were supplemented with 400 μg G418/ml, 50 μg kanamycin/ml, and/or 90 μM DAP where necessary.
[c] These cultures were first diluted from postconjugation cultures at a 1:33 ratio, and the enrichment-growth-phase analysis was performed with G418 and without DAP (to select for exconjugates and against donors, respectively).
[d] *E. coli* strain with donor plasmid; genotype, *thrB1004 pro thi rpsL hsdS lacZ*ΔM15 *RP4-1360*Δ(*araBAD*)*567* Δ*dapA1341*::[*erm pir* (wt)].

high-resolution microarrays (11, 12), transcript start site information (13), affinity-tagged proteins (14), markerless deletion mutants (15), and an isolated library of over 1.2×10^4 individually maintained transposon mutants with known unique insertion sites (http://desulfovibriomaps.biochem.missouri.edu/mutants/). The availability of these tools for confirmation of gene fitness information, combined with the impracticality of employing preexisting Tn-seq methods (2–5) for analysis of DvH, makes it a challenging proof-of-principle organism for the establishment of this technique. Any such protocol adapted for successful use in DvH would have the advantage of being immediately available for a much wider range of anaerobic and/or environmentally relevant bacteria.

Our objective here was to relax the requirements of the traditional Tn-seq procedure to facilitate analysis of a wider range of isolates. This advancement is strongly tied to a combination enrichment/competition phase carried out entirely in liquid culture, resulting in *tra*nsposon *li*quid *e*nrichment *seq*uencing (TnLE-seq). Overnight production of genome-saturating quantities of transposon mutants by a single researcher is made possible through conjugal transfer of a transposon delivery plasmid from an *Escherichia coli* donor. Additional variables associated with freezer storage and maintenance of a library can be eliminated, because the genome is saturated with insertion mutants in each conjugation. Decreases in library generation time and material costs allow more conditions to be sampled. The increased sampling generates well-defined "standard" profiles with reduced noise against which profiles from new growth conditions can be compared to identify conditionally important genes and gene networks.

MATERIALS AND METHODS

Strain information, mutant generation, and media. Throughout the protocol, wild-type DvH carrying the pDV1 native plasmid (ATCC 29579) (16) was grown in rich liquid MOYLS4 (17) medium or plated on the same medium solidified with agar for CFU counting. The conjugative donor *E. coli* BW29427 (18) (also known as WM3064), a diaminopimelic acid (DAP) auxotroph, was used as a host strain that could later be eliminated through growth in the absence of DAP. BW29427 was transformed via the Invitrogen OneShot TOP10 transformation protocol (Life Technologies, Grand Island, NY) with the mobilizable plasmid pRL27 (19), the delivery vector for the Tn-RL27 transposon. Transformants were selected on solidified LC medium (17) (components per liter of medium, 10 g tryptone, 5 g sodium chloride, and 5 g yeast extract) supplemented with 50 μg kanamycin per ml and 90 μM DAP. To prepare the *E. coli* conjugational donors, single colonies of *E. coli* transformants were inoculated into 5 ml LC–Kan–DAP for overnight growth at 37°C with shaking at 200 rpm. A sample of 400 μl from this culture was transferred to 10 ml LC–DAP in a 125-ml flask and grown for 4 h at 37°C with slower shaking (100 rpm) to preserve conjugative pili.

Conjugations were carried out in a 34°C Coy anaerobic chamber (Coy Laboratory Products, Grass Lake, MI) with an atmosphere of a 95:5 N_2:H_2 gas mix. Five 25-mm-diameter nitrocellulose membranes (pore size, 0.22 μm) were arranged on the surface of a 90-mm-diameter MOYLS4 agar plate that had been allowed to dry to ensure that liquid could be absorbed quickly through the membranes. Each of the five membranes was spotted with a 100-μl cell mixture in MOYLS4, which contained resuspended cell pellets from 1.5 ml *E. coli* (from the 4-h, 100-rpm culture) and 3 ml DvH (early-stationary-growth-phase cells in MOYLS4). Membranes were incubated for conjugation in the chamber overnight.

Mutant recovery and enrichment and collection of final bacterial pool. In the anaerobic chamber, each membrane from the overnight conjugation was placed into 3 ml MOYLS4 in a 5-ml tube. Cells were removed from membranes by agitation and allowed to recover for 4 h. Postconjugation cultures (15 ml total) were combined and diluted at a 1:33 ratio to a final volume of 500 ml MOYLS4–400 μg G418 (a kanamycin analog) per ml, without DAP and with 0.38 mM titanium citrate added to lower the redox potential of the medium. This combined culture was grown to an optical density at 600 nm (OD_{600}) of 0.40 to allow DvH exconjugants resistant to G418 an opportunity to outcompete wild-type DvH. Such growth was completed in about 24 h under these standard conditions, and cultures were still in the exponential-growth phase at that time. Doubling times of mutants were determined to be approximately 8. The culture was then removed from the anaerobic chamber, and cells were harvested by centrifugation at 3,696 × *g* at 4°C for 12 min. Cells were washed twice with 25 ml MOYLS4 medium. The MOYLS4 used for washes was autoclaved the day of use and sealed to minimize oxygen absorption. The final cell pellet was resuspended in 1.5 ml of MOYLS4 medium. Ambion Turbo DNase (Life Technologies) (15 μl) and the enzyme buffer (170 μl) were added, and the mixture was incubated at 37°C for 30 min to digest extracellular DNA. After addition of 15 μl fresh Turbo DNase, the exconjugant cells were incubated a further 30 min. Cells were again collected by centrifugation, and the supernatant was discarded. The pellet was resuspended in 500 μl MOYLS4 medium, incubated at 75°C for 10 min to inactivate DNase, and then frozen in aliquots at −20°C for later genomic DNA (gDNA) extraction. All steps from conjugation through pellet freezing were accomplished in 5 days, with the exception of the time needed to quantify the DvH CFU. CFU of donor *E. coli*, wild-type DvH, and DvH resistant to G418 were recorded by serial dilution and plating at three time points: (i) immediately before conjugation, (ii) following membrane recovery, and (iii) at 24 h, when cultures were harvested for genomic DNA (gDNA) isolation and DNA fragment pool preparation (Table 1). Initial transposon incorporation occurred in DvH with a frequency of about one event in 6×10^3 wild-type cells. After dilution and liquid selection to grow transposon mutants while inhibiting wild-type DvH and *E. coli* growth, the final ratio of wild-type to mutant DvH was approximately 1:1.

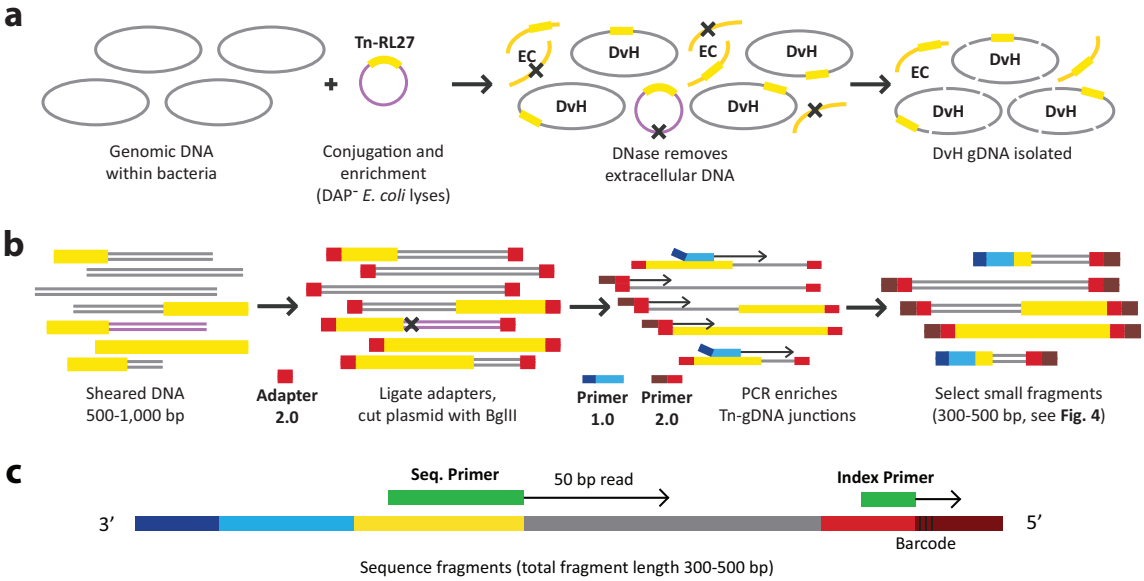

FIG 1 Summary of TnLE-seq workflow for each condition tested. All steps may be performed in parallel with other conditions or background mutant strains. (a) *In vivo* culture phase. DvH DNA remains in cells until the final gDNA isolation step. (b) *In vitro* library preparation phase. BglII cuts 11 bp from the end of Tn-RL27 in the donor plasmid to eliminate PCR amplification of plasmid sequences and cuts 134 times in the DvH genome. (c) Sequencing (Seq.) arrangement.

Preparation of parallel mutant pools. The procedure described above can be expanded to produce multiple mutant pools in parallel by increasing the number of conjugation membranes and enrichment cultures. In order to eliminate the effect of possible variation in conjugation efficiency among membranes, it is important to combine all exconjugants in a proportionately larger culture before taking aliquots for individual pools. Each of these pools of mutants can be diluted into a different experimental medium as described above. The remainder of the protocol proceeds with DNA manipulation of individual pools in parallel, and each ultimately provides a separate fitness profile for the genome. Multiple pools can later be analyzed on the same Illumina lane though use of separate, barcoded Adapter 2.0 sequences (see Table S1 in the supplemental material) with an index sequencing cycle to identify these barcodes (Fig. 1). This process allows rapid, genome-saturating levels of unique insertion mutants across multiple experiments and eliminates the need to freeze away a single mutant pool for growth in future experiments. Therefore, additional selection pressures associated with growing a bacterial population from a frozen sample are avoided.

DNA isolation, fragmentation, and size selection. The final enriched cell pellet from a 500-ml DvH transposon mutant pool was frozen, ready for immediate DNA extraction, library construction, and sequencing. The pellet was thawed at room temperature and gDNA purified with the Gram Negative Bacteria protocol of a Wizard genomic DNA purification kit (Promega Corporation, Madison, WI). Cells were not spun before step 1 of the Wizard protocol; instead, 6 ml of nucleus lysis solution was added directly to the thawed pellet and mixed by pipetting. DNA was recovered according to the Promega Wizard protocol and then rehydrated in 1 ml elution buffer and left at room temperature overnight. DNA concentration was quantified by a NanoDrop (Thermo Fisher Scientific, Waltham, MA) assay. The DNA was diluted to 600 ng/μl, divided into 200-μl aliquots, and fragmented to 500 to 1,000 bp on a Bioruptor standard UCD-200 sonication device (Diagenode, Inc., Denville, NJ). Multiple trials were performed to establish sonication parameters, with the final DNA pool containing 500- to 1,000-bp fragments that were verified by electrophoresis on an agarose gel. After verification, ≥240 μg of fragmented DNA was subjected to electrophoresis on a 2% (wt/vol) agarose gel and the 500- to 1,000-bp band carefully excised. Clean equipment and buffers were used to avoid DNase contamination, and bacterial gDNA to be sequenced was not exposed to UV light during gel excision. Extraction and purification of DNA from the gel slice employed a Wizard SV gel and PCR clean-up system (Promega; centrifugation protocol). The resulting products were purified by application of the standard protocol in a MinElute PCR purification kit (Qiagen, Valencia, CA) to concentrate fragments and eliminate residual ethanol.

Preparation of Illumina fragment library. Purified DNA fragments were diluted such that 5 μg DNA was dissolved in 85 μl MinElute EB buffer (Qiagen). Illumina Adapter 2.0 was created by incubating a mixture of the two Adapter 2.0 oligonucleotides (10 μM each; see Table S1 in the supplemental material) at 70°C for 1 min followed by 39.5°C for 5 min. This double-stranded adapter was attached to the 500- to 1,000-bp fragments by the use of a NEBNext DNA Sample Prep kit as described for the End Repair, dA-Tailing, and Adapter Ligation modules. The fragment pool was digested with BglII (a 6-bp recognition endonuclease with fewer than 150 sites in DvH) for elimination of residual pRL27 which would yield uninformative sequences. Free adaptors and small DNA fragments were eliminated by gel purification. The gel slice containing fragments of 500 to 1,000 bp was excised, and this DNA was isolated. PCR amplification was carried out to enrich Tn-gDNA junctions among DNA fragments and to add Adapter 1.0 (Fig. 1) for cluster generation for Illumina sequencing. PCR parameters (see Tables S2 and S3 in the supplemental material) were designed to amplify the fragment pool from transposon ends preferentially. Products were purified with a final gel electrophoresis and excision procedure, retaining Tn-gDNA junctions in fragments in the 300- to 500-bp range. The reduction in fragment isolation length from 500 to 1,000 bp in the PCR input to 300 to 500 bp in the output further enriches the pool for junction-containing fragments (Fig. 1). This occurs because average junction-containing fragments anneal to Primer 1.0 (Table S1) near the center of the fragment and shorten the resulting amplification product, while fragments annealing only with Primer 2.0 retain their full length. Initial Sanger sequencing of a sample of the enriched library (data not shown) indicated that ≥30% of the DNA fragments would be amplified on the Illumina flowcell and that an accurate junction location would be mapped to the published DvH genome from sequences of these fragments (16).

Sequencing. The final fragment pool, containing at least 30 ng DNA and the Illumina sequencing primer (Fig. 1; see also Table S1 in the sup-

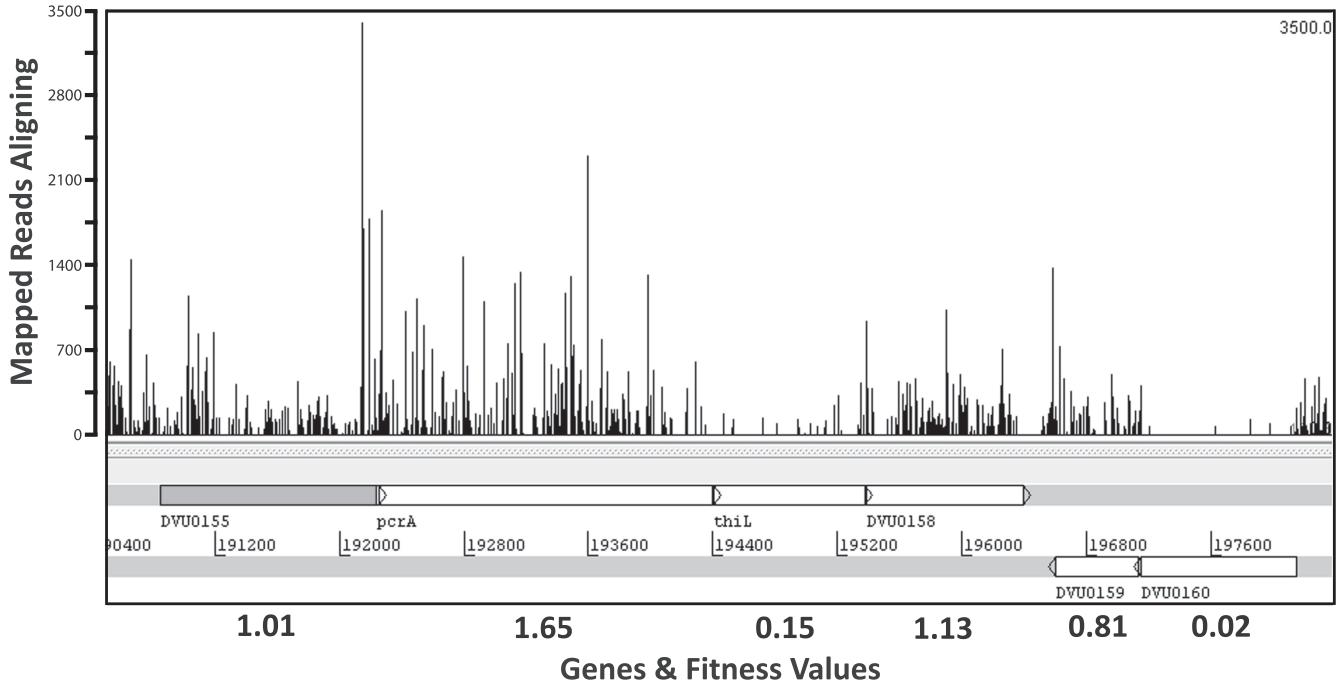

FIG 2 Artemis screenshot of mapped insertions across multiple operons. Predicted genes are shown as gray or white boxes with arrows. Vertical black lines represent insertion points, with height corresponding to the number of reads mapped uniquely to that location by the Bowtie aligner. Numbers below the screenshot indicate relative fitness values calculated for the pictured genes.

plemental material), was submitted for sequencing on an Illumina HiSeq 2000 platform. The sample was quantified precisely by Life Technologies Qubit 2.0 Fluorometer analysis, examined on an Agilent 2100 Bioanalyzer to quantify fragment length distribution, and diluted according to quantitative PCR (qPCR) results determined with a KAPA Biosystems Library quantification kit. Our fragment pool was loaded on a single flowcell lane at 12 pM with 50-bp single-read settings. For read processing and alignment, see Box S1 in the supplemental material.

Fitness determination and statistical analysis of data. The initial test of the protocol consisted of a single mutant pool resuspended from conjugation membranes and grown with MOYLS4 medium for 8 doublings under standard laboratory conditions. This enriched pool was sequenced without multiplexing. This analysis yielded an average of one insertion per 14 bp of the genome, allowing gene-level analysis of the fitness consequences imposed by transposon interruption. To eliminate peripheral insertions that might not disrupt gene function, fitness was calculated for each annotated gene from transposon mutants only in the 5% to 85% region of the coding sequence (3). Briefly, fitness values for genes were calculated by dividing the total number of transposon insertions in the gene by the length (in base pairs) of the 5% to 85% region of the gene (below). This value was normalized to the genome average by dividing it by the average number of insertions per base pair in the 5% to 85% regions of all nonessential genes in the genome according to the following equation:

$$\text{Fitness} = \left(\frac{\#\text{ insertions in gene}}{\text{length of gene}}\right) \Big/ \left(\frac{\#\text{ insertions in all genes}}{\text{length of all genes}}\right)$$

We assumed t_0 for mutant numbers to occur at recovery from conjugation membranes. Our standard outgrowth of ~8 doubling times provided a reproducible benchmark transposon insertion array for lactate/sulfate medium.

The distribution of gene fitness values for each pool is bimodal, with modes corresponding to the essential model at 0 and the nonessential model at 1 (Fig. 2). The probability of each gene being associated with these modes was calculated by an established method used in previous Tn-seq experiments (2, 6). Each of these modes was fitted to a gamma distribution with EasyFit Professional version 5.5, and cumulative probability curves were calculated for each of the two conditions based on the observed gene fitness values (see Fig. S1 in the supplemental material). Genes were called essential if they were at least four times more likely to be essential according to the essential model than according to the nonessential model. The reverse reasoning was used to determine nonessential genes. Genes between these cutoffs could not be associated confidently with either model. The first TnLE-seq pool returned 553 essential genes, 67 that could not be called, and 2,782 nonessential genes. This is a very conservative cutoff parameter, and the essentiality of some genes is not absolute.

Protocol repetition and TnLE-seq analysis of growth in minimal medium. The entire protocol procedure was repeated five times, and these pools were tagged with barcodes within Primer 2.0 to allow multiplexing via pooling of the five libraries on one Illumina HiSeq 2000 lane. One of these libraries represented a biological replicate of the initial library, while another represented growth in medium lacking yeast extract.

RESULTS AND DISCUSSION

To determine the feasibility of selection and enrichment of mutants for gene fitness values in liquid culture, a genome-saturating pool of random transposon mutants of DvH was generated and enriched by growth in lactate/sulfate medium supplemented with antibiotic. DNA was extracted and prepared for Illumina sequencing. The completed DNA fragment libraries were analyzed via single-end sequencing for later alignment to the reference genome and determination of fitness. From the first data set, 1.29×10^8 50-bp reads passed the quality filter of the sequencer (see Box S1 in the supplemental material for all software and version information) and were used as a starting pool for data analysis. By application of the default parameters of the Bowtie aligner (20), 4.80×10^7 (37.2%) reads aligned to the DvH reference genome, which

TABLE 2 Summary of Illumina read alignment and genome coverage

Sequencing lane	Growth medium (date)	No. of 50-bp reads passing quality filter	No. of DvH reads aligned[a]	% DvH reads	No. of unique insertions	Avg. bp per insertion[b]
1	MOYLS4 (November 2011)	128,794,198	47,957,241	37.2	274,488	13.7
2A[c]	MOYLS4 (September 2012)	37,881,964	30,539,030	80.6	343,075	11.0
2B[c]	MOLS4 (September 2012)	42,035,071	14,209,954	33.8	190,430	19.8

[a] All alignments were performed with default Bowtie 2 parameters (see Box S1 in the supplemental material for read processing details).
[b] Data were determined on the basis of the *D. vulgaris* Hildenborough genome size of 3,773,159 bp.
[c] These libraries were sequenced together with three others on one Illumina lane. The total number of reads aligned for this lane was 126,470,203, or 71.5% of all reads passing the quality filter from the lane.

included the native plasmid pDV1, and were visualized by an Artemis Genome Browser (Fig. 2) (21). A total of 3.17×10^7 (24.6%) reads aligned to *E. coli* MG1655, and 7.15×10^6 (5.6%) aligned to the donor plasmid, pRL27 (Table 2). There were 5,838 reads aligning ambiguously to both the DvH and the *E. coli* genomes, with the vast majority (99.2%) of these being found in highly conserved rRNA or tRNA sequences. A total of 2.74×10^5 unique transposon insertion sites were found in DvH DNA, corresponding to an average coverage of one insertion per 13.7 bp of the genome and an average sequencing depth of 175 reads per insertion site. An additional 1.56×10^7 (32.6%) reads were not aligned to any of these references due to small (1- to 3-nucleotide [nt]) sequence mismatches and/or the presence of adapter sequence in the read. This set contained proportions of DvH, *E. coli*, and plasmid reads similar to those of the successfully aligned set.

By comparison, the subsequent multiplexed samples showed improvements in both sequencing and alignment efficiency. These replicates displayed a modest increase in total quality reads (1.37×) and a significant increase in percent reads aligning to DvH (1.92×), allowing an average of 2.5×10^7 reads aligned to DvH in each of the five multiplexed pools for a total of 1.3×10^8 reads (Table 2). The rich-medium and minimal-medium multiplexed pools yielded average sequencing depths of 89 and 75 reads per insertion site, respectively. This coverage was more than adequate to assign gene fitness values by the same approach as that used with the original unmultiplexed pool.

This sequencing depth, coupled with a precise control over population doublings from the time of transposon incorporation, allowed identification of genes across the full spectrum of fitness contributions (Fig. 3). Thus, our data set showed improvement over data determined by previously published techniques that were unable to distinguish between essential genes and those that were expendable but conferred a very significant fitness disadvantage (2–5). Due to the well-characterized random insertion properties of the Tn-RL27 system (19), insertions were observed in high abundance across the genome. Insertion frequency was remarkably consistent across the genome except where insertion in essential genes produced a lethal mutation and prevented cell survival or replication. Though sequencing immediately following conjugation was not feasible due to a low ratio of mutant cells to wild-type cells, the insertion frequency and consistency allow this time point to serve as a starting point for determination of the fitness of the final pool. Polar effects within operons, while possible, were not observed, as many operons contain recovered mutations in nonessential genes upstream of apparent essential genes (Fig. 2). Although insertion of multiple copies of Tn-RL27 in a single bacterium is also possible, the low rate of recovery of transposon mutants, 10^{-3} to 10^{-4} per recipient cell, would cause the occurrence of multiple transposition events to be low. Further evidence for single transposition events was found in preparing the cataloged library of >12,000 mutants. In sequencing insertion locations in this library, multiple priming events (which would be expected for multiple transposons in a single cell) were rarely (frequency, 1% to 2%) encountered. Given the high overall insertion rate and high probability that each gene is independently hit many times, the low level of multiple insertions would not be expected to produce an "essential" designation as a false positive.

Essential gene comparison. The classification of 553 genes of the 3,402 open reading frames (ORFs) in DvH as essential compares to transposon saturation studies in *Caulobacter cresentus* (7) and *Salmonella enterica* serovar Typhi (2), which found 480 of 3,876 and 356 of 4,537 ORFs to be essential for growth, respectively. In contrast to those determinations, our study employed fewer population doublings and liquid-only enrichment to allow a broader range of observed fitness values. As a result of this, many severely impaired mutants survived in low abundance up to the final extraction of DNA in our study, leaving only 135 predicted genes devoid of any reads in the 5% to 85% range of their coding region. Therefore, the histogram of gene fitness (Fig. 3) (used for determining the number of essential genes; see Fig. S1 in the supplemental material) groups genes containing infrequently recovered mutations with those lacking any recovered mutations at all. The time- and strain-dependent nature of this approach makes comparisons across Tn-seq methods difficult, and, as a result, we have been conservative in what we call a "nonessential" gene.

Comparison to cataloged Tn library. Our gene fitness designations can be compared to the recently completed library of indi-

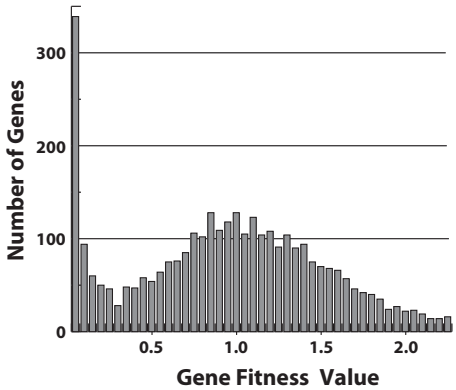

FIG 3 Histogram of fitness values for all DvH genes found by the TnLE-seq method. All genes were reduced to 5% to 85% of their coding region, and genes with fitness values ≤ 0.05 were not considered when determining the genome average.

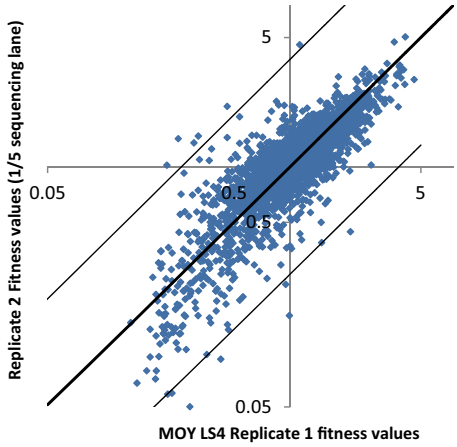

FIG 4 Gene fitness comparison of biological replicates of *D. vulgaris* Hildenborough grown in MOYLS4. Parallel lines represent *P* value cutoffs for $P \leq 10^{-5}$. Axes are shown in $\log_{10}$ format.

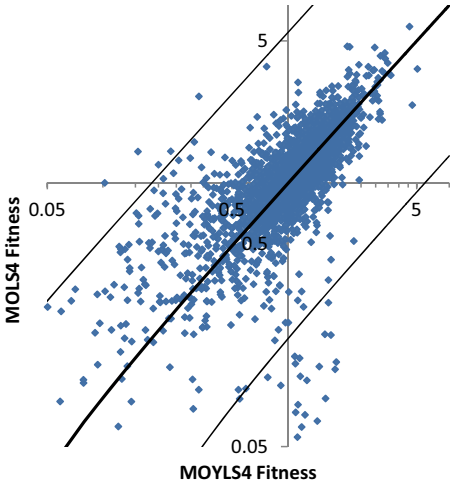

FIG 5 Gene fitness comparison of *D. vulgaris* Hildenborough cultures grown in rich medium (MOYLS4) versus minimal medium (MOLS4). Parallel lines represent *P* value cutoffs for $P \leq 10^{-5}$. Axes are shown in $\log_{10}$ format.

vidually isolated and barcoded transposon mutants of DvH (see Fig. S2 in the supplemental material),which was prepared by a similar conjugation technique with the Tn-RL27 transposon for mutant generation (22). Over 1.2×10^4 unique mutants were isolated and stored individually, and the transposon location for each mutant was determined with Sanger sequencing. A genome-wide map of these mutants is available online (http://desulfovibriomaps.biochem.missouri.edu/mutants/). These approaches serve different purposes, with a cataloged library taking over a year instead of weeks to complete but providing stocks of individual mutants. Nonetheless, the mutants generated in each procedure are comparable and can be used to evaluate the coverage of the TnLE-seq technique. Again counting only the transposons occurring in 5% to 85% of the coding sequence as effective insertions, the cataloged mutant library included 2,238 of 3,402 annotated DvH genes (65.8%). In contrast, the TnLE-seq method identified 2,782 nonessential genes (81.8%) (Fig. S2). This shows that TnLE-seq has greater depth of coverage but identifies the same genes as the individually barcoded library. (See the supplemental material for a complete list of gene fitness values.)

The essential genes correlated very well with genes that DvH traditionally cannot survive without, and this designation was further supported by the lack of recovery of insertion mutants in these genes in the cataloged library. For example, DNA replication machinery genes (including *dnaABEGNXZ* and *gyrAB*) were unable to tolerate transposon insertion and returned very few or no reads in any of our TnLE-seq data sets. Likewise, dissimilatory sulfite reductase (*dsrABCD*) genes essential to sulfate metabolism under these growth conditions returned fitness values very near zero. This pattern continued in genes encoding ribosomal proteins, tRNA synthetases, and transcription/translation machinery. Conversely, genes with transposon insertions in flagellar components and two regions encoding type III secretion functions were found to have fitness values above the genome average (1.5× to 4× the genome average), demonstrating their nonessential status under laboratory conditions. All of the essential genes listed above lack recovered transposon mutants present in the barcoded library, and the data corresponding to the nonessential genes, such as those mentioned above, include at least one isolate present in that library. Taking these results together, the overlap of these data sets lends a high degree of confidence to the biological relevance of our overall growth competition assay.

Fitness differences between pools. To determine reproducibility that would allow use of the standard conditions as a comparison for treatments or mutant analyses, we explored recovery of mutants in lactate/sulfate medium. We also explored the possible loss of data from multiplexing samples when sequencing on the Illumina platform. A comparison was made between the original TnLE-seq pool from cells grown in rich medium (R_A) that was not sequenced on a multiplexed Illumina lane and the biological replicate of this condition (R_B) that was multiplexed. The latter was sequenced with four additional samples on one Illumina lane. $\log_2$ likelihood ratios of fitness values between the pools were calculated for each gene after adding 100 reads to smooth for underrepresented genes (2, 23). Essential genes were removed, and remaining fitness values were fitted to a normal distribution. Genes exhibiting $\log_2$ likelihood ratios with *P* values below 10^{-5} were considered to have significantly altered fitness values as shown by comparisons between the pools (Fig. 4). Significantly altered fitness was seen for only 13 genes in the comparison of biological replicate pools. Of these, one was a direct result of ambiguity involving the multiplex barcode (commonly referred to as barcode bleed [24]) causing incorrect sequence binning for that gene, four were located within two nearly identical 30-kb phage insertion islands (25), and the remaining eight were small genes with an average length of 232 bp. In the case of these small genes, stochastic effects in transposon location may have affected the resulting fitness. Therefore, comparison of biological replicates revealed high reproducibility.

A comparison was also made for the rich medium pool and a defined medium pool (R_B versus D_A) sequenced on the same lane (Fig. 5), which returned 25 genes with significant fitness differences. Of these, 24 are annotated to code for specific biosynthetic enzymes, as would be expected when switching to a minimal (yeast extract-free) growth medium. The remaining gene (DVU1039) is annotated as a putative lipoprotein. This low number of genes might have been influenced by cross-feeding of amino acids from lysed *E. coli* or WT DvH cells. No gene was found to exhibit significant fitness differences in both

TABLE 3 Key changes to previous Tn-seq techniques

Step	Original method (Langridge et al. [2])	Method used in this study (TnLE-seq)	Reasoning
Generation of mutants			
Tn mutant generation	Electroporation with pure plasmid	Conjugation with *E. coli*	Conjugation is possible in many bacterial systems where electroporation efficiency is prohibitively low; mutants are produced more efficiently, thereby lowering costs and saving time
Tn mutant enrichment	Plating, mutants scraped to liquid	Dilution into liquid media	Liquid-only enrichment reduces time and cost associated with preparing and harvesting colonies on $>1 \times 10^3$ plates; many bacteria can be cultured in liquid medium but do not grow with high efficiencies on solidified medium
Removal of extracellular DNA	None	Turbo DNase digestion	Lysis of donor *E. coli* during enrichment without diaminopimelic acid leaves extracellular DNA behind; Tn sequences found in the *E. coli* DNA and originating from the Tn delivery plasmid are not useful, and their elimination via exonuclease digestion increases the proportion of useful fragments in the final pool
Sequencing for transposon location			
Removal of donor plasmid	None	BglII digestion	Donor plasmid-derived fragments are eliminated by restriction endonuclease cleavage near the Tn-gDNA junction at the Tn end used for sequencing.
Template for PCR junction enrichment	100 ng, 250–350 bp	200 ng, 500–1,000 bp	More PCR template (2×) allows an increase in the potentially unique insertions sites; larger input fragments allow elimination of fragments which do not contain junctions and are not amplified by PCR with a transposon-specific primer (see Fig. 1)
Final size fractionation	None	Fragment size of 300–500 bp	PCR enrichment shortens the fragments containing Tn-gDNA junctions; therefore, a further size fractionation retaining only 300- to-500-bp fragments is beneficial before sequencing (see Fig. 1)
Illumina sequencing	GA_{II} platform	HiSeq platform	The Illumina HiSeq platform produces ~10× more reads per lane than previous systems
Sequencing primer position	Reads begin 10 bp before junction	Reads begin at precise junction	The sequencing primer is homologous to the exact end of the transposon (see Fig. 3 and Table S3 in the supplemental material); this prevents cluster-calling errors, which are likely when most reads begin with an identical sequence derived from within the transposon

the control and rich- versus defined-medium analyses. (See the supplemental material for complete gene lists and corresponding fitness values.)

Establishing a surface colony-based pool may impose a selection bias that can be avoided with TnLE-seq. Since TnLE-seq is not reliant on one enriched pool for all subsequent growth experiments, it can detect less-severe fitness defects in genes. Additionally, fitness values could be extraordinarily different under various conditions, highlighting the value of an approach that can quickly generate new genome-saturating pools for each growth condition. It is also important that the perceived severity of a given fitness defect may be amplified as transposon mutants continue to grow in a culture of pooled mutants. Likewise, gene fitness differences between culture conditions may become more pronounced as the number of population doublings increase. Here we have demonstrated the results of an approach using 6 to 8 doubling times of a mutant pool, with a final optical density (OD [measured at 600 nm]) of 0.40 as the target for gene fitness determinations. For quantification of the resulting populations, CFU were determined and found to be consistent at this OD. An increase in culture doubling would almost certainly have increased the number of genes with significant fitness differences between rich and minimal media, as slower-growing mutants would become a smaller fraction of the population. Such a variation in experimental design is now possible and practical in DvH and other organisms as a result of TnLE-seq availability.

Practical considerations and use in other microbes. TnLE-seq provides a rapid, genome-wide screen of gene fitness (Table 3). Bacterial growth and library preparation can be accomplished in 2 weeks by a single researcher, with additional time needed for validation and/or high-throughput sequencing on the Illumina HiSeq platform (see Methods in the supplemental material). In addition, TnLE-seq can easily be multiplexed to maintain its practicality on full-scale sequencing platforms and further reduce overall costs. Gene fitness can be examined under standard laboratory growth conditions, during a stress treatment, with various electron donors and acceptors, or with growth in the presence of other microbes. It can also be adapted as a genetic interaction tool (5) to identify synthetically lethal or compensatory genetic interactions. The latter approach would start with a known background mutant, such as a markerless deletion (15), for TnLE-seq mutagenesis. The fitness data would be compared on a gene-by-gene basis to those from a parallel culture of pooled mutants in the wild-type background. Genes that were differentially lost from the population in the mutant would be candidates for functions required for growth of the mutant but not the wild type. Thus, genes compensating for the functions(s) lost in the mutant would be revealed.

The introduction of the transposon for mutant generation by conjugal transfer of the delivery plasmid is applicable to a wide range of bacterial species, including many of the (Gram-negative) *Proteobacteria*. Similar techniques exist for use in Gram-positive

phyla, including the *Firmicutes* (26) and *Actinobacteria* (27, 28). In addition to the introduction of the genes for the transposon delivery, however, consideration must be given to the ability of the strain to express the transposase and the selectable marker. The G+C content of the recipient genome has been shown to play an important role in expression of foreign DNA (29). As such, it may be necessary to tailor the type of transposon or antibiotic resistance marker and codon usage to accommodate the strain being analyzed by TnLE-seq. Overcoming such roadblocks in new microbes, however, is likely to be easier than development of traditional gene-deletion strategies tailored to each strain. TnLE-seq therefore has the potential to facilitate whole-genome gene fitness analysis of many previously genetically intractable organisms.

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J.D.W. conceived of the project. S.R.F. modified existing techniques and designed the final procedure. S.M.B. provided sequencing expertise. G.M.Z. generated the cataloged mutant pool. S.R.F. and G.M.Z. wrote Perl scripts for data processing. S.R.F. and J.D.W. wrote the paper.

We declare that we have no conflicts of interest.

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Genetic basis for nitrate resistance in *Desulfovibrio* strains

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Nitrate is an inhibitor of sulfate-reducing bacteria (SRB). In petroleum production sites, amendments of nitrate and nitrite are used to prevent SRB production of sulfide that causes souring of oil wells. A better understanding of nitrate stress responses in the model SRB, *Desulfovibrio vulgaris* Hildenborough and *Desulfovibrio alaskensis* G20, will strengthen predictions of environmental outcomes of nitrate application. Nitrate inhibition of SRB has historically been considered to result from the generation of small amounts of nitrite, to which SRB are quite sensitive. Here we explored the possibility that nitrate might inhibit SRB by a mechanism other than through nitrite inhibition. We found that nitrate-stressed *D. vulgaris* cultures grown in lactate-sulfate conditions eventually grew in the presence of high concentrations of nitrate, and their resistance continued through several subcultures. Nitrate consumption was not detected over the course of the experiment, suggesting adaptation to nitrate. With high-throughput genetic approaches employing TnLE-seq for *D. vulgaris* and a pooled mutant library of *D. alaskensis*, we determined the fitness of many transposon mutants of both organisms in nitrate stress conditions. We found that several mutants, including homologs present in both strains, had a greatly increased ability to grow in the presence of nitrate but not nitrite. The mutated genes conferring nitrate resistance included the gene encoding the putative Rex transcriptional regulator (DVU0916/Dde_2702), as well as a cluster of genes (DVU0251-DVU0245/Dde_0597-Dde_0605) that is poorly annotated. Follow-up studies with individual *D. vulgaris* transposon and deletion mutants confirmed high-throughput results. We conclude that, in *D. vulgaris* and *D. alaskensis,* nitrate resistance in wild-type cultures is likely conferred by spontaneous mutations. Furthermore, the mechanisms that confer nitrate resistance may be different from those that confer nitrite resistance.

Keywords: sulfate-reducing bacteria, sulfide control, *Desulfovibrio*, nitrite, nitrate inhibition, stress response, functional genomics, fitness profiling

INTRODUCTION

Sulfate-reducing bacteria (SRB) are environmentally and industrially significant microorganisms that use sulfate as a terminal electron acceptor in anaerobic respiration. These anaerobes produce sulfide as the end product of sulfate respiration (Postgate, 1984). Sulfide is toxic to most organisms (Caffrey and Voordouw, 2010), and its production causes oil souring in the petroleum industry (Ligthelm et al., 1991; Sunde et al., 1993). Despite the undesirable features of this metabolic end product, SRB have been exploited in studies of heavy metal bioremediation (Jiang and Fan, 2008; Martins et al., 2009) because of the ability of sulfide to form insoluble complexes with heavy metals (Jalali and Baldwin, 2000). SRB also precipitate heavy metals by directly changing the metal redox state to a less soluble form (Lovley et al., 1993a,b; Lloyd et al., 1999; Chardin et al., 2003). The metabolism of SRB is studied, therefore, to understand how to minimize the detrimental economic effects of these bacteria and to maximize their positive metabolic traits.

Such traits have been studied extensively in *Desulfovibrio vulgaris* Hildenborough (DvH), a model SRB with a sequenced genome (Heidelberg et al., 2004). DvH has been examined under a variety of stress conditions, including elevated nitrite (He et al., 2006; Bender et al., 2007) or nitrate concentrations (Redding et al., 2006; He et al., 2010a), heat shock (Chhabra et al., 2006), high salt (Mukhopadhyay et al., 2006; He et al., 2010b), oxygen (Mukhopadhyay et al., 2007), or electron donor depletion (Clark et al., 2006). The data obtained help in the prediction of responses of SRB in heavy metal-contaminated sites, which also contain many chemicals that inhibit these bacteria. For example, nitrate concentrations can be greater than 100 mM at US nuclear weapon complexes overseen by the Department of Energy (Green et al., 2012), and these waste sites are also contaminated with heavy metals (Riley and Zachara, 1992). High nitrate inhibits the growth of DvH (He et al., 2010a). Although some SRB can also use nitrate as a terminal electron acceptor (McCready et al., 1983), nitrate is successfully used by the petroleum industry to control the growth

of SRB and the oil souring that their sulfide production causes (Sunde and Torsvik, 2005). The mechanism of nitrate inhibition of SRB is still unclear. In the environment, at least part of the inhibition by nitrate is indirect: nitrate-reducing, sulfide-oxidizing bacteria produce nitrite that is toxic to SRB at much lower concentrations than is nitrate (Haveman et al., 2005; He et al., 2006). Furthermore, in oil wells, heterotrophic nitrate-reducing bacteria can compete with SRB for volatile fatty acid electron donors, further reducing the production of sulfide (Grigoryan et al., 2008). However, nitrate is also inhibitory to DvH in the absence of nitrate-reducing bacteria (Redding et al., 2006; He et al., 2010a).

It has been suggested that this pure culture nitrate inhibition is also a result of nitrite stress, since DvH itself may produce small amounts of nitrite from non-specific reduction of nitrate (Wall et al., 2007). In addition, high concentrations of nitrate could potentially induce a non-specific osmotic shock response in the bacteria (Wall et al., 2007). However, microarray data reveal few common gene expression changes among nitrate, nitrite, and sodium chloride stress conditions (He et al., 2010a). He et al. suggested that unique nitrate stress responses might account for these discrepancies (He et al., 2010a). Understanding the mechanism of nitrate inhibition of DvH and the genes involved in the nitrate stress response should facilitate the prediction and monitoring of the effectiveness of bioremediation strategies that employ SRB (Hazen and Stahl, 2006).

Past studies of the mechanisms of nitrate stress responses in DvH have relied primarily on transcript analyses (He et al., 2010a) and protein determination (Redding et al., 2006) techniques. However, mutant analysis is a more reliable method of determining gene essentiality in a particular stress condition (Price et al., 2013). Fitness profiling of many mutants en masse is a high-throughput approach complementary to classical genetic techniques that has allowed rapid annotation of genes (Deutschbauer et al., 2011). In this study, we used random transposon mutant fitness profiling in two completely sequenced (Heidelberg et al., 2004; Hauser et al., 2011) model SRB, *Desulfovibrio alaskensis* G20 ("G20," formerly called *Desulfovibrio desulfuricans* G20) and DvH, to probe the molecular mechanisms of their nitrate stress responses. Because 58% of G20 genes (1954/3371) are also present in DvH, which has 3503 genes (http://www.microbesonline.org/), we predicted that the strains would have similar nitrate stress responses. Therefore, pools of DvH and G20 transposon mutants with mutations saturating the non-essential genes under permissive growth conditions were subjected to high concentrations of nitrate. Illumina sequencing or microarrays were used to locate the transposons in mutants surviving the nitrate exposure and, by comparison with mutants not exposed to stress, to identify genes essential for survival in high nitrate. Generally, those mutants lost from the stress treatment represent genes whose functions are needed for stress survival. From the fitness profiling reported here, surprisingly we identified mutants with dramatically increased fitness in nitrate stress conditions that we further analyzed in pure cultures. However, the same mutations did not confer resistance to nitrite. These results confirmed the predicted existence of unique nitrate-resistance mechanisms (He et al., 2010a) and suggested that environmental models of nitrate inhibition require expansion.

MATERIALS AND METHODS

STRAINS AND MEDIA

The strains used in this study are listed in **Table 1**. All DvH and G20 strains were grown in defined MOLS4 medium [MO Basal Salts (Zane et al., 2010) with 60 mM sodium lactate and 30 mM sodium sulfate]. The medium used to grow DvH cultures was reduced with 1.2 mM sodium thioglycolate; whereas, the medium for G20 was reduced with 0.38 mM titanium citrate. DvH and G20 manipulations, including setup of growth kinetic studies, were done at about 25°C in an anaerobic growth chamber (Coy Laboratory Products, Inc., Grass Lake, MI) with an atmosphere of approximately 95% N_2 and 5% H_2. Optical densities (600 nm) were determined with a Genesys 20 spectrophotometer (Thermo Scientific, Waltham, MA).

GROWTH KINETICS

Growth kinetic studies with WT G20 were carried out essentially as described below for the G20 fitness profiling, with the following exceptions: No kanamycin was used with the WT cells, and each wild-type G20 freezer stock was pelleted to reduce carryover of glycerol used as the cryoprotectant before inoculation of starter cultures. For all DvH growth kinetics, 5 mL MOLS4 cultures (with 1.2 mM sodium thioglycolate) were started by inoculation with the pelleted cells from a freezer stock. Geneticin (G418) sulfate (400 μg/mL) or spectinomycin dihydrochloride pentahydrate (100 μg/mL) were added to DvH cultures where indicated. Each condition tested was prepared as 14.5 mL of inoculated culture plus 1 mL deionized water (for "no additions" controls) or inhibitory salts (sodium nitrate, sodium nitrite) dissolved in deionized water. Aliquots of 5.1 mL from this 15.5 mL culture were grown as triplicates in 27-mL anaerobic tubes, each capped with a butyl rubber stopper and grown at 34°C. All G20 and DvH inocula were grown to late exponential or stationary phase. 100 mM sodium nitrate was used for experiments with DvH, compared with 150 mM for G20 experiments, due to the greater sensitivity of DvH to nitrate. With a few exceptions, all growth kinetics experiments were repeated at least twice with triplicates in each experiment. Triplicate growth experiments for the DVU0250 transposon mutant and intergenic control transposon mutant experiments were done once. Triplicates of the Δ*rex* mutant in the presence of nitrite were also grown once.

G20 TRANSPOSON MUTANT FITNESS STUDIES

Fitness data were collected with two pools of G20 transposon insertion mutants (4069 and 4056 mutants, respectively) that will be described in more detail elsewhere (Kuehl et al., in revision). Briefly, 1174 strains are present in both pools, leaving 6951 strains that are present only once in the complete library. 498 genes are represented only once in the library. 571 genes are represented twice in the library; that is, either a single strain is present in each of the pools or two different strains with a transposon insertion in the same gene are present in the library. 1341 genes are represented in the library three or more times. A total of 2410 unique genes and 212 unique intergenic regions are represented. Thus, about 71% of G20 genes are represented in the library, providing excellent coverage of non-essential genes. Transposon insertions were mapped to the genome by a two-step arbitrary

Table 1 | Strains and plasmids used in this study.

Strain or plasmid	Genotype or relevant characteristics[a]	Sources and/or references
E. coli		
α-Select (Silver Efficiency)	F$^-$ *deo*R *end*A1 *rec*A1 *rel*A1 *gyr*A96 *hsd*R17(r_k^-, m_k^+) *sup*E44 *thi*-1 *pho*A Δ(*lac*ZYA-*arg*F)U169 Φ80*lac*ZΔM15 λ$^-$	Bioline
D. alaskensis		
G20	Spontaneously nalidixic acid-resistant derivative of *Desulfovibrio desulfuricans* G100A lacking the endogenous cryptic 2.3-kb plasmid, pBG1	Wall et al., 1993
D. vulgaris		
ATCC29579	Wild-type *D. vulgaris* Hildenborough (pDV1); 5-FU^s (Parent for GZ strains)	ATCC
JW710	WT Δ*upp* (pDV1); 5-FU^r (used as "WT" control for DvH growth kinetics in this study; parent strain for deletions)	Keller et al., 2009)
JW3311	JW710 ΔDVU0916::(*npt upp*); Km^r; 5-FU^s(Δ*rex* marker exchange)	This study
GZ9685	DVU0245-773::Tn*5*-RL27;insertion at bp 773/1110 for the gene; Km^r	Wall laboratory
GZ12997	DVU0246-111::Tn*5*-RL27;insertion at bp 111/2235 for the gene; Km^r	Wall laboratory
GZ2640	DVU0247-211::Tn*5*-RL27;insertion at bp 211/360 for the gene; Km^r	Wall laboratory
GZ12015	DVU0250-427::Tn*5*-RL27;insertion at bp 427/588 for the gene; Km^r	Wall laboratory
GZ10694	DVU0251-80::Tn*5*-RL27;insertion at bp 80/963 for the gene; Km^r	Wall laboratory
GZ2179	Genome position 658487::Tn*5*-RL27; insertion at intergenic region 327 bp upstream of VIMSS209534, DVU0590; Km^r (Control strain for transposon mutant growth kinetics)	Wall laboratory
PLASMIDS		
pMO719	pCR8/GW/TOPO containing SRB replicon (pBG1); Sp^r; source of Sp^r and pUC *ori* fragment for marker exchange suicide plasmid construction	Keller et al., 2009
pMO746	*upp* in artificial operon with *npt* and Ap^r-pUC *ori*; P_{npt}-*npt*-*upp*; Km^r; 5-FU^s; for marker exchange suicide plasmid construction	Parks et al., 2013
pMO9075	pMO719 containing P_{npt} for constitutive expression of complementation constructs; pBG1 stable SRB replicon; Sp^r	Keller et al., 2011, 2014
pMO3311	Sp^r and pUC *ori* from pMO719 plus 1630 bp upstream and 1590 bp downstream DNA regions from DVU0916 (*rex)* flanking the artificial operon of P_{npt}-*npt*-*upp* from pMO746; for marker exchange deletion mutagenesis; Sp^r and Km^r	This study
pMO3313	pMO9075 with DVU0916 (*rex*) constitutively expressed from P_{npt}	This study
pRL27	Tn*5*-RL27 (Km^r-*ori*R6 K) delivery vector; for transposon mutagenesis of DvH strains	Larsen et al., 2002

[a] *Km, kanamycin; Sp, spectinomycin; Ap, ampicillin; 5-FU, 5-fluorouracil; superscript "r" or "s," resistance or sensitivity.*

PCR as described previously (Oh et al., 2010). Each mutant has a "TagModule" that contains two different variable segments, an "uptag" and a "downtag"(Oh et al., 2010). Within each pool, each strain has a unique TagModule, so that the abundance of the TagModule is a proxy for the abundance of that strain. Only the uptags are amplified from the "uptag pool," Pool 1 (4069 strains) and only the downtags are amplified from the "downtag pool" Pool 2 (4056 strains). Amplified tags from both pools can be hybridized to the same array because only one tag (up or down) from a TagModule has been shown to be necessary for accurate quantification of strain abundance and there is no overlap of tags in the two pools (Oh et al., 2010; Deutschbauer et al., 2011). Each pool was grown overnight to late log phase (OD about 0.87) in about 10 mL MOLS4 medium amended with titanium citrate (0.38 mM) as reductant and kanamycin (800 μg/mL). 750 μL of each pool was added to 15 mL MOLS4 + 1650 μL sterile MO Basal salts (Zane et al., 2010) or salt (sodium nitrate, sodium chloride, etc.) dissolved in MO Basal Salts. Each amended medium plus mutants (17.4 mL) was aliquoted into three 27-mL anaerobic tubes, about 5.8 mL per tube, each capped with a butyl rubber stopper and grown at 34°C. When the cultures had reached stationary phase (OD > 1), 0.5 mL from each control or stress condition was pelleted and processed as described previously; that is, genomic DNA was extracted (Deutschbauer et al., 2011), and the uptags and downtags were PCR amplified, hybridized to an Affymetrix 16K TAG4 array, and scanned (Pierce et al., 2007). The number of doublings of the population was estimated by using the doubling in OD_{600} to approximate doubling of the cell population.

Fitness data for G20 were analyzed as described for similar experiments with *Shewanella oneidensis* MR-1 (Deutschbauer et al., 2011), with slight modifications (Price et al., 2013). Briefly, strain fitness = $\log_2$(END/START), where those values ("END" and "START") are averages of the gene location-specific uptag and downtag $\log_2$ intensities. Mutant strains with low START values were excluded, leaving measurements for 3726 strains in Pool 1 and 3865 strains in Pool 2. Strain fitness was normalized across the genome so that the median was 0; this was done separately

for the two pools. Since a gene could be mutated at different sites, gene fitness was calculated as the average fitness of strains with mutations in a particular gene. Gene fitness was normalized to remove the effect of chromosomal position on gene fitness and to set the mode of fitness values to zero, as previously described (Price et al., 2013). One difference from the previously described protocol (Price et al., 2013) was that only one Affymetrix chip was used per experiment; up- and downtags were hybridized to the same array. The results of the "MOLS4 no stress" condition were similar to the LS4D controls described previously (Price et al., 2013), including similarly "sick" auxotrophs that would be expected in a defined medium when compared with lactate-sulfate medium containing yeast extract. Two quality metrics were used for each experiment. Strain correlation (Table S1) is the correlation of the strain fitness values for the same strains between the two pools. Operon correlation (Table S1) is the correlation of gene fitness values between adjacent genes predicted (http://www.microbesonline.org/) to be in the same operon. The low quality metrics for the sodium nitrate and potassium nitrate conditions (Table S1) reflect the predominance of a few strains in the culture; essentially only the data for these few strains is biologically meaningful, while the majority of strains did not have the opportunity to grow at all before the culture reached stationary phase. The complete data from these experiments are available at http://www.microbesonline.org/.

DvH TnLE-Seq FITNESS STUDIES

This nitrate resistance study was one of five multiplexed TnLE-seq pools that were part of a protocol described elsewhere (Fels et al., 2013). One advantage of this method is that individual mutants do not need to be isolated and confirmed, as in a catalogued library. They also do not need to be frozen en masse and recovered from the freezer. Rather, hundreds of thousands of unique transposon mutations are created by conjugation at the beginning of each experiment. The only experimental difference between this study and those published was the addition of 100 mM nitrate to the MOLS4 defined medium for growth of the mutant pool. As expected given the strong stress of 100 mM nitrate, this pool was delayed by about 92 h in reaching an OD_{600} of 0.4 compared with only about 40 h in the defined MOLS4 medium without nitrate. However, the nitrate pool was harvested and the fitness values were determined as previously described (Fels et al., 2013). The total number of cells in the final 500 mL culture (1×10^{11} cells) was determined by plating for individual colony-forming units, as previously described (Fels et al., 2013). The number of doublings of the culture was estimated by assuming that only the genes with $\log_2$ fitness scores >0 (38 genes) contributed significantly to the final population. Therefore, the number of unique insertions in these genes (1904) was considered to be number of cells in the starting pool. The complete data from these experiments are available at http://desulfovibriomaps.biochem.missouri.edu/fitness/.

PLASMID AND STRAIN CONSTRUCTION

Genomic DNA from DvH was isolated with the Wizard® Genomic DNA Purification Kit (Promega, USA). Plasmids were isolated from both *E. coli* and DvH with the GeneJET Plasmid Miniprep Kit (Fermentas, Thermo Scientific, Glen Burnie, MD). All primers were obtained from Integrated DNA Technologies (Coralville, IA). The pMO3311 and pMO3313 plasmids were constructed by Sequence- and Ligation-Independent Cloning (SLIC) (Li and Elledge, 2007). PCR products from template plasmids were agarose gel-purified to reduce transformation of the parent plasmid. All products were cleaned with a Wizard® SV Gel and PCR Clean-up System (Promega, USA) before the SLIC procedure. The plasmids were constructed by amplification of DNA regions (Table S2) with Herculase II polymerase (Agilent cat# 600675), as previously described for a similar procedure (Parks et al., 2013). DNA products were transformed into Silver Efficiency α-Select *E. coli* cells (Bioline) and plated on solidified LC medium (Zane et al., 2010). Electroporation procedures were similar to those previously described (Keller et al., 2011) with electroporation parameters 1500 V, 250 Ω, and 25 μF. Cells recovered overnight after electroporation were plated on MOYLS4 with 1.2 mM thioglycolate as reductant and about 0.2% (wt/vol) yeast extract. Sequence confirmation of the mutagenic cassette and the complementing gene was performed at the University of Missouri DNA Core Facility (http://www.biotech.missouri.edu/dnacore/).

NITRATE DETERMINATION

A scaled-down version of a previously described colorimetric method (Cataldo et al., 1975) was used to determine nitrate concentrations. Briefly, 200 μL of salicylic acid solution (1 g salicylic acid dissolved in 20 mL of approximately 98% [vol/vol] sulfuric acid) was added to each 25 μL sample that had been diluted 25-fold in deionized water. This was mixed and incubated 20 min at room temperature and then 4.75 mL of 2 M NaOH was added to each tube. Absorbance at 410 nm was measured with a Genesys 20 spectrophotometer (Thermo Scientific, Waltham, MA). R^2 for a standard curve was >0.99, instrument detection limit 0.1 ± 0.1 mM.

PROTEIN DETERMINATIONS

Whole cell protein concentrations were determined with the Bradford assay (Bradford, 1976) with bovine serum albumin as the standard. Absorbance at 595 nm was measured with a Genesys 20 spectrophotometer (Thermo Scientific, Waltham, MA).

RESULTS

RESPONSE OF DvH TO NITRATE EXPOSURE

It has been reported (Elias et al., 2009; He et al., 2010a) that DvH cells can grow rapidly and abundantly after a long lag phase in high nitrate concentrations. It was unclear, however, whether this rapid growth was due to elimination of the toxic nitrate, some modification of cell metabolism allowing adaptation to the continued presence of nitrate, or outgrowth of preexisting nitrate-resistant mutants. Furthermore, it was not known whether the cells that grew in nitrate had a growth advantage over naïve cells when subcultured into a fresh medium amended with nitrate. To test this, JW710 (**Table 1**), the parent for making marker exchange and markerless deletion strains (Keller et al., 2009), was used. JW710 will therefore be referred to as the wild-type control for all DvH growth kinetics in this study. This wild-type control was

grown in lactate-sulfate medium amended with 100 mM nitrate (**Figure 1A**).

It was determined that, at the end of growth in the presence of 100 mM nitrate, no gross consumption of nitrate was detected (**Table 2**). The persistence of the nitrate suggested that the ability of DvH to grow in the presence of 100 mM nitrate was due to adaptation to nitrate or outgrowth of spontaneous mutants, rather than a detoxification of nitrate itself. To further confirm this lack of nitrate metabolism, nitrite was measured (American Public Health Association, 1992) during the lag/inhibition phase for JW710 cells exposed to 100 mM nitrate and the nitrite concentration was below 15 ± 5 μM (data not shown). This nitrite concentration is below the concentration (40 μM) reported to inhibit plated single colonies of *D. vulgaris* (Haveman et al., 2004). Thus, secondary production of nitrite is not likely the cause of nitrate sensitivity. To begin to test whether the nitrate adaptation was due to a reversible gene regulation or to successful growth of spontaneous mutants in the culture, nitrate-adapted strains were subcultured back into medium with or without nitrate. We found that nitrate-stressed cultures grew without a prolonged lag and maintained nitrate resistance when subcultured into fresh medium with 100 mM nitrate (**Figure 1B**). This resistance continued over the course of three subcultures (data not shown). Further, even nitrate-resistant cultures that were subcultured into medium lacking nitrate retained nitrate resistance when subcultured back into 100 mM nitrate (data not shown). As with the original exposure to nitrate, no gross consumption of nitrate was observed over the course of the subcultures (**Table 2**). We suggest that spontaneous mutations in the culture lead to increased nitrate resistance of some cells which then predominate in the population.

FITNESS PROFILING WITH G20

To test what mutations might be causing this nitrate resistance, we employed transposon mutant fitness profiling. A catalogued transposon mutant library, which enables high-throughput phenotypic screening, had been generated in G20 prior to that produced in DvH (Price et al., 2013). Each mutant strain in the library is identified by two unique DNA barcode sequences or "tags," the "up" tag and the "down" tag (Oh et al., 2010; Deutschbauer et al., 2011). Strain abundance is measured by reading the abundance of the barcodes through fluorescence in microarrays made to detect the barcodes (Pierce et al., 2006, 2007).

We predicted that comparison of fitness profiles of nitrite- and nitrate-stressed G20 cells would reveal mutants with responses unique to nitrate. That is, fitness profiling in the two conditions would allow us to see which mutants differentially increased in relative abundance during a pooled growth competition and which decreased. The fitness of a particular strain is calculated as $\log_2$ of the ratio of the relative abundance of the strain after growth competition to the relative abundance of the strain before growth competition. Therefore, if the relative abundance of a particular strain in the pool remained the same before and after stress, its fitness would be equal to zero (Oh et al., 2010):

$$\text{Fitness of a G20 mutant} = \log_2\left(\frac{\text{barcode microarray signal from cells after stress}}{\text{barcode microarray signal from cells prior to stress}}\right)$$

Table 2 | Nitrate concentrations from stationary phase cultures of *D. vulgaris* Hildenborough grown in MOLS4 medium amended as indicated.

Subculture[a]	Inoculum history	Amendment	$[NO_3^-]^b$ in mM
0-A[c]	Lactate/SO_4^{2-}	none	not measured
0-B[c]	Lactate/SO_4^{2-}	100 mM NO_3^-	101 ± 3
1-A[d]	From 0-B	none	8 ± 1
1-B[d]	From 0-B	100 mM NO_3^-	102 ± 3
2-A	From 1-B	none	6 ± 2
2-B	From 1-B	100 mM NO_3^-	99 ± 1
3-A	From 2-A	none	not detected
3-B	From 2-A	100 mM NO_3^-	101 ± 7
3-C	From 2-B	none	8 ± 2
3-D	From 2-B	100 mM NO_3^-	103 ± 5

[a] *Inocula were 6.5% (vol/vol).*

[b] *Concentrations determined from triplicate determinations with standard deviations shown.*

[c] *Growth curves in* ***Figure 1A****.*

[d] *Growth curves in* ***Figure 1B****.*

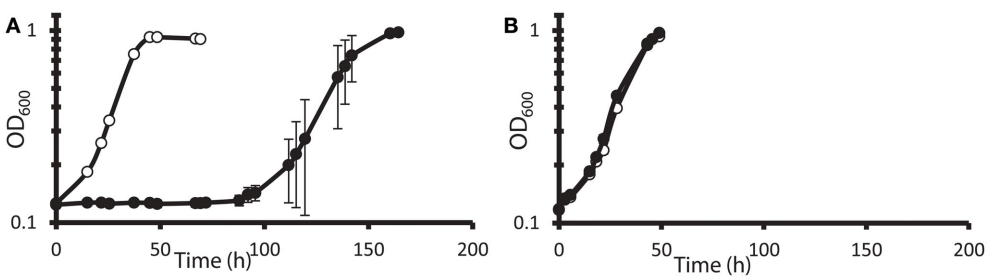

FIGURE 1 | Growth and subculture of wild-type *D. vulgaris* Hildenborough (JW710) in lactate-sulfate medium with inhibitory nitrogen species. (A) Growth of DvH with no additions (○) or 100 mM sodium nitrate (●) **(B)** Growth of DvH subcultured from original 100 mM nitrate culture shown in **(A)** no additions (○), 100 mM sodium nitrate (●). Approximately 6–6.5% (vol/vol) inocula were used for the original culture and subcultures. Readings reflect averages of three samples, and errors bars show standard deviations.

If a strain decreased in relative abundance after the stress condition because it was outcompeted or unable to cope with the stress, it would have negative (<0) fitness. If its relative abundance increased, it would have positive (>0) fitness. For the pools, the fitness calculated for a particular gene, referred to as the "mean log ratio," is expressed as $\log_2$ of the average fitness of strains with a mutation in that particular gene.

The G20 pools were grown in lactate-sulfate medium amended with 150 mM $NaNO_3$, 150 mM KNO_3, 150 mM NaCl, 150 mM KCl, or 0.25 mM $NaNO_2$. NaCl and KCl conditions were osmotic controls; KNO_3 vs. KCl allowed a control for anion specificity. Concentrations of 150 mM nitrate and 0.25 mM nitrite were chosen because these concentrations severely but not completely inhibited wild-type G20 (**Figures 2A,B**). Since a long lag phase had been observed before exponential growth of nitrate-stressed cultures of both DvH and G20 in lactate-sulfate conditions (**Figures 1A**, **2A**), it was reasonable to hypothesize that spontaneous mutants in wild-type cultures were selected in the population after the lag. Therefore, this hypothesis was confirmed when we found that, in the transposon mutant pools, several mutant strains predominated in cultures growing in the presence of nitrate (**Table 3**; Table S3). That is, transposon insertion conferred a growth advantage, and therefore a high fitness, on these particular strains in the nitrate stress condition. The top 10 genes interrupted in the strains that grew abundantly in sodium nitrate had fitness values (mean log ratios) greater than 2 in that condition, but fitness values less than 0.25 in sodium chloride, potassium chloride, sodium nitrite, and in the absence of stress (Table S3). In contrast, interruption of those same genes was advantageous in both sodium nitrate and potassium nitrate

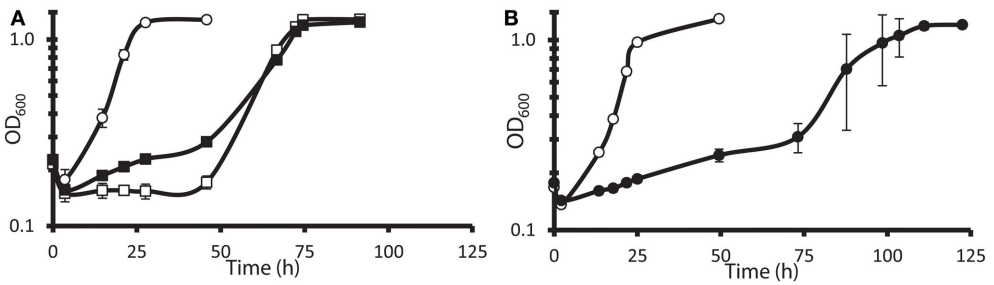

FIGURE 2 | Growth of wild-type *D. alaskensis* G20 in lactate-sulfate medium with inhibitory nitrogen species. (A) Growth of G20 with no additions (○), 150 mM sodium nitrate (□), or 150 potassium nitrate (■). **(B)** Growth of G20 with no additions (○) or 0.25 mM sodium nitrite (●). Approximately 4.5% (vol/vol) inocula were used. Readings reflect averages of three samples, and errors bars show standard deviations.

Table 3 | *Desulfovibrio* genes interrupted in strains with high fitness in lactate-sulfate conditions amended with sodium nitrate.

G20 gene (Dde)	fitness[a]	DvH homolog (DVU)	fitness[b]	Annotations
2702	4.23	0916	3.81	AT-rich DNA binding protein (COG2344); Transcriptional repressor, redox-sensing, Rex (IPR022876)
0597	2.25	no homolog	No data	Uncharacterized protein conserved in archaea (COG2043); Protein of unknown function DUF169 (IPR003748)
0598	3.01	0251	11.44	Transmembrane protein TauE like (IPR002781); predicted permease (COG0730); sulfite exporter TauE/SafE (pfam01925)
0600	2.88	0250	−5.82	Conserved hypothetical protein
0601	3.51	0249	3.86	PtxB, putative (http://microbesonline.org/); ABC-type phosphate/phosphonate transport system, periplasmic component (COG3221); outer membrane-associated homodimer (Walian et al., 2012)
0602	2.34	0248 (pseudo-gene)	1.43	Signal transduction histidine kinase (COG5002); PAS fold (IPR013767); ATPase-like, ATP-binding domain (IPR003594); HAMP linker domain (IPR003660); PAC motif (IPR001610)
0603	3.08	0247	9.14	Signal transduction response regulator, receiver domain (IPR001789); CheY-like superfamily (IPR011006); ntrX (http://microbesonline.org/)
0604	3.41	0246	2.18	Pyruvate phosphate dikinase, PEP/pyruvate-binding (IPR002192); PEP-utilizing enzyme, mobile domain (IPR008279); ATP-grasp fold, subdomain 1 (IPR013815); ATP-grasp fold, subdomain 2 (IPR013816)
0605	2.08	0245	−6.04	Protein-tyrosine/Dual-specificity phosphatase (IPR000387)

[a] *$\log2\left(\frac{\text{barcode microarray signal from cells after stress}}{\text{barcode microarray signal from cells prior to stress}}\right)$; fitness of stationary-phase G20 cultures grown for about 3.3 doublings (about 63 h) in lactate-sulfate medium amended with 150 mM sodium nitrate.*

[b] *$\log2\left[\left(\frac{\text{\# insertions in gene}}{\text{length of gene}}\right) / \left(\frac{\text{\# insertions in all genes}}{\text{length of all genes}}\right)\right]$; fitness determined from mid-log phase DvH cultures grown for about 25.5 doublings (92 h) in lactate-sulfate medium amended with 100 mM nitrate.*

(Table S3). Growth of the mutants in both salts of nitrate supports the specificity of the nitrate anion as the driver for selection of these resistant mutants. The interrupted gene conferring the highest fitness in sodium nitrate was Dde_2702 (**Table 3**), a gene annotated as encoding Rex, a redox-sensing regulatory protein (Ravcheev et al., 2012). Particularly surprising was the high fitness conferred by mutation of a cluster of poorly annotated genes, Dde_0597 through Dde_0605, hereafter called the "nitrate cluster." Both the *rex* gene and the nitrate cluster (**Table 3**) have homologs in DvH. Because of these homologies, including shared synteny of the nitrate cluster in G20 (**Figure 3**), it seemed reasonable that mutations of the homologs in DvH would confer similar nitrate-resistant phenotypes.

FITNESS PROFILING WITH DvH

In order to test the hypothesis that both G20 and DvH used the same mechanisms for nitrate resistance, we had the opportunity to employ a different high-throughput fitness profiling method, Transposon Liquid Enrichment sequencing (TnLE-seq). This method (Fels et al., 2013) is based on deep sequencing of random transposon mutations to query DvH. TnLE-seq is a modification of the HITS (High-throughput Insertion Tracking by deep Sequencing) (Gawronski et al., 2009), Tn-seq (Van Opijnen et al., 2009), and TraDIS (Transposon Directed Insertion-site Sequencing) (Langridge et al., 2009) methods. However, the TnLE-seq method developed for DvH is especially well-adapted to oxygen-sensitive bacteria that have low electroporation efficiency (Fels et al., 2013). The mutated culture is grown in control vs. stress conditions, and deep sequencing then determines the abundance and location of mutations at the end of growth. Because of the differences in methods, the calculation of fitness is also different from that of the mutant library experiment (Fels et al., 2013). The fitness value shown below is in $\log_2$R format, for easier comparison with the G20 pools:

$$\text{Fitness of a DvH gene} = \log_2\left[\left(\frac{\#\text{ insertions in gene}}{\text{length of gene}}\right) / \left(\frac{\#\text{ insertions in } \mathbf{all} \text{ genes}}{\text{length of } \mathbf{all} \text{ genes}}\right)\right]$$

As previously described (Fels et al., 2013), fitness was calculated from insertions only in the 5–85% region of the coding sequence of genes, as such insertions are more likely to impair the function of gene products. As with the G20 pool described above, negative fitness indicates a fitness defect, whereas positive fitness indicates that the mutation confers a fitness advantage in that particular condition. For nitrate stress, the transposon mutants were grown in lactate-sulfate medium amended with 100 mM sodium nitrate. As expected, the results showed that mutations in a predicted *rex* gene annotated as encoding a transcriptional regulator (DVU0916) as well as mutations in homologs of the G20 "nitrate cluster" (DVU0251, DVU0249, DVU0247, and DVU0246) conferred fitness values among the ten highest values (**Table 3**; Table S4). In fact, mutation of DVU0251 led to the highest fitness value, 11.44, or 2780-fold. Essentially, there was a "jackpot effect" in which a small percentage of mutants predominated in the population, a consistent result between the DvH and G20 fitness experiments. Despite these consistencies, in-depth, individual mutant analysis was necessary to confirm and elucidate the results of high-throughput fitness profiling (Deutschbauer et al., 2011).

CONFIRMATION OF FITNESS PROFILING WITH INDIVIDUAL MUTANTS

DvH was chosen for confirmation studies because a catalogued transposon mutant library of DvH was also available, in-frame deletion mutants can be made with greater facility (Keller et al., 2009), and complementation of mutants is readily accomplished. For an initial confirmation of the physiological relevance of the "nitrate cluster" to nitrate resistance, we determined growth kinetics of five DvH isolated mutants with transposon insertions in genes in that cluster (**Figures 4A–E**). The control strain used had a transposon at an intergenic position 327 base pairs upstream of a gene encoding a "random" hypothetical protein, DVU0590, and, therefore, was not predicted to be involved in nitrate stress responses. We found that the mutants with transposon insertions in DVU0246, DVU0247, DVU0250, and DVU0251 grew with indistinguishable kinetics with or without 100 mM nitrate. In contrast, 100 mM nitrate inhibited the control and the DVU0245 transposon mutants (**Figures 4A–F**). Inhibition of the DVU0245 mutant in high nitrate is consistent with the low fitness of the DVU0245 mutant in nitrate (fitness −6.04, **Table 3**) and consistent with the inhibition of a deletion mutant of DVU0245 (data not shown). None of the mutants grew better than the control strain in 1 mM sodium nitrite (**Figures 4A–F**). We interpret these results to mean that the growth advantage of these mutants is specific to nitrate and not simply an advantage in the presence of inhibitory nitrogen species.

The results of the G20 and DvH fitness studies indicated similar responses of homologous genes. In the G20 results, the predicted *rex* mutant had the highest fitness (Dde_2702). The fitness score for the DvH *rex* mutant was also in the top ten fitness scores, along with four DvH "nitrate cluster" (DVU0251, DVU0247, DVU0249, DVU0246) mutants (**Table 3**; Table S2). However, both the DVU0245 and the DVU0250 mutants had low fitness

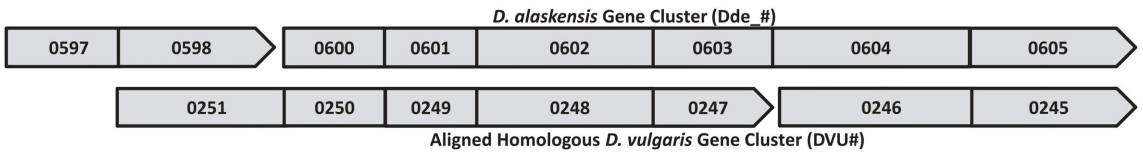

FIGURE 3 | *Desulfovibrio* nitrate resistance gene cluster. Operon predictions were from http://microbesonline.org/; boxes represent predicted genes, arrows indicate direction of transcription, and contiguous boxes ending in an arrow represent predicted operons.

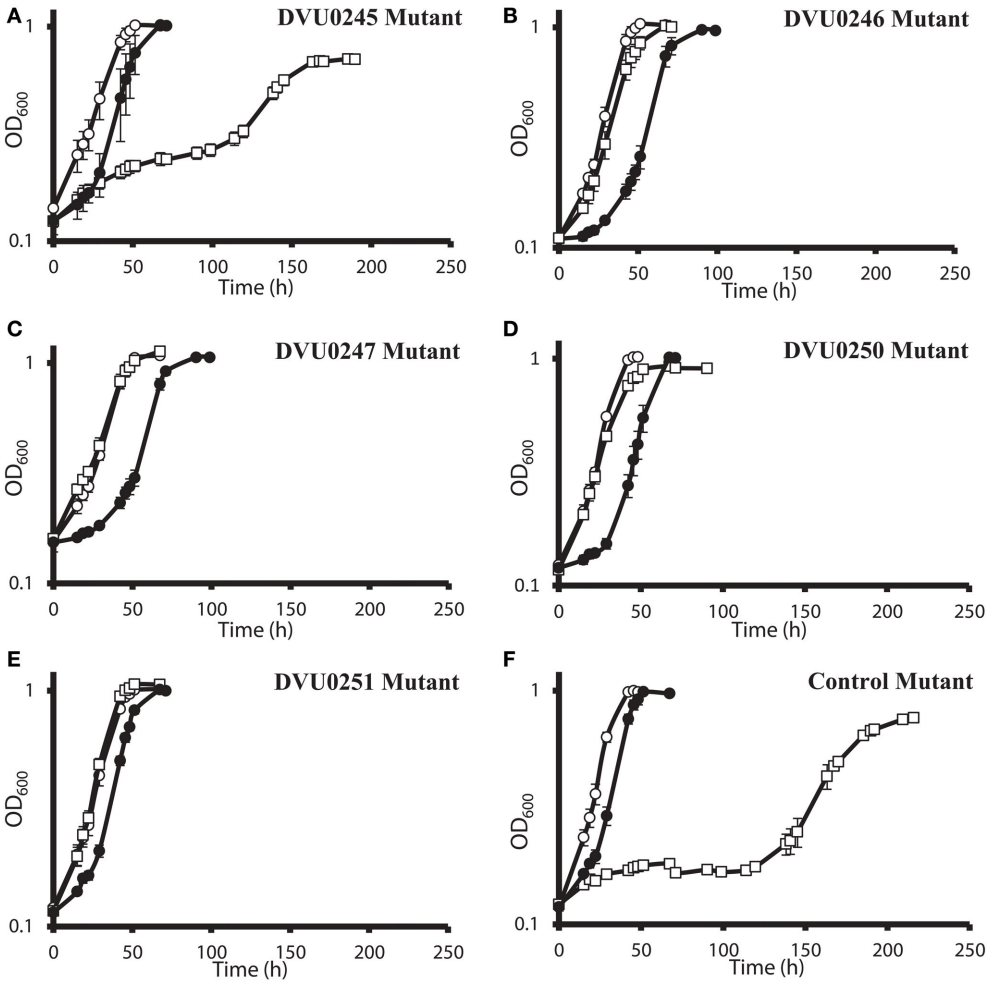

FIGURE 4 | Growth of *D. vulgaris* Hildenborough transposon mutants in lactate-sulfate medium with inhibitory nitrogen species. Growth of the DVU0245 **(A)**, DVU0246 **(B)**, DVU0247 **(C)**, DVU0250 **(D)**, DVU0251 **(E),** and intergenic transposon control **(F)** mutants in the presence of no additions (○), 100 mM sodium nitrate (□), or 1 mM sodium nitrite (●). Approximately 5.3% (vol/vol) inocula were used. Optical density readings reflect averages of three samples, and errors bars show standard deviations.

in nitrate, whereas mutants of their G20 homologs had high fitness in nitrate (**Table 3**). The nitrate resistance of the pooled vs. the isolated DvH mutants was also not entirely consistent. The rapid growth of the isolated DVU0250 mutant (**Figure 4D**) in the presence of nitrate was unexpected because of the low TnLE-seq fitness conferred in the same condition by mutation of DVU0250 (**Table 3**). In addition, preliminary growth kinetic data (not shown) suggest that the transposon mutant of DVU0248, which is annotated as a pseudogene in DvH, has little or no growth advantage over the control strain in the presence of 100 mM nitrate. In contrast, in the pooled experiment the DVU0248 mutations conferred positive fitness in nitrate (**Table 3**). While more data will be needed either to confirm or to change the annotation of DVU0248 as a pseudogene, we suggest that similar nitrate-resistance mechanisms are operating in G20 and DvH. The discrepancies between pooled and individual mutant studies confirm the need for follow-up studies of high-throughput experiments.

Such follow-up was pursued with gene deletion and complementation of the DvH gene encoding the predicted transcription regulator Rex. Interruption of the *rex* gene conferred the highest fitness in G20 but not in DvH (**Table 3**). We found that a deletion of DvH *rex* (DVU0916) had a clear advantage over the JW710 parent strain in lactate-sulfate medium with 100 mM added nitrate (**Figures 5A,B**). Like the "nitrate cluster" transposon mutants described above (**Figures 4A–F**), the *rex* mutant is not demonstrably resistant to nitrite (**Figures 5A,B**). Interestingly, when the mutant was complemented with *rex* expressed from a constitutive promoter, the phenotype in the presence of 100 mM nitrate was different from either parent or mutant phenotypes (**Figure 5C**). In contrast, the parent strain with *rex* overexpressed appeared to be at least as sensitive to nitrate as the parent strain (**Figure 5C**). The unique phenotype of the complemented mutant may result from some of the bacterial population losing the plasmid containing the complemented *rex* gene, in spite of antibiotic selection. While spectinomycin selects for plasmid retention, nitrate should

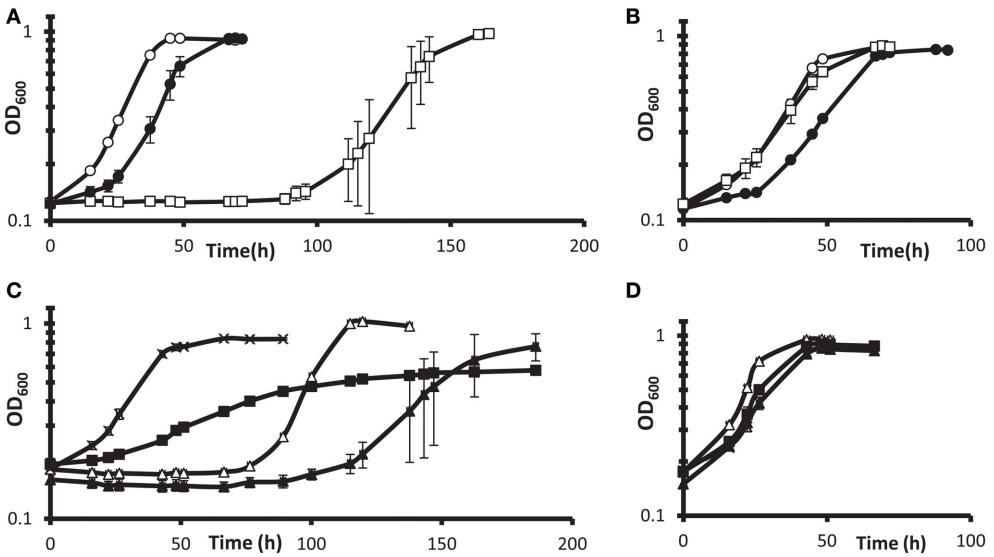

FIGURE 5 | Growth of DvH wild-type vs. Δ*rex* mutant in lactate-sulfate medium with inhibitory nitrogen species. (A,B) Growth of the "wild-type" parental strain JW710 **(A)** vs. Δ*rex* **(B)** mutant in the presence of no additions (○), 100 mM sodium nitrate (□), or 1 mM sodium nitrite (●). Approximately 6% (vol/vol) inocula were used. **(C,D)** show four strains grown with 100 mM nitrate **(C)** or no additions **(D)**. Wild-type with empty vector [JW710(pMO9075)],(△); wild-type with *rex* overexpression plasmid [JW710(pMO3313)], (▲); Δ*rex* strain with empty vector [JW3311(pMO9075)], (x); Δ*rex* strain with *rex* complement plasmid [JW3311(pMO3313)], (■). Approximately 7.5% (vol/vol) inocula were used. Readings reflect averages of three samples, and errors bars, which were often within the symbols, show standard deviations.

select for plasmid loss in a Δ*rex* strain grown in high nitrate. Cells containing the plasmid may produce enough of the antibiotic-modifying enzyme to confer sufficient resistance to allow other cells to survive without containing the plasmid. If this is the case, then the Δ*rex* cells containing the plasmid should grow slowly while those which have lost the plasmid should grow more rapidly in the presence of 100 mM nitrate. The result would be a population growth rate in-between that seen for wild-type vs. Δ*rex* strains. Indeed, the phenotype of the complemented Δ*rex* strain exhibits this growth property (**Figure 5C**). Finally, nitrate concentrations in the cultures with empty vector or *rex* complementing plasmids (**Figures 5C,D**) were measured colorimetrically at the end of growth. As with the wild-type cultures described above, gross consumption of nitrate was not detected for any of these strains (data not shown). This is evidence of genuine nitrate resistance in these strains. Taken together, these growth and gene fitness data support transcriptomic predictions that nitrate stress responses involve mechanisms independent of nitrite stress responses (He et al., 2010a).

DISCUSSION

Whereas Elias et al. (2009) and Bender et al. (2007) reported mutations that led to increased sensitivity to both nitrate and nitrite, here we report the unexpected discovery of DvH mutants with increased resistance to nitrate but not nitrite. The data presented confirm that the *rex* deletion and the "nitrate cluster" transposon mutants, the top candidates from fitness profiling, confer resistance to nitrate in DvH. Such resistance also developed in the non-mutagenized DvH parental strain after subculture from 100 mM nitrate (**Figure 1B**), likely as a result of the outgrowth of preexisting spontaneous nitrate-resistant mutants. The lack of nitrate metabolism of DvH is consistent with a report that 10 mM nitrate did not noticeably inhibit DvH (Haveman et al., 2004). Furthermore, DvH has been shown to reduce nitrite (Haveman et al., 2004), but not nitrate.

The ability of mutations in a subset of non-essential genes to confer nitrate resistance may in part account for the recently reported fluctuating sulfide levels produced by SRB in a bioreactor inoculated with oil from a Canadian oil field (Callbeck et al., 2013). In this bioreactor, sulfide production was completely inhibited during pulses of 100 mM nitrate. However, after each pulse, sulfide production resumed, indicating that some SRB persisted in the presence of the nitrate (Callbeck et al., 2013). The results of the work presented here suggest that persistence of SRB in nitrate-treated oil reservoirs may be the result of mutant resistance. Even if total oil-well nitrate concentrations reach low millimolar levels, the initial concentration of nitrate near the injection site will be much higher than this. For example, the peak nitrate concentration in one study of pulsed nitrate injection was reported as 760 mM (Voordouw et al., 2009). Resistance to nitrate in the presence of a mixed culture is consistent with preliminary fitness profiling data from G20 grown in coculture with the nitrate reducer *Pseudomonas stutzeri* RCH2 in the presence of 100 mM nitrate. Under these mixed-culture conditions, the "nitrate cluster" mutant and the *rex* mutant gained a fitness advantage (A. Deutschbauer, unpublished data) very similar to that observed in pools of G20 mutants alone in the presence of 150 mM nitrate (**Table 3**).

These fitness studies bring clarity to questions that neither transcriptomic nor proteomic data could answer. While "omics"

studies can assist detection and monitoring of changes in the metabolism of bacteria in contaminated environments (Steinberg et al., 2008), they are not sufficient (Torres-García et al., 2009) for elucidating underlying inhibitory mechanisms. In fact, there are poor correlations between the expression of transcripts and the expression of proteins in DvH in response to nitrate stress (Redding et al., 2006; He et al., 2010a). He et al. (2010a) reported 28 genes for which the mRNA and protein levels were both significantly changed in nitrate stress conditions. However, for 7 of these 28 genes, the mRNA was significantly downregulated while the protein was significantly upregulated (He et al., 2010a). Although this poor correlation may be a result of meaningful regulatory mechanisms (Lu et al., 2007), transcript abundance is difficult to interpret and does not always correlate well with gene fitness (Price et al., 2013). For example, there is an upward trend of expression of the "nitrate cluster" genes in both nitrate (He et al., 2010a) and nitrite (He et al., 2006) stress conditions (http://microbesonline.org/). Because mutation of the nitrate cluster genes confers a growth advantage in high nitrate, increased expression of these genes should be detrimental to growth of DvH in high nitrate. This is consistent with the recent deduction (Price et al., 2013) that, counterintuitively, detrimental bacterial genes are often not downregulated. This apparent suboptimal regulation of the nitrate cluster genes in the presence of high concentrations of nitrate likely contributes to the explanation of why their interruption confers such a strong growth advantage.

The roles of the genes of the nitrate cluster in nitrate sensitivity are not immediately obvious from their poor annotation (**Table 3**). The native functions of the nitrate cluster genes are not likely involved with nitrate, since neither DvH (Seitz and Cypionka, 1986; Pereira et al., 2000) nor G20 (Wall, unpublished data) have been shown to use nitrate for energy conservation. We hypothesize that they may allow non-specific nitrate transport by a leaky thiosulfate transporter. The G20 mutants in this cluster were mildly sick when grown with 10 mM thiosulfate as a terminal electron acceptor (A. Deutschbauer, unpublished data), which suggests a possible role for these genes in thiosulfate uptake. Preliminary data also show that the Δ*rex* DvH strain described here grows more slowly than the parent strain with 30 mM thiosulfate as a terminal electron acceptor (Christensen, unpublished data). Therefore, we suggest that mutation of these genes might relieve nitrate inhibition by barring entry of nitrate into the cell. Further study will be needed to explore their native functions.

Several additional genes outside of the "nitrate cluster" appear to have high fitness values during nitrate stress, indicating that their absence may improve growth. Follow-up studies with individual mutants will be necessary to confirm these predictions. The results from this study clearly indicate that DvH and G20 have common nitrate resistance mechanisms that should be considered in environmental modeling.

AUTHOR CONTRIBUTIONS

Hannah L. Korte, Samuel R. Fels and Judy D. Wall designed the experiments. Samuel R. Fels conducted the TnLE-seq experiments and analyzed them. Geoff A. Christensen constructed the Δ*rex* mutant and showed its impairment on thiosulfate. Morgan N. Price and Adam M. Deutschbauer generated and analyzed the G20 fitness profiling data. Jennifer V. Kuehl constructed the G20 transposon mutant library. Grant M. Zane constructed the DvH transposon mutant library, confirmed and provided the individual transposon mutants tested. Adam P. Arkin and Judy D. Wall supervised the project. Hannah L. Korte, Morgan N. Price, and Judy D. Wall interpreted the data and wrote the manuscript.

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SUPPLEMENTARY MATERIAL

The Supplementary Material for this article can be found online at: http://www.frontiersin.org/journal/10.3389/fmicb.2014.00153/abstract

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Appendix G - TnLE-seq data

(shaded genes contain a BglII recognition site)

Gene	Description	WT MOYLS4 (1)	WT MOYLS4 (2)	WT MOLS4	WT MOLS4 + NO_3	JW710 MOLS4	JW3319 MOLS4
DORF10279	hypothetical protein	3.01	2.95	2.17	0.06	3.01	3.46
DORF10286	hypothetical protein	0.60	0.84	1.27	0.01	0.72	0.79
DORF10446	hypothetical protein	0.60	0.81	0.49	0.01	1.29	0.77
DORF10632	hypothetical protein	0.53	0.74	0.71	0.03	0.66	0.67
DORF10862	HesB-like domain	0.42	0.26	0.20	0.00	0.45	0.40
DORF10920	hypothetical protein	0.78	0.52	0.84	0.03	0.77	0.85
DORF11409	hypothetical protein	0.39	0.47	0.21	0.00	0.35	0.27
DORF11799	hypothetical protein	1.18	1.50	0.76	0.05	1.34	1.33
DORF11999	pyridoxamine 5'-phosphate oxidase-related, FMN-binding	1.12	1.16	1.32	0.05	1.02	1.39
DORF123	hypothetical protein	2.64	1.71	1.92	1.34	2.19	2.56
DORF12360	hypothetical protein	0.65	0.86	0.80	0.01	0.68	0.68
DORF12455	helix-turn-helix protein, CopG family	0.51	0.35	0.26	0.00	0.61	0.48
DORF12457	protein of unknown function DUF497	0.87	0.18	0.00	0.00	0.14	0.20
DORF12461	HigA protein (antitoxin to HigB)	0.65	1.19	0.71	0.03	0.91	1.15
DORF12465	hypothetical protein	0.55	0.66	1.18	0.01	1.08	1.11
DORF12467	protein of unknown function DUF497	1.60	1.07	2.94	0.00	1.22	0.95
DORF12469	hypothetical protein	0.16	0.13	0.00	0.04	0.23	0.25
DORF12810	hypothetical protein	1.47	1.45	1.25	0.01	1.26	1.16
DORF13021	hypothetical protein	1.60	1.45	2.60	0.00	1.28	1.59
DORF13417	hypothetical protein	0.18	0.27	0.74	0.01	0.28	0.25
DORF13424	hypothetical protein	0.59	0.81	1.35	0.02	0.80	1.32
DORF14650	hypothetical protein	0.46	0.85	1.10	0.03	0.93	1.38
DORF1474	hypothetical protein	0.12	0.20	0.04	0.01	0.14	0.13
DORF14879	putative anti-sigma regulatory factor, serine/threonine prot	0.16	0.09	0.11	0.00	0.11	0.11
DORF14945	ada metal-binding domain-like, possible truncation	0.12	0.19	0.00	0.02	0.29	0.33
DORF15009	Response regulator containing a CheY-like receiver domain a	0.00	0.12	0.11	0.00	0.11	0.09
DORF15023	conserved hypothetical protein	0.50	0.38	0.11	0.04	0.66	0.52
DORF15085	conserved hypothetical protein	0.02	0.02	0.00	0.00	0.03	0.04
DORF15105	Predicted transcriptional regulator	0.45	0.33	0.06	0.01	0.36	0.31
DORF15206	AAA ATPase	0.94	0.91	0.77	0.03	1.14	1.20
DORF15229	hypothetical protein	0.19	0.32	0.10	0.00	0.40	0.43
DORF15383	hypothetical protein	0.91	1.21	1.35	0.03	1.64	1.77
DORF16094	hypothetical protein	0.79	0.64	1.16	0.04	0.80	1.03
DORF16603	hypothetical protein	0.65	1.19	1.49	0.02	0.95	0.91
DORF17147	TPR domain protein	1.02	0.90	1.15	0.02	1.15	1.10
DORF18707	hypothetical protein	0.14	0.45	1.11	0.06	0.52	0.30
DORF19110	hypothetical protein	0.87	1.02	0.90	0.03	0.95	0.98
DORF19118	hypothetical protein	1.74	2.37	2.56	0.04	1.82	1.66
DORF19125	hypothetical protein	1.28	1.49	1.45	0.03	1.33	1.51
DORF19137	hypothetical protein	1.24	1.32	1.20	0.05	1.31	1.25
DORF19323	hypothetical protein	1.45	1.04	2.63	0.00	1.55	1.80
DORF19328	hypothetical protein	1.76	1.62	1.68	0.04	1.63	1.66
DORF19331	hypothetical protein	0.86	1.27	0.45	0.00	1.00	0.98
DORF1985	hypothetical protein	0.74	1.31	0.75	0.55	1.02	1.23
DORF20226	hypothetical protein	3.06	2.92	1.84	0.03	2.23	3.12
DORF2077	hypothetical protein	0.62	0.98	0.61	0.05	0.95	1.12
DORF2111	hypothetical protein	0.82	1.08	1.07	0.82	1.21	1.13
DORF2116	hypothetical protein	0.89	0.95	1.05	0.61	1.12	0.96
DORF2161	hypothetical protein	0.96	1.14	1.20	0.55	1.17	1.05
DORF2315	hypothetical protein	0.24	0.73	0.23	0.02	0.66	0.67
DORF23513	hypothetical protein	1.05	0.74	0.74	0.01	0.58	0.53
DORF24435	hypothetical protein	1.43	1.55	1.37	0.02	1.43	1.59
DORF24761	hypothetical protein	1.18	0.91	1.02	0.01	0.96	0.93
DORF25031	hypothetical protein	1.58	1.00	1.28	0.03	0.90	1.88
DORF25047	hypothetical protein	2.42	2.61	2.58	0.04	2.95	2.75
DORF25842	hypothetical protein	4.42	2.95	4.66	0.08	4.04	3.27
DORF26313	hypothetical protein	1.93	1.37	1.71	0.02	1.49	1.54
DORF26446	hypothetical protein	0.65	0.45	0.22	0.01	0.35	0.52
DORF26459	hypothetical protein	1.67	1.33	1.40	0.04	1.23	1.29
DORF26503	hypothetical protein	0.93	0.79	1.12	0.01	0.78	0.62
DORF26828	hypothetical protein	1.49	1.28	0.95	0.03	1.37	1.50

DORF26924	Methylase involved in ubiquinone/menaquinone biosynthes		0.01	0.03	0.00	0.00	0.03	0.04
DORF27889	hypothetical protein		1.27	1.11	1.14	0.01	1.35	1.23
DORF28817	hypothetical protein		0.14	0.09	0.00	0.00	0.10	0.12
DORF28911	hypothetical protein		1.08	1.19	0.89	0.01	1.03	1.17
DORF29743	hypothetical protein		0.45	0.72	0.01	0.00	0.53	0.50
DORF31523	hypothetical protein		0.82	0.73	0.74	0.00	0.75	0.96
DORF32061	hypothetical protein		0.58	0.89	1.16	0.01	0.50	0.66
DORF32294	hypothetical protein		0.72	0.84	0.93	0.01	0.79	0.80
DORF34036	hypothetical protein		0.90	0.80	0.92	0.02	1.28	1.47
DORF35362	hypothetical protein		0.10	0.99	0.85	0.03	0.14	0.19
DORF35977	hypothetical protein		1.36	0.90	1.15	0.05	0.85	0.80
DORF36392	hypothetical protein		0.00	0.02	0.17	0.00	0.01	0.05
DORF37046	hypothetical protein		0.53	0.47	0.43	0.17	0.53	0.62
DORF37060	hypothetical protein		0.41	0.28	0.20	0.01	0.42	0.45
DORF37657	Hemolysins and related proteins containing CBS domains		0.21	0.28	0.42	0.02	0.28	0.37
DORF37658	Magnesium and cobalt efflux protein CorC		0.25	0.26	0.30	0.01	0.33	0.36
DORF38058	putative regulatory protein, FmdB family		0.12	0.39	0.52	0.02	0.39	0.31
DORF39356	hypothetical protein		0.77	0.38	0.15	0.04	0.69	0.55
DORF39360	hypothetical protein		0.98	0.72	1.45	0.00	0.78	1.13
DORF3938	hypothetical protein		0.00	0.00	0.08	0.00	0.01	0.00
DORF39640	Flp pilus assembly protein, pilin Flp		1.37	0.76	0.32	0.00	0.65	1.01
DORF40128	hypothetical protein		0.00	0.03	0.00	0.00	0.02	0.01
DORF40861	hypothetical protein		1.10	1.02	1.05	0.03	1.09	1.00
DORF41147	hypothetical protein		0.95	1.34	1.36	0.02	1.06	1.56
DORF41366	hypothetical protein		0.82	1.14	0.89	0.03	1.55	1.62
DORF4170	hypothetical protein		1.00	0.77	0.76	0.00	0.57	0.81
DORF42491	hypothetical protein		1.25	1.61	1.60	0.05	1.37	1.51
DORF43224	hypothetical protein		0.28	0.46	0.00	0.00	0.50	0.55
DORF43274	regulatory protein, LacI		3.33	2.08	2.62	0.02	1.82	2.05
DORF43335	hypothetical protein		0.07	0.02	0.03	0.00	0.15	0.15
DORF43366	hypothetical protein		0.97	1.37	1.65	0.01	1.93	1.89
DORF43423	Uncharacterized protein conserved in archaea		1.11	1.27	1.35	0.02	1.05	1.08
DORF43823	hypothetical protein		1.14	1.09	0.80	0.03	0.75	0.77
DORF4420	hypothetical protein		0.90	0.82	1.15	0.02	1.14	1.54
DORF45242	hypothetical protein		1.14	1.24	1.10	0.03	1.54	1.40
DORF45537	hypothetical protein		3.81	3.10	2.56	0.10	2.90	2.81
DORF46408	hypothetical protein		1.78	2.28	1.41	0.06	1.20	1.31
DORF47110	hypothetical protein		1.15	1.33	1.16	0.02	1.14	1.11
DORF47312	hypothetical protein		0.00	0.01	0.02	0.00	0.00	0.00
DORF526	cyclopropane-fatty-acyl-phospholipid synthase/methyltrans		0.62	0.57	0.60	0.37	0.54	0.50
DORF5389	hypothetical protein		3.06	2.15	3.12	0.05	2.11	2.22
DORF5594	diguanylate phosphodiesterase (EAL domain)		1.10	1.31	1.34	0.03	1.54	1.35
DORF6830	hypothetical protein		1.58	1.27	1.43	0.03	2.35	1.42
DORF702	response regulator receiver protein		0.40	0.72	0.56	0.22	0.64	0.64
DORF7327	putative mitomycin resistance protein		1.82	1.40	0.92	0.02	1.29	1.11
DORF7571	hypothetical protein		0.28	0.77	0.01	0.00	0.40	0.44
DORF765	rhodanese-like protein		0.65	0.76	0.69	0.73	1.02	0.87
DORF768	hypothetical protein		0.44	0.64	0.63	0.45	0.52	0.60
DORF7824	hypothetical protein		0.80	2.14	2.44	0.04	2.06	1.40
DORF7832	hypothetical protein		0.69	0.91	0.86	0.02	0.90	0.90
DORF7930	hypothetical protein		0.67	0.29	0.61	0.02	0.72	0.59
DORF807	hypothetical protein		0.70	0.92	1.14	0.71	1.17	1.05
DORF8192	hypothetical protein		0.17	0.72	0.31	0.01	0.78	1.06
DORF831	NA protein		0.48	0.98	0.74	0.51	1.04	0.94
DORF8571	hypothetical protein		0.09	0.19	0.26	0.00	0.17	0.26
DORF8626	hypothetical protein		1.73	1.69	2.19	0.02	2.07	2.02
DORF9413	hypothetical protein		0.83	0.78	1.07	0.03	0.57	0.86
DORF9582	hypothetical protein		1.29	0.76	1.57	0.02	1.16	1.15
DORF9585			0.89	0.34	0.35	0.00	0.55	0.63
DVU0001	chromosomal replication initiator protein DnaA (T	dnaA-1	0.99	1.00	1.25	0.02	0.72	0.85
DVU0002	DNA polymerase III, beta subunit (TIGR)	dnaN	0.00	0.00	0.00	0.00	0.00	0.00
DVU0003	DNA gyrase, B subunit (TIGR)	gyrB	0.00	0.00	0.03	0.00	0.00	0.00
DVU0004	DNA gyrase, A subunit (TIGR)	gyrA	0.00	0.00	0.03	0.00	0.00	0.00
DVU0005	lipoprotein, putative (TIGR)		2.17	1.81	1.82	0.05	1.93	1.52
DVU0006	universal stress protein family (TIGR)		1.62	1.78	1.94	0.03	1.53	1.64
DVU0007	asparaginyl-tRNA synthetase (TIGR)	asnS	1.79	1.47	1.39	0.05	1.59	1.53
DVU0008	hypothetical protein (TIGR)		0.56	0.34	0.67	0.02	0.47	0.50

DVU0009	DedA family protein (TIGR)	dctM	1.45	1.55	1.53	0.01	1.53	1.23
DVU0010	TRAP transporter, DctQ family (TIGR)		1.23	1.32	1.43	0.02	1.16	1.11
DVU0011	TRAP dicarboxylate family transporter (TIGR)		2.24	2.20	2.00	0.03	2.17	2.08
DVU0012	hypothetical protein (TIGR)		1.61	1.65	1.63	0.03	1.81	1.57
DVU0013	sensory box histidine kinase (TIGR)		1.01	0.98	2.29	0.04	0.93	1.17
DVU0014	translation initiation factor IF-1 (TIGR)	infA-1	1.03	0.38	0.63	0.00	0.41	0.60
DVU0015	prolipoprotein diacylglyceryl transferase (TIGR)	lgt	0.02	0.01	0.10	0.00	0.00	0.00
DVU0016	hypothetical protein (TIGR)		0.41	0.27	0.18	0.02	0.35	0.59
DVU0018	methyl-accepting chemotaxis protein, putative (TIGR)		1.36	1.50	1.42	0.04	1.58	1.52
DVU0019	nigerythrin (TIGR)	ngr	1.95	2.08	2.54	0.06	2.24	2.20
DVU0020	hypothetical protein (TIGR)		3.76	3.42	4.08	0.06	3.27	2.88
DVU0021	conserved domain protein (TIGR)		1.45	1.82	1.49	0.04	1.49	1.54
DVU0022	HAMP domain/GGDEF domain/EAL domain protein (TIGR)		1.97	2.10	1.82	0.05	1.98	1.83
DVU0024	conserved hypothetical protein (TIGR)		0.76	1.13	1.43	0.01	0.72	1.05
DVU0025	sensory box histidine kinase (TIGR)		1.79	1.83	1.43	0.04	1.66	1.65
DVU0026	conserved hypothetical protein (TIGR)		1.88	2.08	1.48	0.02	1.81	1.76
DVU0027	membrane protein, putative (TIGR)		1.45	1.46	1.43	0.04	1.42	1.43
DVU0028	chaperone CsaA (TIGR)	csaA	1.42	0.96	1.80	0.02	1.03	1.12
DVU0029	hydantoinase/oxoprolinase family protein (TIGR)		1.27	0.70	1.11	0.03	0.88	1.35
DVU0030	transcriptional regulator, GntR family (TIGR)		2.15	1.66	1.56	0.05	1.90	1.71
DVU0031	AzlC family protein (TIGR)		2.01	1.49	2.13	0.05	1.65	1.57
DVU0032	conserved hypothetical protein (TIGR)		1.32	1.45	0.91	0.04	1.65	1.45
DVU0033	isochorismatase family protein (TIGR)		1.81	1.09	1.28	0.04	1.18	1.20
DVU0034	DSBA-like thioredoxin domain protein (TIGR)		1.85	2.02	2.11	0.02	1.96	1.86
DVU0035	hypothetical protein (TIGR)		1.53	0.97	0.81	0.07	0.98	1.03
DVU0036	hypothetical protein (TIGR)		1.29	1.53	1.40	0.02	1.21	1.07
DVU0037	conserved hypothetical protein (TIGR)		1.77	1.32	0.85	0.04	1.42	1.54
DVU0038	acyltransferase domain protein (TIGR)		1.67	1.77	2.32	0.03	1.68	1.64
DVU0039	C4-type zinc finger protein, DksA/TraR family (TIGR)		2.25	2.97	2.83	0.05	2.41	2.46
DVU0040	hypothetical protein (TIGR)		1.64	1.56	2.00	0.04	1.90	1.73
DVU0041	transglycosylase, SLT family (TIGR)		2.35	2.57	2.68	0.06	2.50	2.26
DVU0042	RNA methyltransferase, TrmH family, group 3 (TIGR)		2.21	1.92	2.31	0.03	2.13	2.18
DVU0043	flagellar biosynthetic protein FliQ (TIGR)	fliQ	0.80	1.18	1.26	0.04	1.53	1.69
DVU0044	flagellar biosynthetic protein fliP (TIGR)	fliP	1.31	1.12	0.93	0.02	1.34	1.39
DVU0045	flagellar biosynthesis protein, FliO, putative (TIGR)		1.47	1.29	1.00	0.02	1.62	1.20
DVU0046	flagellar motor switch protein FliN (TIGR)	fliN	1.90	1.85	1.60	0.05	2.08	2.17
DVU0047	flagellar protein FliL (TIGR)		0.95	1.05	1.06	0.01	1.35	1.09
DVU0048	chemotaxis protein MotB (TIGR)		1.46	1.69	1.83	0.03	1.60	1.53
DVU0049	OmpA family protein (TIGR)		2.02	1.89	1.67	0.04	1.63	1.65
DVU0050	chemotaxis protein MotA (TIGR)	motA-1	2.13	1.91	2.28	0.03	1.95	1.88
DVU0051	conserved hypothetical protein TIGR00044 (TIGR)		1.73	2.15	2.43	0.05	1.91	1.97
DVU0052	GTP-binding protein Era (TIGR)	era	0.18	0.29	1.35	0.03	0.12	0.14
DVU0053	sulfate permease, putative (TIGR)		1.93	2.23	2.55	0.05	2.32	2.01
DVU0054	dihydrouridine synthase family protein (TIGR)		1.99	1.79	1.63	0.05	1.78	1.66
DVU0055	hydroxymethylbutenyl pyrophosphate reductase (	ispH	0.84	0.67	2.10	0.02	0.25	0.19
DVU0056	chemotaxis protein CheV (TIGR)	cheV-1	1.27	1.44	1.39	0.03	1.36	1.45
DVU0057	transcriptional regulator, TetR family (TIGR)		1.91	1.45	1.82	0.04	1.50	1.43
DVU0058	efflux transporter, RND family, MFP subunit (TIGR)		2.28	2.01	2.15	0.04	2.08	1.89
DVU0059	AcrB/AcrD/AcrF family protein (TIGR)		1.64	1.58	1.36	0.04	1.36	1.19
DVU0060	efflux transporter, RND family, MFP subunit (TIGR	acrA	1.74	1.72	1.41	0.02	1.52	1.58
DVU0061	multidrug resistance protein, putative (TIGR)		2.26	2.12	1.82	0.04	2.18	2.09
DVU0062	RND efflux system, outer membrane protein, NodT family (T		1.38	1.53	1.07	1.16	1.28	1.22
DVU0063	transcriptional regulator, MarR family (TIGR)		0.68	0.87	0.63	0.03	1.21	0.95
DVU0064	hypothetical protein (TIGR)		1.25	1.52	1.45	0.04	1.45	1.55
DVU0065	hypothetical protein (TIGR)		1.81	2.06	2.57	0.04	1.75	1.65
DVU0066	cytidine/deoxycytidylate deaminase domain protein (TIGR)		1.42	1.60	1.55	0.03	1.22	1.14
DVU0067	hypothetical protein (TIGR)		0.90	1.03	0.96	0.01	1.04	0.95
DVU0068	conserved hypothetical protein (TIGR)		1.87	1.83	1.88	0.05	1.87	1.83
DVU0069	hypothetical protein (TIGR)		1.97	2.02	1.91	0.04	1.84	1.64
DVU0070	Ser/Thr protein phosphatase family protein (TIGR)	yhaO	2.06	1.91	1.94	0.04	1.70	1.62
DVU0071	DNA polymerase IV (TIGR)	dinP	2.01	2.12	2.05	0.05	1.84	1.74
DVU0072	glucose-1-phosphate cytidylyl-transferase (TIGR)	mpg	0.87	0.75	0.77	0.02	0.26	0.34
DVU0073	CDP-glucose-4,6-dehydratase, putative (TIGR)		1.07	0.64	1.18	0.01	0.21	0.26
DVU0074	polysaccharide biosynthesis domain protein (TIGR)		1.25	1.42	1.48	0.03	1.51	1.17
DVU0075	aminotransferase, DegT/DnrJ/EryC1/StrS family (T	rfbE	1.33	0.72	1.30	0.03	0.42	0.35
DVU0076	glycosyl transferase, group 2 family protein (TIGR)		0.91	0.64	0.85	0.02	0.37	0.27
DVU0077	conserved hypothetical protein (TIGR)		1.85	1.52	2.09	0.03	1.40	1.37

DVU0078	conserved hypothetical protein (TIGR)		0.98	1.79	1.33	0.03	1.54	1.42
DVU0079	ZIP zinc transporter family protein (TIGR)	gufA	1.36	1.44	1.28	0.03	1.33	1.37
DVU0080	fumarate hydratase, class II (TIGR)	fumC	1.94	1.96	1.59	0.04	1.64	1.73
DVU0081	sensory box histidine kinase/response regulator (TIGR)		1.18	1.19	1.08	0.02	1.15	1.14
DVU0082	conserved hypothetical protein (TIGR)		1.41	1.76	1.46	0.03	1.50	1.48
DVU0083	conserved hypothetical protein (TIGR)		1.84	1.73	0.68	0.03	1.35	1.36
DVU0084	translation initiation factor, aIF-2BI family, putative (TIGR)		1.79	1.71	1.86	0.05	1.52	1.42
DVU0085	tryptophan synthase, beta subunit (TIGR)	trpB-1	2.55	2.23	2.11	0.06	2.17	2.23
DVU0087	conserved domain protein (TIGR)		0.64	0.37	0.40	0.01	0.40	0.42
DVU0088	Sodium/pantothenate symporter (TIGR)		0.75	0.55	0.99	0.01	0.54	0.64
DVU0089	conserved hypothetical protein (TIGR)		0.88	0.94	0.69	0.02	1.13	1.09
DVU0090	GDP-fucose synthetase (TIGR)	wcaG	0.22	0.20	0.45	0.01	0.02	0.08
DVU0091	conserved hypothetical protein (TIGR)		0.90	1.01	0.86	0.03	1.16	1.11
DVU0092	sensory box histidine kinase (TIGR)		1.26	1.42	1.17	0.03	1.45	1.30
DVU0093	conserved domain protein/glycosyl transferase, group 1 fan		1.52	1.54	1.63	0.04	1.59	1.54
DVU0094	methyl-accepting chemotaxis protein (TIGR)		1.35	1.22	1.30	0.03	1.15	1.20
DVU0095	polyamine ABC transporter, periplasmic polyamine	potD-1	1.35	1.20	1.26	0.02	1.37	1.21
DVU0096	polyamine ABC transporter, permease protein (TIC	potC	1.23	1.91	1.49	0.08	2.01	2.18
DVU0097	polyamine ABC transporter, permease protein (TIC	potB	0.96	0.93	0.93	0.02	1.14	1.15
DVU0098	polyamine ABC transporter, ATP-binding protein (T	potA	0.98	1.13	0.80	0.03	1.19	1.09
DVU0099	TonB domain protein (TIGR)		1.58	1.75	1.61	0.04	1.77	1.51
DVU0100	TonB-dependent receptor (TIGR)		1.91	1.88	1.88	0.05	1.77	1.68
DVU0101	methlytransferase, UbiE/COQ5 family (TIGR)		1.76	1.70	1.64	0.04	1.63	1.64
DVU0102	cation ABC transporter, periplasmic binding protein (TIGR)		1.72	1.63	1.52	0.03	1.55	1.54
DVU0103	cation ABC transporter, ATP-binding protein, puta	fepC	1.55	1.50	0.97	0.06	1.22	1.07
DVU0104	cation ABC transporter, permease protein, putative (TIGR)		1.47	1.56	1.29	0.02	1.47	1.44
DVU0105	glutamine ABC transporter, ATP-binding protein (T	glnQ	1.68	1.34	1.34	0.03	1.83	1.49
DVU0106	glutamine ABC transporter, permease protein (TIG	glnP	1.20	1.28	1.19	0.03	1.41	1.37
DVU0107	glutamine ABC transporter, periplasmic glutamine	glnH	1.18	1.16	1.04	0.02	1.16	1.20
DVU0108	hypothetical protein (TIGR)		0.23	0.35	0.72	0.00	0.65	0.81
DVU0109	sensor histidine kinase (TIGR)	hydH	1.74	1.48	1.30	0.03	1.63	1.47
DVU0110	sigma-54 dependent transcriptional regulator/resp	ntrC	1.13	1.09	1.31	0.02	1.20	1.04
DVU0111	response regulator (TIGR)		1.41	1.16	0.76	0.02	0.99	1.05
DVU0112	deoxyribodipyrimidine photolyase, putative (TIGR)	phrB	0.95	1.39	1.04	0.02	1.14	1.07
DVU0113	phosphoribosyl-AMP cyclohydrolase (TIGR)	hisI	1.45	1.73	0.18	0.00	0.01	0.01
DVU0114	ATP phosphoribosyltransferase (TIGR)	hisG	1.73	1.55	0.05	0.01	0.00	0.01
DVU0115	shikimate 5-dehydrogenase (TIGR)	aroE	0.95	0.89	0.49	0.00	0.02	0.02
DVU0116	polysaccharide deacetylase family protein (TIGR)		1.20	1.31	0.64	0.01	1.10	0.92
DVU0117	glycosyl transferase, group 2 family protein (TIGR)		1.52	1.47	1.27	0.05	1.41	1.43
DVU0118	sigma-54 dependent transcriptional regulator/resp	ntrC	1.61	2.15	1.67	0.03	1.98	1.61
DVU0119	sensor histidine kinase (TIGR)		1.41	1.56	1.45	0.03	1.46	1.31
DVU0120	ABC transporter, substrate-binding protein, putative (TIGR)		2.40	1.82	1.30	0.04	1.83	1.63
DVU0121	conserved hypothetical protein (TIGR)		1.38	1.14	1.02	0.03	1.34	1.23
DVU0122	hypothetical protein (TIGR)		1.72	0.89	1.65	0.03	0.98	1.01
DVU0123	membrane protein, putative (TIGR)		1.39	1.62	1.74	8.03	1.58	1.42
DVU0124	hypothetical protein (TIGR)		0.30	0.66	0.33	0.00	0.53	0.50
DVU0125	hypothetical protein (TIGR)		1.46	1.54	1.36	0.05	1.60	1.32
DVU0126	ABC transporter, ATP-binding protein (TIGR)	b3486	1.58	1.41	1.65	0.02	1.38	1.36
DVU0127	membrane protein, putative (TIGR)		2.07	2.03	1.59	0.04	1.75	1.71
DVU0128	membrane protein, putative (TIGR)		1.55	1.80	1.83	0.04	1.47	1.41
DVU0129	sensory box/HDIG domain protein (TIGR)		1.33	1.34	0.90	0.02	1.41	1.22
DVU0130	phosphoglycolate phosphatase, putative (TIGR)		1.47	1.66	1.70	0.02	1.58	1.47
DVU0132	membrane protein, putative (TIGR)		1.04	1.72	1.41	0.02	1.03	1.34
DVU0133	hypothetical protein (TIGR)		1.58	1.38	0.81	0.03	1.09	1.12
DVU0134	glycosyl transferase, group 2 family protein (TIGR)		28.78	1.28	0.99	0.02	1.00	0.91
DVU0135	conserved hypothetical protein (TIGR)		1.23	1.28	1.30	0.03	1.29	1.16
DVU0136	hypothetical protein (TIGR)		2.81	2.04	1.16	0.06	1.61	1.61
DVU0138	response regulator (TIGR)		1.20	1.30	1.23	0.03	1.20	1.29
DVU0139	sensor histidine kinase (TIGR)	cckA	1.97	1.76	1.64	0.03	1.55	1.66
DVU0140	response regulator (TIGR)	cheYI	0.84	0.57	0.68	0.02	0.74	0.76
DVU0141	peptidase, M50 family (TIGR)		0.77	0.77	0.98	0.01	0.33	0.35
DVU0142	tryptophanyl-tRNA synthetase (TIGR)	trpS	0.00	0.03	0.02	0.00	0.00	0.00
DVU0143	conserved hypothetical protein (TIGR)		1.20	1.14	0.73	0.03	1.07	0.97
DVU0144	cytidyltransferase-related domain protein (TIGR)	rfaE	0.08	0.02	0.31	0.00	0.03	0.02
DVU0145	response regulator (TIGR)		0.80	0.70	0.65	0.01	0.89	0.82
DVU0146	hypothetical protein (TIGR)		0.73	0.67	0.43	0.02	0.73	0.64
DVU0147	lipoprotein, putative (TIGR)		0.83	0.82	0.51	0.01	1.05	1.01

DVU0148	lipoprotein, putative (TIGR)		0.85	1.37	0.78	0.15	1.30	1.37
DVU0149	membrane protein, putative (TIGR)		0.97	1.05	0.62	0.02	0.85	0.97
DVU0150	membrane protein, putative (TIGR)		0.76	0.87	1.38	0.01	0.69	0.62
DVU0151	HAMP domain/sigma-54 interaction domain protein (TIGR)		1.33	1.27	1.42	0.02	1.17	1.17
DVU0152	phosphoenolpyruvate synthase-related protein (TI	ppsA	1.33	1.48	1.52	0.03	1.43	1.35
DVU0153	hypothetical protein (TIGR)		2.21	2.47	2.05	0.04	2.32	2.17
DVU0155	type I phosphodiesterase/nucleotide pyrophosphatase fami		1.18	1.32	1.32	0.02	1.49	1.19
DVU0156	ATP-dependent DNA helicase, UvrD/REP family (TI	pcrA	1.98	1.99	2.06	0.04	1.86	1.74
DVU0157	thiamin-monophosphate kinase (TIGR)	thiL	0.19	0.11	0.45	0.00	0.03	0.04
DVU0158	conserved hypothetical protein TIGR00104 (TIGR)		1.44	1.37	1.46	0.02	1.65	1.23
DVU0159	thioesterase family protein (TIGR)		0.94	1.52	1.03	0.05	1.25	1.15
DVU0160	carbohydrate isomerase, KpsF/GutQ family (TIGR)		0.04	0.00	0.00	0.00	0.01	0.00
DVU0161	amidophosphoribosyltransferase (TIGR)	purF	0.25	0.13	0.41	0.01	0.02	0.02
DVU0162	carbamoyl-phosphate synthase, large subunit (TIG	carB	0.49	0.49	0.03	0.01	0.00	0.00
DVU0163	lipoprotein, putative (TIGR)		1.08	0.51	0.65	0.00	0.85	0.69
DVU0164	cation efflux family protein (TIGR)		1.47	1.23	0.72	0.04	1.10	1.09
DVU0165	oligopeptide/dipeptide ABC transporter, ATP-bind	oppF	1.39	1.40	1.70	0.04	1.46	1.51
DVU0166	oligopeptide/dipeptide ABC transporter, ATP-bind	oppD	1.69	1.37	1.36	0.04	1.56	1.64
DVU0167	oligopeptide/dipeptide ABC transporter, permeas	oppC	1.19	1.11	1.65	0.03	1.18	1.30
DVU0168	oligopeptide/dipeptide ABC transporter, permease protein (		1.28	0.96	1.26	0.03	1.01	1.07
DVU0169	oligopeptide/dipeptide ABC transporter, periplasmic oligope		2.03	1.66	1.79	0.04	1.85	1.87
DVU0170	methyl-accepting chemotaxis protein (TIGR)		2.01	1.89	1.58	1.30	1.69	1.69
DVU0171	hemolysin-related protein (TIGR)	patB	1.69	1.49	1.38	0.03	1.50	1.42
DVU0172	thiosulfate reductase (phsB) (Shelley Haveman)	phsB	2.10	2.24	2.58	0.03	1.90	1.04
DVU0173	thiosulfate reductase (Shelley Haveman)	phsA	1.81	1.49	1.25	0.04	1.38	0.79
DVU0174	hypothetical protein (TIGR)		1.90	0.45	0.56	0.00	0.84	1.43
DVU0175	tungsten formylmethanofuran dehydrogenase family protei		2.01	1.54	1.23	0.04	1.49	1.14
DVU0176	glycerophosphoryl diester phosphodiesterase family protein		1.19	1.36	1.37	0.04	1.45	1.27
DVU0177	molybdenum ABC transporter, periplasmic molybc	modA	2.76	2.22	2.95	0.05	2.21	2.19
DVU0179	molybdenum-pterin binding domain protein/site-specific re		1.59	1.45	1.56	0.04	1.50	1.46
DVU0180	ATP-binding component of molybdate ABC transpo	modC	1.53	1.08	1.04	0.02	1.02	1.11
DVU0181	molybdenum ABC transporter, permease protein (	modB	1.26	1.37	1.09	0.04	1.28	1.26
DVU0182	radical SAM domain protein (TIGR)		2.20	1.65	1.45	0.05	1.54	1.59
DVU0183	methyl-accepting chemotaxis protein (TIGR)		1.79	1.26	1.44	0.04	1.29	1.42
DVU0184	hypothetical protein (TIGR)		1.55	0.90	0.94	0.01	1.00	1.29
DVU0185	hypothetical protein (TIGR)		2.39	0.78	0.54	0.03	0.79	1.09
DVU0186	conserved hypothetical protein (TIGR)		0.92	1.36	1.05	0.02	0.95	1.15
DVU0187	GGDEF domain protein (TIGR)		1.71	1.50	1.39	0.04	1.33	1.49
DVU0189	phage/plasmid primase, P4 family (TIGR)		0.91	0.83	0.74	0.01	0.74	0.83
DVU0190	hypothetical protein (TIGR)		0.25	0.44	0.42	0.02	0.17	0.31
DVU0191	conserved hypothetical protein (TIGR)		1.60	1.37	1.67	0.03	1.25	1.40
DVU0192	adenine specific DNA methyltransferase, putative (TIGR)		1.09	0.84	0.97	0.01	0.79	0.92
DVU0193	hypothetical protein (TIGR)		0.90	0.80	1.17	0.03	1.02	1.13
DVU0194	terminase, large subunit, putative (TIGR)		1.80	1.89	1.44	0.05	1.68	1.85
DVU0195	hypothetical protein (TIGR)		2.24	2.39	1.64	0.06	2.32	2.68
DVU0196	hypothetical protein (TIGR)		1.23	0.82	0.88	0.00	0.85	0.68
DVU0197	phage portal protein, lambda family (TIGR)		1.62	1.50	1.43	0.02	1.48	1.51
DVU0198	minor capsid protein C, degenerate (TIGR)		1.03	1.01	0.75	0.02	0.90	0.98
DVU0199	conserved hypothetical protein (TIGR)		0.85	0.72	0.74	0.02	0.80	0.70
DVU0200	major head protein (TIGR)		1.00	0.77	0.68	0.01	0.78	0.80
DVU0201	hypothetical protein (TIGR)		2.43	1.21	0.52	0.04	1.23	1.32
DVU0202	holin (TIGR)		0.28	0.39	0.52	0.01	0.39	0.31
DVU0203	conserved hypothetical protein (TIGR)		2.81	2.21	1.83	0.06	2.18	1.80
DVU0204	lipoprotein, putative (TIGR)		2.52	2.25	1.21	0.09	2.02	1.81
DVU0205	hypothetical protein (TIGR)		2.38	1.78	3.09	0.03	1.96	1.79
DVU0206	hypothetical protein (TIGR)		0.18	0.10	0.07	0.01	0.06	0.07
DVU0207	hypothetical protein (TIGR)		0.11	0.13	0.19	0.00	0.17	0.24
DVU0208	hypothetical protein (TIGR)		1.41	1.08	1.49	0.03	1.15	0.90
DVU0209	conserved hypothetical protein (TIGR)		1.32	0.57	0.86	0.03	0.70	0.80
DVU0210	tail sheath protein, putative (TIGR)		0.74	0.86	0.92	0.03	0.81	0.72
DVU0211	tail tube protein, putative (TIGR)		0.40	0.18	0.10	0.01	0.20	0.18
DVU0212	conserved hypothetical protein (TIGR)		2.26	1.61	1.02	0.02	1.29	1.28
DVU0213	conserved domain protein (TIGR)		1.02	1.03	0.83	0.03	0.81	0.84
DVU0214	tail/DNA circulation protein, putative (TIGR)		1.03	0.75	0.77	0.08	0.75	0.66
DVU0215	tail protein, putative (TIGR)		1.37	1.33	1.38	0.02	1.31	1.18
DVU0216	phage baseplate assembly protein V, putative (TIGR)		0.85	1.15	0.67	0.03	0.84	0.81
DVU0217	tail protein, putative (TIGR)		1.90	2.05	2.15	0.07	2.01	1.84

DVU0218	tail protein, putative (TIGR)		1.80	1.81	1.47	0.03	1.66	1.67
DVU0219	tail protein, putative (TIGR)		0.86	0.85	0.96	0.02	0.89	0.94
DVU0220	tail fiber protein, putative (TIGR)		1.91	1.49	1.81	0.06	1.58	1.59
DVU0221	tail fiber assembly protein, putative (TIGR)		1.37	1.67	1.11	0.03	1.50	1.37
DVU0222	hypothetical protein (TIGR)		0.71	0.68	0.53	0.02	0.56	0.58
DVU0223	conserved hypothetical protein (TIGR)		0.21	0.30	0.17	0.00	0.24	0.44
DVU0224	conserved hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU0226	hypothetical protein (TIGR)		2.17	1.67	1.68	0.05	1.66	1.68
DVU0227	conserved hypothetical protein (TIGR)		0.56	0.36	0.21	0.01	0.25	0.34
DVU0230	transcriptional regulator cII, putative (TIGR)		1.20	1.89	1.61	0.07	1.85	1.94
DVU0231	hypothetical protein (TIGR)		1.79	1.99	1.63	0.03	1.30	1.49
DVU0232	hypothetical protein (TIGR)		0.51	0.89	1.03	0.01	0.56	0.73
DVU0234	hypothetical protein (TIGR)		3.01	3.31	2.01	0.07	2.59	2.58
DVU0235	hypothetical protein (TIGR)		2.36	1.91	1.20	0.03	1.97	2.02
DVU0236	site-specific recombinase, phage integrase family (TIGR)		1.35	1.57	1.91	0.05	1.79	1.54
DVU0237	seryl-tRNA synthetase (TIGR)	serS	0.01	0.01	0.05	0.00	0.00	0.00
DVU0238	hypothetical protein (TIGR)		1.09	1.41	1.43	0.01	1.29	1.28
DVU0240	hypothetical protein (TIGR)		1.63	1.11	0.63	0.01	1.22	1.49
DVU0241	MTH1175-like domain family protein (TIGR)		0.93	1.21	1.29	0.02	1.11	1.33
DVU0242	SEC-C motif domain protein (TIGR)		3.00	2.37	2.33	0.05	3.11	3.07
DVU0243	lipoprotein, putative (TIGR)		1.22	1.91	1.20	0.03	1.48	1.50
DVU0244	hypothetical protein (TIGR)		1.78	1.59	0.89	0.01	1.36	1.26
DVU0245	protein phosphatase, putative (TIGR)		1.26	1.13	1.37	0.02	1.06	0.99
DVU0246	pyruvate phosphate dikinase, PEP/pyruvate binding domain		1.44	1.40	1.28	4.53	1.26	1.15
DVU0247	response regulator (TIGR)	ntrX	1.75	2.62	2.34	563.23	1.75	2.33
DVU0249	conserved hypothetical protein (TIGR)		1.54	1.23	1.20	14.53	1.21	1.13
DVU0250	hypothetical protein (TIGR)		0.53	0.30	0.51	0.02	0.42	1.49
DVU0251	membrane protein, putative (TIGR)		1.10	3.39	4.14	2781.24	2.99	3.13
DVU0252	hypothetical protein (TIGR)		0.64	0.39	0.74	2.52	0.55	1.22
DVU0253	oxidoreductase, FAD/iron-sulfur cluster-binding domain pro		1.43	1.58	1.27	0.03	1.54	1.51
DVU0255	hypothetical protein (TIGR)		1.51	2.14	1.16	0.03	1.58	1.74
DVU0256	ATP-dependent RNA helicase, DEAD/DEAH box family (TIGR)		1.22	1.50	1.24	0.02	1.44	1.34
DVU0257	acetyltransferase, GNAT family (TIGR)		0.61	0.82	0.62	0.02	0.71	0.73
DVU0258	sensory box histidine kinase/response regulator (TIGR)		0.91	1.05	0.64	0.02	1.07	0.92
DVU0259	DNA-binding response regulator (TIGR)	divK	0.79	0.85	0.53	0.01	0.78	0.84
DVU0260	response regulator (TIGR)	mtrA	1.18	1.59	1.21	0.02	1.84	1.74
DVU0261	universal stress protein family (TIGR)		1.30	1.31	1.51	0.04	1.41	1.29
DVU0262	hypothetical protein (TIGR)		1.41	1.95	2.06	0.05	3.10	2.71
DVU0263	Transmembrane complex, tetraheme cytochrome	tmcA	0.00	0.00	0.19	0.00	0.01	0.02
DVU0264	Transmembrane complex, ferredoxin, 2 [4Fe-4S] (S	tmcB	0.08	0.00	0.14	0.00	0.02	0.00
DVU0265	membrane protein, putative (TIGR)		0.08	0.02	0.05	0.00	0.01	0.00
DVU0266	hypothetical protein (TIGR)		0.07	0.00	0.01	0.00	0.01	0.00
DVU0269	transcriptional regulator, rrf2 protein, putative (TIGR)		0.42	0.26	0.43	0.01	0.62	0.26
DVU0270	sensory box histidine kinase (TIGR)		3.93	1.51	1.25	0.02	1.21	1.12
DVU0271	response regulator (TIGR)		1.18	1.40	1.34	0.04	1.42	1.35
DVU0272	hypothetical protein (TIGR)		0.71	1.59	1.24	0.03	1.13	1.18
DVU0273	conserved hypothetical protein (TIGR)		1.00	1.43	1.16	0.03	1.32	1.28
DVU0274	hypothetical protein (TIGR)		0.83	0.87	1.74	0.01	1.00	1.07
DVU0275	polysaccharide deacetylase family protein (TIGR)		0.84	1.40	1.18	0.01	1.16	1.14
DVU0276	conserved hypothetical protein (TIGR)		1.70	1.60	1.41	0.07	1.35	1.27
DVU0277	transcriptional regulator, AraC family (TIGR)		1.27	1.28	1.33	0.05	1.35	1.33
DVU0278	glyoxalase family protein (TIGR)		1.14	1.40	0.99	0.04	1.30	1.33
DVU0279	sulfate permease family protein (TIGR)		1.01	1.32	1.45	0.02	1.13	1.23
DVU0280	glycosyl transferase, group 1 family protein (TIGR)	wbaZ-2	0.84	1.22	0.86	0.02	1.23	1.26
DVU0281	exopolysaccharide biosynthesis protein, putative (TIGR)		1.24	1.48	1.36	0.04	1.38	1.28
DVU0282	A/G-specific adenine glycosylase (TIGR)	mutY	1.38	1.09	1.25	0.03	1.26	1.29
DVU0283	AhpF family protein/thioredoxin reductase (TIGR)		1.58	1.53	1.62	0.04	1.73	1.69
DVU0284	peptidyl-prolyl cis-trans isomerase B (TIGR)	ppiB-1	1.06	1.45	1.10	0.03	1.32	1.52
DVU0285	imidazole glycerol phosphate synthase, glutamine	hisH	2.13	1.90	0.07	0.01	0.00	0.00
DVU0286	imidazoleglycerol phosphate synthase, cyclase sub	hisF	1.24	1.12	0.03	0.00	0.00	0.00
DVU0289	molybdenum cofactor biosynthesis protein C (TIGI	moaC	1.57	1.53	1.62	0.03	1.42	1.22
DVU0290	lipoprotein, putative (TIGR)		0.97	1.20	1.27	0.03	1.26	1.16
DVU0291	ABC transporter, ATP-binding protein (TIGR)	potA	1.38	1.43	1.54	0.03	1.51	1.29
DVU0292	hypothetical protein (TIGR)		1.65	1.65	1.26	0.04	1.56	1.56
DVU0293	prokaryotic dksA/traR C4-type zinc finger family protein (TIC		0.84	0.89	0.91	0.00	1.44	1.09
DVU0294	glycosyl transferase, group 2 family protein (TIGR)		1.36	1.59	1.43	0.03	1.51	1.54
DVU0295	amine oxidase, flavin-containing (TIGR)		1.75	1.79	1.72	0.04	2.22	2.16

DVU0296	peptidase, M24 family (TIGR)		1.16	1.15	1.36	0.03	1.23	1.34
DVU0297	hypothetical protein (TIGR)		4.02	5.55	3.68	0.05	4.99	5.14
DVU0298	hypothetical protein (TIGR)		0.82	0.96	1.11	0.03	0.89	0.99
DVU0299	anaerobic ribonucleoside-triphosphate reductase, putative (		0.86	1.08	0.97	0.02	1.10	1.20
DVU0300	radical SAM domain protein (TIGR)		0.06	0.04	0.68	0.03	2.02	3.13
DVU0301	hypothetical protein (TIGR)		0.32	0.44	0.00	0.04	0.51	0.32
DVU0302	chemotaxis protein CheX, putative (TIGR)		1.27	0.95	0.92	0.03	0.87	0.95
DVU0303	hypothetical protein (TIGR)		0.96	1.40	0.99	0.05	1.37	1.69
DVU0304	hypothetical protein (TIGR)		2.24	2.10	2.31	0.04	1.89	2.63
DVU0305	ferredoxin II (Sean Caffrey)	fd II	1.16	1.20	0.72	0.05	1.03	1.14
DVU0306	hypothetical protein (TIGR)		1.16	1.79	1.26	0.11	1.56	1.63
DVU0307	flagella basal body rod domain protein (TIGR)		1.36	1.19	0.94	0.03	1.90	1.91
DVU0308	membrane protein, putative (TIGR)		0.80	0.92	0.65	0.02	0.65	0.72
DVU0309	transcriptional regulator, LysR family (TIGR)		1.34	1.51	1.61	0.03	1.61	1.31
DVU0310	flagellum-specific ATP synthase FliI (TIGR)	fliI	1.49	1.91	1.47	0.03	2.72	2.45
DVU0311	flagellar assembly protein FliH, putative (TIGR)		1.23	1.15	1.15	0.02	1.88	1.63
DVU0312	flagellar motor switch protein FliG (TIGR)	fliG	1.21	1.54	1.29	0.03	2.04	2.25
DVU0313	flagellar M-ring protein FliF (TIGR)	fliF	1.55	1.73	1.39	0.03	2.06	2.21
DVU0314	flagellar basal body component FliE (TIGR)	fliE	1.18	1.20	1.61	0.02	2.47	2.30
DVU0315	flagellar basal-body rod protein FlgC (TIGR)	flgC	3.00	2.62	2.71	0.05	3.57	3.83
DVU0316	flagellar basal-body rod protein FlgB (TIGR)	flgB	1.44	1.56	1.20	0.03	1.94	2.23
DVU0318	TPR domain protein (TIGR)		0.95	1.19	0.72	0.01	1.27	1.43
DVU0319	NAD-dependent epimerase/dehydratase family protein (TIG		1.25	0.63	1.29	0.02	0.34	0.42
DVU0320	conserved hypothetical protein (TIGR)		1.55	1.50	1.13	0.02	1.21	1.25
DVU0321	transcriptional activator, putative, Baf family (TIGR)		0.16	0.05	0.27	0.00	0.01	0.01
DVU0322	enolase (TIGR)	eno	0.04	0.01	0.13	0.00	0.01	0.01
DVU0323	methylenetetrahydrofolate dehydrogenase/methe	folD	0.21	0.26	0.15	0.00	0.01	0.00
DVU0325	hydrogenase expression/formation protein HypD (	hypD	0.32	0.30	0.89	0.03	0.30	0.40
DVU0326	hydrogenase expression/formation protein HypE (	hypE	0.27	0.39	0.84	0.02	0.25	0.32
DVU0327	exopolysaccharide biosynthesis protein, putative (	pss	1.07	0.53	0.82	0.01	0.31	0.29
DVU0328	glycosyl transferase, group 1 family protein (TIGR)		2.01	1.21	2.27	0.03	0.55	0.53
DVU0330	response regulator (TIGR)		1.82	1.93	1.72	0.09	1.49	1.33
DVU0331	sensory box histidine kinase, putative (TIGR)		1.67	1.85	1.65	0.04	1.56	1.32
DVU0333	hypothetical protein (TIGR)		1.67	1.11	1.54	0.04	1.45	1.49
DVU0334	D-alanine--D-alanine ligase (TIGR)		0.01	0.02	0.44	0.02	0.00	0.00
DVU0335	3-deoxy-D-manno-octulosonic-acid transferase, putative (TI		0.12	0.04	0.23	0.01	0.02	0.02
DVU0336	aminotransferase, DegT/DnrJ/EryC1/StrS family (T	rfbE	1.72	1.09	1.21	0.03	0.68	0.65
DVU0337	hypothetical protein (TIGR)		1.84	1.17	1.26	0.04	0.67	0.64
DVU0338	hydrolase, haloacid dehalogenase-like family (TIGR)		1.50	0.60	1.04	0.01	0.34	0.44
DVU0339	D-isomer specific 2-hydroxyacid dehydrogenase fa	serA	2.51	1.87	1.37	0.04	1.54	1.71
DVU0340	acetyltransferase, CysE/LacA/LpxA/NodL family (TIGR)		1.59	1.23	1.21	0.03	1.06	1.10
DVU0341	3-deoxy-D-manno-octulosonate cytidylyltransfera	kdsB	0.78	0.71	1.39	0.04	0.34	0.26
DVU0342	NAD-dependent epimerase/dehydratase family protein (TIG		1.57	0.67	0.92	0.01	0.39	0.39
DVU0343	HPCH/HPAI aldolase family protein (TIGR)		2.21	1.50	1.49	0.02	0.63	0.67
DVU0344	methyl-accepting chemotaxis protein (TIGR)		1.62	1.58	1.27	0.04	1.62	1.57
DVU0346	membrane protein, putative (TIGR)		0.37	0.22	1.42	0.03	0.09	0.10
DVU0347	transferase, hexapeptide repeat family (TIGR)		1.71	1.17	1.38	0.04	1.28	1.16
DVU0348	hypothetical protein (TIGR)		2.00	1.56	1.42	0.03	1.42	1.11
DVU0349	NeuB family protein (TIGR)		1.16	1.40	1.54	0.04	1.40	1.27
DVU0350	spore coat polysaccharide biosynthesis protein sps	spsF	1.53	2.19	2.10	0.04	2.01	2.08
DVU0351	cytidine 5monophosphate N-acetylneuraminic acid syntheta		1.49	1.24	0.99	0.02	1.18	1.07
DVU0352	aminotransferase, DegT/DnrJ/EryC1/StrS family (T	lpsC	1.80	1.51	1.50	0.04	1.42	1.19
DVU0353	alcohol dehydrogenase, iron-containing (TIGR)		2.21	1.86	1.87	0.03	1.82	1.53
DVU0354	conserved domain protein (TIGR)		1.92	1.87	1.73	0.04	1.94	1.76
DVU0355	sensory box/GGDEF domain protein (TIGR)		1.89	1.67	1.59	0.03	1.63	1.60
DVU0356	DNA-3-methyladenine glycosylase I (TIGR)	tag	2.03	1.66	1.71	0.03	1.88	1.52
DVU0357	conserved hypothetical protein (TIGR)		1.71	1.69	1.25	0.05	1.59	1.73
DVU0358	hypothetical protein (TIGR)		1.65	1.17	1.17	0.03	0.97	1.15
DVU0359	HesB-like domain (TIGR)		0.51	0.81	0.99	0.01	0.80	0.87
DVU0360	acetolactate synthase, large subunit, biosynthetic	ilvB-1	2.27	2.25	2.30	0.05	2.00	1.96
DVU0361	acetolactate synthase III, small subunit, putative (T	ilvH	1.87	1.24	0.92	0.01	1.20	1.16
DVU0362	conserved hypothetical protein (TIGR)		1.39	1.47	1.28	0.03	1.24	1.11
DVU0363	para-aminobenzoate synthase, component I (TIGR	pabB	1.45	1.42	1.42	0.03	1.33	1.16
DVU0364	para-aminobenzoate/anthranilate synthase glutan	pabA	1.11	1.59	1.75	0.02	1.39	1.24
DVU0365	conserved hypothetical protein (TIGR)		1.59	1.49	1.09	0.02	1.33	1.18
DVU0366	5-formyltetrahydrofolate cyclo-ligase family protein (TIGR)		1.28	1.45	1.27	0.04	1.13	1.05
DVU0367	Ser/Thr protein phosphatase family protein (TIGR)		1.42	1.49	1.65	0.05	1.42	1.32

DVU0368	hypothetical protein (TIGR)		0.39	0.40	0.43	0.01	0.60	0.48
DVU0369	hypothetical protein (TIGR)		0.09	0.13	0.00	0.00	0.02	0.18
DVU0370	hypothetical protein (TIGR)		0.04	0.00	0.04	0.00	0.01	0.08
DVU0371	conserved hypothetical protein (TIGR)		1.60	1.62	2.00	0.04	1.49	1.55
DVU0372	membrane protein, putative (TIGR)		2.14	2.45	2.61	0.07	2.43	2.78
DVU0373	CoA-binding domain protein (TIGR)		1.71	1.42	1.49	0.03	1.46	1.51
DVU0374	pyruvate ferredoxin/flavodoxin oxidoreductase family prote		1.64	1.75	1.90	0.04	1.66	1.70
DVU0375	Glu/Leu/Phe/Val dehydrogenase family protein (TIGR)		1.02	1.33	1.87	0.05	1.31	1.27
DVU0376	hypothetical protein (TIGR)		1.08	1.02	0.88	0.05	0.99	0.89
DVU0377	thioredoxin reductase (TIGR)	trxB-1	1.61	1.44	1.81	0.03	1.30	1.33
DVU0378	thioredoxin, putative (TIGR)		0.50	0.69	1.08	0.01	0.59	0.79
DVU0379	transcriptional regulator, putative (TIGR)		0.59	0.53	0.24	0.01	0.43	0.59
DVU0380	sulfatase, putative (TIGR)		1.42	1.55	1.45	0.05	1.33	1.57
DVU0381	Na+/H+ antiporter NhaC (TIGR)	nhaC-1	1.71	1.70	1.26	0.04	1.67	1.77
DVU0382	hypothetical protein (TIGR)		0.53	0.38	0.47	0.01	0.52	0.88
DVU0383	hypothetical protein (TIGR)		3.65	3.14	2.36	0.11	2.74	2.72
DVU0384	flavoredoxin (TIGR)	flr	0.89	0.90	0.63	0.02	0.77	0.78
DVU0386	amino acid ABC transporter, periplasmic amino ac	glnH	1.03	0.75	1.41	0.01	1.01	1.06
DVU0387	amino acid ABC transporter, permease protein, His/Glu/Gln,		1.32	1.23	1.56	0.04	1.84	1.58
DVU0388	amino acid ABC transporter, ATP-binding protein (TIGR)		1.45	1.40	1.82	0.33	1.85	1.78
DVU0389	amino acid ABC tranporter, permease protein, His/Glu/Gln/		1.75	1.64	2.34	0.06	2.39	2.25
DVU0390	glycolate oxidase, subunit GlcD, putative (TIGR)	glcD	1.91	1.39	1.60	0.03	1.70	1.42
DVU0391	hypothetical protein (TIGR)		1.29	1.42	1.29	0.03	1.20	0.98
DVU0392	aromatic aminotransferase (TIGR)		2.11	2.01	1.85	0.06	2.29	2.10
DVU0393	uracil-DNA glycosylase (TIGR)	ung	1.12	1.56	1.94	0.04	1.55	1.53
DVU0394	radical SAM domain protein (TIGR)		0.15	0.04	0.54	0.01	0.01	0.03
DVU0395	HIT family protein (TIGR)	hit	0.63	0.79	0.46	0.01	0.60	0.54
DVU0396	DNA-binding protein HU (TIGR)	hup-1	0.26	0.34	0.34	0.00	0.17	0.12
DVU0397	rare lipoprotein A, putative (TIGR)	rlpA	1.78	1.92	2.08	0.05	1.88	2.14
DVU0398	HMGL-like domain protein (TIGR)		0.63	0.55	0.07	0.00	0.02	0.02
DVU0399	hypothetical protein (TIGR)		1.65	1.68	1.54	0.02	1.58	1.24
DVU0400	hypothetical protein (TIGR)		1.64	1.95	1.78	0.04	2.07	1.70
DVU0401	hypothetical protein (TIGR)		0.81	0.81	1.19	0.02	1.02	0.92
DVU0402	dissimilatory sulfite reductase alpha subunit (TIGR	dsrA	0.02	0.01	0.00	0.00	0.00	0.00
DVU0403	dissimilatory sulfite reductase beta subunit (TIGR)	dvsB	0.00	0.01	0.00	0.00	0.00	0.00
DVU0404	dissimilatory sulfite reductase D (Shelley Haveman	dsrD	0.00	0.00	0.12	0.00	0.00	0.01
DVU0405	cobyrinic acid a,c-diamide synthase (TIGR)	cobB-1	0.05	0.02	0.34	0.01	0.02	0.02
DVU0406	membrane protein, putative (TIGR)		1.03	1.38	1.06	0.03	1.18	1.28
DVU0407	rare lipoprotein A family protein (TIGR)	rlpA	0.25	0.43	0.65	0.02	0.39	0.39
DVU0408	response regulator/sensory box/GGDEF domain/EAL domai		0.96	1.04	0.85	0.02	1.04	1.04
DVU0409	hypothetical protein (TIGR)		0.47	0.93	0.38	0.01	0.77	1.20
DVU0410	hypothetical protein (TIGR)		1.44	1.52	0.69	0.02	1.76	1.83
DVU0411	heptosyltransferase family protein (TIGR)		1.49	1.49	1.40	0.04	1.63	1.70
DVU0412	potassium uptake protein TrkA, putative (TIGR)		1.58	1.18	1.17	0.03	0.94	0.86
DVU0413	potassium uptake protein, TrkH family (TIGR)	trk1	1.20	1.05	1.27	0.02	0.99	0.82
DVU0414	NADP-dependent malic enzyme-related protein (T	tme	2.05	1.75	0.97	0.03	1.53	1.66
DVU0415	cytosol aminopeptidase (TIGR)	pepA	1.39	1.13	1.68	0.05	1.48	1.76
DVU0416	GGDEF domain protein (TIGR)		1.31	1.37	1.27	0.03	1.25	1.31
DVU0417	arginine decarboxylase (TIGR)	speA	1.40	1.02	0.83	0.02	1.06	0.74
DVU0418	saccharopine dehydrogenase (TIGR)	lys1	1.69	1.01	0.70	0.03	0.67	0.39
DVU0419	carboxynorspermidine decarboxylase (TIGR)	nspC	1.54	1.43	1.11	0.02	1.52	1.04
DVU0420	hypothetical protein (TIGR)		0.48	0.92	0.49	0.02	0.72	0.88
DVU0421	agmatinase, putative (TIGR)		1.42	1.05	0.84	0.02	1.36	1.00
DVU0422	sensory box/GGDEF domain/EAL domain protein (TIGR)		1.65	1.64	1.73	0.04	1.73	1.82
DVU0423	universal stress protein family (TIGR)		1.51	1.74	1.27	0.04	1.81	1.77
DVU0424	cardiolipin synthetase (TIGR)	cls	1.85	1.75	1.63	0.04	1.59	1.51
DVU0425	hypothetical protein (TIGR)		1.12	1.15	1.14	0.02	1.22	1.16
DVU0426	chromate transport family protein (TIGR)		1.56	1.28	1.01	0.02	1.43	1.24
DVU0428	conserved hypothetical protein (TIGR)		0.93	1.25	0.57	0.05	1.06	1.18
DVU0429	Ech hydrogenase, subunit EchF, putative (TIGR)		1.36	1.13	0.88	0.03	0.92	1.02
DVU0430	Ech hydrogenase, subunit EchE, putative (TIGR)		1.37	1.52	1.49	0.02	1.47	1.40
DVU0431	Ech hydrogenase, subunit EchD, putative (TIGR)		1.08	0.77	0.61	0.01	0.82	0.94
DVU0432	Ech hydrogenase, subunit EchC, putative (TIGR)		0.95	1.53	1.27	0.02	1.18	1.21
DVU0433	Ech hydrogenase, subunit EchB, putative (TIGR)		1.57	1.63	1.82	0.04	1.76	1.71
DVU0434	Ech hydrogenase, subunit EchA, putative (TIGR)	mnhA	1.81	1.45	1.67	0.04	1.59	1.53
DVU0436	transcriptional regulator, TetR family (TIGR)		0.81	1.24	0.93	0.02	0.92	1.12
DVU0437	efflux transporter, RND family, MFP subunit (TIGR)		1.56	1.61	1.26	0.02	1.35	1.36

DVU0438	AcrB/AcrD/AcrF family protein (TIGR)		1.52	1.52	1.55	0.04	1.57	1.49
DVU0439	YCII-related domain protein (TIGR)		1.32	1.73	1.41	0.03	1.30	1.42
DVU0440	conserved hypothetical protein (TIGR)		1.47	1.49	1.35	0.04	1.62	1.61
DVU0441	adenine deaminase (TIGR)	ade	1.46	1.35	1.50	0.03	1.32	1.32
DVU0442	phoH-related protein (TIGR)		1.32	1.38	1.27	0.03	1.19	1.36
DVU0443	exonuclease, putative (Keith Keller)		1.95	1.64	1.53	0.03	1.40	1.37
DVU0444	CBS domain protein (TIGR)		1.59	1.88	2.01	0.04	1.83	1.73
DVU0445	CBS domain protein (TIGR)		2.05	1.56	1.93	0.04	1.54	1.61
DVU0446	sodium/solute symporter family protein (TIGR)		1.48	1.49	1.21	0.03	1.29	1.43
DVU0447	membrane protein, putative (TIGR)		2.01	0.77	0.75	0.03	0.86	0.81
DVU0448	GDP-mannose 4,6-dehydratase (TIGR)	gmd	1.74	1.81	1.55	0.04	1.77	1.86
DVU0449	sensor/response regulator (TIGR)		1.75	1.57	1.60	0.03	1.52	1.62
DVU0450	riboflavin biosynthesis protein RibF (TIGR)	ribF	0.13	0.01	0.31	0.00	0.01	0.01
DVU0451	chloride channel family protein (TIGR)		1.51	1.71	1.93	0.05	1.63	1.50
DVU0452	hypothetical protein (TIGR)		1.26	1.48	1.33	0.02	1.39	1.30
DVU0453	ATP-dependent DNA helicase, UvrD/REP family (TIGR)		1.28	1.19	1.28	0.03	1.23	1.08
DVU0454	hypothetical protein (TIGR)		1.23	0.96	0.58	0.05	1.12	1.16
DVU0455	hypothetical protein (TIGR)		1.40	1.65	1.46	0.03	0.89	0.48
DVU0456	DHH family protein (TIGR)		1.09	0.70	0.80	0.02	0.80	0.80
DVU0457	EAL domain protein (TIGR)		1.32	1.11	1.33	0.02	1.00	1.15
DVU0458	hypothetical protein (TIGR)		0.06	0.15	0.00	0.00	0.02	0.03
DVU0459	hypothetical protein (TIGR)		0.79	0.40	0.00	0.00	0.05	0.17
DVU0460	predicted phospho-2-dehydro-3-deoxyheptonate aldolase (T		0.97	0.75	0.21	0.00	0.01	0.00
DVU0461	predicted 3-dehydroquinate synthase (TIGR)		1.36	0.97	0.17	0.00	0.00	0.01
DVU0462	chorismate mutase/prephenate dehydratase (TIGR)		1.41	1.54	0.16	0.00	0.00	0.00
DVU0463	3-phosphoshikimate 1-carboxyvinyltransferase (TI	aroA	1.07	1.10	0.10	0.00	0.01	0.01
DVU0464	prephenate dehydrogenase (TIGR)		0.67	0.80	0.31	0.01	0.10	0.14
DVU0465	anthranilate synthase, component I (TIGR)	trpE	1.61	1.69	0.32	0.00	0.05	0.02
DVU0466	anthranilate synthase, glutamine amidotransferas	trpG	1.91	1.51	0.58	0.01	0.17	0.14
DVU0467	anthranilate phosphoribosyltransferase (TIGR)	trpD	1.42	1.46	0.09	0.01	0.02	0.02
DVU0468	indole-3-glycerol phosphate synthase (TIGR)	trpC	1.58	1.81	0.09	0.01	0.03	0.02
DVU0469	N-(5-phosphoribosyl)anthranilate isomerase (TIGR	trpF-1	0.85	0.87	0.28	0.00	0.05	0.04
DVU0470	tryptophan synthase, beta subunit (TIGR)	trpB-2	1.55	1.71	0.15	0.00	0.00	0.00
DVU0471	tryptophan synthase, alpha subunit (TIGR)	trpA	1.20	1.26	0.04	0.00	0.01	0.00
DVU0474	ISDvu4, transposase (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU0475	membrane protein, putative, truncation (TIGR)		0.61	0.63	0.47	0.01	0.57	0.68
DVU0477	isocitrate dehydrogenase, NADP-dependent (TIGR	icd	0.12	0.30	0.03	0.00	0.00	0.00
DVU0478	Ser/Thr protein phosphatase family (TIGR)		1.64	1.54	1.27	0.03	1.71	1.46
DVU0479	serine/threonine protein kinase, putative (TIGR)		0.96	1.19	0.96	0.03	0.98	1.07
DVU0480	hypothetical protein (TIGR)		1.26	0.86	0.93	0.03	0.80	0.84
DVU0481	ADP-L-glycero-D-mannoheptose-6-epimerase (TIG	rfaD	0.02	0.00	0.02	0.00	0.00	0.00
DVU0482	sensory box histidine kinase/response regulator (TIGR)		1.51	1.46	1.26	0.04	1.38	1.41
DVU0483	DNA mismatch repair protein MutL, putative (TIGR)		1.74	1.92	2.00	0.03	1.66	1.53
DVU0484	ABC transporter, ATP-binding protein (TIGR)		1.25	1.06	0.67	0.02	0.98	1.20
DVU0485	membrane protein, putative (TIGR)		1.22	1.30	1.42	0.02	1.35	1.41
DVU0486	hypothetical protein (TIGR)		0.59	0.84	0.89	0.00	0.88	0.77
DVU0487	phosphoribosylaminoimidazole carboxylase, catal	purE	1.29	1.67	1.08	0.03	0.05	0.06
DVU0488	phosphoribosylamine--glycine ligase (TIGR)	purD	0.52	0.43	0.40	0.01	0.03	0.01
DVU0489	phenylacetate-coenzyme A ligase (TIGR)	paaK-1	1.94	1.62	1.80	0.03	1.78	1.62
DVU0491	HDIG domain protein (TIGR)		1.52	1.45	1.30	0.03	1.24	1.38
DVU0492	N-acetyl-gamma-glutamyl-phosphate reductase (T	argC	1.93	1.45	0.03	0.00	0.00	0.01
DVU0493	hypothetical protein (TIGR)		0.75	0.71	0.41	0.00	0.23	0.28
DVU0494	aminotransferase, class V (TIGR)		0.03	0.04	0.06	0.00	0.00	0.00
DVU0495	conserved hypothetical protein (TIGR)		1.21	1.11	0.90	0.02	0.27	0.17
DVU0496	DNA polymerase I (TIGR)	polA	0.29	0.20	0.18	0.01	0.06	0.04
DVU0497	hypothetical protein (TIGR)		0.97	1.49	1.44	0.02	0.97	1.52
DVU0498	iron-sulfur cluster-binding protein, putative (TIGR)		1.25	1.04	1.06	0.03	1.10	1.18
DVU0499	conserved hypothetical protein TIGR00149 (TIGR)		2.33	1.43	2.09	0.05	1.72	1.67
DVU0500	selenocysteine-specific translation elongation fact	selB	1.21	1.09	1.84	0.04	0.98	0.91
DVU0501	conserved hypothetical protein (TIGR)		0.87	1.27	1.25	0.01	1.34	1.19
DVU0502	hypothetical protein (TIGR)		1.60	0.81	0.91	0.01	0.74	1.07
DVU0503	polyribonucleotide nucleotidyltransferase (TIGR)	pnp	0.05	0.02	0.20	0.00	0.02	0.01
DVU0504	ribosomal protein S15 (TIGR)	rpsO	0.00	0.00	0.00	0.00	0.00	0.00
DVU0505	tRNA pseudouridine synthase B (TIGR)	truB	0.64	0.67	0.92	0.01	0.72	0.78
DVU0506	DHH family protein (TIGR)		0.67	0.56	0.68	0.01	0.73	0.78
DVU0507	conserved hypothetical protein (TIGR)		0.87	0.82	1.19	0.03	1.14	0.88
DVU0508	translation initiation factor IF-2 (TIGR)	infB	0.02	0.00	0.06	0.00	0.00	0.00

DVU0509	conserved hypothetical protein (TIGR)		0.64	0.88	0.81	0.02	0.59	0.46
DVU0510	N utilization substance protein A (TIGR)	nusA	0.00	0.00	0.00	0.00	0.01	0.01
DVU0511	conserved hypothetical protein (TIGR)		0.49	0.62	1.00	0.03	0.75	0.71
DVU0512	flagellar basal-body rod protein, putative (TIGR)	flgF	1.33	1.94	1.40	0.05	2.70	2.61
DVU0513	flagellar basal-body rod protein FlgG (TIGR)	flgG	1.32	1.65	1.17	0.03	2.31	2.20
DVU0514	FlgA family protein (TIGR)		1.34	1.61	1.14	0.03	1.91	1.72
DVU0515	flagellar L-ring protein FlgH (TIGR)	flgH	2.61	2.64	2.29	0.04	3.41	3.32
DVU0516	flagellar P-ring protein FlgI (TIGR)	flgI	2.18	2.18	1.61	0.05	2.69	2.55
DVU0517	peptidase, M23/M37 family (TIGR)		1.46	1.29	1.30	0.03	1.64	1.56
DVU0518	hypothetical protein (TIGR)		2.89	2.51	2.60	0.03	3.77	3.91
DVU0519	flagellar hook-associated protein FlgK, putative (TIGR)		2.20	2.23	2.16	0.04	2.95	2.79
DVU0520	flagellar hook-associated protein FlgL, putative (TIGR)		1.52	1.44	1.05	0.02	1.70	1.79
DVU0521	carbon storage regulator (TIGR)	csrA	1.49	0.78	1.06	0.03	0.97	1.04
DVU0522	conserved hypothetical protein (TIGR)	yviF	0.96	1.30	1.38	0.02	1.56	1.73
DVU0523	negative regulator of flagellin synthesis FlgM (TIGF	flgM	3.16	3.18	2.04	0.09	2.36	2.75
DVU0524	hypothetical protein (TIGR)		0.17	0.58	0.21	0.02	0.58	0.50
DVU0525	transcriptional regulator, MarR family (TIGR)		0.90	1.40	1.70	2.12	1.37	1.37
DVU0526	drug resistance transporter, putative (TIGR)		1.01	1.13	1.40	0.04	1.21	1.24
DVU0527	septum formation protein Maf (TIGR)	maF	0.95	1.18	1.39	0.03	1.00	1.12
DVU0528	phosphatidylglycerophosphatase (TIGR)	pgpA	0.11	0.21	0.41	0.01	0.05	0.03
DVU0529	Rrf2 protein (voordouw)	rrf2	1.11	0.60	0.85	0.02	0.98	0.97
DVU0530	Rrf1 protein (voordouw)	rrf1	0.79	1.08	1.00	0.02	0.77	0.75
DVU0531	HmcF, 52.7 kd protein in hmc operon (voordouw)	hmcF	0.91	1.09	1.44	0.04	1.21	1.30
DVU0532	HmcE, 25.3 kd protein in hmc operon (voordouw)	hmcE	1.15	1.19	0.83	0.02	1.48	1.07
DVU0533	HmcD, 5.8 kd protein in hmc operon (voordouw)	hmcD	1.24	1.04	1.39	0.02	1.23	1.20
DVU0534	HmcC, 43.2 kd protein in hmc operon (voordouw)	hmcC	1.08	1.17	1.18	0.04	1.38	1.18
DVU0535	40.1 kd protein in hmc operon (HmcB) (voordouw	hmcB	0.76	0.98	1.15	0.03	1.12	0.95
DVU0536	HmcA; high-molecular-weight cytochrome c (voor	hmcA	1.28	1.37	1.48	0.03	1.57	1.28
DVU0538	AP endonuclease, family 2 (TIGR)		1.70	1.61	1.74	0.03	1.46	1.33
DVU0539	sigma-54 dependent DNA-binding response regulator (TIGR)		1.76	2.06	1.81	0.06	2.08	2.12
DVU0540	sensor histidine kinase (TIGR)		1.79	1.80	1.68	6.83	1.75	1.76
DVU0542	universal stress protein family (TIGR)		0.83	0.62	0.77	0.02	0.51	0.58
DVU0543	conserved hypothetical protein (TIGR)		1.48	1.40	1.87	0.04	1.17	1.39
DVU0544	hypothetical protein (TIGR)		1.93	1.71	1.12	0.05	1.59	1.56
DVU0545	conserved hypothetical protein (TIGR)		2.30	1.46	0.76	0.03	1.66	1.41
DVU0547	high-affinity branched chain amino acid ABC transporter, pe		1.42	1.65	1.81	0.03	1.72	1.28
DVU0548	high-affinity branched-chain amino acid ABC trans	livH	1.21	1.28	1.44	0.04	1.34	1.09
DVU0549	high-affinity branched-chain amino acid ABC transporter, pe		0.72	1.18	1.07	0.03	1.18	0.89
DVU0550	high-affinity branched-chain amino acid ABC trans	livG	1.53	1.57	1.34	0.04	1.55	1.00
DVU0551	high-affinity branched-chain amino acid ABC trans	livF	0.58	1.60	0.87	0.01	1.22	1.05
DVU0552	conserved hypothetical protein (TIGR)		0.24	0.12	0.17	0.01	0.17	0.18
DVU0554	NAD-dependent epimerase/dehydratase family protein (TIG		0.00	0.02	0.00	0.00	0.00	0.00
DVU0555	hypothetical protein (TIGR)		0.17	0.41	0.42	0.00	0.33	0.28
DVU0556	ISDvu3, transposase OrfA (TIGR)		0.24	0.39	0.73	0.00	0.30	0.12
DVU0560	conserved domain protein (TIGR)		0.00	0.06	0.01	0.00	0.06	0.07
DVU0561	glycosyl transferase, group 1 family protein (TIGR)		0.22	0.23	0.22	0.00	0.37	0.29
DVU0562	ISD1, transposase OrfA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU0563	ISD1, transposase OrfB (TIGR)		0.35	0.37	0.13	0.01	0.29	0.31
DVU0564	ISDvu4, transposase, truncation (TIGR)	b0502	0.00	0.00	0.00	0.00	0.00	0.00
DVU0565	glyceraldehyde 3-phosphate dehydrogenase (TIGR	gap-1	0.80	0.99	0.95	0.02	1.22	1.28
DVU0566	GAF domain protein (TIGR)		1.82	1.59	1.66	0.04	1.67	1.62
DVU0567	TerC family protein (TIGR)		1.25	1.02	0.84	0.03	1.26	1.26
DVU0568	rhodanese-like domain protein (TIGR)		1.49	1.57	1.17	0.04	1.36	1.26
DVU0569	sigma-54 dependent transcriptional regulator (TIG	flrA	1.30	1.56	1.25	0.02	1.40	1.48
DVU0570	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.02	0.03
DVU0571	alanine dehydrogenase (TIGR)	ald	1.41	1.60	1.42	0.04	1.48	1.35
DVU0572	hypothetical protein (TIGR)		2.79	2.15	2.37	0.04	2.37	2.52
DVU0573	creA protein (TIGR)	creA	6.13	1.38	1.35	0.02	1.15	1.18
DVU0575	hypothetical protein (TIGR)		0.96	0.93	1.04	0.01	1.10	0.79
DVU0576	peptide methionine sulfoxide reductase MsrB (TIG	msrB	1.00	1.18	1.18	0.02	1.02	1.14
DVU0577	formate dehydrogenase formation protein FdhE, putative (T		1.32	1.63	1.20	0.02	1.72	1.52
DVU0578	formate dehydrogenase accessory protein FdhD, putative (T		1.40	1.42	1.36	0.03	1.53	1.27
DVU0579	molybdopterin-guanine dinucleotide biosynthesis protein A,		1.86	1.55	1.29	0.02	1.53	1.24
DVU0580	molybdenum cofactor biosynthesis protein A (TIGI	moaA	0.94	1.04	1.44	0.02	1.03	0.80
DVU0581	response regulator/anti-anti-sigma factor (TIGR)		1.04	1.10	0.92	0.04	0.93	1.12
DVU0582	sensory box histidine kinase (TIGR)		0.86	1.10	0.74	0.02	0.75	0.99
DVU0583	lipoprotein, putative (TIGR)		1.10	0.75	0.43	0.01	0.70	0.83

DVU0584	transposase, putative (TIGR)		1.62	1.47	1.13	0.02	1.45	1.42
DVU0585	conserved hypothetical protein (TIGR)		1.10	1.17	1.07	0.02	1.18	1.20
DVU0586	hypothetical protein (TIGR)		1.65	2.48	0.91	0.05	2.19	1.84
DVU0587	formate dehydrogenase, alpha subunit, selenocyst	fdnG-1	1.28	1.25	1.00	0.03	1.25	1.28
DVU0588	formate dehydrogenase, beta subunit, putative (TI	hybA	1.76	1.78	1.55	0.03	1.84	1.66
DVU0589	molybdopterin-guanine dinucleotide biosynthesis	protein B,	2.07	2.39	1.86	0.05	2.51	2.48
DVU0590	hypothetical protein (TIGR)		1.10	0.80	0.57	0.03	1.22	1.06
DVU0591	methyl-accepting chemotaxis protein (TIGR)	mcpD	1.32	1.60	1.42	0.03	1.58	1.46
DVU0592	chemotaxis protein CheW (TIGR)	cheW-1	0.65	0.65	0.44	0.02	0.63	0.60
DVU0593	L-lysine exporter, putative (TIGR)	LysE	0.77	1.04	1.31	0.03	1.06	1.00
DVU0594	chromosome initiation inhibitor (TIGR)	iciA	2.13	2.00	1.50	0.04	1.89	1.75
DVU0595	conserved hypothetical protein (TIGR)		0.78	0.88	0.92	0.01	1.08	1.13
DVU0596	DNA-binding response regulator LytR (TIGR)	lytR	0.71	1.22	0.99	0.03	1.04	1.10
DVU0597	regulatory protein LytS (TIGR)	lytS	1.65	1.82	1.49	0.03	1.85	1.71
DVU0598	carbon starvation protein A, putative (TIGR)		0.45	0.83	0.99	0.02	0.71	0.76
DVU0599	carbon starvation protein A, putative (TIGR)		0.62	0.72	0.76	0.01	0.68	0.75
DVU0600	L-lactate dehydrogenase (TIGR)	ldh	1.65	1.85	1.40	0.03	1.92	1.90
DVU0601	phenylacetic acid degradation protein PaaI (TIGR)	b1396	1.42	1.12	1.09	0.01	1.18	1.08
DVU0602	hypothetical protein (TIGR)		0.00	0.00	0.04	0.00	0.00	0.00
DVU0603	hypothetical protein (TIGR)		0.56	0.24	0.35	0.03	0.50	0.82
DVU0604	hypothetical protein (TIGR)		0.10	0.00	0.18	0.00	0.10	0.14
DVU0605	hypothetical protein (TIGR)		0.38	0.07	0.71	0.00	0.16	0.07
DVU0606	transcriptional regulator, ArsR family/methyltrans	ferase, Ub	0.50	0.63	0.79	0.02	0.48	0.52
DVU0607	adenosylhomocysteinase (TIGR)	ahcY	0.29	0.43	0.65	0.02	0.34	0.39
DVU0608	methyl-accepting chemotaxis protein (TIGR)		1.23	1.31	1.31	0.06	1.23	1.29
DVU0609	lipoprotein, putative (TIGR)		1.18	0.97	0.44	0.01	0.94	0.99
DVU0610	conserved hypothetical protein (TIGR)		1.15	1.38	1.27	0.02	1.45	1.29
DVU0611	ABC transporter, ATP-binding protein (TIGR)		1.88	1.78	1.73	0.04	2.15	1.99
DVU0612	STAS domain protein (TIGR)		1.28	1.52	1.34	0.03	1.32	1.43
DVU0614	hypothetical protein (TIGR)		0.97	1.43	1.25	0.05	1.16	1.05
DVU0616	hypothetical protein (TIGR)		0.56	1.02	1.04	0.02	1.01	0.80
DVU0617	hypothetical protein (TIGR)		1.56	1.24	1.42	0.03	1.35	1.57
DVU0618	hypothetical protein (TIGR)		0.14	0.07	0.00	0.00	0.06	0.04
DVU0619	sigma-54 dependent transcriptional regulator (TIGR)		1.29	1.32	1.29	0.02	1.53	1.50
DVU0620	endoribonuclease, L-PSP family (TIGR)		0.42	0.45	0.65	0.03	0.64	0.49
DVU0621	sigma-54 dependent DNA-binding response regulator	(TIGR)	1.95	2.22	2.21	0.03	2.47	2.19
DVU0622	sensor histidine kinase/response regulator (TIGR)		1.52	1.58	1.43	0.04	1.77	1.72
DVU0624	NapC/NirT cytochrome c family protein (TIGR)	nrfH	1.59	1.12	1.18	0.03	1.10	1.11
DVU0625	cytochrome c nitrite reductase, catalytic subunit N	nrfA	0.99	1.17	1.11	0.04	1.29	1.39
DVU0626	acetolactate synthase, small subunit (TIGR)	ilvN-1	2.17	1.78	2.26	0.03	1.78	1.79
DVU0627	phosphotransbutyrylase (TIGR)	ptB	0.66	0.81	0.61	0.02	0.98	0.87
DVU0628	butyrate kinase (TIGR)	buk	0.63	0.86	0.71	0.01	0.73	0.97
DVU0629	transcriptional regulator, TetR family (TIGR)		0.59	0.69	0.60	0.02	0.61	0.79
DVU0630	hypothetical protein (TIGR)		0.10	0.44	0.26	0.00	0.35	0.46
DVU0631	conserved hypothetical protein (TIGR)		0.77	1.05	0.94	0.02	0.97	0.87
DVU0632	cupin family protein (TIGR)		1.36	1.09	1.21	0.02	1.17	1.18
DVU0633	penicillin-binding protein (TIGR)		0.02	0.04	0.42	0.01	0.00	0.00
DVU0634	hypothetical protein (TIGR)		0.90	1.00	1.16	0.02	1.01	0.91
DVU0635	dolichyl-phosphate-mannose-protein mannosyltrans	ferase f	0.97	0.58	1.02	0.02	0.52	0.66
DVU0636	response regulator/GGDEF domain protein (TIGR)		1.28	1.35	0.79	0.02	1.24	1.26
DVU0637	conserved hypothetical protein (TIGR)		1.35	1.30	1.28	0.02	1.22	1.31
DVU0638	membrane protein, putative (TIGR)		1.13	0.96	0.93	0.03	0.78	0.93
DVU0639	chemotaxis protein PomB (TIGR)	pomB	0.73	0.60	0.62	0.02	0.82	0.91
DVU0640	chemotaxis protein PomA (TIGR)	pomA	1.04	1.06	1.15	0.01	1.52	1.61
DVU0641	conserved hypothetical protein (TIGR)		1.51	1.63	1.20	0.03	1.64	1.64
DVU0642	hydrolase, alpha/beta fold family (TIGR)		0.99	1.14	0.77	0.02	0.93	0.97
DVU0643	thiF protein, putative (TIGR)		1.30	1.26	1.07	0.02	1.37	1.34
DVU0645	methyl-accepting chemotaxis protein (TIGR)		1.17	1.18	1.01	0.03	1.08	1.04
DVU0646	precorrin-2 C20-methyltransferase (TIGR)	cobI	0.91	0.98	0.98	0.04	0.54	0.43
DVU0647	iron compound ABC transporter, periplasmic iron	compound	0.78	1.16	0.89	1.42	0.69	0.57
DVU0648	iron compound ABC transporter, ATP-binding prot	fepC	1.01	1.04	1.07	0.02	0.73	0.57
DVU0649	iron compound ABC transporter, permease protein	(TIGR)	0.83	0.96	0.83	0.02	0.51	0.43
DVU0650	chelatase, putative (TIGR)		1.27	1.32	1.36	0.03	0.69	0.45
DVU0651	membrane protein, putative (TIGR)		1.81	1.63	1.70	0.05	1.53	1.52
DVU0652	chemotaxis protein CheV (TIGR)	cheV-2	0.77	0.98	1.00	0.02	1.05	0.90
DVU0653	sigma-54 dependent transcriptional regulator, put	atoC	1.19	1.13	1.24	0.03	1.21	1.05
DVU0654	peptidase, U32 family (TIGR)		1.37	1.63	1.65	0.03	1.60	1.50

DVU0655	PHP domain protein (TIGR)		1.62	1.52	1.85	0.04	1.82	1.43
DVU0656	conserved hypothetical protein (TIGR)		1.11	1.00	2.17	0.04	0.64	0.56
DVU0657	heat shock protein, Hsp20 family (TIGR)		1.06	0.97	1.32	0.02	1.26	0.96
DVU0658	heat shock protein, Hsp20 family (TIGR)		0.66	0.77	0.76	0.02	1.03	1.06
DVU0659	hypothetical protein (TIGR)		1.62	1.81	1.32	0.04	1.56	1.56
DVU0660	phosphoesterase, putative (TIGR)		1.40	1.15	1.52	0.02	1.16	1.19
DVU0661	dihydrouridine synthase family protein (TIGR)		0.80	0.93	0.85	0.01	0.92	0.86
DVU0662	serine O-acetyltransferase (TIGR)	cysE	0.02	0.00	1.04	0.02	0.57	0.77
DVU0663	cysteine synthase A (TIGR)	cysK	0.42	0.19	1.17	0.04	1.02	1.01
DVU0664	cysteine desulfurase (TIGR)		0.34	0.38	0.65	0.01	0.62	0.91
DVU0665	nitrogen fixation protein nifU (TIGR)		0.27	0.30	0.65	0.02	0.87	1.34
DVU0666	HD domain protein (TIGR)		0.81	1.02	1.27	0.01	1.07	1.18
DVU0667	HD domain protein (TIGR)		1.08	1.50	1.31	0.03	1.15	1.44
DVU0668	methyl-accepting chemotaxis protein (TIGR)		0.93	1.03	0.76	0.02	1.03	0.92
DVU0669	hypothetical protein (TIGR)		0.79	1.05	1.02	0.03	1.08	1.37
DVU0670	exopolysaccharide production protein, putative (TIGR)		0.81	0.75	0.67	0.02	0.90	1.08
DVU0671	conserved hypothetical protein (TIGR)		1.26	1.12	1.27	0.03	0.77	0.54
DVU0672	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU0673	hypothetical protein (TIGR)		0.09	0.28	1.01	0.00	0.20	0.19
DVU0674	ABC transporter, permease protein, His/Glu/Gln/Arg/opine		0.97	1.17	0.90	0.02	1.23	1.11
DVU0675	amino acid ABC transporter, periplasmic amino ac	fliY	1.01	0.95	0.72	0.02	1.15	1.13
DVU0676	amino acid ABC transporter, permease protein, Hi	artQ	0.84	0.92	0.72	0.01	1.00	0.89
DVU0677	transglycosylase domain protein (TIGR)		0.59	0.83	0.59	0.01	0.87	0.92
DVU0679	sigma-54 dependent transcriptional regulator/resp	luxO	0.84	1.23	1.07	0.02	1.32	1.15
DVU0680	sensory box histidine kinase (TIGR)		1.60	1.65	1.53	0.04	1.66	1.57
DVU0681	sensor histidine kinase/response regulator (TIGR)		1.32	1.43	1.55	0.03	1.25	0.71
DVU0682	DNA-binding protein, putative (TIGR)		0.64	0.70	0.58	0.03	0.51	0.45
DVU0683	hflC protein, putative (TIGR)		0.88	0.97	1.15	0.02	1.10	1.01
DVU0684	hflK protein, putative (TIGR)	hflK	1.06	1.03	1.00	0.04	1.17	0.93
DVU0685	phosphomannomutase (TIGR)	rfbB	0.03	0.12	0.56	0.01	0.00	0.02
DVU0686	iron-sulfur cluster-binding protein (TIGR)		1.35	1.54	1.46	0.04	1.32	1.51
DVU0687	aldehyde:ferredoxin oxidoreductase, tungsten-cor	aor-2	1.38	1.94	1.67	0.03	1.85	1.83
DVU0688	hypothetical protein (TIGR)		1.01	1.38	0.81	0.02	1.17	0.97
DVU0689	ribonuclease HI (TIGR)	rnhA	0.47	0.67	0.92	0.01	0.76	0.60
DVU0690	conserved hypothetical protein (TIGR)		1.36	1.77	1.14	0.03	1.68	1.62
DVU0691	membrane protein, putative (TIGR)		1.33	1.24	1.34	0.02	1.24	1.04
DVU0692	molybdopterin oxidoreductase, transmembrane subunit, pu		0.83	1.01	1.14	0.02	2.01	0.97
DVU0693	molybdopterin oxidoreductase, iron-sulfur cluster	narH	1.34	1.16	1.02	0.03	2.27	1.31
DVU0694	molybdopterin oxidoreductase, molybdopterin-binding subu		1.03	1.22	1.12	0.03	2.12	1.20
DVU0697	mannose-1-phosphate guanylyltransferase/manno	rfbA	0.02	0.13	0.36	0.00	0.00	0.01
DVU0698	dTDP-4-dehydrorhamnose 3,5-epimerase (TIGR)	rfbC	0.55	0.45	0.81	0.02	0.48	0.78
DVU0700	sensory box sensor histidine kinase/response regulator, autl		1.31	1.31	1.52	0.03	1.37	1.42
DVU0701	malate synthase G (TIGR)	glcB	1.41	1.46	1.50	0.04	1.82	1.95
DVU0702	cytochrome c family protein (TIGR)		0.82	0.83	0.98	0.03	0.79	0.91
DVU0703	GTP-binding protein LepA (TIGR)	lepA	0.72	0.66	1.33	0.03	0.59	0.58
DVU0704	signal peptidase I (TIGR)	lepB	0.00	0.02	0.12	0.00	0.00	0.01
DVU0705	TRAP dicarboxylate transporter, putative (TIGR)	dctM	1.01	1.01	1.05	0.03	1.26	1.15
DVU0706	membrane protein, putative (TIGR)		0.68	0.81	1.31	0.04	1.16	1.14
DVU0707	TRAP dicarboxylate family transporter (TIGR)	dctP	1.31	1.46	0.81	0.02	1.42	1.34
DVU0710	competence protein comM, putative (TIGR)		1.26	1.46	1.36	0.03	1.43	1.47
DVU0711	hypothetical protein (TIGR)		0.96	1.25	0.93	0.03	1.14	1.14
DVU0712	amino acid ABC transporter, periplasmic-binding protein (TI		1.13	1.58	1.52	0.03	2.39	2.28
DVU0713	branched-chain amino acid ABC transporter, perm	livH	1.29	1.24	2.25	0.07	2.65	2.32
DVU0714	branched-chain amino acid ABC transporter, perm	livM	0.83	0.72	0.67	0.02	1.29	1.23
DVU0715	branched-chain amino acid ABC transporter, ATP b	livG	0.92	0.90	1.25	0.03	1.60	1.54
DVU0716	branched-chain amino acid ABC transporter, ATP-b	livF	0.69	0.81	0.84	0.02	1.64	1.13
DVU0717	GGDEF domain/EAL domain protein (TIGR)		0.78	0.86	0.96	0.02	1.01	0.98
DVU0718	ISDvu2, transposase OrfA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU0719	ISDvu2, transposase OrfB (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU0720	HAMP domain protein (TIGR)		1.09	0.90	1.11	0.02	1.05	1.08
DVU0721	sensory box histidine kinase (TIGR)		1.12	1.10	1.23	0.02	1.10	1.10
DVU0722	response regulator (TIGR)		0.52	0.62	0.57	0.01	0.66	0.59
DVU0723	phosphoribosylglycinamide formyltransferase 2 (T	purT	0.89	0.95	1.22	0.01	0.84	0.81
DVU0724	sodium/alanine symporter family protein (TIGR)		0.71	0.83	1.15	0.03	1.19	0.95
DVU0725	conserved hypothetical protein (TIGR)		1.27	1.06	1.13	0.02	1.18	1.15
DVU0726	queuine tRNA-ribosyltransferase (TIGR)	tgt	1.51	1.51	1.33	0.03	1.52	1.54
DVU0727	conserved hypothetical protein (TIGR)		1.05	1.16	0.90	0.04	1.05	1.11

DVU0728	hypothetical protein (TIGR)		0.00	0.00	0.06	0.00	0.05	0.07
DVU0729	hypothetical protein (TIGR)		1.32	1.21	2.31	0.05	1.17	1.26
DVU0730	conserved hypothetical protein (TIGR)		1.09	0.84	1.12	0.02	0.89	0.83
DVU0731	hypothetical protein (TIGR)		0.30	0.14	0.57	0.01	0.06	0.08
DVU0732	valyl-tRNA synthetase (TIGR)	valS	0.02	0.01	0.09	0.00	0.00	0.00
DVU0733	conserved hypothetical protein (TIGR)		1.53	1.15	1.34	0.02	1.27	1.23
DVU0734	uroporphyrinogen III synthase/methyltransferase	cysG-1	0.01	0.00	0.06	0.00	0.00	0.00
DVU0735	MOSC domain protein (TIGR)		1.48	1.28	1.61	0.04	1.13	1.34
DVU0736	phosphoribosylglycinamide formyltransferase (TIG	purN	1.22	1.21	1.12	0.03	0.81	1.04
DVU0737	sensory box histidine kinase (TIGR)		1.65	1.61	1.55	1.13	1.79	1.84
DVU0738	substrate-binding protein, putative (TIGR)		1.57	1.57	1.81	0.03	1.67	1.84
DVU0739	conserved hypothetical protein TIGR00296 (TIGR)		1.27	1.52	1.26	0.04	1.68	1.67
DVU0740	membrane protein, putative (TIGR)		1.29	1.39	1.42	0.04	1.49	1.46
DVU0741	hypothetical protein (TIGR)		1.11	1.37	1.22	0.07	1.18	1.39
DVU0742	hypothetical protein (TIGR)		1.52	1.23	1.19	0.04	1.45	1.35
DVU0743	sensory box histidine kinase (TIGR)		0.93	1.10	0.99	0.02	1.18	1.26
DVU0744	sigma-54 dependent transcriptional regulator/response regu		1.18	1.27	0.96	0.02	0.91	1.05
DVU0745	ABC transporter, periplasmic substrate-binding protein (TIGI		1.42	0.85	0.79	0.03	0.93	0.97
DVU0746	ABC transporter, permease protein (TIGR)	cysW	0.72	0.85	0.71	0.02	0.90	0.82
DVU0747	ABC transporter, ATP-binding protein (TIGR)	cysA	1.05	0.96	1.08	0.01	1.02	0.94
DVU0748	acetyl-CoA synthetase (TIGR)	acs	1.17	0.84	1.07	0.02	0.70	0.68
DVU0749	DNA-binding response regulator (TIGR)		1.24	1.34	1.44	0.02	1.29	1.31
DVU0750	methyl-accepting chemotaxis protein (TIGR)		1.03	1.14	0.91	0.02	1.10	1.14
DVU0751	amino acid ABC transporter, permease protein, His/Glu/Gln,		0.88	0.92	0.86	0.02	0.98	1.03
DVU0752	amino acid ABC transporter, amino acid-binding protein (TIC		1.28	1.23	1.39	0.04	1.32	1.34
DVU0753	amino acid ABC transporter, ATP-binding protein (TIGR)		1.09	1.62	1.37	0.04	1.60	1.46
DVU0754	hypothetical protein (TIGR)		0.09	0.28	0.36	0.02	0.27	0.21
DVU0755	sensor histidine kinase, putative (TIGR)		0.74	0.76	0.98	0.01	0.81	0.79
DVU0756	TPR domain protein (TIGR)		1.01	1.36	1.26	0.03	1.35	1.41
DVU0757	hypothetical protein (TIGR)		0.70	1.08	1.71	0.03	0.99	0.88
DVU0758	hypothetical protein (TIGR)		0.41	0.80	0.27	0.02	0.74	0.62
DVU0759	peptidase, M29 family (TIGR)		1.27	1.19	1.21	0.02	1.18	1.11
DVU0760	hypothetical protein (TIGR)		1.37	1.58	1.74	0.03	1.40	1.48
DVU0761	lipoprotein, putative (TIGR)		1.09	1.05	1.42	0.02	1.45	1.15
DVU0762	conserved hypothetical protein (TIGR)		1.18	1.25	0.54	0.04	1.29	1.25
DVU0763	GGDEF domain protein (TIGR)	gdp	1.08	1.08	1.03	0.03	1.10	1.22
DVU0764	DNA-binding protein HU (TIGR)	hup-2	0.18	0.68	1.13	0.02	0.79	1.06
DVU0765	hydroxypyruvate reductase, putative (TIGR)		1.38	1.47	1.38	0.03	1.59	1.53
DVU0766	transporter, putative (TIGR)		1.04	1.51	1.38	0.03	1.47	1.32
DVU0767	aminotransferase, class V (TIGR)		0.80	1.34	1.17	0.02	1.39	1.31
DVU0768	glutamate racemase (TIGR)	murI	0.01	0.01	0.95	0.02	0.32	0.14
DVU0769	pyridoxal kinase, putative (TIGR)		0.91	1.08	1.16	0.03	1.28	1.18
DVU0770	membrane protein, putative (TIGR)		0.88	0.90	0.70	0.01	0.92	0.98
DVU0771	molybdenum-pterin binding domain protein/site-specific re		0.95	0.98	1.18	0.02	1.16	0.95
DVU0772	hypothetical protein (TIGR)		0.49	0.98	0.86	0.03	0.88	0.91
DVU0773	hypothetical protein (TIGR)		0.24	0.36	0.56	0.00	0.55	0.46
DVU0774	ATP synthase, F1 epsilon subunit (TIGR)	atpC	0.18	0.02	0.16	0.00	0.12	0.17
DVU0775	ATP synthase, F1 beta subunit (TIGR)	atpD	0.05	0.07	0.13	0.00	0.15	0.44
DVU0776	ATP synthase, F1 gamma subunit (TIGR)	atpG	0.07	0.02	0.19	0.01	0.24	0.55
DVU0777	ATP synthase, F1 alpha subunit (TIGR)	atpA	0.14	0.08	0.33	0.01	0.28	0.78
DVU0778	ATP synthase, F1 delta subunit (TIGR)	atpH	0.05	0.05	0.33	0.00	0.17	0.39
DVU0779	ATP synthase F0, B subunit, putative (TIGR)	atpF2	0.07	0.03	0.03	0.00	0.15	0.38
DVU0780	ATP synthase F0, B subunit, putative (TIGR)	atpF1	0.17	0.18	0.28	0.03	0.27	0.73
DVU0784	conserved hypothetical protein (TIGR)		1.10	1.45	1.45	0.04	1.33	1.29
DVU0785	rod shape-determining protein RodA (TIGR)	rodA	0.06	0.09	0.99	0.03	0.03	0.07
DVU0786	penicillin-binding protein (TIGR)		0.06	0.07	0.80	0.03	0.03	0.06
DVU0787	hypothetical protein (TIGR)		0.87	1.03	1.28	0.03	0.89	0.94
DVU0788	rod shape-determining protein MreC (TIGR)	mreC	0.03	0.02	0.93	0.03	0.03	0.05
DVU0789	rod shape-determining protein MreB (TIGR)	mreB-1	0.02	0.01	0.43	0.01	0.01	0.03
DVU0790	radical SAM protein, TIGR01212 family (TIGR)		1.12	1.16	1.14	0.01	0.72	0.97
DVU0791	methylated-DNA--protein-cysteine methyltransfer	ogt	1.20	1.21	1.08	0.03	1.30	1.23
DVU0792	conserved domain protein (TIGR)		3.10	3.24	2.22	0.07	2.98	3.41
DVU0793	hypothetical protein (TIGR)		0.88	0.98	1.27	0.05	0.88	0.73
DVU0794	enoyl-(acyl-carrier-protein) reductase (TIGR)	fabI	0.55	0.25	0.07	0.00	0.24	0.10
DVU0795	phosphoribosylaminoimidazole-succinocarboxami	purC	1.13	1.28	0.21	0.01	0.01	0.01
DVU0796	histidinol dehydrogenase (TIGR)	hisD	0.92	0.92	0.08	0.00	0.01	0.00
DVU0797	conserved hypothetical protein (TIGR)		0.93	0.86	0.79	0.01	0.80	0.72

DVU0798	hypothetical protein (TIGR)		0.68	0.28	0.00	0.00	0.33	0.26
DVU0799	conserved hypothetical protein (TIGR)		0.20	0.12	0.29	0.00	0.24	0.19
DVU0801	excinuclease ABC, C subunit (TIGR)	uvrC	0.91	0.91	0.73	0.02	0.98	1.05
DVU0802	hypothetical protein (TIGR)		1.24	0.80	0.84	0.05	0.71	1.07
DVU0803	sensor histidine kinase (TIGR)		1.82	1.63	1.26	0.03	1.75	1.71
DVU0804	sigma-54 dependent transcriptional regulator/resp	atoC	1.16	1.17	0.90	0.03	1.35	1.29
DVU0805	hypothetical protein (TIGR)		0.98	1.09	1.50	0.04	1.33	1.28
DVU0806	chemotaxis protein CheY, putative (TIGR)		0.57	0.87	0.65	0.01	0.94	1.22
DVU0807	tRNA (5-methylaminomethyl-2-thiouridylate)-met	trmU	0.02	0.01	0.07	0.00	0.02	0.01
DVU0808	glutamyl-tRNA(Gln) amidotransferase, A subunit (T	gatA	0.01	0.00	0.00	0.00	0.00	0.00
DVU0809	glutamyl-tRNA(Gln) amidotransferase, C subunit (T	gatC	0.39	0.08	0.06	0.00	0.01	0.03
DVU0810	hypothetical protein (TIGR)		0.34	0.40	0.72	0.02	0.12	0.07
DVU0811	dnaK protein (TIGR)	dnaK	0.01	0.01	0.04	0.00	0.00	0.00
DVU0812	heat shock protein GrpE (TIGR)	grpE	0.14	0.22	0.22	0.00	0.04	0.13
DVU0813	heat-inducible transcription repressor HrcA (TIGR)	hrcA	1.64	1.31	1.26	0.03	1.32	1.56
DVU0814	bacterioferritin comigratory protein, putative (TIG	bcp	1.83	1.86	1.17	0.03	1.75	1.36
DVU0815	AsmA family protein (TIGR)		0.97	1.44	1.28	0.03	1.35	1.54
DVU0816	cobyric acid synthase CobQ (TIGR)	cobQ	1.58	1.72	1.24	0.05	0.81	0.73
DVU0817	hypothetical protein (TIGR)		1.20	0.89	0.97	0.04	0.94	1.15
DVU0818	conserved domain protein (TIGR)		0.70	0.95	0.85	0.03	0.87	0.84
DVU0819	FMN reductase, NADPH-dependent (TIGR)	isf-1	1.50	0.98	1.00	0.03	0.97	0.95
DVU0821	conserved hypothetical protein (TIGR)		0.09	0.08	0.15	0.00	0.16	0.18
DVU0822	hypothetical protein (TIGR)		0.10	0.07	0.07	0.00	0.18	0.19
DVU0823	arginine biosynthesis bifunctional protein ArgJ (TI	argJ	1.39	1.28	0.04	0.00	0.00	0.00
DVU0825	preprotein translocase, SecA subunit (TIGR)	secA	0.01	0.00	0.02	0.00	0.00	0.00
DVU0826	glycolate oxidase, iron-sulfur subunit, putative (TIGR)		0.98	0.92	0.99	0.02	0.94	0.92
DVU0827	glycolate oxidase, subunit GlcD, putative (TIGR)		0.96	1.20	1.01	2.47	1.26	1.13
DVU0828	SsrA-binding protein (TIGR)	smpB	0.01	0.02	0.29	0.00	0.03	0.05
DVU0829	phosphoenolpyruvate-protein phosphotransferase	ptsI	0.94	1.11	1.04	0.02	1.14	1.27
DVU0830	phosphocarrier protein HPr (TIGR)	ptsH	0.41	0.66	0.96	0.02	0.65	0.92
DVU0831	PTS system, IID component, putative (TIGR)		0.33	0.42	0.33	0.00	0.20	0.09
DVU0832	tetrapyrrole methylase family protein (TIGR)		1.02	1.03	1.12	0.03	0.78	1.01
DVU0833	conserved hypothetical protein TIGR00252 (TIGR)		0.80	1.11	0.68	0.01	1.03	1.10
DVU0834	ribonuclease HII (TIGR)	rnhB	0.86	0.84	0.78	0.01	0.94	0.78
DVU0835	ribosomal protein L19 (TIGR)	rplS	0.00	0.00	0.00	0.00	0.02	0.00
DVU0836	tRNA (guanine-N1)-methyltransferase (TIGR)	trmD	0.16	0.09	0.24	0.00	0.30	0.15
DVU0837	16S rRNA processing protein RimM (TIGR)	rimM	0.00	0.10	0.16	0.00	0.03	0.03
DVU0838	conserved hypothetical protein (TIGR)		0.00	0.00	0.19	0.00	0.06	0.05
DVU0839	ribosomal protein S16 (TIGR)	rpsP	0.00	0.00	0.00	0.00	0.00	0.01
DVU0840	signal recognition particle protein (TIGR)	ffh	0.01	0.00	0.02	0.00	0.00	0.00
DVU0841	aspartate aminotransferase, putative (TIGR)		0.96	0.97	1.24	0.02	0.28	0.16
DVU0842	hypothetical protein (TIGR)		0.80	0.92	0.58	0.04	1.05	1.21
DVU0843	hypothetical protein (TIGR)		0.73	0.60	0.76	0.02	0.52	0.48
DVU0846	adenylylsulphate reductase, beta subunit (TIGR)	ApsB	0.01	0.00	0.00	0.00	0.00	0.01
DVU0847	adenylyl-sulphate reductase, alpha subunit (TIGR)	ApsA	0.01	0.02	0.14	0.00	0.01	0.00
DVU0848	Quinone-interacting membrane-bound oxidoredu	QmoA	0.08	0.06	0.05	0.00	0.00	0.01
DVU0849	Quinone-interacting membrane-bound oxidoredu	QmoB	0.04	0.05	0.18	0.00	0.00	0.01
DVU0850	Quinone-interacting membrane-bound oxidoredu	QmoC	0.02	0.03	0.09	0.00	0.00	0.00
DVU0851	hypothetical protein (TIGR)		0.13	0.08	0.24	0.00	0.05	0.00
DVU0852	extracellular solute-binding protein, putative (TIGR)		1.08	1.09	0.62	0.03	1.12	1.25
DVU0853	conserved hypothetical protein (TIGR)		0.82	0.81	0.99	0.02	1.04	0.98
DVU0854	NirD protein, putative (TIGR)		0.04	0.05	0.00	0.00	0.01	0.01
DVU0855	radical SAM domain protein (TIGR)		0.04	0.02	0.10	0.00	0.01	0.00
DVU0856	porphobilinogen synthase (TIGR)	hemB	0.00	0.00	0.04	0.00	0.00	0.00
DVU0857	radical SAM domain protein (TIGR)	nirJ-1	0.03	0.02	0.04	0.00	0.00	0.00
DVU0858	lipoprotein, putative (TIGR)		1.60	1.62	1.46	0.02	1.93	2.62
DVU0859	hypothetical protein (TIGR)		1.41	1.90	1.18	0.03	1.75	1.29
DVU0861	glycosyl transferase, group 1 family protein (TIGR)		1.21	1.59	1.13	0.03	1.33	1.61
DVU0862	flagellar protein FliS/hypothetical protein, fusion (TIGR)		0.88	1.19	1.34	0.04	1.22	1.26
DVU0863	flagellar hook-associated protein 2, putative (TIGR)		1.11	1.36	1.00	0.01	1.64	1.68
DVU0864	glycoprotease family protein, putative (TIGR)		0.09	0.09	0.43	0.01	0.08	0.10
DVU0865	membrane-associated zinc metalloprotease, putative (TIGR)		0.47	0.54	0.63	0.01	0.77	0.62
DVU0866	1-deoxy-D-xylulose 5-phosphate reductoisomeras	dxr	0.31	0.25	1.28	0.01	0.09	0.07
DVU0867	aromatic amino acid decarboxylase, putative (TIGR)		0.82	1.11	1.06	0.02	0.90	0.97
DVU0868	phosphatidate cytidylyltransferase (TIGR)	cdsA	0.00	0.00	0.00	0.00	0.00	0.00
DVU0869	undecaprenyl diphosphate synthase (TIGR)	uppS	0.25	0.13	1.41	0.05	0.02	0.05
DVU0870	ribosome recycling factor (TIGR)	frr	0.03	0.03	0.19	0.00	0.05	0.01

DVU0871	uridylate kinase (TIGR)	pyrH	0.06	0.02	0.07	0.00	0.00	0.02
DVU0872	glycosyl transferase, group 2 family protein (TIGR)		0.02	0.00	0.21	0.00	0.01	0.01
DVU0873	translation elongation factor Ts (TIGR)	tsf	0.03	0.00	0.09	0.00	0.00	0.00
DVU0874	ribosomal protein S2 (TIGR)	rpsB	0.02	0.01	0.03	0.00	0.00	0.00
DVU0875	fumarylacetoacetate hydrolase family protein (TIGR)		0.95	1.30	1.12	0.05	1.25	1.54
DVU0876	metallo-beta-lactamase family protein (TIGR)		0.80	0.98	0.64	0.02	1.01	0.91
DVU0878	dnaK suppressor protein, putative (TIGR)		2.36	2.49	2.89	0.08	2.50	2.86
DVU0880	hypothetical protein (TIGR)		1.52	1.50	0.71	0.01	1.32	1.50
DVU0881	translation elongation factor G, putative (TIGR)	fusA	0.94	1.20	1.15	0.04	0.57	0.86
DVU0882	hypothetical protein (TIGR)		0.90	1.11	1.02	0.04	0.96	1.05
DVU0883	glutaredoxin, putative (TIGR)	nrdH	1.03	0.75	1.00	0.05	1.20	1.66
DVU0884	conserved hypothetical protein (TIGR)	ftrB	1.13	1.36	1.48	0.02	1.48	1.42
DVU0885	amidohydrolase family protein (TIGR)		0.94	1.07	0.89	0.02	1.24	1.34
DVU0886	thioesterase family protein (TIGR)		1.03	1.27	0.74	0.01	1.22	1.07
DVU0887	transglycosylase, putative (TIGR)	mltA	1.39	1.22	1.47	0.03	1.50	1.63
DVU0888	response regulator (TIGR)		1.20	1.16	1.06	0.57	1.19	1.03
DVU0889	phosphonopyruvate decarboxylase-related protein (TIGR)		1.56	1.80	1.40	0.03	1.71	1.74
DVU0890	homoserine dehydrogenase (TIGR)	hom	0.19	0.11	0.43	0.01	0.12	0.09
DVU0891	aminotransferase, classes I and II (TIGR)		0.39	0.49	0.80	0.01	0.54	0.45
DVU0892	shikimate kinase (TIGR)	aroK-1	0.61	0.52	0.17	0.00	0.01	0.01
DVU0893	universal stress protein family (TIGR)		1.61	1.88	1.41	0.08	1.59	1.44
DVU0894	chorismate synthase (TIGR)	aroC	0.77	0.95	0.17	0.00	0.01	0.01
DVU0895	helicase, RecD/TraA family (TIGR)	recD	0.94	1.08	1.10	0.03	0.96	0.91
DVU0896	lipoprotein, NLP/P60 family (TIGR)		1.31	1.73	1.82	0.03	1.81	1.81
DVU0897	RNA modification enzyme, MiaB-family (TIGR)		0.81	0.96	0.84	0.01	1.24	1.17
DVU0898	conserved hypothetical protein (TIGR)		0.50	1.07	1.01	0.04	1.17	1.07
DVU0899	conserved hypothetical protein (TIGR)		0.19	0.84	1.04	0.01	0.78	0.81
DVU0900	guanylate kinase (TIGR)	gmk	0.03	0.00	0.20	0.01	0.03	0.01
DVU0901	orotidine 5`-phosphate decarboxylase (TIGR)	pyrF	1.47	1.24	0.92	0.02	0.01	0.01
DVU0902	TPR domain protein (TIGR)		0.71	0.59	0.39	0.01	0.71	0.76
DVU0903	HD domain protein (TIGR)		1.23	1.31	0.98	0.05	1.59	1.43
DVU0904	single-stranded-DNA-specific exonuclease RecJ (TI	recJ	0.60	0.80	0.73	0.01	0.87	0.81
DVU0905	lipoic acid synthetase (TIGR)	lipA	1.09	1.11	1.39	0.16	1.29	1.24
DVU0906	lipoate-protein ligase B (TIGR)	lipB	0.22	0.86	0.93	0.01	0.91	0.77
DVU0907	conserved domain protein (TIGR)		0.50	0.69	0.70	0.02	0.72	0.62
DVU0908	iron-sulfur cluster-binding protein, putative (TIGR)		1.05	1.22	0.96	0.02	0.06	0.04
DVU0909	hypothetical protein (TIGR)		1.88	1.72	1.02	0.03	1.68	2.03
DVU0910	flagellar motor switch protein FliM (TIGR)	fliM	1.11	0.73	0.70	0.02	1.49	1.27
DVU0911	tRNA pseudouridine synthase A (TIGR)	truA	1.54	1.64	1.25	0.02	1.38	1.36
DVU0912	conserved domain protein (TIGR)		0.57	1.06	0.64	0.02	1.62	1.14
DVU0913	conserved hypothetical protein (TIGR)		0.76	0.90	0.82	0.06	1.56	1.53
DVU0914	cobalamin-5-phosphate synthase (TIGR)	cobS	0.85	0.68	0.65	0.01	0.50	0.50
DVU0915	conserved hypothetical protein (TIGR)		0.71	0.67	1.00	0.02	0.91	0.69
DVU0916	AT-rich DNA-binding protein (TIGR)		0.05	0.07	0.14	13.99	0.03	0.01
DVU0917	ATP synthase F0, C subunit (TIGR)	atpE	0.00	0.00	0.00	0.00	0.02	0.02
DVU0918	ATP synthase F0, A subunit (TIGR)	atpB	0.00	0.01	0.00	0.00	0.01	0.04
DVU0919	hypothetical protein (TIGR)		0.15	0.14	0.02	0.01	0.16	0.10
DVU0920	ATP synthase protein I (TIGR)	atpI	0.18	0.25	0.39	0.04	0.35	0.07
DVU0921	5-nitroimidazole antibiotic resistance protein, putative (TIGI		1.48	1.81	0.89	0.08	2.01	2.34
DVU0922	cytochrome c family protein (TIGR)		1.38	1.47	1.16	0.04	1.70	1.61
DVU0923	endoribonuclease, L-PSP family (TIGR)		0.13	0.38	0.33	0.02	0.38	0.48
DVU0924	23S rRNA (uracil-5-)-methyltransferase RumA (TIG	rumA	1.53	1.55	1.71	0.04	1.63	1.74
DVU0925	glucose-1-phosphate thymidylyltransferase (TIGR)	rfbA	0.03	0.02	0.33	0.01	0.01	0.02
DVU0926	hypothetical protein (TIGR)		0.61	0.84	0.14	0.09	0.62	0.80
DVU0927	ribosomal protein L21 (TIGR)	rplU	0.00	0.00	0.00	0.00	0.00	0.00
DVU0928	ribosomal protein L27 (TIGR)	rpmA	0.00	0.05	0.08	0.00	0.01	0.01
DVU0929	GTP-binding protein, GTP1/OBG family (TIGR)	obg	0.04	0.02	0.14	0.00	0.01	0.00
DVU0930	glutamate 5-kinase (TIGR)	proB	0.83	0.89	0.16	0.00	0.00	0.01
DVU0931	phosphomethylpyrimidine kinase (TIGR)	thiD	0.06	0.08	0.46	0.01	0.02	0.02
DVU0932	sensor histidine kinase (TIGR)		0.84	0.95	0.95	0.03	1.13	1.11
DVU0933	response regulator (TIGR)		1.41	1.54	1.36	0.04	1.59	1.73
DVU0934	hypothetical protein (TIGR)		0.57	0.90	0.21	0.03	0.64	0.78
DVU0935	methyl-accepting chemotaxis protein (TIGR)		1.26	1.02	1.15	0.02	1.19	1.23
DVU0936	hypothetical protein (TIGR)		2.10	2.40	3.52	0.03	2.85	2.81
DVU0937	hypothetical protein (TIGR)		0.67	0.82	0.37	0.04	0.62	0.91
DVU0938	isoamylase N-terminal domain protein (TIGR)		0.52	0.32	0.86	0.02	0.63	0.68
DVU0939	conserved hypothetical protein (TIGR)		0.64	0.81	0.70	0.05	0.91	0.93

DVU0940	GGDEF domain protein (TIGR)	pleD	1.14	1.61	1.07	0.02	1.85	1.87
DVU0941	metalloprotease, iron-related (Dmitry Rodionov)	pep*	0.87	0.83	0.69	0.02	0.86	0.82
DVU0942	ferric uptake regulator (Dmitry Rodionov)	fur	0.01	0.01	0.05	0.00	0.01	0.02
DVU0943	membrane protein, putative (TIGR)		0.90	0.92	1.00	0.02	1.18	1.28
DVU0944	hypothetical protein (TIGR)		0.54	1.09	1.19	0.04	1.45	1.16
DVU0945	sensor histidine kinase (TIGR)		0.76	1.08	1.11	0.02	1.15	1.15
DVU0946	sigma-54 dependent transcriptional regulator/response regu		0.72	0.64	0.74	0.02	0.73	0.89
DVU0947	membrane protein, putative (TIGR)		0.77	0.73	0.60	0.01	0.71	0.66
DVU0948	conserved hypothetical protein (TIGR)		0.61	0.73	0.91	0.01	1.07	0.95
DVU0949	conserved domain protein (TIGR)		0.92	0.99	0.76	0.02	0.94	1.04
DVU0951	molybdopterin biosynthesis MoeA protein, putativ	moeA-2	1.10	1.25	1.30	0.03	1.31	1.38
DVU0952	conserved hypothetical protein TIGR00282 (TIGR)		0.77	0.99	0.67	0.02	1.09	1.03
DVU0953	tyrosyl-tRNA synthetase (TIGR)	tyrS	0.03	0.01	0.03	0.00	0.00	0.00
DVU0954	organic solvent tolerance protein, putative (TIGR)		0.00	0.00	0.08	0.00	0.00	0.01
DVU0955	alanine racemase (TIGR)	alr	1.13	0.40	1.14	0.02	1.45	1.46
DVU0956	ribosomal protein S6 (TIGR)	rpsF	0.00	0.00	0.11	0.00	0.00	0.00
DVU0957	ribosomal protein S18 (TIGR)	rpsR	0.02	0.00	0.00	0.00	0.01	0.00
DVU0958	ribosomal protein L9 (TIGR)	rplI	0.00	0.00	0.00	0.00	0.03	0.02
DVU0959	replicative DNA helicase (TIGR)	dnaB	0.00	0.00	0.01	0.00	0.00	0.00
DVU0961	conserved hypothetical protein (TIGR)		1.24	1.22	1.21	0.04	1.29	1.40
DVU0963	GTP cyclohydrolase I family protein (TIGR)		1.23	1.29	0.84	0.02	1.24	1.28
DVU0964	Glu/Leu/Phe/Val dehydrogenase family protein (TI	fragment	1.15	1.47	1.30	0.03	1.41	1.41
DVU0965	hypothetical protein (TIGR)		0.36	0.77	0.50	0.03	0.77	0.55
DVU0966	amino acid ABC transporter, periplasmic amino acid-binding		0.87	1.33	1.53	0.04	1.85	1.88
DVU0967	amino acid ABC transporter, permease protein, His/Glu/Gln,		0.98	0.97	1.09	0.04	1.67	1.71
DVU0968	amino acid ABC transporter, ATP-binding protein (TIGR)		0.56	0.77	0.80	0.01	1.21	1.23
DVU0969	efflux protein, LysE family (TIGR)		1.35	1.38	1.15	0.02	1.33	1.36
DVU0970	lipoprotein, putative (TIGR)		0.44	1.06	0.65	0.02	0.77	0.79
DVU0971	molybdenum cofactor biosynthesis protein (TIGR)		0.99	1.16	1.13	0.04	1.28	0.91
DVU0972	HD domain protein (TIGR)		0.83	0.92	0.92	0.02	1.11	1.04
DVU0973	4-hydroxybenzoate octaprenyltransferase, putative (TIGR)		0.37	0.20	0.84	0.04	0.10	0.12
DVU0974	hypothetical protein (TIGR)		0.57	0.75	0.44	0.01	1.01	0.84
DVU0975	conserved hypothetical protein (TIGR)		0.56	0.69	0.89	0.01	0.68	0.57
DVU0976	response regulator (TIGR)		1.19	1.42	1.57	0.04	1.27	1.33
DVU0978	ABC transporter, periplasmic substrate-binding protein, puta		1.70	1.97	1.84	0.04	1.98	2.13
DVU0979	DAK1 domain protein (TIGR)	b1200	1.30	1.44	1.36	0.02	1.47	1.59
DVU0980	DAK2 domain protein (TIGR)	b1199	1.21	1.27	1.14	0.04	1.57	1.54
DVU0981	multiphosphoryl transfer protein, putative (TIGR)	ptsI	1.01	1.08	1.06	0.03	1.19	1.10
DVU0982	PHP domain protein (TIGR)		0.61	0.50	0.26	0.02	0.85	0.87
DVU0983	conserved hypothetical protein (TIGR)		0.97	1.11	0.66	0.02	1.03	1.04
DVU0984	tRNA-i(6)A37 modification enzyme MiaB (TIGR)	miaB	1.08	0.84	0.98	0.04	1.10	1.29
DVU0987	heavy metal-binding domain protein (TIGR)		1.06	1.01	0.77	0.07	1.10	0.96
DVU0988	carbohydrate kinase, PfkB family (TIGR)	cbhK	0.86	0.75	0.87	0.01	0.60	0.68
DVU0989	periplasmic divalent cation tolerance protein cutA, putative		2.11	1.99	1.01	0.03	1.87	1.70
DVU0990	endonuclease III, putative (TIGR)	nth	1.11	1.21	1.28	0.03	1.57	1.43
DVU0991	conserved hypothetical protein (TIGR)		1.09	1.52	1.10	0.04	1.27	1.42
DVU0992	chemotaxis protein CheV (TIGR)	cheV-3	1.06	1.16	1.10	0.02	1.13	1.08
DVU0993	hypothetical protein (TIGR)		0.98	1.04	1.10	0.03	1.14	1.22
DVU0994	hypothetical protein (TIGR)		0.00	0.05	0.01	0.00	0.05	0.01
DVU0995	ThiJ/PfpI family protein (TIGR)		0.50	0.64	0.26	0.00	0.58	0.68
DVU0996	hypothetical protein (TIGR)		0.63	0.90	0.83	0.02	0.94	0.87
DVU0997	5,10-methylenetetrahydrofolate reductase (TIGR)	metF	0.85	1.14	0.32	0.02	0.03	0.01
DVU0998	heptosyltransferase family protein (TIGR)		0.04	0.15	0.49	0.01	0.01	0.05
DVU0999	thio:disulfide interchange protein, putative (TIGR)		0.66	0.86	0.76	0.03	0.93	1.01
DVU1000	peptidase, M24 family (TIGR)		0.72	0.85	0.62	0.03	0.82	0.74
DVU1001	coenzyme A binding protein (TIGR)	b0965	1.07	1.28	1.27	0.03	1.11	1.16
DVU1002	conserved domain protein (TIGR)		1.16	1.13	1.14	0.03	1.61	1.32
DVU1003	dnaJ domain protein (TIGR)		0.57	0.88	0.51	0.02	0.79	0.86
DVU1004	membrane protein, putative (TIGR)		1.23	1.43	1.06	0.01	1.51	1.53
DVU1005	hypothetical protein (TIGR)		0.82	0.84	0.75	0.01	0.87	0.85
DVU1006	hypothetical protein (TIGR)		1.39	1.24	0.58	0.01	1.00	0.94
DVU1007	cobinamide kinase/cobinamide phosphate guanyl	cobU	0.74	0.78	0.69	0.04	0.51	0.34
DVU1008	hypothetical protein (TIGR)		0.83	0.62	0.92	0.03	0.84	0.85
DVU1009	hypothetical protein (TIGR)		0.37	0.68	0.75	0.01	0.67	0.56
DVU1012	hemolysin-type calcium-binding repeat protein (TIGR)		0.97	0.97	0.85	0.02	1.09	1.12
DVU1013	type I secretion outer membrane protein, TolC family (TIGR)		0.82	0.99	1.20	0.01	0.98	0.96
DVU1017	ABC transporter, ATP-binding protein/permease p	rtxB	0.70	1.00	0.60	0.01	1.06	0.95

DVU1018	type I secretion membrane fusion protein, HlyD fa	rtxD	0.77	0.82	0.63	0.02	0.86	0.92
DVU1019	conserved domain protein (TIGR)		0.79	1.01	1.23	0.03	1.40	1.26
DVU1020	HD domain/sensory box protein (TIGR)		0.90	0.94	1.10	0.02	0.99	0.94
DVU1021	conserved hypothetical protein (TIGR)		0.07	0.02	0.05	0.00	0.03	0.03
DVU1022	SUF system FeS assembly ATPase SufC, putative (TIGR)		0.05	0.03	0.10	0.00	0.07	0.03
DVU1023	rhomboid family protein (TIGR)		0.76	0.74	0.66	0.01	0.84	0.93
DVU1024	ribosomal large subunit pseudouridine synthase D	rluD/coaI	0.80	0.68	0.89	0.02	0.29	0.27
DVU1025	uracil phosphoribosyltransferase (TIGR)	upp	0.91	1.08	1.58	0.04	0.00	0.00
DVU1026	uracil permease (TIGR)	uraA	1.20	1.23	1.20	0.03	1.66	1.64
DVU1027	hypothetical protein (TIGR)		0.88	1.03	1.12	0.03	1.22	1.19
DVU1028	cytidylate kinase (TIGR)	cmk	0.06	0.12	0.27	0.00	0.52	0.07
DVU1029	histidinol-phosphate aminotransferase (TIGR)	hisC	0.70	0.53	0.06	0.00	0.00	0.00
DVU1030	universal stress protein family (TIGR)		0.76	0.85	0.98	0.02	1.01	0.87
DVU1032	hypothetical protein (TIGR)		0.59	0.54	0.81	0.02	0.77	0.96
DVU1033	competence/damage-inducible protein CinA prote	cinA	1.21	0.73	1.04	0.01	1.00	0.88
DVU1034	hypothetical protein (TIGR)		0.91	1.05	0.85	0.04	1.00	1.11
DVU1035	glucokinase, putative (TIGR)	glk	0.66	0.76	0.49	0.01	0.98	0.81
DVU1036	membrane protein, putative (TIGR)		0.93	1.04	1.18	0.02	0.92	1.00
DVU1037	mercuric reductase, putative (TIGR)		0.52	0.77	0.76	0.01	0.77	0.76
DVU1038	phosphoribosylformimino-5-aminoimidazole carb	hisA	0.76	1.18	0.01	0.00	0.00	0.00
DVU1039	lipoprotein, putative (TIGR)		0.54	0.75	0.06	0.00	0.00	0.01
DVU1040	imidazoleglycerol-phosphate dehydratase (TIGR)	hisB	1.46	1.12	0.00	0.00	0.01	0.00
DVU1041	Sec-independent protein translocase TatC (TIGR)	tatC	0.05	0.03	0.09	0.01	0.01	0.01
DVU1042	twin-arginine translocation protein TatB (TIGR)	tatB	0.01	0.02	0.62	0.00	0.01	0.02
DVU1043	GMP synthase (TIGR)	guaA	0.03	0.03	0.13	0.00	0.00	0.00
DVU1044	inosine-5`-monophosphate dehydrogenase (TIGR)	guaB	0.00	0.02	0.02	0.00	0.00	0.00
DVU1045	hypothetical protein (TIGR)		1.16	1.11	0.82	0.03	1.50	1.91
DVU1046	hypothetical protein (TIGR)		0.00	0.00	0.29	0.00	0.06	0.00
DVU1047	cytochrome c-type biogenesis protein CcmC (TIGR	ccmC	0.03	0.00	0.18	0.00	0.00	0.00
DVU1048	cytochrome c-type biogenesis protein CcmB (TIGR	ccmB	0.04	0.07	0.19	0.00	0.02	0.02
DVU1049	ABC transporter, ATP-binding protein (TIGR)		0.04	0.02	0.29	0.00	0.03	0.03
DVU1050	cytochrome c-type biogenesis protein CcmF (TIGR	ccmF	0.04	0.02	0.13	0.01	0.02	0.01
DVU1051	cytochrome c-type biogenesis protein CcmE (TIGR	ccmE	0.01	0.02	0.14	0.00	0.00	0.00
DVU1052	CBS domain protein (TIGR)		1.05	0.89	1.01	0.02	1.04	1.31
DVU1054	hydrolase, HAD-superfamily, subfamily IIIA (TIGR)		0.11	0.11	0.42	0.01	0.06	0.07
DVU1055	heptosyltransferase family protein (TIGR)		0.03	0.04	0.14	0.01	0.01	0.01
DVU1056	component of nickel ABC transport system (Dmitr	nikO	1.17	1.13	1.67	0.02	0.88	1.08
DVU1057	component of nickel ABC transport system (Dmitr	nikQ	0.64	0.66	1.33	0.01	0.50	0.63
DVU1058	component of nickel ABC transport system (Dmitr	nikM	0.83	0.86	1.43	0.05	0.34	0.47
DVU1059	aminotransferase, putative (TIGR)		1.15	1.45	1.44	0.03	0.53	0.48
DVU1060	glycosyl transferase, group 1 family protein (TIGR)		0.18	0.34	0.51	0.03	0.02	0.14
DVU1061	glycosyl transferase, group 1 family protein (TIGR)		0.79	0.75	1.40	0.03	1.02	0.95
DVU1062	conserved hypothetical protein (TIGR)		1.22	1.25	1.22	0.03	1.41	1.45
DVU1063	transcriptional regulatory protein (TIGR)	flrC	1.02	1.32	0.62	0.02	0.46	0.51
DVU1064	aconitate hydratase, putative (TIGR)	aco	0.12	0.16	0.02	0.00	0.00	0.00
DVU1065	peptidyl-prolyl cis-trans isomerse domain protein (TIGR)		1.08	0.98	0.97	0.02	1.05	1.18
DVU1066	xanthine-guanine phosphoribosyltransferase (TIGF	gpt	1.00	0.83	1.24	0.02	1.14	1.19
DVU1067	membrane protein, Bmp family (TIGR)		0.88	0.86	0.80	0.02	0.73	0.79
DVU1068	branched-chain amino acid ABC transporter, permease prot		0.62	0.64	0.46	0.01	0.61	0.73
DVU1069	branched chain amino acid ABC transporter, permease prot		0.93	1.03	0.92	0.03	0.74	0.90
DVU1070	branched chain amino acid ABC transporter, ATP-b	rbsA	0.65	0.64	0.61	0.02	0.60	0.69
DVU1071	hypothetical protein (TIGR)		0.57	0.84	0.76	0.01	0.79	0.76
DVU1072	conserved hypothetical protein (TIGR)		1.12	1.12	1.11	0.03	1.02	1.11
DVU1073	conserved domain protein (TIGR)		1.25	1.18	1.28	0.03	1.47	1.45
DVU1074	ribosomal protein L34 (TIGR)	rpmH	0.00	0.04	0.30	0.00	0.08	0.02
DVU1075	ribonuclease P protein component (TIGR)	rnpA	0.03	0.13	0.42	0.01	0.16	0.29
DVU1076	conserved hypothetical protein TIGR00278 (TIGR)		0.93	0.30	0.71	0.02	0.49	0.56
DVU1077	inner membrane protein, 60 kDa (TIGR)	yidC	0.00	0.01	0.06	0.00	0.00	0.00
DVU1078	R3H domain protein (TIGR)		0.48	0.56	0.85	0.03	1.58	1.18
DVU1079	tRNA modification GTPase TrmE (TIGR)	trmE	0.41	0.52	0.43	0.01	0.35	0.53
DVU1080	iron-sulfur cluster-binding protein (TIGR)		0.78	0.77	1.46	0.03	0.97	0.98
DVU1081	iron-sulfur cluster-binding protein (TIGR)		1.40	1.51	1.23	0.04	1.47	1.61
DVU1082	3- 5 exonuclease domain protein (TIGR)		0.94	0.89	1.12	0.02	1.09	1.22
DVU1083	phosphate regulon transcriptional regulator PhoB	phoB	0.38	0.19	0.74	0.02	0.25	0.32
DVU1084	phosphate ABC transporter, ATP-binding protein (	pstB-1	1.67	1.88	1.66	0.05	2.05	2.39
DVU1085	phosphate transport system protein PhoU (TIGR)	phoU	0.87	0.96	0.55	0.03	1.07	1.18
DVU1086	hypothetical protein (TIGR)		0.46	0.77	0.35	0.02	0.84	0.81

DVU1087	conserved hypothetical protein (TIGR)		0.89	0.56	0.80	0.02	0.54	0.72
DVU1088	hypothetical protein (TIGR)		1.77	1.43	0.84	0.01	1.37	1.61
DVU1089	alanyl-tRNA synthetase (TIGR)	alaS	0.01	0.00	0.03	0.00	0.00	0.00
DVU1090	recA protein (TIGR)	recA	0.23	0.16	0.41	0.01	0.04	0.03
DVU1091	conserved hypothetical protein (TIGR)		0.87	0.84	1.03	0.03	1.02	1.10
DVU1092	sodium-dependent symporter family protein (TIGR)		1.50	1.44	1.52	0.02	0.82	0.91
DVU1093	HAD-superfamily hydrolase, subfamily IA, variant 3 (TIGR)		1.66	1.28	1.56	0.04	1.49	1.66
DVU1094	argininosuccinate lyase (TIGR)	argH	1.19	1.16	0.12	0.00	0.01	0.01
DVU1095	argininosuccinate synthase (TIGR)	argG	1.06	1.09	0.11	0.00	0.00	0.00
DVU1096	ornithine carbamoyltransferase (TIGR)	argF	1.06	1.02	0.26	0.01	0.01	0.01
DVU1097	conserved hypothetical protein (TIGR)		1.36	1.26	0.72	0.02	0.33	0.20
DVU1098	adenine specific DNA methyltransferase, putative (TIGR)		1.24	1.35	1.18	0.04	1.24	1.30
DVU1099	tail fiber assembly protein, putative (TIGR)		1.15	1.05	1.06	0.02	1.00	1.17
DVU1100	tail fiber protein, putative (TIGR)		1.69	1.49	1.73	0.04	1.42	1.63
DVU1101	hypothetical protein (TIGR)		1.13	1.32	1.10	0.03	1.47	1.50
DVU1102	baseplate assembly protein, putative (TIGR)		2.18	1.85	2.13	0.07	1.93	2.09
DVU1103	baseplate assembly protein, putative (TIGR)		1.44	1.82	1.88	0.02	1.49	1.68
DVU1104	baseplate assembly protein, putative (TIGR)		1.27	1.27	1.62	0.05	1.21	1.30
DVU1105	hypothetical protein (TIGR)		1.80	1.08	1.38	0.05	1.31	1.40
DVU1106	hypothetical protein (TIGR)		0.76	1.16	1.04	0.02	1.00	1.09
DVU1107	tail tape measure protein (TIGR)		1.39	1.51	1.57	0.04	1.43	1.55
DVU1108	hypothetical protein (TIGR)		3.79	3.60	3.51	0.09	3.23	3.71
DVU1109	ATPase domain protein (TIGR)		0.06	0.03	0.11	0.00	0.08	0.09
DVU1110	hypothetical protein (TIGR)		1.73	1.63	1.66	0.02	1.62	1.77
DVU1111	hypothetical protein (TIGR)		2.07	1.78	1.83	0.06	1.98	2.02
DVU1112	hypothetical protein (TIGR)		1.25	1.92	1.73	0.03	1.96	1.97
DVU1113	hypothetical protein (TIGR)		1.09	1.45	1.24	0.03	1.41	1.43
DVU1114	virion morphogenesis protein (TIGR)		2.26	1.58	1.67	0.01	1.49	1.71
DVU1115	conserved hypothetical protein (TIGR)		0.92	1.08	0.86	0.01	0.95	1.00
DVU1116	hypothetical protein (TIGR)		2.14	1.78	1.98	0.05	1.86	2.05
DVU1117	hypothetical protein (TIGR)		2.14	1.73	2.38	0.02	1.56	1.63
DVU1118	conserved hypothetical protein (TIGR)		2.05	2.25	1.82	0.04	1.94	2.05
DVU1119	virion morphogenesis protein (TIGR)		1.45	1.43	1.38	0.03	1.45	1.26
DVU1120	conserved hypothetical protein (TIGR)		1.27	1.23	1.36	0.04	1.33	1.26
DVU1121	hypothetical protein (TIGR)		1.06	0.91	0.74	0.02	0.75	0.98
DVU1122	portal protein, putative (TIGR)		1.32	1.50	1.69	0.03	1.67	1.81
DVU1123	conserved domain protein (TIGR)		1.19	1.97	1.72	0.03	1.70	1.75
DVU1124	hypothetical protein (TIGR)		3.63	3.20	2.17	0.17	2.85	3.20
DVU1125	conserved domain protein (TIGR)		1.59	1.30	0.96	0.01	1.04	1.33
DVU1126	lipoprotein, putative (TIGR)		1.54	0.93	1.61	0.05	1.30	1.15
DVU1127	hypothetical protein (TIGR)		0.92	1.07	1.49	0.03	1.15	1.36
DVU1128	lysozyme, putative (TIGR)		1.35	1.04	1.21	0.03	1.25	1.32
DVU1129	conserved hypothetical protein (TIGR)		1.33	1.30	1.59	0.02	1.13	1.36
DVU1130	DNA-binding protein (TIGR)		0.90	0.93	1.47	0.01	1.10	1.02
DVU1131	hypothetical protein (TIGR)		1.04	1.06	1.54	0.03	1.18	1.13
DVU1132	conserved hypothetical protein (TIGR)		1.49	1.57	1.21	0.05	1.23	1.66
DVU1133	hypothetical protein (TIGR)		1.30	1.38	1.64	0.05	1.39	1.42
DVU1134	DNA-binding protein HU, beta subunit (TIGR)	hupB	1.17	1.54	2.11	0.03	1.20	1.23
DVU1135	conserved domain protein (TIGR)		0.96	1.08	1.23	0.04	1.17	1.09
DVU1136	host-nuclease inhibitor protein Gam, putative (TIGR)		1.51	1.10	0.89	0.03	1.13	1.33
DVU1137	hypothetical protein (TIGR)		2.77	1.96	1.96	0.03	1.54	1.39
DVU1138	hypothetical protein (TIGR)		0.99	1.47	1.89	0.03	1.22	1.07
DVU1139	bacteriophage DNA transposition B protein, putative (TIGR)		1.48	1.29	1.02	0.02	1.53	1.35
DVU1141	hypothetical protein (TIGR)		0.95	1.48	1.93	0.04	1.13	1.44
DVU1142	transcriptional regulator, putative (TIGR)		1.14	0.63	1.36	0.04	0.94	1.28
DVU1143	hypothetical protein (TIGR)		2.50	1.82	2.16	0.05	2.01	2.54
DVU1144	transcriptional regulator, Cro/CI family (TIGR)		0.00	0.00	0.03	0.00	0.00	0.00
DVU1145	hypothetical protein (TIGR)		0.26	0.08	0.00	0.00	0.16	0.12
DVU1147	alginate o-acetyltransferase AlgI, putative (TIGR)		0.46	0.37	0.32	0.01	0.50	0.58
DVU1148	conserved hypothetical protein (TIGR)		0.17	0.20	0.26	0.01	0.28	0.32
DVU1151	hypothetical protein (TIGR)		0.31	0.27	0.82	0.00	0.12	0.14
DVU1152	hypothetical protein (TIGR)		1.46	1.74	1.72	0.03	1.69	2.08
DVU1153	hypothetical protein (TIGR)		2.30	2.40	1.50	0.05	1.36	1.91
DVU1154	hypothetical protein (TIGR)		0.07	0.23	0.00	0.00	0.23	0.24
DVU1155	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.05	0.07
DVU1156	sigma-54 dependent transcriptional regulator, putative/resp		1.19	1.09	1.00	0.02	1.21	1.30
DVU1157	sensory box histidine kinase (TIGR)		1.13	1.05	1.01	0.02	0.99	1.12

DVU1158	hypothetical protein (TIGR)		0.90	1.43	0.91	0.02	1.33	1.20
DVU1159	hypothetical protein (TIGR)		0.39	0.52	1.05	0.02	0.51	0.37
DVU1160	urea transporter, putative (TIGR)		1.29	1.17	1.36	0.03	1.24	1.38
DVU1161	hypothetical protein (TIGR)		0.04	0.16	0.07	0.00	0.37	0.25
DVU1162	hypothetical protein (TIGR)		0.34	0.30	0.58	0.01	0.43	0.53
DVU1163	major facilitator superfamily protein (TIGR)		0.85	0.89	0.66	0.02	0.81	0.88
DVU1164	aliphatic amidase (TIGR)	amiE	1.47	1.14	1.25	0.03	1.16	1.28
DVU1165	NADH respiratory dehydrogenase (Regina ONeil)	ndh	0.97	0.97	1.12	0.02	1.05	1.05
DVU1166	hypothetical protein (TIGR)		0.10	0.00	0.01	0.00	0.09	0.03
DVU1168	hypothetical protein (TIGR)		1.13	0.66	0.74	0.02	0.93	1.12
DVU1169	methyl-accepting chemotaxis protein (TIGR)		0.86	0.85	0.83	0.02	0.90	1.07
DVU1170	hypothetical protein (TIGR)		0.53	0.49	0.33	0.02	0.99	0.77
DVU1173	integral membrane protein MviN (TIGR)	mviN-1	0.00	0.02	0.16	0.01	0.00	0.01
DVU1174	hypothetical protein (TIGR)		0.70	0.37	0.33	0.02	0.53	0.70
DVU1175	hypothetical protein (TIGR)		0.83	0.60	0.54	0.01	0.70	0.57
DVU1176	hypothetical protein (TIGR)		1.03	1.07	1.59	0.01	1.16	1.21
DVU1177	hypothetical protein (TIGR)		1.07	0.86	0.61	0.01	0.76	0.83
DVU1179	aldehyde:ferredoxin oxidoreductase, tungsten-cor	aor	1.02	1.06	0.98	0.02	1.11	1.07
DVU1180	hypothetical protein (TIGR)		0.39	0.54	0.55	0.01	0.52	0.62
DVU1181	response regulator (TIGR)		0.97	1.13	1.17	0.04	1.27	1.12
DVU1182	hypothetical protein (TIGR)		1.40	1.26	1.30	0.02	1.18	1.36
DVU1183	HD domain protein (TIGR)		1.02	0.84	0.72	0.02	0.97	1.00
DVU1185	colicin V production family protein (TIGR)		0.59	0.66	0.85	0.02	0.60	0.59
DVU1186	MazG family protein (TIGR)	mazG	0.63	0.87	0.13	0.00	0.00	0.00
DVU1187	hypothetical protein (TIGR)		1.01	1.11	0.79	0.41	1.14	1.07
DVU1188	hypothetical protein (TIGR)		1.19	0.95	1.69	0.04	1.25	1.16
DVU1189	conserved hypothetical protein (TIGR)		1.40	1.36	1.46	0.03	1.43	1.36
DVU1190	sensory box/GGDEF domain/EAL domain protein (TIGR)		0.81	0.94	0.94	0.03	1.02	1.09
DVU1191	ATP-dependent protease La, putative (TIGR)	lon	1.05	1.10	1.11	0.02	0.93	1.11
DVU1192	acylphosphatase (TIGR)	acyP	1.49	1.11	1.57	0.05	1.45	1.17
DVU1193	DNA repair protein RadC (TIGR)	radC	1.19	0.93	1.15	0.01	1.04	0.97
DVU1194	hypothetical protein (TIGR)		0.00	0.00	0.07	0.00	0.00	0.00
DVU1195	lipoprotein, putative (TIGR)		0.00	0.01	0.05	0.00	0.00	0.01
DVU1196	leucyl-tRNA synthetase (TIGR)	leuS	0.00	0.01	0.01	0.00	0.00	0.00
DVU1197	N utilization substance protein B (TIGR)	nusB	0.07	0.08	0.37	0.02	0.14	0.09
DVU1198	riboflavin synthase, beta subunit (TIGR)	ribH	0.06	0.00	0.01	0.00	0.00	0.00
DVU1199	3,4-dihydroxy-2-butanone 4-phosphate synthase/(	ribAB	0.02	0.00	0.03	0.00	0.00	0.00
DVU1200	riboflavin synthase, alpha subunit (TIGR)	ribE	0.00	0.00	0.18	0.01	0.00	0.01
DVU1201	riboflavin biosynthesis protein RibD (TIGR)	ribD	0.01	0.01	0.08	0.00	0.00	0.01
DVU1202	cytidine/deoxycytidylate deaminase family protein (TIGR)		0.02	0.06	0.03	0.00	0.04	0.05
DVU1203	serine hydroxymethyltransferase (TIGR)	glyA	0.03	0.02	0.08	0.00	0.00	0.00
DVU1204	3-oxoacyl-(acyl-carrier-protein) synthase II (TIGR)	fabF	0.00	0.00	0.00	0.00	0.00	0.00
DVU1205	acyl carrier protein (TIGR)	acpP	0.00	0.00	0.18	0.00	0.08	0.05
DVU1206	3-oxoacyl-(acyl-carrier-protein) reductase (TIGR)	fabG	0.02	0.09	0.08	0.00	0.01	0.03
DVU1207	3-oxoacyl-(acyl-carrier-protein) synthase III (TIGR)	fabH	0.47	0.23	0.35	0.01	0.02	0.01
DVU1208	fatty acid/phospholipid synthesis protein PlsX (TIG	plsX	0.34	0.08	0.18	0.00	0.07	0.03
DVU1209	ribosomal protein L32 (TIGR)	rpmF	0.03	0.00	0.38	0.00	0.08	0.03
DVU1210	conserved hypothetical protein (TIGR)		0.08	0.25	0.95	0.02	0.50	0.44
DVU1211	ribosomal protein L28 (TIGR)	rpmB	0.00	0.05	0.00	0.00	0.01	0.00
DVU1212	fxsA protein (TIGR)	fsxA	0.84	1.01	1.17	0.02	1.06	1.04
DVU1213	rhomboid family protein (TIGR)		1.11	1.04	1.24	0.03	1.12	1.30
DVU1214	dolichyl-phosphate-mannose-protein mannosyltransferase f		0.88	0.87	1.05	0.02	1.01	0.95
DVU1215	PAP2 family protein (TIGR)		0.60	0.40	0.92	0.02	0.42	0.43
DVU1217	MATE efflux family protein (TIGR)		1.60	1.38	1.46	0.04	1.29	1.41
DVU1218	conserved hypothetical protein (TIGR)		0.61	0.50	0.80	0.00	0.51	0.66
DVU1219	conserved hypothetical protein (TIGR)		1.36	1.30	1.32	0.03	1.40	1.39
DVU1220	nitroreductase family protein (TIGR)		1.01	1.01	1.09	0.03	1.28	1.20
DVU1221	hypothetical protein (TIGR)		0.96	0.80	0.61	0.02	0.91	1.10
DVU1222	hypothetical protein (TIGR)		0.83	0.77	0.81	0.01	0.79	0.87
DVU1223	conserved hypothetical protein (TIGR)		1.23	1.24	1.12	0.02	1.27	1.32
DVU1224	endonuclease IV (TIGR)	nfo	1.74	1.92	1.68	0.06	2.16	1.97
DVU1225	hypothetical protein (TIGR)		0.82	0.91	0.77	0.02	1.05	0.98
DVU1226	hypothetical protein (TIGR)		0.72	0.53	3.29	0.10	1.54	1.68
DVU1228	thiol peroxidase (TIGR)	tpX	0.46	0.59	0.63	0.02	0.72	0.74
DVU1230	hypothetical protein (TIGR)		0.86	0.93	0.72	0.01	0.82	0.82
DVU1231	ammonium transporter (TIGR)	amt	1.24	1.35	1.59	0.02	1.12	1.43
DVU1232	nitrogen regulatory protein P-II (TIGR)	glnB-1	1.18	1.48	1.24	0.04	1.74	2.06

DVU1233	protein-P-II uridylyltransferase, putative (TIGR)	glnD	1.17	1.11	0.97	0.02	1.22	1.27
DVU1234	membrane protein, putative (TIGR)		1.16	1.01	1.38	0.03	1.30	1.16
DVU1235	hypothetical protein (TIGR)		0.91	0.88	0.99	0.02	1.16	1.17
DVU1236	amino acid ABC transporter, ATP-binding protein (TIGR)		0.70	0.80	0.64	0.02	1.17	1.01
DVU1237	amino acid ABC transporter, permease protein, Hi	glnP	0.41	0.68	0.62	0.03	1.08	1.03
DVU1238	amino acid ABC transporter, periplasmic amino acid-binding		0.78	0.71	0.64	0.02	0.73	0.77
DVU1239	membrane protein, putative (TIGR)		0.60	0.75	0.73	0.02	0.90	0.86
DVU1240	hypothetical protein (TIGR)		1.30	1.52	1.01	0.04	1.98	1.67
DVU1241	conserved hypothetical protein (TIGR)		0.65	0.73	0.87	0.03	0.70	0.71
DVU1242	vacJ lipoprotein, putative (TIGR)	vacJhom	0.74	0.83	0.60	0.02	0.95	1.05
DVU1243	conserved hypothetical protein (TIGR)		0.71	0.62	0.74	0.01	0.72	0.83
DVU1244	conserved hypothetical protein (TIGR)		1.10	1.31	1.71	0.01	1.28	1.50
DVU1245	ABC transporter, ATP-binding protein (TIGR)		0.93	0.96	1.09	0.02	1.07	0.93
DVU1246	membrane protein, putative (TIGR)		0.71	0.69	0.38	0.02	0.78	0.74
DVU1247	hypothetical protein (TIGR)		0.67	0.67	0.57	0.02	0.83	0.87
DVU1248	arginyl-tRNA synthetase (TIGR)	argS	0.01	0.02	0.07	0.00	0.00	0.00
DVU1249	malonyl CoA-acyl carrier protein transacylase (TIG	fabD	0.25	0.09	0.98	0.01	0.04	0.04
DVU1250	methyltransferase GidB (TIGR)	gidB	1.10	1.75	1.79	0.04	1.70	1.84
DVU1251	hypothetical protein (TIGR)		0.75	0.43	0.69	0.01	0.89	0.82
DVU1252	membrane protein, putative (TIGR)		0.95	0.72	1.10	0.03	0.34	0.36
DVU1253	hypothetical protein (TIGR)		0.34	0.38	0.25	0.00	0.59	0.50
DVU1254	conserved hypothetical protein (TIGR)		2.00	1.25	1.40	0.05	1.31	1.53
DVU1255	Sua5/YciO/YrdC/YwlC family protein (TIGR)		0.07	0.08	0.25	0.02	0.03	0.06
DVU1256	heptosyltransferase family protein (TIGR)		1.07	1.21	1.26	0.03	1.05	1.15
DVU1257	RNA-binding protein (TIGR)		0.02	0.05	0.25	0.01	0.15	0.18
DVU1258	glutamine synthetase, type III (TIGR)	glnN	0.00	0.01	0.01	0.00	0.00	0.00
DVU1260	outer membrane protein P1, putative (TIGR)		0.98	0.99	0.66	0.03	1.05	1.15
DVU1261	conserved domain protein (TIGR)		1.30	1.13	1.17	0.03	1.17	1.23
DVU1262	twitching motility protein PilT (TIGR)	pilT-1	0.56	0.78	0.46	0.01	0.72	0.76
DVU1263	type IV prepilin-like proteins leader peptidase (TIG	pppA	0.86	1.05	0.65	0.01	0.85	0.89
DVU1264	transglycosylase SLT domain protein (TIGR)		1.97	1.37	1.00	0.04	1.52	1.76
DVU1265	hypothetical protein (TIGR)		0.95	0.74	0.81	0.03	0.77	0.67
DVU1266	hypothetical protein (TIGR)		1.27	1.20	1.13	0.02	1.13	1.17
DVU1267	hypothetical protein (TIGR)		1.57	1.38	1.16	0.05	1.31	1.42
DVU1268	hypothetical protein (TIGR)		1.20	1.00	1.57	0.02	1.12	1.00
DVU1270	twitching motility protein (TIGR)	pilT-1	0.88	0.91	1.27	0.01	1.37	1.16
DVU1271	general secretion pathway protein F, putative (TIGR)		1.05	0.76	0.86	0.02	0.92	0.82
DVU1272	general secretion pathway protein E, putative (TIG	gspE	1.17	1.22	1.18	0.02	1.31	1.17
DVU1273	bacterial type II/III secretion system protein (TIGR)		1.27	1.28	0.99	0.03	1.32	1.19
DVU1274	hypothetical protein (TIGR)		1.50	1.78	1.80	0.04	1.55	1.41
DVU1275	hypothetical protein (TIGR)		1.22	1.08	1.55	0.03	1.10	1.12
DVU1276	hypothetical protein (TIGR)		1.58	1.53	1.45	0.04	1.60	1.61
DVU1277	hypothetical protein (TIGR)		0.32	0.23	0.07	0.00	0.16	0.29
DVU1278	cell division protein FtsH (TIGR)	ftsH	0.01	0.00	0.05	0.00	0.00	0.00
DVU1279	dihydropteroate synthase (TIGR)	folP	0.36	0.41	1.05	0.02	0.11	0.16
DVU1280	conserved hypothetical protein TIGR00159 (TIGR)		0.56	0.90	0.49	0.02	0.68	0.83
DVU1281	conserved hypothetical protein (TIGR)		0.88	0.87	0.66	0.01	0.98	1.09
DVU1282	phosphoglucosamine mutase (TIGR)	glmM	0.00	0.01	0.20	0.00	0.01	0.01
DVU1283	UTP-glucose-1-phosphate uridylyltransferase (TIGI	galU	0.57	0.63	0.32	0.01	0.50	0.56
DVU1284	primosomal protein n (TIGR)	priA	0.13	0.15	0.32	0.00	0.02	0.03
DVU1285	response regulator (TIGR)		0.23	0.31	0.22	0.01	0.41	0.50
DVU1286	Integral membrane protein (Shelley Haveman)	DsrP	0.01	0.02	0.09	0.00	0.00	0.01
DVU1287	Periplasmic (Tat), binds 2[4Fe-4S] (Shelley Havema	DsrO	0.00	0.00	0.08	0.00	0.00	0.01
DVU1288	Periplasmic (Sec) triheme cytochrome c (Shelley H	DsrJ	0.02	0.00	0.00	0.00	0.02	0.03
DVU1289	Cytoplasmic, binds 2 [4Fe-4S] (Shelley Haveman)	DsrK	0.00	0.02	0.07	0.00	0.01	0.01
DVU1290	Inner membrane protein binds 2 heme b (Shelley H	DsrM	0.01	0.02	0.12	0.00	0.00	0.00
DVU1291	hypothetical protein (TIGR)		0.03	0.01	0.19	0.01	0.03	0.05
DVU1292	hypothetical protein (TIGR)		0.14	0.39	0.00	0.00	0.38	0.35
DVU1294	conserved hypothetical protein (TIGR)		0.33	0.30	0.32	0.01	0.36	0.32
DVU1295	sulfate adenylyltransferase (TIGR)	sat	0.02	0.01	0.06	0.00	0.00	0.01
DVU1297	hypothetical protein (TIGR)		0.72	0.66	0.38	0.00	0.57	1.64
DVU1298	ribosomal protein S12 (TIGR)	rpsL	0.00	0.00	0.00	0.01	0.00	0.01
DVU1299	ribosomal protein S7 (TIGR)	rpsG	0.00	0.00	0.00	0.01	0.00	0.00
DVU1300	translation elongation factor G (TIGR)	fusA-1	0.00	0.01	0.05	0.00	0.00	0.00
DVU1301	hypothetical protein (TIGR)		0.31	0.00	0.00	0.00	0.16	0.12
DVU1302	ribosomal protein S10 (TIGR)	rpsJ	0.00	0.00	0.15	0.00	0.00	0.00
DVU1303	ribosomal protein L3 (TIGR)	rplC	0.01	0.00	0.00	0.00	0.00	0.00

DVU1304	ribosomal protein L4 (TIGR)	rplD	0.00	0.00	0.00	0.00	0.00	0.00
DVU1305	ribosomal protein L23 (TIGR)	rplW	0.00	0.00	0.09	0.00	0.00	0.00
DVU1306	ribosomal protein L2 (TIGR)	rplB	0.02	0.00	0.00	0.00	0.00	0.00
DVU1307	ribosomal protein S19 (TIGR)	rpsS	0.03	0.00	0.00	0.00	0.00	0.00
DVU1308	ribosomal protein L22 (TIGR)	rplV	0.00	0.00	0.00	0.00	0.00	0.00
DVU1309	ribosomal protein S3 (TIGR)	rpsC	0.00	0.00	0.00	0.00	0.00	0.00
DVU1310	ribosomal protein L16 (TIGR)	rplP	0.00	0.00	0.00	0.00	0.00	0.00
DVU1311	ribosomal protein L29 (TIGR)	rpmC	0.00	0.00	0.00	0.00	0.00	0.00
DVU1312	ribosomal protein S17 (TIGR)	rpsQ	0.00	0.00	0.00	0.00	0.00	0.00
DVU1313	ribosomal protein L14 (TIGR)	rplN	0.00	0.00	0.00	0.00	0.00	0.00
DVU1314	ribosomal protein L24 (TIGR)	rplX	0.00	0.00	0.00	0.00	0.00	0.00
DVU1315	ribosomal protein L5 (TIGR)	rplE	0.00	0.00	0.00	0.00	0.00	0.00
DVU1316	ribosomal protein S14 (TIGR)	rpsN	0.00	0.00	0.00	0.00	0.00	0.00
DVU1317	ribosomal protein S8 (TIGR)	rpsH	0.00	0.00	0.00	0.00	0.00	0.00
DVU1318	ribosomal protein L6 (TIGR)	rplF	0.00	0.00	0.00	0.00	0.00	0.00
DVU1319	ribosomal protein L18 (TIGR)	rplR	0.00	0.00	0.05	0.00	0.01	0.00
DVU1320	ribosomal protein S5 (TIGR)	rpsE	0.00	0.00	0.00	0.00	0.00	0.00
DVU1321	ribosomal protein L30 (TIGR)	rpmD	0.00	0.00	0.00	0.00	0.00	0.00
DVU1322	ribosomal protein L15 (TIGR)	rplO	0.00	0.00	0.00	0.00	0.00	0.00
DVU1323	preprotein translocase, SecY subunit (TIGR)	secY	0.00	0.00	0.00	0.00	0.00	0.00
DVU1324	methionine aminopeptidase, type I (TIGR)	map	0.13	0.06	0.22	0.00	0.04	0.07
DVU1325	ribosomal protein L36 (TIGR)	rpmJ	0.00	0.00	0.00	0.00	0.00	0.00
DVU1326	ribosomal protein S13 (TIGR)	rpsM	0.00	0.00	0.00	0.00	0.00	0.00
DVU1327	ribosomal protein S11 (TIGR)	rpsK	0.00	0.01	0.00	0.00	0.00	0.00
DVU1328	ribosomal protein S4 (TIGR)	rpsD	0.00	0.00	0.00	0.00	0.00	0.00
DVU1329	DNA-directed RNA polymerase, alpha subunit (TIG	rpoA	0.00	0.00	0.00	0.00	0.00	0.00
DVU1330	ribosomal protein L17 (TIGR)	rplQ	0.00	0.00	0.00	0.00	0.00	0.00
DVU1331	transcriptional regulator, LysR family (TIGR)		0.56	0.98	0.89	0.02	1.08	1.21
DVU1332	selenide, water dikinase, selenocysteine-containin	selD	0.78	0.99	1.01	0.02	1.07	0.92
DVU1333	hypothetical protein (TIGR)		0.00	0.25	0.01	0.00	0.29	0.11
DVU1334	trigger factor (TIGR)	tig	0.04	0.01	0.29	0.01	0.05	0.14
DVU1335	ATP-dependent Clp protease, proteolytic subunit (	clpP	0.53	0.48	0.92	0.03	0.63	0.35
DVU1336	ATP-dependent Clp protease, ATP-binding subunit	clpX	0.32	0.52	0.73	0.01	0.55	0.23
DVU1337	ATP-dependent protease La (TIGR)	lon	0.67	0.99	0.69	0.02	0.71	0.61
DVU1338	conserved hypothetical protein (TIGR)		0.62	1.11	0.87	0.02	1.29	0.90
DVU1339	lipoprotein, putative (TIGR)		1.13	1.12	1.07	0.02	1.37	1.26
DVU1340	Zinc uptake transcriptional regulator ZUR (Fur fam	ZUR	0.65	1.19	1.65	0.01	1.21	1.12
DVU1341	permease component of zinc ABC transporter (Dr	znuC	1.03	1.34	0.96	0.03	1.26	1.08
DVU1342	ATPase component of zinc ABC transporter (Dmitr	znuB	1.33	1.66	1.08	0.02	1.50	1.20
DVU1343	periplasmic component of zinc ABC transporter (D	znuA	0.84	1.24	0.67	0.02	1.11	0.91
DVU1344	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate s	ispG	0.12	0.07	0.49	0.00	0.05	0.04
DVU1345	prolyl-tRNA synthetase (TIGR)	proS	0.03	0.00	0.04	0.00	0.00	0.00
DVU1346	exodeoxyribonuclease VII, large subunit (TIGR)	xseA	0.77	1.06	1.02	0.02	1.15	1.12
DVU1347	peptidase, M23/M37 family (TIGR)		0.73	0.69	0.54	0.02	0.73	0.74
DVU1348	exodeoxyribonuclease VII, small subunit (TIGR)	xseB	0.56	0.53	0.20	0.00	0.61	0.45
DVU1349	geranylgeranyl diphosphate synthase (TIGR)	SelGGPS	0.52	0.31	0.77	0.02	0.32	0.19
DVU1350	deoxyxylulose-5-phosphate synthase (TIGR)	dxs	0.12	0.03	0.21	0.01	0.02	0.02
DVU1351	membrane protein, MarC family (TIGR)		0.42	0.73	0.69	0.01	0.51	0.60
DVU1352	6-pyruvoyl tetrahydrobiopterin synthase, putative	(TIGR)	0.11	0.07	0.41	0.00	0.05	0.07
DVU1353	DNA polymerase III, alpha subunit (TIGR)	dnaE	0.00	0.00	0.00	0.00	0.00	0.00
DVU1355	hypothetical protein (TIGR)		0.53	1.01	0.95	0.03	1.30	0.99
DVU1356	HD domain protein (TIGR)		0.77	1.06	1.22	0.03	0.86	0.96
DVU1357	conserved domain protein (TIGR)		0.18	0.09	0.27	0.01	0.05	0.12
DVU1358	hydrolase, haloacid dehalogenase-like family (TIGR)		0.95	0.97	0.75	0.03	1.14	1.14
DVU1359	hypothetical protein (TIGR)		1.27	1.48	1.15	0.12	2.03	1.67
DVU1360	UDP-glucose 4-epimerase (TIGR)	galE	0.83	1.02	0.96	0.02	1.25	1.48
DVU1361	lipid A disaccharide synthase (TIGR)	lpxB	0.00	0.00	0.02	0.00	0.00	0.00
DVU1362	membrane protein, putative (TIGR)		0.28	0.23	0.22	0.01	0.24	0.29
DVU1363	dTDP-4-dehydrorhamnose reductase (TIGR)	rfbD	1.00	1.31	0.88	0.04	1.30	1.60
DVU1364	dTDP-glucose 4,6-dehydratase (TIGR)	rfbB	0.02	0.00	0.23	0.00	0.00	0.00
DVU1365	heme-binding protein, putative (TIGR)		0.01	0.11	0.30	0.00	0.03	0.04
DVU1366	lipoprotein, putative (TIGR)		1.23	1.41	1.24	0.05	1.25	1.36
DVU1367	twin-arginine translocation protein, TatA/E family	tatA	0.18	0.32	0.11	0.00	0.38	0.33
DVU1368	rhodanese-like domain protein (TIGR)		1.27	1.37	1.23	0.03	1.19	1.28
DVU1369	hypothetical protein (TIGR)		0.85	0.75	1.21	0.01	0.89	0.73
DVU1370	hypothetical protein (TIGR)		1.20	1.40	0.71	0.03	0.83	0.85
DVU1371	HAD-superfamily hydrolase, subfamily IA (TIGR)		0.74	0.89	0.78	0.02	0.48	0.51

DVU1372	membrane protein, putative (TIGR)		0.96	1.82	1.39	0.02	1.58	1.50
DVU1373	cell-division initiation protein DivIVA (TIGR)	divIVA	0.81	1.08	0.80	0.02	0.89	1.18
DVU1374	conserved hypothetical protein (TIGR)		1.01	0.74	1.74	0.08	0.92	1.11
DVU1375	hypothetical protein (TIGR)		1.35	1.14	1.39	0.01	0.81	1.04
DVU1376	acetolactate synthase, large subunit, biosynthetic	ilvB-2	0.55	0.65	0.63	0.01	0.10	0.12
DVU1377	acetolactate synthase, small subunit (TIGR)	ilvN-2	0.66	0.88	0.47	0.01	0.43	0.64
DVU1378	ketol-acid reductoisomerase (TIGR)	ilvC	0.25	0.59	0.54	0.01	0.10	0.13
DVU1380	hypothetical protein (TIGR)		0.39	0.72	0.37	0.00	0.62	0.66
DVU1381	hypothetical protein (TIGR)		0.07	0.16	0.18	0.00	0.16	0.13
DVU1382	HesB family selenoprotein (TIGR)		0.09	0.11	0.21	0.00	0.20	0.11
DVU1384	pyrimidine operon regulatory protein (TIGR)	pyrR	0.57	0.94	0.88	0.03	0.79	0.85
DVU1386	membrane protein, putative (TIGR)		0.81	0.99	0.99	0.02	1.04	1.06
DVU1387	conserved hypothetical protein (TIGR)		0.51	0.64	0.53	0.01	0.62	0.65
DVU1388	conserved hypothetical protein (TIGR)		1.37	1.30	0.85	0.04	1.41	1.42
DVU1389	hypothetical protein (TIGR)		0.55	0.66	0.91	0.02	0.74	0.78
DVU1390	hypothetical protein (TIGR)		0.32	1.00	0.52	0.01	0.91	0.82
DVU1392	NLP/P60 family protein (TIGR)		0.81	0.61	0.81	0.01	1.04	0.76
DVU1393	hypothetical protein (TIGR)		0.40	0.23	0.37	0.01	0.23	0.58
DVU1394	hypothetical protein (TIGR)		0.00	0.04	0.00	0.00	0.02	0.03
DVU1395	C4-type zinc finger protein, DksA/TraR family (TIGR)		0.38	0.70	0.78	0.01	0.79	0.79
DVU1397	bacterioferritin (TIGR)	bfr	0.76	0.74	0.55	0.01	0.74	0.95
DVU1398	ISDvu2, transposase OrfB (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU1399	ISDvu2, transposase OrfA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU1400	methyl-accepting chemotaxis protein (TIGR)		1.10	1.12	1.06	0.02	1.14	1.16
DVU1401	membrane protein, putative (TIGR)		0.53	0.79	0.91	0.02	0.88	0.89
DVU1402	transcriptional regulator, LysR family (TIGR)		0.67	0.74	0.99	0.02	0.84	0.89
DVU1403	cob(I)alamin adenosyltransferase (TIGR)	cobO	0.95	1.22	1.12	0.04	0.80	0.81
DVU1404	radical SAM domain protein (TIGR)	pflA	0.82	1.08	1.14	0.04	1.00	1.02
DVU1405	hypothetical protein (TIGR)		1.15	1.12	1.26	0.02	1.37	1.29
DVU1406	phosphoribosylformylglycinamidine cyclo-ligase (T	purM	0.29	0.16	0.29	0.00	0.01	0.00
DVU1407	radical SAM domain protein (TIGR)		0.71	0.94	0.96	0.02	0.99	0.90
DVU1408	hypothetical protein (TIGR)		0.83	0.68	0.60	0.00	0.78	0.86
DVU1409	hypothetical protein (TIGR)		0.42	0.33	0.54	0.01	0.49	0.62
DVU1410	conserved domain protein (TIGR)		1.21	1.31	0.88	0.15	1.22	1.61
DVU1411	thiamine biosynthesis protein ThiC (TIGR)	thiC	0.04	0.02	0.14	0.00	0.00	0.00
DVU1412	D-isomer specific 2-hydroxyacid dehydrogenase family prote		0.85	0.95	0.86	0.02	1.15	1.26
DVU1413	conserved hypothetical protein (TIGR)		0.87	0.96	1.23	0.02	1.17	1.07
DVU1414	sensory box/GGDEF domain/EAL domain protein (TIGR)		0.96	1.21	1.36	0.67	1.23	1.33
DVU1415	AsmA family protein (TIGR)		0.71	0.88	1.04	0.02	1.03	1.06
DVU1416	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU1418	sensory box histidine kinase (TIGR)	hydH	1.09	1.27	1.16	0.03	1.50	1.66
DVU1419	sigma-54 dependent transcriptional regulator/resp	atoC	0.58	0.67	0.64	0.01	0.62	0.71
DVU1420	Hpt domain protein (TIGR)		0.40	0.49	0.28	0.00	0.48	0.40
DVU1421	hypothetical protein (TIGR)		0.31	0.32	0.27	0.02	0.39	0.62
DVU1422	OmpA family protein (TIGR)		0.75	0.64	0.68	0.01	0.71	0.74
DVU1423	2-oxoglutarate dehydrogenase, E3 component, lip	lpdA	0.81	0.93	1.32	0.01	1.05	0.95
DVU1424	glycine cleavage system P protein, subunit 2 (TIGR	gcvPB	1.21	1.27	1.14	0.01	1.25	1.16
DVU1425	glycine cleavage system P protein, subunit 1 (TIGR	gcvPA	1.60	1.47	1.38	0.03	1.84	1.87
DVU1426	glycine cleavage system H protein (TIGR)	gcvH	0.93	0.98	0.87	0.03	0.90	1.03
DVU1427	response regulator (TIGR)		0.88	0.55	0.91	0.00	0.28	0.09
DVU1428	phosphoglucomutase, alpha-D-glucose phosphate	pgm	1.19	1.24	1.53	0.03	1.31	1.41
DVU1429	GTP-binding protein (TIGR)		0.61	0.93	1.27	0.02	0.89	0.95
DVU1430	peptidase, M16 family (TIGR)		1.60	1.47	1.42	0.03	1.70	1.66
DVU1431	hpt domain protein/STAS domain protein (TIGR)		0.72	1.02	0.89	0.01	1.06	1.08
DVU1432	radical SAM domain protein (TIGR)		0.88	0.84	0.98	0.02	0.85	0.90
DVU1434	hypothetical protein (TIGR)		0.43	0.64	0.32	0.03	0.86	0.91
DVU1435	membrane protein, putative (TIGR)		1.13	1.46	1.68	0.05	1.56	1.63
DVU1436	hypothetical protein (TIGR)		0.74	0.24	0.74	0.00	1.02	1.32
DVU1438	cobyrinic acid a,c-diamide synthase family protein (TIGR)		0.47	0.44	0.80	0.01	0.39	0.44
DVU1440	ribonuclease III (TIGR)	rnc	0.60	0.47	0.41	0.01	0.45	1.27
DVU1441	flagellin (TIGR)	flaB1	0.85	1.32	1.25	0.03	1.43	1.48
DVU1442	flagellin FlaG, putative (TIGR)		0.95	1.35	1.07	0.04	1.03	1.19
DVU1443	flagellar hook protein FlgE (TIGR)	flgE	0.84	1.00	0.77	0.03	1.50	1.66
DVU1444	basal-body rod modification protein FlgD (TIGR)	flgD	0.97	0.85	1.10	0.02	1.60	1.92
DVU1445	flagellar hook-length control domain protein (TIGR)		1.03	1.26	1.17	0.03	1.80	2.07
DVU1446	heptosyltransferase family protein (TIGR)		0.96	0.79	0.70	0.03	1.08	1.23
DVU1447	CgeB family protein (TIGR)		0.69	0.82	0.67	0.02	0.90	1.15

DVU1448	conserved hypothetical protein (TIGR)		0.58	0.70	0.52	0.01	0.70	0.71
DVU1449	anti-anti-sigma factor, putative (TIGR)		0.77	0.84	0.78	0.01	0.78	0.89
DVU1450	anti-sigma factor, putative (TIGR)		0.50	0.62	0.85	0.01	0.69	0.74
DVU1451	response regulator (TIGR)		1.10	1.00	1.00	0.03	1.20	1.03
DVU1452	D-tyrosyl-tRNA(Tyr) deacylase (TIGR)	dtd	0.67	0.74	1.26	0.03	1.09	0.87
DVU1453	long-chain-fatty-acid--CoA ligase (TIGR)	fadD	0.89	1.03	1.10	0.02	1.25	1.14
DVU1454	2-C-methyl-D-erythritol 4-phosphate cytidylyltrans	ispD	0.47	0.34	1.19	0.02	0.16	0.13
DVU1455	conserved hypothetical protein (TIGR)		0.43	0.45	0.45	2.53	0.70	0.57
DVU1456	NIF3 family protein (TIGR)		1.46	1.09	1.36	0.02	1.44	1.21
DVU1457	thioredoxin reductase, putative (TIGR)	trxB	1.10	1.25	0.87	0.04	1.23	1.19
DVU1458	chemotaxis protein CheZ, putative (TIGR)		1.17	1.09	0.78	0.03	1.28	1.20
DVU1459	conserved domain protein (TIGR)		0.13	0.10	0.42	0.01	0.02	0.04
DVU1460	hypothetical protein (TIGR)		0.57	0.63	0.87	0.04	0.41	0.63
DVU1461	glutamyl-tRNA reductase (TIGR)	hemA	0.02	0.00	0.15	0.00	0.00	0.01
DVU1462	cytochrome c assembly protein, putative (TIGR)		0.87	1.04	0.97	0.02	1.19	1.13
DVU1463	siroheme synthase, N-terminal domain protein (TI	cysG-1	0.18	0.14	0.47	0.01	0.06	0.08
DVU1464	heptosyltransferase family protein (TIGR)		1.82	1.69	1.86	0.04	1.75	2.00
DVU1465	CgeB family protein (TIGR)		0.78	1.19	0.87	0.03	1.49	1.65
DVU1466	acetylglutamate kinase (TIGR)	argB	0.37	0.67	0.00	0.00	0.01	0.01
DVU1467	heat shock protein HslVU, ATPase subunit HslU (TI	hslU	1.40	1.06	1.10	0.03	1.31	1.40
DVU1468	peptidase/PDZ domain protein (TIGR)	htrA	1.39	1.29	1.22	0.04	1.69	1.69
DVU1469	ribosomal protein S1, putative (TIGR)	rpsA	1.14	1.20	0.94	0.03	1.04	0.93
DVU1470	peptidyl-prolyl cis-trans isomerase C (TIGR)	ppiC	1.08	0.97	0.93	0.03	1.03	0.95
DVU1471	heat shock protein, Hsp20 family (TIGR)	hspC	0.89	1.13	0.56	0.01	1.15	1.22
DVU1472	ATP-dependent protease, putative (TIGR)		0.96	1.27	1.01	0.03	1.21	1.46
DVU1474	hypothetical protein (TIGR)		0.06	0.03	0.00	0.00	0.02	0.17
DVU1475	PhoU family protein (TIGR)		0.52	0.36	0.74	0.01	0.39	0.69
DVU1476	hypothetical protein (TIGR)		0.70	0.63	0.41	0.00	0.52	0.57
DVU1477	hypothetical protein (TIGR)		0.75	0.94	1.00	0.01	1.13	1.49
DVU1478	hypothetical protein (TIGR)		0.10	0.09	0.06	0.00	0.06	0.12
DVU1479	conserved hypothetical protein (TIGR)		0.21	0.12	0.08	0.00	0.19	0.10
DVU1480	conserved domain protein (TIGR)		0.69	1.35	1.09	0.02	1.27	1.12
DVU1481	nuclease domain protein (TIGR)		1.80	1.94	2.04	0.07	2.71	3.02
DVU1483	tail fiber assembly protein, putative (TIGR)		1.40	1.36	1.38	0.02	1.00	1.40
DVU1484	hypothetical protein (TIGR)		0.45	0.38	0.44	0.00	0.44	0.57
DVU1485	hypothetical protein (TIGR)		0.62	0.60	0.52	0.01	0.58	0.71
DVU1486	tail fiber protein, truncation (TIGR)		1.00	1.08	1.40	0.03	1.13	1.28
DVU1487	conserved domain protein (TIGR)		1.09	1.24	0.97	0.03	1.10	1.36
DVU1488	minor tail protein, putative (TIGR)		0.57	0.84	0.82	0.01	0.78	0.91
DVU1489	hypothetical protein (TIGR)		1.19	1.08	0.81	0.04	1.08	1.03
DVU1490	tail tape measure protein, putative (TIGR)		0.75	0.74	0.82	0.01	0.85	1.04
DVU1491	conserved hypothetical protein (TIGR)		1.20	1.27	1.18	0.08	1.54	1.15
DVU1493	hypothetical protein (TIGR)		1.51	1.68	1.11	0.02	1.56	1.95
DVU1494	hypothetical protein (TIGR)		0.92	1.22	0.95	0.03	1.00	1.17
DVU1495	hypothetical protein (TIGR)		0.53	1.06	1.35	0.05	0.92	1.31
DVU1496	hypothetical protein (TIGR)		0.66	0.93	1.12	0.01	0.94	1.09
DVU1497	head-tail adaptor, putative (TIGR)		1.86	1.12	1.15	0.03	1.29	1.54
DVU1498	conserved hypothetical protein (TIGR)		1.54	1.37	1.17	0.02	1.46	1.84
DVU1499	hypothetical protein (TIGR)		0.95	0.75	1.00	0.04	1.06	1.43
DVU1500	major capsid protein, HK97 family (TIGR)		0.96	1.04	1.39	0.03	1.03	1.13
DVU1501	ClpP protease family protein (TIGR)	clpP	1.20	0.78	0.66	0.02	0.94	1.00
DVU1502	portal protein, HK97 family (TIGR)		1.25	1.01	1.18	0.03	1.04	1.15
DVU1503	terminase, large subunit (TIGR)		0.83	0.82	0.90	0.02	0.90	1.18
DVU1504	terminase, small subunit (TIGR)		0.74	0.87	0.95	0.03	0.83	1.02
DVU1505	holin, putative (TIGR)		1.67	1.38	2.09	0.04	1.72	2.08
DVU1506	hypothetical protein (TIGR)		0.75	0.59	1.02	0.02	0.77	0.73
DVU1507	hypothetical protein (TIGR)		0.34	0.44	0.51	0.02	0.61	0.54
DVU1508	conserved hypothetical protein (TIGR)		0.46	0.43	0.53	0.01	0.69	0.55
DVU1509	conserved hypothetical protein (TIGR)		0.19	0.10	0.13	0.00	0.16	0.08
DVU1510	hypothetical protein (TIGR)		0.08	0.06	0.05	0.00	0.04	0.01
DVU1511	hypothetical protein (TIGR)		0.21	0.67	0.69	0.01	0.75	0.64
DVU1513	conserved hypothetical protein (TIGR)		1.58	1.26	1.44	0.03	1.36	1.79
DVU1514	hypothetical protein (TIGR)		1.20	1.58	2.01	0.02	1.51	1.73
DVU1515	type II DNA modification methyltransferase, putat	dcm	1.04	0.86	1.31	0.03	1.05	1.32
DVU1516	hypothetical protein (TIGR)		1.11	1.07	1.44	0.02	1.26	1.84
DVU1517	transcriptional regulator cII, putative (TIGR)		1.16	1.44	1.51	0.02	1.28	1.50
DVU1518	transcriptional regulator cI, truncation (TIGR)		0.80	0.44	0.34	0.01	1.04	1.18

DVU1519	transcriptional regulator, putative (TIGR)		0.02	0.00	0.08	0.00	0.01	0.01
DVU1520	hypothetical protein (TIGR)		0.07	0.05	0.13	0.00	0.06	0.08
DVU1521	hypothetical protein (TIGR)		0.00	0.13	0.00	0.02	0.04	0.16
DVU1522	hypothetical protein (TIGR)		0.68	1.71	2.27	0.02	1.65	1.69
DVU1523	hypothetical protein (TIGR)		1.06	1.41	1.32	0.03	1.22	1.23
DVU1524	conserved hypothetical protein (TIGR)		1.43	1.56	2.27	0.03	1.51	2.05
DVU1525	conserved domain protein (TIGR)		0.65	1.33	1.27	0.03	1.43	1.37
DVU1526	hypothetical protein (TIGR)		1.08	1.15	2.21	0.03	0.89	1.50
DVU1527	site-specific recombinase, phage integrase family (TIGR)		1.05	1.05	1.23	0.04	1.38	1.32
DVU1528	cytidine/deoxycytidylate deaminase family protein (TIGR)		0.38	0.45	1.06	0.01	0.10	0.17
DVU1529	decarboxylase family protein (TIGR)		0.89	0.82	0.47	0.01	1.00	0.90
DVU1530	metallo-beta-lactamase family protein (TIGR)		0.67	0.99	0.94	0.01	1.11	1.10
DVU1531	methyltransferase, putative (TIGR)		0.85	0.94	0.58	0.02	1.06	1.23
DVU1532	pantetheine-phosphate adenylyltransferase (TIGR)	coaD	0.09	0.09	0.16	0.00	0.00	0.02
DVU1533	tRNA delta(2)-isopentenylpyrophosphate transfer	miaA	0.36	0.34	0.67	0.02	0.35	0.37
DVU1534	membrane protein, putative (TIGR)		0.65	0.67	0.59	0.01	0.77	0.99
DVU1535	membrane protein, putative (TIGR)		0.88	0.83	1.00	0.02	1.01	1.07
DVU1536	transglycosylase, SLT family (TIGR)	mltC	0.60	0.63	0.75	0.02	0.71	0.69
DVU1537	lipoprotein, putative (TIGR)		0.50	0.62	0.73	0.01	0.70	0.89
DVU1538	hypothetical protein (TIGR)		0.62	0.63	0.78	0.01	0.67	0.67
DVU1539	fructose-1,6-bisphosphatase, class II (TIGR)	glpX	0.11	0.17	0.34	0.01	0.22	0.09
DVU1540	formyltetrahydrofolate deformylase (TIGR)	purU	0.76	0.69	0.76	0.01	0.65	0.67
DVU1541	hypothetical protein (TIGR)		0.25	0.22	0.17	0.01	0.50	0.48
DVU1542	hypothetical protein (TIGR)		0.72	0.59	0.46	0.00	0.49	0.72
DVU1543	ATP-dependent helicase HrpB (TIGR)	hrpB	0.89	0.76	0.96	0.02	0.92	0.89
DVU1544	mechanosensitive ion channel family protein (TIGR)		0.77	0.75	0.80	0.02	0.97	0.97
DVU1545	hemolysin-type calcium-binding repeat/calx-beta domain pr		1.15	1.17	1.27	0.02	1.32	1.30
DVU1547	sensory box protein (TIGR)		1.25	1.12	1.28	0.03	1.30	1.45
DVU1548	outer membrane transport protein, OmpP1/FadL/TodX fam		1.15	1.26	1.12	0.03	1.24	1.40
DVU1549	conserved hypothetical protein (TIGR)		1.30	1.41	1.56	0.04	1.62	2.10
DVU1550	phosphoglycerate mutase family protein (TIGR)		1.13	1.35	1.21	0.04	1.27	1.40
DVU1551	HD domain protein (TIGR)		1.32	1.19	1.77	0.02	1.42	1.49
DVU1552	conserved hypothetical protein (TIGR)	b2875	1.29	1.35	1.47	0.03	1.50	1.64
DVU1553	AMP-binding protein (TIGR)	ftsA-3	0.79	1.08	0.90	0.04	1.11	1.16
DVU1554	radical SAM domain protein (TIGR)		1.00	1.21	1.30	0.03	1.31	1.46
DVU1555	hypothetical protein (TIGR)		2.60	2.94	3.59	0.07	2.80	3.28
DVU1556	conserved domain protein (TIGR)		0.75	0.77	0.93	0.02	1.03	1.01
DVU1557	hypothetical protein (TIGR)		0.79	1.22	0.96	0.05	0.87	1.54
DVU1558	cysteine-rich domain/iron-sulfur cluster-binding domain pro		1.44	1.69	1.70	0.04	1.50	1.75
DVU1559	aldehyde oxidoreductase (TIGR)	mop	1.03	1.12	1.17	0.03	1.12	1.25
DVU1560	molybdopterin biosynthesis protein, putative (TIGR)		1.05	1.04	0.99	0.02	1.06	1.25
DVU1561	molybdenum-binding protein, HTH domain (TIGR)		1.10	1.97	2.29	0.03	1.87	2.38
DVU1562	HAMP domain protein (TIGR)		0.45	0.51	0.57	0.01	0.61	0.62
DVU1563	sensory box histidine kinase/response regulator (TIGR)		0.59	0.44	0.68	0.02	0.66	0.79
DVU1566	phosphoadenosine phosphosulfate reductase, put	cysD	0.96	1.07	1.14	0.03	1.49	1.39
DVU1567	hypothetical protein (TIGR)		0.99	0.64	0.61	0.02	0.66	0.93
DVU1568	ferritin (TIGR)	ftn	0.40	0.68	0.68	0.01	0.79	0.84
DVU1569	pyruvate ferredoxin oxidoreductase, alpha subunit	porA	0.91	0.76	0.74	0.02	0.98	0.94
DVU1570	pyruvate ferredoxin oxidoreductase, beta subunit	porB	0.57	0.51	0.94	0.01	0.56	0.85
DVU1571	transcription termination factor Rho (TIGR)	rho	0.04	0.04	0.30	0.00	0.09	0.08
DVU1572	transcriptional regulator, CarD family (TIGR)		0.41	0.49	0.65	0.01	0.24	0.10
DVU1573	peptidyl-tRNA hydrolase (TIGR)	pth	0.03	0.05	0.29	0.01	0.03	0.05
DVU1574	ribosomal protein L25 (TIGR)	rplY	0.14	0.10	0.25	0.00	0.18	0.20
DVU1575	ribose-phosphate pyrophosphokinase (TIGR)	prsA	0.00	0.00	0.00	0.00	0.00	0.00
DVU1576	4-diphosphocytidyl-2C-methyl-D-erythritol kinase	ispE	0.30	0.20	1.08	0.01	0.10	0.09
DVU1577	ATP-dependent protease hslV (TIGR)	hslV	0.63	0.81	0.67	0.02	0.92	0.95
DVU1578	TPR domain protein (TIGR)		0.70	0.62	0.55	0.01	0.78	0.71
DVU1579	cysteinyl-tRNA synthetase (TIGR)	cysS	0.01	0.00	0.08	0.00	0.00	0.00
DVU1580	ribose 5-phosphate isomerase, putative (TIGR)	rpiB	0.18	0.06	0.43	0.01	0.11	0.14
DVU1581	hypothetical protein (TIGR)		0.88	0.91	0.74	0.03	1.23	1.15
DVU1582	hypothetical protein (TIGR)		0.03	0.00	0.16	0.00	0.00	0.00
DVU1583	TPR domain protein (TIGR)		1.26	1.69	1.73	3.51	1.52	1.29
DVU1584	sigma 70 family protein (TIGR)	rpoH	0.05	0.04	0.36	0.01	0.05	0.04
DVU1585	vitamin B12-dependent methionine synthase family protein		0.56	0.79	0.26	0.01	0.02	0.02
DVU1586	thioredoxin family protein (TIGR)	ccmG	0.71	0.81	0.18	0.00	0.13	0.16
DVU1587	acetyltransferase, GNAT family (TIGR)		0.99	1.17	0.00	0.00	0.01	0.03
DVU1588	hypoxanthine phosphoribosyltransferase (TIGR)	hpt	0.55	0.43	0.46	0.03	0.71	0.69

DVU1589	hypothetical protein (TIGR)		0.92	1.05	0.65	0.01	1.01	1.23
DVU1590	DNA repair protein RadA (TIGR)	radA	0.69	0.81	0.72	0.02	0.96	0.93
DVU1591	hypothetical protein (TIGR)		1.31	0.28	0.01	0.03	0.47	0.55
DVU1592	arginine N-succinyltransferase, beta subunit, putative (TIGR)		1.11	1.28	1.25	0.04	1.38	1.52
DVU1593	chemotaxis protein CheY (TIGR)	cheY-1	0.75	0.63	0.99	0.02	0.84	0.93
DVU1594	chemotaxis protein CheA (TIGR)	cheA-1	0.81	0.99	1.05	0.02	0.97	1.17
DVU1595	chemotaxis protein methyltransferase (TIGR)	cheR-1	0.91	1.14	0.89	0.03	1.03	1.21
DVU1596	protein-glutamate methylesterase CheB (TIGR)	cheB-1	1.40	1.49	1.71	0.05	1.66	1.83
DVU1597	sulfite reductase, assimilatory-type (TIGR)	sir	0.68	1.22	1.41	0.04	1.27	1.47
DVU1598	conserved hypothetical protein (TIGR)		1.50	0.87	1.38	0.04	1.28	1.54
DVU1599	crcB protein (TIGR)	crcB	1.12	1.26	0.99	0.02	1.41	1.46
DVU1600	adenylate cyclase (TIGR)		1.12	1.32	2.01	0.05	0.99	1.22
DVU1601	ATP-dependent Clp protease adaptor protein ClpS (TIGR)		2.30	2.16	3.70	0.06	2.42	2.65
DVU1602	ATP-dependent Clp protease, ATP-binding subunit	clpA	0.93	1.01	1.19	0.03	1.13	1.19
DVU1603	leucyl/phenylalanyl-tRNA--protein transferase (TIC	aat	0.82	1.08	0.82	0.04	1.22	1.27
DVU1604	hypothetical protein (TIGR)		0.71	0.65	1.17	0.04	1.24	1.21
DVU1605	excinuclease ABC, B subunit (TIGR)	uvrB	1.07	1.31	1.13	0.02	1.23	1.35
DVU1606	potassium uptake protein, TrkA family (TIGR)		0.71	0.79	0.93	0.02	0.90	0.93
DVU1607	hypothetical protein (TIGR)		0.87	1.08	1.18	0.03	1.25	1.21
DVU1608	DNA ligase, NAD-dependent (TIGR)	ligA	0.00	0.00	0.02	0.00	0.00	0.01
DVU1609	dihydrodipicolinate reductase (TIGR)	dapB	0.24	0.30	0.23	0.00	0.10	0.09
DVU1610	glutamine-dependent NAD+ synthetase (TIGR)	nadE	0.09	0.03	0.13	0.00	0.02	0.02
DVU1611	molybdopterin oxidoreductase domain protein (TIGR)		0.57	0.81	0.63	0.01	0.79	0.80
DVU1612	ACT domain protein (TIGR)		0.34	0.50	1.22	0.01	0.80	0.74
DVU1613	pyridine nucleotide-disulfide oxidoreductase (TIGR)		0.80	1.02	0.62	0.02	0.49	0.47
DVU1614	iron-sulfur cluster-binding protein (TIGR)		1.09	1.16	1.34	0.02	0.54	0.54
DVU1615	phenylacetate-coenzyme A ligase (TIGR)	paaK-2	0.74	0.82	0.82	0.02	0.95	0.90
DVU1617	nitroreductase family protein (TIGR)		1.10	1.24	0.96	0.04	1.25	1.28
DVU1618	iojap-related protein (TIGR)		0.28	0.21	0.09	0.00	0.11	0.17
DVU1619	phosphoglycerate mutase, 2,3-bisphosphoglycerat	gpmA	0.02	0.02	0.10	0.00	0.00	0.00
DVU1620	hypothetical protein (TIGR)		0.95	0.59	0.56	0.00	0.32	0.45
DVU1621	hypothetical protein (TIGR)		0.72	0.84	0.93	0.04	1.05	1.12
DVU1622	phosphoribosylformylglycinamidine synthase I (TIC	purQ	0.40	0.19	0.24	0.01	0.01	0.01
DVU1623	CTP synthase (TIGR)	pyrG	0.01	0.00	0.11	0.00	0.00	0.00
DVU1624	2-dehydro-3-deoxyphosphooctonate aldolase (TIG	kdsA	0.01	0.00	0.15	0.00	0.00	0.00
DVU1625	phosphatase, YrbI family (TIGR)		0.07	0.08	0.12	0.01	0.13	0.13
DVU1626	hypothetical protein (TIGR)		0.11	0.08	0.08	0.00	0.13	0.07
DVU1627	ABC transporter, ATP-binding protein (TIGR)		0.00	0.00	0.09	0.00	0.00	0.00
DVU1628	RNA polymerase sigma-54 factor (TIGR)	rpoN	0.02	0.01	0.03	0.00	0.00	0.00
DVU1629	ribosomal subunit interface protein (TIGR)	yfiA	0.46	0.63	0.37	0.01	0.54	0.59
DVU1630	PTS system, IIA component (TIGR)	ptsN	0.34	0.64	0.72	0.01	0.45	0.49
DVU1631	conserved hypothetical protein (TIGR)		0.63	0.71	0.83	0.02	0.55	1.00
DVU1632	PTS system, IIA component (TIGR)		0.76	0.86	0.37	0.01	0.91	1.28
DVU1633	PTS system, IIB component (TIGR)		0.21	0.19	0.27	0.01	0.11	0.06
DVU1634	membrane protein, putative (TIGR)		0.25	0.19	0.41	0.00	0.09	0.07
DVU1635	hypothetical protein (TIGR)		0.46	0.41	0.66	0.00	0.28	0.55
DVU1636	inorganic pyrophosphatase, manganese-depender	ppaC	0.08	0.04	0.34	0.01	0.00	0.04
DVU1638	conserved domain protein (TIGR)		0.08	0.05	0.00	0.00	0.04	0.04
DVU1639	conserved domain protein (TIGR)		0.62	0.77	0.71	0.03	0.94	0.87
DVU1641	conserved hypothetical protein (TIGR)		0.89	0.79	0.59	0.01	0.44	0.56
DVU1644	permease, putative (TIGR)		0.49	0.59	0.58	0.01	0.60	0.63
DVU1645	transcriptional regulator, ArsR family (TIGR)		0.23	0.17	0.36	0.00	0.26	0.32
DVU1646	arsenate reductase (TIGR)	arsC	0.43	0.39	0.43	0.05	0.52	0.65
DVU1647	diaminopimelate decarboxylase (TIGR)	lysA-1	0.84	0.75	0.63	0.03	0.97	1.07
DVU1648	lipoprotein, putative (TIGR)		0.52	0.62	0.43	0.03	0.77	0.70
DVU1649	DNA mismatch repair protein MutS (TIGR)	mutS	0.80	0.90	0.81	0.02	1.00	1.15
DVU1650	conserved hypothetical protein (TIGR)		1.28	1.30	1.23	0.04	1.41	1.67
DVU1651	conserved hypothetical protein (TIGR)		0.72	0.92	0.89	0.01	0.94	1.21
DVU1652	HIT family protein (TIGR)	hit	0.66	1.05	1.31	0.03	0.73	0.73
DVU1653	polyA polymerase family protein (TIGR)		0.71	0.84	1.23	0.03	0.70	0.85
DVU1654	site-specific recombinase, phage integrase family (	xerD	1.07	1.21	1.46	0.03	0.95	1.10
DVU1655	aminotransferase, classes I and II (TIGR)	aspC4	0.00	0.01	0.00	0.00	0.00	0.00
DVU1656	2-amino-4-hydroxy-6-hydroxymethyldihydropteric	folK	0.05	0.14	0.55	0.01	0.01	0.04
DVU1657	hypothetical protein (TIGR)		0.05	0.19	0.22	0.00	0.12	0.26
DVU1658	transaldolase, putative (TIGR)		0.74	0.86	1.13	0.04	0.89	1.20
DVU1660	undecaprenol kinase, putative (TIGR)		0.86	0.87	0.74	0.04	1.82	1.74
DVU1661	hypothetical protein (TIGR)		0.37	0.23	0.47	0.00	0.54	0.81

DVU1662	permease, putative (TIGR)		0.00	0.01	0.02	0.00	0.00	0.00
DVU1663	permease, putative (TIGR)		0.00	0.00	0.03	0.00	0.00	0.00
DVU1664	GTP-binding protein (TIGR)		0.07	0.07	0.35	0.02	0.06	0.05
DVU1665	3-dehydroquinate dehydratase, type II (TIGR)	aroQ	0.70	0.64	0.16	0.01	0.01	0.02
DVU1666	translation elongation factor P (TIGR)	efp	0.56	0.58	1.00	0.01	0.71	1.62
DVU1667	FtsK/SpoIIIE family protein (TIGR)	ftsK	0.02	0.03	0.07	0.00	0.01	0.01
DVU1668	outer membrane lipoprotein carrier protein, putat	lolA	0.07	0.01	0.12	0.01	0.02	0.02
DVU1669	ribosomal large subunit pseudouridine synthase B	rluB	1.13	1.62	1.72	0.05	1.58	2.16
DVU1670	conserved hypothetical protein (TIGR)		1.40	0.90	0.89	0.03	1.02	1.50
DVU1671	ABC transporter, ATP-binding protein/permease p	msbA	0.01	0.01	0.03	0.00	0.00	0.00
DVU1672	conserved hypothetical protein (TIGR)		0.00	0.01	0.37	0.01	0.02	0.33
DVU1673	acyltransferase, putative (TIGR)		0.23	0.13	0.35	0.01	0.34	0.54
DVU1674	transcriptional regulator, putative (TIGR)		0.60	0.73	0.59	0.01	0.74	1.36
DVU1675	hypothetical protein (TIGR)		0.16	0.52	0.41	0.02	0.49	0.55
DVU1676	preprotein translocase, SecG subunit (TIGR)	secG	0.31	0.11	0.65	0.01	0.20	0.16
DVU1677	triosephosphate isomerase (TIGR)	tpiA	0.06	0.09	0.27	0.00	0.02	0.01
DVU1678	ribosomal-protein-alanine acetyltransferase (TIGR	rimI	0.98	1.21	0.96	0.02	1.16	1.44
DVU1679	isopentenyl-diphosphate delta-isomerase (TIGR)	idi	0.70	0.68	1.17	0.01	1.04	1.20
DVU1680	inositol-1-monophosphatase (TIGR)	suhB	1.07	0.65	0.64	0.02	0.85	0.91
DVU1681	rod shape-determining protein MreB (TIGR)	mreB-2	0.92	0.86	0.98	0.02	1.11	1.08
DVU1682	GAF domain protein (TIGR)		1.23	1.26	1.72	0.04	1.78	2.38
DVU1683	hypothetical protein (TIGR)		0.92	0.91	0.82	0.03	0.98	1.08
DVU1684	glycine cleavage system T protein (TIGR)	gcvT	1.00	1.11	1.26	0.00	1.15	1.43
DVU1685	conserved hypothetical protein TIGR00046 (TIGR)		0.54	1.00	0.82	0.02	0.98	1.10
DVU1686	ATPase, AAA family (TIGR)		1.44	1.09	1.19	0.03	1.46	1.48
DVU1687	glycosyl transferase, group 2 family protein (TIGR)		0.49	0.86	0.66	0.02	0.68	1.00
DVU1688	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative (TI		0.02	0.01	0.09	0.00	0.00	0.00
DVU1690	transcriptional regulator, TetR family (TIGR)		0.23	0.47	0.33	0.00	0.75	0.90
DVU1692	hypothetical protein (TIGR)		0.40	0.43	0.37	0.02	0.66	0.66
DVU1693	glutamyl-tRNA synthetase (TIGR)	gltX-1	1.41	1.04	0.87	0.04	1.47	1.27
DVU1694	C4-type zinc finger protein, DksA/TraR family (TIGR)		1.70	1.44	1.52	0.08	1.98	2.02
DVU1695	tail fiber assembly protein, putative (TIGR)		1.87	1.49	2.17	0.02	1.46	1.73
DVU1696	hypothetical protein (TIGR)		1.40	0.88	1.42	0.02	0.67	0.89
DVU1697	hypothetical protein (TIGR)		0.25	0.47	0.33	0.01	0.51	0.68
DVU1698	hypothetical protein (TIGR)		0.52	0.46	0.44	0.01	0.39	0.46
DVU1699	hypothetical protein (TIGR)		0.06	0.20	0.38	0.00	0.17	0.25
DVU1700	metallo-beta-lactamase family protein (TIGR)		0.23	0.11	0.17	0.00	0.26	0.26
DVU1701	hypothetical protein (TIGR)		0.22	0.00	0.15	0.01	0.07	0.08
DVU1702	conserved hypothetical protein (TIGR)		1.22	0.95	1.06	0.03	0.89	1.12
DVU1703	type I restriction-modification enzyme, R subunit (TIGR)		1.18	1.04	1.04	0.03	1.32	1.47
DVU1704	conserved hypothetical protein (TIGR)		0.61	1.05	0.51	0.02	1.16	1.14
DVU1705	type I restriction-modification enzyme, S subunit (TIGR)		0.12	0.18	0.20	0.01	0.18	0.25
DVU1707	hypothetical protein (TIGR)		0.33	0.20	0.19	0.00	0.24	0.31
DVU1708	conserved hypothetical protein (TIGR)		0.19	0.16	0.14	0.00	0.28	0.34
DVU1709	type I restriction-modification system, M subunit (	hsdM	0.46	0.38	0.60	0.02	0.62	0.75
DVU1710	conserved hypothetical protein (TIGR)		0.73	0.93	1.04	0.03	1.00	1.30
DVU1712	hypothetical protein (TIGR)		1.22	1.19	1.30	0.03	1.17	1.62
DVU1713	hypothetical protein (TIGR)		2.03	1.76	1.87	0.04	1.76	1.99
DVU1714	conserved hypothetical protein (TIGR)		1.10	0.99	1.04	0.03	0.97	1.15
DVU1715	hypothetical protein (TIGR)		1.86	1.40	1.58	0.04	1.49	1.92
DVU1716	hypothetical protein (TIGR)		2.58	3.22	4.32	0.06	2.37	2.95
DVU1717	hypothetical protein (TIGR)		0.93	1.24	1.93	0.04	1.49	1.50
DVU1718	hypothetical protein (TIGR)		1.47	1.52	1.68	0.03	1.48	1.60
DVU1719	conserved domain protein (TIGR)		1.73	1.65	1.60	0.05	1.55	1.65
DVU1720	hypothetical protein (TIGR)		1.17	1.00	1.55	0.06	1.19	1.82
DVU1721	hypothetical protein (TIGR)		1.55	1.54	2.19	0.04	1.45	1.92
DVU1722	hypothetical protein (TIGR)		1.96	1.99	4.61	0.05	2.56	2.92
DVU1723	hypothetical protein (TIGR)		1.47	1.35	1.74	0.04	1.43	1.68
DVU1724	phage uncharacterized protein, putative (TIGR)		2.13	1.93	2.22	0.05	1.68	2.17
DVU1725	conserved hypothetical protein (TIGR)		1.15	0.99	1.51	0.03	1.08	1.32
DVU1726	hypothetical protein (TIGR)		0.57	0.53	1.04	0.03	0.70	0.67
DVU1727	hypothetical protein (TIGR)		0.53	0.37	0.87	0.00	0.40	0.40
DVU1728	conserved hypothetical protein (TIGR)		0.70	1.00	1.43	0.01	1.15	1.27
DVU1729	killer protein, putative (TIGR)		0.74	1.31	1.06	0.01	1.02	1.36
DVU1730	DNA-binding protein (TIGR)		0.50	0.32	0.40	0.00	0.23	0.23
DVU1731	hypothetical protein (TIGR)		0.48	0.63	0.80	0.02	0.62	0.94
DVU1735	hypothetical protein (TIGR)		0.58	0.78	1.14	0.00	0.87	1.07

DVU1736	hypothetical protein (TIGR)		0.92	0.59	1.36	0.05	1.12	0.67
DVU1737	conserved hypothetical protein (TIGR)		1.87	1.59	2.35	0.02	1.83	1.72
DVU1738	site-specific recombinase, phage integrase family (TIGR)		2.20	1.28	1.85	0.02	1.80	1.52
DVU1740	hypothetical protein (TIGR)		1.27	0.80	1.21	0.01	1.18	1.10
DVU1741	hypothetical protein (TIGR)		1.34	1.43	1.29	0.04	1.33	1.84
DVU1742	prevent-host-death family protein (TIGR)		0.93	0.41	0.27	0.00	0.57	0.58
DVU1743	hypothetical protein (TIGR)		0.89	0.77	0.76	0.01	0.65	0.75
DVU1744	DNA-binding protein (TIGR)		0.49	0.93	1.10	0.01	0.77	1.19
DVU1745	DNA-binding protein (TIGR)		1.19	1.40	1.71	0.05	1.56	1.80
DVU1746	C-5 cytosine-specific DNA methylase family protein (TIGR)		0.05	0.07	0.08	0.00	0.30	0.10
DVU1747	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like do		0.69	0.68	0.75	0.02	0.94	1.06
DVU1748	conserved hypothetical protein (TIGR)		0.01	0.03	0.00	0.00	0.04	0.04
DVU1750	hypothetical protein (TIGR)		0.94	0.95	0.91	0.03	1.10	1.27
DVU1751	hypothetical protein (TIGR)		0.10	0.06	0.00	0.00	0.21	0.10
DVU1752	hypothetical protein (TIGR)		2.21	1.18	1.69	0.00	1.21	1.11
DVU1753	hypothetical protein (TIGR)		1.77	1.75	1.50	0.01	1.59	1.76
DVU1754	hypothetical protein (TIGR)		1.10	0.87	0.97	0.01	0.91	0.94
DVU1756	hypothetical protein (TIGR)		0.53	1.09	0.93	0.01	1.25	1.37
DVU1757	site-specific recombinase, phage integrase family (TIGR)		1.25	1.03	1.34	0.04	1.21	1.30
DVU1758	lipoprotein, putative (TIGR)		0.67	0.57	0.99	0.01	0.84	0.84
DVU1759	molybdenum-binding protein, HTH domain (TIGR)	mopB	1.47	1.19	1.21	0.05	1.36	1.38
DVU1760	transcriptional regulator, TetR family (TIGR)		0.33	0.31	0.19	0.01	0.32	0.37
DVU1762	membrane protein, putative (TIGR)		1.07	1.02	0.44	0.02	1.01	0.98
DVU1764	conserved hypothetical protein (TIGR)		0.41	0.88	1.31	0.05	0.81	0.88
DVU1765	thiH protein, putative (TIGR)	thiH	0.56	0.95	1.00	0.03	1.21	1.17
DVU1766	aspartate ammonia-lyase, putative (TIGR)	aspA	1.07	1.20	1.48	0.04	1.23	1.28
DVU1767	radical SAM domain protein (TIGR)		0.94	1.46	1.38	0.03	1.41	1.54
DVU1768	GTP-binding protein (TIGR)		1.21	1.12	1.53	0.03	1.21	0.96
DVU1769	periplasmic [Fe] hydrogenase, large subunit (TIGR)	hydA	1.45	1.72	2.03	2.49	1.98	2.23
DVU1770	periplasmic [Fe] hydrogenase, small subunit (TIGR)	hydB	2.42	2.31	2.06	0.06	2.51	2.61
DVU1771	[Fe] hydrogenase gamma (TIGR)	hydC	1.10	1.24	1.26	0.02	1.31	1.28
DVU1772	pyridine nucleotide-disulfide oxidoreductase (TIGR	gltD	0.83	1.05	1.04	0.02	1.05	1.02
DVU1774	hypothetical protein (TIGR)		0.99	1.19	1.38	0.02	1.31	1.22
DVU1775	3,4-dihydroxy-2-butanone 4-phosphate synthase (	ribB	1.60	1.37	1.03	0.04	1.45	1.59
DVU1776	hypothetical protein (TIGR)		0.18	0.22	0.01	0.00	0.06	0.10
DVU1777	carbonic anhydrase (TIGR)	cynT	0.69	0.68	0.89	0.01	0.39	0.24
DVU1778	cation efflux family protein (TIGR)		0.69	0.98	0.79	0.02	0.95	1.01
DVU1779	hypothetical protein (TIGR)		0.68	0.30	0.37	0.00	0.45	0.74
DVU1780	conserved hypothetical protein (TIGR)		1.05	1.20	0.88	0.02	1.21	1.09
DVU1781	conserved hypothetical protein (TIGR)		0.85	0.75	1.17	0.02	0.84	1.04
DVU1782	iron-sulfur cluster-binding protein (TIGR)		0.87	1.06	1.05	0.02	1.05	1.16
DVU1783	cysteine-rich domain protein (TIGR)		0.73	1.17	0.82	0.04	1.09	1.31
DVU1784	oxidoreductase, short-chain dehydrogenase/reductase fami		1.07	1.15	1.29	0.02	1.35	1.21
DVU1785	membrane protein, MarC family (TIGR)		0.95	0.81	1.33	0.01	1.00	1.05
DVU1786	GGDEF domain protein (TIGR)		0.69	0.61	0.74	0.02	0.73	0.85
DVU1787	nuclease domain protein (TIGR)		0.99	1.18	0.81	0.02	1.15	1.28
DVU1788	RNA polymerase sigma-70 factor (TIGR)	rpoD	0.01	0.00	0.05	0.00	0.00	0.00
DVU1789	DNA primase (TIGR)	dnaG	0.01	0.00	0.00	0.00	0.00	0.00
DVU1790	MutS2 family protein (TIGR)		0.96	1.14	0.55	0.02	1.39	1.34
DVU1791	GatB/Yqey family protein (TIGR)		0.90	0.73	0.99	0.02	1.05	1.24
DVU1792	ribosomal protein S21 (TIGR)	rpsU	0.00	0.00	0.00	0.00	0.00	0.00
DVU1794	hypothetical protein (TIGR)		0.92	1.19	1.42	0.03	1.66	2.01
DVU1795	DNA-binding protein HU (TIGR)	hup-3	0.72	0.36	0.89	0.03	0.61	1.01
DVU1796	hypothetical protein (TIGR)		1.29	0.39	0.52	0.03	0.80	1.14
DVU1797	dimethyladenosine transferase (TIGR)	ksgA	0.47	0.82	1.08	0.02	1.31	0.89
DVU1798	conserved hypothetical protein (TIGR)		0.70	0.78	0.60	0.02	0.95	1.02
DVU1799	translation elongation factor G (TIGR)	fusA-2	1.30	0.92	1.14	0.02	1.14	1.16
DVU1801	hypothetical protein (TIGR)		0.80	0.88	0.80	0.02	0.99	1.06
DVU1802	conserved hypothetical protein (TIGR)		0.72	1.04	0.83	0.02	0.98	1.04
DVU1803	glycosyl transferase, group 1 family protein (TIGR)		1.03	1.02	0.94	0.03	1.12	1.23
DVU1804	glycosyl transferase, group 1 family protein (TIGR)		1.09	1.32	1.13	0.05	1.25	1.43
DVU1805	GGDEF domain protein (TIGR)		0.90	0.92	0.75	0.03	1.00	1.07
DVU1806	magnesium transporter (TIGR)	mgtE	0.70	0.77	0.85	0.03	1.06	0.97
DVU1807	nicotinate-nucleotide pyrophosphorylase (TIGR)	nadC	0.05	0.03	0.05	0.01	0.01	0.00
DVU1808	quinolinate synthetase complex, subunit A (TIGR)	nadA	0.00	0.00	0.00	0.00	0.00	0.00
DVU1809	L-aspartate oxidase (TIGR)	nadB	0.05	0.03	0.21	0.00	0.02	0.03
DVU1810	hypothetical protein (TIGR)		0.68	1.00	0.53	0.02	1.02	0.97

DVU1811	protoheme IX farnesyltransferase, putative (TIGR)		0.64	0.67	0.62	0.02	0.74	0.89
DVU1812	cytochrome c oxidase, subunit II, putative (TIGR)	coxB	0.86	0.78	0.48	0.01	0.88	0.95
DVU1813	hypothetical protein (TIGR)		0.51	0.66	0.37	0.02	0.53	0.55
DVU1814	cytochrome c oxidase, subunit III, putative (TIGR)		0.37	0.41	0.33	0.00	0.47	0.60
DVU1815	cytochrome c oxidase, subunit I, putative (TIGR)		0.62	0.68	0.58	0.01	0.64	0.70
DVU1816	conserved hypothetical protein (TIGR)		0.60	0.72	0.90	0.02	0.78	0.86
DVU1817	cytochrome c-553 (TIGR)	cyf	0.82	0.71	0.59	0.00	0.75	0.96
DVU1818	protein-export membrane protein SecF (TIGR)	secF	0.00	0.01	0.13	0.00	0.01	0.01
DVU1819	protein-export membrane protein SecD (TIGR)	secD	0.01	0.00	0.08	0.00	0.00	0.01
DVU1820	preprotein translocase, YajC subunit (TIGR)	yajC	0.07	0.35	0.55	0.01	0.22	0.46
DVU1821	glutamate synthase, large subunit (VIMSS_AUTO)	gltB	0.74	1.29	1.22	0.03	1.32	1.28
DVU1822	glutamate synthase, amidotransferase subunit, putative (TIC		0.76	1.01	0.98	0.02	1.00	1.10
DVU1823	glutamate synthase, iron-sulfur cluster-binding sut	gltB-1	1.05	0.88	1.10	0.03	1.17	1.12
DVU1824	conserved hypothetical protein (TIGR)		1.26	1.43	1.20	0.05	1.48	1.61
DVU1825	amidohydrolase family protein (TIGR)		2.25	1.87	2.02	0.03	2.04	2.03
DVU1826	hypothetical protein (TIGR)		0.01	0.02	0.06	0.00	0.06	0.03
DVU1827	acetylornithine deacetylase/succinyl-diaminopimelate desuc		0.71	0.64	0.48	0.01	0.63	0.78
DVU1828	glucose inhibited division protein A (TIGR)	gidA	0.40	0.35	0.47	0.02	0.22	0.36
DVU1830	hypothetical protein (TIGR)		0.63	0.80	0.88	1.50	0.90	0.82
DVU1832	hypothetical protein (TIGR)		0.00	0.10	0.00	0.03	0.05	0.08
DVU1833	phosphoenolpyruvate synthase, putative (TIGR)	ppsA	0.00	0.00	0.00	0.00	0.00	0.00
DVU1834	pyruvate carboxylase, putative (TIGR)	pyc	0.01	0.01	0.03	0.00	0.00	0.00
DVU1835	biotin--acetyl-CoA-carboxylase ligase (TIGR)		0.23	0.22	0.49	0.01	0.05	0.07
DVU1836	tRNA nucleotidyltransferase, putative (TIGR)	cca	0.86	0.91	0.80	0.02	0.99	1.09
DVU1837	competence protein, putative (TIGR)		0.01	0.07	0.02	0.00	0.10	0.04
DVU1838	thioredoxin reductase (TIGR)	trxB-2	0.42	0.52	0.51	0.02	0.59	0.56
DVU1839	thioredoxin (TIGR)	trx	0.00	0.00	0.00	0.00	0.00	0.00
DVU1840	metalloendopeptidase, putative, glycoprotease fa	gcp	0.01	0.01	0.17	0.00	0.02	0.02
DVU1841	fructose-1,6-bisphosphatase (TIGR)	fbp	0.19	0.13	0.24	0.01	0.06	0.25
DVU1842	lipoprotein, putative (TIGR)		0.38	0.31	0.04	0.00	0.17	0.30
DVU1843	hypothetical protein (TIGR)		0.47	0.51	0.41	0.03	0.60	0.56
DVU1844	septum formation initiator family protein (TIGR)		0.25	0.23	0.42	0.01	0.09	0.25
DVU1845	hypothetical protein (TIGR)		0.38	0.50	1.13	0.00	0.43	0.53
DVU1846	CDP-diacylglycerol--glycerol-3-phosphate 3-phosp	pgsA	0.07	0.00	0.13	0.00	0.02	0.02
DVU1847	conserved hypothetical protein (TIGR)		0.03	0.01	0.23	0.00	0.02	0.05
DVU1848	conserved hypothetical protein (TIGR)		0.94	1.13	1.30	0.03	1.17	1.14
DVU1849	protein-L-isoaspartate O-methyltransferase (TIGR)	pcm	0.78	0.60	0.61	0.00	0.50	0.36
DVU1850	CBS domain protein (TIGR)		0.56	0.58	0.20	0.01	0.63	0.65
DVU1851	peptidase, M23/M37 family (TIGR)		0.68	0.91	0.91	0.02	1.07	1.14
DVU1852	conserved hypothetical protein (TIGR)		0.34	0.33	0.39	0.01	0.56	0.73
DVU1853	hypothetical protein (TIGR)		0.09	0.43	0.65	0.02	0.64	0.76
DVU1854	hypothetical protein (TIGR)		0.53	0.63	0.75	0.01	0.83	0.75
DVU1855	integrase, truncation (TIGR)		1.12	0.74	1.05	0.00	0.82	1.18
DVU1857	methyl-accepting chemotaxis protein (TIGR)		0.98	1.10	0.88	0.02	1.03	1.17
DVU1858	cold shock domain protein (TIGR)		0.79	0.90	1.03	0.02	1.05	1.21
DVU1859	hypothetical protein (TIGR)		0.22	0.39	0.21	0.00	0.48	0.51
DVU1860	apolipoprotein N-acyltransferase (TIGR)	cutE	0.22	0.24	1.12	0.02	0.14	0.16
DVU1861	peptide chain release factor 2, programmed frame	prfB	0.01	0.00	0.07	0.01	0.00	0.00
DVU1862	GGDEF domain protein (TIGR)		1.11	1.21	1.11	0.02	1.76	1.38
DVU1863	flagellar synthesis regulator FleN, putative (TIGR)		0.80	0.90	1.02	0.00	1.08	1.09
DVU1864	DNA-binding protein HU, beta subunit, putative (T	ihfB	0.22	0.25	0.10	0.00	0.21	0.18
DVU1865	hypothetical protein (TIGR)		0.39	0.82	0.35	0.01	1.12	1.08
DVU1866	hypothetical protein (TIGR)		0.85	1.10	1.47	0.02	1.08	1.10
DVU1867	diaminopimelate epimerase (TIGR)	dapF	0.00	0.02	0.00	0.01	0.00	0.00
DVU1868	dihydrodipicolinate synthase (TIGR)	dapA	0.08	0.02	0.07	0.00	0.00	0.00
DVU1869	methyl-accepting chemotaxis protein (TIGR)		0.62	0.70	0.66	0.02	0.72	0.66
DVU1870	cyclase, putative (TIGR)		0.97	1.21	1.01	0.02	1.21	1.20
DVU1871	aspartate ammonia-lyase (TIGR)	aspA	0.57	0.57	0.50	0.01	0.78	0.72
DVU1873	peptidyl-prolyl cis-trans isomerase B (TIGR)	ppiB-2	0.77	0.60	0.48	0.01	0.74	0.72
DVU1874	ATP-dependent Clp protease, ATP-binding subunit	clpB	0.98	1.24	0.92	0.03	1.09	1.17
DVU1875	dafA protein (TIGR)		1.04	0.97	0.59	0.02	0.99	1.34
DVU1876	dnaJ protein, putative (TIGR)	dnaJ	0.88	1.12	1.03	0.03	0.94	1.11
DVU1877	polysaccharide deacetylase family protein (TIGR)		0.12	0.16	0.58	0.01	0.02	0.11
DVU1878	threonine aldolase, low-specificity (TIGR)	ltaE	0.74	1.04	1.18	0.04	1.02	1.05
DVU1879	glycosyl transferase, group 1 family protein (TIGR)		0.05	0.04	0.40	0.01	0.01	0.04
DVU1880	hypothetical protein (TIGR)		0.50	0.73	0.59	0.02	0.58	0.71
DVU1881	phoH family protein (TIGR)	phoH	1.07	1.26	0.99	0.02	1.43	1.44

DVU1882	HDIG domain protein (TIGR)		0.69	0.78	0.76	0.02	0.91	0.82
DVU1883	conserved hypothetical protein (TIGR)		0.07	0.11	0.11	0.02	0.18	0.16
DVU1884	methyl-accepting chemotaxis protein (TIGR)		0.67	0.89	0.92	0.02	0.84	0.96
DVU1885	glutamyl-tRNA(Gln) amidotransferase, B subunit (T	gatB	0.02	0.02	0.00	0.00	0.00	0.00
DVU1886	hypothetical protein (TIGR)		0.03	0.07	0.50	0.00	0.01	0.03
DVU1887	hypothetical protein (TIGR)		1.09	1.04	1.10	0.02	1.12	1.28
DVU1888	ATP-NAD kinase domain protein (TIGR)		0.02	0.03	0.11	0.00	0.01	0.01
DVU1889	phosphoheptose isomerase (TIGR)	gmhA	0.03	0.01	0.00	0.00	0.00	0.00
DVU1890	porphobilinogen deaminase (TIGR)	hemC	0.00	0.02	0.18	0.00	0.00	0.00
DVU1891	conserved hypothetical protein (TIGR)		1.01	1.11	1.79	0.03	1.24	1.14
DVU1892	glycosyl transferase, group 2 family protein (TIGR)		1.68	1.17	1.31	0.04	1.57	1.73
DVU1893	ATP-dependent protease, putative (TIGR)		0.77	1.12	1.01	0.02	0.98	1.02
DVU1894	hypothetical protein (TIGR)		1.10	0.67	0.42	0.01	1.21	1.08
DVU1895	major facilitator superfamily protein (TIGR)		0.69	0.99	1.12	0.02	1.01	0.85
DVU1896	ribosomal protein S20 (TIGR)	rpsT	0.00	0.00	0.08	0.00	0.03	0.00
DVU1897	glycyl-tRNA synthetase, beta subunit (TIGR)	glyS	0.00	0.01	0.04	0.00	0.00	0.00
DVU1898	glycyl-tRNA synthetase, alpha subunit (TIGR)	glyQ	0.00	0.01	0.02	0.00	0.00	0.00
DVU1899	DNA repair protein RecO, putative (TIGR)		1.08	1.11	1.00	0.03	1.23	1.15
DVU1900	conserved hypothetical protein (TIGR)		0.57	0.76	1.46	0.03	1.55	1.37
DVU1901	peptidyl-prolyl cis-trans isomerase domain protein (TIGR)		0.12	0.01	0.07	0.00	0.01	0.02
DVU1902	conserved hypothetical protein (TIGR)		0.75	1.01	0.98	0.02	1.20	1.28
DVU1903	transcription-repair coupling factor (TIGR)	mfd	0.83	1.15	1.10	0.03	1.17	1.14
DVU1904	chemotaxis protein CheW (TIGR)	cheW-2	0.76	0.57	0.76	0.04	0.81	0.81
DVU1905	hypothetical protein (TIGR)		0.47	0.45	0.25	0.02	0.51	0.63
DVU1907	UDP-glucose 6-dehydrogenase (TIGR)	ugd	0.04	0.00	0.17	0.00	0.00	0.00
DVU1908	pyridoxal phosphate biosynthetic protein PdxJ (TIC	pdxJ	0.76	0.86	1.00	0.02	0.96	0.69
DVU1909	holo-(acyl-carrier-protein) synthase (TIGR)	acpS	0.08	0.12	0.00	0.00	0.03	0.00
DVU1910	YjeF-related protein (TIGR)		1.62	1.54	1.49	0.03	1.64	1.68
DVU1911	CBS domain protein (TIGR)		0.23	0.16	0.64	0.00	0.26	0.33
DVU1912	conserved hypothetical protein TIGR00150 (TIGR)		0.03	0.02	0.65	0.00	0.05	0.04
DVU1913	aspartate kinase, monofunctional class (TIGR)		0.21	0.12	0.10	0.00	0.01	0.02
DVU1914	2-isopropylmalate synthase/homocitrate synthase family pr		0.84	1.01	1.11	0.02	0.38	0.40
DVU1915	hypothetical protein (TIGR)		0.32	0.32	0.10	0.01	0.33	0.30
DVU1916	hypothetical protein (TIGR)		0.00	0.00	0.25	0.00	0.17	0.06
DVU1917	periplasmic [NiFeSe] hydrogenase, small subunit (T	hysB	0.71	0.71	0.54	0.02	0.88	0.97
DVU1918	periplasmic [NiFeSe] hydrogenase, large subunit, s	hysA	0.67	0.69	0.94	0.02	0.82	0.94
DVU1919	hydrogenase expression/formation protein, putative (TIGR)		0.46	0.45	0.52	0.01	0.54	0.55
DVU1921	periplasmic [NiFe] hydrogenase, small subunit, iso	hynB-1	0.72	0.66	0.75	0.01	0.84	0.92
DVU1922	periplasmic [NiFe] hydrogenase, large subunit, iso	hynA-1	1.20	1.17	1.50	0.03	1.40	1.50
DVU1923	hydrogenase expression/formation protein HupD (	hupD	0.79	0.85	0.88	0.03	1.10	1.10
DVU1924	hydrogenase assembly chaperone hypC/hupF (TIG	hypC	0.15	0.20	0.17	0.00	0.14	0.29
DVU1925	lipase, GDSL family (TIGR)	tesA	0.73	0.98	1.03	0.02	1.22	1.26
DVU1926	conserved hypothetical protein (TIGR)		1.34	1.37	1.16	0.03	1.20	1.48
DVU1927	isoleucyl-tRNA synthetase (TIGR)	ileS	0.00	0.00	0.02	0.00	0.00	0.00
DVU1928	lipoprotein signal peptidase (TIGR)	lspA	0.00	0.00	0.02	0.00	0.01	0.01
DVU1929	hypothetical protein (TIGR)		0.42	0.25	0.55	0.01	0.53	0.41
DVU1930	TPR domain protein (TIGR)		0.09	0.09	0.33	0.01	0.00	0.00
DVU1931	iron-sulfur cluster-binding protein (TIGR)		0.48	0.95	1.00	0.01	0.23	0.21
DVU1932	adenylate kinase (TIGR)	adk	0.02	0.00	0.07	0.00	0.00	0.01
DVU1933	peptidase, PfpI family (TIGR)		0.33	0.45	0.68	0.01	0.59	0.40
DVU1934	phosphonate ABC transporter, permease protein (	phnE	0.57	0.78	0.48	0.02	0.81	0.74
DVU1935	phosphonate ABC transporter, permease protein (	phnE	0.56	0.78	0.86	0.02	0.94	0.90
DVU1936	phosphonate ABC transporter, ATP-binding protei	phnC	0.72	0.87	0.98	0.03	1.04	1.14
DVU1937	phosphonate ABC transporter, periplasmic phosphonate-bir		0.96	1.15	1.51	0.03	1.69	1.72
DVU1938	hypothetical protein (TIGR)		1.02	0.75	0.87	0.02	0.81	0.87
DVU1939	anaerobic glycerol-3-phosphate dehydrogenase, B subunit,		0.79	0.94	1.18	0.02	1.32	1.20
DVU1940	anaerobic glycerol-3-phosphate dehydrogenase, A	glpA	1.12	1.24	1.00	0.02	1.20	1.34
DVU1941	HAD-superfamily hydrolase, subfamily IIA (TIGR)		0.78	0.87	1.37	0.03	1.24	1.36
DVU1942	DAK2 domain/degV family protein (TIGR)		0.64	0.98	1.11	0.01	1.13	1.08
DVU1943	hypothetical protein (TIGR)		1.05	0.52	1.14	0.01	0.80	0.68
DVU1944	pyruvate ferredoxin oxidoreductase, iron-sulfur bi	oorD	1.19	1.44	1.18	0.03	1.29	1.59
DVU1945	pyruvate ferredoxin oxidoreductase, alpha subunit	oorA	0.83	1.23	1.19	0.03	1.28	1.36
DVU1946	pyruvate ferredoxin oxidoreductase, beta subunit,	oorB	1.11	1.53	1.29	3.06	1.54	1.56
DVU1947	pyruvate ferredoxin oxidoreductase, gamma subu	oorC	0.88	0.78	1.01	0.01	0.93	1.24
DVU1948	conserved hypothetical protein (TIGR)		0.14	0.55	0.68	0.01	0.64	0.70
DVU1949	nif-specific regulatory protein (TIGR)	nifA-1	0.33	0.39	0.54	0.00	0.10	0.03
DVU1950	indolepyruvate ferredoxin oxidoreductase, beta subunit, pu		0.87	0.97	1.45	0.04	0.86	0.61

DVU1951	indolepyruvate ferredoxin oxidoreductase, alpha subunit, pu		0.70	0.43	0.73	0.02	0.29	0.15
DVU1952	hypothetical protein (TIGR)		0.70	0.86	1.12	0.01	0.62	0.61
DVU1953	gamma-glutamyl phosphate reductase (TIGR)	proA	1.17	1.17	0.24	0.00	0.01	0.00
DVU1954	nicotinate (nicotinamide) nucleotide adenylyltrans	nadD	0.14	0.08	0.10	0.00	0.01	0.02
DVU1955	TPR domain protein (TIGR)		1.18	1.05	0.98	0.02	1.26	1.29
DVU1956	heptosyltransferase family protein (TIGR)		0.04	0.00	0.20	0.00	0.01	0.02
DVU1958	sensory box histidine kinase (TIGR)		1.06	1.13	1.11	0.02	1.12	1.15
DVU1959	EAL domain/GGDEF domain protein (TIGR)		0.92	0.95	0.84	0.02	0.98	1.11
DVU1960	chemotaxis protein CheA (TIGR)	cheA-2	1.07	0.97	0.77	0.03	0.96	1.04
DVU1961	chemotaxis protein CheW (TIGR)	cheW-3	1.18	0.81	0.99	0.01	0.87	1.00
DVU1962	methyl-accepting chemotaxis protein (TIGR)		0.98	1.07	1.11	0.02	1.13	1.20
DVU1964	transcriptional regulator, rrf2 protein, putative (TIGR)		0.16	0.15	0.32	0.01	0.10	0.03
DVU1967	transcriptional regulator, rrf2 protein, putative (TI	rrf2	0.55	0.75	0.90	0.01	0.56	0.64
DVU1968	oxidoreductase, putative (TIGR)		0.62	0.82	1.03	0.03	0.78	0.98
DVU1969	hypothetical protein (TIGR)		0.88	1.27	0.89	0.03	0.82	1.04
DVU1970	response regulator (TIGR)		0.98	0.82	0.62	0.02	0.91	1.11
DVU1971	conserved domain protein (TIGR)		1.41	1.34	1.54	0.03	1.17	1.32
DVU1972	hypothetical protein (TIGR)		1.13	1.33	1.65	0.05	1.97	2.31
DVU1973	rhodanese-like domain protein (TIGR)		0.79	0.95	0.82	0.03	1.01	0.98
DVU1974	pyridine nucleotide-disulfide oxidoreductase (TIGR)		0.87	0.67	0.73	0.02	0.87	0.86
DVU1975	methyl-accepting chemotaxis protein (TIGR)		0.60	0.72	0.72	0.01	0.76	0.84
DVU1976	chaperonin, 60 kDa (TIGR)	groEL	0.00	0.01	0.00	0.00	0.00	0.00
DVU1977	chaperonin, 10 kDa (TIGR)	groES	0.00	0.00	0.00	0.00	0.00	0.00
DVU1978	methionine transporter from the Na+/H+ antiport	metT	3.13	0.62	0.54	0.01	0.63	0.71
DVU1979	ABC transporter, ATP-binding protein (TIGR)		0.73	0.78	0.98	0.02	0.93	0.88
DVU1980	hypothetical protein (TIGR)		1.15	1.13	1.49	0.02	1.24	1.35
DVU1981	conserved hypothetical protein (TIGR)	rhlE	1.16	1.15	0.90	0.04	1.03	1.04
DVU1982	ATP-dependent RNA helicase RhlE (TIGR)		0.82	1.20	1.66	0.02	1.32	1.23
DVU1983	hypothetical protein (TIGR)	msrA	1.62	1.92	1.87	0.02	2.15	1.88
DVU1984	peptide methionine sulfoxide reductase MsrA (TIGR)		0.61	0.66	0.74	0.01	0.68	0.78
DVU1985	conserved domain protein (TIGR)		0.56	0.58	0.74	0.02	0.61	0.66
DVU1986	conserved hypothetical protein (TIGR)	uvrA	1.59	1.14	0.84	0.01	1.16	1.06
DVU1987	excinuclease ABC, A subunit (TIGR)		1.35	1.26	1.44	0.06	1.33	1.31
DVU1988	membrane protein, putative (TIGR)		0.80	0.84	0.67	0.03	1.07	0.94
DVU1990	hypothetical protein (TIGR)		0.91	0.88	1.18	0.01	0.93	0.90
DVU1991	hypothetical protein (TIGR)	cat	0.83	0.85	0.64	0.01	0.77	0.95
DVU1992	antibiotic acetyltransferase (TIGR)	ctpF	0.99	1.02	0.96	0.02	0.96	1.06
DVU1993	cation-transporting ATPase, E1-E2 family (TIGR)	rsbV	1.22	1.15	1.06	0.03	1.16	1.20
DVU1995	anti-anti-sigma factor (TIGR)		1.01	1.02	0.81	0.02	0.97	1.02
DVU1996	quaternary ammonium compound-resistance protein	QacC,	0.22	0.25	0.13	0.00	0.26	0.30
DVU1999	sulfate transporter family protein (TIGR)		0.63	0.74	0.57	4.59	0.84	0.92
DVU2000	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.01
DVU2003	transposase, IS5 family, truncation (TIGR)		0.68	0.90	0.67	0.04	0.89	0.86
DVU2004	ISDvu4, transposase (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2006	hypothetical protein (TIGR)		0.06	0.00	0.00	0.00	0.13	0.11
DVU2007	nuclease, putative (TIGR)		0.27	0.33	0.24	0.00	0.22	0.25
DVU2008	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.05
DVU2009	conserved domain protein (TIGR)		0.08	0.39	0.01	0.00	0.23	0.22
DVU2010	ISD1, transposase OrfB (TIGR)		0.43	0.44	0.28	0.02	0.32	0.45
DVU2011	ISD1, transposase OrfA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2012	hypothetical protein (TIGR)		0.83	0.57	0.34	0.00	0.83	0.69
DVU2013	hybrid cluster protein (TIGR)	fprA-1	0.95	0.79	0.96	0.02	1.13	1.00
DVU2014	metallo-beta-lactamase family protein (TIGR)		0.79	0.75	0.73	0.04	0.97	1.04
DVU2016	GGDEF domain protein (TIGR)		0.04	0.01	0.04	0.00	0.08	0.06
DVU2017	ISDvu5, transposase (TIGR)		1.33	1.10	0.96	0.03	1.19	1.16
DVU2019	conserved hypothetical protein (TIGR)		0.66	0.81	0.97	0.04	0.81	0.93
DVU2020	conserved hypothetical protein (TIGR)		0.62	0.51	0.54	0.01	0.89	0.81
DVU2021	hypothetical protein (TIGR)		0.26	0.29	0.24	0.01	0.32	0.43
DVU2022	conserved hypothetical protein (TIGR)		0.52	0.40	0.34	0.01	0.76	0.79
DVU2023	hypothetical protein (TIGR)		0.88	0.80	0.87	0.02	0.83	1.06
DVU2024	conserved hypothetical protein (TIGR)		1.09	0.89	0.95	0.02	1.57	1.64
DVU2025	conserved hypothetical protein (TIGR)		0.65	0.46	0.41	0.01	0.89	0.91
DVU2026	conserved hypothetical protein (TIGR)		0.18	0.13	0.20	0.00	0.24	0.24
DVU2028	conserved domain protein (TIGR)		0.87	0.76	0.44	0.03	1.09	1.08
DVU2029	ISDvu2, transposase OrfA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2030	ISDvu2, transposase OrfB (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2032	ERF family protein (TIGR)		1.27	1.34	1.26	0.04	1.51	1.77

DVU2033	hypothetical protein (TIGR)		1.39	1.27	1.24	0.02	1.21	1.45
DVU2034	hypothetical protein (TIGR)		1.10	0.60	0.88	0.00	0.58	0.60
DVU2035	plasmid stabilization system family protein (TIGR)		0.46	0.71	0.82	0.01	0.66	0.94
DVU2036	helix-turn-helix protein, CopG family (TIGR)		0.00	0.00	0.00	0.00	0.01	0.02
DVU2037	cobS protein, putative (TIGR)		1.55	1.08	1.47	0.04	1.36	1.45
DVU2038	hypothetical protein (TIGR)		1.66	1.90	2.66	0.01	2.10	2.59
DVU2039	hypothetical protein (TIGR)		1.58	1.25	1.66	0.01	1.26	1.82
DVU2040	hypothetical protein (TIGR)		1.68	0.88	0.78	0.04	0.86	1.17
DVU2041	conserved hypothetical protein (TIGR)		1.51	1.27	1.29	0.04	1.51	1.54
DVU2042	Fic family protein (TIGR)		0.41	0.34	0.35	0.01	0.34	0.19
DVU2043	conserved hypothetical protein (TIGR)		1.16	0.99	1.39	0.02	1.10	1.10
DVU2044	hypothetical protein (TIGR)		0.99	1.35	0.87	0.01	1.21	0.89
DVU2045	hypothetical protein (TIGR)		0.51	0.70	0.89	0.02	0.85	0.92
DVU2046	hypothetical protein (TIGR)		0.48	0.34	0.34	0.00	0.15	0.25
DVU2048	hypothetical protein (TIGR)		0.06	0.13	0.25	0.00	0.11	0.29
DVU2051	hypothetical protein (TIGR)	dmt	0.14	0.08	0.12	0.01	0.17	0.15
DVU2052	glycosyl transferase, group 2 family protein (TIGR)		0.13	0.04	0.21	0.00	0.01	0.02
DVU2053	membrane protein, putative (TIGR)		0.65	0.23	0.65	0.01	0.09	0.14
DVU2054	hypothetical protein (TIGR)	metG	0.54	0.09	0.57	0.01	0.20	0.23
DVU2055	methionyl-tRNA synthetase (TIGR)		0.03	0.06	0.09	0.00	0.06	0.06
DVU2057	conserved hypothetical protein (TIGR)		0.57	0.66	1.00	0.02	0.62	0.46
DVU2058	HDIG domain protein (TIGR)		1.18	1.39	1.30	0.02	1.37	1.42
DVU2059	glycosyl transferase, group 2 family protein (TIGR)		0.96	0.94	1.14	0.03	1.47	1.05
DVU2060	hypothetical protein (TIGR)	pfkA	0.79	0.00	0.38	0.01	0.47	0.25
DVU2061	6-phosphofructokinase (TIGR)		1.19	1.03	1.02	0.02	1.09	1.14
DVU2062	ATP-dependent DNA helicase, UvrD/REP family (TIGR)		0.66	0.77	0.86	0.02	0.45	0.58
DVU2063	conserved hypothetical protein (TIGR)	fabK	0.87	0.88	0.86	0.02	0.59	0.71
DVU2064	oxidoreductase, 2-nitropropane dioxygenase famil	xerC	0.37	0.37	0.38	0.01	0.11	0.02
DVU2066	site-specific recombinase, phage integrase family (TIGR)		0.57	0.61	0.84	0.02	0.47	0.37
DVU2067	GGDEF domain protein (TIGR)		0.73	0.60	0.92	0.02	0.71	0.72
DVU2068	HD domain protein (TIGR)	dprA	0.61	0.83	0.84	0.02	0.90	1.04
DVU2069	DNA processing protein DprA, putative (TIGR)		0.81	0.84	0.93	0.02	0.97	0.94
DVU2070	TPR domain protein (TIGR)		0.58	0.78	1.09	0.00	0.83	0.85
DVU2071	membrane protein, putative (TIGR)	cheA-3	0.02	0.00	0.05	0.00	0.00	0.00
DVU2072	chemotaxis protein CheA (TIGR)	cheY-2	0.42	0.54	0.45	0.01	0.57	0.47
DVU2073	chemotaxis protein CheY (TIGR)		1.27	1.50	1.35	0.00	1.80	1.46
DVU2074	chemotaxis protein CheW (TIGR)	parA	0.33	0.52	0.94	0.01	0.65	0.63
DVU2075	ParA family protein (TIGR)	cheR-2	0.69	0.99	1.00	0.01	0.97	0.97
DVU2076	chemotaxis protein methyltransferase (TIGR)		0.84	1.06	0.95	0.01	1.23	1.19
DVU2077	conserved hypothetical protein (TIGR)	cheB-2	1.15	1.06	1.03	0.02	1.10	1.08
DVU2078	protein-glutamate methylesterase CheB (TIGR)		0.93	0.99	0.97	0.02	1.06	0.98
DVU2079	sensory box histidine kinase (TIGR)		0.81	0.88	0.86	0.02	0.78	1.05
DVU2081	hypothetical protein (TIGR)	flaD	0.48	0.75	0.73	0.02	0.96	0.80
DVU2082	flagellin, putative (TIGR)	relA	1.58	1.47	1.54	0.08	1.69	1.79
DVU2083	GTP pyrophosphokinase (TIGR)	appA	0.59	0.85	0.82	0.02	0.56	0.69
DVU2084	oligopeptide-binding protein, putative (TIGR)		1.08	1.20	1.13	0.02	1.13	1.13
DVU2085	Snf2 family protein (TIGR)		0.20	0.36	0.56	0.01	0.53	0.76
DVU2086	transcriptional regulator, GntR family (TIGR)		0.68	0.80	0.74	0.02	0.85	0.92
DVU2087	hypothetical protein (TIGR)		1.04	0.94	1.02	0.02	0.84	1.06
DVU2088	membrane protein, putative (TIGR)		0.77	1.07	0.76	0.02	0.98	1.10
DVU2090	EF hand domain protein (TIGR)	thiE-1	0.44	0.66	0.68	0.01	0.65	0.85
DVU2091	thiamine-phosphate pyrophosphorylase (TIGR)	moeB	0.48	0.81	0.60	0.02	0.62	0.88
DVU2092	thiF family protein (TIGR)	thiH	0.80	0.68	0.57	0.01	0.74	0.67
DVU2093	thiH protein (TIGR)	thiG	1.43	1.30	1.07	0.02	1.21	1.21
DVU2094	thiG protein (TIGR)	thiS	0.43	0.50	0.36	0.00	0.52	0.52
DVU2095	thiamine biosynthesis protein ThiS (TIGR)		0.36	0.47	0.76	0.01	0.46	0.47
DVU2096	hypothetical protein (TIGR)		0.33	0.45	0.86	0.05	0.28	0.54
DVU2097	transcriptional regulator, putative (TIGR)	cooS	0.16	0.17	0.12	0.00	0.19	0.24
DVU2098	carbon monoxide dehydrogenase (TIGR)	cooC-2	0.69	0.77	0.48	0.02	0.77	0.82
DVU2099	carbon monoxide dehydrogenase accessory protein	CooC, p	0.92	1.19	0.90	0.04	1.14	1.25
DVU2100	universal stress protein family (TIGR)		0.92	1.18	1.06	0.04	1.61	1.47
DVU2101	conserved hypothetical protein (TIGR)		0.86	1.16	0.94	0.02	1.12	1.10
DVU2102	outer membrane protein, OMP85 family (TIGR)		0.99	1.31	1.26	0.11	1.39	1.37
DVU2103	iron-sulfur cluster-binding/ATPase domain protein (TIGR)		0.45	0.21	0.23	0.00	0.31	0.18
DVU2104	iron-sulfur cluster-binding/ATPase domain protein (TIGR)		0.71	0.44	0.54	0.01	0.54	0.32
DVU2105	hypothetical protein (TIGR)	flrC	1.37	1.34	1.09	0.03	1.44	1.12
DVU2106	sigma-54 dependent transcriptional regulator (TIGR)		0.44	0.17	0.74	0.01	0.30	0.16

DVU2107	hypothetical protein (TIGR)		1.16	1.06	1.36	0.04	0.86	1.11
DVU2108	MTH1175-like domain family protein (TIGR)	mrp	0.16	0.10	0.30	0.00	0.20	0.19
DVU2109	MTH1175-like domain family protein (TIGR)	b2975	0.46	0.30	0.31	0.01	0.31	0.10
DVU2110	L-lactate permease (TIGR)		0.86	0.97	0.69	0.02	1.11	1.13
DVU2111	transcriptional regulator, LysR family (TIGR)		1.81	1.53	0.85	0.03	1.79	1.82
DVU2112	hypothetical protein (TIGR)		0.59	0.50	0.73	0.00	0.62	0.60
DVU2113	xanthine/uracil permease family protein (TIGR)	atoC	0.70	0.97	0.84	0.01	1.02	1.00
DVU2114	sigma-54 dependent transcriptional regulator/response regu		0.81	1.08	0.80	0.02	0.88	1.00
DVU2115	hypothetical protein (TIGR)		0.57	0.29	0.48	0.01	0.43	0.57
DVU2116	pilin, putative (TIGR)		1.25	1.02	1.03	0.03	0.70	1.21
DVU2117	membrane protein, putative (TIGR)		0.71	0.63	0.79	0.01	0.69	0.88
DVU2118	conserved hypothetical protein (TIGR)	cpaC	1.25	1.71	1.24	0.02	1.63	1.75
DVU2119	type II/III secretion system protein (TIGR)		1.02	1.13	1.02	0.04	1.00	1.06
DVU2120	hypothetical protein (TIGR)		1.29	0.77	0.58	0.05	0.68	0.90
DVU2121	response regulator (TIGR)	cpaF	0.84	0.72	0.64	0.01	0.73	0.86
DVU2122	type II/IV secretion system protein (TIGR)		0.87	1.01	0.86	0.02	0.80	0.99
DVU2123	membrane protein, putative (TIGR)		1.02	1.23	0.92	0.02	0.98	1.11
DVU2124	conserved hypothetical protein (TIGR)		0.69	1.04	1.12	0.01	0.82	1.06
DVU2125	TPR domain protein (TIGR)		1.17	1.20	0.89	0.02	1.10	1.25
DVU2126	hypothetical protein (TIGR)		0.84	1.23	1.53	0.05	1.01	1.33
DVU2127	von Willebrand factor type A domain protein (TIGR)		1.13	0.97	1.11	0.04	0.96	1.08
DVU2128	hypothetical protein (TIGR)	cckA	1.06	1.01	0.75	0.02	0.97	0.97
DVU2129	sensory box histidine kinase/response regulator (TIGR)		1.41	1.22	1.07	0.02	1.25	1.29
DVU2130	hypothetical protein (TIGR)		0.92	0.80	1.09	0.02	0.99	1.06
DVU2131	hypothetical protein (TIGR)		2.34	2.21	1.49	0.03	1.69	1.91
DVU2132	hypothetical protein (TIGR)		1.79	1.23	1.37	0.03	1.29	1.37
DVU2133	membrane protein, putative (TIGR)		1.09	1.17	0.96	0.03	1.18	1.36
DVU2134	hypothetical protein (TIGR)		0.00	0.00	0.00	0.00	0.07	0.00
DVU2135	hypothetical protein (TIGR)		1.17	1.53	1.05	0.02	1.51	1.71
DVU2136	hypothetical protein (TIGR)	sucCD	1.28	1.54	1.36	0.02	1.53	1.82
DVU2137	succinyl-CoA synthetase, alpha/beta subunit (sucCD) (Chris I		0.92	0.88	0.83	0.01	0.88	0.88
DVU2138	conserved hypothetical protein (TIGR)	aphA	0.56	0.50	0.43	0.02	0.55	0.62
DVU2139	histone deacetylase family protein (TIGR)	tmk	0.78	0.90	0.95	0.02	0.89	0.99
DVU2140	thymidylate kinase (TIGR)		0.08	0.01	0.00	0.00	0.02	0.09
DVU2141	nucleic acid-binding protein, putative (TIGR)	surE	1.62	1.78	1.81	0.04	1.26	1.65
DVU2142	stationary-phase survival protein SurE (TIGR)	fba	1.57	1.14	1.28	0.02	1.44	1.23
DVU2143	fructose-1,6-bisphosphate aldolase, class II (TIGR)	gap-2	0.05	0.02	0.04	0.00	0.00	0.00
DVU2144	glyceraldehyde 3-phosphate dehydrogenase (TIGR)		0.02	0.02	0.00	0.00	0.00	0.00
DVU2145	chloramphenicol acetyltransferase, putative (TIGR)		0.21	0.15	0.28	0.00	0.21	0.22
DVU2146	hypothetical protein (TIGR)	sda	0.21	0.14	0.00	0.00	0.21	0.06
DVU2147	L-serine dehydratase, putative (TIGR)		1.29	1.07	1.11	0.02	1.24	1.18
DVU2148	CBS/transporter associated domain protein (TIGR)		0.81	0.85	0.78	0.02	0.86	1.05
DVU2149	conserved hypothetical protein (TIGR)	dksA	2.02	1.96	2.29	0.04	2.03	2.04
DVU2150	dnaK suppressor protein, putative (TIGR)		0.40	0.17	0.33	0.00	0.11	0.05
DVU2151	conserved hypothetical protein (TIGR)		1.57	1.19	1.45	0.02	1.25	1.69
DVU2152	hypothetical protein (TIGR)		1.22	0.82	0.83	0.02	0.87	0.93
DVU2153	tail fiber protein, putative (TIGR)		1.46	1.35	1.52	0.04	1.47	1.50
DVU2154	tail assembly protein, putative (TIGR)		0.89	1.08	1.72	0.04	1.28	1.50
DVU2155	hypothetical protein (TIGR)		2.59	2.08	2.24	0.04	1.81	2.39
DVU2156	hypothetical protein (TIGR)		3.40	2.30	2.90	0.05	2.63	3.00
DVU2157	tail tape meausure protein, putative (TIGR)		1.34	1.16	1.25	0.03	1.31	1.34
DVU2158	hypothetical protein (TIGR)		1.70	1.47	1.98	0.03	1.63	1.76
DVU2159	hypothetical protein (TIGR)		1.90	1.48	2.16	1.19	1.56	1.71
DVU2160	hypothetical protein (TIGR)		1.62	1.01	1.02	0.02	0.94	1.10
DVU2161	hypothetical protein (TIGR)		0.97	0.96	0.97	0.03	1.11	1.10
DVU2162	hypothetical protein (TIGR)		2.44	1.54	1.54	0.01	1.60	1.82
DVU2164	lipoprotein, putative (TIGR)		1.95	1.57	2.41	0.05	1.98	1.95
DVU2165	lysozyme, putative (TIGR)		0.93	0.69	0.91	0.01	0.66	0.78
DVU2166	holin (TIGR)		2.08	1.53	2.55	0.04	1.98	2.12
DVU2167	hypothetical protein (TIGR)		0.59	0.99	0.94	0.03	0.90	0.74
DVU2168	major head protein (TIGR)		1.36	1.14	1.37	0.02	1.06	1.19
DVU2169	conserved hypothetical protein (TIGR)		1.67	1.71	2.11	0.03	1.71	1.93
DVU2170	minor capsid protein C (TIGR)		1.53	1.35	1.53	0.03	1.32	1.47
DVU2171	portal protein (TIGR)		1.06	1.16	1.17	0.02	1.18	1.20
DVU2172	hypothetical protein (TIGR)		0.93	1.37	2.09	0.01	1.41	1.62
DVU2173	hypothetical protein (TIGR)		0.14	0.17	0.00	0.01	0.30	0.29
DVU2174	hypothetical protein (TIGR)		0.09	0.10	0.04	0.00	0.06	0.08

DVU2175	adenine specific DNA methyltransferase, putative (TIGR)		0.97	0.79	0.76	0.03	0.90	0.95
DVU2176	hypothetical protein (TIGR)		0.99	1.00	0.42	0.02	1.06	0.94
DVU2177	hypothetical protein (TIGR)		0.08	0.02	0.08	0.00	0.11	0.08
DVU2178	ISDvu2, transposase OrfB (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2179	ISDvu2, transposase OrfA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2180	hypothetical protein (TIGR)		0.20	0.17	0.22	0.00	0.14	0.31
DVU2181	antirepressor, putative (TIGR)		1.30	1.44	1.94	0.03	1.68	1.71
DVU2183	hypothetical protein (TIGR)		0.06	0.04	0.02	0.00	0.01	0.06
DVU2184	DNA-binding domain, excisionase family (TIGR)		2.21	1.23	2.02	0.08	2.15	2.31
DVU2185	terminase, large subunit, putative (TIGR)		1.60	1.23	1.45	0.04	1.51	1.52
DVU2186	hypothetical protein (TIGR)		1.16	1.23	1.16	0.03	1.10	1.40
DVU2187	hypothetical protein (TIGR)		0.97	1.33	0.95	0.02	1.41	1.29
DVU2188	primase, putative (TIGR)		0.97	1.33	1.46	0.03	1.37	1.72
DVU2189	transcriptional regulator cII, putative (TIGR)		0.82	0.52	0.29	0.01	0.64	0.80
DVU2190	transcriptional regulator, putative (TIGR)		0.60	0.38	0.16	0.01	0.40	0.68
DVU2191	hypothetical protein (TIGR)		2.34	2.23	2.97	0.05	2.78	2.85
DVU2192	hypothetical protein (TIGR)		1.81	1.00	1.59	0.10	1.27	1.90
DVU2193	hypothetical protein (TIGR)		1.25	1.15	1.80	0.04	1.35	1.69
DVU2194	hypothetical protein (TIGR)		1.36	0.98	1.05	0.03	1.17	1.14
DVU2195	hypothetical protein (TIGR)		1.75	1.55	1.01	0.02	2.59	2.20
DVU2196	hypothetical protein (TIGR)		1.08	0.99	0.89	0.03	1.03	1.20
DVU2197	site-specific recombinase, phage integrase family (TIGR)		1.53	1.77	1.94	0.06	2.21	2.22
DVU2198	hypothetical protein (TIGR)		0.24	0.50	0.09	0.02	0.43	0.40
DVU2200	hypothetical protein (TIGR)	b3011	0.40	0.27	0.16	0.00	0.33	0.39
DVU2201	alcohol dehydrogenase, iron-containing (TIGR)		1.59	1.37	1.56	0.04	1.48	1.40
DVU2202	transglycosylase SLT domain/bacterial extracellular solute-b		1.44	1.44	1.25	0.03	1.62	1.69
DVU2203	endoribonuclease, L-PSP family (TIGR)	tnaA	0.56	0.67	0.96	0.03	1.02	0.92
DVU2204	tryptophanase (TIGR)	mtr	1.13	1.00	0.78	0.03	1.09	1.30
DVU2205	tryptophan-specific transport protein (TIGR)		1.31	1.04	1.00	0.03	1.16	1.35
DVU2206	conserved hypothetical protein (TIGR)		0.71	0.70	0.65	0.02	0.90	0.84
DVU2207	hypothetical protein (TIGR)		0.84	0.63	0.71	0.01	0.83	0.70
DVU2208	hypothetical protein (TIGR)		0.32	0.33	0.76	0.00	0.28	0.31
DVU2209	conserved hypothetical protein (TIGR)		1.07	0.92	1.56	0.01	1.50	2.22
DVU2210	TPR domain protein (TIGR)		1.22	1.03	0.94	0.02	1.82	2.55
DVU2211	hypothetical protein (TIGR)		0.88	0.83	1.05	0.02	0.92	1.27
DVU2212	conserved hypothetical protein (TIGR)		1.10	1.31	0.80	0.02	1.22	1.17
DVU2213	nuclease domain protein (TIGR)		1.13	0.92	1.44	0.04	1.09	1.10
DVU2214	hypothetical protein (TIGR)		1.03	0.79	1.17	0.04	1.19	1.19
DVU2215	RNA-binding protein (TIGR)	infA-2	0.02	0.06	0.15	0.00	0.09	0.16
DVU2216	translation initiation factor IF-1 (TIGR)		0.38	0.50	0.90	0.00	0.78	0.51
DVU2217	acetyltransferase, GNAT family (TIGR)		0.81	0.92	0.40	0.02	0.89	0.88
DVU2218	GTP-binding protein, putative (TIGR)		0.69	0.70	0.71	0.01	0.64	0.85
DVU2220	conserved hypothetical protein (TIGR)		0.66	0.92	0.93	0.04	1.21	1.11
DVU2221	hypothetical protein (TIGR)	ssb	0.08	0.26	0.32	0.00	0.49	0.62
DVU2222	single-strand binding protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2223	hypothetical protein (TIGR)		0.50	0.42	0.56	0.03	0.72	0.57
DVU2224	hypothetical protein (TIGR)		0.13	0.04	0.12	0.00	0.02	0.01
DVU2225	acetyl-CoA carboxylase, carboxyl transferase, alph	accC	0.02	0.02	0.21	0.01	0.00	0.00
DVU2226	acetyl-CoA carboxylase, biotin carboxylase, putative (TIGR)		0.04	0.04	0.25	0.00	0.00	0.01
DVU2227	hypothetical protein (TIGR)		2.54	1.82	1.94	0.05	2.01	2.10
DVU2228	motB protein, putative (TIGR)	motA-2	0.75	0.87	1.01	0.01	0.84	1.11
DVU2229	chemotaxis protein MotA (TIGR)	deoD	1.05	0.83	0.86	0.02	1.10	1.05
DVU2230	purine nucleoside phosphorylase (TIGR)	typA	1.34	0.98	1.08	0.02	1.24	1.31
DVU2231	GTP-binding protein TypA (TIGR)		0.90	0.97	1.10	0.03	1.12	1.11
DVU2232	hypothetical protein (TIGR)		0.88	0.81	1.15	0.03	1.18	1.12
DVU2233	conserved hypothetical protein (TIGR)		0.78	1.12	1.17	0.01	1.13	1.00
DVU2234	conserved hypothetical protein TIGR00275 (TIGR)		0.63	0.88	0.86	0.01	1.07	1.08
DVU2235	conserved hypothetical protein (TIGR)		0.42	0.75	0.83	0.00	0.53	0.74
DVU2236	hypothetical protein (TIGR)	cbiB	1.08	1.03	1.88	0.00	0.74	0.53
DVU2237	cobalamin biosynthesis protein CobD, putative (TIGR)		1.07	1.11	1.00	0.02	0.73	0.54
DVU2238	RNA methyltransferase, TrmH family (TIGR)		1.03	0.91	0.84	0.02	0.90	1.01
DVU2239	glycosyl hydrolase, family 3 (TIGR)		0.81	0.99	0.81	0.01	1.02	0.96
DVU2240	hydantoinase/oxoprolinase family protein (TIGR)	pdxA	0.91	1.08	1.07	0.02	1.19	1.21
DVU2241	pyridoxal phosphate biosynthetic protein PdxA (TIGR)		1.54	1.49	1.83	0.04	1.83	1.74
DVU2242	asparaginase family protein (TIGR)	glgB	0.90	1.02	0.77	0.01	1.09	1.04
DVU2243	1,4-alpha-glucan branching enzyme (TIGR)	glgA	0.90	1.04	0.69	0.01	1.03	1.02
DVU2244	glycogen synthase (TIGR)		1.23	1.37	1.47	0.03	1.65	1.64

DVU2245	mutT/nudix family protein (TIGR)		0.75	1.09	0.79	0.02	1.16	1.20
DVU2246	S1 RNA binding domain protein (TIGR)	ahpC	1.10	1.05	0.82	0.03	1.20	1.08
DVU2247	alkyl hydroperoxide reductase C (Dmitry Rodionov)		0.70	1.05	0.91	0.02	1.12	1.25
DVU2250	AMP-binding protein (TIGR)		0.79	1.02	0.90	0.02	1.22	1.20
DVU2251	DNA-binding protein (TIGR)	dnaA-2	0.59	0.94	0.59	0.02	0.92	0.84
DVU2252	chromosomal replication initiator protein DnaA (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2253	hypothetical protein (TIGR)	thyX	0.07	0.04	0.00	0.00	0.10	0.31
DVU2254	thymidylate synthase ThyX (TIGR)	ruvB	0.00	0.05	0.04	0.00	0.01	0.00
DVU2255	Holliday junction DNA helicase RuvB (TIGR)	ruvA	0.45	0.64	0.60	0.01	0.19	0.14
DVU2256	Holliday junction DNA helicase RuvA (TIGR)		0.28	0.43	0.25	0.01	0.12	0.04
DVU2257	hypothetical protein (TIGR)	ruvC	1.31	2.28	1.31	0.06	1.80	1.76
DVU2258	crossover junction endodeoxyribonuclease RuvC (TIGR)		0.93	1.09	1.03	0.02	0.62	0.52
DVU2259	conserved hypothetical protein TIGR01033 (TIGR)	rrmJ	0.37	0.40	0.74	0.02	0.16	0.45
DVU2260	ribosomal RNA large subunit methyltransferase J (TIGR)		0.60	0.86	0.86	0.01	0.88	0.94
DVU2261	hypothetical protein (TIGR)		1.48	1.49	1.52	0.04	1.54	1.72
DVU2263	outer membrane autotransporter barrel domain protein (TI		1.72	1.71	1.63	0.03	1.81	2.01
DVU2264	hypothetical protein (TIGR)		0.53	0.70	0.15	0.00	0.57	0.89
DVU2267	hypothetical protein (TIGR)		0.58	1.02	1.12	0.02	0.77	0.99
DVU2268	hypothetical protein (TIGR)		1.13	1.31	1.91	0.02	1.45	1.47
DVU2269	hypothetical protein (TIGR)		1.25	0.90	1.42	0.06	1.13	1.53
DVU2270	hypothetical protein (TIGR)	pflA	0.48	0.96	0.74	0.00	0.46	0.75
DVU2271	pyruvate formate-lyase activating enzyme, putative (TIGR)		1.46	1.69	1.35	0.03	1.58	1.85
DVU2272	formate acetyltransferase, putative (TIGR)		0.98	1.13	1.00	0.02	1.08	1.21
DVU2274	hypothetical protein (TIGR)	rocR	0.46	0.74	0.19	0.00	0.93	1.13
DVU2275	sigma-54 dependent transcriptional regulator (TIGR)		0.90	1.13	0.97	0.03	1.11	1.26
DVU2276	membrane protein, putative (TIGR)		1.17	1.30	1.10	0.04	1.73	1.51
DVU2277	hypothetical protein (TIGR)		1.28	1.34	1.34	0.04	1.26	1.35
DVU2278	membrane protein, putative (TIGR)		0.98	1.15	1.20	0.03	1.23	1.33
DVU2279	hypothetical protein (TIGR)		0.10	0.07	0.16	0.00	0.04	0.06
DVU2280	amino acid permease family protein (TIGR)	torS	1.33	1.29	1.61	0.04	1.31	1.34
DVU2281	sensor histidine kinase/response regulator (TIGR)		1.01	0.99	0.92	0.01	0.93	1.03
DVU2282	hypothetical protein (TIGR)		1.00	1.19	0.97	0.03	1.36	1.22
DVU2283	hypothetical protein (TIGR)		0.77	0.95	1.57	0.00	1.15	1.30
DVU2284	hypothetical protein (TIGR)		1.53	1.24	0.82	0.02	1.18	1.16
DVU2285	L-lactate permease family protein (TIGR)		0.58	0.51	0.77	0.02	0.69	0.59
DVU2286	hydrogenase, CooM subunit, putative (TIGR)		0.14	0.26	0.42	0.01	0.19	0.26
DVU2287	hydrogenase, CooK subunit, selenocysteine-containing, puta		0.13	0.14	0.29	0.01	0.13	0.17
DVU2288	hydrogenase, CooL subunit, putative (TIGR)	b2488	0.09	0.04	0.24	0.00	0.10	0.09
DVU2289	hydrogenase, CooX subunit, putative (TIGR)		0.09	0.18	0.35	0.01	0.16	0.22
DVU2290	hydrogenase, CooU subunit, putative (TIGR)		0.14	0.12	0.33	0.00	0.14	0.13
DVU2291	carbon monoxide-induced hydrogenase CooH, put	hypA	0.10	0.10	0.24	0.00	0.09	0.13
DVU2292	hydrogenase nickel insertion protein HypA (TIGR)	cooF	0.21	0.10	0.42	0.01	0.29	0.31
DVU2293	iron-sulfur protein CooF (TIGR)		0.05	0.18	0.21	0.02	0.14	0.16
DVU2294	femAB family protein (TIGR)		1.17	0.93	1.07	0.02	1.03	0.96
DVU2295	methyl-accepting chemotaxis protein (TIGR)	mtgA	0.96	1.03	1.03	0.03	1.08	0.97
DVU2296	monofunctional biosynthetic peptidoglycan transglycosylase		0.86	0.94	0.66	0.02	0.93	0.88
DVU2297	glycine/betaine/L-proline ABC transporter, peripla	opuBB	0.60	0.58	0.78	0.02	0.64	0.72
DVU2298	glycine/betaine/L-proline ABC transporter, permea	proV	0.65	1.03	0.75	0.02	1.00	0.89
DVU2299	glycine/betaine/L-proline ABC transporter, ATP binding prot		0.79	0.86	1.05	0.02	1.10	0.95
DVU2300	hypothetical protein (TIGR)		0.61	0.52	0.54	0.03	0.60	0.46
DVU2301	lipoprotein, putative (TIGR)		0.43	1.05	1.48	0.00	0.74	1.06
DVU2302	glutathione-regulated potassium-efflux system protein KefB		1.60	1.57	1.33	0.03	1.56	1.54
DVU2303	conserved domain protein (TIGR)		0.71	0.84	1.37	0.04	0.61	0.79
DVU2305	conserved hypothetical protein (TIGR)		0.44	0.32	0.13	0.00	0.28	0.41
DVU2306	phosphate transporter family protein (TIGR)		0.46	0.40	0.63	0.01	0.32	0.41
DVU2307	C4-type zinc finger protein, DksA/TraR family (TIGR)		1.46	1.01	1.28	0.03	0.96	0.73
DVU2308	conserved hypothetical protein TIGR00022 (TIGR)		0.62	0.89	0.72	0.02	0.85	0.73
DVU2309	methyl-accepting chemotaxis protein, putative (TIGR)		0.84	0.90	0.96	0.02	0.94	0.92
DVU2310	metallo-beta-lactamase family protein (TIGR)		1.00	1.03	0.77	0.02	1.04	1.13
DVU2312	hypothetical protein (TIGR)	pgl	1.08	0.87	0.97	0.04	1.06	1.18
DVU2313	6-phosphogluconolactonase (TIGR)		1.51	1.72	1.86	0.03	1.74	1.79
DVU2315	conserved hypothetical protein TIGR00257 (TIGR)	topB	0.88	1.01	0.93	0.02	1.02	1.06
DVU2316	DNA topoisomerase III (TIGR)		1.22	1.24	1.27	0.03	1.23	1.26
DVU2317	methyl-accepting chemotaxis protein, putative (TI	rbr2	1.19	1.36	1.23	0.02	1.29	1.35
DVU2318	rubrerythrin, putative (TIGR)		0.75	0.92	0.79	0.03	1.03	0.95
DVU2319	transcriptional regulator domain protein (TIGR)		0.86	1.15	1.27	2.45	1.08	1.00
DVU2320	3-octaprenyl-4-hydroxybenzoate carboxy-lyase family prote		0.33	0.23	0.76	0.02	0.08	0.11

DVU2322	UTP--glucose-1-phosphate uridylyltransferase, putative (TIG		0.85	1.04	1.11	0.02	1.16	1.17
DVU2323	hypothetical protein (TIGR)		0.39	0.64	0.74	0.01	0.67	0.52
DVU2324	copper-translocating P-type ATPase (TIGR)	merP	1.03	1.15	1.17	0.02	1.14	1.08
DVU2325	mercuric transport protein periplasmic component (TIGR)		1.37	1.35	0.84	0.02	1.36	1.11
DVU2326	conserved domain protein (TIGR)	hypA	1.36	0.95	1.16	0.02	1.19	1.19
DVU2328	hydrogenase nickel insertion protein HypA, putati	hypB	0.66	0.55	0.68	0.01	0.73	0.79
DVU2329	hydrogenase accessory protein HypB (TIGR)	E.coliMin	0.14	0.19	0.55	0.02	0.19	0.25
DVU2330	MRP family protein (TIGR)		0.56	0.66	1.07	0.02	0.89	1.04
DVU2331	Smr family protein (TIGR)	proC	0.87	0.94	0.52	0.01	0.92	0.87
DVU2332	pyrroline-5-carboxylate reductase (TIGR)	ndk	0.46	0.73	0.60	0.00	0.02	0.01
DVU2333	nucleoside diphosphate kinase (TIGR)		1.42	1.40	1.42	0.05	1.32	1.42
DVU2335	conserved domain protein (TIGR)		0.64	1.03	0.77	0.03	1.01	0.90
DVU2336	carboxyl-terminal protease (TIGR)		1.81	1.89	2.48	0.06	1.38	0.85
DVU2337	peptidase, M23/M37 family (TIGR)		1.44	1.61	1.67	0.04	1.58	1.47
DVU2338	DNA repair protein, HhH-GPD family (TIGR)	prmA	1.12	1.07	0.92	0.02	1.06	1.06
DVU2339	ribosomal protein L11 methyltransferase, putative (TIGR)		0.63	0.93	1.27	0.02	1.07	1.00
DVU2340	amino acid ABC transporter, permease protein, His/Glu/Gln,		1.03	0.87	0.63	0.03	3.03	2.30
DVU2341	amino acid ABC transproter, permease protein, His/Glu/Gln,		0.74	0.99	0.67	0.02	3.43	3.25
DVU2342	amino acid ABC transporter, periplasmic amino ac	glnQ	2.17	2.13	1.58	0.03	4.56	4.71
DVU2343	amino acid ABC transporter, ATP-binding protein (TIGR)		1.26	1.52	1.56	0.04	4.78	3.30
DVU2345	hypothetical protein (TIGR)	argD	0.53	0.84	0.70	0.02	0.73	0.49
DVU2347	acetylornithine aminotransferase (TIGR)	dut	1.33	1.32	0.02	0.01	0.00	0.00
DVU2348	deoxyuridine 5-triphosphate nucleotidohydrolase (TIGR)		0.34	0.43	0.76	0.01	0.37	0.25
DVU2349	carbohydrate phosphorylase family protein (TIGR)	gid	1.06	1.15	1.27	0.03	1.21	1.21
DVU2350	gid protein (TIGR)		0.80	1.11	1.08	0.02	1.15	0.99
DVU2351	hypothetical protein (TIGR)		0.53	0.71	0.92	0.01	0.64	0.75
DVU2352	glycosyl transferase, group 2 family protein (TIGR)		1.38	1.46	1.31	0.03	1.65	1.55
DVU2353	glycosyl transferase, group 2 family protein (TIGR)		1.34	1.26	1.36	0.03	1.44	1.51
DVU2354	glycosyl transferase, group 2 family protein (TIGR)	trmH	1.54	1.46	1.40	0.04	1.57	1.58
DVU2355	tRNA (guanosine-2-O-)-methyltransferase (TIGR)		1.36	1.20	1.94	0.03	1.25	1.50
DVU2356	membrane protein, putative (TIGR)		0.76	1.03	0.88	0.02	1.21	1.10
DVU2357	HD domain protein (TIGR)		0.74	0.81	0.57	0.01	0.99	0.86
DVU2359	sigma-54 dependent transcriptional regulator (TIGR)		0.78	0.71	0.86	0.02	0.94	0.91
DVU2360	oxidoreductase, FAD/NAD-binding family (TIGR)	thiE-2	0.71	1.09	0.98	0.03	1.27	1.34
DVU2362	thiamine-phosphate pyrophosphorylase (TIGR)	thiM	1.24	0.94	1.10	0.01	1.18	1.01
DVU2363	hydroxyethylthiazole kinase (TIGR)		0.97	0.99	0.73	0.03	0.97	1.06
DVU2364	aminotransferase, classes I and II (TIGR)		1.00	1.18	1.23	0.04	1.42	1.25
DVU2365	conserved hypothetical protein (TIGR)	lpxA	0.00	0.00	0.00	0.00	0.00	0.00
DVU2367	acyl-(acyl-carrier-protein)--UDP-N-acetylglucosam	fabZ	0.00	0.00	0.07	0.00	0.00	0.01
DVU2368	beta-hydroxyacyl-(acyl-carrier-protein) dehydratas	lpxD	0.00	0.00	0.04	0.01	0.00	0.01
DVU2369	UDP-3-O-(R-3-hydroxymyristoyl)-glucosamine N-acyltransfe		0.02	0.01	0.12	0.00	0.01	0.00
DVU2370	outer membrane protein OmpH, putative (TIGR)	amiA	0.00	0.00	0.06	0.01	0.03	0.01
DVU2371	N-acetylmuramoyl-L-alanine amidase, putative (TIGR)		0.90	0.57	1.40	0.03	0.59	0.53
DVU2372	hypothetical protein (TIGR)		1.71	1.47	2.71	0.03	1.90	1.97
DVU2373	outer membrane protein, OMP85 family (TIGR)	lolD	0.01	0.00	0.12	0.00	0.00	0.00
DVU2374	lipoprotein releasing system, ATP-binding protein (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2375	lipoprotein releasing system, permease protein (TI	lysS	0.00	0.01	0.06	0.00	0.00	0.00
DVU2376	lysyl-tRNA synthetase (TIGR)		0.02	0.01	0.03	0.00	0.00	0.00
DVU2377	hypothetical protein (TIGR)	foxR	1.30	0.92	1.15	0.04	0.93	1.94
DVU2378	transcriptional regulator, AraC family (TIGR)	pqqL	1.11	1.38	1.62	0.04	1.41	1.45
DVU2379	peptidase, M16 family, putative (TIGR)	atpX	0.86	1.02	1.01	0.02	1.10	1.21
DVU2380	ABC transporter, ATP-binding protein (TIGR)		1.06	1.35	1.02	0.04	1.58	1.52
DVU2381	conserved hypothetical protein (TIGR)		1.36	1.25	1.49	0.04	1.48	1.46
DVU2382	conserved domain protein (TIGR)		1.43	1.45	1.57	0.03	1.72	1.85
DVU2383	tonB dependent receptor domain protein (TIGR)		1.07	1.16	1.28	0.03	1.23	1.41
DVU2384	ABC transporter, periplasmic substrate-binding protein (TIGI		0.99	0.84	0.74	0.02	1.00	1.17
DVU2385	ABC transporter, permease protein (TIGR)	oppC	1.14	1.05	0.91	0.02	1.21	1.24
DVU2386	ABC transporter, permease protein (TIGR)		0.76	0.96	1.03	0.02	1.18	1.39
DVU2387	ABC transporter, ATP-binding protein (TIGR)	tolQ-1	1.29	1.53	1.09	0.03	1.81	1.88
DVU2388	tolQ protein (TIGR)	tolR	1.43	1.63	1.13	0.04	1.61	1.79
DVU2389	biopolymer transport protein, ExbD/TolR family (TIGR)		0.81	0.86	0.99	0.02	0.74	1.07
DVU2390	TonB domain protein (TIGR)		1.09	1.22	1.06	0.04	1.30	1.39
DVU2391	hypothetical protein (TIGR)		0.12	0.56	0.66	0.00	0.21	0.38
DVU2392	type III secretion chaperone, CesT family (TIGR)	ntrC1	0.30	0.54	0.38	0.01	0.76	0.78
DVU2394	sigma-54 dependent transcriptional regulator/response regu		1.32	1.50	1.54	0.05	0.93	1.03
DVU2395	sensor histidine kinase (TIGR)	adh	0.81	1.35	1.66	0.03	0.91	0.94
DVU2396	alcohol dehydrogenase (Chris Hemme)		0.97	1.11	1.58	0.02	0.93	0.90

DVU2397	hypothetical protein (TIGR)		0.59	0.52	0.42	0.01	1.25	1.30
DVU2398	conserved hypothetical protein (TIGR)		0.42	0.96	0.65	0.03	1.54	1.40
DVU2399	hydrogenase, putative (TIGR)		1.37	1.28	1.03	0.03	1.25	1.24
DVU2400	hydrogenase, putative (TIGR)		0.77	0.75	0.73	0.02	0.79	0.61
DVU2401	hydrogenase, iron-sulfur cluster-binding subunit, p	hdrA	1.06	0.87	0.58	0.02	0.86	0.69
DVU2402	heterodisulfide reductase, A subunit (TIGR)	hdrB	0.99	1.12	0.71	0.02	0.94	0.91
DVU2403	heterodisulfide reductase, B subunit (TIGR)	hdrC	1.20	1.18	0.87	0.02	1.01	0.94
DVU2404	heterodisulfide reductase, C subunit (TIGR)		1.04	0.52	0.24	0.00	0.86	0.74
DVU2405	alcohol dehydrogenase, iron-containing (TIGR)		1.55	1.27	1.20	0.03	1.38	1.63
DVU2407	conserved hypothetical protein (TIGR)		1.43	1.54	1.45	0.04	1.84	1.96
DVU2408	hypothetical protein (TIGR)		0.64	1.42	1.69	0.03	0.98	1.31
DVU2409	bacterial extracellular solute-binding proteins, fam	sodB	0.97	1.11	0.93	0.02	1.15	1.24
DVU2410	superoxide dismutase, Fe (TIGR)		0.95	1.20	0.69	0.02	1.28	1.36
DVU2411	EF hand domain protein (TIGR)		0.65	0.98	0.57	0.00	1.09	0.99
DVU2412	sensory box histidine kinase (TIGR)		1.04	1.38	1.09	0.05	1.53	1.37
DVU2413	radical SAM domain protein (TIGR)		1.15	1.31	1.00	0.02	1.46	1.41
DVU2414	hypothetical protein (TIGR)		1.07	1.18	1.10	0.02	1.25	1.19
DVU2415	hypothetical protein (TIGR)		1.02	1.34	0.97	0.01	1.27	1.19
DVU2416	conserved hypothetical protein (TIGR)		0.79	0.88	0.99	0.01	1.15	1.05
DVU2417	SlyX protein (TIGR)		0.65	0.94	1.08	0.01	1.05	1.04
DVU2418	vanZ-like family protein (TIGR)		0.63	0.44	0.68	0.02	0.70	0.69
DVU2419	conserved domain protein (TIGR)		1.04	0.97	0.83	0.02	1.29	1.11
DVU2420	conserved hypothetical protein (TIGR)	dmpI	0.28	0.61	0.74	0.01	0.80	0.65
DVU2421	4-oxalocrotonate tautomerase family protein (TIGR)		1.06	1.24	1.73	0.03	1.10	1.31
DVU2422	nitroreductase family protein (TIGR)		1.08	1.31	1.03	0.02	1.34	1.33
DVU2423	transcriptional regulator, putative (TIGR)		0.74	0.95	1.11	0.03	0.70	0.83
DVU2424	membrane protein, putative (TIGR)	rarD	0.91	1.23	1.32	0.03	1.17	1.39
DVU2425	rarD protein (TIGR)		0.77	1.00	0.87	0.00	1.16	1.00
DVU2427	hypothetical protein (TIGR)		1.04	1.09	0.79	0.02	1.37	1.16
DVU2428	lipoprotein, putative (TIGR)		1.00	1.28	1.07	0.01	1.46	1.39
DVU2429	hypothetical protein (TIGR)		0.02	0.36	0.00	0.00	0.06	0.13
DVU2430	RNA-binding protein (TIGR)		0.35	0.60	0.56	0.02	0.70	0.64
DVU2431	hypothetical protein (TIGR)		0.48	1.40	1.40	0.10	1.55	2.14
DVU2432	sensory box/GGDEF domain/EAL domain protein (TIGR)		0.84	1.17	0.96	0.02	1.20	1.21
DVU2434	hypothetical protein (TIGR)	corA	1.11	1.53	1.03	0.04	1.63	1.51
DVU2435	transporter, CorA family (TIGR)		0.78	0.78	0.65	0.01	0.90	0.81
DVU2436	conserved hypothetical protein (TIGR)		0.67	0.67	0.60	0.03	0.83	0.70
DVU2437	ABC transporter, permease protein (TIGR)		0.66	1.11	0.84	0.02	1.11	1.07
DVU2439	efflux transporter, RND family, MFP subunit (TIGR)		0.53	0.67	0.77	0.02	0.85	0.81
DVU2440	hypothetical protein (TIGR)	hspC	0.66	1.21	0.91	0.01	1.09	1.10
DVU2441	heat shock protein, Hsp20 family (TIGR)		0.17	0.02	0.00	0.00	0.10	0.07
DVU2442	heat shock protein, Hsp20 family (TIGR)		0.57	0.89	0.53	0.02	0.94	0.81
DVU2443	conserved hypothetical protein (TIGR)	flaB3	0.66	0.75	0.56	0.02	0.88	0.64
DVU2444	flagellin (TIGR)	panB	0.68	0.80	0.72	0.01	0.78	0.87
DVU2446	3-methyl-2-oxobutanoate hydroxymethyltransferase (TIGR)		1.22	1.33	1.02	0.04	1.51	1.30
DVU2447	hypothetical protein (TIGR)	panC	1.15	1.09	1.04	0.01	0.98	0.90
DVU2448	pantoate--beta-alanine ligase (TIGR)	metK	1.31	1.79	1.44	0.02	1.72	1.46
DVU2449	S-adenosylmethionine synthetase (TIGR)		0.00	0.00	0.01	0.00	0.00	0.00
DVU2450	conserved hypothetical protein (TIGR)		0.09	0.35	0.20	0.01	0.43	0.29
DVU2451	L-lactate permease family protein (TIGR)		0.53	0.56	0.64	0.02	0.59	0.51
DVU2454	hypothetical protein (TIGR)		1.09	0.63	0.67	0.03	0.73	0.81
DVU2455	NAD-dependent epimerase/dehydratase family protein (TIG		0.36	0.43	0.31	0.01	0.50	0.52
DVU2459	hypothetical protein (TIGR)		0.28	0.22	0.49	0.01	0.53	0.51
DVU2460	hypothetical protein (TIGR)	appB	0.32	0.34	0.63	0.03	0.51	0.44
DVU2461	oligopeptide ABC transporter, permease protein (TIGR)		1.12	1.58	1.06	0.03	1.11	1.10
DVU2462	oligopeptide ABC transporter, permease protein (T	recN	0.68	0.82	0.47	0.01	0.86	0.82
DVU2463	DNA repair protein RecN (TIGR)		0.95	1.38	1.11	0.03	1.35	1.24
DVU2464	hypothetical protein (TIGR)		0.52	0.98	0.77	0.02	0.96	0.81
DVU2466	flocculin repeat domain (TIGR)	rnr	0.81	1.20	0.94	0.04	1.06	0.97
DVU2467	ribonuclease R (TIGR)	lpxK	0.61	0.84	0.80	0.01	0.84	0.81
DVU2468	tetraacyldisaccharide 4-kinase (TIGR)	b0786	0.11	0.08	0.18	0.01	0.01	0.01
DVU2470	membrane protein, putaive (TIGR)		0.65	0.73	0.44	0.04	0.71	0.77
DVU2471	oxidoreductase, selenocysteine-containing (TIGR)		0.96	1.39	0.98	0.03	1.20	1.28
DVU2472	conserved hypothetical protein (TIGR)		0.65	0.87	0.84	0.02	0.94	0.93
DVU2473	hypothetical protein (TIGR)		0.84	1.10	0.64	0.04	0.98	0.91
DVU2474	hypothetical protein (TIGR)		0.32	0.64	0.67	0.01	0.47	0.51
DVU2475	oxidoreductase, NAD-binding, putative (TIGR)	gltA	0.61	1.09	0.78	0.01	0.87	0.82

DVU2476	glutamate synthase, small subunit (TIGR)	pstS	1.39	1.29	0.76	0.02	1.35	1.34
DVU2477	phosphate ABC transporter, periplasmic phosphat	pstC-2	0.75	0.89	0.73	0.02	1.05	0.85
DVU2478	phosphate ABC transporter, permease protein, pu	pstA-2	0.52	0.84	0.76	0.01	1.13	0.97
DVU2479	phosphate ABC transporter, permease protein, pu	fdoH	1.42	1.32	1.16	0.03	1.26	1.32
DVU2481	formate dehydrogenase, beta subunit, putative (TI	fdnG-2	0.87	1.26	1.29	0.04	1.33	1.43
DVU2482	formate dehydrogenase, alpha subunit, selenocysteine-cont		0.85	1.07	1.15	0.03	1.10	1.09
DVU2483	cytochrome c family protein (TIGR)		0.77	1.05	0.95	0.03	1.11	1.03
DVU2484	cytochrome c family protein (TIGR)		0.73	0.85	0.77	0.02	0.93	0.80
DVU2485	membrane protein, putative (TIGR)		0.97	1.22	0.73	0.03	1.24	1.06
DVU2486	acetyltransferase, GNAT family (TIGR)		1.93	1.75	2.05	0.03	1.77	1.73
DVU2487	hypothetical protein (TIGR)		1.15	1.28	0.93	0.02	1.28	1.22
DVU2489	hypothetical protein (TIGR)		1.53	1.71	1.61	0.03	1.57	1.90
DVU2490	Histidinol phosphatase (Natalia Ivanova)		0.03	0.06	0.17	0.00	0.00	0.00
DVU2491	ABC transporter, ATP-binding protein (TIGR)	trpF-2	0.90	1.10	1.08	0.02	1.11	1.12
DVU2492	N-(5-phosphoribosyl)anthranilate isomerase (TIGR	b0992	0.91	1.01	0.78	0.03	0.89	0.97
DVU2493	iron-sulfur cluster-binding protein (TIGR)		0.74	1.13	1.05	0.02	1.11	1.10
DVU2494	peptidase, M48 family (TIGR)		0.62	0.75	0.73	0.01	0.70	0.73
DVU2495	thioesterase family protein (TIGR)		0.35	0.61	0.49	0.02	0.55	0.46
DVU2496	lipoprotein, putative (TIGR)		0.34	0.75	1.08	0.02	1.13	0.67
DVU2497	lipoprotein, putative (TIGR)		0.52	0.90	0.84	0.01	1.09	1.11
DVU2498	hypothetical protein (TIGR)	ftsZ	0.10	0.27	0.15	0.00	0.17	0.15
DVU2499	cell division protein FtsZ (TIGR)	ftsA	0.01	0.02	0.14	0.00	0.00	0.01
DVU2500	cell division protein FtsA (TIGR)		0.02	0.04	1.02	0.02	0.02	0.08
DVU2501	cell division protein FtsQ, putative (TIGR)	murB	0.02	0.10	0.88	0.01	0.07	0.08
DVU2502	UDP-N-acetylenolpyruvoylglucosamine reductase	murC	0.00	0.00	0.00	0.00	0.00	0.00
DVU2503	UDP-N-acetylmuramate--alanine ligase (TIGR)	murG	0.00	0.01	0.28	0.00	0.00	0.00
DVU2504	UDP-N-acetylglucosamine--N-acetylmuramyl-(pen	ftsW	0.00	0.02	0.32	0.00	0.01	0.01
DVU2505	cell cycle protein, FtsW/RodA/SpoVE family (TIGR)	murD	0.06	0.10	1.35	0.01	0.09	0.15
DVU2506	UDP-N-acetylmuramoylalanine--D-glutamate ligas	mraY	0.04	0.01	0.08	0.00	0.01	0.00
DVU2507	phospho-N-acetylmuramoyl-pentapeptide-transfe	murF	0.00	0.01	0.14	0.01	0.00	0.00
DVU2508	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-dian	murE	0.01	0.00	0.09	0.00	0.00	0.00
DVU2509	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopim		0.01	0.02	0.24	0.01	0.00	0.01
DVU2510	penicillin-binding protein (TIGR)		0.04	0.05	0.67	0.01	0.03	0.07
DVU2511	hypothetical protein (TIGR)	mraW	0.69	0.91	2.17	0.06	1.18	1.63
DVU2512	S-adenosyl-methyltransferase MraW (TIGR)	mraZ	1.00	1.43	1.54	0.04	1.96	2.25
DVU2513	conserved hypothetical protein TIGR00242 (TIGR)	pyk	0.61	0.82	0.63	0.03	0.90	0.93
DVU2514	pyruvate kinase (TIGR)		0.90	0.95	1.07	0.03	1.05	1.00
DVU2515	HD domain protein (TIGR)		1.04	1.01	0.94	7.71	1.08	1.05
DVU2516	CBS domain protein (TIGR)		1.32	1.53	1.76	0.05	2.05	1.73
DVU2517	conserved hypothetical protein (TIGR)	rplM	0.75	0.74	0.52	0.01	0.83	0.89
DVU2518	ribosomal protein L13 (TIGR)	rpsI	0.00	0.00	0.00	0.00	0.01	0.00
DVU2519	ribosomal protein S9 (TIGR)	aroK-2	0.00	0.00	0.00	0.00	0.00	0.00
DVU2521	shikimate kinase (TIGR)		0.03	0.11	0.22	0.01	0.05	0.04
DVU2522	hypothetical protein (TIGR)		1.13	1.55	1.97	0.03	1.86	1.77
DVU2523	lipoprotein, putative (TIGR)		0.55	0.76	0.23	0.01	0.70	0.67
DVU2524	cytochrome c3, putative (TIGR)	hynB-2	0.95	1.21	1.11	0.01	1.20	1.06
DVU2525	periplasmic [NiFe] hydrogenase, small subunit, iso	hynA-2	1.14	1.07	0.76	0.02	1.16	1.06
DVU2526	periplasmic [NiFe] hydrogenase, large subunit, isozyme 2 (TI		0.73	0.77	0.94	0.02	0.91	1.02
DVU2527	transcriptional regulator, putative (TIGR)		0.32	0.11	0.00	0.01	0.25	0.26
DVU2528	hypothetical protein (TIGR)	pgk	0.14	0.27	0.10	0.00	0.18	0.27
DVU2529	phosphoglycerate kinase (TIGR)	tkt	0.04	0.03	0.05	0.00	0.00	0.00
DVU2530	transketolase (TIGR)	rpe	0.05	0.01	0.09	0.00	0.00	0.00
DVU2531	ribulose-phosphate 3-epimerase (TIGR)		0.05	0.03	0.25	0.00	0.00	0.00
DVU2532	transcriptional regulator, MerR family (TIGR)	pheT	0.68	0.98	0.96	0.02	0.71	0.71
DVU2533	phenylalanyl-tRNA synthetase, beta subunit (TIGR)	pheS	0.01	0.01	0.04	0.00	0.00	0.00
DVU2534	phenylalanyl-tRNA synthetase, alpha subunit (TIGF	rplT	0.01	0.00	0.04	0.01	0.00	0.01
DVU2535	ribosomal protein L20 (TIGR)	rpmI	0.00	0.00	0.09	0.00	0.00	0.00
DVU2536	ribosomal protein L35 (TIGR)	infC	0.04	0.03	0.37	0.00	0.13	0.01
DVU2537	translation initiation factor IF-3 (TIGR)	thrS	0.00	0.00	0.00	0.00	0.00	0.00
DVU2538	threonyl-tRNA synthetase (TIGR)		0.01	0.01	0.04	0.00	0.00	0.00
DVU2539	hypothetical protein (TIGR)		1.45	1.36	1.04	0.02	1.06	1.31
DVU2540	lyase, putative (TIGR)		1.18	1.22	1.21	0.03	1.03	1.07
DVU2541	CoA-substrate-specific enzyme activase, putative (	b0873	1.37	1.70	1.76	0.04	1.46	1.65
DVU2543	hybrid cluster protein (TIGR)		0.86	1.16	0.98	0.03	1.09	1.27
DVU2544	iron-sulfur cluster-binding protein (TIGR)		1.37	1.52	1.22	0.02	1.44	1.53
DVU2545	alcohol dehydrogenase, iron-containing (TIGR)		1.33	1.30	0.98	0.05	1.30	1.25
DVU2546	sensory box histidine kinase (TIGR)		0.80	0.74	0.75	0.01	0.89	0.84

DVU2547	transcriptional regulator, putative (TIGR)	acpD	1.76	1.42	1.38	0.03	2.00	1.59
DVU2548	acyl carrier protein phosphodiesterase (TIGR)		1.04	1.30	0.94	0.06	1.06	1.27
DVU2549	hypothetical protein (TIGR)		2.35	3.22	3.31	0.07	3.62	3.32
DVU2550	hypothetical protein (TIGR)		1.20	1.05	1.25	0.03	1.13	1.15
DVU2551	HD domain protein (TIGR)	gltX-2	0.98	1.05	1.03	0.02	1.04	1.10
DVU2552	glutamyl-tRNA synthetase (TIGR)	nifU-3	0.01	0.00	0.10	0.00	0.00	0.00
DVU2553	NifU family protein (TIGR)		0.41	0.65	0.90	0.01	0.65	0.93
DVU2554	conserved hypothetical protein (TIGR)		1.38	1.54	1.75	0.03	1.66	1.51
DVU2555	MATE efflux family protein (TIGR)		0.77	1.15	0.78	0.02	1.03	1.06
DVU2556	hypothetical protein (TIGR)	birA	0.74	0.95	1.33	0.03	1.03	0.86
DVU2557	birA bifunctional protein (TIGR)	bioB	0.87	1.18	0.92	0.04	1.17	1.21
DVU2558	biotin synthase (Dmitry Rodionov)	bioA	1.04	1.31	1.51	0.03	1.46	1.46
DVU2559	adenosylmethionine--8-amino-7-oxononanoate aminotrans		1.10	1.21	0.98	0.02	1.24	1.28
DVU2560	conserved domain protein (TIGR)		1.02	1.52	1.55	0.03	1.36	1.21
DVU2561	oxidoreductase, short chain dehydrogenase/reduc	acpP	1.37	1.50	1.55	0.04	1.55	1.51
DVU2562	acyl carrier protein (TIGR)	fabF	0.70	0.97	1.06	0.04	1.08	1.09
DVU2563	beta-ketoacyl synthase, putative (TIGR)	bioF	1.10	1.39	1.30	0.03	1.53	1.30
DVU2564	8-amino-7-oxononanoate synthase (Dmitry Rodior	bioD	1.30	1.36	1.07	0.03	1.24	1.22
DVU2565	dethiobiotin synthetase (TIGR)	lysA-2	1.59	1.19	1.16	0.01	1.32	1.41
DVU2566	diaminopimelate decarboxylase (TIGR)	lysX	0.75	0.88	0.80	0.02	0.81	0.66
DVU2567	predicted transcriptional regulator for lysine biosy	cpsA	0.55	0.96	1.22	0.01	0.95	0.95
DVU2568	peptidase, M20/M25/M40 family (TIGR)	slyD	1.07	1.14	1.13	0.03	1.25	1.25
DVU2569	peptidyl-prolyl cis-trans isomerase, FKBP-type (TIG	pleD	0.64	0.59	0.74	0.01	0.83	1.03
DVU2570	GGDEF domain/HAMP domain protein (TIGR)	feoB	0.93	1.06	1.26	0.04	1.20	1.30
DVU2571	ferrous iron transport protein B (TIGR)	feoA	0.02	0.00	0.04	0.00	0.00	0.00
DVU2572	ferrous iron transport protein A (Dmitry Rodionov)		0.00	0.00	0.09	0.00	0.01	0.01
DVU2573	hypothetical protein (TIGR)	feoA	0.71	0.53	0.71	0.01	0.82	0.71
DVU2574	ferrous iron transporter component feoA (Dmitry Rodionov)		0.00	0.01	0.00	0.00	0.06	0.02
DVU2575	peptidase, M20/M25/M40 family (TIGR)		1.50	1.93	1.82	0.04	1.93	1.87
DVU2576	oligopeptide ABC transporter, ATP-binding protein (TIGR)		1.63	1.52	1.34	0.04	1.70	1.68
DVU2577	DNA-binding response regulator, LuxR family (TIGR)		0.97	0.81	0.67	0.00	0.71	0.68
DVU2578	response regulator (TIGR)		0.96	1.17	0.95	0.02	1.05	0.97
DVU2579	TPR domain protein (TIGR)		1.23	0.91	0.87	0.02	1.19	1.37
DVU2580	response regulator (TIGR)	cheYIV	1.33	1.31	1.22	0.03	1.00	0.77
DVU2581	response regulator (TIGR)		0.90	0.64	0.56	0.02	0.94	0.96
DVU2582	transcriptional regulator, TetR family (TIGR)		1.42	1.72	1.03	0.02	1.39	0.87
DVU2583	lipoprotein, putative (TIGR)	corA	1.64	1.86	1.42	0.01	1.66	1.47
DVU2584	transporter, CorA family (TIGR)		0.64	0.76	0.90	0.02	0.91	0.90
DVU2585	methyl-accepting chemotaxis protein (TIGR)		1.69	1.55	1.41	0.04	1.61	1.50
DVU2586	ABC transporter, ATP-binding protein (TIGR)	vicK	0.70	0.72	0.90	0.02	0.96	0.75
DVU2587	sensor histidine kinase (TIGR)	trcR	1.85	2.00	1.65	0.06	1.84	1.94
DVU2588	DNA-binding response regulator (TIGR)		1.16	1.27	1.15	0.03	1.30	1.32
DVU2590	sensory box protein (TIGR)		1.06	1.21	1.00	0.04	1.15	1.12
DVU2591	tail fiber assembly protein, putative (TIGR)		1.83	1.19	2.41	0.04	1.37	1.40
DVU2592	hypothetical protein (TIGR)		0.19	0.69	0.15	0.01	0.55	0.58
DVU2595	hypothetical protein (TIGR)		1.05	1.36	1.73	0.03	1.52	1.55
DVU2596	hypothetical protein (TIGR)		1.00	1.56	1.77	0.02	1.22	1.10
DVU2598	hypothetical protein (TIGR)		2.63	2.14	1.77	0.07	1.86	2.27
DVU2599	hypothetical protein (TIGR)		1.10	1.18	0.76	0.03	0.84	1.18
DVU2600	hypothetical protein (TIGR)		1.35	1.04	1.39	0.03	0.93	1.33
DVU2602	conserved domain protein (TIGR)		0.96	1.31	0.80	0.03	1.11	1.20
DVU2603	hypothetical protein (TIGR)		0.89	1.16	1.47	0.04	1.40	1.45
DVU2604	conserved hypothetical protein (TIGR)		1.27	1.42	1.25	0.04	1.44	1.43
DVU2605	hypothetical protein (TIGR)		0.93	1.41	1.55	0.04	1.54	1.42
DVU2606	hypothetical protein (TIGR)		1.60	1.28	1.34	0.03	1.18	1.15
DVU2607	hypothetical protein (TIGR)	motA-3	1.09	1.16	0.73	0.03	1.16	1.17
DVU2608	chemotaxis protein MotA (TIGR)		0.70	1.12	1.09	0.02	1.04	1.22
DVU2609	chemotaxis MotB protein, putative (TIGR)		0.38	0.76	0.67	0.02	0.83	0.68
DVU2610	hypothetical protein (TIGR)		1.21	0.89	1.05	0.04	1.28	0.97
DVU2611	conserved hypothetical protein (TIGR)		1.22	1.53	1.87	0.03	1.62	1.57
DVU2612	conserved hypothetical protein (TIGR)		0.74	0.92	0.98	0.04	1.06	1.26
DVU2613	hypothetical protein (TIGR)		1.38	1.47	2.07	0.05	0.90	1.57
DVU2614	hypothetical protein (TIGR)		0.72	1.06	1.59	0.04	0.52	0.97
DVU2615	bacterial extracellular solute-binding protein, family 3 (TIGR		2.37	1.85	2.02	0.04	2.15	2.06
DVU2616	sensory box histidine kinase/response regulator (TIGR)		1.05	1.21	1.24	0.03	1.17	1.19
DVU2617	sodium/calcium exchanger family protein (TIGR)		0.94	1.13	1.08	0.03	1.04	1.21
DVU2619	conserved hypothetical protein (TIGR)		0.95	1.17	1.22	0.01	1.46	1.21

DVU2620	conserved hypothetical protein (TIGR)		1.17	1.15	1.07	0.02	1.70	1.50
DVU2621	hypothetical protein (TIGR)		1.48	1.05	0.96	0.01	1.07	1.17
DVU2622	hypothetical protein (TIGR)		1.68	1.26	1.93	0.01	1.61	1.32
DVU2623	hypothetical protein (TIGR)		0.99	1.28	1.60	0.03	1.13	1.16
DVU2624	hypothetical protein (TIGR)		1.00	1.07	0.95	0.04	1.31	1.20
DVU2625	hypothetical protein (TIGR)		0.35	0.05	0.00	0.00	0.20	0.09
DVU2626	hypothetical protein (TIGR)		1.57	0.98	0.96	0.03	1.33	1.45
DVU2627	conserved domain protein (TIGR)		0.82	0.86	0.60	0.02	0.87	0.94
DVU2628	TPR domain protein (TIGR)		1.55	1.13	2.24	0.05	0.73	1.34
DVU2629	hypothetical protein (TIGR)		1.41	1.53	1.43	0.03	1.60	1.65
DVU2630	lipoprotein, putative (TIGR)		1.47	1.45	1.53	0.03	1.70	1.52
DVU2631	hypothetical protein (TIGR)		1.79	1.24	1.28	0.01	1.43	1.22
DVU2633	transcriptional regulator, putative (TIGR)		0.00	0.00	0.05	0.01	0.01	0.00
DVU2634	hypothetical protein (TIGR)		0.54	0.51	0.52	0.02	0.79	0.69
DVU2635	glycosyl transferase, group 1 family protein (TIGR)		0.47	0.39	1.43	0.03	0.23	0.26
DVU2636	hypothetical protein (TIGR)		1.22	1.21	1.25	0.03	1.28	1.09
DVU2637	HAMP domain protein (TIGR)		1.22	1.42	1.32	0.03	1.51	1.45
DVU2638	conserved domain protein (TIGR)		0.77	0.97	1.03	0.02	1.00	1.01
DVU2639	conserved hypothetical protein (TIGR)		1.17	0.81	1.02	0.02	0.75	0.79
DVU2640	hypothetical protein (TIGR)		2.28	1.85	1.93	0.06	2.25	2.24
DVU2641	lipoprotein, putative (TIGR)		1.60	1.12	0.55	0.02	0.96	0.95
DVU2642	alanyl-tRNA synthetase family protein, putative (T	htpG	0.91	0.99	1.26	0.02	1.04	0.92
DVU2643	heat shock protein HtpG (TIGR)		1.03	0.90	0.88	0.02	0.98	0.99
DVU2644	transcriptional regulator, GntR family (TIGR)		0.97	0.66	0.87	0.02	0.69	0.62
DVU2645	Na+/H+ antiporter family protein (TIGR)		1.25	1.29	1.19	0.02	1.15	1.04
DVU2646	1-aminocyclopropane-1-carboxylate deaminase (TIGR)		1.36	1.28	1.04	0.02	1.33	1.13
DVU2647	endoribonuclease, L-PSP family (TIGR)		1.06	1.24	1.31	0.01	1.10	1.14
DVU2648	hypothetical protein (TIGR)		1.05	1.14	1.35	0.02	1.28	1.49
DVU2649	hypothetical protein (TIGR)		0.26	0.37	0.22	0.01	0.46	0.46
DVU2650	hypothetical protein (TIGR)		0.17	0.33	0.15	0.01	0.30	0.21
DVU2651	hypothetical protein (TIGR)		0.09	0.04	0.09	0.00	0.11	0.16
DVU2652	hypothetical protein (TIGR)	dacA	0.57	0.54	0.28	0.02	0.64	0.44
DVU2655	D-alanyl-D-alanine carboxypeptidase family protein (TIGR)		1.00	0.85	0.70	0.02	1.04	1.00
DVU2657	6-pyruvoyl tetrahydrobiopterin synthase, putative (TIGR)		0.65	0.91	0.81	0.02	0.93	1.01
DVU2658	conserved hypothetical protein (TIGR)		1.49	0.94	0.72	0.03	1.18	0.96
DVU2659	exsB protein (TIGR)	CueO	0.88	0.60	0.51	0.01	0.81	0.61
DVU2661	twin-arginine translocation pathway signal sequence domai		1.06	1.22	1.43	0.03	1.37	1.29
DVU2662	conserved hypothetical protein (TIGR)		1.31	1.41	1.79	0.02	1.48	1.36
DVU2663	conserved hypothetical protein (TIGR)	pstB-2	1.61	1.92	1.75	0.03	2.12	2.02
DVU2664	phosphate ABC transporter, ATP-binding protein (TIGR)		1.46	1.46	1.75	0.02	1.39	1.31
DVU2665	phosphate ABC transporter, permease protein, putative (TIC		1.50	1.39	1.68	0.04	1.37	1.43
DVU2666	phosphate ABC transporter, permease protein, pu	pstS	1.36	1.44	1.07	0.05	1.26	1.05
DVU2667	phosphate ABC transporter, periplasmic phosphat	glmU	1.12	1.01	0.78	0.03	1.00	1.06
DVU2668	UDP-N-acetylglucosamine pyrophosphorylase, putative (TIG		0.00	0.02	0.17	0.01	0.01	0.01
DVU2669	conserved domain protein (TIGR)		0.80	0.82	0.58	0.00	0.74	0.57
DVU2670	hypothetical protein (TIGR)		0.38	0.63	0.49	0.03	0.31	0.63
DVU2671	HDIG/HD/KH domain protein (TIGR)		0.11	0.08	0.22	0.01	0.04	0.02
DVU2672	membrane protein, putative (TIGR)	glpA	1.26	1.42	1.10	0.03	1.41	1.58
DVU2673	anaerobic glycerol-3-phosphate dehydrogenase, s	sdhB	1.37	1.26	1.13	0.04	1.45	1.21
DVU2674	succinate dehydrogenase and fumarate reductase iron-sulfu		1.22	1.06	1.27	0.02	1.14	1.03
DVU2675	DNA-binding response regulator, LuxR family (TIGR)		1.30	1.44	1.57	0.04	1.59	1.32
DVU2676	hypothetical protein (TIGR)		0.43	0.40	0.62	0.02	0.77	0.71
DVU2677	sensor histidine kinase/response regulator (TIGR)		1.32	1.30	0.98	0.02	1.43	1.34
DVU2678	RNA pseudouridine synthase family protein (TIGR)		1.07	1.38	1.63	0.03	1.58	1.34
DVU2679	sensory box histidine kinase/response regulator (T	fld	1.41	1.32	1.63	0.03	1.29	1.36
DVU2680	flavodoxin, iron-repressed (Dmitry Rodionov)		0.95	0.78	0.42	0.01	0.83	0.89
DVU2682	DedA family protein (TIGR)		0.80	0.58	0.66	0.02	0.77	0.94
DVU2683	L-lactate permease family protein (TIGR)		1.05	1.37	1.77	0.03	1.48	1.67
DVU2684	hypothetical protein (TIGR)		0.67	1.10	1.31	0.03	1.16	1.10
DVU2686	peptidase, S24 family (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2687	hypothetical protein (TIGR)		0.87	0.99	0.81	0.01	0.86	0.97
DVU2688	bacteriophage transposase A protein (TIGR)		1.64	1.40	1.45	0.03	1.45	1.46
DVU2689	bacteriophage DNA transposition B protein (TIGR)		1.48	1.50	1.76	0.02	1.29	1.60
DVU2690	hypothetical protein (TIGR)		1.71	1.50	1.48	0.01	1.23	1.29
DVU2691	hypothetical protein (TIGR)		1.12	0.81	1.31	0.03	0.82	0.84
DVU2692	conserved domain protein (TIGR)		1.02	1.02	0.82	0.00	0.93	1.01
DVU2693	hypothetical protein (TIGR)		1.07	1.15	0.81	0.00	1.31	1.43

DVU2694	hypothetical protein (TIGR)		0.89	1.24	1.54	0.06	1.16	1.04
DVU2695	conserved hypothetical protein (TIGR)		1.91	1.66	1.92	0.04	1.41	1.76
DVU2696	conserved hypothetical protein (TIGR)		2.55	1.77	2.66	0.09	1.65	2.29
DVU2697	hypothetical protein (TIGR)		0.73	0.72	0.95	0.02	0.70	0.55
DVU2698	lipoprotein, putative (TIGR)	slt	2.06	1.35	2.14	0.04	1.68	1.86
DVU2699	transglycosylase SLT domain protein (TIGR)		1.59	0.96	1.54	0.04	1.51	1.26
DVU2700	hypothetical protein (TIGR)		2.60	1.85	1.98	0.06	1.79	1.84
DVU2701	hypothetical protein (TIGR)		1.31	1.15	1.57	0.03	1.17	1.05
DVU2702	conserved hypothetical protein (TIGR)		1.59	1.37	1.45	0.02	1.26	1.16
DVU2703	hypothetical protein (TIGR)		1.18	1.49	0.65	0.01	1.40	1.18
DVU2704	conserved hypothetical protein (TIGR)		1.11	0.95	1.30	0.04	1.23	1.28
DVU2705	phage uncharacterized protein (TIGR)		2.24	1.83	1.83	0.06	1.86	2.13
DVU2706	conserved hypothetical protein (TIGR)		1.80	1.47	1.44	0.04	1.55	1.50
DVU2707	virion morphogenesis protein (TIGR)		1.44	1.24	1.30	0.02	1.16	1.16
DVU2708	virion morphogenesis protein (TIGR)		1.63	1.19	0.76	0.03	1.32	1.18
DVU2710	conserved hypothetical protein (TIGR)		2.07	1.71	2.02	0.04	1.78	1.67
DVU2711	major head subunit, putative (TIGR)		1.69	1.39	1.97	0.04	1.24	1.38
DVU2712	hypothetical protein (TIGR)		1.53	1.33	1.30	0.03	1.57	1.40
DVU2713	conserved hypothetical protein (TIGR)		2.31	2.29	1.52	0.06	2.05	2.20
DVU2714	conserved hypothetical protein (TIGR)		0.96	1.30	1.94	0.03	1.47	1.40
DVU2715	conserved hypothetical protein (TIGR)		0.97	0.86	1.60	0.06	0.97	0.87
DVU2716	tail sheath protein, putative (TIGR)		2.02	2.12	1.98	0.04	2.08	1.97
DVU2717	hypothetical protein (TIGR)		0.05	0.06	0.10	0.00	0.07	0.05
DVU2719	conserved hypothetical protein (TIGR)		1.63	0.98	0.80	0.03	0.78	0.94
DVU2720	hypothetical protein (TIGR)		0.96	1.68	1.28	0.03	1.27	1.30
DVU2721	phage tail tape measure protein, TP901 family, putative (TIG		1.47	1.18	1.39	0.04	1.16	1.18
DVU2722	conserved hypothetical protein (TIGR)		1.56	1.48	1.98	0.03	1.58	1.63
DVU2723	tail protein, putative (TIGR)		1.30	1.29	1.42	0.02	1.30	1.42
DVU2724	phage baseplate assembly protein V, putative (TIGR)		1.28	1.28	1.35	0.03	1.29	1.24
DVU2725	membrane protein, putative (TIGR)		0.21	0.18	0.43	0.02	0.26	0.28
DVU2727	conserved hypothetical protein (TIGR)		0.59	0.83	0.92	0.01	0.88	0.83
DVU2728	tail protein, putative (TIGR)		0.74	0.98	1.17	0.02	1.55	1.64
DVU2729	tail protein, putative (TIGR)	svQ	0.72	0.40	0.39	0.01	0.34	0.23
DVU2730	tail fiber protein, putative (TIGR)		2.18	1.91	2.26	0.04	1.78	1.87
DVU2731	tail fiber assembly protein, putative (TIGR)		2.60	3.14	3.25	0.10	3.17	3.16
DVU2732	conserved hypothetical protein (TIGR)		3.74	3.08	3.04	0.09	2.89	4.04
DVU2733	adenine specific DNA methyltransferase, putative	paaK-3	1.47	1.16	1.15	0.03	1.29	1.42
DVU2735	phenylacetate-coenzyme A ligase (TIGR)		1.93	1.83	2.09	0.04	2.06	2.10
DVU2736	hypothetical protein (TIGR)		1.08	1.13	1.21	0.01	1.11	1.09
DVU2737	RNA methyltransferase, TrmH family (TIGR)		1.72	1.61	1.63	0.05	1.56	1.48
DVU2738	methyl-accepting chemotaxis protein (TIGR)		1.07	1.09	0.97	0.03	1.20	1.16
DVU2739	pyruvate phosphate dikinase, PEP/pyruvate bindin	livF	1.27	1.25	1.38	0.02	1.36	1.40
DVU2740	high-affinity branched-chain amino acid ABC trans	livG	0.80	0.89	1.04	0.02	1.03	1.16
DVU2741	high-affinity branched chain amino acid ABC trans	livM	1.29	1.40	1.53	0.03	1.49	1.35
DVU2742	high-affinity branched chain amino acid ABC trans	livH	0.98	0.82	0.95	0.02	0.76	0.97
DVU2743	high-affinity branched-chain amino acid ABC ransporter, per		1.42	1.19	1.25	0.02	1.32	1.42
DVU2744	high-affinity branched-chain amino acid ABC transporter, pe		1.00	1.17	1.46	0.03	1.42	1.40
DVU2746	conserved hypothetical protein (TIGR)		1.57	1.47	1.31	0.04	1.47	1.51
DVU2747	hypothetical protein (TIGR)	cobM	1.05	0.93	1.22	0.03	0.99	0.94
DVU2748	precorrin-4 C11-methyltransferase (TIGR)	cobL	1.10	1.21	1.12	0.02	0.57	0.42
DVU2749	precorrin-6Y C5,15-methyltransferase (decarboxyl	cbiD	1.05	1.14	0.99	0.03	0.72	0.55
DVU2750	cobalamin biosynthesis protein CbiD (TIGR)		1.48	1.51	1.57	0.05	0.85	0.75
DVU2751	hypothetical protein (TIGR)		1.77	2.16	1.85	0.05	2.19	2.15
DVU2752	rhodanese-like domain protein (TIGR)		0.69	0.76	0.98	0.05	0.73	0.87
DVU2753	C_GCAxxG_C_C family protein (TIGR)	qor	1.24	1.42	1.18	0.03	1.36	1.33
DVU2754	quinone oxidoreductase (TIGR)		1.24	1.38	1.22	0.03	1.47	1.27
DVU2755	conserved hypothetical protein (TIGR)		0.66	0.72	1.36	0.03	0.61	0.51
DVU2756	radical SAM domain protein (TIGR)		0.86	0.45	1.35	0.04	0.70	0.61
DVU2757	radical SAM domain protein (TIGR)		0.64	0.61	1.90	0.03	0.63	0.47
DVU2758	conserved hypothetical protein (TIGR)		0.45	0.62	1.08	0.04	0.62	0.38
DVU2760	hypothetical protein (TIGR)		1.15	1.41	1.35	0.05	1.49	1.34
DVU2761	hypothetical protein (TIGR)		0.27	0.44	0.88	0.00	0.65	0.68
DVU2762	membrane protein, putative (TIGR)		1.04	0.92	1.07	0.03	0.74	0.65
DVU2763	TPR/GGDEF domain protein (TIGR)		1.68	1.58	1.60	0.03	1.32	0.89
DVU2764	nitroreductase family protein (TIGR)		0.94	0.99	0.56	0.02	0.84	1.01
DVU2765	metallo-beta-lactamase family protein (TIGR)		0.83	1.11	0.86	0.02	1.15	1.20
DVU2766	hypothetical protein (TIGR)		0.75	1.39	0.78	0.03	1.27	1.49

DVU2767	iron-sulfur flavoprotein, putative (TIGR)		0.97	0.87	0.73	0.03	0.14	0.16
DVU2768	comF family protein (TIGR)	nikK	1.38	1.29	1.70	0.03	1.08	1.24
DVU2769	additional component of nickel ABC transporter (Dmitry Roc		1.24	1.16	1.24	0.05	1.25	1.39
DVU2770	response regulator (TIGR)		0.64	0.95	1.29	0.01	1.08	1.13
DVU2771	conserved hypothetical protein (TIGR)		0.54	0.73	0.86	0.02	0.96	0.77
DVU2772	conserved hypothetical protein (TIGR)		1.21	1.26	1.48	0.02	1.28	1.39
DVU2773	membrane protein, putative (TIGR)		1.11	1.70	1.61	0.04	1.59	1.53
DVU2774	CBS domain protein/ACT domain protein (TIGR)		0.50	0.97	0.42	0.00	0.70	0.84
DVU2775	hypothetical protein (TIGR)	dsrC	0.24	0.51	0.54	0.00	0.47	0.56
DVU2776	dissimilatory sulfite reductase, gamma subunit (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU2777	hypothetical protein (TIGR)		2.42	3.01	2.86	0.05	3.09	2.96
DVU2778	hypothetical protein (TIGR)		0.53	0.81	0.41	0.00	0.70	0.81
DVU2779	extracellular solute-binding protein, putative (TIGR)		1.09	0.92	0.87	0.03	1.12	1.06
DVU2780	membrane protein, putative (TIGR)		0.92	1.25	1.15	0.04	1.18	1.29
DVU2781	hypothetical protein (TIGR)		1.12	1.18	0.92	0.02	1.55	1.10
DVU2783	membrane protein, putative (TIGR)	lldD	0.94	1.07	0.78	0.03	1.13	0.90
DVU2784	dehydrogenase, FMN-dependent family (TIGR)	pdhR	1.32	1.13	1.37	0.02	1.18	1.16
DVU2785	transcriptional regulator, GntR family (TIGR)		0.92	1.09	1.08	0.02	0.90	0.89
DVU2786	hypothetical protein (TIGR)		0.25	0.40	0.50	0.02	0.45	0.38
DVU2787	conserved domain protein (TIGR)	smtB	1.51	1.61	1.26	0.03	1.38	1.30
DVU2788	transcriptional regulator, ArsR family (TIGR)		1.20	1.47	1.21	0.02	1.36	1.17
DVU2789	Gpr1/Fun34/YaaH family protein (TIGR)		1.71	1.60	1.34	0.05	1.51	1.54
DVU2790	hypothetical protein (TIGR)	dhcA	0.00	0.07	0.42	0.00	0.18	0.22
DVU2791	Decaheme cytochrome c associated with Rnf complex (Shell		1.69	1.31	1.00	0.03	1.46	1.49
DVU2792	NADH:quinone oxidoreductase subunit RnfC (Shelley Haverr		1.33	0.96	0.80	0.02	1.28	1.37
DVU2793	electron transport complex protein RnfD, putative (TIGR)		1.12	1.06	0.63	0.02	1.39	1.43
DVU2794	NADH:quinone oxidoreductase subunit RnfG (Shel	nqr4	1.29	1.23	1.11	0.03	1.46	1.63
DVU2795	NADH:quinone oxidoreductase subunit RnfE (Shell	b1627	1.58	1.13	0.84	0.01	1.26	1.48
DVU2796	NADH:quinone oxidoreductase subunit RnfA (Shelley Haverr		1.62	1.41	0.46	0.01	1.54	1.69
DVU2797	NADH:quinone oxidoreductase subunit RnfB (Shelley Haverr		1.71	1.38	1.11	0.03	1.57	1.76
DVU2798	ApbE family protein (TIGR)		1.00	0.99	0.77	0.02	1.33	1.42
DVU2799	transcriptional regulator, MarR family (TIGR)		1.17	1.13	0.61	0.04	1.34	1.45
DVU2800	heavy metal translocating P-type ATPase (TIGR)		1.60	1.76	1.46	0.04	1.68	1.75
DVU2801	hypothetical protein (TIGR)		0.41	0.61	0.72	0.01	0.60	0.59
DVU2802	transcriptional regulator, GntR family (TIGR)		2.80	2.61	1.90	0.06	3.35	2.42
DVU2803	membrane protein, putative (TIGR)		2.06	1.67	1.51	0.05	2.32	1.84
DVU2804	metallo-beta-lactamase family protein (TIGR)		1.59	1.59	1.43	0.04	1.91	1.44
DVU2805	cobalamin synthesis protein/P47K family (TIGR)		1.34	1.48	1.43	0.03	1.62	1.22
DVU2806	MotA/TolQ/ExbB proton channel family protein (TIGR)		0.86	1.11	0.72	0.02	1.32	1.18
DVU2807	biopolymer transport protein, ExbD/TolR family (TIGR)		1.68	1.57	2.03	0.05	1.90	1.44
DVU2808	TonB domain protein (TIGR)		1.34	0.91	0.99	0.04	1.25	0.98
DVU2809	cytochrome c3 (TIGR)		0.88	1.00	0.97	0.01	1.08	0.92
DVU2810	formate dehydrogenase formation protein FdhE, putative (T		1.34	1.30	1.77	0.04	1.30	1.39
DVU2811	formate dehydrogenase, beta subunit, putative (TI	fdnG-3	1.06	1.07	1.27	0.04	0.96	1.00
DVU2812	formate dehydrogenase, alpha subunit, selenocysteine-cont		1.33	1.33	1.28	0.03	1.44	1.44
DVU2815	outer membrane efflux protein (TIGR)		1.54	1.40	1.58	0.04	1.63	1.59
DVU2816	multidrug resistance protein (TIGR)	acrA	1.45	1.55	1.63	0.03	1.53	1.56
DVU2817	multidrug resistance protein (TIGR)		1.60	1.59	1.49	0.03	1.73	1.62
DVU2818	hypothetical protein (TIGR)		1.10	0.85	1.02	0.02	0.60	0.91
DVU2819	transcriptional regulator, TetR family (TIGR)		1.23	1.27	1.17	0.02	1.00	1.19
DVU2820	amidohydrolase family protein (TIGR)		2.14	1.57	1.19	0.04	1.50	1.64
DVU2821	hypothetical protein (TIGR)		0.48	0.64	1.00	0.00	0.68	0.68
DVU2822	TRAP dicarboxylate family transporter (TIGR)	dctM	1.59	1.32	1.49	0.02	1.30	1.33
DVU2823	TRAP dicarboxylate transporter family protein (TIGR)		1.19	1.17	1.16	0.02	1.17	1.15
DVU2824	formate acetyltransferase (TIGR)		1.53	1.44	1.32	0.03	1.61	1.64
DVU2825	pyruvate formate-lyase 1 activating enzyme, putative (TIGR)		0.70	0.74	0.95	0.01	1.45	0.89
DVU2827	sigma-54 dependent transcriptional regulator (TIGR)		1.15	1.08	1.19	0.02	1.24	1.16
DVU2828	site-specific recombinase, phage integrase family (TIGR)		1.94	2.35	2.18	0.06	2.51	2.38
DVU2829	hypothetical protein (TIGR)		1.45	1.63	3.53	0.02	1.71	1.69
DVU2830	hypothetical protein (TIGR)		2.30	1.64	1.67	0.07	1.78	1.84
DVU2831	hypothetical protein (TIGR)		1.77	1.78	2.38	0.06	1.65	1.65
DVU2832	transcriptional regulator cII, putative (TIGR)		3.60	2.93	3.49	0.08	3.12	3.15
DVU2833	hypothetical protein (TIGR)		1.70	1.41	1.97	0.01	1.37	1.90
DVU2835	transcriptional regulator, putative (TIGR)		1.09	1.13	0.86	0.05	1.21	1.25
DVU2836	hypothetical protein (TIGR)		0.12	0.07	0.45	0.01	0.10	0.04
DVU2837	conserved hypothetical protein (TIGR)		1.52	1.16	1.32	0.02	1.62	1.47
DVU2838	conserved hypothetical protein (TIGR)		0.55	0.36	0.37	0.01	0.47	0.46

DVU2839	conserved hypothetical protein (TIGR)		0.85	0.28	0.21	0.01	0.45	0.68
DVU2840	conserved hypothetical protein (TIGR)		0.09	0.09	0.08	0.00	0.19	0.21
DVU2841	type II restriction endonuclease, putative (TIGR)	dcm	0.81	0.76	0.60	0.02	0.76	0.78
DVU2842	type II DNA modification methyltransferase, putat	vsr	0.00	0.00	0.00	0.00	0.01	0.01
DVU2843	DNA mismatch endonuclease Vsr, putative (TIGR)		0.54	0.51	0.98	0.01	0.51	0.66
DVU2844	hypothetical protein (TIGR)	hit	0.79	0.92	0.85	0.03	1.01	1.07
DVU2845	HIT family protein (TIGR)		1.45	1.60	1.49	0.03	1.15	1.26
DVU2846	hypothetical protein (TIGR)		0.73	0.39	0.25	0.02	0.54	0.53
DVU2847	hypothetical protein (TIGR)		0.90	1.10	1.27	0.02	1.03	1.31
DVU2848	tail fiber assembly protein, putative (TIGR)	b1157	2.14	2.19	1.72	0.05	2.17	2.30
DVU2849	tail fiber protein, putative (TIGR)		1.84	1.27	1.21	0.03	1.26	1.15
DVU2850	tail protein, putative (TIGR)		1.24	1.21	1.06	0.02	1.26	1.15
DVU2851	tail protein, putative (TIGR)		1.98	1.37	1.66	0.02	1.70	1.33
DVU2852	tail protein, putative (TIGR)		2.24	1.99	2.90	0.02	2.20	1.80
DVU2853	phage baseplate assembly protein V, putative (TIGR)		1.12	1.23	0.91	0.02	1.03	0.76
DVU2854	tail protein, putative (TIGR)		1.53	1.09	1.11	0.03	1.26	1.19
DVU2855	tail/DNA circulation protein, putative (TIGR)		0.52	0.51	0.34	0.02	0.61	0.59
DVU2856	conserved domain protein (TIGR)		0.98	0.76	0.80	0.04	0.90	0.93
DVU2857	conserved hypothetical protein (TIGR)		0.97	1.45	0.92	0.03	1.14	1.24
DVU2858	tail tube protein, putative (TIGR)		0.11	0.17	0.19	0.00	0.18	0.13
DVU2859	tail sheath protein, putative (TIGR)		1.22	1.04	0.91	0.02	1.02	0.94
DVU2860	conserved hypothetical protein (TIGR)		0.73	0.53	1.03	0.04	0.57	0.55
DVU2861	hypothetical protein (TIGR)		1.16	1.48	1.79	0.02	1.53	1.34
DVU2862	hypothetical protein (TIGR)		0.24	0.26	0.28	0.00	0.16	0.27
DVU2863	hypothetical protein (TIGR)		0.34	0.23	0.09	0.00	0.20	0.21
DVU2864	hypothetical protein (TIGR)		1.56	1.54	1.23	0.09	1.43	1.78
DVU2865	lipoprotein, putative (TIGR)		1.23	1.63	1.57	0.03	1.38	1.15
DVU2866	conserved hypothetical protein (TIGR)		1.72	1.72	1.91	0.02	1.58	1.53
DVU2867	holin (TIGR)		0.49	0.48	0.27	0.02	0.45	0.53
DVU2868	hypothetical protein (TIGR)		0.75	0.78	1.25	0.03	1.05	1.00
DVU2869	major head protein (TIGR)		0.44	0.54	0.43	0.02	0.68	0.62
DVU2870	conserved hypothetical protein (TIGR)		0.86	0.73	0.40	0.02	0.87	0.48
DVU2871	minor capsid protein C (TIGR)		1.03	1.00	0.84	0.02	0.91	0.95
DVU2872	phage portal protein, lambda family (TIGR)		1.62	1.36	1.62	0.02	1.43	1.51
DVU2873	hypothetical protein (TIGR)		0.66	1.04	0.64	0.01	0.60	0.67
DVU2874	hypothetical protein (TIGR)		1.72	1.27	1.43	0.02	1.16	1.34
DVU2875	DNA-binding domain, excisionase family (TIGR)		1.32	1.63	1.38	0.01	1.38	1.47
DVU2876	terminase, large subunit, putative (TIGR)		1.61	1.55	1.41	0.03	1.43	1.47
DVU2877	hypothetical protein (TIGR)		0.76	0.66	0.71	0.02	0.87	0.95
DVU2878	adenine specific DNA methyltransferase, putative (TIGR)		1.33	0.93	0.86	0.03	1.02	1.01
DVU2879	conserved hypothetical protein (TIGR)		1.43	1.19	1.31	0.03	1.34	1.28
DVU2880	hypothetical protein (TIGR)		0.46	0.38	0.43	0.01	0.35	0.68
DVU2881	phage/plasmid primase, P4 family (TIGR)	folC	0.65	0.52	0.60	0.01	0.53	0.64
DVU2882	folylpolyglutamate synthase (TIGR)	selA	0.49	0.44	0.98	0.02	0.06	0.08
DVU2883	L-seryl-tRNA selenium transferase (TIGR)		1.21	0.91	1.91	0.02	0.98	0.84
DVU2884	peptidase, M18 family (TIGR)	dhaT	1.99	1.80	1.47	0.05	1.76	1.82
DVU2885	alcohol dehydrogenase, iron-containing (TIGR)		1.91	1.51	2.01	0.05	1.67	1.54
DVU2886	transcriptional regulator, AraC family (TIGR)		2.23	1.71	1.96	0.04	1.85	1.91
DVU2887	membrane protein, putative (TIGR)		1.13	1.31	1.37	0.02	1.30	1.28
DVU2888	cobalt ABC transporter, ATP-binding protein, putative (TIGR		1.51	1.09	0.75	0.01	1.19	1.22
DVU2889	BioY family protein (TIGR)		1.68	1.09	1.19	0.03	1.49	1.22
DVU2890	conserved domain protein (TIGR)	nikR	2.00	1.32	2.16	0.02	1.71	1.55
DVU2891	nickel responsive regulator (TIGR)		1.09	1.52	1.14	0.03	1.24	1.64
DVU2892	conserved hypothetical protein (TIGR)	flgG	0.33	0.25	0.58	0.01	0.12	0.07
DVU2893	flagellar basal-body rod protein, putative (TIGR)	flrA	1.50	2.00	1.40	0.03	1.72	1.37
DVU2894	sigma-54 dependent transcriptional regulator (TIGR)		1.06	1.09	1.21	0.02	1.44	1.25
DVU2895	hypothetical protein (TIGR)		2.28	1.85	2.92	0.07	2.05	2.60
DVU2896	TPR domain protein (TIGR)		1.52	1.61	1.30	0.03	2.15	1.91
DVU2897	conserved hypothetical protein (TIGR)		1.40	1.27	1.00	0.02	1.24	1.15
DVU2898	conserved hypothetical protein (TIGR)		1.37	1.25	1.26	0.03	1.49	1.35
DVU2899	hypothetical protein (TIGR)		1.23	1.59	1.43	0.05	1.66	1.87
DVU2900	amidohydrolase family protein (TIGR)	pyrB	0.68	0.80	0.99	0.04	0.65	0.49
DVU2901	aspartate carbamoyltransferase (TIGR)	pyrC	1.75	1.69	0.50	0.01	0.01	0.01
DVU2902	dihydroorotase (TIGR)	pcnB2	1.85	1.62	0.80	0.02	0.01	0.02
DVU2903	HD domain protein (TIGR)		0.96	1.00	1.07	0.02	1.12	1.02
DVU2904	radical SAM enzyme, Cfr family (TIGR)		1.49	1.33	1.07	0.02	1.33	1.36
DVU2905	alcohol dehydrogenase, iron-containing (TIGR)	umuC	1.36	1.44	1.14	0.03	1.27	1.29

DVU2906	umuC protein (TIGR)	umuD	1.56	1.40	1.61	0.04	1.46	1.38
DVU2907	umuD protein (TIGR)		1.18	0.94	0.49	0.02	1.13	1.25
DVU2908	hypothetical protein (TIGR)		1.98	1.90	2.01	0.03	1.79	1.59
DVU2909	transcriptional regulator, MarR family (TIGR)		3.55	5.06	2.61	0.05	2.82	2.59
DVU2910	membrane protein, putative (TIGR)		1.32	1.54	0.87	0.03	1.42	1.32
DVU2911	hemolysin A (TIGR)	rpmE	1.30	1.02	1.00	0.03	1.25	1.10
DVU2912	ribosomal protein L31 (TIGR)		0.11	0.14	0.10	0.00	0.12	0.06
DVU2913	lipoprotein, putative (TIGR)	prfA	1.10	1.21	1.04	0.05	1.27	1.33
DVU2914	peptide chain release factor 1 (TIGR)		0.02	0.01	0.12	0.00	0.00	0.00
DVU2915	hypothetical protein (TIGR)	hemK	1.78	1.68	2.91	0.04	1.34	1.35
DVU2916	hemK protein (TIGR)	lpxC	1.24	0.83	1.93	0.03	0.54	0.48
DVU2917	UDP-3-0-acyl N-acetylglucosamine deacetylase (TIGR)		0.00	0.01	0.04	0.00	0.01	0.02
DVU2918	hypothetical protein (TIGR)	tuf	1.50	2.27	1.35	0.03	2.15	1.88
DVU2920	translation elongation factor Tu (TIGR)	rpmG	0.00	0.00	0.00	0.00	0.00	0.00
DVU2921	ribosomal protein L33 (TIGR)	secE	0.00	0.00	0.12	0.00	0.00	0.00
DVU2922	preprotein translocase, SecE subunit (TIGR)	nusG	0.00	0.00	0.00	0.00	0.00	0.00
DVU2923	transcription antitermination protein NusG (TIGR)	rplK	0.03	0.01	0.00	0.00	0.01	0.00
DVU2924	ribosomal protein L11 (TIGR)	rplA	0.00	0.00	0.00	0.00	0.00	0.00
DVU2925	ribosomal protein L1 (TIGR)	rplJ	0.00	0.02	0.00	0.00	0.00	0.00
DVU2926	ribosomal protein L10 (TIGR)	rplL	0.00	0.00	0.00	0.00	0.00	0.00
DVU2927	ribosomal protein L7/L12 (TIGR)	rpoB	0.00	0.00	0.00	0.00	0.00	0.00
DVU2928	DNA-directed RNA polymerase, beta subunit (TIGR	rpoC	0.00	0.00	0.01	0.00	0.00	0.00
DVU2929	DNA-directed RNA polymerase, beta prime subunit (TIGR)		0.01	0.00	0.01	0.00	0.00	0.00
DVU2930	hypothetical protein (TIGR)		0.66	0.31	0.56	0.00	0.65	0.63
DVU2931	sensory box histidine kinase (TIGR)		0.93	0.75	1.14	0.02	0.69	0.61
DVU2932	conserved hypothetical protein TIGR01777 (TIGR)		1.22	1.07	0.98	0.03	0.96	1.00
DVU2933	response regulator/sensory box/HDIG domain pro	ntrX	0.96	1.20	1.12	0.02	1.09	0.99
DVU2934	sigma-54 dependent transcriptional regulator/resp	gpm	0.11	0.06	0.19	0.01	0.00	0.00
DVU2935	phosphoglycerate mutase (TIGR)		1.43	1.61	1.81	0.05	1.69	1.70
DVU2937	TPR domain protein/response regulator receiver domain pr		0.90	1.12	1.09	0.03	1.43	1.42
DVU2938	conserved hypothetical protein (TIGR)		1.09	1.08	0.83	0.01	0.15	0.05
DVU2939	conserved hypothetical protein (TIGR)		1.68	1.66	1.76	0.04	1.70	1.54
DVU2940	hypothetical protein (TIGR)		0.32	0.44	0.00	0.00	0.47	0.52
DVU2941	conserved hypothetical protein (TIGR)	purB	0.53	0.72	0.60	0.00	0.12	0.08
DVU2942	adenylosuccinate lyase (TIGR)	pyrE	0.00	0.00	0.00	0.00	0.01	0.00
DVU2943	orotate phosphoribosyltransferase (TIGR)		1.41	1.77	0.37	0.02	0.00	0.01
DVU2944	ErfK/YbiS/YcfS/YnhG family protein (TIGR)		1.09	1.19	1.24	0.03	1.49	1.24
DVU2945	conserved domain protein (TIGR)		0.40	0.55	0.60	0.02	0.61	0.60
DVU2946	hypothetical protein (TIGR)		0.77	1.31	1.15	0.00	1.45	1.43
DVU2947	anaerobic ribonucleoside-triphosphate reductase, putative (		0.11	0.06	0.50	0.01	1.19	1.32
DVU2948	bacterial flagellin N-terminal domain protein (TIGR)		1.25	1.39	1.03	0.03	1.09	1.23
DVU2949	membrane protein, putative (TIGR)	glnS	1.24	1.81	1.40	0.04	1.67	2.11
DVU2951	glutaminyl-tRNA synthetase (TIGR)		0.01	0.00	0.08	0.00	0.00	0.00
DVU2952	membrane protein, putative (TIGR)		1.87	1.95	1.28	0.02	2.01	1.86
DVU2953	transcriptional regulator, GntR family (TIGR)		1.28	1.44	1.13	0.04	1.74	1.55
DVU2954	GGDEF domain protein (TIGR)	flrA	1.11	1.24	1.00	0.02	1.22	1.29
DVU2956	sigma-54 dependent transcriptional regulator (TIGR)		0.31	0.39	0.52	0.01	0.47	0.51
DVU2957	hypothetical protein (TIGR)		0.10	0.00	0.00	0.00	0.13	0.03
DVU2958	membrane protein, putative (TIGR)		0.25	0.15	0.28	0.01	0.19	0.19
DVU2959	conserved hypothetical protein (TIGR)	ntrC	0.16	0.19	0.48	0.00	0.15	0.11
DVU2960	sigma-54 dependent transcriptional regulator (TIGR)		1.98	2.33	2.06	0.03	2.12	2.15
DVU2961	hypothetical protein (TIGR)		1.46	1.17	1.07	0.02	1.12	1.13
DVU2962	sensor histidine kinase (TIGR)		0.54	0.62	0.80	0.01	0.78	0.60
DVU2963	response regulator (TIGR)		0.73	0.86	0.64	0.04	0.86	0.83
DVU2964	hypothetical protein (TIGR)		0.74	0.72	0.57	0.02	1.11	0.96
DVU2965	hypothetical protein (TIGR)		1.30	1.61	0.97	0.05	1.79	1.86
DVU2966	response regulator (TIGR)		0.88	1.32	0.86	0.03	1.24	0.84
DVU2967	sensor histidine kinase/response regulator (TIGR)		0.91	0.98	0.76	0.02	0.86	0.82
DVU2968	sensor histidine kinase/response regulator (TIGR)		0.97	1.41	1.16	0.02	1.21	1.26
DVU2969	acetoacetyl-CoA synthase (TIGR)		1.55	1.64	1.46	0.03	1.58	1.51
DVU2970	acetyltransferase, GNAT family (TIGR)		1.15	1.29	1.42	0.04	1.36	1.29
DVU2971	glycosyl transferase, family 8 (TIGR)		0.77	0.89	1.31	0.03	0.93	1.05
DVU2972	chemotaxis protein CheD, putative (TIGR)	hup	0.73	0.64	0.45	0.03	0.68	0.75
DVU2973	integration host factor, beta subunit (TIGR)		0.86	1.06	0.52	0.01	0.78	0.72
DVU2974	hypothetical protein (TIGR)		0.23	0.56	0.61	0.02	0.73	0.89
DVU2975	hydrolase, putative (TIGR)		1.52	1.61	1.60	0.04	1.75	1.74
DVU2976	conserved hypothetical protein (TIGR)		1.88	1.70	1.60	0.03	1.64	1.46

DVU2978	hydrolase, haloacid dehalogenase-like family (TIGR)		1.19	1.65	2.03	0.03	1.98	1.80
DVU2979	phosphatidylserine decarboxylase-related protein	pssA	0.03	0.00	0.06	0.00	0.00	0.00
DVU2980	CDP-diacylglycerol--serine O-phosphatidyltransfer	leuA	0.00	0.00	0.04	0.00	0.00	0.00
DVU2981	2-isopropylmalate synthase (TIGR)	leuC	1.06	1.22	0.59	0.01	0.36	0.11
DVU2982	3-isopropylmalate dehydratase, large subunit, put	leuD	0.73	1.02	0.85	0.01	0.11	0.03
DVU2983	3-isopropylmalate dehydratase, small subunit (TIGR)		1.04	0.75	0.32	0.02	0.06	0.01
DVU2984	conserved hypothetical protein (TIGR)	leuB	1.11	1.16	0.99	0.01	0.61	0.65
DVU2985	3-isopropylmalate dehydrogenase (TIGR)	pspC	1.28	1.62	0.90	0.01	0.14	0.06
DVU2986	phage shock protein C (TIGR)		0.82	0.72	0.25	0.02	0.88	0.96
DVU2987	hypothetical protein (TIGR)	pspA	1.49	2.14	2.15	0.03	1.47	1.72
DVU2988	phage shock protein A (TIGR)	pspF	0.96	1.03	0.66	0.02	0.99	1.11
DVU2989	psp operon transcriptional activator (TIGR)	moeA	1.52	1.98	1.27	0.03	1.86	1.86
DVU2990	molybdopterin biosynthesis MoeA protein (TIGR)		1.39	1.69	1.80	0.04	1.87	1.83
DVU2991	hypothetical protein (TIGR)		1.06	1.33	0.85	0.02	1.19	1.27
DVU2992	glycosyl transferase, group 2 family protein (TIGR)		1.46	1.54	1.20	0.03	1.42	1.68
DVU2993	glycosyl transferase, group 1/2 family protein (TIGR)		1.77	1.69	1.58	0.03	1.83	1.94
DVU2994	glycosyl transferase, group 2 family protein (TIGR)		0.78	0.94	0.98	0.02	1.18	0.99
DVU2995	glycosyl transferase, group 1 family protein (TIGR)		1.05	1.30	1.15	0.01	1.24	1.43
DVU2996	NAD-dependent epimerase/dehydratase family protein (TIG		0.94	0.86	0.77	0.02	1.06	1.17
DVU2997	hypothetical protein (TIGR)		1.60	1.82	1.89	0.04	1.99	1.95
DVU2998	hypothetical protein (TIGR)		1.27	1.39	1.28	0.04	1.43	1.34
DVU2999	methionyl-tRNA formyltransferase, putative (TIGR)		1.49	1.40	1.28	0.04	1.42	1.31
DVU3000	hypothetical protein (TIGR)		1.13	1.14	1.11	0.02	1.08	1.04
DVU3001	conserved domain protein (TIGR)		0.90	1.06	1.01	0.02	1.12	1.06
DVU3002	conserved domain protein (TIGR)		1.46	1.34	1.37	0.04	1.34	1.30
DVU3003	radical SAM domain protein (TIGR)		1.84	1.28	1.38	0.02	1.21	1.28
DVU3004	radical SAM domain protein (TIGR)	rfbE	1.90	1.83	2.01	0.03	1.86	1.64
DVU3005	aminotransferase, DegT/DnrJ/EryC1/StrS family (T	spsF	1.17	0.91	1.19	0.02	0.94	1.00
DVU3006	polysaccharide biosynthesis protein/methyltransferase, puta		1.43	1.18	1.69	0.03	1.33	1.33
DVU3007	hypothetical protein (TIGR)		1.90	1.87	1.84	0.03	1.75	1.91
DVU3008	NeuB family protein (TIGR)		1.57	1.59	1.66	0.02	1.69	1.62
DVU3009	radical SAM domain protein (TIGR)	lpsC	1.35	1.27	1.51	0.02	1.66	1.73
DVU3010	aminotransferase, DegT/DnrJ/EryC1/StrS family (TIGR)		1.32	1.27	1.34	0.03	1.34	1.37
DVU3011	conserved hypothetical protein (TIGR)		1.85	1.66	1.81	0.05	1.66	1.61
DVU3012	membrane protein, putative (TIGR)	dmt	1.74	1.57	1.33	0.04	1.62	1.60
DVU3013	glycosyl transferase, group 2 family protein (TIGR)		1.44	1.42	1.31	2.46	1.41	1.33
DVU3014	asparagine synthetase, glutamine-hydrolyzing (TIGR)		1.43	1.43	1.17	0.03	1.26	1.23
DVU3015	conserved domain protein (TIGR)		1.03	1.13	1.47	0.03	1.14	1.21
DVU3016	B12 binding domain protein/radical SAM domain protein (TI		0.44	0.33	0.42	0.00	0.43	0.39
DVU3017	conserved domain protein (TIGR)		1.60	1.65	1.56	0.04	1.66	1.74
DVU3018	radical SAM domain protein (TIGR)		1.32	1.63	1.68	0.03	1.61	1.56
DVU3019	radical SAM/B12 binding domain protein (TIGR)		1.41	1.44	1.49	0.03	1.54	1.74
DVU3020	hypothetical protein (TIGR)		1.38	1.46	0.58	0.04	1.36	1.63
DVU3021	HDIG domain protein (TIGR)		1.38	1.56	1.61	0.03	1.67	1.38
DVU3022	sensory box histidine kinase/response regulator (T	atoC	0.38	0.37	0.82	0.02	0.12	0.16
DVU3023	sigma-54 dependent DNA-binding response regulator (TIGR)		0.35	0.22	0.55	0.01	0.04	0.07
DVU3024	hypothetical protein (TIGR)	por	0.20	0.23	0.30	0.00	0.18	0.24
DVU3025	pyruvate-ferredoxin oxidoreductase (TIGR)		0.01	0.01	0.06	0.00	0.00	0.00
DVU3026	L-lactate permease family protein (TIGR)	glcD	0.82	0.61	0.89	0.03	0.24	0.18
DVU3027	glycolate oxidase, subunit GlcD (TIGR)		0.77	0.71	0.91	0.01	0.22	0.17
DVU3028	iron-sulfur cluster-binding protein (TIGR)	pta	0.58	0.73	1.44	0.02	0.58	0.55
DVU3029	phosphate acetyltransferase (TIGR)	ackA	0.02	0.00	0.11	0.00	0.00	0.00
DVU3030	acetate kinase (TIGR)		0.00	0.00	0.00	0.00	0.00	0.00
DVU3031	conserved hypothetical protein (TIGR)		0.60	0.48	0.57	0.01	0.50	0.47
DVU3032	conserved hypothetical protein (TIGR)		0.95	1.05	1.60	0.02	1.07	1.12
DVU3033	iron-sulfur cluster-binding protein (TIGR)		1.54	1.36	1.59	0.05	1.35	1.33
DVU3035	methyl-accepting chemotaxis protein, putative (TIGR)		0.87	0.87	1.05	0.03	0.90	0.84
DVU3036	conserved hypothetical protein (TIGR)		1.26	1.66	1.85	0.02	1.70	1.60
DVU3037	rhodanese-like domain protein (TIGR)		1.77	1.44	1.70	0.03	1.51	1.39
DVU3039	conserved hypothetical protein (TIGR)		1.78	2.04	1.89	0.06	2.03	1.85
DVU3041	cytochrome c553 (TIGR)		1.99	1.97	3.15	0.01	2.65	2.62
DVU3042	lipoprotein, putative (TIGR)		0.56	0.39	0.36	0.01	0.60	0.53
DVU3043	hypothetical protein (TIGR)	fexB	1.48	1.42	1.68	0.05	1.49	1.24
DVU3045	sensory box histidine kinase/response regulator (TIGR)		1.27	1.23	1.31	0.03	1.21	1.07
DVU3046	glycosyl transferase, group 1 family protein (TIGR)		1.18	0.82	0.99	0.02	1.02	1.04
DVU3047	aminotransferase, class IV (TIGR)	asd	1.04	0.78	1.08	0.02	0.90	1.01
DVU3048	aspartate-semialdehyde dehydrogenase (TIGR)		0.17	0.06	0.08	0.00	0.00	0.01

DVU3049	hemerythrin family protein (TIGR)		0.70	0.72	0.87	0.05	0.80	0.78
DVU3050	membrane protein, putative (TIGR)	mutT	1.25	0.89	0.88	0.02	0.99	1.01
DVU3051	mutator mutT protein (TIGR)		1.62	2.13	1.62	0.06	1.57	1.59
DVU3052	ABC transporter, ATP-binding protein (TIGR)		1.39	1.10	1.27	0.03	1.12	1.08
DVU3053	conserved hypothetical protein (TIGR)		1.34	1.35	1.66	0.04	1.29	1.36
DVU3054	radical SAM domain protein (TIGR)	rne	1.45	1.51	1.30	0.04	1.52	1.55
DVU3055	ribonuclease, Rne/Rng family (TIGR)		0.10	0.09	0.53	0.01	0.10	0.07
DVU3056	conserved hypothetical protein (TIGR)		1.46	1.01	1.25	0.02	1.28	1.15
DVU3057	oxygen-independent coproporphyrinogen III oxidase, putati		1.19	1.12	1.30	0.03	1.17	1.05
DVU3058	sensory box histidine kinase/response regulator (T	ftsY	1.17	1.34	1.21	0.03	1.35	1.20
DVU3059	signal recognition particle-docking protein FtsY (TIGR)		0.01	0.01	0.00	0.00	0.00	0.00
DVU3061	sensory box histidine kinase (TIGR)		1.38	1.46	1.18	0.04	1.44	1.65
DVU3062	sensor histidine kinase/response regulator (TIGR)	mviN-2	1.29	1.26	1.37	0.03	1.35	1.27
DVU3063	integral membrane protein MviN (TIGR)		1.03	0.96	1.03	0.02	1.08	1.02
DVU3064	sensory box/GGDEF domain/EAL domain protein (TIGR)		1.38	1.43	1.65	0.04	1.52	1.60
DVU3065	AMP-binding enzyme family protein (TIGR)		1.33	1.41	1.36	0.03	1.59	1.40
DVU3066	DNA-binding protein (TIGR)	hypF	0.38	0.59	0.83	0.01	0.93	1.02
DVU3067	[NiFe] hydrogenase maturation protein HypF (TIGR)		0.36	0.50	1.28	0.03	0.49	0.55
DVU3068	GAF domain/sensory box/EAL domain protein (TIGR)		1.60	1.58	1.43	0.03	1.76	1.68
DVU3069	conserved hypothetical protein TIGR00247 (TIGR)		0.99	0.75	0.74	0.02	0.98	0.85
DVU3070	conserved hypothetical protein (TIGR)		0.16	0.16	0.19	0.01	0.01	0.04
DVU3071	oxidoreductase, FAD/iron-sulfur cluster-binding domain pro		0.01	0.01	0.01	0.00	0.00	0.00
DVU3072	ABC transporter, permease protein, putative (TIGR)		1.95	2.00	1.90	0.04	2.04	1.79
DVU3073	conserved domain protein (TIGR)		1.83	2.42	1.39	0.04	2.03	1.96
DVU3074	membrane protein, putative (TIGR)		2.67	2.22	1.86	0.05	1.98	2.00
DVU3076	conserved hypothetical protein (TIGR)		1.18	1.18	1.05	0.02	1.37	1.36
DVU3077	AhpC/TSA family protein (TIGR)		1.53	1.56	1.12	0.03	1.46	1.25
DVU3079	glyoxalase family protein (TIGR)		1.36	1.37	0.85	0.03	1.21	1.48
DVU3080	transcriptional regulator, putative (TIGR)		0.60	0.35	0.30	0.00	0.42	0.36
DVU3081	membrane protein, putative (TIGR)		1.48	1.41	1.36	0.02	1.31	1.28
DVU3082	methyl-accepting chemotaxis protein (TIGR)		1.02	1.02	1.29	0.02	1.06	1.05
DVU3084	transcriptional regulator, putative (TIGR)		0.53	0.37	0.29	0.00	0.35	0.40
DVU3085	hypothetical protein (TIGR)	cobB-2	0.81	1.42	0.76	0.03	0.83	0.94
DVU3086	cobyrinic acid a,c-diamide synthase (TIGR)	cobH	1.52	1.42	1.23	0.03	0.74	0.61
DVU3087	precorrin-8X methylmutase (TIGR)	deaD	1.66	1.56	1.29	0.04	0.98	0.61
DVU3088	ATP-dependent RNA helicase, DEAD/DEAH box family (TIGR)		1.32	1.52	1.09	0.03	1.13	1.29
DVU3089	hypothetical protein (TIGR)		0.55	1.30	0.97	0.03	1.00	0.92
DVU3090	outer membrane protein, OMPP1/FadL/TodX family (TIGR)		0.89	0.97	0.98	0.02	1.03	1.05
DVU3091	conserved hypothetical protein (TIGR)		0.92	1.17	0.95	0.03	1.23	1.21
DVU3092	hypothetical protein (TIGR)	rdl	0.90	1.63	1.34	0.01	1.12	1.33
DVU3093	rubredoxin-like protein (TIGR)	rbr	0.84	0.71	0.56	0.04	0.78	0.94
DVU3094	rubrerythrin (TIGR)	PerR	0.49	0.57	0.43	0.01	0.47	0.50
DVU3095	peroxide-responsive regulator PerR (Dmitry Rodionov)		0.16	0.18	0.29	0.00	0.11	0.23
DVU3097	outer membrane efflux protein (TIGR)		1.61	1.68	1.28	0.03	1.89	1.41
DVU3098	hypothetical protein (TIGR)	tolQ-2	1.29	0.79	0.51	0.00	1.01	0.74
DVU3099	tolQ protein (TIGR)	tolR	0.07	0.00	0.09	0.00	0.00	0.00
DVU3100	biopolymer transport protein, ExbD/TolR family (TIGR)		0.04	0.05	0.09	0.00	0.06	0.02
DVU3101	tonB protein, putative (TIGR)		0.08	0.03	0.18	0.00	0.00	0.00
DVU3102	hypothetical protein (TIGR)		1.86	1.88	0.92	0.02	2.10	1.72
DVU3103	tolB protein, putative (TIGR)	pal	0.05	0.03	0.26	0.00	0.00	0.00
DVU3104	peptidoglycan-associated lipoprotein, putative (TIGR)		0.01	0.00	0.00	0.00	0.00	0.00
DVU3106	GGDEF domain protein (TIGR)		2.10	1.71	1.45	0.03	1.71	1.47
DVU3107	cytochrome c family protein (TIGR)	nhaC-2	1.78	1.95	1.70	0.04	1.80	1.74
DVU3108	Na+/H+ antiporter NhaC (TIGR)		2.17	2.17	2.24	0.04	2.22	2.12
DVU3109	iron-sulfur cluster-binding protein (TIGR)		1.70	1.41	1.74	0.01	1.45	1.49
DVU3110	L-aspartate oxidase, putative (TIGR)		1.21	1.17	0.96	0.03	1.12	1.16
DVU3111	transcriptional regulator, Crp/Fnr family (TIGR)		1.36	1.03	1.17	0.02	1.12	1.30
DVU3112	TPR domain protein (TIGR)	carA	0.92	1.01	0.99	0.03	0.97	0.97
DVU3113	carbamoyl-phosphate synthase, small subunit (TIG	kdsB	0.54	0.59	0.06	0.00	0.00	0.00
DVU3114	3-deoxy-manno-octulosonate cytidylyltransferase	prfC	0.02	0.08	0.46	0.00	0.02	0.04
DVU3116	peptide chain release factor 3 (TIGR)		1.40	1.53	1.06	0.04	1.57	1.28
DVU3117	hypothetical protein (TIGR)		0.43	0.62	0.85	0.02	0.72	0.60
DVU3118	conserved hypothetical protein (TIGR)		1.82	1.96	1.50	0.08	1.92	1.60
DVU3119	AMP-binding enzyme family protein (TIGR)		1.01	1.31	1.47	0.03	1.39	1.39
DVU3121	aminotransferase, class V (TIGR)		1.69	1.67	1.92	0.03	1.85	1.68
DVU3122	hypothetical protein (TIGR)		0.11	0.08	0.24	0.00	0.36	0.02
DVU3123	HD domain protein (TIGR)		0.84	1.18	0.68	0.02	1.20	1.00

DVU3125	lipoprotein, putative (TIGR)	pqiB	1.42	1.91	1.40	0.03	1.77	1.36
DVU3127	paraquat-inducible protein B (TIGR)		1.19	1.36	0.92	0.02	1.31	1.38
DVU3128	lipoprotein, putative (TIGR)		1.76	1.37	1.76	0.04	1.69	1.48
DVU3129	hypothetical protein (TIGR)		0.74	0.40	0.59	0.01	0.47	0.37
DVU3130	hypothetical protein (TIGR)		0.17	0.15	0.33	0.01	0.09	0.16
DVU3131	transcriptional regulator, putative (TIGR)		1.19	1.15	1.56	0.04	1.13	1.33
DVU3132	glycerol-3-phosphate dehydrogenase, FAD-depenc	glpF	1.62	1.76	1.69	0.03	1.98	1.78
DVU3133	glycerol uptake facilitator protein (TIGR)	glpK	1.26	1.39	1.03	0.04	1.31	1.19
DVU3134	glycerol kinase (TIGR)	mdaB	1.22	1.58	1.43	0.03	1.46	1.34
DVU3135	flavodoxin-like fold domain protein (TIGR)		1.58	1.04	1.13	0.03	1.21	1.23
DVU3136	nitroreductase family protein (TIGR)	fabG	1.10	1.31	1.47	0.03	1.51	1.77
DVU3137	oxidoreductase, short chain dehydrogenase/reductase famil		1.72	1.94	1.80	0.07	1.92	1.77
DVU3139	bacterial extracellular solute-binding protein, family 3 (TIGR		0.17	0.10	0.09	0.00	0.14	0.13
DVU3140	capsular polysaccharide transport protein, putative (TIGR)		1.37	1.30	1.70	0.03	1.55	1.45
DVU3141	lipoprotein, putative (TIGR)		1.20	0.97	0.62	0.01	0.79	0.68
DVU3142	sigma-54 dependent transcriptional regulator (TIGR)		1.43	1.24	1.31	0.04	1.31	1.29
DVU3143	iron-sulfur cluster-binding protein (TIGR)		1.59	1.52	1.46	0.04	1.70	1.48
DVU3144	cytochrome c family protein (TIGR)	b1670	1.22	1.21	1.16	0.02	1.28	1.15
DVU3145	hydrogenase, b-type cytochrome subunit, putative (TIGR)		2.09	1.67	2.05	0.04	2.07	1.87
DVU3146	hypothetical protein (TIGR)		1.64	1.43	1.89	0.03	1.62	1.49
DVU3147	6-phosphofructo-2-kinase/fructose-2,6-biphospha	malQ	1.26	1.16	1.08	0.03	1.14	1.17
DVU3148	4-alpha-glucanotransferase (TIGR)	sppA	0.73	1.16	1.22	0.02	1.05	1.05
DVU3149	signal peptide peptidase SppA, 36K type (TIGR)	rpsA	0.50	0.60	0.49	0.01	0.62	0.57
DVU3150	ribosomal protein S1 (TIGR)		0.06	0.02	0.08	0.00	0.00	0.00
DVU3151	MiaB-like tRNA modifying enzyme YliG, TIGR01125 (TIGR)		2.39	2.03	2.30	0.05	2.23	2.02
DVU3152	sensory box histidine kinase (TIGR)		2.19	1.76	1.43	0.04	1.89	1.83
DVU3153	hypothetical protein (TIGR)		2.07	2.90	3.16	0.03	2.82	3.06
DVU3154	HAM1 family protein (TIGR)	dcrH	0.39	0.30	1.59	0.01	0.39	0.08
DVU3155	methyl-accepting chemotaxis protein DcrH (TIGR)	glmS	2.18	1.87	1.90	0.04	1.97	1.94
DVU3156	glucosamine--fructose-6-phosphate aminotransferase (isom		0.00	0.00	0.10	0.00	0.00	0.00
DVU3157	conserved hypothetical protein (TIGR)	vacJhom	1.31	1.24	1.01	0.03	1.31	1.12
DVU3158	vacJ lipoprotein, putative (TIGR)	gpsA	1.64	1.36	1.70	0.01	1.53	1.24
DVU3159	glycerol-3-phosphate dehydrogenase (NAD(P)+) (TIGR)		1.85	1.83	2.15	0.03	2.22	2.26
DVU3161	ABC transporter, ATP-binding protein (TIGR)		1.74	1.64	1.26	0.03	1.65	1.74
DVU3162	ABC transporter, periplasmic substrate-binding protein (TIG		1.80	1.87	1.76	0.04	1.73	1.74
DVU3163	ABC transporter, permease protein (TIGR)		1.23	1.09	1.16	0.04	1.39	1.29
DVU3164	ABC transporter, permease protein (TIGR)		1.68	1.85	1.52	0.03	1.68	1.68
DVU3165	conserved domain protein (TIGR)		1.84	1.82	1.90	0.03	1.63	1.47
DVU3166	alanyl-tRNA synthetase family protein, putative (TIGR)		3.26	3.74	3.45	0.08	3.92	3.68
DVU3167	heme biosynthesis protein, putative (TIGR)	hemL	0.13	0.03	0.00	0.01	0.00	0.01
DVU3168	glutamate-1-semialdehyde-2,1-aminomutase (TIG	cbiG	0.01	0.01	0.05	0.01	0.00	0.01
DVU3169	cobalamin biosynthesis protein CbiG (TIGR)	cobJ	1.57	1.46	1.39	0.04	0.93	0.82
DVU3170	precorrin-3b C17-methyltransferase (TIGR)		1.81	2.18	1.81	0.03	1.01	0.89
DVU3171	cytochrome c3 (TIGR)		0.01	0.03	0.16	0.00	0.03	0.01
DVU3172	hypothetical protein (TIGR)		1.23	1.04	0.92	0.04	0.79	0.82
DVU3173	hypothetical protein (TIGR)	ubiE	0.00	0.37	0.00	0.00	0.24	0.23
DVU3174	ubiquinone/menaquinone biosynthesis methlytransferase U		0.43	0.25	0.93	0.02	0.26	0.20
DVU3175	membrane protein, putative (TIGR)		0.66	0.94	0.85	0.01	0.90	1.05
DVU3176	UDP-glucose/GDP-mannose dehydrogenase family protein (		0.04	0.05	0.60	0.01	0.05	0.11
DVU3177	hypothetical protein (TIGR)		0.76	0.63	0.19	0.00	0.84	0.56
DVU3178	conserved hypothetical protein (TIGR)	ispB	0.78	0.74	1.66	0.03	0.82	0.57
DVU3179	octaprenyl-diphosphate synthase (TIGR)		0.12	0.08	0.50	0.01	0.04	0.04
DVU3180	GGDEF domain protein (TIGR)	purL	1.72	1.47	1.72	0.04	1.57	1.38
DVU3181	phosphoribosylformylglycinamidine synthase II (TI	dcrA	0.60	0.57	0.53	0.01	0.01	0.02
DVU3182	methyl-accepting chemotaxis protein DcrA (TIGR)	rbO	1.69	1.62	1.42	0.03	1.40	1.48
DVU3183	desulfoferrodoxin (TIGR)		0.41	0.44	0.84	0.03	0.72	0.71
DVU3184	rubredoxin (TIGR)	roO	0.47	0.73	0.39	0.00	0.90	1.02
DVU3185	rubredoxin-oxygen oxidoreductase (TIGR)		1.23	1.69	1.66	0.04	1.67	1.61
DVU3186	hypothetical protein (TIGR)	hup-4	1.23	1.47	1.40	0.04	1.29	1.09
DVU3187	DNA-binding protein HU (TIGR)		0.35	0.80	0.80	0.05	0.95	1.07
DVU3188	NLP/P60 family protein (TIGR)		1.03	1.20	1.31	0.04	1.21	1.09
DVU3189	NOL1/NOP2/sun family protein (TIGR)		1.29	1.59	1.32	0.03	1.84	1.77
DVU3190	hypothetical protein (TIGR)	rluC	0.01	0.00	0.00	0.00	0.00	0.00
DVU3191	ribosomal large subunit pseudouridine synthase C (TIGR)		1.23	0.87	0.96	0.04	0.77	0.96
DVU3192	glycosyl transferase, group 1 family protein (TIGR)		0.10	0.01	0.32	0.01	0.01	0.02
DVU3193	DNA-binding domain, excisionase family (TIGR)	engA	0.99	1.18	1.27	0.02	1.18	0.98
DVU3194	GTP-binding protein EngA (TIGR)		0.03	0.05	0.30	0.01	0.01	0.01

DVU3195	lipoprotein, putative (TIGR)		0.92	1.06	1.03	0.02	1.00	0.93
DVU3196	twin-arginine translocation pathway signal sequen	ilvE	1.28	1.31	1.41	0.03	1.48	1.23
DVU3197	branched-chain amino acid aminotransferase (TIG	dnaZX	1.66	1.80	1.89	0.03	0.10	0.07
DVU3198	DNA polymerase III, gamma and tau subunits, putative (TIGF		0.00	0.00	0.03	0.00	0.00	0.00
DVU3199	conserved hypothetical protein TIGR00103 (TIGR)	recR	0.87	0.85	0.98	0.01	0.60	0.77
DVU3200	recombination protein RecR (TIGR)		1.29	1.55	1.59	0.04	1.66	1.60
DVU3201	hypothetical protein (TIGR)		1.37	1.92	1.47	0.03	1.74	1.56
DVU3202	hydrolase, TatD family (TIGR)	holB	1.15	1.50	0.88	0.01	0.98	0.92
DVU3203	DNA polymerase III, delta prime subunit, putative	purA	0.05	0.01	0.09	0.00	0.02	0.01
DVU3204	adenylosuccinate synthetase (TIGR)		0.00	0.02	0.00	0.00	0.00	0.00
DVU3205	transglycosylase SLT domain protein (TIGR)	purH	1.51	1.68	1.33	0.04	1.71	1.59
DVU3206	phosphoribosylaminoimidazolecarboxamide formyltransfera		0.79	1.21	0.09	0.00	0.01	0.01
DVU3207	RNB-like family protein (TIGR)		0.95	1.26	1.72	0.04	1.40	1.01
DVU3208	membrane protein, putative (TIGR)	thrC	0.39	0.48	0.41	0.01	0.50	0.44
DVU3210	threonine synthase (TIGR)	nox	0.18	0.11	0.02	0.00	0.03	0.02
DVU3212	pyridine nucleotide-disulfide oxidoreductase (TIGR)		0.08	0.06	0.17	0.00	0.13	0.07
DVU3213	hypothetical protein (TIGR)		0.86	0.80	1.36	0.00	1.13	0.89
DVU3214	phosphoenolpyruvate synthase-related protein (TI	drrA	0.76	0.77	1.04	0.02	0.88	0.95
DVU3215	response regulator (TIGR)	cckA	1.03	0.98	1.13	0.04	1.01	0.95
DVU3216	sensor histidine kinase (TIGR)		1.13	1.07	0.98	0.02	1.11	1.00
DVU3217	hypothetical protein (TIGR)	pncA	0.81	0.65	0.83	0.03	0.82	0.77
DVU3218	pyrazinamidase/nicotinamidase (TIGR)		1.84	1.42	1.32	0.03	1.79	1.46
DVU3219	hypothetical protein (TIGR)	atoC	0.97	1.34	1.21	0.03	1.17	1.36
DVU3220	sigma-54 dependent transcriptional regulator/response regu		0.00	0.00	0.08	0.00	0.00	0.00
DVU3221	sensor histidine kinase (TIGR)	pgi	0.14	0.08	0.39	0.00	0.01	0.01
DVU3222	glucose-6-phosphate isomerase (TIGR)	aspB	0.09	0.04	0.41	0.00	0.01	0.02
DVU3223	aspartate aminotransferase (TIGR)	sfsA	1.83	2.25	4.79	0.10	3.51	2.91
DVU3224	sugar fermentation stimulation protein (TIGR)		1.44	1.43	1.42	0.04	1.44	1.46
DVU3225	hypothetical protein (TIGR)		0.81	0.90	1.20	0.01	0.89	1.01
DVU3226	hypothetical protein (TIGR)		1.38	1.52	1.25	0.04	1.76	1.59
DVU3227	flagellar basal body-associated protein, putative (T	cheY-3	1.14	1.25	1.24	0.04	1.54	1.62
DVU3228	chemotaxis protein CheY (TIGR)	fliA	1.39	0.67	0.88	0.02	0.90	0.93
DVU3229	RNA polymerase sigma factor for flagellar operon FliA (TIGR		1.19	1.05	0.73	0.04	1.44	1.61
DVU3230	flagellar synthesis regulator FleN (TIGR)		1.25	0.56	0.41	0.01	0.35	0.44
DVU3231	flagellar biosynthesis protein FlhF, putative (TIGR)	flhA	1.45	1.69	1.51	0.04	1.48	1.47
DVU3232	flagellar biosynthetic protein FlhA (TIGR)	flhB	1.54	2.01	2.11	0.04	2.54	2.33
DVU3233	flagellar biosynthetic protein FlhB (TIGR)		1.70	1.47	1.45	0.03	2.11	2.08
DVU3234	flagellar biosynthetic protein FliR (TIGR)	purH	1.27	1.39	1.47	0.03	1.73	1.68
DVU3235	IMP cyclohydrolase, putative (TIGR)	hflX	1.50	1.46	0.54	0.00	0.02	0.02
DVU3236	GTP-binding protein HflX (TIGR)		1.37	1.71	1.50	0.04	1.60	1.46
DVU3237	phosphoenolpyruvate synthase-related protein (TIGR)		2.06	1.97	2.09	0.04	2.03	2.02
DVU3238	response regulator (TIGR)		1.34	0.99	1.74	0.07	1.20	1.05
DVU3239	PAP2 family protein (TIGR)		1.04	1.45	1.37	0.03	1.18	1.08
DVU3240	peptidase, M23/M37 family (TIGR)		1.31	1.27	1.84	0.02	1.50	1.57
DVU3241	conserved hypothetical protein (TIGR)	rpoZ	2.05	1.73	1.67	0.05	1.74	1.70
DVU3242	DNA-directed RNA polymerase, omega subunit (TI	dnaJ	0.53	0.39	0.84	0.02	0.53	0.58
DVU3243	dnaJ protein (TIGR)	greA	0.91	0.83	1.07	0.02	0.78	0.94
DVU3245	transcription elongation factor GreA (TIGR)		1.02	1.55	1.55	0.03	1.04	1.22
DVU3246	RND efflux system, outer membrane protein, NodT family (T		1.42	1.38	1.58	0.03	1.65	1.56
DVU3247	efflux transporter, RND family, MFP subunit (TIGR)		1.91	2.07	1.84	0.05	2.14	1.98
DVU3248	AcrB/AcrD/AcrF family protein (TIGR)		1.65	1.53	1.56	0.03	1.44	1.42
DVU3249	lipoprotein, putative (TIGR)		2.37	2.18	2.46	0.04	2.21	2.19
DVU3250	hypothetical protein (TIGR)		1.70	1.93	2.13	0.05	1.85	1.84
DVU3251	membrane protein, HPP family (TIGR)		1.68	2.35	2.36	0.05	2.04	2.13
DVU3252	hypothetical protein (TIGR)		0.93	0.82	0.44	0.02	0.86	0.71
DVU3253	phenylacetate-coenzyme A ligase, putative (TIGR)		0.33	0.30	0.16	0.00	0.30	0.45
DVU3254	PDZ domain protein (TIGR)		1.01	1.37	1.07	0.03	1.44	1.28
DVU3255	transcriptional regulator, CopG family (TIGR)	mutM	1.88	1.63	1.20	0.05	1.46	1.54
DVU3256	formamidopyrimidine-DNA glycosylase (TIGR)		1.87	1.94	1.47	0.04	1.80	1.83
DVU3257	DNA internalization-related competence protein C	murA	1.76	1.76	2.00	0.04	1.84	1.67
DVU3258	UDP-N-acetylglucosamine 1-carboxyvinyltransfera	xth	0.00	0.00	0.14	0.00	0.00	0.00
DVU3259	exodeoxyribonuclease III (TIGR)		1.32	1.23	1.36	0.02	1.30	1.45
DVU3260	hypothetical protein (TIGR)	frdC	0.79	0.86	1.97	0.02	0.96	0.93
DVU3261	fumarate reductase, cytochrome b subunit (TIGR)	fdrA	2.53	1.91	2.02	0.05	1.73	1.69
DVU3262	fumarate reductase, flavoprotein subunit (TIGR)	frdB	2.15	2.16	1.97	0.05	2.38	2.23
DVU3263	fumarate reductase, iron-sulfur protein (TIGR)		1.46	1.17	1.82	0.04	1.52	1.41
DVU3264	tartrate dehydratase alpha subunit, putative (TIGR)		1.08	1.30	1.50	0.04	1.21	1.16

DVU3265	tartrate dehydratase beta subunit, putative (TIGR)		1.47	1.76	1.82	0.03	1.92	1.82
DVU3266	conserved hypothetical protein (TIGR)		1.11	1.42	0.96	0.03	1.38	1.53
DVU3267	hypothetical protein (TIGR)		1.01	1.28	0.76	0.05	1.38	1.19
DVU3268	conserved hypothetical protein (TIGR)		2.04	1.82	1.83	0.04	1.74	1.74
DVU3269	sensory box histidine kinase/response regulator (T	cydB	3.82	3.61	4.04	0.09	3.79	3.76
DVU3270	cytochrome d ubiquinol oxidase, subunit II (TIGR)	cydA	2.99	3.00	3.73	0.07	3.12	3.20
DVU3271	cytochrome d ubiquinol oxidase, subunit I (TIGR)		2.24	2.21	1.68	0.05	2.08	2.14
DVU3272	TPR domain protein (TIGR)		1.57	1.49	2.17	0.03	1.46	1.48
DVU3273	conserved hypothetical protein (TIGR)		1.38	1.31	1.75	0.03	1.29	1.31
DVU3274	hypothetical protein (TIGR)		0.30	0.33	0.61	0.03	0.29	0.26
DVU3275	hypothetical protein (TIGR)		0.65	0.59	0.94	0.02	1.28	0.73
DVU3276	ferredoxin I (TIGR)		0.00	0.00	0.21	0.00	0.01	0.03
DVU3277	hypothetical protein (TIGR)	htrA	1.68	1.29	0.97	0.05	1.18	1.63
DVU3278	peptidase/PDZ domain protein (TIGR)	cobT	2.01	2.29	1.94	0.05	2.15	2.06
DVU3279	nicotinate-nucleotide--dimethylbenzimidazole phosphoribos		1.47	1.48	2.22	0.02	1.23	1.06
DVU3281	hypothetical protein (TIGR)		0.83	0.64	0.92	0.04	1.07	1.27
DVU3282	ADP-ribosylglycohydrolase family protein (TIGR)		2.53	2.26	3.17	0.04	1.92	1.87
DVU3283	hypothetical protein (TIGR)	b2975	1.08	1.05	1.27	1.78	1.17	1.43
DVU3284	L-lactate permease (TIGR)		2.45	2.22	1.94	0.04	1.98	1.86
DVU3285	hypothetical protein (TIGR)		0.01	0.13	0.16	0.01	0.13	0.19
DVU3287	glycosyl transferase, group 2 family protein (TIGR)		2.13	2.04	1.61	0.03	2.20	2.60
DVU3289	hypothetical protein (TIGR)		2.47	1.20	1.14	0.02	1.34	1.64
DVU3290	conserved domain protein (TIGR)		2.60	2.37	2.24	0.05	2.03	1.98
DVU3291	glutamate synthase, iron-sulfur cluster-binding subunit, puta		2.57	2.25	2.11	0.06	2.33	2.14
DVU3292	pyridine nucleotide-disulfide oxidoreductase (TIGR)		2.05	1.92	1.98	0.04	1.87	1.72
DVU3293	thiamine pyrophosphate-requiring enzyme (TIGR)	areC	2.02	1.76	1.54	0.04	1.66	1.73
DVU3294	aldehyde dehydrogenase (NADP) family protein (TIGR)		1.96	1.58	1.48	0.04	1.58	1.52
DVU3295	hemolysin III (TIGR)		2.07	2.11	2.08	0.03	2.30	1.90
DVU3296	membrane protein, putative (TIGR)	mtr	1.56	1.24	1.13	0.02	1.59	1.39
DVU3297	tryptophan-specific transport protein (TIGR)		1.67	1.54	1.70	0.03	1.54	1.48
DVU3298	hypothetical protein (TIGR)		2.08	2.28	1.79	0.04	1.82	1.79
DVU3299	membrane protein, putative (TIGR)		1.50	0.83	1.15	0.02	0.36	0.16
DVU3300	hypothetical protein (TIGR)		1.33	1.61	1.06	0.01	0.44	0.33
DVU3301	hypothetical protein (TIGR)		1.90	1.66	1.71	0.05	1.41	1.43
DVU3302	hypothetical protein (TIGR)	lon	0.38	0.35	0.77	0.02	0.40	0.25
DVU3303	ATP-dependent protease La, truncation (TIGR)		2.00	1.84	1.51	0.03	1.65	1.35
DVU3304	sensor histidine kinase	atoC	1.62	1.76	1.77	0.04	1.39	1.26
DVU3305	sigma-54 dependent transcriptional regulator/response regu		1.67	1.64	1.51	0.04	1.34	1.34
DVU3306	hypothetical protein (TIGR)	ubiX	1.77	1.66	2.45	0.04	1.71	1.70
DVU3307	3-octaprenyl-4-hydroxybenzoate carboxy-lyase (TIGR)		1.13	0.77	1.03	0.02	0.30	0.32
DVU3308	metallo-beta-lactamase family protein (TIGR)		1.33	1.69	1.36	0.03	1.41	1.12
DVU3309	endo/excinuclease amino terminal domain protein	deaD	2.20	2.66	1.55	0.03	1.83	1.45
DVU3310	ATP-dependent RNA helicase, DEAD/DEAH family (TIGR)		2.28	2.34	0.51	0.01	0.27	0.11
DVU3311	hypothetical protein (TIGR)		3.66	2.07	3.34	0.12	2.36	2.28
DVU3312	conserved hypothetical protein (TIGR)		1.80	1.20	1.26	0.13	1.33	1.50
DVU3313	transcriptional regulator, LysR family (TIGR)		2.30	2.29	1.64	0.05	1.85	1.86
DVU3314	peptidase, U32 family (TIGR)	pyrK	1.17	1.16	1.12	0.02	0.78	0.57
DVU3315	dihydroorotate dehydrogenase, electron transfer s	pyrD	1.06	0.79	0.82	0.02	0.00	0.01
DVU3316	dihydroorotate dehydrogenase (TIGR)		0.64	0.79	0.30	0.01	0.00	0.00
DVU3318	hypothetical protein (TIGR)	putA	0.90	0.95	1.17	0.11	1.07	1.18
DVU3319	proline dehydrogenase/delta-1-pyrroline-5-carboxylate deh		1.31	1.31	1.24	0.02	1.34	1.27
DVU3320	conserved domain protein (TIGR)		2.06	1.76	0.95	0.06	1.61	1.85
DVU3322	conserved domain protein (TIGR)		1.37	1.16	1.17	0.01	1.30	1.18
DVU3323	ABC transporter, permease protein (TIGR)		1.77	1.64	1.91	0.03	1.49	1.49
DVU3324	ABC transporter, ATP-binding protein (TIGR)		2.04	1.90	2.36	0.04	1.50	1.76
DVU3325	hypothetical protein (TIGR)		1.44	1.04	0.20	0.00	0.77	0.35
DVU3326	multidrug resistance protein, Smr family (TIGR)		1.37	1.58	1.40	0.03	1.65	1.21
DVU3327	multidrug resistance protein, Smr family (TIGR)		1.86	1.73	1.54	0.06	1.60	1.55
DVU3329	hypothetical protein (TIGR)		0.43	1.02	0.62	0.00	0.47	0.48
DVU3330	hypothetical iron-regulated P-type ATPase (Dmitry Rodionov		3.05	3.11	3.17	0.06	2.12	2.22
DVU3331	hypothetical protein (TIGR)		1.51	1.65	2.39	0.02	1.80	1.77
DVU3332	heavy metal translocating P-type ATPase (TIGR)		1.53	1.40	1.35	0.04	1.54	1.48
DVU3333	hypothetical protein (TIGR)		1.96	2.53	2.27	0.06	1.76	2.00
DVU3334	sigma-54 dependent DNA-binding response regulator (TIGR)		1.74	1.82	1.92	0.03	1.79	1.81
DVU3335	sensory box histidine kinase (TIGR)	kdpD	2.00	1.50	1.42	0.03	1.55	1.42
DVU3336	potassium channel histidine kinase domain protein	kdpC	1.91	1.62	1.67	0.05	1.41	1.10
DVU3337	potassium-transporting ATPase, C subunit (TIGR)	kdpB	3.07	2.34	2.39	0.05	2.25	2.51

DVU3338	potassium-transporting ATPase, B subunit (TIGR)	kdpA	2.35	1.77	1.68	0.05	1.65	1.68
DVU3339	potassium-transporting ATPase, A subunit (TIGR)	kdpF	1.77	1.53	1.85	0.04	1.49	1.47
DVU3339.1	potassium-transporting ATPase, KdpF subunit (TIGR)		0.80	0.90	0.99	0.00	1.08	0.73
DVU3342	hypothetical protein (TIGR)		1.73	1.45	1.55	0.02	1.38	1.32
DVU3343	hypothetical protein (TIGR)		1.77	1.55	1.16	0.02	1.85	1.68
DVU3344	hypothetical protein (TIGR)		1.87	1.70	2.53	0.05	1.91	1.85
DVU3347	pyruvate ferredoxin/flavodoxin oxidoreductase family prote		1.28	1.11	0.99	0.03	1.15	1.03
DVU3348	pyruvate ferredoxin/flavodoxin oxidoreductase, beta subuni		1.42	1.23	1.03	0.03	1.10	1.15
DVU3349	pyruvate flavodoxin/ferredoxin oxidoreductase, th	oorD	1.32	1.16	1.12	0.03	1.15	1.20
DVU3350	iron-sulfur cluster-binding protein (TIGR)	queA	3.95	3.44	3.47	0.10	4.51	3.66
DVU3351	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (T		2.93	2.60	2.66	0.06	2.66	2.64
DVU3352	lipoprotein, putative (TIGR)	coaBC	0.95	1.07	0.63	0.01	0.67	0.67
DVU3353	phosphopantothenoylcysteine decarboxylase/pho	ebs	0.16	0.12	0.45	0.01	0.02	0.03
DVU3355	SPFH domain/Band 7 family protein (TIGR)		2.40	2.51	2.17	0.05	2.11	2.60
DVU3356	NAD-dependent epimerase/dehydratase family protein (TIG		0.31	0.32	2.74	0.08	0.73	1.72
DVU3357	hypothetical protein (TIGR)	parA	1.34	0.99	1.10	0.00	0.73	0.87
DVU3358	ParA family protein (TIGR)		2.97	2.73	3.49	0.12	3.33	3.44
DVU3359	hypothetical protein (TIGR)	parB	0.35	0.13	0.27	0.04	0.17	1.33
DVU3360	ParB family protein (TIGR)	rfaE	2.57	2.21	2.32	0.06	2.72	3.28
DVU3361	ADP-heptose synthase, putative (TIGR)		0.06	0.02	0.22	0.01	0.01	0.03
DVU3362	conserved hypothetical protein (TIGR)	sun	1.20	0.98	0.89	0.03	1.35	1.60
DVU3363	sun protein (TIGR)		2.21	1.79	1.69	0.04	2.29	2.37
DVU3364	conserved hypothetical protein (TIGR)	fmt	2.57	2.54	1.35	0.03	2.00	2.56
DVU3365	methionyl-tRNA formyltransferase (TIGR)	def	0.21	0.33	0.44	0.02	0.14	0.10
DVU3366	polypeptide deformylase (TIGR)	aspS	0.29	0.12	0.54	0.00	0.12	0.07
DVU3367	aspartyl-tRNA synthetase (TIGR)	hisS	0.00	0.01	0.08	0.00	0.00	0.00
DVU3368	histidyl-tRNA synthetase (TIGR)		0.03	0.02	0.03	0.00	0.00	0.00
DVU3369	conserved domain protein (TIGR)	metE	1.16	0.89	1.07	0.04	1.34	1.07
DVU3371	5-methyltetrahydropteroyltriglutamate-homocysteine S-me		2.78	2.26	2.51	0.04	2.08	2.07
DVU3372	hypothetical protein (TIGR)	ilvD	2.77	2.37	1.36	0.04	1.99	1.78
DVU3373	dihydroxy-acid dehydratase (TIGR)		1.78	1.77	1.59	0.02	0.20	0.26
DVU3374	permease, putative (TIGR)	ftsE	2.37	2.15	1.59	0.05	1.68	1.72
DVU3375	cell division ATP-binding protein FtsE, putative (TIGR)		1.35	1.34	1.81	0.03	1.36	1.33
DVU3376	sulfatase family protein (TIGR)	dgkA	1.13	1.05	0.77	0.03	1.13	1.23
DVU3377	diacylglycerol kinase (TIGR)		2.08	2.04	1.99	0.01	2.01	2.40
DVU3378	YbaK/EbsC protein (TIGR)		1.50	1.79	1.22	0.03	1.55	1.51
DVU3379	ribonucleoside-diphosphate reductase (TIGR)		1.70	1.60	1.36	0.03	1.58	1.57
DVU3380	hypothetical protein (TIGR)	ntrC	1.98	1.59	1.47	0.00	1.38	1.81
DVU3381	transcriptional regulatory protein zraR (TIGR)	zraS	2.57	2.13	2.50	0.03	2.22	2.10
DVU3382	sensor protein ZraS (TIGR)	zraP	1.62	1.52	1.31	0.03	1.54	1.39
DVU3384	zinc resistance-associated protein (TIGR)		1.81	1.74	1.48	0.05	1.62	1.57
DVU3386	permease, putative (TIGR)		2.12	1.84	2.11	0.04	1.76	1.53
DVU3387	hypothetical protein (TIGR)		1.99	2.10	2.18	0.03	2.33	2.04
DVU3388	lipoprotein, putative (TIGR)	topA	1.30	1.15	1.19	0.05	1.35	1.15
DVU3389	DNA topoisomerase I (TIGR)	glnA	0.03	0.00	0.02	0.00	0.00	0.00
DVU3392	glutamine synthetase, type I (TIGR)		1.71	1.93	1.53	0.03	1.00	0.99
DVU3393	hypothetical protein (TIGR)		1.35	1.43	2.37	0.03	1.04	1.13
DVU3394	hypothetical protein (TIGR)		0.49	0.52	0.71	0.03	0.79	0.78
DVU3395	peptidase, M23/M37 family (TIGR)		1.73	1.36	1.27	0.05	1.47	1.41
DVUA0001	hypothetical protein (TIGR)	soj	0.17	0.05	0.00	0.00	0.07	0.23
DVUA0002	ParA family protein (TIGR)		0.18	0.10	0.25	0.19	0.07	0.10
DVUA0003	hypothetical protein (TIGR)		0.02	0.01	0.02	0.01	0.01	0.00
DVUA0004	DNA-binding protein HU, putative (TIGR)		0.44	0.69	1.40	0.43	0.49	0.60
DVUA0005	universal stress protein family (TIGR)	mgtE	1.09	0.87	0.72	0.54	0.81	1.02
DVUA0006	magnesium transporter MgtE, putative (TIGR)	nifB	0.87	0.78	0.62	0.55	0.66	0.69
DVUA0007	nitrogenase cofactor biosynthesis protein NifB (TI	nifN	1.22	1.30	1.50	1.00	1.25	1.19
DVUA0008	nitrogenase molybdenum-iron cofactor biosynthes	nifE	1.46	1.27	1.45	0.86	1.29	1.23
DVUA0009	nitrogenase MoFe cofactor biosynthesis protein NifE domai		1.33	1.50	1.40	0.80	1.39	1.40
DVUA0010	ferredoxin, 2fe-2s (TIGR)	nifK	0.93	0.88	0.46	0.21	0.76	0.64
DVUA0011	nitrogenase molybdenum-iron protein beta chain	nifD	1.03	1.23	1.44	0.71	1.06	1.11
DVUA0012	nitrogenase molybdenum-iron protein alpha chain	glnB-2	0.81	0.97	0.79	0.68	0.93	1.02
DVUA0013	nitrogen regulatory protein P-II (TIGR)	glnB-3	1.03	0.78	0.76	0.19	0.85	0.79
DVUA0014	nitrogen regulatory protein P-II (TIGR)	nifH	1.03	1.94	1.34	1.12	1.43	1.36
DVUA0015	nitrogenase iron protein (TIGR)	nifV	1.41	1.67	1.47	0.80	1.64	1.59
DVUA0016	homocitrate synthase (TIGR)		1.60	1.51	1.28	0.77	1.63	1.55
DVUA0019	type II DNA modification methyltransferase, putative (TIGR)		0.01	0.00	0.01	0.00	0.00	0.00
DVUA0020	type II restriction endonuclease, putative (TIGR)		0.51	0.33	0.52	0.19	0.53	0.52

DVUA0020.1	Abortive infection protein		1.25	1.03	0.82	0.69	1.19	1.06
DVUA0021	conserved hypothetical protein (TIGR)		1.14	1.08	0.99	0.52	1.12	0.98
DVUA0022	ABC transporter, ATP-binding protein (TIGR)		1.56	1.16	1.60	0.95	1.16	1.16
DVUA0023	ABC transporter, permease protein, putative (TIGF	atoC	1.17	1.30	1.13	68.39	1.40	1.15
DVUA0024	sigma-54 interaction domain protein (TIGR)		0.95	1.12	1.20	0.96	1.18	1.18
DVUA0025	response regulator receiver domain protein (TIGR)		2.47	1.80	2.37	1.18	2.08	2.07
DVUA0028	hypothetical protein (TIGR)		0.05	0.24	0.30	0.16	0.24	0.22
DVUA0029	hypothetical protein (TIGR)		0.35	0.48	0.56	0.57	0.42	0.42
DVUA0030	hypothetical protein (TIGR)		1.04	1.18	1.43	1.12	1.27	1.56
DVUA0031	hypothetical protein (TIGR)		0.97	1.14	1.30	0.98	1.06	1.19
DVUA0032	hypothetical protein (TIGR)		1.43	1.29	1.04	0.98	1.41	1.43
DVUA0034	conserved domain protein (TIGR)		1.16	1.16	1.14	0.80	1.07	1.17
DVUA0036	TPR domain protein (TIGR)		1.45	1.26	1.25	0.58	1.27	1.20
DVUA0037	sugar transferase domain protein (TIGR)	b0983	1.08	1.36	1.15	0.32	1.18	1.13
DVUA0038	capsular polysaccharide transport protein (TIGR)		1.32	1.45	1.37	0.42	1.25	1.26
DVUA0039	chain length determinant family protein (TIGR)		1.33	1.53	1.67	0.66	1.31	1.31
DVUA0040	polysaccharide biosynthesis protein, putative (TIG	exeA	1.71	1.64	1.93	1.26	1.69	1.62
DVUA0041	conserved domain protein (TIGR)		1.34	1.18	1.15	0.98	1.23	1.35
DVUA0042	lipoprotein, putative (TIGR)		1.10	0.82	0.73	0.50	0.94	0.92
DVUA0043	polysaccharide deacetylase family protein (TIGR)		1.50	1.17	1.43	0.78	1.09	1.11
DVUA0044	conserved hypothetical protein (TIGR)		1.61	1.07	1.24	0.67	1.37	1.13
DVUA0045	aminotransferase, DegT/DnrJ/EryC1/StrS family (TIGR)		1.32	1.51	1.15	0.86	1.36	1.14
DVUA0046	glycosyl transferase, group 2 family protein (TIGR)		1.03	1.12	1.17	0.71	1.09	0.99
DVUA0047	hypothetical protein (TIGR)		1.05	1.13	0.91	0.60	0.99	1.01
DVUA0048	exopolysaccharide production protein, putative (TIGR)		1.54	1.49	1.56	0.44	1.41	1.38
DVUA0049	polysaccharide biosynthesis family protein (TIGR)		1.88	1.72	1.90	0.79	1.68	1.68
DVUA0050	conserved hypothetical protein (TIGR)		1.02	1.02	1.04	0.56	1.18	1.02
DVUA0051	glycosyl transferase, group 1 family protein (TIGR)		1.14	1.10	1.39	0.45	1.16	0.98
DVUA0052	conserved hypothetical protein (TIGR)		1.39	1.17	1.07	0.64	1.14	1.55
DVUA0053	conserved hypothetical protein (TIGR)		1.29	1.08	1.31	0.33	1.06	0.96
DVUA0054	glycosyl transferase, group 1 family protein (TIGR)		1.12	1.12	1.18	0.60	1.08	0.88
DVUA0055	membrane protein, putative (TIGR)		1.21	1.27	1.32	0.62	1.30	1.22
DVUA0056	hypothetical protein (TIGR)	atoC	1.45	1.49	1.52	0.55	1.33	1.27
DVUA0057	sigma-54 dependent transcriptional regulator/response regu		0.90	0.72	0.76	0.42	0.85	0.80
DVUA0058	BNR/Asp-box repeat protein (TIGR)		1.17	1.01	1.12	0.65	1.08	1.00
DVUA0059	conserved hypothetical protein (TIGR)		1.23	1.27	1.28	0.61	1.13	1.02
DVUA0060	membrane protein, putative (TIGR)		1.27	1.16	1.64	0.82	1.21	1.20
DVUA0061	membrane protein, putative (TIGR)		1.12	1.27	1.34	0.88	1.21	1.11
DVUA0062	conserved domain protein (TIGR)		1.05	1.12	1.07	0.85	1.14	1.07
DVUA0063	Orn/DAP/Arg family decarboxylase (TIGR)		1.42	1.21	0.97	0.67	1.12	1.03
DVUA0063.1	Methicillin resistance protein		1.05	1.26	1.15	0.45	1.32	1.10
DVUA0064	conserved domain protein (TIGR)		1.09	1.17	1.37	0.54	1.14	1.00
DVUA0065	sensor histidine kinase (TIGR)		0.95	1.00	1.04	0.56	1.11	1.12
DVUA0066	phospholipase, patatin family (TIGR)		1.56	1.55	1.42	0.61	1.38	1.32
DVUA0067	membrane protein, putative (TIGR)		0.06	0.08	0.14	0.14	0.09	0.13
DVUA0068	membrane protein, putative (TIGR)		1.01	0.89	0.85	0.46	0.94	0.85
DVUA0069	GtrA family protein, selenocysteine-containing (TIGR)		0.49	0.92	0.82	0.37	0.93	0.92
DVUA0070	conserved domain protein (TIGR)		0.70	0.62	0.81	0.51	0.43	0.60
DVUA0071	glycosyl transferase, group 1/2 family protein (TIGR)		0.80	0.86	0.76	0.45	0.92	0.99
DVUA0072	glycosyl transferase, group 1 family protein (TIGR)		0.24	0.17	0.50	0.40	0.02	0.03
DVUA0073	asparagine synthase (glutamine-hydrolyzing), putative (TIGR		0.68	0.63	0.78	0.43	0.15	0.57
DVUA0074	sulfotransferase family protein (TIGR)		0.58	0.55	0.46	0.69	0.57	0.79
DVUA0075	radical SAM domain protein (TIGR)		0.63	0.48	0.50	0.37	0.20	0.56
DVUA0076	ABC transporter, ATP-binding protein (TIGR)		0.70	0.59	0.81	0.31	0.15	0.59
DVUA0077	ABC transporter, permease protein (TIGR)	cysC	0.86	0.62	0.86	0.51	0.14	0.55
DVUA0079	adenylylsulfate kinase (TIGR)		0.43	0.38	0.56	0.42	0.44	0.56
DVUA0080	glycosyl transferase, group 2 family protein (TIGR)		1.06	0.89	0.68	0.27	1.05	1.15
DVUA0081	glycosyl transferase, group 1/2 family protein (TIG	xerD	0.79	0.70	0.91	0.26	0.82	0.92
DVUA0082	site-specific recombinase, phage integrase family (TIGR)		0.76	1.09	0.93	0.58	1.01	0.94
DVUA0084	transcriptional regulator, AbrB family (TIGR)		0.42	0.20	0.14	0.05	0.47	0.57
DVUA0085	conserved hypothetical protein (TIGR)		0.37	0.34	0.30	0.18	0.48	0.52
DVUA0086	response regulator (TIGR)		0.95	0.67	0.56	0.30	0.90	0.89
DVUA0087	sensory box histidine kinase (TIGR)		0.88	0.99	0.96	0.42	1.08	1.09
DVUA0088	conserved hypothetical protein (TIGR)		1.03	1.12	1.27	0.59	1.02	1.06
DVUA0089	hypothetical protein (TIGR)		0.43	0.40	0.35	0.25	0.33	0.45
DVUA0090	membrane protein, putative (TIGR)	katA	0.71	0.64	1.05	0.48	0.72	0.62
DVUA0091	catalase (TIGR)		0.98	0.90	0.99	0.60	1.08	0.99

DVUA0092	hypothetical protein (TIGR)		0.56	0.66	0.48	0.29	0.71	0.75
DVUA0093	chromate transport family protein (TIGR)	chrB	0.68	0.99	1.04	0.75	1.01	1.09
DVUA0094	chrB protein (TIGR)		0.97	1.27	1.02	0.75	1.06	1.14
DVUA0096	major facilitator superfamily protein (TIGR)		0.83	1.08	0.64	0.73	0.81	0.85
DVUA0097	radical SAM domain protein (TIGR)		1.03	0.99	0.91	0.57	1.16	1.13
DVUA0098	dehydrogenase, putative (TIGR)		0.99	1.09	0.99	0.47	1.13	1.06
DVUA0099	HAMP domain protein (TIGR)	flrC	1.04	1.21	1.29	0.82	1.25	1.13
DVUA0100	sigma-54 dependent transcriptional regulator (TIG	flhB	0.74	0.93	0.83	0.43	1.10	1.06
DVUA0101	type III secretion protein, hrpY/hrcU family (TIGR)	escT	0.84	0.90	0.86	0.46	0.78	0.97
DVUA0102	type III secretion inner membrane protein (TIGR)	invX	1.41	1.52	1.47	1.00	1.90	1.83
DVUA0103	type III secretion protein, HrpO family (TIGR)	sctV	4.04	2.86	2.03	0.91	3.03	3.37
DVUA0104	type III secretion inner membrane protein, HrcV family (TIGI		1.07	1.13	1.14	0.42	1.22	1.18
DVUA0104.1	Tetratricopeptide TPR_4		1.35	1.75	2.66	0.81	2.00	1.82
DVUA0105	conserved hypothetical protein (TIGR)		0.65	1.19	0.99	0.32	1.30	1.27
DVUA0106	type III secretion target, YopN family (TIGR)		1.60	1.61	1.30	1.01	1.61	1.66
DVUA0108	hypothetical protein (TIGR)		1.06	1.15	0.92	0.46	0.99	1.27
DVUA0109	type III secretion system chaperone, LcrH/SycD family (TIGR		1.26	1.03	0.81	0.06	1.12	1.10
DVUA0110	type III secretion system target, YopB family (TIGR)		0.72	1.18	1.35	1.78	1.14	1.29
DVUA0111	type III secretion system protein, IpaC family, putative (TIGR		0.76	0.72	0.69	0.58	0.88	0.89
DVUA0111.1	Tir chaperone family protein		0.84	0.76	0.38	0.27	0.68	0.73
DVUA0112	type III secretion system protein, YscC family (TIGR)		0.88	1.09	0.95	0.42	1.01	1.03
DVUA0113	type III secretion protein, YscD family (TIGR)		1.00	1.07	1.04	0.35	1.02	1.08
DVUA0114	hypothetical protein (TIGR)		0.98	0.92	1.03	0.42	0.93	0.64
DVUA0115	type III secretion system protein, YscF family (TIGR)		2.58	2.39	3.11	1.62	2.95	3.16
DVUA0116	conserved hypothetical protein (TIGR)	escJ	0.75	0.87	0.51	0.43	0.87	0.80
DVUA0117	type III secretion lipoprotein (TIGR)		0.98	1.18	0.82	0.79	1.08	1.06
DVUA0118	type III secretion protein, YopL family (TIGR)	sctN	0.84	0.85	0.98	1.81	1.05	1.03
DVUA0119	type III secretion system ATPase (TIGR)		0.84	1.05	1.05	0.56	1.03	1.14
DVUA0119.1	type III secretion YscO fmaily protein		1.26	1.05	0.86	0.24	1.15	1.24
DVUA0120	type III secretion protein, putative (TIGR)		0.94	1.00	1.02	0.72	0.88	0.72
DVUA0121	type III secretion system protein, YopQ family (TIG	yscR	0.98	1.02	0.91	0.80	1.12	1.03
DVUA0122	type III secretion system protein, YscR family (TIGR)		0.72	0.80	0.65	0.35	0.85	0.86
DVUA0123	anti-anti-sigma factor (TIGR)		0.80	0.95	0.85	0.35	0.56	0.58
DVUA0124	sigma factor serine-protein kinase (TIGR)	slt	0.11	0.11	0.06	0.10	0.04	0.06
DVUA0125	transglycosylase, SLT family (TIGR)		1.21	1.14	1.00	0.46	1.16	1.17
DVUA0126	conserved hypothetical protein (TIGR)	cas3	1.19	1.35	1.36	0.62	1.16	1.24
DVUA0129	CRISPR-associated helicase Cas3 domain protein (TIGR)		1.29	1.18	1.10	0.82	1.25	1.38
DVUA0130	CRISPR-associated protein, CT1134 family (TIGR)		0.96	0.89	0.76	0.14	0.80	0.84
DVUA0131	CRISPR-associated protein, CT1133 family (TIGR)		1.09	1.02	1.00	0.44	1.05	1.12
DVUA0132	CRISPR-associated protein, TM1801 family (TIGR)		1.31	1.33	0.87	0.64	1.33	1.44
DVUA0133	CRISPR-associated protein Cas4 (TIGR)	cas1	0.80	1.16	0.98	1.00	1.21	1.06
DVUA0134	CRISPR-associated protein Cas1 (TIGR)		1.07	1.17	1.19	0.81	1.25	1.23
DVUA0135	CRISPR-associated protein Cas2 (TIGR)	zupT	0.62	0.94	0.81	0.27	0.94	1.07
DVUA0136	zinc transporter (TIGR)		0.65	0.80	1.21	0.51	0.98	0.94
DVUA0137	response regulator (TIGR)		1.53	1.30	0.88	0.70	1.13	1.36
DVUA0138	sensor histidine kinase (TIGR)		0.92	1.15	1.11	0.63	1.20	1.16
DVUA0139	outer membrane autotransporter barrel domain protein (TI		0.98	0.82	0.74	0.34	0.96	1.04
DVUA0141	hypothetical protein (TIGR)	nifA-2	0.07	0.17	0.07	0.26	0.28	0.22
DVUA0143	nif-specific regulatory protein (TIGR)		1.20	1.19	1.20	0.52	1.17	1.21
DVUA0144	hypothetical protein (TIGR)		2.87	1.95	1.44	0.71	2.19	1.84
DVUA0145	conserved domain protein (TIGR)		1.27	1.26	1.38	0.69	1.36	1.31
DVUA0146	hypothetical protein (TIGR)		0.93	0.81	1.03	0.13	1.03	0.89
DVUA0147	conserved hypothetical protein (TIGR)		1.52	1.33	1.80	1.05	1.58	1.47
DVUA0148	major facilitator superfamily protein (TIGR)		1.12	1.08	1.05	0.86	1.22	1.11
DVUA0149	hypothetical protein (TIGR)		1.19	1.20	1.32	0.51	1.17	1.05
DVUA0150	bacterial extracellular solute-binding protein, family 3 (TIGR		1.24	1.20	0.94	0.64	1.18	1.21
DVUA0151	DNA-binding protein, putative (TIGR)		0.06	0.06	0.00	0.00	0.02	0.00
DVUA0152	conserved domain protein (TIGR)		1.08	1.24	0.85	0.47	0.91	0.77

Appendix H - Total RNA-seq data

				Normalized Transcripts Per Million (TPM)					
Gene	Name		Length	710-2	710-3	710-4	9005-1	9005-2	9005-3
DVU0001	dnaA-1 CDS	dnaA-1	1,314	194	223.8	194.2	203.3	201.9	215.1
DVU0002	dnaN CDS	dnaN	1,155	344.6	370.8	349.9	194.6	207.1	189.3
DVU0003	gyrB CDS	gyrB	2,397	417.7	457.6	437.6	310.1	321.7	272.7
DVU0004	gyrA CDS	gyrA	2,571	417.8	434.3	419.8	377.3	379.1	284.1
DVU0005	lipoprotein, putative (TIGR) CDS		786	198.7	198.2	201.5	452.9	414.6	412.3
DVU0006	universal stress protein family (TIGR) CDS		465	194.7	178.1	149.6	252	265.6	355.6
DVU0007	asnS CDS	asnS	1,386	249	225.8	201.3	178	165.8	170.4
DVU0008	hypothetical protein (TIGR) CDS		126	12.6	14.1	6.3	1.4	2.1	0
DVU0009	dctM CDS	dctM	1,281	47.2	54.5	47.9	55	59.6	44.6
DVU0010	TRAP transporter, DctQ family (TIGR) CDS		567	50.8	64.2	51.8	68.5	66.6	67
DVU0011	TRAP dicarboxylate family transporter (TIGR) CDS		1,026	80.3	94.1	79.1	83.5	84.4	90.6
DVU0012	hypothetical protein (TIGR) CDS		1,203	150.1	151.9	137.8	164.1	180.7	173.1
DVU0013	sensory box histidine kinase (TIGR) CDS		1,809	86.7	78.7	81.4	126.9	134.5	117.1
DVU0014	infA-1 CDS	infA-1	219	1329.1	1200.3	1401.1	1727	1763.1	2461.5
DVU0015	lgt CDS	lgt	792	179.9	181.1	169.1	317.5	312.5	236.3
DVU0016	hypothetical protein (TIGR) CDS		105	19.9	23.4	17.7	32.6	40.4	44.3
DVU0018	methyl-accepting chemotaxis protein, putative (TIGR) CDS		2,250	64.2	66.9	56	74.9	72.1	65.4
DVU0019	ngr CDS	ngr	609	607.2	668.6	631.8	376.1	356.1	509.2
DVU0020	hypothetical protein (TIGR) CDS		147	24.5	36.8	30.6	24.5	29.3	17.6
DVU0022	HAMP domain/GGDEF domain/EAL domain protein (TIGR) CDS		2,382	30.7	38.4	33.6	41.7	40.3	34.5
DVU0024	conserved hypothetical protein (TIGR) CDS		171	899.5	927.4	761.5	782.3	1049.6	1275.5
DVU0025	sensory box histidine kinase (TIGR) CDS		2,160	150.7	126.6	121.8	86.2	98.5	82.1
DVU0026	conserved hypothetical protein (TIGR) CDS		573	59.7	59.9	55.3	95.5	111	82.1
DVU0027	membrane protein, putative (TIGR) CDS		1,425	430.2	437.2	375.1	402.2	380	358.4
DVU0028	csaA CDS	csaA	378	193.7	193.3	184.4	108.8	113.1	87.5
DVU0029	hydantoinase/oxoprolinase family protein (TIGR) CDS		1,713	155.7	148.5	145.8	152.4	153.9	142.1
DVU0030	transcriptional regulator, GntR family (TIGR) CDS		1,503	98.4	97	96.7	80.3	88.5	54.7
DVU0032	conserved hypothetical protein (TIGR) CDS		336	97.3	65.8	77.9	96.7	135.3	89.2
DVU0033	isochorismatase family protein (TIGR) CDS		615	180.8	153.6	151.7	118.4	120.6	124.4
DVU0034	DSBA-like thioredoxin domain protein (TIGR) CDS		786	385.2	366.5	349.6	256.8	260.5	253.9
DVU0035	hypothetical protein (TIGR) CDS		174	329.2	361.3	268.8	525.3	488.4	748.6
DVU0036	hypothetical protein (TIGR) CDS		456	504.9	742.6	740.7	3813.7	3649.9	5852
DVU0037	conserved hypothetical protein (TIGR) CDS		417	320.2	251.8	263.4	315.3	272.8	223.1
DVU0038	acyltransferase domain protein (TIGR) CDS		1,851	6.3	6.5	5.5	5.6	5.6	4.2
DVU0039	C4-type zinc finger protein, DksA/TraR family (TIGR) CDS		531	9.2	13.3	9.8	14.1	11.9	12.6
DVU0040	hypothetical protein (TIGR) CDS		615	94.2	96	102.9	183.6	195.6	180.7
DVU0041	transglycosylase, SLT family (TIGR) CDS		1,764	242.1	252.3	234.7	435.1	404.7	443
DVU0043	fliQ CDS	fliQ	270	100.2	94.4	83.8	130.8	129.8	120.6
DVU0044	fliP CDS	fliP	708	133.2	119.1	121.1	307.3	293.8	417.5
DVU0045	flagellar biosynthesis protein, FliO, putative (TIGR) CDS		522	166.5	167.8	142.1	462.4	467.2	577.2
DVU0046	fliN CDS	fliN	513	286.3	279.1	252.1	514.3	487.3	564.2
DVU0047	flagellar protein FliL (TIGR) CDS		516	285.6	296.4	270.3	627.7	668.4	769.3
DVU0048	chemotaxis protein MotB (TIGR) CDS		741	206.7	186.8	174.8	206.6	188.6	209.9
DVU0049	OmpA family protein (TIGR) CDS		1,095	69.6	83.9	67.9	120.1	107.4	93.7
DVU0050	motA-1 CDS	motA-1	759	112.3	124.8	107.6	220.6	198.6	220.9
DVU0052	era CDS	era	927	428.6	417.3	398.2	474	456.9	572
DVU0054	dihydrouridine synthase family protein (TIGR) CDS		1,260	223.5	213.4	214.5	263.1	268.7	266.6
DVU0055	ispH CDS	ispH	873	157.7	152	140.8	122.6	157.3	141.5
DVU0056	cheV-1 CDS	cheV-1	954	343	316.5	308	439.8	401.5	423.7
DVU0057	transcriptional regulator, TetR family (TIGR) CDS		642	72.6	74.1	68.5	108	114.2	124
DVU0058	efflux transporter, RND family, MFP subunit (TIGR) CDS		1,152	65	68.3	68.4	77.6	78.1	67.9
DVU0059	AcrB/AcrD/AcrF family protein (TIGR) CDS		3,711	59.5	62.5	63.2	79.1	76	88.5
DVU0060	acrA CDS	acrA	1,185	358.7	380	351.7	439.3	421	770.9
DVU0061	multidrug resistance protein, putative (TIGR) CDS		3,141	256.5	260.4	245.8	732	692.5	1334.8
DVU0062	RND efflux system, outer membrane protein, NodT family (TIG		1,515	267.1	282.6	258.7	303.5	297.9	477.1
DVU0063	transcriptional regulator, MarR family (TIGR) CDS		441	247.9	249.2	238.5	271.6	285.2	423.7
DVU0064	hypothetical protein (TIGR) CDS		909	440.4	475.3	449.9	386.8	378.2	514.6
DVU0065	hypothetical protein (TIGR) CDS		798	34.8	42.5	33.7	46.5	44.8	42.7
DVU0066	cytidine/deoxycytidylate deaminase domain protein (TIGR) CD		570	85.2	84.8	81.6	54.1	47.8	53.5
DVU0067	hypothetical protein (TIGR) CDS		309	67.3	81.8	75.9	173.9	154.8	152.2
DVU0068	conserved hypothetical protein (TIGR) CDS		1,536	48.3	51.3	52.2	71.4	74.6	65.3
DVU0069	hypothetical protein (TIGR) CDS		4,404	57	59.9	59.2	61.4	60.8	59.4

DVU0070	yhaO CDS	yhaO	1,356	75.1	79.3	69.3	44.4	50.7	42.7
DVU0071	dinP CDS	dinP	1,161	62.2	61.9	59.3	76.5	82.4	66.4
DVU0072	mpg CDS	mpg	780	306.4	325.1	292.2	370.5	333.7	524.5
DVU0073	CDP-glucose-4,6-dehydratase, putative (TIGR) CDS		1,107	336	346	325.1	486.1	464.7	444.5
DVU0074	polysaccharide biosynthesis domain protein (TIGR) CDS		444	310.2	337.3	348.4	339	319.5	355.6
DVU0075	rfbE CDS	rfbE	1,134	161.6	181.1	151.7	229	227.3	260.7
DVU0076	glycosyl transferase, group 2 family protein (TIGR) CDS		1,038	152.1	169.3	154.7	131.2	140.1	124.5
DVU0077	conserved hypothetical protein (TIGR) CDS		1,083	134.7	141	132.4	102.7	92.8	92.1
DVU0078	conserved hypothetical protein (TIGR) CDS		342	40	31.1	34.7	86.2	75.6	59
DVU0079	gufA CDS	gufA	804	136	145.8	108.9	235.9	261.5	196.1
DVU0080	fumC CDS	fumC	1,407	110.7	104	92	372.4	379.4	347.5
DVU0081	sensory box histidine kinase/response regulator (TIGR) CDS		1,731	70.3	76.6	71.3	193	189.6	173.1
DVU0082	conserved hypothetical protein (TIGR) CDS		1,593	63.7	70.1	63.9	226.6	204.7	193.7
DVU0083	conserved hypothetical protein (TIGR) CDS		420	45.7	48.5	48.1	47	58.4	48
DVU0084	translation initiation factor, aIF-2BI family, putative (TIGR) CDS		1,053	191.9	167	155.5	172.6	166.1	197.8
DVU0085	trpB-1 CDS	trpB-1	1,245	93.7	252.5	120.6	279.7	268	404
DVU0087	conserved domain protein (TIGR) CDS		495	163.6	149.4	140.2	119.1	108.3	106.5
DVU0088	Sodium/pantothenate symporter (TIGR) CDS		1,488	131.2	105.5	102.7	133	128.3	114.6
DVU0089	conserved hypothetical protein (TIGR) CDS		804	88.1	73.9	71.5	87.3	85.5	70.7
DVU0090	wcaG CDS	wcaG	972	182.7	165.6	148.3	251	243.8	236.1
DVU0091	conserved hypothetical protein (TIGR) CDS		723	250.6	251.9	210.6	221.6	201.3	232.3
DVU0092	sensory box histidine kinase (TIGR) CDS		3,318	112.7	102.8	95.5	173.4	176.8	187.4
DVU0093	conserved domain protein/glycosyl transferase, group 1 family		2,451	15.2	13.5	11.3	14.7	17.4	15.6
DVU0094	methyl-accepting chemotaxis protein (TIGR) CDS		2,163	34.1	33.9	27.5	27.1	33.7	22.9
DVU0095	potD-1 CDS	potD-1	1,038	265.9	239.2	196.2	77.2	76.7	109.1
DVU0096	potC CDS	potC	774	119.4	120.5	93.4	66.7	72.4	115.5
DVU0097	potB CDS	potB	888	98.8	107.7	81.2	114.3	126.1	130.4
DVU0098	potA CDS	potA	1,107	109.7	115.5	105.1	100.9	93.7	140.1
DVU0099	TonB domain protein (TIGR) CDS		1,161	46.6	55.5	41.8	207.2	229.6	292
DVU0100	TonB-dependent receptor (TIGR) CDS		1,950	172.4	182	135.8	434.9	432.8	549.7
DVU0101	methlytransferase, UbiE/COQ5 family (TIGR) CDS		1,527	98.8	115.9	87.2	301.2	311.7	304.6
DVU0102	cation ABC transporter, periplasmic binding protein (TIGR) CDS		993	114.7	132.4	100.2	253.8	274.7	236.8
DVU0103	fepC CDS	fepC	942	92.2	100.7	85.9	266.6	281.9	220
DVU0104	cation ABC transporter, permease protein, putative (TIGR) CDS		837	66.9	77.5	58.5	155.8	172.8	127.8
DVU0105	glnQ CDS	glnQ	735	309.1	354.4	343.5	305.8	329.4	274.3
DVU0106	glnP CDS	glnP	672	464.2	498	482.9	832.3	748.7	1112.9
DVU0107	glnH CDS	glnH	750	1067.2	1101	1010.3	597.7	607.9	752.5
DVU0108	hypothetical protein (TIGR) CDS		108	10	11.9	9	10.8	5.6	9.6
DVU0110	ntrC CDS	ntrC	1,431	156.5	146.9	145.4	128.9	131	121.9
DVU0111	response regulator (TIGR) CDS		807	213.3	200.9	198.2	166.5	168.4	145.4
DVU0112	phrB CDS	phrB	1,425	109.8	101.4	95.9	148	133.1	135.3
DVU0113	hisI CDS	hisI	381	354.8	393.9	355.6	545	555.1	446.3
DVU0114	hisG CDS	hisG	882	355.7	392.4	377.3	404.3	413.2	390.9
DVU0115	aroE CDS	aroE	906	51.2	54.4	60.4	36.5	44.4	43.3
DVU0116	polysaccharide deacetylase family protein (TIGR) CDS		1,077	97.2	103.3	105.5	88.1	97.5	72.5
DVU0117	glycosyl transferase, group 2 family protein (TIGR) CDS		918	86.1	90.4	88.7	77.3	85	74.9
DVU0118	ntrC CDS	ntrC	1,365	80.1	73.4	68.8	80.7	78.2	65.3
DVU0119	sensor histidine kinase (TIGR) CDS		1,665	68.5	78.5	72	95.9	102.3	84.9
DVU0120	ABC transporter, substrate-binding protein, putative (TIGR) CDS		939	56.4	51.8	48.6	77.3	73.1	62.2
DVU0121	conserved hypothetical protein (TIGR) CDS		444	117.9	116.9	109.3	426.3	425.6	386.5
DVU0122	hypothetical protein (TIGR) CDS		99	30.8	52.2	31.2	12.7	15.6	2.6
DVU0123	membrane protein, putative (TIGR) CDS		1,083	18.6	26.7	17.1	19.6	22.7	18.9
DVU0124	hypothetical protein (TIGR) CDS		189	17.1	15.3	18.9	10	12.1	10.9
DVU0125	hypothetical protein (TIGR) CDS		1,134	65.3	57.1	53	105.5	109.3	82.7
DVU0126	b3486 CDS	b3486	3,516	35.3	36.2	29.7	62.5	69.2	52.6
DVU0127	membrane protein, putative (TIGR) CDS		1,113	94.2	86.6	87.4	129.1	130.5	112.2
DVU0128	membrane protein, putative (TIGR) CDS		1,059	203.7	215.1	190.7	276.3	264.3	200.1
DVU0129	sensory box/HDIG domain protein (TIGR) CDS		1,359	168.5	151.1	135.2	145	144.5	136.9
DVU0130	phosphoglycolate phosphatase, putative (TIGR) CDS		663	132.5	143.8	140.9	233.8	215.8	223.8
DVU0132	membrane protein, putative (TIGR) CDS		1,125	468.8	422.4	408	1094.4	986.3	1271.4
DVU0133	hypothetical protein (TIGR) CDS		723	359.5	367.4	299.5	370.8	367.1	509.3
DVU0134	glycosyl transferase, group 2 family protein (TIGR) CDS		1,038	41.9	40.3	37	30.4	30.9	25.9
DVU0135	conserved hypothetical protein (TIGR) CDS		912	146.1	162.3	143.2	92.6	84.7	84.5
DVU0136	hypothetical protein (TIGR) CDS		219	198.3	210.7	176.1	120.2	121.5	165.2
DVU0138	response regulator (TIGR) CDS		381	532.4	492.6	455	763.9	766.2	956.4
DVU0139	cckA CDS	cckA	1,713	45	50.3	40.8	107.5	105.7	93.5
DVU0140	cheYI CDS	cheYI	414	72.6	70.8	65	85.6	113.4	94.9

DVU0141	peptidase, M50 family (TIGR) CDS		675	201.3	238.4	216.9	313	332.7	319.3
DVU0142	trpS CDS	trpS	990	387.9	393	354.2	274.1	250.4	250.6
DVU0143	conserved hypothetical protein (TIGR) CDS		777	408.7	379.1	370.7	544.9	550.4	540.1
DVU0144	rfaE CDS	rfaE	603	119.3	102	106.6	166.9	171.3	201.5
DVU0145	response regulator (TIGR) CDS		408	23.8	28.9	20.4	48	40.9	46.9
DVU0146	hypothetical protein (TIGR) CDS		810	13.9	13.8	11.5	55	52.6	50.4
DVU0147	lipoprotein, putative (TIGR) CDS		261	72.1	53.9	44.9	25.6	27.2	21.8
DVU0148	lipoprotein, putative (TIGR) CDS		612	47.9	46.7	37.3	50.7	54.6	34.6
DVU0149	membrane protein, putative (TIGR) CDS		1,053	35.2	33	35.8	60.5	53.4	49.6
DVU0150	membrane protein, putative (TIGR) CDS		297	71.4	83.5	83.8	141.8	123.9	127
DVU0151	HAMP domain/sigma-54 interaction domain protein (TIGR) CD		2,874	125.4	117.6	116.6	198.4	208.7	199.1
DVU0152	ppsA CDS	ppsA	2,562	117.7	107.6	114.1	164.6	176	146.9
DVU0153	hypothetical protein (TIGR) CDS		384	256.6	293	300.8	276.9	264.8	304.2
DVU0155	type I phosphodiesterase/nucleotide pyrophosphatase family		1,389	195.1	208.4	198.8	225.6	228.1	250.8
DVU0156	pcrA CDS	pcrA	2,160	173.9	181.9	175.4	330.9	314.6	376.4
DVU0157	thiL CDS	thiL	972	206.9	196.5	186	439.5	443.5	415
DVU0158	conserved hypothetical protein TIGR00104 (TIGR) CDS		999	214.3	208.9	202.6	337.7	349.5	379.5
DVU0159	thioesterase family protein (TIGR) CDS		522	174	171.3	182.2	207.5	216.6	204
DVU0160	carbohydrate isomerase, KpsF/GutQ family (TIGR) CDS		996	176.9	194.5	200.1	205.1	189.8	216.4
DVU0161	purF CDS	purF	1,389	433.4	516.2	468.7	230.3	242.5	236.7
DVU0162	carB CDS	carB	3,234	392.9	491.7	451	315.2	303.2	336.1
DVU0163	lipoprotein, putative (TIGR) CDS		561	66.8	59.1	65.1	62	47.7	39.6
DVU0164	cation efflux family protein (TIGR) CDS		909	49.2	45.6	42.3	75.1	79.3	66.6
DVU0165	oppF CDS	oppF	1,014	360.4	423.7	374.3	283.7	293.7	205.9
DVU0166	oppD CDS	oppD	987	372.9	437.5	391.6	267.7	271	234.1
DVU0167	oppC CDS	oppC	921	290.6	337	327.4	185.1	186.9	155.7
DVU0168	oligopeptide/dipeptide ABC transporter, permease protein (TI		978	257.3	296.8	260.8	202.3	211	206.9
DVU0169	oligopeptide/dipeptide ABC transporter, periplasmic oligopept		1,563	1439.9	1540.1	1356.1	617.9	561.4	652.7
DVU0170	methyl-accepting chemotaxis protein (TIGR) CDS		2,070	19.3	32.2	21.9	88.2	66.9	38.2
DVU0171	patB CDS	patB	1,182	55.9	57.9	46.9	55.6	54.9	38.4
DVU0172	phsB CDS	phsB	1,002	299.5	309.8	152	229.1	243.8	133.1
DVU0174	hypothetical protein (TIGR) CDS		108	76.6	103	88.2	68.4	105.4	95.7
DVU0175	tungsten formylmethanofuran dehydrogenase family protein/		1,632	167.5	158.4	131.2	143.9	143.3	158
DVU0176	glycerophosphoryl diester phosphodiesterase family protein (T		900	139.2	146.3	130	196.5	194.4	256.2
DVU0177	modA CDS	modA	810	9.5	8.3	9	6.7	6.8	6.4
DVU0179	molybdenum-pterin binding domain protein/site-specific reco		1,398	51.9	43.3	46.1	63.3	71.3	59.7
DVU0180	modC CDS	modC	762	34.8	31	34.3	40.3	46.5	34.3
DVU0181	modB CDS	modB	702	11.4	7.1	7.2	7.9	8.7	10.3
DVU0182	radical SAM domain protein (TIGR) CDS		924	164.7	169	156.1	164.6	162.7	156.6
DVU0183	methyl-accepting chemotaxis protein (TIGR) CDS		1,770	8.6	8.5	8.2	39.7	40.6	44.4
DVU0184	hypothetical protein (TIGR) CDS		420	5.9	10.2	7.5	10.5	7.5	6.1
DVU0185	hypothetical protein (TIGR) CDS		66	5.1	21.6	11.3	8.2	5.1	0
DVU0186	conserved hypothetical protein (TIGR) CDS		780	1077.3	953.9	351.9	297.7	441.9	117.9
DVU0187	GGDEF domain protein (TIGR) CDS		1,092	71.5	70	63.5	74.4	75.1	100.8
DVU0189	phage/plasmid primase, P4 family (TIGR) CDS		1,686	1.6	53.8	45.7	13.4	11.1	16.6
DVU0190	hypothetical protein (TIGR) CDS		213	6.6	56.1	42	14	13.1	24.3
DVU0191	conserved hypothetical protein (TIGR) CDS		1,560	9.4	37.9	35.9	13.7	13	11.9
DVU0192	adenine specific DNA methyltransferase, putative (TIGR) CDS		1,359	1.6	32.9	32.1	7.1	6.2	8.3
DVU0193	hypothetical protein (TIGR) CDS		732	7.6	36	39	37.3	41.8	27.2
DVU0194	terminase, large subunit, putative (TIGR) CDS		1,959	15.7	33.5	31.9	27	27.9	22.9
DVU0195	hypothetical protein (TIGR) CDS		219	18.5	29	18.5	5.8	2.1	10.6
DVU0197	phage portal protein, lambda family (TIGR) CDS		1,701	26	172.3	159.6	33.3	27.8	31.6
DVU0198	minor capsid protein C, degenerate (TIGR) CDS		1,320	0.9	227.3	207.2	50.7	36.4	50.3
DVU0199	conserved hypothetical protein (TIGR) CDS		384	0.1	359.8	335.6	57.7	33.3	55.2
DVU0200	major head protein (TIGR) CDS		1,005	0.6	460.9	405.7	45.7	33.9	54.8
DVU0201	hypothetical protein (TIGR) CDS		321	26.3	444.1	404.9	41.1	21.4	49.9
DVU0202	holin (TIGR) CDS		489	5.3	233.8	220.2	37.6	27	47.1
DVU0203	conserved hypothetical protein (TIGR) CDS		549	12.1	225.9	192.5	51	32.3	41.5
DVU0204	lipoprotein, putative (TIGR) CDS		411	7.2	303	262.9	37.8	24.2	48.4
DVU0205	hypothetical protein (TIGR) CDS		168	1.5	273.1	253.9	32.7	21.8	26.1
DVU0206	hypothetical protein (TIGR) CDS		594	0.4	194.7	189.3	26.1	23.1	17.8
DVU0207	hypothetical protein (TIGR) CDS		327	0	162.4	148.5	15.9	13.9	25.3
DVU0208	hypothetical protein (TIGR) CDS		558	1.8	245.8	224.1	23.2	14.5	20.4
DVU0209	conserved hypothetical protein (TIGR) CDS		192	0	251.3	219.9	23.3	14	33.6
DVU0210	tail sheath protein, putative (TIGR) CDS		1,464	2.6	219	203.6	29.6	24.4	20.1
DVU0211	tail tube protein, putative (TIGR) CDS		366	0	168.2	135.9	26.2	25	35.3
DVU0212	conserved hypothetical protein (TIGR) CDS		261	0.3	184.5	156.5	24.7	18.9	29.7

DVU0213	conserved domain protein (TIGR) CDS		1,491	42.5	116.8	115.2	32.6	26.8	25.3
DVU0214	tail/DNA circulation protein, putative (TIGR) CDS		1,200	1.6	63.7	58.4	29.1	24.2	23.2
DVU0215	tail protein, putative (TIGR) CDS		1,134	2	78.3	74.5	26.3	21.4	21.9
DVU0216	phage baseplate assembly protein V, putative (TIGR) CDS		639	1.9	74.9	77	19.9	20	16.6
DVU0217	tail protein, putative (TIGR) CDS		477	4.6	72.3	68.6	30.1	33.1	15.7
DVU0218	tail protein, putative (TIGR) CDS		1,062	1.9	85.6	82.4	32.7	31.4	22.4
DVU0219	tail protein, putative (TIGR) CDS		627	2.3	100.3	103.6	19.3	14	13.2
DVU0220	tail fiber protein, putative (TIGR) CDS		1,017	90	125.6	125.6	36.6	34.3	25.9
DVU0221	tail fiber assembly protein, putative (TIGR) CDS		444	100.4	145.1	127.9	52.1	47.9	40.2
DVU0222	hypothetical protein (TIGR) CDS		330	27.9	126.9	117.8	75.5	82.6	66.6
DVU0223	conserved hypothetical protein (TIGR) CDS		183	548	503.4	521.9	291.4	339	343.1
DVU0224	conserved hypothetical protein (TIGR) CDS		396	207.7	221.2	251.2	176.3	198.3	179.5
DVU0226	hypothetical protein (TIGR) CDS		1,140	416.6	426.6	384	274.6	265.8	253.9
DVU0227	conserved hypothetical protein (TIGR) CDS		531	391.9	391.8	326.9	57.9	73.4	70.1
DVU0230	transcriptional regulator cII, putative (TIGR) CDS		465	33.4	41.9	38.7	20.7	20	28.9
DVU0231	hypothetical protein (TIGR) CDS		225	50.7	61.4	60.2	35.4	26.7	32.2
DVU0232	hypothetical protein (TIGR) CDS		249	75.6	89.1	74.2	23	19.5	29.1
DVU0234	hypothetical protein (TIGR) CDS		324	103.4	110.2	101.8	34.1	29.8	35.1
DVU0235	hypothetical protein (TIGR) CDS		564	96.4	103.1	98.5	42.8	44.5	41.3
DVU0236	site-specific recombinase, phage integrase family (TIGR) CDS		1,143	174	170.4	183.1	90.5	92.8	87.3
DVU0237	serS CDS	serS	1,275	525.3	554.6	562.2	673.7	655.4	707
DVU0238	hypothetical protein (TIGR) CDS		390	170.6	210.2	198.1	646.9	657.4	766
DVU0241	MTH1175-like domain family protein (TIGR) CDS		378	1069.6	1149.1	1015.7	1167.7	1153.3	1316.7
DVU0242	SEC-C motif domain protein (TIGR) CDS		489	1071.7	1127.1	1044.7	826.4	810.2	762
DVU0243	lipoprotein, putative (TIGR) CDS		669	315	299.9	324.9	340.3	351.6	252.6
DVU0244	hypothetical protein (TIGR) CDS		858	111.5	112.2	107.1	156.6	165.3	126.5
DVU0245	protein phosphatase, putative (TIGR) CDS		1,110	64.3	48.7	44.3	83	84.1	85.2
DVU0246	pyruvate phosphate dikinase, PEP/pyruvate binding domain pr		2,235	92.8	76.9	69.6	144.8	136.7	132.7
DVU0247	ntrX CDS	ntrX	360	259.1	215.9	183.5	133.2	148.7	137.8
DVU0249	conserved hypothetical protein (TIGR) CDS		972	116.4	122.3	66.8	114.1	118.3	92
DVU0250	hypothetical protein (TIGR) CDS		588	197.3	227.7	111.2	140.7	173.5	132.7
DVU0251	membrane protein, putative (TIGR) CDS		963	1378.2	1273.2	521.2	455.7	519.7	197
DVU0252	hypothetical protein (TIGR) CDS		210	156.7	202.9	161.4	151.1	161	194.4
DVU0253	oxidoreductase, FAD/iron-sulfur cluster-binding domain protei		2,826	299	330	255.7	440.4	391.3	537.1
DVU0255	hypothetical protein (TIGR) CDS		555	193.6	206.2	169.8	228.7	219.1	262.6
DVU0256	ATP-dependent RNA helicase, DEAD/DEAH box family (TIGR) C		3,366	77.6	81.6	76.8	154.9	158.1	149.4
DVU0257	acetyltransferase, GNAT family (TIGR) CDS		465	62.2	60.5	48.8	36.9	50.1	35.5
DVU0258	sensory box histidine kinase/response regulator (TIGR) CDS		1,974	146.3	147.4	137.8	192.5	186	237.6
DVU0259	divK CDS	divK	390	1781.2	1707.1	1503.4	875.1	847.7	1316
DVU0260	mtrA CDS	mtrA	402	1512.4	1437.9	1207.2	870.1	846.2	1045.3
DVU0261	universal stress protein family (TIGR) CDS		927	1643.6	1635.3	1388.5	655.4	623.1	860.6
DVU0262	hypothetical protein (TIGR) CDS		555	1262.2	1272.1	1079.2	1433.5	1365.4	1839.7
DVU0263	tmcA CDS	tmcA	381	1658.5	1606.1	1410.8	624	578.2	1009.3
DVU0264	tmcB CDS	tmcB	1,320	1299.8	1231.5	1106.3	1173.9	1083.4	1709.7
DVU0265	membrane protein, putative (TIGR) CDS		660	1002.7	1041.6	928.2	656.4	548.7	757.6
DVU0266	hypothetical protein (TIGR) CDS		1,257	1318.2	1315.8	1163.1	845.5	806.7	1104.8
DVU0269	transcriptional regulator, rrf2 protein, putative (TIGR) CDS		498	591.4	505.8	488.1	692.9	697.5	590.6
DVU0270	sensory box histidine kinase (TIGR) CDS		2,271	263.1	253.1	238	296.6	300.3	287.1
DVU0271	response regulator (TIGR) CDS		1,491	207.4	208.8	185.8	141.5	154.4	112.8
DVU0272	hypothetical protein (TIGR) CDS		96	41.8	38.9	33.1	31.9	30.2	26.9
DVU0273	conserved hypothetical protein (TIGR) CDS		1,518	130.4	111.9	102.6	69.9	75.2	106.9
DVU0274	hypothetical protein (TIGR) CDS		372	249.4	262.6	234.1	145.2	150.3	122.3
DVU0275	polysaccharide deacetylase family protein (TIGR) CDS		696	120.8	116.2	108.5	121.1	114.9	152.2
DVU0276	conserved hypothetical protein (TIGR) CDS		399	215.1	216.9	183.1	189.7	188.2	222.8
DVU0277	transcriptional regulator, AraC family (TIGR) CDS		981	179.2	184.7	161.8	108.9	110.5	102.2
DVU0278	glyoxalase family protein (TIGR) CDS		423	137.4	154.9	142.6	209.5	199	271.3
DVU0279	sulfate permease family protein (TIGR) CDS		1,707	65.3	60.5	58.7	58.3	56	58.8
DVU0280	wbaZ-2 CDS	wbaZ-2	1,140	208.9	233.5	205	314.6	330.6	328.7
DVU0282	mutY CDS	mutY	1,122	119.4	103.2	110.3	254.6	248.3	208.2
DVU0284	ppiB-1 CDS	ppiB-1	507	422.2	391.8	346.3	372.2	380.1	442.4
DVU0285	hisH CDS	hisH	642	195.6	197.6	168.9	169.1	169.3	166.3
DVU0286	hisF CDS	hisF	780	212	196.4	185.2	211.4	216.1	154.7
DVU0290	lipoprotein, putative (TIGR) CDS		609	169.1	163.4	131.2	257.7	267.3	269.5
DVU0291	potA CDS	potA	1,065	55.8	60.6	53.6	72.8	76.5	81
DVU0292	hypothetical protein (TIGR) CDS		1,107	77.5	81.6	73.1	149.8	146	187.4
DVU0293	prokaryotic dksA/traR C4-type zinc finger family protein (TIGR		342	310.1	337.2	245.4	483.9	447.6	563.7
DVU0295	amine oxidase, flavin-containing (TIGR) CDS		1,350	137.4	123.5	112.1	163.3	168.9	139.7

DVU0296	peptidase, M24 family (TIGR) CDS		1,071	353.8	344.9	350.5	214.6	209.2	218.7
DVU0298	hypothetical protein (TIGR) CDS		786	57.2	65.5	43.7	96.4	116.4	82.8
DVU0299	anaerobic ribonucleoside-triphosphate reductase, putative (TI		2,046	344	308.4	259.5	347.9	348.8	452.7
DVU0300	radical SAM domain protein (TIGR) CDS		738	472.2	446.1	365.4	329.4	314.1	477.6
DVU0301	hypothetical protein (TIGR) CDS		150	31.2	42	34.8	13.8	11.7	13.8
DVU0302	chemotaxis protein CheX, putative (TIGR) CDS		468	710.6	609.2	662.8	1199.6	1167.2	1679.8
DVU0303	hypothetical protein (TIGR) CDS		318	37.4	36.5	28.6	41.5	69.2	73.1
DVU0304	hypothetical protein (TIGR) CDS		282	70.6	50.6	40.3	65.6	107.1	183.2
DVU0305	fd II CDS	fd II	195	1001.2	1461.1	959.2	423	417.9	604.3
DVU0306	hypothetical protein (TIGR) CDS		618	173.9	163.3	163.8	271.7	274.7	250
DVU0307	flagella basal body rod domain protein (TIGR) CDS		1,497	223.3	244.3	212.9	451.6	460.4	563.2
DVU0308	membrane protein, putative (TIGR) CDS		435	36.6	29.4	27.2	16.5	23.9	27.3
DVU0309	transcriptional regulator, LysR family (TIGR) CDS		921	46.4	43.6	45.7	57.6	66.5	57.2
DVU0310	fliI CDS	fliI	1,314	97.4	93.2	88.5	129.8	134.6	110.3
DVU0311	flagellar assembly protein FliH, putative (TIGR) CDS		753	163.4	169.4	146.5	263.7	282.4	253.7
DVU0312	fliG CDS	fliG	1,017	235.3	251.7	241.6	294.7	287.7	275.7
DVU0313	fliF CDS	fliF	1,617	128.8	137.5	120.3	334	333.9	316.3
DVU0314	fliE CDS	fliE	336	128.2	135.6	116.2	302.3	294.4	373
DVU0315	flgC CDS	flgC	438	87.2	101.1	87.3	360.9	343.5	427.2
DVU0316	flgB CDS	flgB	411	157	199.6	175.7	494.8	481.5	585.3
DVU0318	TPR domain protein (TIGR) CDS		564	450.2	522.8	456.2	2317	2135.7	4257.6
DVU0319	NAD-dependent epimerase/dehydratase family protein (TIGR)		1,026	301.5	334.1	291.9	618.3	593.5	753.1
DVU0320	conserved hypothetical protein (TIGR) CDS		261	131.8	136.4	96	1025	813.8	1204
DVU0321	transcriptional activator, putative, Baf family (TIGR) CDS		789	319.2	323.8	305.7	327.1	306.5	327.5
DVU0322	eno CDS	eno	1,314	735.4	769.3	706.2	561.4	555.3	758
DVU0323	folD CDS	folD	861	200.1	205.1	203.2	97.9	109.8	88.2
DVU0325	hypD CDS	hypD	1,098	185.7	161.8	150.3	168.9	161	166.7
DVU0326	hypE CDS	hypE	1,026	192.5	167.4	159.3	178.1	187.1	146
DVU0327	pss CDS	pss	1,266	212.9	219.8	219.2	159	150.7	157.2
DVU0328	glycosyl transferase, group 1 family protein (TIGR) CDS		1,146	215.1	220.2	217	226.5	221.6	267.9
DVU0330	response regulator (TIGR) CDS		1,239	18.3	24.2	18	98	91.2	74.3
DVU0331	sensory box histidine kinase, putative (TIGR) CDS		2,922	40.1	46.6	38.5	148.3	129.8	118.7
DVU0333	hypothetical protein (TIGR) CDS		657	238.2	210.2	216.9	204.7	213.3	257.2
DVU0334	D-alanine--D-alanine ligase (TIGR) CDS		912	169.4	189.8	172.2	126.5	131.1	132.6
DVU0335	3-deoxy-D-manno-octulosonic-acid transferase, putative (TIGF		1,593	109	105.6	106.5	49.9	56.9	50.3
DVU0336	rfbE CDS	rfbE	1,341	138.6	153.7	145.9	116.6	124.2	104.3
DVU0337	hypothetical protein (TIGR) CDS		1,971	136	158.5	148.8	115.1	122.7	96.7
DVU0338	hydrolase, haloacid dehalogenase-like family (TIGR) CDS		642	272.9	325.8	277.1	191.5	196.1	179.9
DVU0339	serA CDS	serA	906	368.8	388.4	351.1	244.5	231.2	270.1
DVU0340	acetyltransferase, CysE/LacA/LpxA/NodL family (TIGR) CDS		594	367.2	408.7	397.4	356.3	354.2	325
DVU0341	kdsB CDS	kdsB	771	391.3	415.1	350.8	279.8	290.1	327.5
DVU0342	NAD-dependent epimerase/dehydratase family protein (TIGR)		915	291	302.1	274	353.4	350	380.7
DVU0343	HPCH/HPAI aldolase family protein (TIGR) CDS		783	231.7	254.9	218.3	373.9	362.9	433
DVU0346	membrane protein, putative (TIGR) CDS		1,539	69.4	61.2	57.1	75.5	76.5	56.8
DVU0347	transferase, hexapeptide repeat family (TIGR) CDS		672	73.9	76.5	65.7	75.3	76.1	66.1
DVU0348	hypothetical protein (TIGR) CDS		1,725	104.5	111.9	90.7	115.5	117	105.7
DVU0349	NeuB family protein (TIGR) CDS		1,059	167.1	177.1	151.4	123.4	117.3	119.1
DVU0350	spsF CDS	spsF	684	133.8	130.2	99.5	145.4	133.8	152.6
DVU0351	cytidine 5monophosphate N-acetylneuraminic acid synthetase		1,635	128	134.4	120.9	97.2	103.4	99.6
DVU0352	lpsC CDS	lpsC	1,182	175	183.3	147.6	147.5	135.6	154
DVU0353	alcohol dehydrogenase, iron-containing (TIGR) CDS		1,074	332.8	363.7	306.3	158.9	167.1	207.4
DVU0355	sensory box/GGDEF domain protein (TIGR) CDS		1,824	59.6	64	63.6	125.3	127.2	102.3
DVU0356	tag CDS	tag	576	190.4	150.2	164.9	309.3	281.2	296.2
DVU0357	conserved hypothetical protein (TIGR) CDS		918	145.9	138.5	146.5	168.8	167.5	158.8
DVU0358	hypothetical protein (TIGR) CDS		744	36.8	42	35.8	69.5	73	72.9
DVU0359	HesB-like domain (TIGR) CDS		327	33.4	30.4	36.4	67.8	82.6	53.8
DVU0360	ilvB-1 CDS	ilvB-1	1,692	23.2	25.3	21.5	24.4	29.9	36.1
DVU0361	ilvH CDS	ilvH	324	31.7	29	35.1	16.8	13.8	23.1
DVU0362	conserved hypothetical protein (TIGR) CDS		780	68.7	70.3	64.1	46	53	43.4
DVU0364	pabA CDS	pabA	555	58.1	60.5	56.3	40.6	50	58.6
DVU0365	conserved hypothetical protein (TIGR) CDS		756	54	59.7	48.3	38	37.5	45.8
DVU0366	5-formyltetrahydrofolate cyclo-ligase family protein (TIGR) CD		852	91.3	103.3	93.7	63.1	66.8	78.2
DVU0367	Ser/Thr protein phosphatase family protein (TIGR) CDS		735	96.9	89	86.6	130.7	119.8	125.2
DVU0368	hypothetical protein (TIGR) CDS		105	12.8	23.4	24.4	8.6	2.6	0
DVU0369	hypothetical protein (TIGR) CDS		99	8.5	9	4.4	0	0	0
DVU0370	hypothetical protein (TIGR) CDS		144	16.6	15.3	10.8	2.9	3.7	3.5
DVU0371	conserved hypothetical protein (TIGR) CDS		1,425	33.8	32.7	33.5	24.4	29.1	24.3

DVU0372	membrane protein, putative (TIGR) CDS		693	6.7	10.9	9.5	6.5	3.5	0
DVU0373	CoA-binding domain protein (TIGR) CDS		2,313	33	33.3	31.7	28.1	27.7	23.4
DVU0374	pyruvate ferredoxin/flavodoxin oxidoreductase family protein		2,499	29.4	31	28	19.5	20	15.1
DVU0375	Glu/Leu/Phe/Val dehydrogenase family protein (TIGR) CDS		1,230	28.1	28.8	26.8	38.4	39.3	26
DVU0376	hypothetical protein (TIGR) CDS		267	40.5	40.7	45.8	51.5	56.4	16.5
DVU0377	trxB-1 CDS	trxB-1	918	88.4	67.5	84.3	109	102.2	81.7
DVU0378	thioredoxin, putative (TIGR) CDS		315	42.4	52.2	49.4	46.6	33.5	32.8
DVU0379	transcriptional regulator, putative (TIGR) CDS		678	69.6	65	76.9	110.8	119.5	119.3
DVU0380	sulfatase, putative (TIGR) CDS		1,563	36.5	35.1	35.3	28	27.1	24.8
DVU0381	nhaC-1 CDS	nhaC-1	1,392	18.1	23.5	20.2	40.6	42.3	37.5
DVU0382	hypothetical protein (TIGR) CDS		300	20.4	21	18	11.7	13.3	6.9
DVU0383	hypothetical protein (TIGR) CDS		390	39	42.9	34.7	41.3	40.9	33.1
DVU0384	flr CDS	flr	573	182.8	201.7	182	135	137.4	97.4
DVU0386	glnH CDS	glnH	750	695.6	655	555	262.9	285.6	237.7
DVU0387	amino acid ABC transporter, permease protein, His/Glu/Gln/A		678	274.8	297.7	278.9	261.7	278.1	344.9
DVU0388	amino acid ABC transporter, ATP-binding protein (TIGR) CDS		768	299.8	299	309.3	429.6	453.1	564.3
DVU0389	amino acid ABC tranporter, permease protein, His/Glu/Gln/Ar		675	296.9	275	291.6	227.6	241.1	254.6
DVU0390	glcD CDS	glcD	1,383	184.6	174.2	171	186.2	187.1	192.3
DVU0391	hypothetical protein (TIGR) CDS		942	40.2	46	48.2	69.4	72	62
DVU0392	aromatic aminotransferase (TIGR) CDS		1,200	148.1	147.5	144.3	116.2	126.4	128.8
DVU0394	radical SAM domain protein (TIGR) CDS		1,023	98.9	100.9	101.5	113.8	119.7	106.6
DVU0395	hit CDS	hit	420	1025.8	1073	1031.8	1245.3	1152.3	1457.7
DVU0396	hup-1 CDS	hup-1	288	1729.4	2080.6	1765.6	1854.3	1729.4	2839.9
DVU0397	rlpA CDS	rlpA	732	305.7	324.8	322.2	193.1	178.6	206.2
DVU0398	HMGL-like domain protein (TIGR) CDS		1,827	310.7	311.3	297.9	229.9	243.4	258.2
DVU0399	hypothetical protein (TIGR) CDS		789	231	250.3	235.1	212.5	196.9	290.8
DVU0400	hypothetical protein (TIGR) CDS		552	202.5	227.2	210.5	210.8	222.3	169
DVU0402	dsrA CDS	dsrA	1,314	3976.9	4232.6	3598.1	1462.4	1348.3	2000.3
DVU0403	dvsB CDS	dvsB	1,146	4242.7	4468	3794.7	1628	1499	2271.5
DVU0404	dsrD CDS	dsrD	237	5232.1	5807.2	5152.2	1623.9	1600.4	2708.6
DVU0405	cobB-1 CDS	cobB-1	1,407	113.8	127.8	136.3	148.2	152.9	132.2
DVU0406	membrane protein, putative (TIGR) CDS		939	37.8	38.4	34.1	29.1	29.6	24.2
DVU0407	rlpA CDS	rlpA	645	1135.6	1294.3	1289.4	1382.8	1324.9	2459.2
DVU0408	response regulator/sensory box/GGDEF domain/EAL domain p		2,148	330.1	341.2	334	612	580.6	628.1
DVU0409	hypothetical protein (TIGR) CDS		351	392.6	428.3	375.5	1347.3	1239.4	1926
DVU0410	hypothetical protein (TIGR) CDS		606	342.5	374.2	317.9	711.2	670.3	1259.8
DVU0411	heptosyltransferase family protein (TIGR) CDS		1,674	77	86.4	78.5	123.7	120.1	139.1
DVU0412	potassium uptake protein TrkA, putative (TIGR) CDS		666	296.5	287	295	359.1	372.2	310.8
DVU0413	trk1 CDS	trk1	1,338	216.4	221.1	216	404.9	378.2	394.4
DVU0414	tme CDS	tme	1,320	375.4	364.3	327.9	395.1	379.8	343.8
DVU0415	pepA CDS	pepA	1,524	464.1	397.7	392.5	211.3	221.7	191.6
DVU0416	GGDEF domain protein (TIGR) CDS		1,119	117.4	138.7	105.7	137.2	139.9	123.3
DVU0417	speA CDS	speA	1,980	257.7	231.3	205.3	273.2	257.8	304.9
DVU0418	lys1 CDS	lys1	1,191	226.1	193.7	162.6	121.6	122.5	126.7
DVU0419	nspC CDS	nspC	1,173	81.4	89.1	69.7	125.7	123.1	120.5
DVU0420	hypothetical protein (TIGR) CDS		177	133	163.1	114.9	487.6	484.1	294.9
DVU0421	agmatinase, putative (TIGR) CDS		873	169.6	208.4	186.4	308	301.7	217.3
DVU0422	sensory box/GGDEF domain/EAL domain protein (TIGR) CDS		3,219	48.5	69.8	61.9	68.8	66	47.4
DVU0423	universal stress protein family (TIGR) CDS		426	423.6	411	352.7	523.3	532	475.6
DVU0424	cls CDS	cls	1,446	188.6	190	169	420.2	417.4	403.1
DVU0425	hypothetical protein (TIGR) CDS		807	91.5	104.7	88.2	382.9	396	372.1
DVU0426	chromate transport family protein (TIGR) CDS		1,353	68.4	67.4	61.1	83.5	79	72.2
DVU0428	conserved hypothetical protein (TIGR) CDS		321	125.1	86.1	97.1	170.7	200.1	191.6
DVU0429	Ech hydrogenase, subunit EchF, putative (TIGR) CDS		402	144.8	131.7	110.4	121.5	121.9	86.8
DVU0430	Ech hydrogenase, subunit EchE, putative (TIGR) CDS		1,077	118.1	128.8	111.5	66.5	77.3	59.1
DVU0431	Ech hydrogenase, subunit EchD, putative (TIGR) CDS		393	152.6	148.6	132.7	64.1	70.7	76.3
DVU0432	Ech hydrogenase, subunit EchC, putative (TIGR) CDS		474	125	110.1	113	149.9	171.2	135.2
DVU0433	Ech hydrogenase, subunit EchB, putative (TIGR) CDS		849	94.2	91	72.7	65.1	61.8	45.9
DVU0434	mnhA CDS	mnhA	1,947	90	88.9	77.7	75	71.8	57.1
DVU0437	efflux transporter, RND family, MFP subunit (TIGR) CDS		1,461	85.3	84.7	82	64.1	79.7	54.8
DVU0438	AcrB/AcrD/AcrF family protein (TIGR) CDS		3,126	67.1	74.1	66.4	68.9	75.8	72
DVU0439	YCII-related domain protein (TIGR) CDS		291	123.1	121.7	128	89.2	88.8	48.9
DVU0440	conserved hypothetical protein (TIGR) CDS		1,332	98.2	101.2	97.1	72.2	76.6	48.5
DVU0441	ade CDS	ade	1,728	122.1	124	100	188.6	158.8	214.8
DVU0442	phoH-related protein (TIGR) CDS		1,197	9.9	12.3	10.8	10	11.8	6.5
DVU0443	exonuclease, putative (Keith Keller) CDS		735	17.6	16.4	15.6	20	23.3	12
DVU0444	CBS domain protein (TIGR) CDS		2,223	12.8	14.5	13	12.9	13.8	10.3

DVU0445	CBS domain protein (TIGR) CDS		1,725	19.5	18.9	19.6	24.3	30.8	35.5
DVU0446	sodium/solute symporter family protein (TIGR) CDS		1,548	11.2	12.6	9.1	8.2	9.1	5
DVU0447	membrane protein, putative (TIGR) CDS		318	11.8	11.6	8.6	10.7	6.9	17.9
DVU0448	gmd CDS	gmd	1,146	495.4	497.8	478.3	261.5	265.5	263.3
DVU0449	sensor/response regulator (TIGR) CDS		4,542	61.9	64.2	63.5	81.3	79.7	63.8
DVU0450	ribF CDS	ribF	945	315.4	335.1	335.3	329.7	338.4	422.2
DVU0451	chloride channel family protein (TIGR) CDS		1,812	249.5	250.3	259.8	233.2	244.7	229.9
DVU0453	ATP-dependent DNA helicase, UvrD/REP family (TIGR) CDS		3,384	161.8	145	137	216.5	215.4	201.8
DVU0454	hypothetical protein (TIGR) CDS		249	169.3	156.1	166.2	657.2	688.1	817.9
DVU0455	hypothetical protein (TIGR) CDS		768	148.8	154	134.7	242.8	253.1	256.4
DVU0456	DHH family protein (TIGR) CDS		1,008	264.7	242.8	233.2	235.9	246.2	318.5
DVU0457	EAL domain protein (TIGR) CDS		1,251	41.9	41.2	34.9	57.2	59.9	42.9
DVU0458	hypothetical protein (TIGR) CDS		168	13.9	25.7	21	7.8	7.6	0
DVU0459	hypothetical protein (TIGR) CDS		102	2856.2	2952.3	2899.4	3489.3	3268.3	5720.8
DVU0460	predicted phospho-2-dehydro-3-deoxyheptonate aldolase (TIG		801	807.4	739.6	664.3	624.1	633	664.9
DVU0461	predicted 3-dehydroquinate synthase (TIGR) CDS		972	696.1	632.9	549.5	560.4	571.2	658.6
DVU0462	chorismate mutase/prephenate dehydratase (TIGR) CDS		1,176	617.9	606	541.1	381.3	399.8	451
DVU0463	aroA CDS	aroA	1,320	593.4	587.9	488.4	400.2	421.9	379.6
DVU0464	prephenate dehydrogenase (TIGR) CDS		768	638	645.4	517.3	596	563.7	816.7
DVU0465	trpE CDS	trpE	1,599	44.7	228.5	79	55.8	62.9	83
DVU0466	trpG CDS	trpG	630	47.4	260	72.1	79.2	94.4	102.1
DVU0467	trpD CDS	trpD	999	44.5	329	75.2	79.5	74.8	121
DVU0468	trpC CDS	trpC	774	38.8	328.8	73.7	84.6	88.4	101.9
DVU0469	trpF-1 CDS	trpF-1	855	46.9	381.6	77.9	55.6	60	70.4
DVU0470	trpB-2 CDS	trpB-2	1,188	49.9	659.6	81.9	62	66.7	89.4
DVU0471	trpA CDS	trpA	774	83.3	959.8	197.7	77.3	82.1	83.4
DVU0474	ISDvu4, transposase (TIGR) CDS		1,050	1.9	90.1	71.1	110.9	103.6	91
DVU0475	membrane protein, putative, truncation (TIGR) CDS		441	104.3	120.9	98.4	23.9	26.8	17.6
DVU0477	icd CDS	icd	1,143	452.8	449.8	431.3	147.1	158.3	169.1
DVU0478	Ser/Thr protein phosphatase family (TIGR) CDS		864	96.4	102.1	82.8	159.1	165.1	186.1
DVU0479	serine/threonine protein kinase, putative (TIGR) CDS		1,500	119.9	104.3	104.5	111.6	123.5	99.3
DVU0480	hypothetical protein (TIGR) CDS		732	151.8	108.2	124.1	154.4	164.3	122.8
DVU0481	rfaD CDS	rfaD	972	232.9	222.2	216.8	209.7	216.8	222.3
DVU0482	sensory box histidine kinase/response regulator (TIGR) CDS		1,449	62.7	65.5	56	237.6	228.6	308.6
DVU0483	DNA mismatch repair protein MutL, putative (TIGR) CDS		2,235	137.3	151.5	141.9	274.6	270.1	253.2
DVU0484	ABC transporter, ATP-binding protein (TIGR) CDS		795	64.7	59.1	63.1	56.6	63.9	55.9
DVU0485	membrane protein, putative (TIGR) CDS		786	51.2	46.7	41.7	72.2	76.5	56.6
DVU0486	hypothetical protein (TIGR) CDS		330	255.4	263.8	210.8	499.5	418.2	651.5
DVU0487	purE CDS	purE	501	545.2	576.1	489.7	364.6	322.7	313.7
DVU0488	purD CDS	purD	1,275	485.4	473.4	468.8	272.6	265.1	270
DVU0489	paaK-1 CDS	paaK-1	1,299	258	280.6	262	173	176.9	206.5
DVU0491	HDIG domain protein (TIGR) CDS		1,206	252.2	243.7	224.3	159.4	167.4	121.7
DVU0492	argC CDS	argC	1,065	244.4	245.8	223.9	179.1	178.5	178.6
DVU0493	hypothetical protein (TIGR) CDS		309	382.4	402.1	365.5	425.1	454.5	419.8
DVU0494	aminotransferase, class V (TIGR) CDS		1,170	242.1	259.5	229.1	357.3	334.2	346.6
DVU0495	conserved hypothetical protein (TIGR) CDS		1,197	197.5	205.3	204.1	199.1	207.5	193.7
DVU0496	polA CDS	polA	3,048	150	158.2	136.4	176	172.9	177.7
DVU0497	hypothetical protein (TIGR) CDS		249	36.9	40.3	29.4	54	46.6	60.2
DVU0498	iron-sulfur cluster-binding protein, putative (TIGR) CDS		1,506	64.9	61.6	63.1	152.8	152.4	135.9
DVU0499	conserved hypothetical protein TIGR00149 (TIGR) CDS		396	38.4	42.4	38.8	56.4	54.1	61.4
DVU0500	selB CDS	selB	1,929	221.1	201.7	208.6	247.7	259.1	205.7
DVU0501	conserved hypothetical protein (TIGR) CDS		822	604.6	622.5	563.7	252.5	253.8	309.7
DVU0503	pnp CDS	pnp	2,283	700.4	769.8	683.5	0.7	0.8	1.1
DVU0504	rpsO CDS	rpsO	270	2950.5	2939.7	2690	719.4	663.3	888.2
DVU0505	truB CDS	truB	915	1292.6	1325.6	1224.9	1482.8	1455.4	2164.3
DVU0506	DHH family protein (TIGR) CDS		1,002	211.4	273	252.9	326.6	332.7	227.2
DVU0507	conserved hypothetical protein (TIGR) CDS		291	341.5	446	405.2	224.7	232	195.3
DVU0508	infB CDS	infB	3,240	733.6	853.9	776.2	420.7	406.6	577.7
DVU0509	conserved hypothetical protein (TIGR) CDS		231	845	978.7	907.5	348.9	347.7	413.9
DVU0510	nusA CDS	nusA	1,287	793.4	909.2	864.2	402.6	431.7	454.6
DVU0511	conserved hypothetical protein (TIGR) CDS		519	964.3	1229.8	1132.6	355.1	383.6	284.8
DVU0512	flgF CDS	flgF	783	95.7	91.5	80.5	340.8	316.4	376.9
DVU0513	flgG CDS	flgG	783	100.7	110	90.1	372.9	371.9	359.1
DVU0514	FlgA family protein (TIGR) CDS		933	64.6	71.4	63.5	290.4	301	223.6
DVU0515	flgH CDS	flgH	717	117.1	130.8	118.6	498.1	492.4	584.6
DVU0516	flgI CDS	flgI	1,137	106.4	108.1	101.7	253.5	263.7	232.1
DVU0517	peptidase, M23/M37 family (TIGR) CDS		1,833	87.2	93	84.7	248.5	241.6	258.6

DVU0518	hypothetical protein (TIGR) CDS		465	131.8	142.2	135.7	458.7	456.5	592.4
DVU0519	flagellar hook-associated protein FlgK, putative (TIGR) CDS		2,097	116.7	120	105.4	530.1	508.2	715.8
DVU0520	flagellar hook-associated protein FlgL, putative (TIGR) CDS		1,572	150	144.1	134.1	397.6	402.2	493
DVU0521	csrA CDS	csrA	237	192.5	194.7	179.4	225.9	229.6	229
DVU0522	yviF CDS	yviF	522	165.3	182.6	162.6	231.5	214.4	249
DVU0523	flgM CDS	flgM	315	948.8	1173	1022.4	923.9	979.1	1117.3
DVU0524	hypothetical protein (TIGR) CDS		417	731.9	759.9	754.8	987.2	934.8	1367.2
DVU0525	transcriptional regulator, MarR family (TIGR) CDS		669	54.9	49.1	48.5	39.7	45.4	27.8
DVU0526	drug resistance transporter, putative (TIGR) CDS		1,404	49.6	41.2	41.7	57.3	52	42.3
DVU0527	maF CDS	maF	633	157.3	147.4	145.7	153.7	173	141.3
DVU0528	pgpA CDS	pgpA	480	193.5	177.6	175.3	158.2	167.7	133.5
DVU0529	rrf2 CDS	rrf2	453	35.8	34.9	43.3	90.9	107.3	65
DVU0530	rrf1 CDS	rrf1	417	55.4	58.7	81.3	112.6	124.3	156.2
DVU0531	hmcF CDS	hmcF	1,386	61.4	79.4	99.9	67.2	78.3	56.4
DVU0532	hmcE CDS	hmcE	681	34	55.5	68.3	53.5	62.1	47.8
DVU0533	hmcD CDS	hmcD	144	46.4	67.6	83	47.2	54.7	46.7
DVU0534	hmcC CDS	hmcC	1,167	50.7	65	78.8	50.5	62.3	48.5
DVU0535	hmcB CDS	hmcB	1,113	66.5	76	106.7	77.6	92.1	66.9
DVU0536	hmcA CDS	hmcA	1,683	56.1	71.6	91.5	43.4	50.7	45.3
DVU0538	AP endonuclease, family 2 (TIGR) CDS		789	77.9	75.4	70.7	112.4	115.4	82.8
DVU0539	sigma-54 dependent DNA-binding response regulator (TIGR) C		1,404	63.8	67.1	67.4	79.1	86	81.8
DVU0540	sensor histidine kinase (TIGR) CDS		2,412	47.2	51.5	49.1	56.2	57.3	44.9
DVU0542	universal stress protein family (TIGR) CDS		423	44.9	61.4	52.4	44.5	55.2	44.6
DVU0543	conserved hypothetical protein (TIGR) CDS		1,110	17.1	23.8	18	25.4	27	11.9
DVU0544	hypothetical protein (TIGR) CDS		402	31.4	32.1	24.7	26	25.7	21.9
DVU0545	conserved hypothetical protein (TIGR) CDS		426	43.2	36.6	36.3	53.4	58.6	32.7
DVU0547	high-affinity branched chain amino acid ABC transporter, perip		1,119	1034.1	949.1	902.7	579.7	568.3	647.1
DVU0548	livH CDS	livH	909	306.7	313	300.5	304.9	311.3	303.9
DVU0549	high-affinity branched-chain amino acid ABC transporter, pern		1,224	312.7	298.9	305.4	353.5	329.6	288.2
DVU0550	livG CDS	livG	789	349.9	366.5	344.4	255.2	268.6	259.1
DVU0551	livF CDS	livF	705	365.3	374.7	369.4	631.7	555.8	571.5
DVU0552	conserved hypothetical protein (TIGR) CDS		966	215.8	261.2	230.4	143.2	164.5	120.9
DVU0554	NAD-dependent epimerase/dehydratase family protein (TIGR)		939	254.8	260.8	248.2	118.6	122.4	115
DVU0555	hypothetical protein (TIGR) CDS		255	267.1	271	240.3	29.8	23.5	32.4
DVU0556	ISDvu3, transposase OrfA (TIGR) CDS		264	481.1	521.7	500.6	120.8	118.1	148.8
DVU0561	glycosyl transferase, group 1 family protein (TIGR) CDS		1,104	272	304.2	268.3	98.5	112.1	86.6
DVU0562	ISD1, transposase OrfA (TIGR) CDS		267	33	338.4	307.7	104.3	114.8	71.7
DVU0563	ISD1, transposase OrfB (TIGR) CDS		825	9.8	205.4	196.7	160.8	205.4	126.3
DVU0564	ylbG CDS	ylbG	396	39.3	110	109.1	91.5	104.3	67.2
DVU0565	gap-1 CDS	gap-1	1,017	606.2	597	495.9	386.8	410	534.9
DVU0566	GAF domain protein (TIGR) CDS		558	508.1	485.3	399.3	292.2	291.4	334.8
DVU0567	TerC family protein (TIGR) CDS		1,080	153	182.3	163.5	280.1	277.9	240.7
DVU0568	rhodanese-like domain protein (TIGR) CDS		1,041	54.2	65.4	53.2	96.6	96.9	94.4
DVU0569	flrA CDS	flrA	1,581	52.8	46.8	45.2	55.5	65	44.5
DVU0570	hypothetical protein (TIGR) CDS		177	25.4	26.7	20.2	2.3	8.6	0
DVU0571	ald CDS	ald	1,113	67	55.8	56.5	90.2	97.2	67.8
DVU0572	hypothetical protein (TIGR) CDS		339	74.6	87.6	77.3	590.6	590.5	512.3
DVU0573	creA CDS	creA	426	277	260.2	240.7	403.7	381	337.3
DVU0575	hypothetical protein (TIGR) CDS		282	444.2	467.9	418	771.3	765.4	670.8
DVU0576	msrB CDS	msrB	432	90.6	98.8	62.3	254.3	269.3	250
DVU0577	formate dehydrogenase formation protein FdhE, putative (TIG		882	272	286.8	236.1	574.8	569.9	747.4
DVU0578	formate dehydrogenase accessory protein FdhD, putative (TIG		789	205.5	209.6	188.1	1042.1	1037.1	1160.5
DVU0579	molybdopterin-guanine dinucleotide biosynthesis protein A, pu		669	165.6	151.9	129.2	916.4	905	953.4
DVU0580	moaA CDS	moaA	1,026	166.8	156.1	140.3	590.9	586.2	554.6
DVU0581	response regulator/anti-anti-sigma factor (TIGR) CDS		702	109.3	105.9	101.3	258.3	256.4	248.1
DVU0582	sensory box histidine kinase (TIGR) CDS		2,019	72.5	73.6	65.9	74.8	74.1	57.5
DVU0583	lipoprotein, putative (TIGR) CDS		1,272	110.1	105.2	99.8	159.2	152	174.1
DVU0585	conserved hypothetical protein (TIGR) CDS		2,394	87.5	83.7	82.3	94.6	95.2	76.7
DVU0586	hypothetical protein (TIGR) CDS		225	585.3	527.6	365.5	5586.5	4805.1	11886.3
DVU0587	fdnG-1 CDS	fdnG-1	3,018	553.8	504.6	376.3	3392	3056	5171.5
DVU0588	hybA CDS	hybA	711	576.5	472.4	387.1	2483.7	2346.3	2918.3
DVU0589	molybdopterin-guanine dinucleotide biosynthesis protein B, pu		741	121.3	123.1	104.9	205.3	218.1	209.9
DVU0591	mcpD CDS	mcpD	1,959	110.7	110.7	98.7	149.4	132.7	74.5
DVU0592	cheW-1 CDS	cheW-1	522	135.2	136.4	124.2	216.8	184.8	81.7
DVU0593	LysE CDS	LysE	621	93.3	70.4	76.4	16.2	23.3	18.3
DVU0594	iciA CDS	iciA	903	243	259.2	244.1	138.2	149.5	115
DVU0595	conserved hypothetical protein (TIGR) CDS		348	372.7	434.7	401.4	206.4	221	286.7

DVU0596	lytR CDS	lytR	774	169.5	193	171	159.9	161.7	189.6
DVU0597	lytS CDS	lytS	1,716	103.6	108.3	107.3	143.5	151.6	100.6
DVU0598	carbon starvation protein A, putative (TIGR) CDS		1,422	13.9	37.3	33.6	50.6	53.2	86.5
DVU0599	carbon starvation protein A, putative (TIGR) CDS		1,422	31.1	69.7	60.8	222.2	216.7	338.8
DVU0600	ldh CDS	ldh	930	75.1	68.6	68.6	123.5	135.3	121.2
DVU0601	b1396 CDS	b1396	435	80.3	61.7	71.4	107.9	124.4	114.1
DVU0602	hypothetical protein (TIGR) CDS		363	332.8	360.5	344.4	364.7	366.4	343.1
DVU0603	hypothetical protein (TIGR) CDS		267	114	146.3	146.9	46.9	44.8	58
DVU0604	hypothetical protein (TIGR) CDS		132	96.7	90.2	108.6	109.3	91.6	142.9
DVU0605	hypothetical protein (TIGR) CDS		129	56	44.2	51.3	37.7	29.7	10
DVU0606	transcriptional regulator, ArsR family/methyltransferase, UbiE		924	280	274	258.3	275.4	289.9	278
DVU0607	ahcY CDS	ahcY	1,440	445.3	433.4	441.2	254.2	249.6	221.1
DVU0608	methyl-accepting chemotaxis protein (TIGR) CDS		2,034	66.3	59.8	58.7	179.7	182.5	171.3
DVU0609	lipoprotein, putative (TIGR) CDS		636	140.4	140.1	138.8	160.2	155.3	170.6
DVU0610	conserved hypothetical protein (TIGR) CDS		921	105.3	101.6	92.5	142.8	133.7	145.1
DVU0611	ABC transporter, ATP-binding protein (TIGR) CDS		828	108.6	107.7	113.4	132.7	129.5	111.8
DVU0614	hypothetical protein (TIGR) CDS		282	171.5	177.3	156.8	1192.9	1168.6	1468.1
DVU0616	hypothetical protein (TIGR) CDS		393	51.7	55.3	56.4	121.4	129.8	138.1
DVU0617	hypothetical protein (TIGR) CDS		291	43.9	52.3	49.9	57	62.2	80.8
DVU0618	hypothetical protein (TIGR) CDS		156	49	69.6	47.5	20	22.9	8.3
DVU0619	sigma-54 dependent transcriptional regulator (TIGR) CDS		1,440	74.7	76.4	69.2	62.1	69.6	58.9
DVU0620	endoribonuclease, L-PSP family (TIGR) CDS		384	357.3	310	305.4	242.9	220.1	214
DVU0621	sigma-54 dependent DNA-binding response regulator (TIGR) C		1,398	74.1	72.8	69.2	63.8	68.1	62.5
DVU0622	sensor histidine kinase/response regulator (TIGR) CDS		2,499	56.7	54.3	49.3	82.8	88	71.6
DVU0624	nrfH CDS	nrfH	480	500.3	509.2	453.1	511.6	519.9	567.9
DVU0625	nrfA CDS	nrfA	1,575	491.7	513.7	463.2	326.4	297.1	286.7
DVU0626	ilvN-1 CDS	ilvN-1	480	250.8	235.4	204.7	323.9	332.4	330
DVU0627	ptB CDS	ptB	1,032	190.3	190.1	163.9	243.7	262.6	216.6
DVU0628	buk CDS	buk	1,119	109.1	105.7	96.7	172.6	190.5	175.9
DVU0629	transcriptional regulator, TetR family (TIGR) CDS		561	264.2	273.8	230.9	465.1	416.2	508.6
DVU0630	hypothetical protein (TIGR) CDS		177	284.7	259.8	237.8	594.1	537.2	852.6
DVU0631	conserved hypothetical protein (TIGR) CDS		1,566	132.2	131	125.2	231.5	206.9	209.6
DVU0632	cupin family protein (TIGR) CDS		618	62	74.3	64.4	44.3	43.8	20.9
DVU0633	penicillin-binding protein (TIGR) CDS		2,424	134.5	144.4	139.1	210.6	224.2	174
DVU0634	hypothetical protein (TIGR) CDS		567	57.9	66.2	54.6	71.3	72.5	61
DVU0635	dolichyl-phosphate-mannose-protein mannosyltransferase far		1,587	94.5	97.6	92.4	154.4	161.8	160.5
DVU0636	response regulator/GGDEF domain protein (TIGR) CDS		1,314	75.8	66.7	57.7	87.2	95.1	87.7
DVU0637	conserved hypothetical protein (TIGR) CDS		1,389	201.4	212.5	215.1	195.7	188.6	171.9
DVU0638	membrane protein, putative (TIGR) CDS		867	270.1	255.2	221.5	678.8	601.4	903.7
DVU0639	pomB CDS	pomB	774	126.3	136.9	127.8	118.6	125.9	97.8
DVU0640	pomA CDS	pomA	753	140.8	150.1	154.5	138.6	139.8	147.9
DVU0641	conserved hypothetical protein (TIGR) CDS		1,149	171.7	165.4	156	165.7	178.5	186.3
DVU0642	hydrolase, alpha/beta fold family (TIGR) CDS		813	298.2	255.5	266.2	391	398.6	356.7
DVU0645	methyl-accepting chemotaxis protein (TIGR) CDS		2,040	410.8	306.3	276.9	91.5	95	61.6
DVU0646	cobI CDS	cobI	771	138.1	147.4	139.9	48.7	57.7	65.7
DVU0647	iron compound ABC transporter, periplasmic iron compount-b		915	97.2	97.9	93.8	82.1	85.5	68
DVU0648	fepC CDS	fepC	816	131.5	131.8	148.2	252.7	248	267
DVU0649	iron compound ABC transporter, permease protein (TIGR) CDS		1,056	219.1	232.2	239.6	179.2	178.2	187.4
DVU0650	chelatase, putative (TIGR) CDS		894	468.6	521.4	503.2	287.9	289.9	394.3
DVU0651	membrane protein, putative (TIGR) CDS		1,089	41.8	42.2	38.9	71.7	67	44.6
DVU0652	cheV-2 CDS	cheV-2	951	54.2	45.5	48.5	76.1	81	85.3
DVU0653	atoC CDS	atoC	1,686	87	91.5	92.3	99.3	100.1	75.1
DVU0654	peptidase, U32 family (TIGR) CDS		1,227	146.8	163.6	146.8	215.6	212.3	175.2
DVU0655	PHP domain protein (TIGR) CDS		867	167	187.1	159.8	264.8	249.2	310.5
DVU0656	conserved hypothetical protein (TIGR) CDS		210	355.9	362.1	313.8	336.9	347.6	374.1
DVU0657	heat shock protein, Hsp20 family (TIGR) CDS		414	252.5	274.8	250.9	336.8	348.3	290.8
DVU0658	heat shock protein, Hsp20 family (TIGR) CDS		462	157.4	157.7	160.7	207.8	197.4	204.7
DVU0659	hypothetical protein (TIGR) CDS		771	154.9	136.3	143.2	177.4	192.3	178.3
DVU0660	phosphoesterase, putative (TIGR) CDS		567	143.6	150.3	146.3	88.8	99.7	59.3
DVU0661	dihydrouridine synthase family protein (TIGR) CDS		999	104.9	106.9	97.8	103	110.5	79.2
DVU0662	cysE CDS	cysE	972	236	320	301.7	273.3	266.8	277.6
DVU0663	cysK CDS	cysK	927	218	261	212.4	292.1	278.6	274.9
DVU0664	cysteine desulfurase (TIGR) CDS		1,185	493.4	541.2	445	570.1	532.6	627.2
DVU0665	nitrogen fixation protein nifU (TIGR) CDS		846	476.1	524.9	415.7	545	540.4	745.4
DVU0666	HD domain protein (TIGR) CDS		999	182.8	202	175.9	255.9	255.3	317.6
DVU0667	HD domain protein (TIGR) CDS		990	44.9	53.2	44.2	47.4	50.6	46.5
DVU0668	methyl-accepting chemotaxis protein (TIGR) CDS		1,587	87.9	95.7	90.6	200.9	213.5	196.1

DVU0669	hypothetical protein (TIGR) CDS		771	226.2	237.7	212.6	176.2	183.1	190.4
DVU0670	exopolysaccharide production protein, putative (TIGR) CDS		1,272	98.7	107.1	101.9	186.5	200.4	150.3
DVU0671	conserved hypothetical protein (TIGR) CDS		1,638	278.5	279.1	242.9	205	230.7	117.7
DVU0672	hypothetical protein (TIGR) CDS		153	1.1	0.6	1.2	0	0.8	0
DVU0673	hypothetical protein (TIGR) CDS		168	9.9	12.9	7.9	1.6	1.6	0
DVU0674	ABC transporter, permease protein, His/Glu/Gln/Arg/opine far		816	134.5	132.4	112.9	189.2	194.7	147.3
DVU0675	fliY CDS	fliY	822	262.1	279.7	230.8	225.8	217.8	205.3
DVU0676	artQ CDS	artQ	888	231.9	224.3	206.2	231.9	239.3	197.3
DVU0677	transglycosylase domain protein (TIGR) CDS		1,050	195	208	210.5	360.1	355.6	411.5
DVU0679	luxO CDS	luxO	1,467	66.6	69.5	65.9	37.1	38.8	28.3
DVU0680	sensory box histidine kinase (TIGR) CDS		2,073	110.8	106.7	111.1	72.5	79.5	52.8
DVU0681	sensor histidine kinase/response regulator (TIGR) CDS		2,004	115.4	127.3	106.4	268.7	262.1	293.3
DVU0683	hflC protein, putative (TIGR) CDS		852	755.7	793.9	718.4	512.7	510.5	614.8
DVU0685	rfbB CDS	rfbB	1,362	196	175.5	174.4	194.9	196.9	171.9
DVU0686	iron-sulfur cluster-binding protein (TIGR) CDS		489	179	163.2	156.1	249	268.5	228.9
DVU0687	aor-2 CDS	aor-2	1,785	185.5	173.7	169.6	139.8	145.9	137.4
DVU0688	hypothetical protein (TIGR) CDS		501	173.9	175.6	165.5	203.2	200.2	133.5
DVU0689	rnhA CDS	rnhA	471	213.5	214	208.9	169.3	203	137.7
DVU0690	conserved hypothetical protein (TIGR) CDS		672	307.3	322.8	297.9	420.3	406.2	423
DVU0691	membrane protein, putative (TIGR) CDS		960	98.4	109.7	104.7	109.5	108.7	95.8
DVU0692	qrcD CDS	qrcD	1,260	957.8	990.7	905.1	1335.6	1233.9	1201.6
DVU0693	qrcC CDS	qrcC	768	974.5	1010.9	934.7	1490.8	1496.6	1974.5
DVU0694	qrcB CDS	qrcB	2,076	951	1039.2	941.7	734	677.1	864.7
DVU0697	rfbA CDS	rfbA	1,419	342.9	354.5	316.8	253.5	245.3	252.6
DVU0698	rfbC CDS	rfbC	573	265.5	269.9	242.9	289.2	260.7	346
DVU0700	methyl-accepting chemotaxis protein (TIGR) CDS		2,457	11.1	13.5	10.9	55.5	45.3	29.9
DVU0701	glcB CDS	glcB	2,190	251.5	227.6	228.2	250.2	249.6	241.7
DVU0702	cytochrome c family protein (TIGR) CDS		447	280	312.5	286	629.1	630.7	486.8
DVU0703	lepA CDS	lepA	1,806	424.9	443.3	429.2	264.9	270.6	286.2
DVU0704	lepB CDS	lepB	600	491.5	474.2	478.2	301.1	316.6	258.5
DVU0705	dctM CDS	dctM	1,284	45.3	41	44.1	83.5	85.4	62.2
DVU0706	membrane protein, putative (TIGR) CDS		471	64.9	62.2	53.4	68.6	95.9	54.3
DVU0707	dctP CDS	dctP	1,017	107.2	101.3	102.2	67.5	76.8	57.4
DVU0710	competence protein comM, putative (TIGR) CDS		1,665	42.3	44.2	41.7	35.3	41.4	24.5
DVU0711	hypothetical protein (TIGR) CDS		642	99.3	88.4	94	184.2	182.1	144.9
DVU0712	amino acid ABC transporter, periplasmic-binding protein (TIGR		1,131	676	661.1	575.6	455.7	435.5	385.6
DVU0713	livH CDS	livH	906	270.2	243.5	243	379.3	374.4	233.7
DVU0714	livM CDS	livM	954	237.1	241.4	226.8	316.5	315.5	208.3
DVU0715	livG CDS	livG	768	227.5	247.6	221.6	149.9	171.3	140.3
DVU0716	livF CDS	livF	717	307.5	300.2	293.3	537.2	554.3	387.4
DVU0717	GGDEF domain/EAL domain protein (TIGR) CDS		1,509	6.3	10.6	10.3	12.8	15.7	10.9
DVU0718	ISDvu2, transposase OrfA (TIGR) CDS		399	0.4	92.7	85.8	133.2	133.8	86.8
DVU0719	ISDvu2, transposase OrfB (TIGR) CDS		843	3.9	72.3	68.4	70.7	74.4	58.9
DVU0720	HAMP domain protein (TIGR) CDS		1,290	100.7	102.1	97.1	147.8	148.6	105.4
DVU0722	response regulator (TIGR) CDS		1,557	65.1	67.8	56.8	115.7	117	82.6
DVU0723	purT CDS	purT	1,182	172.6	169.6	149.8	183	179.6	114.6
DVU0724	sodium/alanine symporter family protein (TIGR) CDS		1,407	274.3	322.9	289.1	263.2	258.9	222.6
DVU0725	conserved hypothetical protein (TIGR) CDS		2,148	51.7	52.5	46.1	170.5	150.9	146.6
DVU0726	tgt CDS	tgt	1,128	207.1	235	207	323.9	329.4	351
DVU0727	conserved hypothetical protein (TIGR) CDS		675	35.6	43.3	33.3	62.7	65.5	51.7
DVU0728	hypothetical protein (TIGR) CDS		171	17.1	26.1	15	9.2	9.5	13.6
DVU0729	hypothetical protein (TIGR) CDS		456	78.3	88.7	73.1	1546.5	1424.4	1733
DVU0730	conserved hypothetical protein (TIGR) CDS		966	64.8	87.5	79.5	71.1	74.1	59.2
DVU0731	hypothetical protein (TIGR) CDS		1,362	139.1	142.4	137.2	440.3	420.3	525.8
DVU0732	valS CDS	valS	2,655	403.3	412.4	398	326.5	325.2	339.7
DVU0733	conserved hypothetical protein (TIGR) CDS		489	104.6	92.4	84.5	118	124.8	72.9
DVU0734	cysG-1 CDS	cysG-1	1,512	451.5	470.7	426.1	192.9	197	193.4
DVU0735	MOSC domain protein (TIGR) CDS		435	147.8	146.1	133.3	257.8	260	202
DVU0736	purN CDS	purN	678	205.7	198.6	191.7	310	301	269.9
DVU0737	sensory box histidine kinase (TIGR) CDS		2,241	56	59.9	55.3	119	120	96.7
DVU0738	substrate-binding protein, putative (TIGR) CDS		1,122	75.4	79.3	71.3	169.3	164.5	136.8
DVU0739	conserved hypothetical protein TIGR00296 (TIGR) CDS		573	67.5	67	49.9	60.4	60.7	65.8
DVU0740	membrane protein, putative (TIGR) CDS		1,176	37	41.3	30.4	59.4	62.6	62
DVU0741	hypothetical protein (TIGR) CDS		477	220.3	254.1	211.9	126.8	124.9	162.5
DVU0742	hypothetical protein (TIGR) CDS		837	155.9	147.1	123.4	275.6	293.3	239.3
DVU0743	sensory box histidine kinase (TIGR) CDS		1,998	130.4	121.6	111.5	185.5	198	177.2
DVU0744	sigma-54 dependent transcriptional regulator/response regula		1,710	72.3	69.7	68	89.3	93.2	70.8

DVU0745	ABC transporter, periplasmic substrate-binding protein (TIGR)		819	191.7	187.5	165.4	164.6	160.1	260.6
DVU0746	cysW CDS	cysW	747	52.2	54.4	50	82.3	91.8	83.8
DVU0747	cysA CDS	cysA	639	58.2	53.4	51.5	56.1	54.7	62.3
DVU0748	acs CDS	acs	1,947	77.2	70.6	64.3	54.1	59.8	54.2
DVU0749	DNA-binding response regulator (TIGR) CDS		930	56.3	58.7	53.5	97.3	110.2	92.8
DVU0750	methyl-accepting chemotaxis protein (TIGR) CDS		2,010	29.3	29.5	28.6	19.3	18	17.2
DVU0751	amino acid ABC transporter, permease protein, His/Glu/Gln/A		1,791	110.8	115.5	114.5	53.4	55.7	42.4
DVU0752	amino acid ABC transporter, amino acid-binding protein (TIGR		828	716.9	705.3	652.7	114.4	127.8	82.4
DVU0753	amino acid ABC transporter, ATP-binding protein (TIGR) CDS		732	239.6	259.5	249.9	158.5	173.6	153.2
DVU0754	hypothetical protein (TIGR) CDS		135	116.6	123.9	123.2	157	162.4	141.7
DVU0755	sensor histidine kinase, putative (TIGR) CDS		1,368	153.5	159.4	136.8	272.4	259.5	282.2
DVU0756	TPR domain protein (TIGR) CDS		714	217.6	216.2	211.9	130.2	144.4	89.4
DVU0757	hypothetical protein (TIGR) CDS		321	152.2	161.5	163.4	103.7	117.4	79.7
DVU0758	hypothetical protein (TIGR) CDS		450	102	133.6	128.2	77.3	74.4	66
DVU0759	peptidase, M29 family (TIGR) CDS		1,206	83.2	104.6	72.1	77.2	83.7	76.5
DVU0760	hypothetical protein (TIGR) CDS		1,131	56.7	72.2	55.8	84	87.5	64
DVU0761	lipoprotein, putative (TIGR) CDS		591	353.3	350.6	284.7	137.5	119.2	176.7
DVU0762	conserved hypothetical protein (TIGR) CDS		471	223.6	223.7	203.4	333.5	314.9	307.3
DVU0763	gdp CDS	gdp	936	14.3	16.4	18.3	21.4	26.8	11.6
DVU0765	hydroxypyruvate reductase, putative (TIGR) CDS		1,365	76.9	73.1	69.3	135.7	128.5	118.9
DVU0766	transporter, putative (TIGR) CDS		531	365	329.8	332.3	415.1	433.5	390.3
DVU0767	aminotransferase, class V (TIGR) CDS		1,107	159.6	140.6	135.4	115.3	105.2	100.8
DVU0768	murI CDS	murI	849	114.2	113.9	100.8	73.4	79.7	75.2
DVU0769	pyridoxal kinase, putative (TIGR) CDS		879	107.9	108.9	87.9	81	81	90.2
DVU0770	membrane protein, putative (TIGR) CDS		951	64.8	76	75.7	73.2	81.6	55.4
DVU0771	molybdenum-pterin binding domain protein/site-specific reco		1,071	79.3	73.4	71.5	80.4	83.5	57.9
DVU0772	hypothetical protein (TIGR) CDS		348	1249.6	1151.1	782.9	1207	1386.8	1382.7
DVU0773	hypothetical protein (TIGR) CDS		240	891	1327.3	1095.5	1056.5	1079	1109.1
DVU0774	atpC CDS	atpC	405	2152.2	2213.3	2079.3	1574.5	1429.3	1048.4
DVU0775	atpD CDS	atpD	1,413	2409.5	2681.3	2409.1	963.1	952	1054.7
DVU0776	atpG CDS	atpG	876	2079.2	2206.6	2027.3	1031.7	981.4	1052.2
DVU0777	atpA CDS	atpA	1,509	2119.3	2345.9	2112.9	853.2	814.7	788.3
DVU0778	atpH CDS	atpH	552	1791.4	1919.3	1789.3	1079.6	947.5	902.7
DVU0779	atpF2 CDS	atpF2	531	1857.7	1977.4	1848.5	1016.2	1028.7	1214.7
DVU0780	atpF1 CDS	atpF1	396	1906.9	2067.9	1958.6	1473.8	1518.1	2097.4
DVU0784	conserved hypothetical protein (TIGR) CDS		348	159	173.1	140.7	98	102.8	75.7
DVU0785	rodA CDS	rodA	1,116	107.6	131.9	120.2	97.4	96.8	76.9
DVU0786	penicillin-binding protein (TIGR) CDS		1,788	172.2	182.4	184.5	136.1	145.5	121.9
DVU0787	hypothetical protein (TIGR) CDS		471	122.4	157	145.6	159	149.5	132.2
DVU0788	mreC CDS	mreC	915	386.5	443	424.1	339.6	345.8	360.1
DVU0789	mreB-1 CDS	mreB-1	1,041	486.2	563.5	486.2	741.2	740.6	1113.9
DVU0790	radical SAM protein, TIGR01212 family (TIGR) CDS		1,056	175.9	188.7	183.1	309.2	318.9	324
DVU0791	ogt CDS	ogt	486	215	217.5	216.2	157.4	186.1	106.4
DVU0792	conserved domain protein (TIGR) CDS		333	243.1	245.6	248.2	160	163.6	124.2
DVU0793	hypothetical protein (TIGR) CDS		96	869.8	868	832.7	533.7	521.2	358
DVU0794	fabI CDS	fabI	765	450.1	480.5	454.2	181.6	184.3	183.4
DVU0795	purC CDS	purC	897	282.2	317.4	293.8	105.3	102.3	105.1
DVU0796	hisD CDS	hisD	1,311	147.3	167.6	147.4	222.2	211	206.8
DVU0797	conserved hypothetical protein (TIGR) CDS		1,431	3957.9	4792.5	4338.6	923	856.9	846.3
DVU0798	hypothetical protein (TIGR) CDS		96	126.2	124	102.9	41.3	59.7	26.9
DVU0799	conserved hypothetical protein (TIGR) CDS		1,401	5453.9	6077.3	5521.9	3639.7	3251.6	5803
DVU0801	uvrC CDS	uvrC	2,109	61.5	66.5	64.1	94.2	103.4	77.9
DVU0802	hypothetical protein (TIGR) CDS		117	20.4	33.7	25.6	32	27.3	17.7
DVU0803	sensor histidine kinase (TIGR) CDS		1,266	148.2	137.9	125	129.3	130.2	109
DVU0804	atoC CDS	atoC	1,473	98.1	89.3	86.9	151.3	156.3	122.8
DVU0805	hypothetical protein (TIGR) CDS		297	212.1	228.4	235.3	211.7	207.7	175.7
DVU0806	chemotaxis protein CheY, putative (TIGR) CDS		411	157.3	139.4	154.7	280.6	305	257.8
DVU0807	trmU CDS	trmU	1,041	175.3	185.3	192.2	125.7	143.5	88.9
DVU0808	gatA CDS	gatA	1,470	236.7	287.1	252.3	125.4	134.1	116.8
DVU0809	gatC CDS	gatC	285	222.3	289.2	233	118.5	131.1	122.4
DVU0810	hypothetical protein (TIGR) CDS		2,061	241	281.8	263.3	212.9	219.4	190.9
DVU0811	dnaK CDS	dnaK	1,911	973.3	1353.2	905.8	1188.4	1099	1528.4
DVU0812	grpE CDS	grpE	576	438.5	511.7	443.4	321.9	323.5	313.1
DVU0813	hrcA CDS	hrcA	1,068	315.3	370.4	313.9	611.2	611.2	633.5
DVU0814	bcp CDS	bcp	486	143.8	155	133.6	277.2	294.6	264.8
DVU0815	AsmA family protein (TIGR) CDS		2,106	53.5	61.9	54.1	94.4	94.5	116.8
DVU0816	cobQ CDS	cobQ	1,632	92.2	99.3	85	125.5	124.5	126.7

DVU0817	hypothetical protein (TIGR) CDS		468	405.6	431.8	415.5	304.1	333	451.7
DVU0818	conserved domain protein (TIGR) CDS		1,749	63.4	57.8	57.5	72.8	80.3	60.6
DVU0819	isf-1 CDS	isf-1	618	357.1	325.5	290.5	216.1	222	279.3
DVU0821	conserved hypothetical protein (TIGR) CDS		600	66.6	95.5	67.5	26	23.1	25
DVU0822	hypothetical protein (TIGR) CDS		657	84.6	111.2	97.5	90.4	75.5	67.6
DVU0823	argJ CDS	argJ	1,182	157.6	151.9	140.2	92.5	90.2	101.5
DVU0825	secA CDS	secA	2,502	241.4	257.3	205	388.1	376	434.2
DVU0826	glycolate oxidase, iron-sulfur subunit, putative (TIGR) CDS		1,323	100.6	123.6	101.5	54.4	52.2	37.9
DVU0827	glycolate oxidase, subunit GlcD, putative (TIGR) CDS		1,416	201.9	209.9	214.8	172.4	193.9	161.4
DVU0828	smpB CDS	smpB	465	402.9	435	377.2	320.3	321.4	336.8
DVU0829	ptsI CDS	ptsI	1,773	180.8	191.1	170.2	268.3	274.7	258.2
DVU0830	ptsH CDS	ptsH	261	336.4	360.3	355.8	591.8	579.7	635.7
DVU0831	PTS system, IID component, putative (TIGR) CDS		759	143.9	163.3	142.1	167.2	184.9	118.4
DVU0832	tetrapyrrole methylase family protein (TIGR) CDS		828	165.8	172.9	153.5	241.6	260.9	193.2
DVU0833	conserved hypothetical protein TIGR00252 (TIGR) CDS		405	126.3	122.2	117.6	205.2	229.2	279.5
DVU0834	rnhB CDS	rnhB	663	196.9	197.2	206.8	258.4	282.2	306
DVU0835	rplS CDS	rplS	348	2149.7	2295.5	2125.3	1231.4	1166.4	1834.3
DVU0836	trmD CDS	trmD	1,278	754.9	819.7	814.5	699.9	656.7	866.1
DVU0837	rimM CDS	rimM	531	582.3	699.7	614.5	567.6	484.9	571.4
DVU0838	conserved hypothetical protein (TIGR) CDS		234	2630.7	3024.1	2750.5	1628.2	1599.8	2033.1
DVU0839	rpsP CDS	rpsP	240	2607	2965.7	2658.3	1388.1	1424.4	1688.4
DVU0840	ffh CDS	ffh	1,527	481.4	544.4	500	1038.8	990.5	1390.1
DVU0841	aspartate aminotransferase, putative (TIGR) CDS		1,182	302.2	292.5	266.6	179.2	188.9	150
DVU0842	hypothetical protein (TIGR) CDS		231	420.6	465	376	514.1	516.5	450.9
DVU0843	hypothetical protein (TIGR) CDS		1,599	364.4	427.1	358.1	428.6	417.4	358.7
DVU0846	ApsB CDS	ApsB	504	5610.7	6432.9	5696.7	1911.7	1638.1	1894.1
DVU0847	ApsA CDS	ApsA	1,995	5080.5	5823	5302.6	1829.3	1684.9	1882.7
DVU0848	QmoA CDS	QmoA	1,239	1040.2	1197.8	1135.2	586.2	553.5	506
DVU0849	QmoB CDS	QmoB	2,277	1098.7	1267	1239.8	579.3	582.9	475.1
DVU0850	QmoC CDS	QmoC	1,155	1230.1	1437	1408.8	859.3	835.3	702.5
DVU0851	hypothetical protein (TIGR) CDS		747	1190.7	1329.8	1331.1	1055.3	988.9	812.3
DVU0852	extracellular solute-binding protein, putative (TIGR) CDS		798	85.3	88.9	82.7	165.9	171.7	141.2
DVU0854	NirD protein, putative (TIGR) CDS		531	561.9	595.1	525.1	604.3	576.8	743.7
DVU0856	hemB CDS	hemB	993	623.7	674.3	555.4	467.6	470.7	587.9
DVU0857	nirJ-1 CDS	nirJ-1	1,182	733.3	801.9	689.9	627.4	580.6	777.6
DVU0858	lipoprotein, putative (TIGR) CDS		684	104.3	109.7	111.4	191.2	179.3	186.7
DVU0861	glycosyl transferase, group 1 family protein (TIGR) CDS		1,119	57.1	56.5	52.7	61.9	57.5	49.4
DVU0862	flagellar protein FliS/hypothetical protein, fusion (TIGR) CDS		906	123.1	145.6	135.2	331.3	315.6	376.3
DVU0863	flagellar hook-associated protein 2, putative (TIGR) CDS		1,728	184.3	198.7	160.1	383.5	363.7	452.9
DVU0864	glycoprotease family protein, putative (TIGR) CDS		786	184.6	198.9	178.6	205.9	204.2	140.7
DVU0865	membrane-associated zinc metalloprotease, putative (TIGR) C		1,065	268.1	290.3	253.1	324.5	312.8	231.5
DVU0866	dxr CDS	dxr	1,227	147.9	161.3	140.6	253.1	239.2	284.1
DVU0867	aromatic amino acid decarboxylase, putative (TIGR) CDS		1,494	176.3	200.7	173.9	162.7	165.1	123.3
DVU0868	cdsA	cdsA	807	225.9	239.5	222.7	242.6	248.1	148.5
DVU0869	uppS CDS	uppS	744	249.9	275.4	245.1	154	175.6	175.7
DVU0870	frr CDS	frr	561	728.9	782.1	658.1	305.4	300	406.3
DVU0871	pyrH CDS	pyrH	717	657	654.3	594.4	1081.2	1052	1622.6
DVU0872	glycosyl transferase, group 2 family protein (TIGR) CDS		768	219.6	230.6	214	196.2	200.4	152.1
DVU0873	tsf CDS	tsf	864	1449.6	1613.9	1459.5	873.2	874.2	810.9
DVU0874	rpsB CDS	rpsB	765	1702.9	1986.3	1740.3	758.5	718.6	956.3
DVU0875	fumarylacetoacetate hydrolase family protein (TIGR) CDS		780	159.2	169.1	142.6	195.7	191.7	220.3
DVU0876	metallo-beta-lactamase family protein (TIGR) CDS		1,665	333.4	335.4	306	265.2	256.1	256.9
DVU0878	dnaK suppressor protein, putative (TIGR) CDS		357	191.4	207.5	190.8	134.5	147.9	228.8
DVU0881	fusA CDS	fusA	2,067	284.9	319	244.6	500	507.8	508.4
DVU0882	hypothetical protein (TIGR) CDS		465	202.2	168.2	170.8	214.6	209.3	176.8
DVU0883	nrdH CDS	nrdH	258	440.7	422.5	389.8	201.4	219.6	241.4
DVU0884	ftrB CDS	ftrB	345	295.9	270.3	238.8	284.6	306.8	391.8
DVU0885	amidohydrolase family protein (TIGR) CDS		789	110.2	124.1	107.4	142.8	159.5	122.5
DVU0886	thioesterase family protein (TIGR) CDS		411	141.2	140.5	132.9	369.6	364.1	443.9
DVU0887	mltA CDS	mltA	1,275	50.1	56.4	51.6	70.6	76.8	50.6
DVU0888	response regulator (TIGR) CDS		1,713	81.5	79.1	76.1	80.3	79.2	62.2
DVU0889	phosphonopyruvate decarboxylase-related protein (TIGR) CDS		1,140	85.3	75.2	77.9	109.7	103.9	81.4
DVU0890	hom CDS	hom	1,275	449.2	443	427.1	453.8	462.1	493.6
DVU0891	aminotransferase, classes I and II (TIGR) CDS		1,194	508.5	510.9	433.8	371.4	361.5	532
DVU0892	aroK-1 CDS	aroK-1	528	95.2	79.4	80.6	215.7	254.4	234
DVU0893	universal stress protein family (TIGR) CDS		483	279.5	310	295.1	257.3	255.2	281.5
DVU0894	aroC CDS	aroC	1,065	254.1	256.8	245.6	278.5	287.8	308.1

DVU0895	recD CDS	recD	2,229	167.8	183.2	168.2	226.2	228.2	201.2
DVU0896	lipoprotein, NLP/P60 family (TIGR) CDS		1,395	211.8	215.1	208.8	99.4	106	63.5
DVU0897	RNA modification enzyme, MiaB-family (TIGR) CDS		1,377	150.9	161.5	166.5	160.4	158.8	89.7
DVU0898	conserved hypothetical protein (TIGR) CDS		882	259.5	255.8	235.1	158.6	161.1	129
DVU0899	conserved hypothetical protein (TIGR) CDS		261	278.6	343.5	301	160.4	182.8	166.4
DVU0900	gmk CDS	gmk	624	252.8	296.1	252.3	201.9	191	162.7
DVU0901	pyrF CDS	pyrF	708	279.7	275	259.5	240.7	247	184.3
DVU0902	TPR domain protein (TIGR) CDS		858	470.5	486.8	458.7	245.3	250.5	253.9
DVU0903	HD domain protein (TIGR) CDS		858	223.7	225.7	222.1	346.9	368.5	259.9
DVU0904	recJ CDS	recJ	1,716	126.9	132.7	130.4	74.3	77.8	54.5
DVU0905	lipA CDS	lipA	897	64.9	60.6	55.6	58	46.6	41.8
DVU0906	lipB CDS	lipB	657	89.1	87.7	82.8	51.7	49.9	42.9
DVU0907	conserved domain protein (TIGR) CDS		2,940	78.2	144.8	126.4	138.9	149.5	132.9
DVU0908	iron-sulfur cluster-binding protein, putative (TIGR) CDS		1,632	109.9	113.9	107.6	99.9	101.1	113.3
DVU0909	hypothetical protein (TIGR) CDS		396	205.6	206.9	190.3	328.7	358.2	268.9
DVU0910	fliM CDS	fliM	981	250.5	293.7	262.8	738.3	720.1	855
DVU0911	truA CDS	truA	894	86	103.1	101.9	158.4	168.4	115.9
DVU0912	conserved domain protein (TIGR) CDS		585	83	86	91	248.3	251	174.5
DVU0913	conserved hypothetical protein (TIGR) CDS		438	76.7	87.4	76.5	182.7	195	194.7
DVU0914	cobS CDS	cobS	738	29.9	40.5	35	40.1	45.5	31.6
DVU0915	conserved hypothetical protein (TIGR) CDS		789	173.5	206.2	193.8	244	253.6	227.3
DVU0916	AT-rich DNA-binding protein (TIGR) CDS		645	715.7	826.2	738.6	473.4	456.7	593.8
DVU0917	atpE CDS	atpE	249	2439.6	2691.3	2324.8	1388.2	1159.5	1255.8
DVU0918	atpB CDS	atpB	702	1047.9	1161.2	1042.7	864.5	778	814.3
DVU0919	hypothetical protein (TIGR) CDS		435	1059.5	1153.7	1101	1352.7	1309.2	1164.4
DVU0921	5-nitroimidazole antibiotic resistance protein, putative (TIGR)		468	83.9	76	68.5	50.8	50.2	51.9
DVU0922	cytochrome c family protein (TIGR) CDS		558	81.3	87.2	63.8	81.4	82.5	99.1
DVU0923	endoribonuclease, L-PSP family (TIGR) CDS		399	202.3	228.3	212.1	92.7	98.6	130.8
DVU0924	rumA CDS	rumA	1,407	102	108.6	101.5	96	92.3	85.2
DVU0925	rfbA CDS	rfbA	909	176.2	180.6	185	311.5	304.7	275.7
DVU0926	hypothetical protein (TIGR) CDS		192	25.2	40.4	35.4	47.9	46.3	51.1
DVU0927	rplU CDS	rplU	309	2535.6	2819.8	2550.6	2120.7	2039.6	2647
DVU0928	rpmA CDS	rpmA	264	2700.8	3072.4	2796.2	2546.7	2510.7	3992.8
DVU0929	obg CDS	obg	1,101	368.6	367	364.1	291	287.7	278.3
DVU0930	proB CDS	proB	1,143	249.4	223.5	235.2	204	208.2	171.8
DVU0931	thiD CDS	thiD	807	230.4	214.3	226.8	200.4	213.8	164.6
DVU0932	sensor histidine kinase (TIGR) CDS		1,176	207.1	191.3	189.9	186.4	191.7	143.2
DVU0933	response regulator (TIGR) CDS		1,245	164.4	142.3	140.1	129.4	133.7	85.5
DVU0934	hypothetical protein (TIGR) CDS		261	108.6	111.8	102.9	66.3	78.7	36.7
DVU0935	methyl-accepting chemotaxis protein (TIGR) CDS		2,505	248.2	223.2	216.3	256.8	269.4	255.5
DVU0937	hypothetical protein (TIGR) CDS		387	460.6	499.5	469.2	401.2	421.1	413.4
DVU0938	isoamylase N-terminal domain protein (TIGR) CDS		369	272.2	300.8	285	315.3	319.5	407.6
DVU0939	conserved hypothetical protein (TIGR) CDS		750	207.9	223.4	221.5	206.8	206.3	239.2
DVU0940	pleD CDS	pleD	732	145.9	146.4	137	245	263.7	170.1
DVU0941	pep* CDS	pep*	2,895	236.5	239.5	209.1	164.4	162.7	169.3
DVU0942	fur CDS	fur	435	524.3	463.8	460.2	715.3	685.3	676.1
DVU0944	hypothetical protein (TIGR) CDS		258	265.1	230	167.6	541.5	603.2	673.1
DVU0945	sensor histidine kinase (TIGR) CDS		2,433	131.6	111.4	99.5	228.3	218.8	213.9
DVU0946	sigma-54 dependent transcriptional regulator/response regula		1,431	162.6	141.8	132.7	154.5	160.7	124.8
DVU0947	membrane protein, putative (TIGR) CDS		906	155.6	140	122.2	225.3	222.6	274.4
DVU0948	conserved hypothetical protein (TIGR) CDS		429	304.7	320.3	292.7	516.4	562.9	1015.1
DVU0949	conserved domain protein (TIGR) CDS		762	156.1	198.3	137.1	468.3	516.8	743.7
DVU0952	conserved hypothetical protein TIGR00282 (TIGR) CDS		873	177.8	149.6	150.8	155.1	176.3	165.2
DVU0953	tyrS CDS	tyrS	1,197	474	465.2	457.1	367.5	367.2	395.5
DVU0954	organic solvent tolerance protein, putative (TIGR) CDS		2,295	210.1	226.7	202.3	267.8	275.8	270.4
DVU0955	alr CDS	alr	1,131	149.4	137.9	135.9	150	153.1	122.5
DVU0956	rpsF CDS	rpsF	306	1690.4	1919.3	1746	799.8	742.3	1202.6
DVU0957	rpsR CDS	rpsR	264	2580.7	2780.7	2586.7	1615.8	1495.8	2396.3
DVU0958	rplI CDS	rplI	504	1656.1	1840.9	1690.4	1218.8	1089.6	1436.7
DVU0959	dnaB CDS	dnaB	1,482	443	469.7	454.7	388.8	384.7	476.1
DVU0961	conserved hypothetical protein (TIGR) CDS		4,065	161.7	162.8	140.8	156.4	153.5	189.3
DVU0963	GTP cyclohydrolase I family protein (TIGR) CDS		498	138.6	131	87.2	102.2	104.9	134.9
DVU0964	fragments CDS	fragments	2,994	135.5	122.2	103.5	222.3	227.5	236.9
DVU0965	hypothetical protein (TIGR) CDS		177	503.8	473.6	454.1	224	223.3	268.7
DVU0966	amino acid ABC transporter, periplasmic amino acid-binding p		819	1220.4	1101.8	1049.7	202.7	207.3	247.4
DVU0967	amino acid ABC transporter, permease protein, His/Glu/Gln/A		1,014	250	249.4	238.4	209.2	203.2	187.6
DVU0968	amino acid ABC transporter, ATP-binding protein (TIGR) CDS		741	223	208.7	193.3	156.9	156.8	132.5

DVU0969	efflux protein, LysE family (TIGR) CDS		747	174.6	172.8	164.2	169.5	165.3	153.5
DVU0970	lipoprotein, putative (TIGR) CDS		540	132.2	132.4	120.9	128.4	137.6	79
DVU0971	molybdenum cofactor biosynthesis protein (TIGR) CDS		780	165	154.6	149.4	123.6	142.1	106.4
DVU0972	HD domain protein (TIGR) CDS		1,266	117.4	119.8	118.5	100.1	101.7	77.8
DVU0973	4-hydroxybenzoate octaprenyltransferase, putative (TIGR) CDS		870	166.8	173.1	157.3	74.9	74.8	51.4
DVU0974	hypothetical protein (TIGR) CDS		339	205.3	181.9	187.8	446.5	451.1	397.2
DVU0975	conserved hypothetical protein (TIGR) CDS		561	241	258.1	238.1	247.7	243	217.9
DVU0976	response regulator (TIGR) CDS		1,164	79.4	88.4	82.9	183.1	196.3	159.8
DVU0978	ABC transporter, periplasmic substrate-binding protein, putati		855	57.4	62.4	53.7	46.9	51.6	35.1
DVU0979	b1200 CDS	b1200	1,065	310.6	339.1	272.3	333.3	342.9	290.7
DVU0980	b1199 CDS	b1199	633	176.4	195.1	163.6	186.2	203.1	125.7
DVU0981	ptsI CDS	ptsI	2,565	115.4	136.6	119.6	166	179.5	116.6
DVU0982	PHP domain protein (TIGR) CDS		660	124	142	123.7	263.8	264	230.2
DVU0983	conserved hypothetical protein (TIGR) CDS		546	195.9	203.5	176.8	257.9	245.7	217.2
DVU0984	miaB CDS	miaB	1,350	153	180.3	155.2	165.4	170.6	185.6
DVU0987	heavy metal-binding domain protein (TIGR) CDS		204	906.3	902.3	852.4	308	339.1	339.5
DVU0988	cbhK CDS	cbhK	927	242.8	231.4	198.8	185.7	216	176.2
DVU0990	nth CDS	nth	858	146.1	173.5	143.3	83.3	90.6	62.6
DVU0991	conserved hypothetical protein (TIGR) CDS		819	148.7	142	136.4	208.4	203.9	251.2
DVU0992	cheV-3 CDS	cheV-3	963	196.9	193.8	170.4	217.2	211.5	185.7
DVU0993	hypothetical protein (TIGR) CDS		723	154	148.3	137.2	223.5	229	188.8
DVU0994	hypothetical protein (TIGR) CDS		180	450.4	671.7	583.3	968.5	959.7	760.9
DVU0995	ThiJ/PfpI family protein (TIGR) CDS		588	327.1	337.2	264.9	270.1	266.6	294.5
DVU0996	hypothetical protein (TIGR) CDS		876	127	132.9	124.5	269.4	272.9	226.6
DVU0997	metF CDS	metF	876	111.3	105.8	94.3	174.1	178.3	134.5
DVU0998	heptosyltransferase family protein (TIGR) CDS		1,056	137.7	120.6	131.5	103.8	103.6	86.7
DVU0999	thio:disulfide interchange protein, putative (TIGR) CDS		2,160	124.3	112.2	115.7	258.1	263.5	198.1
DVU1000	peptidase, M24 family (TIGR) CDS		1,224	84.1	89.8	79.1	79.2	83.9	88.7
DVU1001	b0965 CDS	b0965	405	252.7	275	238.5	149.6	165.4	169.7
DVU1002	conserved domain protein (TIGR) CDS		456	276.9	275.6	273	205.5	222.4	189.8
DVU1003	dnaJ domain protein (TIGR) CDS		987	232.8	216.5	221.8	273.8	286.8	213.3
DVU1004	membrane protein, putative (TIGR) CDS		885	105.2	94.2	92.7	118.5	115.6	110.9
DVU1005	hypothetical protein (TIGR) CDS		1,221	380	392.8	395.2	391.7	403.2	419.1
DVU1006	hypothetical protein (TIGR) CDS		450	132.1	115	111.5	204.3	217.1	214.8
DVU1007	cobU CDS	cobU	537	79.6	77.4	65.9	91	107.3	66.5
DVU1008	hypothetical protein (TIGR) CDS		804	263.7	234.5	230.6	167.9	190.5	129.9
DVU1009	hypothetical protein (TIGR) CDS		615	123.5	155	135.3	64	61.9	32.8
DVU1012	hemolysin-type calcium-binding repeat protein (TIGR) CDS		9,117	537.3	616.6	546.6	627.1	604.6	728
DVU1013	type I secretion outer membrane protein, TolC family (TIGR) C		1,371	675.3	740.7	622.9	767.6	745.5	878
DVU1017	rtxB CDS	rtxB	2,331	199.2	202.1	185.6	219.5	220.6	211.2
DVU1018	rtxD CDS	rtxD	1,347	190.2	189.6	175.6	191.7	207.5	203.6
DVU1019	conserved domain protein (TIGR) CDS		1,221	149.7	160.4	147.3	151.6	164.9	119.2
DVU1020	HD domain/sensory box protein (TIGR) CDS		2,106	192.9	215.4	189.8	242.1	261.9	199.4
DVU1021	conserved hypothetical protein (TIGR) CDS		1,167	390.8	387.3	367.5	463.5	451.8	434.3
DVU1022	SUF system FeS assembly ATPase SufC, putative (TIGR) CDS		777	367.2	362.5	338.1	562.2	522.4	711.4
DVU1023	rhomboid family protein (TIGR) CDS		741	23.9	23.3	24.3	33.9	36.8	31.4
DVU1024	rluD/coaE CDS	rluD/coaE	1,626	17.3	20.8	17.6	137.9	142.2	144
DVU1025	upp CDS	upp	627	0.5	14.4	13.9	545.2	577.1	617.4
DVU1026	uraA CDS	uraA	1,260	109.1	109.6	95.6	87.5	86.1	66.5
DVU1027	hypothetical protein (TIGR) CDS		972	302.3	327.8	330.9	409.2	384	471.7
DVU1028	cmk CDS	cmk	699	225	207.4	199.6	161.8	166.6	137.5
DVU1029	hisC CDS	hisC	1,122	128.9	125.6	101.3	122.6	124.5	126.7
DVU1030	universal stress protein family (TIGR) CDS		444	692.8	771.5	643.1	653.1	651.9	768.3
DVU1032	hypothetical protein (TIGR) CDS		510	640.5	480.4	542.2	1296.9	1207.5	1334.7
DVU1033	cinA CDS	cinA	495	345.5	375.3	346.2	302.6	339.6	359.2
DVU1034	hypothetical protein (TIGR) CDS		786	167.7	152.7	155	176.1	197.1	145.6
DVU1035	glk CDS	glk	1,065	110.2	103.9	98.6	114.5	111.8	109
DVU1036	membrane protein, putative (TIGR) CDS		885	72	73.8	68.2	117.3	116.8	102.5
DVU1037	mercuric reductase, putative (TIGR) CDS		1,443	90.4	75.8	74.6	126.3	131.4	97.9
DVU1038	hisA CDS	hisA	750	334.4	351.5	329.4	653.6	625.4	553.7
DVU1039	lipoprotein, putative (TIGR) CDS		642	377.8	395.8	373.4	511.3	482.2	444
DVU1040	hisB CDS	hisB	609	332.3	385.1	354.1	516.9	530	702.3
DVU1041	tatC CDS	tatC	774	278.7	337.6	285.9	249.8	238.9	262.7
DVU1042	tatB CDS	tatB	369	999	1035.2	959.4	776	706	689.8
DVU1043	guaA CDS	guaA	1,548	700.5	816	737.1	624	627.5	623.6
DVU1044	guaB CDS	guaB	1,458	724.9	821.5	751.9	376.1	395.9	359.1
DVU1045	hypothetical protein (TIGR) CDS		597	418	457.8	399.8	223.2	227.3	203.9

DVU1046	hypothetical protein (TIGR) CDS		138	210.8	255.6	216.4	460.1	448.5	359.5
DVU1047	ccmC CDS	ccmC	675	236.6	246.5	229	368.6	348.4	297.5
DVU1048	ccmB CDS	ccmB	678	299.1	283.4	285	494.6	480.2	372.7
DVU1049	ABC transporter, ATP-binding protein (TIGR) CDS		651	279.1	321.4	293	696	660.3	730
DVU1050	ccmF CDS	ccmF	1,896	340.6	378.2	346.3	514.2	509.1	474.5
DVU1051	ccmE CDS	ccmE	414	553.5	624.9	504.5	542.3	551.4	526.8
DVU1052	CBS domain protein (TIGR) CDS		1,065	75.4	87.4	75.2	91.2	83.8	69.4
DVU1054	hydrolase, HAD-superfamily, subfamily IIIA (TIGR) CDS		639	98.5	94.4	89.2	95.5	101.4	73.6
DVU1055	heptosyltransferase family protein (TIGR) CDS		1,035	109.4	100.3	98.7	53.5	63	39.5
DVU1056	nikO CDS	nikO	822	86.5	87.3	71.9	127.7	126.6	122.6
DVU1057	nikQ CDS	nikQ	771	73.3	77.6	59.8	161.3	161.5	168.2
DVU1058	nikM CDS	nikM	615	103.8	123.6	97.1	323.6	310.4	400
DVU1059	aminotransferase, putative (TIGR) CDS		1,173	79.2	92	87.7	68.9	73.5	52.9
DVU1060	glycosyl transferase, group 1 family protein (TIGR) CDS		1,104	112.3	127.3	119.6	84	96.2	51.3
DVU1061	glycosyl transferase, group 1 family protein (TIGR) CDS		1,062	98.7	125.6	108.6	87.6	86.6	76.7
DVU1062	conserved hypothetical protein (TIGR) CDS		771	274.5	282.2	282.6	541.3	551.7	406.3
DVU1064	aco CDS	aco	1,929	387.9	396.4	365.7	428.7	417.2	400.7
DVU1065	peptidyl-prolyl cis-trans isomerse domain protein (TIGR) CDS		1,890	535.6	539.6	523.1	587.8	607.2	539.4
DVU1066	gpt CDS	gpt	492	177	206.8	180.1	148.4	149.4	102.9
DVU1067	membrane protein, Bmp family (TIGR) CDS		1,149	686	687.6	649.1	372.6	360.1	264.5
DVU1068	branched-chain amino acid ABC transporter, permease protein		1,065	121.5	132.1	113.9	109.6	119.5	60.9
DVU1069	branched chain amino acid ABC transporter, permease protein		921	169.1	168.2	181.6	168	170.9	92
DVU1070	rbsA CDS	rbsA	1,575	130.8	155.6	144.4	82.8	86.4	59.3
DVU1071	hypothetical protein (TIGR) CDS		591	319.2	310.5	271.3	179.9	187.5	186.3
DVU1072	conserved hypothetical protein (TIGR) CDS		663	162.7	147.9	123	190.9	182.4	205
DVU1073	conserved domain protein (TIGR) CDS		927	187.8	201.7	193	271.2	291	232
DVU1074	rpmH CDS	rpmH	135	2321.9	2452.2	2173	584.9	660	658.5
DVU1075	rnpA CDS	rnpA	291	831.6	1018.9	902.7	757.5	759.3	859.6
DVU1076	conserved hypothetical protein TIGR00278 (TIGR) CDS		261	618.8	715.1	684.8	386.1	376.5	404.9
DVU1077	yidC CDS	yidC	1,605	514.9	586.2	569.3	441.8	443.5	453.3
DVU1078	R3H domain protein (TIGR) CDS		1,293	410.1	465.2	445.9	364.5	361.9	349.4
DVU1079	trmE CDS	trmE	1,374	57.6	64.8	61.7	59.3	72.5	51.6
DVU1080	iron-sulfur cluster-binding protein (TIGR) CDS		543	37.9	29.3	32.7	85.7	74.3	86.2
DVU1081	iron-sulfur cluster-binding protein (TIGR) CDS		1,620	32.6	37.4	29.4	69.4	72.3	66.6
DVU1082	3- 5 exonuclease domain protein (TIGR) CDS		609	222.6	255.3	236.2	313	309.3	304.7
DVU1083	phoB CDS	phoB	690	127.4	114.3	124.3	245.3	248.3	177.5
DVU1084	pstB-1 CDS	pstB-1	768	119.7	120.6	116	104.6	104.4	97.3
DVU1085	phoU CDS	phoU	666	84.3	96.6	91.3	116.2	129.5	92.7
DVU1087	conserved hypothetical protein (TIGR) CDS		981	226.6	225.9	223.6	274.7	282.5	217.3
DVU1088	hypothetical protein (TIGR) CDS		177	201.7	205.6	221.8	251.3	261.8	129.9
DVU1089	alaS CDS	alaS	2,640	329.3	342.5	306.1	224.8	223.9	213.6
DVU1090	recA CDS	recA	1,074	412.8	442.3	370	350.1	339.9	302.2
DVU1091	conserved hypothetical protein (TIGR) CDS		1,107	142.1	145	146	127.6	129.3	102.7
DVU1092	sodium-dependent symporter family protein (TIGR) CDS		1,362	205.6	196	180.8	169.6	170.6	119.2
DVU1093	HAD-superfamily hydrolase, subfamily IA, variant 3 (TIGR) CDS		531	223.3	200.2	199.8	494.8	467.6	430.2
DVU1094	argH CDS	argH	1,383	438.1	401.4	380.1	309.8	311.5	335
DVU1095	argG CDS	argG	1,191	443.5	435	361.2	209	228.1	280.1
DVU1096	argF CDS	argF	903	461.1	454.9	417.1	682.6	669.2	861.4
DVU1097	conserved hypothetical protein (TIGR) CDS		750	74.7	64.7	71.8	87.4	90.8	68.2
DVU1098	adenine specific DNA methyltransferase, putative (TIGR) CDS		744	48.6	66.1	55.5	23.5	27.9	17.4
DVU1099	tail fiber assembly protein, putative (TIGR) CDS		447	54	68.2	63.1	51.3	54.2	38.8
DVU1100	tail fiber protein, putative (TIGR) CDS		1,518	20.5	24.9	24.6	24.9	26.8	20.9
DVU1101	hypothetical protein (TIGR) CDS		657	8.3	12.2	9	17.9	16.2	11
DVU1102	baseplate assembly protein, putative (TIGR) CDS		1,155	8.8	11.2	8.3	10.5	13.1	10.5
DVU1103	baseplate assembly protein, putative (TIGR) CDS		435	5.4	8.4	9.3	12.5	21	5.3
DVU1104	baseplate assembly protein, putative (TIGR) CDS		732	8.5	11.6	8.3	12.7	14.3	6.4
DVU1105	hypothetical protein (TIGR) CDS		801	5.2	9.3	5.9	9.4	10.4	7.7
DVU1106	hypothetical protein (TIGR) CDS		552	9.3	23.3	17.1	10.8	14.3	13.1
DVU1107	tail tape measure protein (TIGR) CDS		2,343	7.7	12.9	9.5	14.9	14.9	14.6
DVU1108	hypothetical protein (TIGR) CDS		333	24.8	32.5	33.7	17	13.9	31
DVU1109	ATPase domain protein (TIGR) CDS		1,023	436.5	403.4	368.9	108.4	109.9	94.5
DVU1110	hypothetical protein (TIGR) CDS		447	265.9	299.7	256.5	216.2	210.5	123.1
DVU1111	hypothetical protein (TIGR) CDS		1,686	51	58.9	54.3	42.8	45.8	46.6
DVU1112	hypothetical protein (TIGR) CDS		381	27.2	43.9	30.1	26	22.5	31.3
DVU1113	hypothetical protein (TIGR) CDS		537	16.8	21.1	13.3	19.8	21.9	21.1
DVU1114	virion morphogenesis protein (TIGR) CDS		441	10.6	18.6	16.4	10.6	17.8	13.4
DVU1115	conserved hypothetical protein (TIGR) CDS		432	19.6	31.6	17.1	26.5	18.1	13.1

DVU1116	hypothetical protein (TIGR) CDS		996	34.4	60.7	32.7	30.6	21.8	36.9
DVU1117	hypothetical protein (TIGR) CDS		348	29.7	58.6	36.1	18.6	16.3	29.7
DVU1118	conserved hypothetical protein (TIGR) CDS		951	27.3	50.4	35.4	46.2	39.1	32.1
DVU1119	virion morphogenesis protein (TIGR) CDS		1,302	24.1	25.6	24	52	58	54
DVU1120	conserved hypothetical protein (TIGR) CDS		1,593	13.2	15.3	16.2	11.9	10.5	10.1
DVU1121	hypothetical protein (TIGR) CDS		621	262.9	354.7	317.3	202.4	185.1	157.3
DVU1122	portal protein, putative (TIGR) CDS		1,485	14.4	19.8	18.4	20.3	24.1	27.2
DVU1123	conserved domain protein (TIGR) CDS		570	11.2	17.8	13	13.8	14	8.1
DVU1124	hypothetical protein (TIGR) CDS		243	12.2	23.3	13.1	6.1	7.9	13.9
DVU1125	conserved domain protein (TIGR) CDS		474	18.9	31.4	18.6	24.2	21.4	32.7
DVU1126	lipoprotein, putative (TIGR) CDS		306	10.1	23	20.4	12.6	5.5	12.7
DVU1127	hypothetical protein (TIGR) CDS		414	13.6	20.1	13.3	10.2	9.4	15
DVU1128	lysozyme, putative (TIGR) CDS		666	10.2	17.8	15.7	18.7	16.9	14.4
DVU1129	conserved hypothetical protein (TIGR) CDS		369	17.3	31.9	16.5	24.2	22.8	37.1
DVU1130	DNA-binding protein (TIGR) CDS		465	20.1	23.7	21.3	46.8	47	55.5
DVU1131	hypothetical protein (TIGR) CDS		366	11.4	18	15.7	31.6	39.1	32.5
DVU1132	conserved hypothetical protein (TIGR) CDS		510	14.2	18.5	24.1	37.5	31.7	61.4
DVU1133	hypothetical protein (TIGR) CDS		459	19.2	20.3	21.6	36	29.6	30.9
DVU1134	hupB CDS	hupB	288	71.3	89.1	86.2	177.8	158.5	173.1
DVU1135	conserved domain protein (TIGR) CDS		240	48.5	67.4	73.9	73.2	74.6	109.8
DVU1136	host-nuclease inhibitor protein Gam, putative (TIGR) CDS		513	39.1	58.7	55.7	55.8	47.4	85.1
DVU1137	hypothetical protein (TIGR) CDS		189	42.9	56.5	67.2	94	80.5	203.8
DVU1138	hypothetical protein (TIGR) CDS		633	31	55.9	46.4	42.4	46.2	56.4
DVU1139	bacteriophage DNA transposition B protein, putative (TIGR) CI		738	34.4	60.6	57.4	82.5	87.8	96.3
DVU1141	hypothetical protein (TIGR) CDS		432	41	75.1	65.6	205.1	198.6	293.1
DVU1142	transcriptional regulator, putative (TIGR) CDS		270	64.3	78.3	95.1	342.5	354.6	381
DVU1143	hypothetical protein (TIGR) CDS		426	94.7	134.4	134.9	551.2	461.7	840.8
DVU1144	transcriptional regulator, Cro/CI family (TIGR) CDS		768	146.8	135.2	119.2	120.7	126.6	109.1
DVU1145	hypothetical protein (TIGR) CDS		141	30.2	36.3	36.3	26.9	35.3	22
DVU1147	alginate o-acetyltransferase AlgI, putative (TIGR) CDS		1,380	82.6	80.3	73.9	31.8	28.3	25.8
DVU1148	conserved hypothetical protein (TIGR) CDS		1,047	105.3	106.6	94.7	22.1	24.1	21.3
DVU1151	hypothetical protein (TIGR) CDS		153	12.6	12.2	15	25.9	18.5	20.3
DVU1152	hypothetical protein (TIGR) CDS		615	25.1	30.3	30.1	44.8	42.4	27.7
DVU1153	hypothetical protein (TIGR) CDS		111	24.1	37.3	31.8	60.9	81.3	93.1
DVU1154	hypothetical protein (TIGR) CDS		138	25.4	38.5	28.8	52.9	39.5	56.1
DVU1155	hypothetical protein (TIGR) CDS		105	10.3	18.7	11.8	6.8	6.4	0
DVU1156	sigma-54 dependent transcriptional regulator, putative/respor		1,440	21.5	23.6	21.4	15	16.7	18.1
DVU1157	sensory box histidine kinase (TIGR) CDS		3,258	21.6	23.5	23.1	32.8	33.9	27.7
DVU1158	hypothetical protein (TIGR) CDS		315	6.1	8.8	10.1	14.9	11.2	14.8
DVU1159	hypothetical protein (TIGR) CDS		147	13.6	8	5.4	6.2	2.8	0
DVU1160	urea transporter, putative (TIGR) CDS		1,014	11.7	12.7	11.6	14	16.6	13.2
DVU1161	hypothetical protein (TIGR) CDS		231	4	6.6	6	7	7.9	9
DVU1162	hypothetical protein (TIGR) CDS		192	9	11.5	5.3	6.6	2.8	2.7
DVU1163	major facilitator superfamily protein (TIGR) CDS		1,275	6.5	10.1	9.6	7.3	9.5	6.5
DVU1164	amiE CDS	amiE	1,005	12.2	13.4	11.1	22.1	19.8	18
DVU1165	ndh CDS	ndh	1,320	53.9	46.9	49.6	169.6	156.1	71.3
DVU1166	hypothetical protein (TIGR) CDS		153	103.2	101	87.6	73.1	85	54.1
DVU1168	hypothetical protein (TIGR) CDS		417	101.1	169.4	165.2	144.2	156.5	125.2
DVU1169	methyl-accepting chemotaxis protein (TIGR) CDS		2,415	271.9	352.8	359.7	144.5	171.5	169.5
DVU1170	hypothetical protein (TIGR) CDS		189	270.4	262.9	219.8	523.7	605.4	418.4
DVU1173	mviN-1 CDS	mviN-1	1,557	69.8	61.3	56.8	82.7	82.7	45.5
DVU1174	hypothetical protein (TIGR) CDS		378	294.2	331.6	345.1	177.8	189.4	188
DVU1176	hypothetical protein (TIGR) CDS		558	449.5	437.3	413.5	320.8	346	303.8
DVU1177	hypothetical protein (TIGR) CDS		663	123.6	121.3	108.5	97.4	109	139.6
DVU1179	aor CDS	aor	1,731	1492.8	1599.9	1458	1040.3	1010.4	1090.7
DVU1180	hypothetical protein (TIGR) CDS		225	320.2	265.2	295.7	419.6	405.2	260.7
DVU1181	response regulator (TIGR) CDS		1,071	131.7	153.5	132.3	170.6	175.2	188.4
DVU1182	hypothetical protein (TIGR) CDS		915	101	118.3	109.5	122.3	124.4	121.5
DVU1183	HD domain protein (TIGR) CDS		1,248	136.9	149.2	135.2	147.1	148.7	125.1
DVU1185	colicin V production family protein (TIGR) CDS		480	103.8	106.6	103	271.6	271.2	147
DVU1186	mazG CDS	mazG	804	239.5	223.1	218.3	213.7	218	173.2
DVU1187	hypothetical protein (TIGR) CDS		825	136.2	124.1	121.6	111.3	125.2	80.8
DVU1188	hypothetical protein (TIGR) CDS		222	70.5	74.4	67	56.2	74.2	50.1
DVU1189	conserved hypothetical protein (TIGR) CDS		1,200	89.1	81.2	80.3	125	130.8	85.1
DVU1190	sensory box/GGDEF domain/EAL domain protein (TIGR) CDS		2,781	146.1	140.6	139.9	270.9	267.4	204.1
DVU1191	lon CDS	lon	2,571	191.6	218.1	199.1	243.3	239.2	185.1
DVU1192	acyP CDS	acyP	303	166.3	202.8	155.5	248.4	297.1	151.8

DVU1193	radC CDS	radC	678	148.9	159	139.5	194.4	221.1	165
DVU1195	lipoprotein, putative (TIGR) CDS		519	405.4	400.5	381.2	405.9	413	342.1
DVU1196	leuS CDS	leuS	2,490	464.3	477.5	439.6	295.2	289.9	296
DVU1197	nusB CDS	nusB	462	495.6	522.6	474	368.1	340.5	435.8
DVU1198	ribH CDS	ribH	471	554.2	597.6	537.4	288.6	287.9	335.7
DVU1199	ribAB CDS	ribAB	1,230	478.9	495.6	451.8	476.6	497.3	510.5
DVU1200	ribE CDS	ribE	663	258.7	262.5	245.3	278.4	286.2	297.4
DVU1201	ribD CDS	ribD	1,134	158.3	180.9	164.5	234.6	243.7	207.6
DVU1202	cytidine/deoxycytidylate deaminase family protein (TIGR) CDS		531	221.8	238.5	221.8	294	286.2	289.1
DVU1203	glyA CDS	glyA	1,239	589	624	537.4	259.5	268	209.4
DVU1204	fabF CDS	fabF	1,248	947.9	938.9	824.2	518.5	505.5	499.8
DVU1205	acpP CDS	acpP	231	2764.3	2996.1	2679.7	381.3	370.3	413.9
DVU1207	fabH CDS	fabH	993	510.2	600.8	568.1	222	217.7	200.9
DVU1208	plsX CDS	plsX	1,038	671.5	794.9	713.4	745	714.6	860.7
DVU1209	rpmF CDS	rpmF	180	1815.7	2031.3	1829.3	901.3	906.2	1224.6
DVU1210	conserved hypothetical protein (TIGR) CDS		537	1066.2	1102.1	1017.3	1101.6	1136.7	1720
DVU1211	rpmB CDS	rpmB	210	1869.7	2190.6	1900.7	1468.3	1541.3	2404.6
DVU1212	fsxA CDS	fsxA	561	115.8	127.1	95.6	224.5	227.8	218.8
DVU1213	rhomboid family protein (TIGR) CDS		1,014	45.3	51.6	38.8	82.1	85.2	56.4
DVU1217	MATE efflux family protein (TIGR) CDS		1,410	150.3	149.9	145.2	109.7	120.1	79.2
DVU1218	conserved hypothetical protein (TIGR) CDS		300	162.3	145.3	152.3	225.6	234.8	174
DVU1219	conserved hypothetical protein (TIGR) CDS		2,196	113.5	111.9	101.4	93.9	96	78.9
DVU1220	nitroreductase family protein (TIGR) CDS		825	288.1	262.7	265.7	221.4	233.4	151.9
DVU1221	hypothetical protein (TIGR) CDS		246	275.1	285.5	233.7	154.8	169.7	200.6
DVU1222	hypothetical protein (TIGR) CDS		528	266.3	241.8	230.4	120.3	154.8	125.3
DVU1224	nfo CDS	nfo	849	85.3	71.3	69	84	88.9	61.5
DVU1225	hypothetical protein (TIGR) CDS		453	181.6	200.9	193	133.7	131.3	114.7
DVU1226	hypothetical protein (TIGR) CDS		96	33	56.4	42.2	16	20.7	18.9
DVU1228	tpX CDS	tpX	519	1046.1	1103.1	860	802.3	773.4	1127.3
DVU1230	hypothetical protein (TIGR) CDS		111	10.5	9.7	13.2	24.8	22.5	34.9
DVU1231	amt CDS	amt	1,209	30	33.7	33.8	27	34.9	18.1
DVU1232	glnB-1 CDS	glnB-1	339	217.5	175.9	147.1	133.5	146.4	141.8
DVU1233	glnD CDS	glnD	2,721	50	53.1	49.7	92.3	100.7	60.9
DVU1234	membrane protein, putative (TIGR) CDS		732	88.7	94.7	88.7	101.4	99	46.6
DVU1235	hypothetical protein (TIGR) CDS		621	66.7	73	66.8	27	36.9	15
DVU1236	amino acid ABC transporter, ATP-binding protein (TIGR) CDS		744	279	275.7	255.2	517.9	515.9	605
DVU1237	glnP CDS	glnP	771	206.9	219.5	192.3	119.3	121.9	115.3
DVU1238	amino acid ABC transporter, periplasmic amino acid-binding p		741	869.8	842.6	656.4	307.5	318.4	316
DVU1239	membrane protein, putative (TIGR) CDS		603	86.6	71.8	69.8	192.9	191.4	111.9
DVU1240	hypothetical protein (TIGR) CDS		408	88.3	85	67.5	63.9	55.9	34.8
DVU1241	conserved hypothetical protein (TIGR) CDS		318	62.7	64	66	210.9	207.4	336.5
DVU1242	vacJhomolog CDS	vacJhomolc	822	344.2	364.3	340.8	427.1	386.8	367.5
DVU1243	conserved hypothetical protein (TIGR) CDS		633	369.5	424.2	386.8	251.8	236.2	318.5
DVU1244	conserved hypothetical protein (TIGR) CDS		447	249.2	297.4	238.6	204.5	212.1	184.4
DVU1245	ABC transporter, ATP-binding protein (TIGR) CDS		825	162	188	192	313.2	343.2	242.1
DVU1246	membrane protein, putative (TIGR) CDS		804	213.9	259.9	254.4	142.1	134	127.6
DVU1247	hypothetical protein (TIGR) CDS		822	412.4	441.3	431.8	235.8	260.8	232.6
DVU1248	argS CDS	argS	1,656	422.8	470.1	454.4	261.1	264.8	290.8
DVU1249	fabD CDS	fabD	954	353.6	376.4	353.9	210.2	225.6	154.4
DVU1250	gidB CDS	gidB	657	393.9	381.3	392.2	314.5	327.6	198.2
DVU1251	hypothetical protein (TIGR) CDS		219	298.9	295.8	307.6	95.1	126.4	68.4
DVU1252	membrane protein, putative (TIGR) CDS		2,277	104.1	97.7	98.6	145.7	150.8	85.5
DVU1253	hypothetical protein (TIGR) CDS		129	161.8	183.4	170.3	144.3	138.9	92.2
DVU1254	conserved hypothetical protein (TIGR) CDS		471	136.3	142.8	128.3	189.2	204.3	156.9
DVU1255	Sua5/YciO/YrdC/YwlC family protein (TIGR) CDS		633	74.1	73.3	78.7	82	89.7	49
DVU1257	RNA-binding protein (TIGR) CDS		273	2710.3	2779.5	2603.6	1468.9	1334.1	2139.4
DVU1258	glnN CDS	glnN	2,181	184.4	201.8	142.9	95	118	60.6
DVU1260	outer membrane protein P1, putative (TIGR) CDS		1,284	1137	1049.2	981.2	163.6	183.8	133.7
DVU1261	conserved domain protein (TIGR) CDS		1,761	61.1	62.5	56.1	35.2	39.3	18.4
DVU1262	pilT-1 CDS	pilT-1	1,110	49.5	59.1	51.9	73.2	77.1	46.1
DVU1263	pppA CDS	pppA	804	58	61.1	55.8	80.2	86.9	57.8
DVU1264	transglycosylase SLT domain protein (TIGR) CDS		762	57.9	67.1	55	56.7	59.9	49.9
DVU1265	hypothetical protein (TIGR) CDS		750	80.5	83.1	81.9	115.3	106.1	85.1
DVU1266	hypothetical protein (TIGR) CDS		3,438	81.2	84.6	80.3	69.7	71.2	51.1
DVU1267	hypothetical protein (TIGR) CDS		684	75.6	87.3	70.3	83.3	90.8	62.7
DVU1268	hypothetical protein (TIGR) CDS		414	50.4	48.7	44	63.5	69	39.9
DVU1270	pilT-1 CDS	pilT-1	1,281	84.6	94	83.1	100.4	94.5	85.5

DVU1271	general secretion pathway protein F, putative (TIGR) CDS		1,227	117.4	123.2	116.3	141.7	136.9	92.5
DVU1272	gspE CDS	gspE	1,722	126	138.4	124.8	108.5	106.2	83
DVU1273	bacterial type II/III secretion system protein (TIGR) CDS		1,575	181.6	198.9	166.3	107.1	107.8	70.2
DVU1274	hypothetical protein (TIGR) CDS		444	516.7	449.3	508	255.7	259.5	213
DVU1275	hypothetical protein (TIGR) CDS		561	164.7	182.4	168	195.7	217.9	140
DVU1276	hypothetical protein (TIGR) CDS		1,920	135.3	158.1	142.6	146.1	144.4	110.3
DVU1277	hypothetical protein (TIGR) CDS		138	86.5	73.4	74.2	13.7	27.8	30
DVU1278	ftsH CDS	ftsH	1,971	507.5	526.5	447.6	856.1	809.2	916.4
DVU1279	folP CDS	folP	861	151.7	173.9	149.2	334	350.3	325
DVU1280	conserved hypothetical protein TIGR00159 (TIGR) CDS		747	148.3	183.8	153.7	229.2	234.8	260.8
DVU1281	conserved hypothetical protein (TIGR) CDS		903	169.1	209.1	188.3	208.1	221.4	157.9
DVU1282	glmM CDS	glmM	1,353	258.8	321.8	300.8	280.5	282.6	208.3
DVU1283	galU CDS	galU	879	390.4	442.9	390.4	555.6	566.6	469.5
DVU1284	priA CDS	priA	2,379	136.4	151.9	146	121.2	125.8	67.7
DVU1286	DsrP CDS	DsrP	1,164	853.4	935	812.2	349.5	337	215.3
DVU1287	DsrO CDS	DsrO	786	920	988.1	851.6	201.8	200.9	166.4
DVU1288	DsrJ CDS	DsrJ	381	972	1011.3	914.4	397.4	414.3	257.1
DVU1289	DsrK CDS	DsrK	1,611	829.3	870.9	783	239.7	250.5	202.6
DVU1290	DsrM CDS	DsrM	1,005	812.3	884.2	772.9	250.2	246.8	217
DVU1292	hypothetical protein (TIGR) CDS		174	235.2	268.3	237.6	62.4	56	52
DVU1294	conserved hypothetical protein (TIGR) CDS		699	57.1	58	51.2	19.9	26.6	19.3
DVU1295	sat CDS	sat	1,284	3104.5	3537.4	3308.9	1634.3	1537.1	1314.7
DVU1297	hypothetical protein (TIGR) CDS		153	8.2	9	8.6	4.8	3.1	0
DVU1298	rpsL CDS	rpsL	372	2916.4	3133.2	2781.4	1295.2	1213.9	1830.5
DVU1299	rpsG CDS	rpsG	471	2648.8	2822.2	2575.4	866.6	787.6	987
DVU1300	fusA-1 CDS	fusA-1	2,076	2217.8	2377.2	2109.3	1719.2	1576.7	2044.5
DVU1301	hypothetical protein (TIGR) CDS		183	2632.8	2833	2656.3	754.5	741.4	793.6
DVU1302	rpsJ CDS	rpsJ	318	2549.5	2728.6	2573.9	1298.7	1145.7	1248.2
DVU1303	rplC CDS	rplC	630	2632.9	2737.1	2528.1	1239.5	1190.8	1622.4
DVU1304	rplD CDS	rplD	621	2404.3	2502.4	2331.3	1441.8	1283.9	2141
DVU1305	rplW CDS	rplW	339	2554.7	2644.8	2456.3	910.6	865.2	1594.8
DVU1306	rplB CDS	rplB	831	2146.5	2182.7	2013.7	1946.6	1804.7	2783.9
DVU1307	rpsS CDS	rpsS	282	1738.6	1770.8	1600.8	512.2	510.1	496.7
DVU1308	rplV CDS	rplV	339	2412.3	2477.9	2249.5	1274.5	1221.2	1429.3
DVU1309	rpsC CDS	rpsC	639	1702.6	1729.6	1517.5	2051.7	1689.5	2797
DVU1310	rplP CDS	rplP	414	1991.1	2001.2	1801.3	723.7	720.5	795.2
DVU1311	rpmC CDS	rpmC	186	2171.3	2169.4	1938.4	397.1	385.1	643.3
DVU1312	rpsQ CDS	rpsQ	267	2030.3	2082.4	1874.8	427.7	414.5	544
DVU1313	rplN CDS	rplN	369	2128.6	2210.6	1925.9	2300.7	2214.6	2925.3
DVU1314	rplX CDS	rplX	324	2099.3	2217.1	1829	1376.1	1300.5	1363.9
DVU1315	rplE CDS	rplE	540	2098.5	2163.2	1839.6	1355.3	1234.8	1748.2
DVU1316	rpsN CDS	rpsN	186	2390.3	2469.5	2144.7	1268.2	1206.2	1664.5
DVU1317	rpsH CDS	rpsH	381	2068.8	2128	1785.3	848.4	883.6	1044.5
DVU1318	rplF CDS	rplF	540	1985	2004.4	1670.8	1020.7	975.1	1298.3
DVU1319	rplR CDS	rplR	360	2205.6	2202.2	1860.9	1254.2	1218.9	1218.9
DVU1320	rpsE CDS	rpsE	492	1964	1961.9	1657	1368.3	1312.8	1523.2
DVU1321	rpmD CDS	rpmD	171	2343.7	2372.6	2038.3	412.4	417	674
DVU1322	rplO CDS	rplO	447	1968.4	2029.9	1707.4	1470.2	1371.5	2021.8
DVU1323	secY CDS	secY	1,314	2040.2	2158.6	1868.4	1181.3	1084.7	1550.4
DVU1324	map CDS	map	780	1330.1	1402.9	1183.2	727.8	674.6	829.9
DVU1325	rpmJ CDS	rpmJ	114	3399.4	3693.5	3201.7	1305	1316.8	1811.2
DVU1326	rpsM CDS	rpsM	369	2082.8	2315.5	2016.9	1090.1	1107.5	1293.5
DVU1327	rpsK CDS	rpsK	390	2740.7	3170.6	2782.6	1246.4	1141.9	1298.7
DVU1328	rpsD CDS	rpsD	627	2510.6	2856.3	2510.5	974.7	943	1103
DVU1329	rpoA CDS	rpoA	1,044	2180.9	2372.8	2112.2	4214.1	3579.6	6252.2
DVU1330	rplQ CDS	rplQ	402	2072.2	2354.5	2065.2	2087.2	1905.3	3155.1
DVU1331	transcriptional regulator, LysR family (TIGR) CDS		927	120.5	115.8	124.1	33.7	38.3	33.1
DVU1332	selD CDS	selD	1,056	147.7	152.7	147.3	144.7	145.1	82.5
DVU1333	hypothetical protein (TIGR) CDS		126	342.7	388.8	369.4	309.4	256.5	418.4
DVU1334	tig CDS	tig	1,302	1167.5	1281	1171.8	603.9	621.2	657
DVU1335	clpP CDS	clpP	606	411	420.5	369.4	212.3	237.1	206.4
DVU1336	clpX CDS	clpX	1,254	524.7	580.8	512.3	440	433.3	432.7
DVU1337	lon CDS	lon	2,466	459.3	519.8	411.5	420.3	416.9	423.6
DVU1338	conserved hypothetical protein (TIGR) CDS		585	96.7	99.1	83.1	121.1	124.6	123.2
DVU1339	lipoprotein, putative (TIGR) CDS		831	125.4	123.2	124.3	248.7	247.1	208.3
DVU1340	ZUR CDS	ZUR	495	127.1	173.9	117.2	164.9	151.3	206.3
DVU1341	znuC CDS	znuC	825	170.7	193	152.5	232.3	228.6	222.4

DVU1342	znuB CDS	znuB	807	221.7	227.8	199.7	276.8	268	326.3
DVU1343	znuA CDS	znuA	1,008	253.8	276.2	206.1	364.8	378	513.8
DVU1345	proS CDS	proS	1,725	451	483.2	472.8	381.5	390.3	337.5
DVU1346	xseA CDS	xseA	1,398	147.5	172.2	177.4	110.1	112.9	71.6
DVU1347	peptidase, M23/M37 family (TIGR) CDS		915	106.6	107.7	113.1	122.6	130.7	97.4
DVU1348	xseB CDS	xseB	246	143.9	143	163	63	53.6	44.2
DVU1349	SelGGPS CDS	SelGGPS	864	167.5	144.4	163.9	85	95.5	70
DVU1350	dxs CDS	dxs	1,926	179.2	182.7	190.6	101.2	106	79.1
DVU1351	membrane protein, MarC family (TIGR) CDS		603	136.7	147	152.3	129.1	130.6	77.2
DVU1352	6-pyruvoyl tetrahydrobiopterin synthase, putative (TIGR) CDS		390	113	121.1	133.1	105.2	107.6	102.1
DVU1353	dnaE CDS	dnaE	3,495	161.1	171.9	159.4	99.6	108.6	96.9
DVU1355	hypothetical protein (TIGR) CDS		369	121.8	122.1	118.1	104.5	115.4	109.3
DVU1356	HD domain protein (TIGR) CDS		804	93.1	84.7	97.4	91.8	101.1	79.7
DVU1357	conserved domain protein (TIGR) CDS		627	93.7	80	77.3	112.4	126.7	77.5
DVU1360	galE CDS	galE	996	205.2	212.1	204.5	299.7	299.9	237.2
DVU1361	lpxB CDS	lpxB	1,131	95.8	105	94.1	127	119.5	103.8
DVU1362	membrane protein, putative (TIGR) CDS		969	113.5	125.8	110.7	158.5	159.2	128.9
DVU1363	rfbD CDS	rfbD	876	226.5	233.5	221.7	473.8	447.5	492.9
DVU1364	rfbB CDS	rfbB	1,023	129.7	133.3	120.2	186.1	182	155.6
DVU1365	heme-binding protein, putative (TIGR) CDS		849	166.5	157.8	147.4	160.3	170.8	139.4
DVU1366	lipoprotein, putative (TIGR) CDS		906	222.2	188.7	201.1	445.3	446.4	379.4
DVU1367	tatA CDS	tatA	198	1341.9	1335.6	1215.6	1211	1071.1	978.9
DVU1368	rhodanese-like domain protein (TIGR) CDS		1,623	207.8	181.9	182.5	160.7	174.4	107
DVU1369	hypothetical protein (TIGR) CDS		375	172.2	149.1	145.4	132.7	125.9	95.1
DVU1370	hypothetical protein (TIGR) CDS		873	202.3	194.6	182.2	194.8	189	106.9
DVU1371	HAD-superfamily hydrolase, subfamily IA (TIGR) CDS		675	167.1	167.2	152.9	168.5	183.1	120.6
DVU1372	membrane protein, putative (TIGR) CDS		303	385.5	393.8	358.3	141	156.1	131.4
DVU1373	divIVA CDS	divIVA	510	365.3	321.8	317.1	377.8	405.2	338.5
DVU1374	conserved hypothetical protein (TIGR) CDS		321	548.6	531.5	500.9	662	703.3	694.7
DVU1375	hypothetical protein (TIGR) CDS		231	1168.1	1176.5	1051.7	551.7	598.3	883.8
DVU1376	ilvB-2 CDS	ilvB-2	1,692	605.9	633.3	620.8	499.5	512.7	590.3
DVU1377	ilvN-2 CDS	ilvN-2	489	912	939.4	905.9	731.5	748	824.4
DVU1378	ilvC CDS	ilvC	996	1417.6	1368	1254.9	1134.9	1064.4	1165
DVU1380	hypothetical protein (TIGR) CDS		231	140.4	161.4	144.8	168.4	213.3	249.5
DVU1381	hypothetical protein (TIGR) CDS		216	224	267.9	209.2	376.6	384.3	465.4
DVU1382	HesB family selenoprotein (TIGR) CDS		324	1221.9	1437.7	1251.8	814.6	748.3	791.2
DVU1384	pyrR CDS	pyrR	537	173.5	174.1	158.2	183.8	184.6	155.9
DVU1386	membrane protein, putative (TIGR) CDS		1,551	45.3	57.4	51.2	50.3	54.3	34.7
DVU1387	conserved hypothetical protein (TIGR) CDS		1,329	140.2	141.7	146.9	70.5	75.1	56
DVU1388	conserved hypothetical protein (TIGR) CDS		756	286.9	280	299.9	247.4	250.8	179.8
DVU1389	hypothetical protein (TIGR) CDS		1,134	100.4	117.6	107.3	79.7	87.1	55.6
DVU1390	hypothetical protein (TIGR) CDS		468	118.1	121.5	105.4	175.9	183.2	108.2
DVU1394	hypothetical protein (TIGR) CDS		159	39.8	31.5	28.7	21	27.6	23.9
DVU1395	C4-type zinc finger protein, DksA/TraR family (TIGR) CDS		222	104.1	96.6	85.9	30.7	41.5	7.7
DVU1397	bfr CDS	bfr	540	486.4	591.7	472.7	272.8	298.4	267
DVU1398	ISDvu2, transposase OrfB (TIGR) CDS		843	6.9	79.3	70.8	65.6	76.1	63.4
DVU1399	ISDvu2, transposase OrfA (TIGR) CDS		399	1.9	90.4	73.8	138.3	125.2	83.5
DVU1400	methyl-accepting chemotaxis protein (TIGR) CDS		1,893	9.5	11.1	9.7	21.6	24.8	15.5
DVU1401	membrane protein, putative (TIGR) CDS		966	49.7	53.9	56.1	117.5	131.6	88.2
DVU1402	transcriptional regulator, LysR family (TIGR) CDS		996	54.3	69.1	61.9	51	55.2	39.2
DVU1403	cobO CDS	cobO	504	81.8	102	88.5	104.2	106.8	74.9
DVU1404	pflA CDS	pflA	1,107	65.4	72.5	71.4	110.4	106.9	83.5
DVU1405	hypothetical protein (TIGR) CDS		504	77.7	89.5	78.3	170.3	159.6	132.8
DVU1406	purM CDS	purM	1,053	551.9	575.1	539.4	1135	1075	1206.9
DVU1407	radical SAM domain protein (TIGR) CDS		1,476	407.1	258.4	318.8	118.4	116.5	98.8
DVU1408	hypothetical protein (TIGR) CDS		303	418.7	432.6	395.1	716.3	654.2	719
DVU1409	hypothetical protein (TIGR) CDS		465	337.4	343.5	338.9	279.3	295.7	208.4
DVU1410	conserved domain protein (TIGR) CDS		873	80	83.6	72.9	160.3	160	135.5
DVU1411	thiC CDS	thiC	1,290	1519.3	1708.5	1440.8	569.1	553.2	576.2
DVU1412	D-isomer specific 2-hydroxyacid dehydrogenase family protein		981	126.3	121.2	102.6	74.2	82.1	61.7
DVU1413	conserved hypothetical protein (TIGR) CDS		1,293	103.9	105.6	114.5	200.7	201.8	141.3
DVU1414	sensory box/GGDEF domain/EAL domain protein (TIGR) CDS		2,994	36.9	42.1	41.1	35.3	37	15.1
DVU1415	AsmA family protein (TIGR) CDS		3,585	55.4	51.9	49.1	49.7	51	28.5
DVU1416	hypothetical protein (TIGR) CDS		978	30.5	30.7	27.3	23.4	28	17.4
DVU1418	hydH CDS	hydH	1,740	79.8	73.7	67.6	139.3	149.2	82.7
DVU1419	atoC CDS	atoC	1,380	142.1	138.6	134.9	193	198.5	148.1
DVU1420	Hpt domain protein (TIGR) CDS		372	275.6	270.3	268.7	363.2	396.7	237.6

DVU1421	hypothetical protein (TIGR) CDS		462	804.5	811.9	757.8	300	306.3	242.7
DVU1422	OmpA family protein (TIGR) CDS		1,074	2760.7	3064.8	2631.4	1237.8	1069	1470.2
DVU1423	lpdA CDS	lpdA	1,371	291	303.9	263.3	590.1	548.7	760
DVU1424	gcvPB CDS	gcvPB	1,446	220.3	256.4	222.9	414.8	403	442.8
DVU1425	gcvPA CDS	gcvPA	1,332	214.3	233.1	201.1	172.8	185	203.8
DVU1426	gcvH CDS	gcvH	384	259.5	283	235.7	180.2	204.6	197.8
DVU1427	response regulator (TIGR) CDS		414	432	452.7	436.9	395.1	415.6	436.9
DVU1428	pgm CDS	pgm	1,656	140	149.6	139	174.9	174.6	154.8
DVU1429	GTP-binding protein (TIGR) CDS		1,101	288.1	287.9	300.3	157.1	176.7	132.8
DVU1430	peptidase, M16 family (TIGR) CDS		2,607	158.2	186.3	157.9	136.2	131.1	125.3
DVU1431	hpt domain protein/STAS domain protein (TIGR) CDS		2,196	132.4	115	111.8	408.5	388.7	285.5
DVU1432	radical SAM domain protein (TIGR) CDS		2,595	179.4	207.1	171.6	109.7	116.6	98.5
DVU1434	hypothetical protein (TIGR) CDS		366	601.1	647	522.9	401.4	395.5	622.7
DVU1435	membrane protein, putative (TIGR) CDS		1,185	51.1	44.1	46.8	54.2	53.4	50.1
DVU1436	hypothetical protein (TIGR) CDS		96	184.4	149.6	131.4	290.1	296	290.7
DVU1438	cobyrinic acid a,c-diamide synthase family protein (TIGR) CDS		1,065	185.9	189.6	154.8	216.7	212.2	227.1
DVU1440	rnc CDS	rnc	762	137.2	123.2	126.8	286.2	285.8	260.4
DVU1441	flaB1 CDS	flaB1	897	451.5	482.6	446.9	1043.9	956.2	1117.9
DVU1442	flagellin FlaG, putative (TIGR) CDS		375	163.5	147.7	140.9	441.3	430.8	406.6
DVU1443	flgE CDS	flgE	1,695	245.9	240.8	215.9	440.8	445.6	401.9
DVU1444	flgD CDS	flgD	798	167.8	161.8	148.9	512.1	530.8	426.8
DVU1445	flagellar hook-length control domain protein (TIGR) CDS		1,596	95	96.3	90.4	290.2	296.2	251.6
DVU1446	heptosyltransferase family protein (TIGR) CDS		1,404	52	60	54.1	87.2	84.9	63.9
DVU1447	CgeB family protein (TIGR) CDS		1,710	103.1	108.9	84.9	131.4	134.3	91.5
DVU1448	conserved hypothetical protein (TIGR) CDS		1,137	199.5	191.1	174.6	245.9	256.8	196.6
DVU1449	anti-anti-sigma factor, putative (TIGR) CDS		345	222.6	230.8	214.6	239.2	237.5	211.3
DVU1450	anti-sigma factor, putative (TIGR) CDS		441	130.8	153	140.7	78.6	84.2	86.8
DVU1451	response regulator (TIGR) CDS		1,170	100.8	111.1	96.9	126.9	120.8	109.4
DVU1452	dtd CDS	dtd	489	210.4	206.2	195.9	265.8	288.5	207.2
DVU1453	fadD CDS	fadD	1,695	262.9	286.7	238.8	233.3	245.1	265
DVU1454	ispD CDS	ispD	1,188	122.3	116.3	115.6	102.3	103.5	84.8
DVU1455	conserved hypothetical protein (TIGR) CDS		744	565.1	625.9	550.8	123.8	126.2	139
DVU1456	NIF3 family protein (TIGR) CDS		1,011	370.7	398.9	368.6	256.4	258.9	242.8
DVU1457	trxB CDS	trxB	930	295.9	346.5	257.8	352.5	350.3	305.6
DVU1458	chemotaxis protein CheZ, putative (TIGR) CDS		747	367.5	353.3	310.6	239.9	226.2	237.3
DVU1459	conserved domain protein (TIGR) CDS		1,173	79.1	93.8	89.2	171.5	171.6	115.2
DVU1460	hypothetical protein (TIGR) CDS		336	251.9	267.3	233.7	390.6	388.2	303.8
DVU1461	hemA CDS	hemA	1,323	239.5	267.6	228.6	271.7	278.3	293.3
DVU1462	cytochrome c assembly protein, putative (TIGR) CDS		732	218.1	236.3	206	773.5	756.2	602.3
DVU1463	cysG-1 CDS	cysG-1	678	128.3	143.5	128.7	178.9	170.6	195.9
DVU1464	heptosyltransferase family protein (TIGR) CDS		1,236	133.2	121.2	108.1	171.3	176.5	146.8
DVU1465	CgeB family protein (TIGR) CDS		1,329	125.4	123.3	115.9	124	136.9	113.1
DVU1466	argB CDS	argB	927	213.7	233.8	208	110.4	107.1	100.9
DVU1467	hslU CDS	hslU	1,326	178.3	190.5	161	102.2	105.8	117
DVU1468	htrA CDS	htrA	1,449	462.5	506	407	715.8	663.7	749.1
DVU1469	rpsA CDS	rpsA	1,464	684.2	692.5	674	345.4	354.3	344.9
DVU1470	ppiC CDS	ppiC	285	1288.3	1027.9	947	834.9	732.6	883.2
DVU1471	hspC CDS	hspC	429	247.6	273.6	240	246.4	240.1	250.6
DVU1474	hypothetical protein (TIGR) CDS		114	10.2	8.7	13.9	4.8	5.9	0
DVU1475	PhoU family protein (TIGR) CDS		678	98.4	89.5	76.2	139.5	131.3	147.1
DVU1476	hypothetical protein (TIGR) CDS		210	5.9	18.7	13.1	30.5	28.9	54.2
DVU1479	conserved hypothetical protein (TIGR) CDS		1,008	102.1	131.8	112.1	79.3	82.1	68.8
DVU1480	conserved domain protein (TIGR) CDS		360	207.6	309.2	315.8	285.8	286.7	205.3
DVU1483	tail fiber assembly protein, putative (TIGR) CDS		510	27.9	127.4	103.2	50.3	50.6	30.9
DVU1484	hypothetical protein (TIGR) CDS		339	5.1	102.5	80.9	37.2	45.4	32
DVU1485	hypothetical protein (TIGR) CDS		636	20.7	91	80	13.8	13.9	10.9
DVU1486	tail fiber protein, truncation (TIGR) CDS		2,313	17.5	53.7	46.8	26.9	25.5	17
DVU1487	conserved domain protein (TIGR) CDS		429	10.9	59.3	49.7	11.3	14	4.8
DVU1488	minor tail protein, putative (TIGR) CDS		906	14.3	59.9	48.5	31.9	33.6	11.5
DVU1489	hypothetical protein (TIGR) CDS		351	13.3	55	47.4	5.2	6	8.9
DVU1490	tail tape measure protein, putative (TIGR) CDS		2,799	8.4	38.6	32.7	12.4	12.1	6.3
DVU1491	conserved hypothetical protein (TIGR) CDS		183	962.8	1118.2	1289.2	1021	818.1	1242.7
DVU1493	hypothetical protein (TIGR) CDS		384	13.8	131.9	95.1	11	9.9	2.7
DVU1494	hypothetical protein (TIGR) CDS		1,164	13.3	112.2	82.7	11.2	11.9	4.5
DVU1495	hypothetical protein (TIGR) CDS		345	13.9	87	73.4	20.6	15.7	28.4
DVU1496	hypothetical protein (TIGR) CDS		498	10.6	95.9	78.8	12.7	13.7	8.3
DVU1497	head-tail adaptor, putative (TIGR) CDS		327	12	103.9	69.5	7	6.6	1.6

DVU1498	conserved hypothetical protein (TIGR) CDS		558	9.9	116.4	96.7	4.6	3.6	1.9
DVU1499	hypothetical protein (TIGR) CDS		270	20.3	234.3	180.9	6.8	4.3	0
DVU1500	major capsid protein, HK97 family (TIGR) CDS		1,197	19	236.1	173.6	16.5	13.4	5.2
DVU1501	clpP CDS	clpP	735	17.3	105.7	85.3	14.7	16.3	2.1
DVU1502	portal protein, HK97 family (TIGR) CDS		1,260	13.7	66.4	59.1	31.1	32.8	30.5
DVU1503	terminase, large subunit (TIGR) CDS		1,698	10.5	60.4	48	11.2	9.1	10.2
DVU1504	terminase, small subunit (TIGR) CDS		468	12.2	74	58	10.1	8.7	15.4
DVU1505	holin, putative (TIGR) CDS		399	15.6	91.6	74.5	5.8	8.7	6.5
DVU1506	hypothetical protein (TIGR) CDS		249	15.3	139.1	99.7	9.6	9.5	16.6
DVU1507	hypothetical protein (TIGR) CDS		351	1.5	85.7	51.2	10.8	13.5	15.4
DVU1508	conserved hypothetical protein (TIGR) CDS		408	12.7	190.4	137.3	38.2	45.5	47.5
DVU1509	conserved hypothetical protein (TIGR) CDS		390	509.3	520.8	503.4	187.4	179.2	182.2
DVU1510	hypothetical protein (TIGR) CDS		564	426.7	587.6	488.5	265	276.6	334.9
DVU1511	hypothetical protein (TIGR) CDS		231	35.8	66	61.5	60	74.4	40.3
DVU1513	conserved hypothetical protein (TIGR) CDS		495	13.6	44.6	41.7	29	31.6	17.7
DVU1514	hypothetical protein (TIGR) CDS		1,218	11.1	42.4	32.7	15.6	13.8	11
DVU1515	dcm CDS	dcm	1,464	13	41.4	29.5	15.7	16.4	9.6
DVU1516	hypothetical protein (TIGR) CDS		360	14.1	65.2	48.4	25.3	35	30.1
DVU1517	transcriptional regulator cII, putative (TIGR) CDS		414	8.5	61	34.7	16.5	15.1	8.8
DVU1518	transcriptional regulator cI, truncation (TIGR) CDS		291	11.2	22	17.6	6.8	7.2	3.5
DVU1520	hypothetical protein (TIGR) CDS		987	123.5	120.9	110.4	33.8	36.2	35.6
DVU1521	hypothetical protein (TIGR) CDS		180	104.6	101.7	84.6	50.1	43.2	17.2
DVU1522	hypothetical protein (TIGR) CDS		396	11	103.9	43.9	17.7	23.1	17
DVU1523	hypothetical protein (TIGR) CDS		1,029	7.3	81.4	34.7	11.5	10.6	17.3
DVU1524	conserved hypothetical protein (TIGR) CDS		897	14.3	98.4	41.9	18.8	18.4	13.5
DVU1525	conserved domain protein (TIGR) CDS		993	11.8	110.3	56	6.7	6.9	3.1
DVU1526	hypothetical protein (TIGR) CDS		219	26.9	92.1	49.5	22.4	19.5	23.6
DVU1527	site-specific recombinase, phage integrase family (TIGR) CDS		1,194	25.1	45.2	30.6	22.6	21.1	19.9
DVU1528	cytidine/deoxycytidylate deaminase family protein (TIGR) CDS		486	64.3	55.9	56.6	103.1	102.1	87.2
DVU1529	decarboxylase family protein (TIGR) CDS		657	337.3	303.5	257.1	207.6	198.7	178.6
DVU1530	metallo-beta-lactamase family protein (TIGR) CDS		1,611	315.5	270.1	251.9	197.4	211.1	196.1
DVU1531	methyltransferase, putative (TIGR) CDS		573	300	289.1	288.8	152.1	149	89.3
DVU1532	coaD CDS	coaD	561	168.1	189	183.5	132.9	138.7	114.3
DVU1533	miaA CDS	miaA	930	165.5	165.9	156.7	116.3	121.3	98.3
DVU1534	membrane protein, putative (TIGR) CDS		513	227.3	260.8	236.1	150.9	149.5	65.5
DVU1535	membrane protein, putative (TIGR) CDS		522	194.8	230.1	202.3	233.1	202.1	80.2
DVU1536	mltC CDS	mltC	1,137	157.2	163	150.6	269.9	280.9	198.2
DVU1537	lipoprotein, putative (TIGR) CDS		567	836.5	849.7	751.7	559.8	531.1	578.9
DVU1538	hypothetical protein (TIGR) CDS		525	147.9	160	135.8	71.6	71.8	65.9
DVU1539	glpX CDS	glpX	984	543.8	602.4	557.4	325.7	332.7	295.2
DVU1540	purU CDS	purU	855	224.3	230.8	222.6	189.2	183.1	202.5
DVU1541	hypothetical protein (TIGR) CDS		402	120.2	135	110.9	248.3	227	231.5
DVU1542	hypothetical protein (TIGR) CDS		228	24.2	30.6	23.6	18.1	13	13.6
DVU1543	hrpB CDS	hrpB	2,544	68.3	71.3	64.7	54.6	61.5	34.6
DVU1545	hemolysin-type calcium-binding repeat/calx-beta domain prot		7,245	320.2	314.8	278.9	240.2	250.2	184.4
DVU1547	sensory box protein (TIGR) CDS		1,626	34.5	41.7	47.4	88.6	77.8	87.1
DVU1548	outer membrane transport protein, OmpP1/FadL/TodX family		1,215	53.7	69.1	74.3	312	249.5	332.6
DVU1549	conserved hypothetical protein (TIGR) CDS		753	70.3	65.6	59.4	61.1	69.2	34.3
DVU1550	phosphoglycerate mutase family protein (TIGR) CDS		657	74.3	64.2	72	114.1	122.1	85.7
DVU1551	HD domain protein (TIGR) CDS		1,407	57.2	54	52	43.1	46.4	23.5
DVU1552	b2875 CDS	b2875	1,131	13.9	14	18.1	25.5	26.4	11.9
DVU1553	ftsA-3 CDS	ftsA-3	1,350	21.5	22.3	19.5	29	26.5	11.9
DVU1554	radical SAM domain protein (TIGR) CDS		1,632	23.6	19.9	18.2	15.2	15.7	11
DVU1555	hypothetical protein (TIGR) CDS		453	17.3	20.8	13.6	7.8	11.2	10.3
DVU1556	conserved domain protein (TIGR) CDS		894	11.2	14.9	12.6	9.5	10.7	7.2
DVU1557	hypothetical protein (TIGR) CDS		216	10.2	14.6	15.7	7.3	8.6	10.7
DVU1558	cysteine-rich domain/iron-sulfur cluster-binding domain prote		2,394	13.7	14.9	13.9	19.4	18.7	16.5
DVU1559	mop CDS	mop	2,721	22.3	21.4	19.9	27.6	29.9	21.5
DVU1560	molybdopterin biosynthesis protein, putative (TIGR) CDS		1,020	10.3	9.9	9.7	10.9	11.9	11.1
DVU1561	molybdenum-binding protein, HTH domain (TIGR) CDS		372	102.6	104.5	100.8	39.5	45.1	40.3
DVU1562	HAMP domain protein (TIGR) CDS		2,895	43.7	41	40.7	42.1	44.8	41.8
DVU1563	sensory box histidine kinase/response regulator (TIGR) CDS		3,120	40.8	44.3	40.4	90.3	88.9	70.1
DVU1567	hypothetical protein (TIGR) CDS		213	109.4	116.2	107.5	35.7	49.9	36.4
DVU1568	ftn CDS	ftn	510	642.9	702.4	514	225.7	224.9	169.3
DVU1569	porA CDS	porA	1,737	175.2	183.8	141	229.8	238.7	166.2
DVU1570	porB CDS	porB	855	160.2	164.6	133	241.3	257.5	240.8
DVU1572	transcriptional regulator, CarD family (TIGR) CDS		516	668.9	687.5	659.1	1651.8	1465.2	2250.7

DVU1573	pth CDS	pth	606	214.8	236	239.2	209	223.5	226.9
DVU1574	rplY CDS	rplY	573	1586.1	1773.1	1624.3	918.2	937.5	1414.3
DVU1575	prsA CDS	prsA	939	1062.2	1256.1	1144.4	1140.7	1035.5	1441
DVU1576	ispE CDS	ispE	861	997.1	1106.2	1015.7	3135.3	2328.9	7084.6
DVU1577	hslV CDS	hslV	546	127.2	145.3	144.5	117	138.9	95.6
DVU1578	TPR domain protein (TIGR) CDS		1,446	101.8	111	99.6	116.1	116.3	94
DVU1579	cysS CDS	cysS	1,458	350.9	399.1	358.4	189.6	197	155.6
DVU1580	rpiB CDS	rpiB	444	290.9	351.9	315.7	353.6	326.4	358.6
DVU1581	hypothetical protein (TIGR) CDS		351	276.3	330.3	293.1	326.6	308.1	390.2
DVU1582	hypothetical protein (TIGR) CDS		840	250.2	267	262.5	464.1	467.4	426.4
DVU1583	TPR domain protein (TIGR) CDS		1,689	225.6	271.7	226.4	195.4	198	179.2
DVU1584	rpoH CDS	rpoH	1,071	289.7	315.2	278.6	224.8	216.8	218.9
DVU1585	vitamin B12-dependent methionine synthase family protein (T		2,415	296.9	284.3	281.6	236.9	251.6	180.6
DVU1586	ccmG CDS	ccmG	468	204.3	221.9	196	622	633.8	516.3
DVU1587	acetyltransferase, GNAT family (TIGR) CDS		465	221.3	237.1	232.7	372.1	381.1	196.2
DVU1588	hpt CDS	hpt	531	297.3	294.8	278.4	631.5	633	467.2
DVU1589	hypothetical protein (TIGR) CDS		789	509	496.9	471.2	556.5	542.1	473.6
DVU1590	radA CDS	radA	1,371	212.6	229.5	213.1	242.6	251.2	190.7
DVU1591	hypothetical protein (TIGR) CDS		132	89.1	98.4	100.2	88.1	90.8	97.9
DVU1592	arginine N-succinyltransferase, beta subunit, putative (TIGR) C		1,743	136.8	127.9	122.6	219	223	150.6
DVU1593	cheY-1 CDS	cheY-1	363	188.7	180.8	170.9	296.9	323.1	175.1
DVU1594	cheA-1 CDS	cheA-1	2,127	120.7	112.3	102.8	157.1	159.2	115
DVU1595	cheR-1 CDS	cheR-1	876	70.9	71.2	57.8	158.8	159	94.7
DVU1596	cheB-1 CDS	cheB-1	1,074	171.7	172.3	162	338.2	348.5	250
DVU1597	sir CDS	sir	657	442.6	459.7	433.3	197	213.3	159.3
DVU1598	conserved hypothetical protein (TIGR) CDS		345	106.1	103.9	92.3	133.5	133.2	125.1
DVU1599	crcB CDS	crcB	375	116.4	132.2	112.2	132.3	136.3	102
DVU1600	adenylate cyclase (TIGR) CDS		612	72	75.4	62.7	48	61.4	34.2
DVU1601	ATP-dependent Clp protease adaptor protein ClpS (TIGR) CDS		315	128.4	144.9	124.5	170.8	191.7	207.5
DVU1602	clpA CDS	clpA	2,331	162.3	162.9	137.6	195	215.1	151.5
DVU1603	aat CDS	aat	705	141.6	162.8	152.1	222.7	210.8	175.9
DVU1605	uvrB CDS	uvrB	2,034	103.6	117.7	106.7	138.1	149.9	126.6
DVU1606	potassium uptake protein, TrkA family (TIGR) CDS		1,053	157	158.2	166.4	123.7	129.1	109.7
DVU1607	hypothetical protein (TIGR) CDS		747	139.5	140.4	141.1	153.8	164.7	82
DVU1608	ligA CDS	ligA	2,400	128.9	142.7	138	141.3	144.2	65
DVU1609	dapB CDS	dapB	780	270.9	271.5	259.6	186	192.8	156.4
DVU1610	nadE CDS	nadE	1,680	214.5	211.7	201.7	118	121.5	88.9
DVU1611	molybdopterin oxidoreductase domain protein (TIGR) CDS		1,929	122.2	115.6	118.5	150.3	154.7	116.8
DVU1612	ACT domain protein (TIGR) CDS		432	616.2	640.6	560.4	395.2	407.8	539.6
DVU1613	pyridine nucleotide-disulfide oxidoreductase (TIGR) CDS		1,059	246.7	248.4	240.3	749	749.8	715.8
DVU1614	iron-sulfur cluster-binding protein (TIGR) CDS		531	278.3	252.6	242.5	450.6	471.8	428.8
DVU1615	paaK-2 CDS	paaK-2	1,308	265.9	265.5	235.9	294	287.3	322.4
DVU1617	nitroreductase family protein (TIGR) CDS		594	336.8	334.9	296.3	227.7	235.7	201.5
DVU1618	iojap-related protein (TIGR) CDS		405	440.5	429.7	387.3	304.2	313.3	273.8
DVU1619	gpmA CDS	gpmA	1,536	240	228.1	223.8	287.8	286.5	199.7
DVU1620	hypothetical protein (TIGR) CDS		243	228.5	222.2	226.5	296.5	265.1	243.6
DVU1621	hypothetical protein (TIGR) CDS		423	159.1	170.9	142.8	57.8	64	57.4
DVU1622	purQ CDS	purQ	810	326.4	340	305.4	262	257.5	256.5
DVU1623	pyrG CDS	pyrG	1,644	630.8	686.1	594.4	391.3	397	386.4
DVU1624	kdsA CDS	kdsA	822	361.5	395.2	363.5	231	241	174.8
DVU1625	phosphatase, YrbI family (TIGR) CDS		528	246.3	266.8	245.9	187.3	203	123.3
DVU1626	hypothetical protein (TIGR) CDS		645	254.9	265.7	248.2	117	119.8	95
DVU1627	ABC transporter, ATP-binding protein (TIGR) CDS		726	260	283.4	284.4	311.7	330.1	190.1
DVU1628	rpoN CDS	rpoN	1,431	411.8	466.9	419.2	439.7	406.6	450.4
DVU1629	yfiA CDS	yfiA	540	547.4	590	495.6	645.9	681.7	681.9
DVU1630	ptsN CDS	ptsN	450	224.7	234.8	218.8	198.9	238	221.1
DVU1631	conserved hypothetical protein (TIGR) CDS		912	165.5	173.3	150.2	170.7	163.3	148.4
DVU1632	PTS system, IIA component (TIGR) CDS		438	177.8	188.7	191.9	200.3	192.4	118
DVU1633	PTS system, IIB component (TIGR) CDS		462	176.2	176.8	159.2	134.2	153.8	111.9
DVU1634	membrane protein, putative (TIGR) CDS		672	66.3	79.3	73.3	47.1	57.3	40.7
DVU1635	hypothetical protein (TIGR) CDS		105	59.2	61.8	87.8	16.7	18.6	27.1
DVU1636	ppaC CDS	ppaC	921	1609.2	2021.8	1936.8	1139.4	1061.5	706.3
DVU1638	conserved domain protein (TIGR) CDS		597	58.4	67.7	66.6	65.3	62.7	76.1
DVU1639	conserved domain protein (TIGR) CDS		996	33.8	41.1	44.8	81	93.8	40.5
DVU1641	conserved hypothetical protein (TIGR) CDS		324	35.3	44.3	42.6	62.1	73.5	55
DVU1644	permease, putative (TIGR) CDS		1,116	61.9	59.4	57.9	74	75.5	47.5
DVU1645	transcriptional regulator, ArsR family (TIGR) CDS		345	112	101.8	102.8	39	32.8	33.8

DVU1646	arsC CDS	arsC	444	91.6	96.2	89.5	50.2	54	33.8
DVU1647	lysA-1 CDS	lysA-1	1,239	176.2	177.2	171.6	135	137.2	124.3
DVU1648	lipoprotein, putative (TIGR) CDS		441	222.8	224.4	204.2	305.2	298.9	280.1
DVU1649	mutS CDS	mutS	2,718	116.8	128.7	118.3	102.4	109.1	73.5
DVU1650	conserved hypothetical protein (TIGR) CDS		1,125	323.9	268.3	287.7	243.4	245.6	137.6
DVU1651	conserved hypothetical protein (TIGR) CDS		372	383.1	418.3	346.8	90.2	80.7	88.2
DVU1652	hit CDS	hit	525	239	243.1	204.9	321.1	311	343.6
DVU1653	polyA polymerase family protein (TIGR) CDS		2,715	82.4	90.4	81.9	105.5	107.3	81.6
DVU1654	xerD CDS	xerD	885	192.6	162.9	175.3	414.5	356	474.5
DVU1655	aspC4 CDS	aspC4	1,167	732.9	705.6	629.8	552.5	530.7	555.9
DVU1656	folK CDS	folK	426	583.7	607.2	533.8	640.3	611.4	567.2
DVU1657	hypothetical protein (TIGR) CDS		300	598.7	557.6	543.6	308.4	326.5	324.7
DVU1658	transaldolase, putative (TIGR) CDS		648	280.9	291.5	250.4	245.2	245.7	224.9
DVU1660	undecaprenol kinase, putative (TIGR) CDS		798	75.4	80.6	79.6	70	80.9	46.7
DVU1661	hypothetical protein (TIGR) CDS		195	274.7	318.9	271	311.5	387	409.5
DVU1662	permease, putative (TIGR) CDS		1,143	171.1	187.4	169.7	192.3	187	136.2
DVU1663	permease, putative (TIGR) CDS		1,083	161.5	170.9	153.4	191.6	204	176.4
DVU1664	GTP-binding protein (TIGR) CDS		651	316.8	294.9	297.9	187.4	182.3	166.7
DVU1665	aroQ CDS	aroQ	468	258.2	267.2	264.7	191.9	191.1	173.3
DVU1666	efp CDS	efp	558	574.4	661.5	647.8	184.4	188	115.7
DVU1667	ftsK CDS	ftsK	2,331	169.8	182	177.2	221.9	236.7	205.7
DVU1668	lolA CDS	lolA	678	288.5	273.5	260.4	191.2	204.9	160.8
DVU1669	rluB CDS	rluB	879	134	145.5	141.6	173.1	177.7	119.9
DVU1670	conserved hypothetical protein (TIGR) CDS		639	47.6	49.1	50.8	53.7	61.2	49.4
DVU1671	msbA CDS	msbA	1,806	147.1	161.9	153	154.6	158.2	117.6
DVU1672	conserved hypothetical protein (TIGR) CDS		627	121.5	128.8	120.3	160.7	169.8	89.9
DVU1673	acyltransferase, putative (TIGR) CDS		945	115.9	137.5	128.6	116.1	112	74.4
DVU1674	transcriptional regulator, putative (TIGR) CDS		615	147	169.7	157.8	262.8	274.6	284.9
DVU1675	hypothetical protein (TIGR) CDS		165	144.2	152.1	159.9	231.1	234.7	222.4
DVU1676	secG CDS	secG	351	1159.8	1151.8	1175.4	1694	1506.1	1976.9
DVU1677	tpiA CDS	tpiA	756	328.9	339.9	314.8	326.5	322.4	345.2
DVU1678	rimI CDS	rimI	495	281.3	264.3	259.1	298.6	305.5	286.1
DVU1679	idi CDS	idi	537	295.1	288.5	306.3	154.1	166.1	117.9
DVU1680	suhB CDS	suhB	792	217.8	207.5	217.6	167.4	184.7	157.6
DVU1681	mreB-2 CDS	mreB-2	1,023	187.2	211.3	200.8	337.5	355.7	272.6
DVU1682	GAF domain protein (TIGR) CDS		1,035	267	255.5	233.7	398.6	398.8	274.2
DVU1683	hypothetical protein (TIGR) CDS		1,737	168.6	170	160.9	198.8	196.7	211.3
DVU1684	gcvT CDS	gcvT	1,131	281.2	298.6	264.4	138.1	137.1	123.3
DVU1685	conserved hypothetical protein TIGR00046 (TIGR) CDS		750	167	174.6	164.8	303.9	293.2	150.5
DVU1686	ATPase, AAA family (TIGR) CDS		1,236	128.6	151.3	122.9	129.1	129.8	102.4
DVU1687	glycosyl transferase, group 2 family protein (TIGR) CDS		708	107.7	116.5	98.6	89.4	102	70.1
DVU1688	1-acyl-sn-glycerol-3-phosphate acyltransferase, putative (TIGR		810	129.5	130.1	134.3	74.9	80.1	86.5
DVU1690	transcriptional regulator, TetR family (TIGR) CDS		570	414.5	431.8	401.5	152.3	160.9	117.9
DVU1692	hypothetical protein (TIGR) CDS		396	376.2	371.1	352.2	801.7	762.9	1040.3
DVU1693	gltX-1 CDS	gltX-1	975	74.7	79.4	78.3	120.3	122	107.6
DVU1694	C4-type zinc finger protein, DksA/TraR family (TIGR) CDS		210	31.6	34	27.6	41.8	37.4	23.3
DVU1695	tail fiber assembly protein, putative (TIGR) CDS		510	15.7	20.1	24.6	24	21.7	27.9
DVU1696	hypothetical protein (TIGR) CDS		369	9.6	16.1	16.9	11.5	9.3	11.3
DVU1698	hypothetical protein (TIGR) CDS		486	10.9	10.1	16.6	3.7	4.5	0
DVU1699	hypothetical protein (TIGR) CDS		120	25	24.6	24.3	7.5	7.9	8.6
DVU1700	metallo-beta-lactamase family protein (TIGR) CDS		1,248	47.7	62.5	58.7	21.3	20.3	20.3
DVU1701	hypothetical protein (TIGR) CDS		318	54.7	59.7	54.9	11.3	11	1.7
DVU1702	conserved hypothetical protein (TIGR) CDS		744	78.5	105.6	110.3	71.9	77.1	56.6
DVU1703	type I restriction-modification enzyme, R subunit (TIGR) CDS		3,300	88	118	109.5	64.3	66.3	43
DVU1704	conserved hypothetical protein (TIGR) CDS		228	775.7	1006.6	1085.2	121.8	150.9	104.3
DVU1705	type I restriction-modification enzyme, S subunit (TIGR) CDS		1,251	64.5	70.2	66.5	19	20.1	6.6
DVU1707	hypothetical protein (TIGR) CDS		210	47.9	77.6	53.8	16.3	20.5	18.4
DVU1708	conserved hypothetical protein (TIGR) CDS		1,014	61.7	80.9	68.8	23.7	30.6	17.3
DVU1709	hsdM CDS	hsdM	1,521	74.6	76.5	72.3	25.8	23.4	12.7
DVU1710	conserved hypothetical protein (TIGR) CDS		579	66.4	63.9	60	108.3	103.1	74.1
DVU1712	hypothetical protein (TIGR) CDS		1,602	2.2	2.4	3.9	2.9	2.8	3.9
DVU1713	hypothetical protein (TIGR) CDS		636	1.5	2.1	2.2	2.1	3.3	0.4
DVU1714	conserved hypothetical protein (TIGR) CDS		2,094	2.6	4.3	2	3.1	3.5	2.8
DVU1715	hypothetical protein (TIGR) CDS		588	3.5	6.8	5.1	19.8	20.2	11.5
DVU1716	hypothetical protein (TIGR) CDS		345	5.8	6.5	5.1	1.4	2.8	6
DVU1717	hypothetical protein (TIGR) CDS		402	4	7.3	5.3	4.6	4.1	2.6
DVU1718	hypothetical protein (TIGR) CDS		933	2.9	3.9	4.1	0.9	3	2.2

DVU1719	conserved domain protein (TIGR) CDS		840	2.8	3.9	2.9	3.1	1.6	3.6
DVU1720	hypothetical protein (TIGR) CDS		333	0.5	2.1	1.3	0	1	0
DVU1721	hypothetical protein (TIGR) CDS		1,653	1	1.5	1.7	1.9	2.7	0
DVU1723	hypothetical protein (TIGR) CDS		555	2	0.8	0.2	4.5	2.9	1.9
DVU1724	phage uncharacterized protein, putative (TIGR) CDS		1,605	1.6	1.6	2.2	4.8	5.5	5.9
DVU1725	conserved hypothetical protein (TIGR) CDS		609	0.4	1	1.1	1.5	2.1	0.4
DVU1726	hypothetical protein (TIGR) CDS		249	2.8	1.2	4	0.8	1.1	4.2
DVU1727	hypothetical protein (TIGR) CDS		351	0.6	3.9	1.7	2.6	1.1	0
DVU1728	conserved hypothetical protein (TIGR) CDS		417	0.4	9.2	5	8.2	11.4	12.4
DVU1729	killer protein, putative (TIGR) CDS		279	118.5	104.2	102.6	108.4	114.4	105.6
DVU1730	DNA-binding protein (TIGR) CDS		306	67.1	74.7	54	81.1	82.3	87.8
DVU1731	hypothetical protein (TIGR) CDS		171	2.9	4.6	5.7	1	0	0
DVU1735	hypothetical protein (TIGR) CDS		144	32.7	49.2	39.2	29.1	34.9	19.8
DVU1736	hypothetical protein (TIGR) CDS		195	25	33.3	34.4	29.8	30.8	30.5
DVU1737	conserved hypothetical protein (TIGR) CDS		219	13.2	24.4	16.1	37.1	32.3	36.6
DVU1738	site-specific recombinase, phage integrase family (TIGR) CDS		645	14.2	14.5	9	20.3	21.7	20.4
DVU1740	hypothetical protein (TIGR) CDS		402	17.4	26.4	25.1	22.2	19.5	4.5
DVU1741	hypothetical protein (TIGR) CDS		972	7.5	10.9	11.2	6.9	4.9	3.4
DVU1742	prevent-host-death family protein (TIGR) CDS		240	16.2	12.3	10.3	42.1	42.1	55.9
DVU1743	hypothetical protein (TIGR) CDS		438	5.1	9	6.6	9	16.7	15.3
DVU1744	DNA-binding protein (TIGR) CDS		243	13.4	13.3	6.9	7	10.5	4.3
DVU1746	C-5 cytosine-specific DNA methylase family protein (TIGR) CDS		1,110	67.3	77.1	68.7	70.4	77.8	54.9
DVU1747	ATPase, histidine kinase-, DNA gyrase B-, and HSP90-like doma		2,946	163.5	203.3	175.3	121.6	124.7	91.4
DVU1748	conserved hypothetical protein (TIGR) CDS		1,773	194.6	196.9	188.4	40.9	40.2	36.6
DVU1750	hypothetical protein (TIGR) CDS		783	19.7	23.5	21.1	18.3	19.8	14.5
DVU1751	hypothetical protein (TIGR) CDS		147	50.6	54.9	79.2	1.2	1.9	0
DVU1752	hypothetical protein (TIGR) CDS		240	13.3	16.4	12.5	12.4	20.2	8.6
DVU1753	hypothetical protein (TIGR) CDS		174	9.2	11.3	10.9	27.9	23.4	23.8
DVU1754	hypothetical protein (TIGR) CDS		408	22.9	26	22	14.3	20.7	1.3
DVU1756	hypothetical protein (TIGR) CDS		264	66.4	68	64.3	38.4	30.6	31.4
DVU1757	site-specific recombinase, phage integrase family (TIGR) CDS		1,122	72.3	74.6	72.4	92.4	88.6	83.3
DVU1758	lipoprotein, putative (TIGR) CDS		708	198.8	199.2	167.2	113.7	114.9	116
DVU1759	mopB CDS	mopB	369	52	57	38.5	21.9	18	16.8
DVU1760	transcriptional regulator, TetR family (TIGR) CDS		585	133	111	124.4	749.6	602.7	1362.4
DVU1762	membrane protein, putative (TIGR) CDS		459	289.3	259.6	254.3	174.6	188.1	179.1
DVU1764	conserved hypothetical protein (TIGR) CDS		270	246.6	205.8	189.4	587.7	661.4	879.6
DVU1765	thiH CDS	thiH	1,395	167.7	164.4	124.6	128.8	140	149.7
DVU1766	aspA CDS	aspA	1,413	109.2	105.7	89.8	168.9	174.8	168
DVU1767	radical SAM domain protein (TIGR) CDS		969	81.7	74.8	63.8	82.7	76.2	91.3
DVU1768	GTP-binding protein (TIGR) CDS		1,233	59	64.6	54.7	82.1	88.5	104
DVU1769	hydA CDS	hydA	1,266	111	108.1	89.3	92.3	113.6	106.4
DVU1770	hydB CDS	hydB	372	120.8	101.6	76.7	71	74.2	78.5
DVU1771	hydC CDS	hydC	1,821	101	89.4	85.5	139.6	143	112.5
DVU1772	gltD CDS	gltD	2,022	109.5	99.4	89.3	90.1	98.8	78.1
DVU1774	hypothetical protein (TIGR) CDS		882	90.9	109.9	105.2	174.5	165	174.1
DVU1775	ribB CDS	ribB	645	282.8	378.9	351.4	369.8	407.1	299.7
DVU1776	hypothetical protein (TIGR) CDS		114	63.7	68.2	53.4	8.7	22.5	13.6
DVU1777	cynT CDS	cynT	738	182.6	175.4	168.2	158.1	167.2	120.4
DVU1778	cation efflux family protein (TIGR) CDS		1,446	56.8	55.9	51.2	96.2	96.9	57.9
DVU1779	hypothetical protein (TIGR) CDS		207	64.5	50.9	46.5	531.7	456.2	486.9
DVU1780	conserved hypothetical protein (TIGR) CDS		306	58.9	46.2	42.7	111.6	116.6	70.9
DVU1781	conserved hypothetical protein (TIGR) CDS		666	284	261.1	238.6	306.4	286	327.1
DVU1782	iron-sulfur cluster-binding protein (TIGR) CDS		1,428	123.7	122.8	100.4	222.4	232.5	245.5
DVU1783	cysteine-rich domain protein (TIGR) CDS		753	106.6	106.7	94	301.8	316.4	346.6
DVU1784	oxidoreductase, short-chain dehydrogenase/reductase family		762	293.5	311.8	276.2	133.7	134.1	95
DVU1785	membrane protein, MarC family (TIGR) CDS		603	150.9	158.4	152.4	117.8	146.3	96.9
DVU1786	GGDEF domain protein (TIGR) CDS		1,059	236.1	243.9	234.6	464.2	492.9	315.3
DVU1787	nuclease domain protein (TIGR) CDS		627	105	121.2	122.6	55.6	73.7	35.4
DVU1788	rpoD CDS	rpoD	1,773	340	419.6	358.5	181.1	198.3	161.2
DVU1789	dnaG CDS	dnaG	1,719	212.4	238	213	485.7	491.7	325.1
DVU1790	MutS2 family protein (TIGR) CDS		2,316	315.3	359.1	345.7	314	320.4	250.8
DVU1791	GatB/Yqey family protein (TIGR) CDS		450	545.1	634	590.2	259.3	286.1	307.2
DVU1792	rpsU CDS	rpsU	204	4724.1	5425.7	4695.6	2058.6	2000.3	2148.4
DVU1794	hypothetical protein (TIGR) CDS		204	1230.2	1336.8	1182.5	360.1	377.5	423.1
DVU1795	hup-3 CDS	hup-3	273	1736.1	1799.3	1596.4	1368.6	1375.7	1392.5
DVU1796	hypothetical protein (TIGR) CDS		123	1286.2	1215.8	1049	1176.9	1195.3	1149.2
DVU1798	conserved hypothetical protein (TIGR) CDS		516	106.8	116.4	114	161.4	154	132.7

DVU1799	fusA-2 CDS	fusA-2	2,049	119.3	117.7	102.7	102.3	111.4	73.2
DVU1801	hypothetical protein (TIGR) CDS		1,188	263.5	272.7	281.6	207.9	208	142.7
DVU1802	conserved hypothetical protein (TIGR) CDS		861	97.7	95.5	80.8	198.2	191.1	165.4
DVU1803	glycosyl transferase, group 1 family protein (TIGR) CDS		1,089	95.3	93.2	91.2	206.9	223.7	138.1
DVU1805	GGDEF domain protein (TIGR) CDS		1,464	143.6	132.6	122.2	401.2	386.6	390.4
DVU1806	mgtE CDS	mgtE	1,371	88.3	91.1	97.9	102.8	106.1	64.8
DVU1807	nadC CDS	nadC	888	179.4	191.7	157.9	253.5	270.9	244.2
DVU1808	nadA CDS	nadA	1,077	189.9	180	173.9	248.6	249.7	178.6
DVU1809	nadB CDS	nadB	1,587	172.9	176.5	157.6	132.2	137.1	95.6
DVU1810	hypothetical protein (TIGR) CDS		423	125.3	144.9	122.6	212.3	237.8	128.3
DVU1811	protoheme IX farnesyltransferase, putative (TIGR) CDS		864	73.7	100.2	90.8	160.9	169.6	97.8
DVU1812	coxB CDS	coxB	1,281	136.6	169.1	151.9	279	287.1	135.5
DVU1813	hypothetical protein (TIGR) CDS		294	92.5	129.6	96.2	84.2	87.6	55.4
DVU1814	cytochrome c oxidase, subunit III, putative (TIGR) CDS		612	96.1	118.4	106.7	151.1	160.2	100.1
DVU1815	cytochrome c oxidase, subunit I, putative (TIGR) CDS		1,626	111.7	126.8	110.4	290.1	273.3	202.2
DVU1817	cyf CDS	cyf	312	1412.3	1739.9	1403.2	356.5	346.4	314.7
DVU1818	secF CDS	secF	1,089	467.7	446.3	442.2	491.1	495.8	534
DVU1819	secD CDS	secD	1,599	434	424	403.3	403.4	390.2	335.5
DVU1820	yajC CDS	yajC	366	1026.7	1092.7	960.9	743.2	770.8	876.9
DVU1821	gltB CDS	gltB	756	126.3	139.8	132.5	123.1	142.1	66.4
DVU1822	glutamate synthase, amidotransferase subunit, putative (TIGR		1,095	133.9	144.7	137.7	121.7	129.6	99.2
DVU1823	gltB-1 CDS	gltB-1	1,524	108.9	126.6	125.5	128.4	141.9	96.4
DVU1824	conserved hypothetical protein (TIGR) CDS		765	27.1	30.9	24.7	80	83.8	64.9
DVU1825	amidohydrolase family protein (TIGR) CDS		1,329	127.6	121.1	116.7	168.8	178.2	175.4
DVU1826	hypothetical protein (TIGR) CDS		273	1356.5	1537.3	1406.5	794.1	791.6	958
DVU1827	acetylornithine deacetylase/succinyl-diaminopimelate desucci		1,224	306.6	370.7	344.9	181.6	194	195.7
DVU1828	gidA CDS	gidA	1,890	198	247.3	225.3	91.2	93.5	80.5
DVU1830	hypothetical protein (TIGR) CDS		1,065	91.7	96.4	87.5	148.9	163.5	148.5
DVU1832	hypothetical protein (TIGR) CDS		102	113	145.6	147.1	40.7	43.6	55.7
DVU1833	ppsA CDS	ppsA	3,576	728.2	762.1	708	725.3	700	780.1
DVU1834	pyc CDS	pyc	3,705	444.8	445.6	407.4	508.5	517.4	483.5
DVU1836	cca CDS	cca	1,152	98.6	95	92.3	137	145.1	123.3
DVU1837	competence protein, putative (TIGR) CDS		783	660	710.5	625.6	337.2	339.1	341
DVU1838	trxB-2 CDS	trxB-2	924	653.1	676.8	606.4	698.7	671.4	537
DVU1839	trx CDS	trx	324	862.4	1036	872.5	497.7	489.6	498.5
DVU1840	gcp CDS	gcp	1,086	276	296.3	284.1	254.8	274.6	187.5
DVU1841	fbp CDS	fbp	1,014	325.1	364.8	348.1	154.1	160.6	115.7
DVU1842	lipoprotein, putative (TIGR) CDS		957	401.4	468.8	444.2	278.4	269.1	191.7
DVU1843	hypothetical protein (TIGR) CDS		954	485.4	521.7	496	585	576.2	445.9
DVU1844	septum formation initiator family protein (TIGR) CDS		330	533.5	598.5	547	457	466.3	390
DVU1845	hypothetical protein (TIGR) CDS		273	657.9	728.8	662.7	589.2	554.6	555.7
DVU1846	pgsA CDS	pgsA	558	363.8	408.4	369.2	213	238.6	244.1
DVU1847	conserved hypothetical protein (TIGR) CDS		894	391	437.8	388.3	231.2	250.6	197.7
DVU1848	conserved hypothetical protein (TIGR) CDS		594	112.1	109.1	113.2	172.5	195.1	94.4
DVU1849	pcm CDS	pcm	633	168.9	182	178.9	229.7	249.2	167
DVU1850	CBS domain protein (TIGR) CDS		429	724.3	713.2	730.3	1743.9	1554.8	2107.2
DVU1851	peptidase, M23/M37 family (TIGR) CDS		1,323	373.3	418	415.1	256.4	249.9	284.8
DVU1852	conserved hypothetical protein (TIGR) CDS		612	83.8	79.4	77.9	152.6	141.9	118.2
DVU1853	hypothetical protein (TIGR) CDS		297	66.3	76.8	69.5	157.8	174.4	140.9
DVU1854	hypothetical protein (TIGR) CDS		693	132	115.1	130.3	300.7	277.9	302.8
DVU1855	integrase, truncation (TIGR) CDS		321	21.3	18.4	20.6	51.4	55.8	48.3
DVU1857	methyl-accepting chemotaxis protein (TIGR) CDS		2,088	111.8	110.1	95.5	243.7	240	168
DVU1858	cold shock domain protein (TIGR) CDS		537	46.4	58.2	46.2	26.7	33.3	11.6
DVU1859	hypothetical protein (TIGR) CDS		126	28.8	31.6	10.5	53.7	52.9	43
DVU1860	cutE CDS	cutE	1,509	170.7	195.3	160.7	269.2	248.5	318.3
DVU1861	prfB CDS	prfB	1,117	359.6	401.9	347.3	236.2	251.5	193.1
DVU1862	GGDEF domain protein (TIGR) CDS		996	281.5	307.6	289.3	142.1	142.1	109.5
DVU1863	flagellar synthesis regulator FleN, putative (TIGR) CDS		819	222.2	259.1	216.6	225.1	221.3	168.1
DVU1864	ihfB CDS	ihfB	282	630.6	710.4	650.9	124.4	147.9	132
DVU1865	hypothetical protein (TIGR) CDS		141	567	612.2	627.9	424.5	386.9	223.6
DVU1866	hypothetical protein (TIGR) CDS		702	351.7	390.7	362.7	278.2	307	279.4
DVU1867	dapF CDS	dapF	849	344.1	373.8	352.6	287.2	303.5	282.2
DVU1868	dapA CDS	dapA	879	342.5	354.6	310.9	643.3	614.3	794.4
DVU1869	methyl-accepting chemotaxis protein (TIGR) CDS		2,316	130.8	128.9	120	213.9	212.1	194
DVU1870	cyclase, putative (TIGR) CDS		798	94.2	79.3	74.8	86.6	99.8	75.1
DVU1871	aspA CDS	aspA	1,407	70.2	62.1	52.2	80.6	83.9	64.3
DVU1874	clpB CDS	clpB	2,598	195.6	305.8	248.7	294.1	309.9	259.3

DVU1875	dafA protein (TIGR) CDS		318	225.6	282.9	198.1	391.7	409.2	327.5
DVU1876	dnaJ CDS	dnaJ	951	160.2	198.3	157.3	579.1	598.6	438.6
DVU1877	polysaccharide deacetylase family protein (TIGR) CDS		1,101	182.1	169.6	168.3	139.4	140.9	109.8
DVU1878	ltaE CDS	ltaE	1,023	170.4	168.5	164.8	149.4	160.1	108.1
DVU1879	glycosyl transferase, group 1 family protein (TIGR) CDS		1,101	170.1	154.4	164.3	151.7	165.3	132.8
DVU1880	hypothetical protein (TIGR) CDS		642	149	138.5	127.1	422	411.1	438.8
DVU1881	phoH CDS	phoH	1,017	181.9	191.6	160.9	313.9	318.6	377.1
DVU1882	HDIG domain protein (TIGR) CDS		2,361	124	122.9	111.7	227.4	233.8	237.5
DVU1883	conserved hypothetical protein (TIGR) CDS		489	87.4	82.9	75.4	451.7	456.1	450.2
DVU1884	methyl-accepting chemotaxis protein (TIGR) CDS		2,403	12.1	12.5	13.1	17.1	17.4	12.9
DVU1885	gatB CDS	gatB	1,431	243.4	236	233.8	294	299.4	227.4
DVU1886	hypothetical protein (TIGR) CDS		678	240.6	251.4	233.3	247.5	248.9	226.4
DVU1887	hypothetical protein (TIGR) CDS		1,743	160.7	161.9	144	158.8	182.5	184.9
DVU1888	ATP-NAD kinase domain protein (TIGR) CDS		900	122.7	129.3	120.5	335.8	343.3	286.6
DVU1889	gmhA CDS	gmhA	627	344	346.7	336.6	338.3	364.4	334.7
DVU1890	hemC CDS	hemC	948	398.9	442.6	405.5	253.7	262.9	222.2
DVU1891	conserved hypothetical protein (TIGR) CDS		762	182.2	180.2	174.3	325.9	308.2	291.4
DVU1892	glycosyl transferase, group 2 family protein (TIGR) CDS		750	172.2	136	140.7	228.4	248.3	171.3
DVU1893	ATP-dependent protease, putative (TIGR) CDS		2,421	242.2	274.1	257.7	249.9	249.6	240.4
DVU1895	major facilitator superfamily protein (TIGR) CDS		1,167	105.8	114.2	94.8	122.7	123.9	128
DVU1896	rpsT CDS	rpsT	264	2253.9	2523.9	2253.5	1687.7	1564.8	2143.8
DVU1897	glyS CDS	glyS	2,091	331.4	338.8	336.1	332.3	334.9	265.2
DVU1898	glyQ CDS	glyQ	870	348.8	363.6	353.8	678.3	596.5	1127.6
DVU1899	DNA repair protein RecO, putative (TIGR) CDS		756	127.9	127.9	118.3	101.6	114.7	84.5
DVU1900	conserved hypothetical protein (TIGR) CDS		942	350.8	353.2	342	405.9	408.1	311.9
DVU1902	conserved hypothetical protein (TIGR) CDS		939	161.5	164.9	156.6	213.8	227.5	146.4
DVU1903	mfd CDS	mfd	3,483	160.8	176.9	165.8	197.8	206	166.5
DVU1904	cheW-2 CDS	cheW-2	477	928.5	875.1	861.9	680.4	661.3	612.2
DVU1907	ugd CDS	ugd	1,338	390.7	405.5	392.2	467.1	476.9	402.9
DVU1908	pdxJ CDS	pdxJ	726	157.3	148.2	133.5	268.6	282.4	308.2
DVU1909	acpS CDS	acpS	375	149.5	141.8	143.5	185.4	211.6	206.8
DVU1910	YjeF-related protein (TIGR) CDS		1,725	180.6	180.5	166.2	279.6	269.4	368
DVU1911	CBS domain protein (TIGR) CDS		453	659.2	708.4	596.8	320	345.8	478
DVU1912	conserved hypothetical protein TIGR00150 (TIGR) CDS		489	494.2	468	449.5	383.4	401.7	365.2
DVU1913	aspartate kinase, monofunctional class (TIGR) CDS		1,227	331.4	315.8	268.4	231.2	238.2	239.7
DVU1914	2-isopropylmalate synthase/homocitrate synthase family prot		1,617	279.1	255.3	235.8	206.3	229	214.3
DVU1915	hypothetical protein (TIGR) CDS		276	41.1	53.4	40.3	48.6	56	68.3
DVU1916	hypothetical protein (TIGR) CDS		132	35.8	49.5	32.4	32.1	41.5	50.9
DVU1917	hysB CDS	hysB	954	1198.7	1200.9	1134.6	493.7	492.5	478.7
DVU1918	hysA CDS	hysA	1,533	1215.7	1245.2	1171.4	243.6	236.9	220
DVU1919	hydrogenase expression/formation protein, putative (TIGR) CD		471	149.8	158.3	146.1	266.8	292.9	177.7
DVU1921	hynB-1 CDS	hynB-1	954	105.1	128.9	96.8	111.4	107.6	88.3
DVU1922	hynA-1 CDS	hynA-1	1,701	90.8	114.1	88.2	64.6	65.9	54.1
DVU1923	hupD CDS	hupD	498	463.2	464.5	425.4	383.2	390.5	402.7
DVU1924	hypC CDS	hypC	252	385.2	396.6	337.5	309.1	291.9	256.4
DVU1925	tesA CDS	tesA	642	165.5	191.8	154.8	271	260.3	252
DVU1926	conserved hypothetical protein (TIGR) CDS		489	60.6	64	49.3	85.7	80.8	77.2
DVU1927	ileS CDS	ileS	2,817	395	439	391.9	349.3	333.4	404.2
DVU1928	lspA CDS	lspA	498	226.3	259.2	240.6	398.4	403.6	436.4
DVU1929	hypothetical protein (TIGR) CDS		198	268.8	353	275.6	137.7	157.8	139.7
DVU1930	TPR domain protein (TIGR) CDS		939	435.8	495.9	418.5	292.3	278.7	337.1
DVU1931	iron-sulfur cluster-binding protein (TIGR) CDS		444	505.6	530.8	482.9	181.5	186.8	189.2
DVU1932	adk CDS	adk	672	1684.7	1906.7	1803.3	922.1	938.7	704.5
DVU1933	peptidase, PfpI family (TIGR) CDS		522	286.5	276.8	227.1	178.7	177.6	140.6
DVU1934	phnE CDS	phnE	801	345.5	341	328.1	386.6	398.2	294.9
DVU1935	phnE CDS	phnE	798	285.1	297.7	272.2	119.2	118.7	95.2
DVU1936	phnC CDS	phnC	798	369.4	370.5	332.4	177.4	197.1	165.8
DVU1937	phosphonate ABC transporter, periplasmic phosphonate-bindi		1,014	864.4	775.1	679.6	293	281.9	262
DVU1938	hypothetical protein (TIGR) CDS		276	20.6	12.2	8.6	12.1	11	0
DVU1939	anaerobic glycerol-3-phosphate dehydrogenase, B subunit, pu		1,284	187.8	179.6	176.5	163.7	184.3	124.4
DVU1940	glpA CDS	glpA	1,551	204.4	207.1	189.8	186.9	195.2	141.5
DVU1941	HAD-superfamily hydrolase, subfamily IIA (TIGR) CDS		768	173.3	190.5	167.9	119.9	128.9	92.5
DVU1942	DAK2 domain/degV family protein (TIGR) CDS		1,914	180	192.7	183.4	148.1	156.7	147.2
DVU1943	hypothetical protein (TIGR) CDS		234	791.8	727.4	749.5	1538.4	1536.9	1535.1
DVU1944	oorD CDS	oorD	273	134.7	152.8	139.3	104.3	104.8	117.4
DVU1945	oorA CDS	oorA	1,149	132.6	134.3	113.6	108.2	116.1	93.8
DVU1946	oorB CDS	oorB	831	122.3	125.4	113	83.6	91	85.5

DVU1947	oorC CDS	oorC	624	220	208.6	190.6	220	210	187.2
DVU1948	conserved hypothetical protein (TIGR) CDS		291	432.1	418.9	359.9	225.2	255.1	262.8
DVU1949	nifA-1 CDS	nifA-1	1,590	398.3	412.3	403	263.6	265.9	229.7
DVU1950	indolepyruvate ferredoxin oxidoreductase, beta subunit, putat		597	306.9	305.6	306.8	270.3	281.5	205.2
DVU1951	indolepyruvate ferredoxin oxidoreductase, alpha subunit, puta		1,851	360.5	380.3	363.1	320.3	320.4	298.9
DVU1952	hypothetical protein (TIGR) CDS		696	360.6	392	372.1	345.3	337	362.4
DVU1953	proA CDS	proA	1,260	217.6	227.2	205.9	159.5	173.1	145.8
DVU1954	nadD CDS	nadD	705	415	388.2	399.5	307.7	288.3	257
DVU1955	TPR domain protein (TIGR) CDS		834	125.4	136.2	127.1	150	151.7	102.9
DVU1956	heptosyltransferase family protein (TIGR) CDS		1,056	122.1	117	114.2	183.1	191.6	111.2
DVU1958	sensory box histidine kinase (TIGR) CDS		2,598	91.7	83.2	75.9	212.6	217.9	198.3
DVU1959	EAL domain/GGDEF domain protein (TIGR) CDS		2,394	19.2	18.8	17.8	16.5	18.7	8.9
DVU1960	cheA-2 CDS	cheA-2	2,094	85.3	81.4	77.6	112.1	123.3	95.4
DVU1961	cheW-3 CDS	cheW-3	504	89.1	84.7	82	79.3	89.2	69.2
DVU1962	methyl-accepting chemotaxis protein (TIGR) CDS		2,163	100.5	99.6	90.4	134.3	151.8	111.4
DVU1964	transcriptional regulator, rrf2 protein, putative (TIGR) CDS		513	393.1	358.4	316.8	490.7	440.9	482.6
DVU1967	rrf2 CDS	rrf2	522	16.2	12.3	15.8	31.7	28.3	7.9
DVU1968	oxidoreductase, putative (TIGR) CDS		1,242	22.2	18	17.7	15.9	22.1	15.8
DVU1969	hypothetical protein (TIGR) CDS		696	10.7	13.3	11.8	13.2	13.9	13.3
DVU1970	response regulator (TIGR) CDS		408	23.6	25.7	24.6	28.6	29.7	25.3
DVU1971	conserved domain protein (TIGR) CDS		564	367.6	369.7	379.9	187.2	223	180.5
DVU1972	hypothetical protein (TIGR) CDS		195	30.8	46.9	37.3	31.2	27.8	51.7
DVU1973	rhodanese-like domain protein (TIGR) CDS		849	96.3	100.4	83.2	118.8	127.1	119.9
DVU1974	pyridine nucleotide-disulfide oxidoreductase (TIGR) CDS		1,104	75.3	72.5	69.3	117	123.3	119.6
DVU1976	groEL CDS	groEL	1,644	2888.5	4248.6	3831.6	2275.1	2081.2	3664.5
DVU1977	groES CDS	groES	288	2951.3	4134.4	3553.6	2374.7	2221.1	2189.4
DVU1978	metT CDS	metT	1,323	141.1	153.2	147.7	98.8	99.2	71.1
DVU1979	ABC transporter, ATP-binding protein (TIGR) CDS		1,926	227.9	197.8	208.9	169.5	186.6	140.1
DVU1980	hypothetical protein (TIGR) CDS		393	176.5	163.9	152.6	244.7	234.4	288
DVU1981	conserved hypothetical protein (TIGR) CDS		492	294.4	329.1	301.4	132.4	157	160.7
DVU1982	rhlE CDS	rhlE	1,389	72.6	75.4	70.8	111.6	116.5	81.1
DVU1983	hypothetical protein (TIGR) CDS		1,224	67.9	73.1	64.4	65.5	67.9	60.4
DVU1984	msrA CDS	msrA	627	118.6	125.2	114.1	207.7	204.4	165.7
DVU1985	conserved domain protein (TIGR) CDS		1,257	619.4	700	602.8	797.6	775.7	772.2
DVU1986	conserved hypothetical protein (TIGR) CDS		432	166	207.4	178.3	115.8	124.7	75.4
DVU1987	uvrA CDS	uvrA	2,871	171.3	202.7	159.9	147.6	154.3	127.8
DVU1988	membrane protein, putative (TIGR) CDS		687	280.4	202.8	238.3	136.7	133.6	85.7
DVU1990	hypothetical protein (TIGR) CDS		648	285.2	279.8	255.4	200.8	192.2	249.7
DVU1991	hypothetical protein (TIGR) CDS		996	13.9	16.7	14.3	33.1	33.7	22.8
DVU1992	cat CDS	cat	645	84.6	76.3	79.1	67.3	76.7	66.5
DVU1993	ctpF CDS	ctpF	2,754	106	132.5	119.2	164.6	164.7	113.8
DVU1995	rsbV CDS	rsbV	330	110.3	97.5	90.9	42.8	50.8	43.9
DVU1996	quaternary ammonium compound-resistance protein QacC, pu		330	126.2	116.8	111.4	18.4	17.6	11.8
DVU1999	sulfate transporter family protein (TIGR) CDS		2,145	70	74.1	73	79.4	81.4	60.7
DVU2000	hypothetical protein (TIGR) CDS		90	75.1	74.3	48	22	19.4	0
DVU2003	transposase, IS5 family, truncation (TIGR) CDS		1,263	31.8	43.8	38.6	31	27.6	18.4
DVU2004	ISDvu4, transposase (TIGR) CDS		1,050	9.7	124.5	109.2	119.2	116	85.6
DVU2006	hypothetical protein (TIGR) CDS		156	263.4	292	224.5	102.9	118.3	46.4
DVU2007	nuclease, putative (TIGR) CDS		417	134.2	133	127.4	43.9	45.4	34.7
DVU2008	hypothetical protein (TIGR) CDS		135	35	24.4	24.9	3.7	3.3	0
DVU2009	conserved domain protein (TIGR) CDS		384	54	62.3	51.8	23.9	21.2	9.4
DVU2010	ISD1, transposase OrfB (TIGR) CDS		825	4.5	118.1	113.9	133.6	142.9	98
DVU2011	ISD1, transposase OrfA (TIGR) CDS		267	16	300.7	286	99.8	133.7	80.3
DVU2012	hypothetical protein (TIGR) CDS		186	123.4	132.2	129.5	119.7	140.5	161.2
DVU2013	hybrid cluster protein (TIGR) CDS		1,662	530.3	601.7	540.5	218.3	222.7	182.2
DVU2014	fprA-1 CDS	fprA-1	1,176	391.8	430.4	412.9	205.6	224.1	198.7
DVU2016	GGDEF domain protein (TIGR) CDS		882	47.7	42.6	45.3	5.3	8.8	5.5
DVU2017	ISDvu5, transposase (TIGR) CDS		1,242	67.6	72.4	73.3	139.2	149.1	100.5
DVU2019	conserved hypothetical protein (TIGR) CDS		2,070	72.9	90.4	74.7	75.7	79.2	63.1
DVU2020	conserved hypothetical protein (TIGR) CDS		2,499	74.1	80.3	77.1	136.5	145.7	93.3
DVU2021	hypothetical protein (TIGR) CDS		468	53.4	56	64.2	24	23.4	22.6
DVU2022	conserved hypothetical protein (TIGR) CDS		3,477	51.7	59.4	54.1	62.1	65.2	33.2
DVU2023	hypothetical protein (TIGR) CDS		540	38.1	46.6	42.8	38	38.5	17.7
DVU2024	conserved hypothetical protein (TIGR) CDS		1,065	48.2	58.5	49.9	28	32.8	24.5
DVU2025	conserved hypothetical protein (TIGR) CDS		3,552	34.2	39.8	35.8	33.8	36.6	26
DVU2026	conserved hypothetical protein (TIGR) CDS		591	20.7	28.7	25.3	29.6	33.9	22.7
DVU2028	conserved domain protein (TIGR) CDS		228	11.7	21.2	25.7	15.8	15.2	23.8

DVU2029	ISDvu2, transposase OrfA (TIGR) CDS		399	1.5	90.2	73.7	133.5	139.5	100.4
DVU2030	ISDvu2, transposase OrfB (TIGR) CDS		843	5	70.4	64.9	76.4	73.9	59.2
DVU2032	ERF family protein (TIGR) CDS		714	13.1	12.9	11.6	15.9	19.2	13
DVU2033	hypothetical protein (TIGR) CDS		1,272	24.6	23.5	22.7	22.4	21.9	21.1
DVU2034	hypothetical protein (TIGR) CDS		366	52	55.5	48.2	43.3	50.1	40.9
DVU2035	plasmid stabilization system family protein (TIGR) CDS		288	64.1	82	68.7	98.2	130.6	84.4
DVU2036	helix-turn-helix protein, CopG family (TIGR) CDS		240	102.6	98.7	82.6	185.2	209.5	150.7
DVU2037	cobS protein, putative (TIGR) CDS		975	7.6	10.4	10.3	18.2	18.1	15.4
DVU2038	hypothetical protein (TIGR) CDS		297	19.4	20.5	21.4	10.6	16.5	7
DVU2039	hypothetical protein (TIGR) CDS		276	2.1	5.5	2.9	8.4	6.1	0
DVU2040	hypothetical protein (TIGR) CDS		288	4.7	3.9	3.6	7.7	8.6	10.7
DVU2041	conserved hypothetical protein (TIGR) CDS		996	16.8	21.1	20.7	18.1	18.5	12.5
DVU2043	conserved hypothetical protein (TIGR) CDS		1,602	6.2	9.8	6.1	14.5	9.7	8.4
DVU2044	hypothetical protein (TIGR) CDS		126	24.6	18	22.4	2.5	5.4	0
DVU2045	hypothetical protein (TIGR) CDS		183	39.3	58.1	41	21.5	21.7	17
DVU2046	hypothetical protein (TIGR) CDS		171	13.9	22.1	16.5	11.3	11.8	3
DVU2048	hypothetical protein (TIGR) CDS		171	29.8	30.8	33.5	4.8	9.5	0
DVU2051	hypothetical protein (TIGR) CDS		1,299	95	74.3	72.1	29	24.6	21
DVU2052	dmt CDS	dmt	723	283.2	325.8	304.6	433.7	418.4	422.5
DVU2053	membrane protein, putative (TIGR) CDS		681	143.8	168.3	156.5	83.5	96.9	69.1
DVU2054	hypothetical protein (TIGR) CDS		99	109.2	117.8	125.7	42.8	56.4	31.4
DVU2055	metG CDS	metG	1,992	273.3	290.9	271.9	242.6	248.7	197.7
DVU2057	conserved hypothetical protein (TIGR) CDS		1,464	279.6	311.9	283	259.6	270.8	251.7
DVU2059	glycosyl transferase, group 2 family protein (TIGR) CDS		993	377.9	383.6	335.9	248.9	236	235.5
DVU2060	hypothetical protein (TIGR) CDS		105	135.2	164.5	150.8	161.8	194.1	147.7
DVU2061	pfkA CDS	pfkA	1,335	174.6	185.8	145.6	238.8	230	215.2
DVU2062	ATP-dependent DNA helicase, UvrD/REP family (TIGR) CDS		3,459	101.2	110.5	106	83.7	84.3	64
DVU2063	conserved hypothetical protein (TIGR) CDS		2,955	87.4	100.6	89.9	91.1	96.6	64.6
DVU2064	fabK CDS	fabK	1,122	888.8	892	822.3	490.4	479.6	424.7
DVU2066	xerC CDS	xerC	1,425	89	90	83.8	95.3	107.4	83.2
DVU2067	GGDEF domain protein (TIGR) CDS		1,122	155.5	145.2	152.3	147.5	153	99.3
DVU2068	HD domain protein (TIGR) CDS		843	143.7	154.1	149.7	215.5	218.4	166.2
DVU2069	dprA CDS	dprA	1,992	161.4	154.6	149.8	79.5	90.5	62.5
DVU2070	TPR domain protein (TIGR) CDS		774	288	301.5	260.7	228.4	236.5	164.9
DVU2071	membrane protein, putative (TIGR) CDS		957	54	51.6	43.3	59.9	57.8	64.8
DVU2072	cheA-3 CDS	cheA-3	3,270	423.9	437.8	402	497.9	488.2	468.1
DVU2073	cheY-2 CDS	cheY-2	369	453.2	459.6	400.6	339.6	325	363.5
DVU2074	chemotaxis protein CheW (TIGR) CDS		651	347.8	349.8	308	603.4	605	556.6
DVU2075	parA CDS	parA	777	324.1	348.1	309	362.7	365.9	341
DVU2076	cheR-2 CDS	cheR-2	879	504.4	492.4	431.1	349.1	363.8	360.1
DVU2077	conserved hypothetical protein (TIGR) CDS		1,929	520.9	532.6	447	415.9	428.6	378.1
DVU2078	cheB-2 CDS	cheB-2	1,104	404.6	437.6	349.3	338.8	342.7	368.9
DVU2081	hypothetical protein (TIGR) CDS		309	87.6	97.2	94.6	249.4	262.7	403.1
DVU2082	flaD CDS	flaD	894	511.2	579.7	545.9	508.4	510.3	699
DVU2083	relA CDS	relA	2,154	175.1	162.6	153	219.6	232.8	221.5
DVU2084	appA CDS	appA	1,698	143.3	141.8	135.1	208.1	220.1	228.9
DVU2085	Snf2 family protein (TIGR) CDS		3,216	357	425.4	395.3	357.1	347.5	357.3
DVU2086	transcriptional regulator, GntR family (TIGR) CDS		1,443	37.2	34	39.1	29.8	33.6	21.9
DVU2087	hypothetical protein (TIGR) CDS		810	21.7	23.9	18	23.1	20.9	14.1
DVU2088	membrane protein, putative (TIGR) CDS		921	26.1	30.7	26.7	14.9	19.5	15.1
DVU2090	EF hand domain protein (TIGR) CDS		837	123.5	131.3	123.6	294.2	273.5	222.9
DVU2091	thiE-1 CDS	thiE-1	681	525.3	506.9	484.4	445.7	474.3	360.5
DVU2092	moeB CDS	moeB	642	618.1	617.8	531.7	1212.7	1202.8	955.2
DVU2093	thiH CDS	thiH	1,335	830.1	765.5	673.8	1127.6	1126	1008.7
DVU2094	thiG CDS	thiG	798	1922	2069	1771.7	1677.9	1675.9	1709.6
DVU2095	thiS CDS	thiS	201	4288.7	4782.4	4010.2	2001.6	2058	2487.8
DVU2096	hypothetical protein (TIGR) CDS		93	13.4	12.7	5.7	27.2	20.3	50
DVU2097	transcriptional regulator, putative (TIGR) CDS		672	22.4	22.4	20.4	13.8	18	13.9
DVU2098	cooS CDS	cooS	1,890	31.2	23.9	25.3	29.5	35	17.5
DVU2099	cooC-2 CDS	cooC-2	882	43.3	34.6	35.4	105.1	121.7	72.1
DVU2100	universal stress protein family (TIGR) CDS		417	456.4	539.3	439.5	721.1	753.1	723.8
DVU2101	conserved hypothetical protein (TIGR) CDS		5,352	70.5	70.5	73.1	107.1	113.1	68.1
DVU2102	outer membrane protein, OMP85 family (TIGR) CDS		2,331	124.2	130.2	124.1	162.8	177.1	146.2
DVU2103	iron-sulfur cluster-binding/ATPase domain protein (TIGR) CDS		864	2247.2	2492.8	2270.1	1725.5	1626.3	3540.5
DVU2104	iron-sulfur cluster-binding/ATPase domain protein (TIGR) CDS		906	1900	2122.6	1764.9	1317.2	1329.4	2293.6
DVU2105	hypothetical protein (TIGR) CDS		513	1922.9	2045.7	1724	2537.3	2491.7	4000.8
DVU2106	flrC CDS	flrC	1,377	32.4	30.5	30	38	38.5	33.8

DVU2108	MTH1175-like domain family protein (TIGR) CDS		360	1996.5	2141.8	1838.2	2139.4	2029.3	3450.7
DVU2109	mrp CDS	mrp	1,464	2206.5	2379.6	2038.3	1150	1100.3	1982.5
DVU2110	b2975 CDS	b2975	1,638	400.9	372.4	368.8	234.6	245.5	172.9
DVU2111	transcriptional regulator, LysR family (TIGR) CDS		903	125	127.8	115.5	130	128.2	101.4
DVU2112	hypothetical protein (TIGR) CDS		420	146.7	158.4	145.7	97.2	120.6	84.9
DVU2113	xanthine/uracil permease family protein (TIGR) CDS		1,332	192	199.8	180.9	67.7	66.5	55.1
DVU2114	atoC CDS	atoC	1,389	63.5	56.4	57.7	85.9	86.6	85.2
DVU2115	hypothetical protein (TIGR) CDS		192	27.4	27.2	26.7	30.5	31.9	21.6
DVU2116	pilin, putative (TIGR) CDS		174	6	23.2	15.7	37.3	32	23.8
DVU2117	membrane protein, putative (TIGR) CDS		567	25.2	26	26	48.1	47.3	25.9
DVU2118	conserved hypothetical protein (TIGR) CDS		819	11.7	15	14.3	34.7	39.3	27.8
DVU2119	cpaC CDS	cpaC	1,455	8.4	11.4	5.9	26.2	23.4	21.5
DVU2120	hypothetical protein (TIGR) CDS		405	10	13.7	5.4	11.2	13.3	9.6
DVU2121	response regulator (TIGR) CDS		1,215	10.4	13.4	8.7	30.1	24	14.3
DVU2122	cpaF CDS	cpaF	1,434	12.3	13.2	11.4	30.1	28.7	12.6
DVU2123	membrane protein, putative (TIGR) CDS		966	7.9	7.4	6.9	11.8	11.4	6.5
DVU2124	conserved hypothetical protein (TIGR) CDS		855	8	5.3	5.5	19.9	16.8	0
DVU2125	TPR domain protein (TIGR) CDS		1,116	9.7	9.3	8.2	29.4	29.6	16.7
DVU2126	hypothetical protein (TIGR) CDS		390	12.4	13.9	13.5	29.4	34.9	10.6
DVU2127	von Willebrand factor type A domain protein (TIGR) CDS		1,263	15.2	16.2	12.5	25.7	29	15.5
DVU2128	hypothetical protein (TIGR) CDS		495	152.5	124.2	121	186.3	211.4	193.1
DVU2129	cckA CDS	cckA	2,472	67.8	66.9	60.5	95.4	93.6	82
DVU2130	hypothetical protein (TIGR) CDS		663	337.3	301.6	257.9	707.6	641.7	861.4
DVU2131	hypothetical protein (TIGR) CDS		480	102.3	114.2	98.3	158.1	149.5	125.9
DVU2132	hypothetical protein (TIGR) CDS		258	105.8	74.7	80.1	120.6	130	80.1
DVU2133	membrane protein, putative (TIGR) CDS		1,740	11.1	15.9	14.4	21	19.5	12.5
DVU2134	hypothetical protein (TIGR) CDS		129	9.7	9.9	9.6	2.8	2.6	0
DVU2135	hypothetical protein (TIGR) CDS		552	46.6	50.8	46.8	174.5	173	159.2
DVU2136	hypothetical protein (TIGR) CDS		1,182	141.3	142.3	123.4	219.6	222.1	191.1
DVU2137	sucCD CDS	sucCD	2,130	28.2	27.8	25.5	24.8	29.2	21.4
DVU2138	conserved hypothetical protein (TIGR) CDS		654	252	260.8	233.2	209.9	217.2	158
DVU2139	aphA CDS	aphA	1,320	171.1	177.9	167.3	284.6	295.1	299.9
DVU2140	tmk CDS	tmk	675	261.7	276.2	257.4	345.9	352.7	232.4
DVU2141	nucleic acid-binding protein, putative (TIGR) CDS		1,038	240.8	257.6	236	207.5	212.7	169.6
DVU2142	surE CDS	surE	753	227.7	214.3	213	242.8	247.8	231.3
DVU2143	fba CDS	fba	924	408.1	451.4	429	349.3	369.3	327
DVU2144	gap-2 CDS	gap-2	1,002	565.6	644.2	574.1	549.8	546.1	491.8
DVU2145	chloramphenicol acetyltransferase, putative (TIGR) CDS		651	88.9	81.6	84.7	35.6	41.8	30.9
DVU2146	hypothetical protein (TIGR) CDS		156	66.3	51.8	55.4	7.5	4.3	0
DVU2147	sda CDS	sda	1,509	43.8	39.2	41.3	36.4	41.8	24.7
DVU2148	CBS/transporter associated domain protein (TIGR) CDS		1,395	93.8	98.6	94.6	123.7	128.4	107.4
DVU2149	conserved hypothetical protein (TIGR) CDS		1,740	200.2	220	208.3	190	183.8	157.3
DVU2150	dksA CDS	dksA	363	1031.8	1113.8	1073.3	661.3	678.6	615.8
DVU2151	conserved hypothetical protein (TIGR) CDS		360	38.3	52.3	56.3	437.3	385.4	361.8
DVU2152	hypothetical protein (TIGR) CDS		1,017	21.4	31.6	39.6	415.8	359.4	289.4
DVU2153	tail fiber protein, putative (TIGR) CDS		4,041	10	14	16.4	379	334.3	245.8
DVU2154	tail assembly protein, putative (TIGR) CDS		426	10.5	12.8	16.8	429.7	380.9	302.1
DVU2155	hypothetical protein (TIGR) CDS		426	13.9	15.8	15.3	315.2	273.1	266.3
DVU2156	hypothetical protein (TIGR) CDS		366	10.4	14.1	17.9	586.4	508.8	399
DVU2157	tail tape meausure protein, putative (TIGR) CDS		2,922	11	13.7	18.6	482.4	397.4	324.1
DVU2158	hypothetical protein (TIGR) CDS		351	21.1	36.2	37	526.3	432	427.7
DVU2159	hypothetical protein (TIGR) CDS		945	20.6	26	40.1	879.4	685.9	647.3
DVU2160	hypothetical protein (TIGR) CDS		468	17.4	21	30.2	1141.8	973.4	1058.6
DVU2161	hypothetical protein (TIGR) CDS		711	14.4	15.7	27.5	700.1	576.8	576.1
DVU2162	hypothetical protein (TIGR) CDS		330	30.8	34.6	37.3	942.7	769.8	462
DVU2164	lipoprotein, putative (TIGR) CDS		411	25.8	37.8	44.8	906	762.3	713.1
DVU2165	lysozyme, putative (TIGR) CDS		501	18	23.8	31.3	925.1	756.1	643.3
DVU2166	holin (TIGR) CDS		399	25.7	32.8	45.7	1100.8	896.8	863.4
DVU2167	hypothetical protein (TIGR) CDS		210	34	54.1	62.8	1952.8	1519.4	1241.6
DVU2168	major head protein (TIGR) CDS		1,026	30.1	47.1	68.5	1880.9	1471.6	1439.4
DVU2169	conserved hypothetical protein (TIGR) CDS		369	26.4	36.4	60.1	1505.6	1198.6	1334.1
DVU2170	minor capsid protein C (TIGR) CDS		1,221	20.7	30.4	40.5	1219.3	1005.3	1015.7
DVU2171	portal protein (TIGR) CDS		1,554	15	22.3	35.6	1433.7	1174	1192.4
DVU2172	hypothetical protein (TIGR) CDS		222	21.2	24.8	31.6	1057	882.5	712.4
DVU2173	hypothetical protein (TIGR) CDS		126	12.3	15.2	17.5	9.3	7	16.5
DVU2174	hypothetical protein (TIGR) CDS		678	80.8	82.4	69.1	16.9	17.8	13.8
DVU2175	adenine specific DNA methyltransferase, putative (TIGR) CDS		4,788	134.2	135.7	123.8	115.4	106.4	90.7

DVU2176	hypothetical protein (TIGR) CDS		180	26.9	47.5	44.2	38.6	47.9	31.6
DVU2177	hypothetical protein (TIGR) CDS		1,314	134.9	120	125.2	41.5	38.3	23.6
DVU2178	ISDvu2, transposase OrfB (TIGR) CDS		843	13.8	85.8	77.3	94.4	99	67.7
DVU2179	ISDvu2, transposase OrfA (TIGR) CDS		399	0.4	77.1	72	125.4	126.4	82.3
DVU2180	hypothetical protein (TIGR) CDS		141	107.2	115.1	141.4	416.1	354.9	271.3
DVU2181	antirepressor, putative (TIGR) CDS		879	34.9	51.9	42.3	321.4	256.2	278.7
DVU2183	hypothetical protein (TIGR) CDS		732	148.5	106.1	115.4	30.4	19.1	15.2
DVU2184	DNA-binding domain, excisionase family (TIGR) CDS		219	21.9	31	24.4	195.9	177.9	119.2
DVU2185	terminase, large subunit, putative (TIGR) CDS		1,926	11.6	14.3	13.7	120.4	96.9	71.9
DVU2186	hypothetical protein (TIGR) CDS		1,014	5.2	7.5	9.6	196.9	161	124.4
DVU2187	hypothetical protein (TIGR) CDS		531	4.1	7.2	12.7	166.8	148.2	97.3
DVU2188	primase, putative (TIGR) CDS		2,493	11	16.6	18.7	377.6	309.8	278.2
DVU2189	transcriptional regulator cII, putative (TIGR) CDS		441	11.4	12.5	17	210.7	180.5	153.5
DVU2190	transcriptional regulator, putative (TIGR) CDS		195	20.9	36.8	35.3	392.5	328.1	243.9
DVU2191	hypothetical protein (TIGR) CDS		357	2.7	4.1	9.9	881.2	766.4	981.6
DVU2192	hypothetical protein (TIGR) CDS		156	4	7.8	10.8	101.7	104.7	129.2
DVU2193	hypothetical protein (TIGR) CDS		555	6.3	8.5	9.1	83.7	62.8	51.3
DVU2194	hypothetical protein (TIGR) CDS		690	9.4	11.9	11.7	81.8	76.5	54.3
DVU2195	hypothetical protein (TIGR) CDS		258	13.9	15	25.3	73.7	48.1	31
DVU2196	hypothetical protein (TIGR) CDS		546	12.5	20.2	30.2	109.7	98.2	61
DVU2197	site-specific recombinase, phage integrase family (TIGR) CDS		930	53.8	50.1	57.8	72.9	79.9	54.2
DVU2198	hypothetical protein (TIGR) CDS		198	127.8	169.4	130.1	219	216.7	250.6
DVU2200	hypothetical protein (TIGR) CDS		381	214.3	194.7	182.5	80.2	100.8	90.8
DVU2201	b3011 CDS	b3011	1,158	527.7	598.7	507.6	288.2	280.2	275.4
DVU2202	transglycosylase SLT domain/bacterial extracellular solute-bin		1,518	39.8	41.7	39.5	47	52.8	29.6
DVU2203	endoribonuclease, L-PSP family (TIGR) CDS		375	57.5	63.2	51.7	65.4	75.5	30.3
DVU2204	tnaA CDS	tnaA	1,389	59.1	55.9	51.7	87.6	95.5	37.9
DVU2205	mtr CDS	mtr	1,278	48.1	44.8	37.1	35.7	36.3	23.9
DVU2206	conserved hypothetical protein (TIGR) CDS		672	121.9	145.6	143.4	200.4	209.7	146.9
DVU2207	hypothetical protein (TIGR) CDS		174	10.3	6.8	5.3	16.3	16.8	3
DVU2208	hypothetical protein (TIGR) CDS		114	9.8	5.2	5	18.6	18.6	0
DVU2209	conserved hypothetical protein (TIGR) CDS		723	183.7	213.9	189.5	198.8	211.2	139.8
DVU2210	TPR domain protein (TIGR) CDS		1,728	196.4	199	178.6	196.1	186.7	162.8
DVU2211	hypothetical protein (TIGR) CDS		2,619	96.2	94.2	87	167.2	170.8	138.4
DVU2212	conserved hypothetical protein (TIGR) CDS		363	249.5	244.7	234.8	389.1	387.7	372.3
DVU2213	nuclease domain protein (TIGR) CDS		702	6	8.1	8.6	23	21.6	19.2
DVU2214	hypothetical protein (TIGR) CDS		174	8.7	3.9	4.6	21.3	26.3	20.8
DVU2215	RNA-binding protein (TIGR) CDS		270	4017.1	4602.3	4419.9	4418	4236.1	6162
DVU2216	infA-2 CDS	infA-2	264	772.4	848.9	799.1	294.3	264.2	487.5
DVU2217	acetyltransferase, GNAT family (TIGR) CDS		507	48.1	42.5	55.2	40.6	50.4	40.7
DVU2218	GTP-binding protein, putative (TIGR) CDS		1,047	8.7	10.6	10.6	9.4	12.5	4.9
DVU2220	conserved hypothetical protein (TIGR) CDS		270	559.1	629	632.8	171.6	161.7	122.5
DVU2221	hypothetical protein (TIGR) CDS		141	209.7	225.4	224.9	49.2	49.6	38.4
DVU2222	ssb CDS	ssb	531	788.3	864.5	806.7	183	217.7	218
DVU2223	hypothetical protein (TIGR) CDS		345	809.4	853.3	803.1	888.6	825.2	851.7
DVU2224	hypothetical protein (TIGR) CDS		651	663.1	676	600.4	456.6	470.5	356.5
DVU2225	acetyl-CoA carboxylase, carboxyl transferase, alpha/beta subu		2,256	578	609	558.5	388.8	378.9	308.6
DVU2226	accC CDS	accC	1,416	576.5	609.2	553.4	335.5	336	326
DVU2227	hypothetical protein (TIGR) CDS		444	492	482.7	441.4	463.1	511.5	543
DVU2228	motB protein, putative (TIGR) CDS		735	226.9	255.2	223.7	578.5	615.8	564.7
DVU2229	motA-2 CDS	motA-2	762	249.6	266.5	244.2	379.8	389.9	443.3
DVU2230	deoD CDS	deoD	825	251.8	225.9	224.9	170.6	169	137.8
DVU2231	typA CDS	typA	1,842	431.4	503.2	469.7	194.4	208	138
DVU2232	hypothetical protein (TIGR) CDS		369	68.3	84.8	64.8	388.4	335.3	393.6
DVU2233	conserved hypothetical protein (TIGR) CDS		978	77.5	70.3	72.7	100.4	97.4	85.1
DVU2234	conserved hypothetical protein TIGR00275 (TIGR) CDS		1,170	86	86.1	81.8	91.4	100.1	76.9
DVU2235	conserved hypothetical protein (TIGR) CDS		210	259.8	265.4	276.5	146.4	154.8	115.6
DVU2236	hypothetical protein (TIGR) CDS		105	211.1	233.8	230.2	74.7	77.9	49.3
DVU2237	cbiB CDS	cbiB	963	117.5	105.5	114.8	114.9	125.8	86.7
DVU2238	RNA methyltransferase, TrmH family (TIGR) CDS		480	82.1	85.3	83.5	98.7	114.6	55.4
DVU2239	glycosyl hydrolase, family 3 (TIGR) CDS		1,446	154.6	145.2	144.8	268.8	269.2	264
DVU2240	hydantoinase/oxoprolinase family protein (TIGR) CDS		1,653	171.3	168.3	164.4	278.6	287.3	254.5
DVU2241	pdxA CDS	pdxA	1,221	188.5	207.7	176.2	312	316.4	323.7
DVU2242	asparaginase family protein (TIGR) CDS		948	125.3	109.3	111.9	113	122.8	83.4
DVU2243	glgB CDS	glgB	1,923	157.3	166	152.9	349	355.9	232.1
DVU2244	glgA CDS	glgA	1,470	161.1	181.1	163.3	286.5	281.4	235.4
DVU2245	mutT/nudix family protein (TIGR) CDS		417	433	471.4	441.1	420	406.6	360.6

DVU2246	S1 RNA binding domain protein (TIGR) CDS		2,172	91.3	91.1	82.2	114.6	121	103.5
DVU2247	ahpC CDS	ahpC	615	734.7	692.8	520.2	365.9	622.4	453.8
DVU2250	AMP-binding protein (TIGR) CDS		1,656	344.4	291.7	272.4	474.7	475.5	526.5
DVU2251	DNA-binding protein (TIGR) CDS		561	284.3	233.2	216.3	528.8	538.6	533.5
DVU2252	dnaA-2 CDS	dnaA-2	1,476	553.1	598.4	504.4	302.6	311.9	474.5
DVU2253	hypothetical protein (TIGR) CDS		183	99.7	97.6	94.5	35.9	38.3	56.5
DVU2254	thyX CDS	thyX	738	162.5	166.3	153.6	161.8	182.7	109.9
DVU2255	ruvB CDS	ruvB	963	151.1	170.2	156.4	142.6	159.3	121.6
DVU2256	ruvA CDS	ruvA	609	187.7	194.5	185.4	275	281.1	203.2
DVU2257	hypothetical protein (TIGR) CDS		159	164.9	165.8	159.5	197	255.4	78
DVU2258	ruvC CDS	ruvC	501	326.4	303.2	305	346.9	392.2	236.3
DVU2259	conserved hypothetical protein TIGR01033 (TIGR) CDS		744	740.3	807.4	805.3	485	535.5	374.4
DVU2260	rrmJ CDS	rrmJ	615	361.9	415.1	393.8	515.1	506.7	296.7
DVU2261	hypothetical protein (TIGR) CDS		1,815	30.2	29.6	27.3	42.8	43.1	30.7
DVU2263	outer membrane autotransporter barrel domain protein (TIGR		1,926	52.6	47.6	52.8	33.6	37.7	32.2
DVU2264	hypothetical protein (TIGR) CDS		153	85.6	93.9	86.5	48.9	59.4	70.9
DVU2267	hypothetical protein (TIGR) CDS		294	29.8	30.9	27.9	61.9	62.6	65
DVU2268	hypothetical protein (TIGR) CDS		120	32.1	46.4	50	48.8	50.5	8.6
DVU2269	hypothetical protein (TIGR) CDS		168	15.4	17.9	13.9	39.7	42.8	30.7
DVU2270	hypothetical protein (TIGR) CDS		114	22	29.3	19.8	22.5	23.1	4.6
DVU2271	pflA CDS	pflA	894	10.7	10.3	7.8	25.9	22.6	15.6
DVU2272	formate acetyltransferase, putative (TIGR) CDS		2,454	18.6	16.9	17.4	63.2	61.1	53.3
DVU2274	hypothetical protein (TIGR) CDS		138	118.6	112.6	105.5	253.4	251.3	239.7
DVU2275	rocR CDS	rocR	1,455	247.9	334.2	344.9	117.6	132.5	81.7
DVU2276	membrane protein, putative (TIGR) CDS		747	206.2	280.9	311.5	115.7	128.3	88.5
DVU2277	hypothetical protein (TIGR) CDS		612	42.9	57.3	60.1	21.4	28.3	18.5
DVU2278	membrane protein, putative (TIGR) CDS		852	17.1	26.5	29.8	17.6	21.8	17.6
DVU2279	hypothetical protein (TIGR) CDS		165	20.8	25.1	20.8	12	4.1	6.3
DVU2280	amino acid permease family protein (TIGR) CDS		1,509	13.5	17.3	14.6	33.3	32.4	26
DVU2281	torS CDS	torS	2,202	8.7	15.5	11.3	60	46.7	22.8
DVU2282	hypothetical protein (TIGR) CDS		1,551	70.8	79.6	65.4	142	134.4	114.3
DVU2283	hypothetical protein (TIGR) CDS		102	50.8	53	51.1	29.2	38.9	35.4
DVU2284	hypothetical protein (TIGR) CDS		513	99.6	106	95.8	174.1	160.8	109.8
DVU2285	L-lactate permease family protein (TIGR) CDS		1,521	503.7	539.7	500.3	287	277.8	224.9
DVU2286	hydrogenase, CooM subunit, putative (TIGR) CDS		3,762	644.4	695.7	668.2	717.7	692.3	611.7
DVU2287	hydrogenase, CooK subunit, selenocysteine-containing, putati		966	754.6	825.1	828.9	728.5	682.5	487.1
DVU2288	hydrogenase, CooL subunit, putative (TIGR) CDS		435	643.2	739.5	677.9	637.1	630.2	542.4
DVU2289	b2488 CDS	b2488	636	691.5	786.7	743.6	493.1	469.8	480.2
DVU2290	hydrogenase, CooU subunit, putative (TIGR) CDS		546	916.8	1027	934.5	589.4	598.7	571.3
DVU2291	carbon monoxide-induced hydrogenase CooH, putative (TIGR)		1,101	791.5	864.3	827.8	1110.8	1043.4	1468.8
DVU2292	hypA CDS	hypA	363	745.4	829.6	776.4	564.1	532.2	434.3
DVU2293	cooF CDS	cooF	522	1013	1105.2	985.2	713	743.4	742.6
DVU2294	femAB family protein (TIGR) CDS		1,080	40.3	38.9	37.9	44.1	44.8	29.2
DVU2295	methyl-accepting chemotaxis protein (TIGR) CDS		2,331	110.2	105.3	104.1	126.8	131.8	105.1
DVU2296	mtgA CDS	mtgA	747	74.9	76.1	80.6	153.5	158.8	153.5
DVU2297	glycine/betaine/L-proline ABC transporter, periplasmic-bindin		858	432.4	428.6	480.1	288.9	290.5	246.4
DVU2298	opuBB CDS	opuBB	852	439.6	447.9	481.9	366.9	377.2	328.1
DVU2299	proV CDS	proV	1,194	485.7	508.4	522.5	432.6	415.3	429.4
DVU2300	hypothetical protein (TIGR) CDS		156	707.1	708.2	720.5	1206.2	1114.2	1597
DVU2301	lipoprotein, putative (TIGR) CDS		138	5.7	9.3	4.8	10.5	10.5	11.3
DVU2302	glutathione-regulated potassium-efflux system protein KefB, p		2,019	106.4	106.9	94.7	157.7	162.4	128.8
DVU2303	conserved domain protein (TIGR) CDS		1,428	86.8	88.7	82.9	101.3	100.2	75.6
DVU2305	conserved hypothetical protein (TIGR) CDS		630	255.2	278	289.2	98.4	97.3	56.6
DVU2306	phosphate transporter family protein (TIGR) CDS		1,011	185.3	185.3	208.8	141.2	148.2	121.7
DVU2307	C4-type zinc finger protein, DksA/TraR family (TIGR) CDS		222	409.8	525.8	398	442	523.6	398.1
DVU2308	conserved hypothetical protein TIGR00022 (TIGR) CDS		492	354.8	396.6	333.3	562.9	496.2	460.1
DVU2309	methyl-accepting chemotaxis protein, putative (TIGR) CDS		2,088	45.3	53.3	41.9	103	98.4	95.8
DVU2310	metallo-beta-lactamase family protein (TIGR) CDS		747	165.2	201.4	170.7	373.9	346.3	323.8
DVU2312	hypothetical protein (TIGR) CDS		468	188.6	187.5	154.6	377.7	369.1	337.9
DVU2313	pgl CDS	pgl	750	209.4	208.1	160.8	346.6	340.8	412.1
DVU2315	conserved hypothetical protein TIGR00257 (TIGR) CDS		729	62.7	58.9	57.1	165.7	161.3	150.3
DVU2316	topB CDS	topB	2,589	68.6	72.4	62.4	70.8	68.5	50.7
DVU2317	methyl-accepting chemotaxis protein, putative (TIGR) CDS		1,770	95.4	83.3	73.2	65.5	67.6	56
DVU2318	rbr2 CDS	rbr2	495	2213.1	2089.8	1432	827.2	1009.6	1264.4
DVU2320	3-octaprenyl-4-hydroxybenzoate carboxy-lyase family protein		1,839	226.1	223.3	218.3	370.5	376.2	308.6
DVU2322	UTP--glucose-1-phosphate uridylyltransferase, putative (TIGR)		1,440	145.2	156.5	136.9	192.2	176	152.9
DVU2323	hypothetical protein (TIGR) CDS		423	398.8	432.1	405.9	411.9	407.6	626.8

DVU2324	copper-translocating P-type ATPase (TIGR) CDS		2,718	78.7	100.6	89.7	168.3	185.1	134.8
DVU2325	merP CDS	merP	198	534.8	576.3	538.7	254.5	266.3	365.4
DVU2326	conserved domain protein (TIGR) CDS		903	353.6	348.7	338.1	286.9	289.4	261.6
DVU2328	hypA CDS	hypA	354	858.7	646.4	632.3	886.2	862.6	659.2
DVU2329	hypB CDS	hypB	675	648.7	619.9	538.3	367.2	357.5	401.3
DVU2330	E.coliMinDlike) CDS	E.coliMinDl	882	635.7	574.2	529.4	595.6	601	673.6
DVU2331	Smr family protein (TIGR) CDS		1,230	142	164	150.2	74.9	71.6	66.4
DVU2332	proC CDS	proC	798	279.6	288.7	294.4	167.5	181.1	100.7
DVU2333	ndk CDS	ndk	420	249.5	295.8	289	106.7	121.5	79.4
DVU2335	conserved domain protein (TIGR) CDS		1,551	205.8	194.9	215.2	151.1	165.4	113.3
DVU2336	carboxyl-terminal protease (TIGR) CDS		1,287	407.1	408.8	375.8	640.4	642.2	684.5
DVU2337	peptidase, M23/M37 family (TIGR) CDS		1,152	108.6	105.8	97.2	140.6	150.9	120.9
DVU2338	DNA repair protein, HhH-GPD family (TIGR) CDS		681	167.6	174.5	176.4	178.3	192.1	126.8
DVU2339	prmA CDS	prmA	852	318.2	327.6	325.1	257.8	245.6	216.6
DVU2340	amino acid ABC transporter, permease protein, His/Glu/Gln/A		693	109.4	123.9	108.1	224.6	220.1	127.2
DVU2341	amino acid ABC transproter, permease protein, His/Glu/Gln/A		702	99.2	116.8	93.4	195.5	189.9	90.2
DVU2342	amino acid ABC transporter, periplasmic amino acid-binding p		813	278.6	303.8	243.1	122.3	127.7	59.8
DVU2343	glnQ CDS	glnQ	729	146.2	162.9	154.9	246.2	257.8	96.5
DVU2345	hypothetical protein (TIGR) CDS		321	24.7	32.2	29.4	144.9	128.6	57.9
DVU2347	argD CDS	argD	1,200	172.9	158.1	152.6	133.5	139.7	186.1
DVU2349	carbohydrate phosphorylase family protein (TIGR) CDS		2,568	158.9	172.4	148.5	429	404.6	379.6
DVU2350	gid CDS	gid	1,425	95.3	95.6	89.1	57.8	62.1	55.8
DVU2351	hypothetical protein (TIGR) CDS		369	247.1	181.1	195.1	332	368.7	323.6
DVU2352	glycosyl transferase, group 2 family protein (TIGR) CDS		1,638	69.4	59.7	61.6	111.4	114	102.8
DVU2354	glycosyl transferase, group 2 family protein (TIGR) CDS		1,248	145.5	150.2	138.7	160	166.7	121.8
DVU2355	trmH CDS	trmH	591	149.2	162.3	131.7	126.7	138	105.8
DVU2356	membrane protein, putative (TIGR) CDS		1,428	449.9	525.8	501.8	569.9	533.9	501
DVU2357	HD domain protein (TIGR) CDS		1,110	140.5	145.6	126.9	462.1	451.4	426.8
DVU2359	sigma-54 dependent transcriptional regulator (TIGR) CDS		1,656	83	91.1	100.6	188.5	200.9	127.6
DVU2360	oxidoreductase, FAD/NAD-binding family (TIGR) CDS		807	66.8	66.4	63.1	120.4	110.1	105.6
DVU2362	thiE-2 CDS	thiE-2	660	56.2	59.9	50.9	133.1	137.6	99.5
DVU2363	thiM CDS	thiM	804	72.4	89.8	73.2	104.2	116.3	81
DVU2364	aminotransferase, classes I and II (TIGR) CDS		1,167	285.3	325.2	306.5	304.2	307.6	255.7
DVU2365	conserved hypothetical protein (TIGR) CDS		825	173.5	177.8	182.1	318.1	294.1	265.3
DVU2367	lpxA CDS	lpxA	804	472.2	524.3	494.2	529.6	496.3	467.3
DVU2368	fabZ CDS	fabZ	465	538.6	612.7	535.9	862.8	811.2	769.7
DVU2369	lpxD CDS	lpxD	1,035	494.2	532.1	484.5	1256.2	1168.2	1069.1
DVU2370	outer membrane protein OmpH, putative (TIGR) CDS		528	928.2	1005.9	891.8	781.2	818.1	830.6
DVU2371	amiA CDS	amiA	1,632	265.6	254.5	271.2	366.8	378.1	349.9
DVU2372	hypothetical protein (TIGR) CDS		366	166.2	160.6	169.9	238.4	257.9	176.5
DVU2374	lolD CDS	lolD	702	405.3	398.9	382.5	576.1	598.6	543.4
DVU2375	lipoprotein releasing system, permease protein (TIGR) CDS		1,236	287.4	293.3	277.1	278.5	282.6	212.4
DVU2377	hypothetical protein (TIGR) CDS		132	3.8	7.4	4	2.1	4.1	7.8
DVU2378	foxR CDS	foxR	693	2.7	5.8	5.8	4.8	4.9	6.7
DVU2379	pqqL CDS	pqqL	3,018	4.9	5.9	6	3.9	4.2	2.2
DVU2380	atpX CDS	atpX	906	5	4.7	8.5	7.3	9.5	6.9
DVU2381	conserved hypothetical protein (TIGR) CDS		669	2.5	3.7	3.2	2.6	3.8	3.1
DVU2382	conserved domain protein (TIGR) CDS		1,365	4.7	4.9	5	3.6	2.4	3
DVU2383	tonB dependent receptor domain protein (TIGR) CDS		2,628	6.9	7.9	6.2	5.8	7.1	3.1
DVU2384	ABC transporter, periplasmic substrate-binding protein (TIGR)		1,920	2.6	3.3	3	4.8	3.3	3.8
DVU2385	ABC transporter, permease protein (TIGR) CDS		1,122	1.9	3	3.9	3.6	5.7	3.2
DVU2386	oppC CDS	oppC	1,032	5.1	3	3	5.1	5.1	3.5
DVU2387	ABC transporter, ATP-binding protein (TIGR) CDS		1,779	3.7	6	3.1	4.8	4.9	7.1
DVU2388	tolQ-1 CDS	tolQ-1	954	9.7	9.8	8	19.1	19.8	22.7
DVU2389	tolR CDS	tolR	414	8	13.5	8.4	5.1	5.4	16.3
DVU2390	TonB domain protein (TIGR) CDS		909	13.8	15.6	17.9	39.1	37.6	25.3
DVU2391	hypothetical protein (TIGR) CDS		144	22	23.9	23.9	0.7	4.6	0
DVU2392	type III secretion chaperone, CesT family (TIGR) CDS		453	62.3	66.7	56.1	43.1	45.4	44.5
DVU2394	ntrC1 CDS	ntrC1	1,392	100.3	97.5	96.3	174.1	175.2	116.8
DVU2395	sensor histidine kinase (TIGR) CDS		1,257	81.7	85	80.6	126.5	126.3	84.1
DVU2396	adh CDS	adh	1,143	88.5	99.9	89.1	217.8	228.5	163.2
DVU2397	hypothetical protein (TIGR) CDS		744	107.9	102.2	102.1	667	603.5	404.3
DVU2398	conserved hypothetical protein (TIGR) CDS		492	204.2	174.9	179.7	1285	1244.7	896.1
DVU2399	hydrogenase, putative (TIGR) CDS		888	241.4	235	191.1	1504.6	1406.8	1211.8
DVU2400	hydrogenase, putative (TIGR) CDS		1,083	193.7	174.8	153.5	1904.7	1678.9	1649.6
DVU2401	hydrogenase, iron-sulfur cluster-binding subunit, putative (TIG		1,485	209.7	195.7	182.3	1269	1208.9	884.9
DVU2402	hdrA CDS	hdrA	1,959	204.7	183.6	162.1	1630.9	1559.5	1259.4

DVU2403	hdrB CDS	hdrB	1,005	201.9	183.3	165.9	1940.9	1764.8	1464.9
DVU2404	hdrC CDS	hdrC	561	286.7	270.2	250.9	1890.8	1772.1	1763.3
DVU2405	alcohol dehydrogenase, iron-containing (TIGR) CDS		1,182	20.2	26.5	21.5	3128.8	2699.2	3717.2
DVU2407	conserved hypothetical protein (TIGR) CDS		501	86.9	86.8	83.5	207.1	236.4	167.6
DVU2408	hypothetical protein (TIGR) CDS		279	54	56.4	58.5	91.1	110.5	114
DVU2409	bacterial extracellular solute-binding proteins, family 3 (TIGR)		813	103	97.2	100.7	138.1	134.3	108.8
DVU2411	EF hand domain protein (TIGR) CDS		417	674.8	635.3	528.4	503.8	521.5	577.5
DVU2413	radical SAM domain protein (TIGR) CDS		2,043	165	186.5	176.6	132.1	136.4	127.3
DVU2414	hypothetical protein (TIGR) CDS		1,761	64.1	64.9	65	139.8	135.4	90.9
DVU2416	conserved hypothetical protein (TIGR) CDS		483	299.7	312.4	295.8	193	199.1	219.9
DVU2417	SlyX protein (TIGR) CDS		222	354.5	366.1	359.3	246.1	287.8	322.4
DVU2418	vanZ-like family protein (TIGR) CDS		423	80.4	69.1	71.7	94.6	88.2	72.1
DVU2419	conserved domain protein (TIGR) CDS		555	163.7	148.6	140.7	179.3	201.6	197.4
DVU2420	conserved hypothetical protein (TIGR) CDS		330	336.3	322.2	285.6	89.6	94.1	72.1
DVU2421	dmpI CDS	dmpI	198	692.7	644.4	564.4	365.8	355	437.2
DVU2422	nitroreductase family protein (TIGR) CDS		510	386.1	341.8	286.3	197.7	193	261
DVU2423	transcriptional regulator, putative (TIGR) CDS		480	143.7	158.4	145.6	266.1	303.5	307.9
DVU2424	membrane protein, putative (TIGR) CDS		915	86	81.7	78.7	55.9	63.6	53.6
DVU2425	rarD CDS	rarD	888	123.7	111.2	103.3	102.7	119.3	87.9
DVU2427	hypothetical protein (TIGR) CDS		642	553.8	575.5	510	546.8	513.3	560.3
DVU2428	lipoprotein, putative (TIGR) CDS		459	994.6	974.5	969.5	866.6	856.5	834.4
DVU2429	hypothetical protein (TIGR) CDS		111	161.3	177.7	175.7	32.5	36.4	20.9
DVU2430	RNA-binding protein (TIGR) CDS		267	263.2	291.7	310	43.2	46.9	47.4
DVU2431	hypothetical protein (TIGR) CDS		150	14.2	26.6	25.6	23.8	32.5	22.4
DVU2432	sensory box/GGDEF domain/EAL domain protein (TIGR) CDS		4,242	68.3	68.9	60.5	112.6	112.9	93.2
DVU2434	hypothetical protein (TIGR) CDS		408	412.4	358	361.1	109.4	124	133
DVU2436	conserved hypothetical protein (TIGR) CDS		633	153.9	157.5	134.4	105.4	101.6	105.3
DVU2437	ABC transporter, permease protein (TIGR) CDS		1,221	98.1	103.7	98.4	163.4	173.6	124.5
DVU2439	efflux transporter, RND family, MFP subunit (TIGR) CDS		1,236	116.9	121.6	113.4	312.1	312	254.7
DVU2440	hypothetical protein (TIGR) CDS		924	65.5	60.5	62.3	45.4	48.5	34.2
DVU2441	hspC CDS	hspC	411	262.3	479.2	359.3	638.2	681.4	647.6
DVU2442	heat shock protein, Hsp20 family (TIGR) CDS		354	370.8	688.9	566.5	676.3	734	665.8
DVU2443	conserved hypothetical protein (TIGR) CDS		627	122.3	110.5	117.1	112.9	125.8	84.9
DVU2444	flaB3 CDS	flaB3	894	1688.2	1909.6	1712.7	773.9	754.8	1030.3
DVU2446	panB CDS	panB	924	77.4	78.7	70.8	125.3	114.7	120.8
DVU2447	hypothetical protein (TIGR) CDS		576	94.1	89	80	185.7	176.9	237.8
DVU2448	panC CDS	panC	852	330.6	288.9	267.9	621.2	608.1	696.4
DVU2449	metK CDS	metK	1,176	677.7	661.5	585	355.4	369.5	381.1
DVU2450	conserved hypothetical protein (TIGR) CDS		207	50	47.1	42.6	34.9	29.9	22.5
DVU2451	L-lactate permease family protein (TIGR) CDS		1,713	539.5	494.5	497.6	403	414.9	445.3
DVU2454	hypothetical protein (TIGR) CDS		270	110.4	52.8	72.2	48.1	50.1	23
DVU2455	NAD-dependent epimerase/dehydratase family protein (TIGR)		951	132.7	146.5	125.9	106.5	119.2	102.2
DVU2459	hypothetical protein (TIGR) CDS		615	215.6	205.8	187.5	137.3	131.1	124.4
DVU2460	hypothetical protein (TIGR) CDS		594	202	186.5	193.7	292.2	292.1	280.2
DVU2461	appB CDS	appB	1,020	131.7	130.3	132.7	242.1	257.3	223.2
DVU2462	oligopeptide ABC transporter, permease protein (TIGR) CDS		903	98.4	97.6	104.9	115.2	120.1	77
DVU2463	recN CDS	recN	1,620	125.8	132.3	125.5	111.9	117.3	92.4
DVU2464	hypothetical protein (TIGR) CDS		1,584	107.5	111.2	103.6	124.5	133.4	121.6
DVU2466	flocculin repeat domain (TIGR) CDS		870	24.6	29.4	32.9	27.6	25.4	17.2
DVU2467	rnr CDS	rnr	2,661	220.1	252.1	232.1	216.1	215.4	200.1
DVU2468	lpxK CDS	lpxK	1,065	221.5	251.6	245.9	651.8	640.8	876.7
DVU2470	b0786 CDS	b0786	702	639.2	631.5	592.6	710.8	698.9	765.7
DVU2471	oxidoreductase, selenocysteine-containing (TIGR) CDS		1,299	257.8	281.3	254.7	119.2	130.5	103.9
DVU2472	conserved hypothetical protein (TIGR) CDS		2,340	56.7	54.9	45.5	117	113.6	129.4
DVU2473	hypothetical protein (TIGR) CDS		144	103.5	84	86.4	177.5	214.9	328.5
DVU2474	hypothetical protein (TIGR) CDS		483	216	251.8	232.9	609.4	551.3	674.7
DVU2475	oxidoreductase, NAD-binding, putative (TIGR) CDS		843	184.2	173.9	148.5	144.7	159.8	142.5
DVU2476	gltA CDS	gltA	1,431	187.4	174.1	176	223.6	225.9	204.3
DVU2477	pstS CDS	pstS	813	60.5	73.3	68.9	77.1	86.3	73.8
DVU2478	pstC-2 CDS	pstC-2	888	63	65.4	56	40.7	37.7	22.7
DVU2479	pstA-2 CDS	pstA-2	930	45	47.2	40.5	60.5	63.3	43.9
DVU2481	fdoH CDS	fdoH	783	333.5	377	360.7	288.8	275.6	199.4
DVU2482	fdnG-2 CDS	fdnG-2	3,012	343.1	397.4	350.1	259.2	260.5	223.9
DVU2483	cytochrome c family protein (TIGR) CDS		1,746	317	363.1	343	253.6	259	213.4
DVU2484	cytochrome c family protein (TIGR) CDS		1,293	228.7	253.4	241.8	227	211.6	166.7
DVU2485	membrane protein, putative (TIGR) CDS		1,065	201.8	230.2	212.2	274.3	254	213.8
DVU2486	acetyltransferase, GNAT family (TIGR) CDS		546	98.4	123.6	112	79	95.1	57.7

DVU2487	hypothetical protein (TIGR) CDS		1,188	189.2	225.2	191.4	195	210	192.3
DVU2490	Histidinol phosphatase (Natalia Ivanova) CDS		825	113.9	130.4	118.8	190.8	190.4	152.2
DVU2491	ABC transporter, ATP-binding protein (TIGR) CDS		1,899	114.5	98.2	100.4	91.3	92.1	82.7
DVU2494	peptidase, M48 family (TIGR) CDS		861	175.8	223.5	157.4	604.1	524.1	600.9
DVU2495	thioesterase family protein (TIGR) CDS		534	64	75.9	64.6	122.7	108.6	86.7
DVU2496	lipoprotein, putative (TIGR) CDS		453	559.7	567.5	527.2	1003.4	957	1334.3
DVU2497	lipoprotein, putative (TIGR) CDS		735	116.4	125.1	109.5	281.1	292	268.7
DVU2498	hypothetical protein (TIGR) CDS		294	43.1	50.4	47.5	34.8	27.2	21.1
DVU2499	ftsZ CDS	ftsZ	1,350	1083.3	1142.4	1070.5	1161.3	1073.8	1606.9
DVU2500	ftsA CDS	ftsA	1,227	669.2	713.6	679.1	958.1	922.1	928.6
DVU2501	cell division protein FtsQ, putative (TIGR) CDS		837	577.2	593.7	594.7	753.6	726.1	777.7
DVU2502	murB CDS	murB	891	279.6	282	268.3	376.7	391.9	206.5
DVU2503	murC CDS	murC	1,365	275.3	327	291.9	227	238	167
DVU2504	murG CDS	murG	1,098	175.7	204.9	182.1	236.8	231.7	132
DVU2505	ftsW CDS	ftsW	1,134	167.8	205.7	198.1	406.3	379.1	425.2
DVU2506	murD CDS	murD	1,302	299.5	309.4	297.1	397.7	418	262.2
DVU2507	mraY CDS	mraY	1,077	205.4	244.4	227.7	351.9	377.6	214.3
DVU2508	murF CDS	murF	1,437	243.4	266.1	231.8	445.2	451.4	273.1
DVU2509	murE CDS	murE	1,461	260.7	288.4	271.4	490.7	512.5	358.9
DVU2510	penicillin-binding protein (TIGR) CDS		2,073	401.3	425.2	402	331.6	368.4	316.4
DVU2511	hypothetical protein (TIGR) CDS		288	400.8	453.5	410.4	288.5	312.6	354.4
DVU2512	mraW CDS	mraW	972	407.2	451.9	401.5	544.3	528.7	507.3
DVU2513	mraZ CDS	mraZ	450	479.4	525.1	486.2	516.6	497.1	460.5
DVU2514	pyk CDS	pyk	1,410	419.6	424.9	352.9	594.6	556.3	591.6
DVU2515	HD domain protein (TIGR) CDS		1,056	359.6	338.9	304	398.6	335.9	555.5
DVU2516	CBS domain protein (TIGR) CDS		486	385.7	348.8	336.1	352.6	372.5	340.3
DVU2517	conserved hypothetical protein (TIGR) CDS		1,242	120	117.6	119.7	232.2	240.4	268.5
DVU2518	rplM CDS	rplM	435	2911.3	3188	2835.5	1865.9	1894.6	3371.9
DVU2519	rpsI CDS	rpsI	393	2265.2	2552.7	2263.4	1171	1148.7	1429.6
DVU2521	aroK-2 CDS	aroK-2	543	230.7	227.4	226	218.6	212.7	224.6
DVU2522	hypothetical protein (TIGR) CDS		603	150.3	157.2	131.9	154.4	168.3	166.3
DVU2523	lipoprotein, putative (TIGR) CDS		477	175.3	161.6	143.1	423.7	382.5	488.7
DVU2524	cytochrome c3, putative (TIGR) CDS		498	12.1	13	13.2	13	9.6	9.4
DVU2525	hynB-2 CDS	hynB-2	915	10.3	14.8	11	16.6	16.6	10.2
DVU2526	hynA-2 CDS	hynA-2	1,650	20.9	26.2	20.8	35.2	33.1	27.6
DVU2527	transcriptional regulator, putative (TIGR) CDS		399	279.6	300.6	279.5	134.6	151.2	117.9
DVU2528	hypothetical protein (TIGR) CDS		198	8.5	12	9.8	4.6	7.8	0
DVU2529	pgk CDS	pgk	1,182	247	250.4	233	126.2	131.1	98.3
DVU2530	tkt CDS	tkt	1,995	454.3	499.1	413.2	318	297	287.6
DVU2531	rpe CDS	rpe	669	267.7	285.3	262	116.6	123.1	108.1
DVU2532	transcriptional regulator, MerR family (TIGR) CDS		384	582.8	618	584.1	1077	1029.1	1336.5
DVU2533	pheT CDS	pheT	2,397	381.6	406.7	371.4	245.6	246.5	215
DVU2534	pheS CDS	pheS	1,038	421.1	474.7	415.5	245.9	249.4	219.1
DVU2535	rplT CDS	rplT	354	2277.7	2383.6	2150.7	795.7	758	1138.8
DVU2536	rpmI CDS	rpmI	198	2587.3	2826.2	2555.5	1130.4	1155.1	2255.3
DVU2537	infC CDS	infC	531	1508.2	1746.8	1606.8	1247.9	1250.6	1545.2
DVU2538	thrS CDS	thrS	1,935	958.7	1082.6	988.7	706	669	739
DVU2539	hypothetical protein (TIGR) CDS		123	17.3	23.2	15.7	29.4	34.5	16.8
DVU2540	lyase, putative (TIGR) CDS		1,143	8.9	10.4	8	13.2	15.2	7.7
DVU2541	CoA-substrate-specific enzyme activase, putative (TIGR) CDS		810	2.9	6.5	4.1	6.1	5.5	5.1
DVU2543	b0873 CDS	b0873	1,701	59	92.9	61.4	308.3	265.6	529.3
DVU2544	iron-sulfur cluster-binding protein (TIGR) CDS		816	41.2	50.3	35.4	247.4	243	331.9
DVU2545	alcohol dehydrogenase, iron-containing (TIGR) CDS		1,161	148.9	162.2	137.1	262	247.1	291.8
DVU2546	sensory box histidine kinase (TIGR) CDS		1,623	103.4	104.7	93.3	243.7	231.5	206.9
DVU2547	transcriptional regulator, putative (TIGR) CDS		687	199.5	208.3	160.1	298.5	319.5	272
DVU2548	acpD CDS	acpD	630	328.1	336.6	298.4	361.3	366.9	321.2
DVU2549	hypothetical protein (TIGR) CDS		276	208.1	216.7	215.8	267.2	284.8	267.8
DVU2550	hypothetical protein (TIGR) CDS		168	138.4	146.4	149.9	334.8	339.3	286.2
DVU2552	gltX-2 CDS	gltX-2	1,392	375.9	395	399.6	368.2	376.7	316
DVU2553	nifU-3 CDS	nifU-3	246	312.9	363.5	292.3	187.6	206.4	264.7
DVU2554	conserved hypothetical protein (TIGR) CDS		885	135.6	170.1	138.3	131.4	139.4	106.3
DVU2555	MATE efflux family protein (TIGR) CDS		1,422	96.6	97.3	76.8	105.1	105.8	80.7
DVU2556	hypothetical protein (TIGR) CDS		369	234.4	245	220.2	398.6	390.9	254.9
DVU2557	birA CDS	birA	993	190.1	174.3	160.3	187.2	185.5	159.8
DVU2558	bioB CDS	bioB	933	142.1	125.9	119	223.4	222	226.1
DVU2559	bioA CDS	bioA	1,629	52.9	56.8	50.1	39	42.9	34.8
DVU2560	conserved domain protein (TIGR) CDS		387	50.9	63.7	53.4	43.4	50.4	27.4

DVU2561	oxidoreductase, short chain dehydrogenase/reductase family (		1,029	40.7	45	39.1	42.3	41.6	18.5
DVU2562	acpP CDS	acpP	408	46.5	63	47.6	10.8	11.5	12.7
DVU2563	fabF CDS	fabF	1,449	24.6	31.4	25.2	13.5	16.5	11.5
DVU2564	bioF CDS	bioF	1,275	27	29.1	29.6	15	13.1	13.1
DVU2565	bioD CDS	bioD	741	186.3	172.8	203.3	32.6	30.9	32.8
DVU2566	lysA-2 CDS	lysA-2	1,266	59.2	63.2	58.4	38.7	42.4	35.1
DVU2567	lysX CDS	lysX	705	62.3	66	59.2	50.8	55.8	35.2
DVU2568	cpsA CDS	cpsA	1,239	68.9	75.2	74	81.5	82.3	45.4
DVU2569	slyD CDS	slyD	426	333.2	351.2	277.5	334.7	332.2	486.5
DVU2570	pleD CDS	pleD	1,653	55.2	52.3	49	63.7	67.1	47.2
DVU2571	feoB CDS	feoB	2,199	109.9	87.5	111.9	56.7	61.3	66.7
DVU2572	feoA CDS	feoA	261	132.8	116.6	154.4	168.4	197.4	119.8
DVU2573	hypothetical protein (TIGR) CDS		156	189.5	162	181.5	227.1	242.9	213.7
DVU2574	feoA CDS	feoA	237	306.2	251.6	297.1	609.7	652.8	491.8
DVU2575	peptidase, M20/M25/M40 family (TIGR) CDS		1,101	141.5	148.4	141.6	115.5	122.7	100.2
DVU2576	oligopeptide ABC transporter, ATP-binding protein (TIGR) CDS		966	111.2	110.1	110.7	87.4	89.8	71.5
DVU2577	DNA-binding response regulator, LuxR family (TIGR) CDS		651	1001.8	1079.5	978.8	1203.2	1146.2	1498.1
DVU2578	response regulator (TIGR) CDS		690	86.9	94.4	85.2	76	106.5	98.1
DVU2579	TPR domain protein (TIGR) CDS		630	233.1	228	209.5	116.2	126.6	127.2
DVU2580	response regulator (TIGR) CDS		4,122	140.2	136.8	126.9	210.8	203.6	191.1
DVU2581	cheYIV CDS	cheYIV	441	137.6	124.5	127.8	144.3	147.8	139.5
DVU2582	transcriptional regulator, TetR family (TIGR) CDS		588	285.9	304.7	260.5	139.9	157.9	120.4
DVU2583	lipoprotein, putative (TIGR) CDS		507	89.7	90.6	79	209.4	207.6	222.2
DVU2584	corA CDS	corA	933	60	40.8	35.7	105.2	97.4	166.8
DVU2585	methyl-accepting chemotaxis protein (TIGR) CDS		1,881	41.2	57.1	50.6	37.7	35	27.2
DVU2586	ABC transporter, ATP-binding protein (TIGR) CDS		1,683	362.6	393.9	367.2	302.8	313.2	308.7
DVU2587	vicK CDS	vicK	1,386	45.2	45.2	37.2	73.6	78	70.1
DVU2588	trcR CDS	trcR	681	72.2	73.9	61.2	115.6	121.2	90.3
DVU2590	sensory box protein (TIGR) CDS		1,566	279.6	265.9	244.6	235.6	241.2	290.1
DVU2591	tail fiber assembly protein, putative (TIGR) CDS		510	18.3	25.3	19.2	15.1	16.4	14.2
DVU2592	hypothetical protein (TIGR) CDS		339	0.8	19.2	8.8	22.2	22.7	18.3
DVU2595	hypothetical protein (TIGR) CDS		576	1.3	1	3.9	1.5	2.2	0
DVU2596	hypothetical protein (TIGR) CDS		780	2	4.3	2.6	2.9	2.4	0
DVU2598	hypothetical protein (TIGR) CDS		555	2.1	3.3	3.6	1.7	2	0.9
DVU2599	hypothetical protein (TIGR) CDS		444	2.6	3.2	2	2.6	5.7	5.8
DVU2600	hypothetical protein (TIGR) CDS		402	7.9	10.4	10.9	6	4.6	11.6
DVU2602	conserved domain protein (TIGR) CDS		684	2.5	3.3	4.5	0.6	0.6	0
DVU2603	hypothetical protein (TIGR) CDS		408	1.1	4.4	2.2	0.9	1.3	1.3
DVU2604	conserved hypothetical protein (TIGR) CDS		1,710	2.4	4.1	4.8	4.1	5.4	4.3
DVU2605	hypothetical protein (TIGR) CDS		435	2.2	1	1	1.6	3.1	0
DVU2606	hypothetical protein (TIGR) CDS		300	8.2	6.6	5.6	17.8	22.7	25.8
DVU2607	hypothetical protein (TIGR) CDS		627	236.9	220.8	204.5	389.1	392.6	409.7
DVU2608	motA-3 CDS	motA-3	846	235.6	245.6	238.5	260.9	262.9	275.5
DVU2609	chemotaxis MotB protein, putative (TIGR) CDS		732	197.8	211.7	195.3	162.3	167	148.2
DVU2610	hypothetical protein (TIGR) CDS		678	101.4	84.9	86	70.7	76.2	66.4
DVU2611	conserved hypothetical protein (TIGR) CDS		1,560	9.5	11.1	10.1	8.3	13.2	8.6
DVU2612	conserved hypothetical protein (TIGR) CDS		390	1063.1	1268.7	1086.4	828.2	849.5	1085.4
DVU2613	hypothetical protein (TIGR) CDS		567	243	329.2	288.9	246.8	246.5	284.4
DVU2614	hypothetical protein (TIGR) CDS		618	173.9	227.5	224.7	133.9	146.8	114.6
DVU2615	bacterial extracellular solute-binding protein, family 3 (TIGR) C		849	36.8	66.5	53.6	105.1	91.3	51.8
DVU2616	sensory box histidine kinase/response regulator (TIGR) CDS		3,003	20	32.8	23.1	57	48.1	28.4
DVU2617	sodium/calcium exchanger family protein (TIGR) CDS		1,221	93.1	124	112.7	164.6	152.5	207.8
DVU2619	conserved hypothetical protein (TIGR) CDS		729	72.8	85.2	76.2	179.9	160.6	204.2
DVU2620	conserved hypothetical protein (TIGR) CDS		1,161	109.5	108.6	120.7	211.4	221.5	144.3
DVU2621	hypothetical protein (TIGR) CDS		813	259.4	269.4	249.1	519.8	563.2	539.4
DVU2622	hypothetical protein (TIGR) CDS		189	29.6	35.3	28.7	49.9	49.7	36.9
DVU2623	hypothetical protein (TIGR) CDS		348	8.4	7.9	5.6	4.9	7.3	11.9
DVU2624	hypothetical protein (TIGR) CDS		498	15.6	16.8	20.9	10.4	11.5	11.5
DVU2625	hypothetical protein (TIGR) CDS		102	72.9	78.6	65.3	57.5	62.7	78.5
DVU2626	hypothetical protein (TIGR) CDS		207	107.3	116.4	103.1	156.6	157	152.3
DVU2627	conserved domain protein (TIGR) CDS		378	192.7	174.5	168.4	199.2	191.3	205.7
DVU2628	TPR domain protein (TIGR) CDS		579	125.6	122.8	116.3	141.9	145.6	152.6
DVU2629	hypothetical protein (TIGR) CDS		552	13.3	14.2	13.6	15.9	20.6	16.9
DVU2630	lipoprotein, putative (TIGR) CDS		876	92.5	94.6	87.5	109	113	96.8
DVU2631	hypothetical protein (TIGR) CDS		372	28.5	26.5	34.2	43.1	46	41.7
DVU2634	hypothetical protein (TIGR) CDS		252	66.3	108.6	76.1	83.1	76.1	82.1
DVU2635	glycosyl transferase, group 1 family protein (TIGR) CDS		1,134	100.1	98.7	90.9	225.1	221.2	216.1

DVU2636	hypothetical protein (TIGR) CDS		1,170	67.5	66.9	58.5	195.6	196	156.8
DVU2638	conserved domain protein (TIGR) CDS		1,089	70.3	60.7	62.6	77.5	88.9	59.8
DVU2639	conserved hypothetical protein (TIGR) CDS		303	239.5	249.3	246.6	79.1	94.1	37.5
DVU2640	hypothetical protein (TIGR) CDS		741	93.6	112.1	91	89.8	79.2	68
DVU2641	lipoprotein, putative (TIGR) CDS		735	185.1	210	203.8	291.8	289.8	198.7
DVU2642	alanyl-tRNA synthetase family protein, putative (TIGR) CDS		444	56.8	59.8	59	94.8	91.6	76.9
DVU2643	htpG CDS	htpG	1,914	337.5	610.7	605.7	177.6	171.6	163.7
DVU2644	transcriptional regulator, GntR family (TIGR) CDS		672	124.5	113.6	117	261	273	247.6
DVU2645	Na+/H+ antiporter family protein (TIGR) CDS		1,401	21.7	24.8	21.9	26	29.9	29.5
DVU2646	1-aminocyclopropane-1-carboxylate deaminase (TIGR) CDS		999	17	17.7	15	11.8	12.9	10.3
DVU2647	endoribonuclease, L-PSP family (TIGR) CDS		390	5.7	9.1	12	6	6.6	5.3
DVU2648	hypothetical protein (TIGR) CDS		327	27.9	28.5	26	17.1	19.6	11
DVU2649	hypothetical protein (TIGR) CDS		261	6	28.5	32.6	32.8	23.7	15.8
DVU2650	hypothetical protein (TIGR) CDS		606	2590.4	3090.5	2867.6	2658	2316	3052.4
DVU2651	hypothetical protein (TIGR) CDS		177	31.2	26.1	26.4	17.9	14.5	20.4
DVU2652	hypothetical protein (TIGR) CDS		582	204.4	211.1	239.4	235.2	230.8	174.9
DVU2655	dacA CDS	dacA	1,326	438.8	489.2	431.5	745.3	721.2	1032.9
DVU2657	6-pyruvoyl tetrahydrobiopterin synthase, putative (TIGR) CDS		363	167.5	163.2	169.6	97.1	95.7	91.2
DVU2658	conserved hypothetical protein (TIGR) CDS		651	105.4	109.2	103.4	217.3	222.5	151.7
DVU2659	exsB protein (TIGR) CDS		729	119	140	131.2	152.5	180.1	148.1
DVU2661	CueO CDS	CueO	1,566	51.4	50.6	40	67.1	60.8	43.9
DVU2662	conserved hypothetical protein (TIGR) CDS		765	112.4	109.9	117	184.3	189.5	191.6
DVU2663	conserved hypothetical protein (TIGR) CDS		477	51.2	56.8	52.9	118.5	111.3	108.9
DVU2664	pstB-2 CDS	pstB-2	867	19.7	15.6	21.6	26.1	24.5	19.1
DVU2665	phosphate ABC transporter, permease protein, putative (TIGR		885	9.9	9.9	9.7	39.1	36.7	26.9
DVU2666	phosphate ABC transporter, permease protein, putative (TIGR		876	7.7	7.7	7.8	16.1	17.7	15.3
DVU2667	pstS CDS	pstS	879	25.6	23.6	17.1	36	32.8	38.9
DVU2668	glmU CDS	glmU	1,368	217.6	236	220.2	283.8	308.2	317.2
DVU2669	conserved domain protein (TIGR) CDS		237	910.3	970.7	907.8	1206.4	1137.6	1781.8
DVU2670	hypothetical protein (TIGR) CDS		264	1306.8	1343.7	1241	1520.2	1517.5	1927.4
DVU2671	HDIG/HD/KH domain protein (TIGR) CDS		1,560	638.6	645.2	624	856.9	825.7	1124.4
DVU2672	membrane protein, putative (TIGR) CDS		624	87.5	85	89.4	117.9	129.5	149.9
DVU2673	glpA CDS	glpA	1,170	190.3	196.2	166.8	262.7	251.4	253.8
DVU2674	sdhB CDS	sdhB	720	142	156.6	137.9	190.9	190.7	237.2
DVU2675	DNA-binding response regulator, LuxR family (TIGR) CDS		684	128.3	160.6	130.2	180.9	195.3	97.5
DVU2676	hypothetical protein (TIGR) CDS		267	84.1	217.4	148.4	208.6	191.9	75.5
DVU2677	sensor histidine kinase/response regulator (TIGR) CDS		1,464	123.3	136.8	121.8	126.2	129.5	100.4
DVU2678	RNA pseudouridine synthase family protein (TIGR) CDS		1,203	111.9	109.4	107.2	78.9	78.9	42.7
DVU2679	sensory box histidine kinase/response regulator (TIGR) CDS		3,018	32.8	32.7	27.6	57.9	58.3	37.3
DVU2680	fld CDS	fld	447	78.8	63.2	60	47.2	66.3	90.2
DVU2682	DedA family protein (TIGR) CDS		642	118.8	123.7	118.4	151.3	161.6	166.7
DVU2683	L-lactate permease family protein (TIGR) CDS		1,551	185.1	137.3	119.7	151.5	145.6	108.7
DVU2686	peptidase, S24 family (TIGR) CDS		783	183.6	179.2	143.4	127.9	128.2	102.9
DVU2688	bacteriophage transposase A protein (TIGR) CDS		2,043	7.8	10.6	9.5	68.1	60.9	109.6
DVU2689	bacteriophage DNA transposition B protein (TIGR) CDS		786	9.1	11.9	10.6	64.9	59.6	163.4
DVU2690	hypothetical protein (TIGR) CDS		588	8.3	16.2	10.9	26.1	27.7	60.2
DVU2691	hypothetical protein (TIGR) CDS		534	13	18	17.3	36.8	33.5	77
DVU2692	conserved domain protein (TIGR) CDS		237	26.4	29.3	25.3	40.7	33.6	68.6
DVU2693	hypothetical protein (TIGR) CDS		240	9.4	12.3	13.2	14.6	22.5	34.5
DVU2694	hypothetical protein (TIGR) CDS		435	5.8	8.4	13.2	47.9	46.4	52.9
DVU2695	conserved hypothetical protein (TIGR) CDS		417	10.7	12.7	9.5	42.5	49.8	107.8
DVU2696	conserved hypothetical protein (TIGR) CDS		489	52.1	60.7	49.5	133.2	126.8	179.7
DVU2697	hypothetical protein (TIGR) CDS		339	247.2	305	251.8	51	55.3	67.8
DVU2698	lipoprotein, putative (TIGR) CDS		363	14.9	16.5	14.8	41.1	33.3	53.4
DVU2699	slt CDS	slt	648	4.3	10.7	8.1	26.6	26.8	22
DVU2700	hypothetical protein (TIGR) CDS		420	2.3	7.8	6	30.4	23.2	30.7
DVU2701	hypothetical protein (TIGR) CDS		219	5.9	8.6	7.9	26.5	31.8	14.2
DVU2702	conserved hypothetical protein (TIGR) CDS		282	5.1	7	7.5	19.9	18.9	34.8
DVU2703	hypothetical protein (TIGR) CDS		216	4.5	8.1	4.3	23	18.4	20.3
DVU2704	conserved hypothetical protein (TIGR) CDS		519	6.6	6.8	7.5	22.2	19.7	30.8
DVU2705	phage uncharacterized protein (TIGR) CDS		1,677	5.3	4.9	4.1	13.4	14.7	21.8
DVU2706	conserved hypothetical protein (TIGR) CDS		1,719	5.6	6.6	4.2	15.2	16.1	26.6
DVU2707	virion morphogenesis protein (TIGR) CDS		1,251	9.7	14.4	12.1	21.2	22	27.9
DVU2708	virion morphogenesis protein (TIGR) CDS		489	33.6	44.4	41.5	30.2	33.4	21.1
DVU2710	conserved hypothetical protein (TIGR) CDS		1,161	6.2	8.8	10.2	51.7	43.1	93.2
DVU2711	major head subunit, putative (TIGR) CDS		930	7.1	12.7	10.3	38.9	39.8	70.8
DVU2712	hypothetical protein (TIGR) CDS		330	14.4	22.5	20.1	27.5	24.1	29.8

DVU2713	conserved hypothetical protein (TIGR) CDS		432	9.7	12.5	9.2	31.8	28.6	46
DVU2714	conserved hypothetical protein (TIGR) CDS		630	8.4	10.3	10.2	31.2	32.1	39
DVU2715	conserved hypothetical protein (TIGR) CDS		186	7.4	16.1	9.2	18.9	15.2	33.3
DVU2716	tail sheath protein, putative (TIGR) CDS		1,422	7.7	9.5	8.9	28	23.8	33.8
DVU2717	hypothetical protein (TIGR) CDS		828	197.5	175.7	171.4	52.4	59.5	63
DVU2719	conserved hypothetical protein (TIGR) CDS		375	28.5	26.2	27.6	69	65.9	100.6
DVU2720	hypothetical protein (TIGR) CDS		330	38	46	35.8	71.5	75.9	100.2
DVU2721	phage tail tape measure protein, TP901 family, putative (TIGR)		1,941	16.5	16.7	15.3	36.3	41.2	40.5
DVU2722	conserved hypothetical protein (TIGR) CDS		1,341	11.8	15.2	15.2	18.1	14.4	26.3
DVU2723	tail protein, putative (TIGR) CDS		1,125	14.4	16.6	15.6	23	23.2	28
DVU2724	phage baseplate assembly protein V, putative (TIGR) CDS		627	58.7	60.2	56.9	75.4	75.1	59.8
DVU2727	conserved hypothetical protein (TIGR) CDS		357	30	34.1	31.5	58.7	55.1	98.4
DVU2728	tail protein, putative (TIGR) CDS		1,062	9.5	10.7	9.6	34.8	32.3	72.3
DVU2729	tail protein, putative (TIGR) CDS		594	9.1	11.2	9.4	22.3	23.1	24.8
DVU2730	svQ CDS	svQ	891	10.6	9.5	13.9	16.2	15	33.3
DVU2731	tail fiber assembly protein, putative (TIGR) CDS		540	8.5	16.1	16.7	38.3	36.2	57
DVU2732	conserved hypothetical protein (TIGR) CDS		201	18	21.5	16.4	11.2	15.2	15.4
DVU2733	adenine specific DNA methyltransferase, putative (TIGR) CDS		750	13.8	17.1	17.1	37.3	36.4	31.7
DVU2735	paaK-3 CDS	paaK-3	1,299	171.5	159.1	140	110.7	121.1	101.5
DVU2736	hypothetical protein (TIGR) CDS		510	130	125.7	105.7	47.5	51.2	33.4
DVU2737	RNA methyltransferase, TrmH family (TIGR) CDS		765	84.8	91.2	98.7	48.5	56.6	40.5
DVU2738	methyl-accepting chemotaxis protein (TIGR) CDS		2,406	439.2	467.9	456.5	455.3	449.9	570.1
DVU2740	livF CDS	livF	726	122.2	116.9	128.5	24.1	24.7	16
DVU2741	livG CDS	livG	768	113.4	102.3	113.1	22.9	28.8	26.3
DVU2742	livM CDS	livM	1,077	83.8	87.4	98.6	20.2	22.7	10.3
DVU2743	livH CDS	livH	921	91.7	84.5	84.3	33.8	29.6	25.2
DVU2744	high-affinity branched-chain amino acid ABC transporter, peris		1,158	305.7	222.5	260.1	60.5	56	43.8
DVU2746	conserved hypothetical protein (TIGR) CDS		945	49.3	54.6	51	37.4	37.2	35.5
DVU2747	hypothetical protein (TIGR) CDS		3,045	207.3	220.2	201.4	224.5	224.6	258.1
DVU2748	cobM CDS	cobM	774	171.7	168.8	156.1	193.1	210	121.9
DVU2749	cobL CDS	cobL	1,461	178.3	181.9	166	126.4	140	74.5
DVU2750	cbiD CDS	cbiD	1,170	137.4	116.8	115.5	377.2	378.2	282.7
DVU2751	hypothetical protein (TIGR) CDS		561	117	101.6	91.6	97.2	105.4	146
DVU2752	rhodanese-like domain protein (TIGR) CDS		522	94	80.7	68.3	47.3	43.8	42.1
DVU2753	C GCAxxG C C family protein (TIGR) CDS		828	74.6	60.1	50.1	74.9	76.5	53.6
DVU2754	qor CDS	qor	978	131.5	111.6	105.8	179.9	186.9	176.5
DVU2755	conserved hypothetical protein (TIGR) CDS		843	88.9	74.2	84.8	113.2	123.6	112.8
DVU2756	radical SAM domain protein (TIGR) CDS		1,119	193.3	197.7	190.6	211.9	215.3	325.4
DVU2757	radical SAM domain protein (TIGR) CDS		1,128	218.3	227.3	203.8	248.1	234.1	211.5
DVU2758	conserved hypothetical protein (TIGR) CDS		843	119.4	128.8	109.8	137.5	132.1	133
DVU2760	hypothetical protein (TIGR) CDS		612	43.2	41.8	39.6	52.9	61.6	60
DVU2761	hypothetical protein (TIGR) CDS		186	57.9	69.8	53.6	99.9	101.8	61.1
DVU2762	membrane protein, putative (TIGR) CDS		921	111.2	102.4	89.8	394.7	376.2	231.2
DVU2764	nitroreductase family protein (TIGR) CDS		519	207.6	204	193	287.3	294.6	361
DVU2765	metallo-beta-lactamase family protein (TIGR) CDS		627	175.6	193.3	165.4	135.7	141.9	140.5
DVU2766	hypothetical protein (TIGR) CDS		168	150.1	154.9	137.1	296.1	322.7	283
DVU2767	iron-sulfur flavoprotein, putative (TIGR) CDS		615	94.9	108.7	99.5	181.2	193.3	200.8
DVU2768	comF family protein (TIGR) CDS		897	21.8	27.5	22.4	23.4	23.2	20.2
DVU2769	nikK CDS	nikK	783	510.1	571.2	460.4	490.3	459.4	523.5
DVU2770	response regulator (TIGR) CDS		399	1120	1175.9	995.9	1095	1115.1	1906.8
DVU2771	conserved hypothetical protein (TIGR) CDS		966	847.6	920.8	816.2	783.2	739.7	797.7
DVU2772	conserved hypothetical protein (TIGR) CDS		1,323	77.8	69.4	71.2	79.2	87.8	47.7
DVU2773	membrane protein, putative (TIGR) CDS		867	76.4	72.4	68	55.4	64.5	54.3
DVU2774	CBS domain protein/ACT domain protein (TIGR) CDS		684	534.5	505.4	418.2	209.7	212	271.3
DVU2775	hypothetical protein (TIGR) CDS		276	36	45.9	35.8	663	711.8	895.2
DVU2776	dsrC CDS	dsrC	318	6092	6579.6	5626.1	2382.4	2298.5	3683
DVU2777	hypothetical protein (TIGR) CDS		267	61.6	49.4	49.2	112.8	128.9	164.6
DVU2778	hypothetical protein (TIGR) CDS		273	245	248.3	237.5	203	232.4	249.9
DVU2779	extracellular solute-binding protein, putative (TIGR) CDS		1,386	156.2	136.2	133.3	231.6	234.2	148.4
DVU2780	membrane protein, putative (TIGR) CDS		876	104.2	101.6	89.4	87.4	91.6	70.2
DVU2781	hypothetical protein (TIGR) CDS		567	190.4	179.3	161.4	264	260.2	286.3
DVU2783	membrane protein, putative (TIGR) CDS		801	995.5	780.9	852	924.3	807.4	866.9
DVU2784	lldD CDS	lldD	1,026	511.8	498	469.3	616.6	597.4	696.4
DVU2785	pdhR CDS	pdhR	714	311.9	305.7	305.7	538.6	491.5	927.7
DVU2786	hypothetical protein (TIGR) CDS		99	150.5	155	146.6	126.5	101.4	200.9
DVU2787	conserved domain protein (TIGR) CDS		459	242.3	208.4	205.2	321.3	315.9	253.3
DVU2788	smtB CDS	smtB	363	332.4	332	336.8	177.6	182.9	178

DVU2789	Gpr1/Fun34/YaaH family protein (TIGR) CDS		552	130.1	110.3	117.6	63.8	61.2	44.9
DVU2790	hypothetical protein (TIGR) CDS		141	10.6	18.8	20.6	12.2	7.6	14.7
DVU2791	dhcA CDS	dhcA	780	399.7	340.8	247.9	460.3	461.3	696.4
DVU2792	NADH:quinone oxidoreductase subunit RnfC (Shelley Havemar		1,206	398.8	318.9	248.4	620	583.9	605.6
DVU2793	electron transport complex protein RnfD, putative (TIGR) CDS		957	297.5	251.2	196.7	298.4	278.7	330.2
DVU2794	NADH:quinone oxidoreductase subunit RnfG (Shelley Havemar		576	379	330	247.4	374.5	334.2	346.8
DVU2795	nqr4 CDS	nqr4	672	321	289	226.6	328	324.5	279.2
DVU2796	b1627 CDS	b1627	576	336.4	281.7	227.9	268.9	225.3	250.3
DVU2797	NADH:quinone oxidoreductase subunit RnfB (Shelley Havemar		888	345.7	317.9	249	376.2	345.3	353
DVU2798	ApbE family protein (TIGR) CDS		1,011	270.3	264.4	205.9	345.9	322	357.1
DVU2799	transcriptional regulator, MarR family (TIGR) CDS		417	358.1	240.8	252.4	153.2	132.5	140.6
DVU2800	heavy metal translocating P-type ATPase (TIGR) CDS		1,902	37.8	29.9	34.5	17.5	18.2	14
DVU2802	transcriptional regulator, GntR family (TIGR) CDS		696	298.5	972.5	1055.3	481.4	581.6	408.5
DVU2803	membrane protein, putative (TIGR) CDS		1,410	666.5	2835.8	3461.7	303.4	301.6	273
DVU2804	metallo-beta-lactamase family protein (TIGR) CDS		1,158	813.6	3312	3969.9	410.1	413.1	347.2
DVU2805	cobalamin synthesis protein/P47K family (TIGR) CDS		1,947	201.8	842.2	1061.6	197.9	226.3	163.7
DVU2806	MotA/TolQ/ExbB proton channel family protein (TIGR) CDS		750	202.7	794.9	1025.5	220.7	218.1	148.1
DVU2807	biopolymer transport protein, ExbD/TolR family (TIGR) CDS		411	118.6	555.3	682.6	125.9	138.5	91.2
DVU2808	TonB domain protein (TIGR) CDS		510	104.8	495.3	626.6	55.3	65.3	26.4
DVU2809	cytochrome c3 (TIGR) CDS		435	34.3	81.9	115.3	35.3	41.8	35.6
DVU2810	formate dehydrogenase formation protein FdhE, putative (TIG		948	12.9	32.1	44.6	28.2	27.5	18
DVU2811	formate dehydrogenase, beta subunit, putative (TIGR) CDS		660	11.8	14.2	15.6	19.3	18.6	14.9
DVU2812	fdnG-3 CDS	fdnG-3	3,039	16.1	15	13.6	27.8	24.4	17.8
DVU2815	outer membrane efflux protein (TIGR) CDS		1,611	33.2	25.9	26.7	16.8	18.3	16
DVU2816	multidrug resistance protein (TIGR) CDS		3,213	25.4	23.5	22.3	16	16.8	18.9
DVU2817	acrA CDS	acrA	1,254	25.9	26.7	24.5	26.4	28.6	15.6
DVU2818	hypothetical protein (TIGR) CDS		219	36.2	36.8	28.2	16.4	19.3	21.3
DVU2819	transcriptional regulator, TetR family (TIGR) CDS		609	57.7	63.2	52.9	55.8	53.7	49.3
DVU2820	amidohydrolase family protein (TIGR) CDS		837	46.8	40	43.7	62.5	64.1	54.4
DVU2821	hypothetical protein (TIGR) CDS		222	28.4	27.7	31.4	49.3	38.9	25.6
DVU2822	TRAP dicarboxylate family transporter (TIGR) CDS		1,011	66.1	58.8	55.6	65	67.6	50.1
DVU2823	dctM CDS	dctM	1,776	32.6	34.2	27.6	57.4	58	36.7
DVU2824	formate acetyltransferase (TIGR) CDS		2,487	62.6	63.3	47.1	58	56.6	57.6
DVU2825	pyruvate formate-lyase 1 activating enzyme, putative (TIGR) C		924	42.3	34.6	35.1	66.2	71.5	61.6
DVU2827	sigma-54 dependent transcriptional regulator (TIGR) CDS		1,422	119.4	121	114.6	46.6	45.4	58.9
DVU2828	site-specific recombinase, phage integrase family (TIGR) CDS		1,185	142.5	151.5	121.6	140.7	145.5	142.2
DVU2829	hypothetical protein (TIGR) CDS		243	101.5	110.9	98.2	181.7	167.4	125.5
DVU2830	hypothetical protein (TIGR) CDS		366	45.2	59.7	66	34.5	23.3	31
DVU2831	hypothetical protein (TIGR) CDS		195	8.6	7.6	12.7	15	13.5	7.9
DVU2832	transcriptional regulator cII, putative (TIGR) CDS		462	10.5	16	9.9	12.5	16.2	14.6
DVU2833	hypothetical protein (TIGR) CDS		330	53.9	82.2	63.1	49.4	48.6	50.1
DVU2835	transcriptional regulator, putative (TIGR) CDS		273	41	53.7	48.2	73.3	69.3	53
DVU2836	hypothetical protein (TIGR) CDS		447	451.5	515.9	448.2	231.2	251	256.7
DVU2837	conserved hypothetical protein (TIGR) CDS		1,074	312.9	355.2	310.4	278.1	282.3	290.6
DVU2838	conserved hypothetical protein (TIGR) CDS		1,338	275.2	298.5	260.9	129.9	132	211.3
DVU2839	conserved hypothetical protein (TIGR) CDS		525	707.6	735.7	638.4	462.7	455.7	554.3
DVU2840	conserved hypothetical protein (TIGR) CDS		702	109.6	106.7	95.2	22.1	19.7	24
DVU2841	type II restriction endonuclease, putative (TIGR) CDS		1,200	124.2	116.7	105.1	95.8	96	91.6
DVU2842	dcm CDS	dcm	1,077	153.1	164.7	157	93.4	93.9	86.4
DVU2843	vsr CDS	vsr	411	108.9	124.9	112.8	115.3	118.6	89.9
DVU2844	hypothetical protein (TIGR) CDS		864	87	93.6	88.7	93.4	104.6	110.9
DVU2845	hit CDS	hit	429	81.5	100.5	86.9	78.9	95	73.4
DVU2846	hypothetical protein (TIGR) CDS		174	70.3	97.3	74.5	36.5	53.6	26.8
DVU2847	hypothetical protein (TIGR) CDS		330	22.8	81.5	80.9	119.5	121.3	93.2
DVU2848	tail fiber assembly protein, putative (TIGR) CDS		540	11.5	27.7	28.5	67.7	57.7	56.5
DVU2849	stfE CDS	stfE	816	16.4	22	26.7	28.7	21.7	11.7
DVU2850	tail protein, putative (TIGR) CDS		627	0.1	16.9	14.3	12.4	13.3	7.8
DVU2851	tail protein, putative (TIGR) CDS		1,062	0.3	9.8	7.4	22.1	14.6	8.5
DVU2852	tail protein, putative (TIGR) CDS		477	0.5	7.9	7.4	26.6	13.9	3.2
DVU2853	phage baseplate assembly protein V, putative (TIGR) CDS		639	0.4	20.2	13.6	26.1	15.6	13.8
DVU2854	tail protein, putative (TIGR) CDS		1,134	0	15.3	10.7	21.3	14.4	5.5
DVU2855	tail/DNA circulation protein, putative (TIGR) CDS		1,200	0.1	13.9	12.3	19.6	13	9.5
DVU2856	conserved domain protein (TIGR) CDS		1,491	2.4	22.6	15.4	21.6	15.4	10.7
DVU2857	conserved hypothetical protein (TIGR) CDS		261	0	21.9	24.2	24.9	13.9	4
DVU2858	tail tube protein, putative (TIGR) CDS		366	0	69.3	50.5	39.6	22.1	24
DVU2859	tail sheath protein, putative (TIGR) CDS		1,464	0.1	49.1	42.1	31.1	20.5	19.9
DVU2860	conserved hypothetical protein (TIGR) CDS		192	0	115.2	100.4	33.3	10.3	16.1

DVU2861	hypothetical protein (TIGR) CDS		558	0.2	39.9	33.7	28.2	16.4	14.4
DVU2862	hypothetical protein (TIGR) CDS		327	0	88.3	65.6	19.3	9.8	23.8
DVU2863	hypothetical protein (TIGR) CDS		594	0	91.4	72.4	33.7	19.7	22.2
DVU2864	hypothetical protein (TIGR) CDS		144	0	32.5	25.7	35.7	17.8	12.6
DVU2865	lipoprotein, putative (TIGR) CDS		411	0.7	32.1	15.1	38.9	21.8	15.1
DVU2866	conserved hypothetical protein (TIGR) CDS		549	0.5	32.6	25.9	38.5	27.3	13.2
DVU2867	holin (TIGR) CDS		489	0.4	76.6	56.2	45.6	24.4	20.1
DVU2868	hypothetical protein (TIGR) CDS		348	4.3	31.2	20.4	40.6	23.3	26.8
DVU2869	major head protein (TIGR) CDS		1,005	0	163	131.4	43.7	28.7	46.6
DVU2870	conserved hypothetical protein (TIGR) CDS		384	0	163.7	138.8	57.3	28.3	18.9
DVU2871	minor capsid protein C (TIGR) CDS		1,320	0.3	55	46	51.7	29.1	32.3
DVU2872	phage portal protein, lambda family (TIGR) CDS		1,701	1.3	15.9	11.7	38.9	18.8	14.9
DVU2873	hypothetical protein (TIGR) CDS		276	8	18	14.4	33.6	19.4	35.6
DVU2874	hypothetical protein (TIGR) CDS		429	13.6	14.7	13.9	9.2	14.6	14.5
DVU2875	DNA-binding domain, excisionase family (TIGR) CDS		219	13.3	13.4	13.2	4.1	6.8	0
DVU2876	terminase, large subunit, putative (TIGR) CDS		1,887	4.3	9.3	9.5	12.2	11.6	13.1
DVU2877	hypothetical protein (TIGR) CDS		723	1.8	9	8.4	12.9	11.5	12.9
DVU2878	adenine specific DNA methyltransferase, putative (TIGR) CDS		1,359	0.1	9.5	5.3	7.8	6.8	3.9
DVU2879	conserved hypothetical protein (TIGR) CDS		1,557	8.4	33.3	31.3	20.9	22.2	20.9
DVU2880	hypothetical protein (TIGR) CDS		129	1.3	6.9	4.8	8.4	6.2	0
DVU2881	phage/plasmid primase, P4 family (TIGR) CDS		1,686	0.3	14.1	10.7	10.5	10.2	7.4
DVU2882	folC CDS	folC	1,497	31.8	32.8	30.4	125.2	121.8	116
DVU2883	selA CDS	selA	1,410	180	181.9	180.8	136.9	135	118.8
DVU2884	peptidase, M18 family (TIGR) CDS		1,404	244.9	239.3	222.5	122.6	124.5	121.2
DVU2885	dhaT CDS	dhaT	1,194	108.1	105.2	105.7	65.3	66	58.9
DVU2886	transcriptional regulator, AraC family (TIGR) CDS		840	57.1	55.9	43.8	56.9	58.9	51.7
DVU2887	membrane protein, putative (TIGR) CDS		969	83.5	72.3	74.5	54.3	58.3	35.7
DVU2888	cobalt ABC transporter, ATP-binding protein, putative (TIGR) C		828	67.3	63.7	63.5	79.5	83.1	57.4
DVU2889	BioY family protein (TIGR) CDS		549	77.4	70.4	65.2	67.4	67.4	60.2
DVU2891	nikR CDS	nikR	420	361.5	418.3	336.3	113.1	116	183.3
DVU2892	conserved hypothetical protein (TIGR) CDS		801	295.4	330.4	281.4	145.1	148.5	112.6
DVU2893	flgG CDS	flgG	378	374	361.4	358.2	925.4	972.1	1175.2
DVU2894	flrA CDS	flrA	1,050	337.2	325.1	302.1	394.1	399.4	415.4
DVU2895	hypothetical protein (TIGR) CDS		303	295.3	297.4	250.3	175.2	185.6	169.7
DVU2896	TPR domain protein (TIGR) CDS		3,231	129	148.2	121.1	285.2	262.1	267.5
DVU2897	conserved hypothetical protein (TIGR) CDS		990	149.5	175	150.7	227.8	232.9	227.1
DVU2898	conserved hypothetical protein (TIGR) CDS		1,002	168.4	187.7	172.3	192.1	180.4	175.8
DVU2899	hypothetical protein (TIGR) CDS		861	67.4	69	70.2	52.1	52.2	49.3
DVU2900	amidohydrolase family protein (TIGR) CDS		1,200	181.8	204.5	199.3	156.4	163	166.9
DVU2901	pyrB CDS	pyrB	954	186.5	220.3	188.1	180.1	174.5	130.5
DVU2902	pyrC CDS	pyrC	1,269	238.2	264.7	235.4	247.3	266.7	180.2
DVU2903	pcnB2 CDS	pcnB2	1,329	647.3	659.7	626.8	789.8	780.1	1097.1
DVU2904	radical SAM enzyme, Cfr family (TIGR) CDS		1,095	118.8	123.5	114.1	116.2	124.3	103.9
DVU2905	alcohol dehydrogenase, iron-containing (TIGR) CDS		1,179	56.4	54.6	47.3	73.4	74	59.6
DVU2906	umuC CDS	umuC	1,404	25	26.9	24.7	48	47.9	47.1
DVU2907	umuD CDS	umuD	495	29.5	26	28.1	32	40	37.6
DVU2908	hypothetical protein (TIGR) CDS		753	62.1	61.8	63.6	215	208.5	190.1
DVU2909	transcriptional regulator, MarR family (TIGR) CDS		414	90.4	103.8	99.8	124.2	152.4	93
DVU2910	membrane protein, putative (TIGR) CDS		606	112.6	128.3	121	99	96.2	51.6
DVU2911	hemolysin A (TIGR) CDS		762	77.2	76.3	74.8	69.9	68.1	44.1
DVU2912	rpmE CDS	rpmE	216	1532.9	1689.8	1384.7	599.7	536.6	866.2
DVU2913	lipoprotein, putative (TIGR) CDS		1,008	443.4	499.6	450.2	614.5	570.3	827
DVU2914	prfA CDS	prfA	1,074	394	417	418.7	344.5	355.6	387.4
DVU2915	hypothetical protein (TIGR) CDS		165	34.9	28	33.7	37.7	41.6	31.4
DVU2916	hemK CDS	hemK	888	39.1	53.7	44.6	32.1	32.7	34.9
DVU2917	lpxC CDS	lpxC	927	389.2	328.3	280.7	1295.3	1121.9	1616.9
DVU2918	hypothetical protein (TIGR) CDS		237	53.9	40.6	45	102.7	123.9	119.9
DVU2920	tuf CDS	tuf	1,194	4239.9	4939	4274	2408.8	2209.6	4103.9
DVU2921	rpmG CDS	rpmG	150	4834.8	5515.7	4668.7	2181.6	2063.7	3295.8
DVU2922	secE CDS	secE	252	2648.2	2943.1	2633	2900.8	2639.3	3427.2
DVU2923	nusG CDS	nusG	552	2190.1	2392.3	2172.4	1152	1092.9	1275.3
DVU2924	rplK CDS	rplK	423	2391.8	2693.7	2336.7	1872.9	1827.1	2503.6
DVU2925	rplA CDS	rplA	708	2061	2416.3	1992.8	825.9	818.2	1160
DVU2926	rplJ CDS	rplJ	522	3113.7	3459.4	3001.7	1393.2	1328.3	1912
DVU2927	rplL CDS	rplL	384	3519.5	4011.4	3378.6	628.8	626.3	822.3
DVU2928	rpoB CDS	rpoB	4,119	693.6	820.7	710.1	599.7	572.1	658.7
DVU2929	rpoC CDS	rpoC	4,158	783.4	812.8	713.3	679.9	647.1	754.6

DVU2930	hypothetical protein (TIGR) CDS		441	185.9	197.9	191.9	344.8	301.9	295.3
DVU2931	sensory box histidine kinase (TIGR) CDS		2,202	127.7	128.1	111.1	182.1	190.4	133.1
DVU2932	conserved hypothetical protein TIGR01777 (TIGR) CDS		927	188.7	226.1	200.9	239.1	246.2	222.7
DVU2933	response regulator/sensory box/HDIG domain protein (TIGR) (		1,377	132.2	151.2	138.2	170.8	180.2	158
DVU2934	ntrX CDS	ntrX	1,419	135.5	141.6	136.2	146.5	149	99.6
DVU2935	gpm CDS	gpm	753	235.3	243	210.4	286.7	264.1	369.3
DVU2937	TPR domain protein/response regulator receiver domain prote		1,356	173.6	195.6	157.5	209.9	228.7	254.2
DVU2938	conserved hypothetical protein (TIGR) CDS		1,173	358.1	357.9	320.3	494.5	493.9	588.5
DVU2939	conserved hypothetical protein (TIGR) CDS		888	34.5	24.7	25.2	31.6	33.7	25.3
DVU2941	conserved hypothetical protein (TIGR) CDS		300	702.3	862.8	756.7	962	1020.3	1214.6
DVU2942	purB CDS	purB	1,293	336.7	375.1	344.2	197.5	201.2	178.9
DVU2943	pyrE CDS	pyrE	561	416.7	434.1	388.1	641.9	642.7	868.3
DVU2944	ErfK/YbiS/YcfS/YnhG family protein (TIGR) CDS		1,290	270.7	321.4	302.5	309.9	330.3	262.2
DVU2945	conserved domain protein (TIGR) CDS		858	153.5	179.4	173	396.7	407.3	366.6
DVU2946	hypothetical protein (TIGR) CDS		243	428.9	422.7	387.7	149.4	171.3	95.7
DVU2947	anaerobic ribonucleoside-triphosphate reductase, putative (TI		2,070	726.7	735.2	662.5	287.8	294.1	349.6
DVU2948	bacterial flagellin N-terminal domain protein (TIGR) CDS		849	78.4	101.3	89.8	108.5	121	98.7
DVU2949	membrane protein, putative (TIGR) CDS		354	69.4	73.1	72.6	83.8	76.9	99.3
DVU2951	glnS CDS	glnS	1,713	232.3	255.3	228.1	306.6	321.1	301.4
DVU2952	membrane protein, putative (TIGR) CDS		1,038	81.5	59.5	59.3	67.9	68.9	56.3
DVU2953	transcriptional regulator, GntR family (TIGR) CDS		1,563	21.8	24.1	21.7	37.6	45.4	34.1
DVU2954	GGDEF domain protein (TIGR) CDS		1,680	23	23.2	26.8	39.1	35.4	33.9
DVU2956	flrA CDS	flrA	1,038	116.7	113.8	115.4	45.1	57.5	30.8
DVU2957	hypothetical protein (TIGR) CDS		141	348.5	488.1	411.7	398.9	388	515
DVU2958	membrane protein, putative (TIGR) CDS		999	454.4	644.3	589.4	588.5	525.8	416.7
DVU2959	conserved hypothetical protein (TIGR) CDS		417	766.6	1060.6	988.5	374.9	398.4	319.8
DVU2960	ntrC CDS	ntrC	1,425	207.1	290.4	275.9	555.6	543.4	428.7
DVU2961	hypothetical protein (TIGR) CDS		348	151.8	158.4	190.3	245.4	242.2	215.3
DVU2962	sensor histidine kinase (TIGR) CDS		1,734	133.4	190.1	186.5	212.2	210.4	177.8
DVU2963	response regulator (TIGR) CDS		387	243.9	335.5	329.9	207	214.5	154.3
DVU2964	hypothetical protein (TIGR) CDS		660	187.6	253.4	273.3	206.6	219.2	138.7
DVU2965	hypothetical protein (TIGR) CDS		300	921.9	1059.2	1026.4	794.4	774.5	515.1
DVU2966	response regulator (TIGR) CDS		456	811.8	1018.6	968	921.4	925.8	817.8
DVU2967	sensor histidine kinase/response regulator (TIGR) CDS		1,125	364.8	444.5	445.4	437.5	398	299.3
DVU2968	sensor histidine kinase/response regulator (TIGR) CDS		1,197	151.7	136.3	131.6	410.1	388.6	402.8
DVU2969	acetoacetyl-CoA synthase (TIGR) CDS		1,986	35.3	36.4	33.4	155.3	148.3	138.2
DVU2970	acetyltransferase, GNAT family (TIGR) CDS		2,697	121.8	119.8	106	189.8	189.4	163.4
DVU2971	glycosyl transferase, family 8 (TIGR) CDS		912	146.9	159.6	158.3	163.8	172.3	160.4
DVU2972	chemotaxis protein CheD, putative (TIGR) CDS		600	232.7	257.2	218.2	499.5	471.1	556.5
DVU2973	hup CDS	hup	276	676.6	657.4	554.3	542.5	553.8	696.6
DVU2974	hypothetical protein (TIGR) CDS		180	74.7	89.3	59.8	121.7	147.4	86.2
DVU2975	hydrolase, putative (TIGR) CDS		1,041	97.7	106.7	88.5	369.4	357.7	438.9
DVU2976	conserved hypothetical protein (TIGR) CDS		1,113	130.6	121.5	118	224.9	216.7	212.2
DVU2978	hydrolase, haloacid dehalogenase-like family (TIGR) CDS		633	111.2	130	95.2	150.4	146.5	182.9
DVU2979	phosphatidylserine decarboxylase-related protein (TIGR) CDS		654	555.9	605.9	553.5	816.2	771	1263.7
DVU2980	pssA CDS	pssA	750	902.6	1038.5	950.6	1447.6	1325.2	2081.1
DVU2981	leuA CDS	leuA	1,530	65.9	79.3	68.9	746.1	682.6	815.5
DVU2982	leuC CDS	leuC	1,260	66	65.2	59	720.8	685.7	660.7
DVU2983	leuD CDS	leuD	504	67.4	59.6	70	668.2	620.9	549.2
DVU2984	conserved hypothetical protein (TIGR) CDS		1,008	58.7	64.1	62.7	605.2	562.3	520.4
DVU2985	leuB CDS	leuB	1,074	91.6	89.4	85.8	582.8	565.8	499.5
DVU2986	pspC CDS	pspC	423	281.5	277.9	240.3	872.6	1007.1	975.1
DVU2987	hypothetical protein (TIGR) CDS		300	162.3	159.7	144.1	754.4	869.7	730.5
DVU2988	pspA CDS	pspA	666	209.1	192.8	188.3	830.1	934.9	919.6
DVU2989	pspF CDS	pspF	1,146	39.2	46.1	39.1	19.3	17.4	17.2
DVU2990	moeA CDS	moeA	1,953	187.4	190.4	177.9	212.1	218.8	231.1
DVU2992	glycosyl transferase, group 2 family protein (TIGR) CDS		1,617	46.9	51.2	41.1	79.9	70.8	97.5
DVU2993	glycosyl transferase, group 1/2 family protein (TIGR) CDS		2,664	50.4	55.5	50.4	81.8	82.8	82.3
DVU2994	glycosyl transferase, group 2 family protein (TIGR) CDS		1,029	39.1	35.9	32.9	87.6	91.5	99.5
DVU2995	glycosyl transferase, group 1 family protein (TIGR) CDS		1,164	98.6	89	87.4	116.7	127.5	87.9
DVU2996	NAD-dependent epimerase/dehydratase family protein (TIGR)		924	75	72.9	75.4	87.7	98.7	64.1
DVU2997	hypothetical protein (TIGR) CDS		777	106.4	99.8	97	173.4	174.6	151.7
DVU2998	hypothetical protein (TIGR) CDS		1,335	127	107.6	114.7	160.6	166	132
DVU2999	methionyl-tRNA formyltransferase, putative (TIGR) CDS		828	59.5	52	53	75.2	75.5	58.3
DVU3000	hypothetical protein (TIGR) CDS		1,191	50.4	48	45.4	82.1	87.8	83.5
DVU3001	conserved domain protein (TIGR) CDS		798	100.8	96	99.4	143.5	156.5	143.1
DVU3002	conserved domain protein (TIGR) CDS		1,149	139.7	126.8	135	209.8	214.5	248

DVU3003	radical SAM domain protein (TIGR) CDS		1,113	127.4	132.4	117.2	266.7	235.2	293.5
DVU3005	rfbE CDS	rfbE	1,035	142.4	146.5	136.2	219.7	213	231.5
DVU3006	spsF CDS	spsF	1,362	76.6	83.4	75.9	200.7	215	210.9
DVU3007	hypothetical protein (TIGR) CDS		1,224	61.3	64	57.7	133.2	134.9	127.1
DVU3008	NeuB family protein (TIGR) CDS		1,077	68	77.3	61	140.1	143.4	189.3
DVU3009	radical SAM domain protein (TIGR) CDS		984	98.7	92.7	93.8	129.1	134	135.7
DVU3010	lpsC CDS	lpsC	1,179	90.5	99.7	93	134.1	136.1	115.3
DVU3011	conserved hypothetical protein (TIGR) CDS		795	70.1	68.8	68.5	126.3	128.5	96.3
DVU3012	membrane protein, putative (TIGR) CDS		1,800	56.4	59.9	55.9	117.9	115.2	101.7
DVU3013	dmt CDS	dmt	1,707	85.6	91.1	80.3	243.2	226	291.5
DVU3014	asparagine synthetase, glutamine-hydrolyzing (TIGR) CDS		2,094	84.2	86.4	79.3	106.3	109.1	108.9
DVU3015	conserved domain protein (TIGR) CDS		567	93.1	89.7	89	181.3	171	170.9
DVU3016	B12 binding domain protein/radical SAM domain protein (TIGF		1,446	69.6	79.6	66.8	108.5	105	117.8
DVU3018	radical SAM domain protein (TIGR) CDS		1,134	94.6	93.8	87.8	216.3	216.7	207.8
DVU3019	radical SAM/B12 binding domain protein (TIGR) CDS		1,458	183.1	170.1	158.7	408.9	399.1	482.6
DVU3020	hypothetical protein (TIGR) CDS		369	260.4	236.5	215.3	488	499.7	611.4
DVU3021	HDIG domain protein (TIGR) CDS		1,371	105.5	104.6	109.2	141.3	138.1	123.7
DVU3022	sensory box histidine kinase/response regulator (TIGR) CDS		3,420	157	162.2	151.2	276.5	266.3	331.7
DVU3023	atoC CDS	atoC	1,425	238.4	236.7	230.4	173.6	178.3	154.7
DVU3024	hypothetical protein (TIGR) CDS		168	1547.3	1619.7	1430	384.4	361.8	666.1
DVU3025	por CDS	por	3,648	2664.7	2827.1	2436.3	788.4	755.5	1221.2
DVU3026	L-lactate permease family protein (TIGR) CDS		1,713	517.8	566.4	480.5	539.3	495.2	817.3
DVU3027	glcD CDS	glcD	1,386	1287.3	1282.4	1092.3	526.7	503.3	750.9
DVU3028	iron-sulfur cluster-binding protein (TIGR) CDS		1,269	1067.7	1014.7	888.6	555.2	538.6	695.5
DVU3029	pta CDS	pta	2,115	884.8	937.4	814.7	607.1	611.3	868.5
DVU3030	ackA CDS	ackA	1,209	1374.1	1454	1301	321.9	320.6	485.6
DVU3031	conserved hypothetical protein (TIGR) CDS		1,092	617.7	628	570.2	420.9	442.4	582.1
DVU3032	conserved hypothetical protein (TIGR) CDS		630	1114.4	1077.8	945.9	229.3	216	252.3
DVU3033	iron-sulfur cluster-binding protein (TIGR) CDS		2,154	1105.2	1095.5	978.6	246.7	259.8	280.6
DVU3035	methyl-accepting chemotaxis protein, putative (TIGR) CDS		1,812	154.6	135.8	129.3	99	103.4	107
DVU3036	conserved hypothetical protein (TIGR) CDS		993	114.5	109.5	99	287.6	284.1	233.1
DVU3037	rhodanese-like domain protein (TIGR) CDS		873	142.8	160.3	136.1	145.5	164.8	164.6
DVU3039	conserved hypothetical protein (TIGR) CDS		726	115.5	103.1	113	179.2	166.2	159.5
DVU3041	cytochrome c553 (TIGR) CDS		282	129.4	141.5	130	263.4	263.8	262.1
DVU3042	lipoprotein, putative (TIGR) CDS		237	198	233.5	204.9	112.6	107.5	117.7
DVU3043	hypothetical protein (TIGR) CDS		1,032	57.1	61.5	57.8	101.1	92.6	105.2
DVU3045	fexB CDS	fexB	2,868	160.7	183.9	161.8	287.3	290.8	348.1
DVU3046	glycosyl transferase, group 1 family protein (TIGR) CDS		1,107	154.5	145.9	140.5	161.3	167	138.2
DVU3047	aminotransferase, class IV (TIGR) CDS		948	218	213.5	193.5	244	245.8	224.1
DVU3048	asd CDS	asd	1,050	638.9	623	562.2	278.6	278.9	334.5
DVU3049	hemerythrin family protein (TIGR) CDS		414	764.3	748.5	677.3	401.5	443.6	396.4
DVU3050	membrane protein, putative (TIGR) CDS		435	88.7	111	110.1	73.7	81.3	41.6
DVU3051	mutT CDS	mutT	390	166.1	189.2	167	120.6	108.2	44.4
DVU3052	ABC transporter, ATP-binding protein (TIGR) CDS		1,980	192.5	211.9	202.5	120.3	143.8	87.8
DVU3053	conserved hypothetical protein (TIGR) CDS		894	326.7	338.7	320.3	293.7	291.8	216.8
DVU3054	radical SAM domain protein (TIGR) CDS		1,095	441.6	477	464.3	543.2	551.3	549.9
DVU3055	rne CDS	rne	1,470	349.8	410.9	395.3	205.5	220	192.8
DVU3056	conserved hypothetical protein (TIGR) CDS		654	302.7	348.7	358.3	292.7	300.6	222.5
DVU3057	oxygen-independent coproporphyrinogen III oxidase, putative		1,494	63.6	74.4	71	77.7	85.4	73.9
DVU3058	sensory box histidine kinase/response regulator (TIGR) CDS		3,672	40.4	44.1	39.3	50.6	53.4	37
DVU3059	ftsY CDS	ftsY	1,467	256.8	271.6	263.2	283.6	294	308.7
DVU3061	sensory box histidine kinase (TIGR) CDS		2,295	122.9	113.8	104.4	291.9	279.7	270.7
DVU3062	sensor histidine kinase/response regulator (TIGR) CDS		3,243	61.9	58.3	57.8	124.4	136	98.1
DVU3063	mviN-2 CDS	mviN-2	1,689	57.7	53.9	54.6	92.7	91.6	56.9
DVU3064	sensory box/GGDEF domain/EAL domain protein (TIGR) CDS		1,731	112.3	124.2	116.4	193.1	199.4	199.5
DVU3065	AMP-binding enzyme family protein (TIGR) CDS		1,653	386.7	368	342.3	286.2	302.7	314.1
DVU3066	DNA-binding protein (TIGR) CDS		570	517.4	543.5	479.3	241.1	252.7	255.2
DVU3068	GAF domain/sensory box/EAL domain protein (TIGR) CDS		2,484	97.9	90.8	75.2	121.9	117.1	141.3
DVU3069	conserved hypothetical protein TIGR00247 (TIGR) CDS		1,323	175.5	184.1	177.5	137.9	137.7	148.2
DVU3070	conserved hypothetical protein (TIGR) CDS		429	212.6	211.8	212.4	155.3	190.1	218.7
DVU3071	oxidoreductase, FAD/iron-sulfur cluster-binding domain protei		3,564	411.2	428.6	408.1	392.6	404.1	565.4
DVU3072	ABC transporter, permease protein, putative (TIGR) CDS		1,935	43.3	40.6	39.3	60.6	65.9	36.4
DVU3073	conserved domain protein (TIGR) CDS		912	70.4	72.1	67.1	74.1	72	56.1
DVU3074	membrane protein, putative (TIGR) CDS		888	52.6	50.2	46.6	49.2	45.5	35.5
DVU3076	conserved hypothetical protein (TIGR) CDS		582	68	77.3	61.2	673.5	616.7	956.4
DVU3077	AhpC/TSA family protein (TIGR) CDS		762	60.5	72.6	61.8	380.5	355.4	411.7
DVU3079	glyoxalase family protein (TIGR) CDS		603	90.8	94.5	84.8	99.3	92.6	75.4

DVU3080	transcriptional regulator, putative (TIGR) CDS		399	918.8	951.5	793.6	406.6	390.4	540.1
DVU3081	membrane protein, putative (TIGR) CDS		903	84.8	92.8	94.5	253.1	244.5	170.5
DVU3082	methyl-accepting chemotaxis protein (TIGR) CDS		1,764	171.1	173.8	166	194.8	207.5	185.7
DVU3084	transcriptional regulator, putative (TIGR) CDS		387	947.2	980	981	618.6	590.1	918.8
DVU3085	hypothetical protein (TIGR) CDS		246	212.1	234	226.4	113.4	123	161.8
DVU3086	cobB-2 CDS	cobB-2	1,824	94.1	110.5	99.6	150.5	146.1	134.3
DVU3087	cobH CDS	cobH	642	149	124.2	139.1	86.7	94	76.5
DVU3088	deaD CDS	deaD	1,734	393.2	417.3	406	244.6	245.2	269.3
DVU3089	hypothetical protein (TIGR) CDS		507	299.6	340.5	351.7	183.6	187.3	209.5
DVU3090	outer membrane protein, OMPP1/FadL/TodX family (TIGR) CD		1,206	286.8	252.8	256.9	109.2	122.8	103.8
DVU3091	conserved hypothetical protein (TIGR) CDS		1,347	91.3	84.8	84.3	147.7	132.6	156.2
DVU3092	hypothetical protein (TIGR) CDS		648	96.6	82.5	92.4	33	45.5	45.4
DVU3093	rdl CDS	rdl	228	2244.1	2278.3	1962.9	1176.9	1280.5	1861.1
DVU3094	rbr CDS	rbr	576	2469.4	2645.1	2261.7	989.3	1055.3	1643.4
DVU3095	PerR CDS	PerR	387	1246.9	1185.4	1000.2	1318.3	1429.9	1771.5
DVU3097	outer membrane efflux protein (TIGR) CDS		1,320	196.4	183.3	184.3	332.8	326.1	339.5
DVU3098	hypothetical protein (TIGR) CDS		204	172.2	168.1	160.7	221.6	250.6	276.2
DVU3099	tolQ-2 CDS	tolQ-2	693	257.6	256.6	228.4	560.7	546.6	515
DVU3100	tolR CDS	tolR	420	323.2	355.1	304.5	283.4	304.9	377.8
DVU3101	tonB protein, putative (TIGR) CDS		1,026	571.5	571.5	562.3	523.8	529	503
DVU3102	hypothetical protein (TIGR) CDS		588	326.6	322.6	277.4	496.8	500	367.4
DVU3103	tolB protein, putative (TIGR) CDS		1,371	501.7	522.4	485.1	485.3	484.3	441.8
DVU3104	pal CDS	pal	504	3628.1	4039.8	3749	2420.5	2201.4	2968.8
DVU3107	cytochrome c family protein (TIGR) CDS		1,770	17.5	29	19.5	117.8	86.8	55.2
DVU3108	nhaC-2 CDS	nhaC-2	1,428	18.3	22.5	17.9	31.4	32.3	23.5
DVU3109	iron-sulfur cluster-binding protein (TIGR) CDS		201	6.8	9.7	6.1	7.6	11.4	5.1
DVU3110	L-aspartate oxidase, putative (TIGR) CDS		1,722	9.3	11.1	12.1	20.2	22.7	16.5
DVU3112	TPR domain protein (TIGR) CDS		804	491	565.8	503.1	953.8	859.4	1093.8
DVU3113	carA CDS	carA	1,128	498.1	560.5	518.7	412.2	419.3	430.8
DVU3114	kdsB CDS	kdsB	759	289.7	316.1	299.8	293.7	287.4	301
DVU3116	prfC CDS	prfC	1,590	186.5	204.8	206.9	101.7	105.1	107.9
DVU3117	hypothetical protein (TIGR) CDS		585	1043.6	1186.6	1074.6	1125.4	1021.5	1627.4
DVU3118	conserved hypothetical protein (TIGR) CDS		306	517.9	508.9	427.6	289	290.5	334.4
DVU3119	AMP-binding enzyme family protein (TIGR) CDS		1,695	118.3	123.6	115.5	146.6	141.6	118
DVU3121	aminotransferase, class V (TIGR) CDS		1,131	138.2	102.8	84.8	51.7	61.8	51.7
DVU3122	hypothetical protein (TIGR) CDS		108	17.1	13.7	24.5	2.5	4.4	19.2
DVU3123	HD domain protein (TIGR) CDS		696	15	21.2	19.7	23.5	26.1	26
DVU3125	lipoprotein, putative (TIGR) CDS		621	216.6	224.7	190.4	220	219.5	256.4
DVU3127	pqiB CDS	pqiB	1,632	62.4	84.6	77.9	86.7	87.5	74.7
DVU3128	lipoprotein, putative (TIGR) CDS		618	264.4	259.6	291.1	111.8	133.6	107.1
DVU3129	hypothetical protein (TIGR) CDS		168	78.5	91	89.3	44.6	45.7	18.4
DVU3130	hypothetical protein (TIGR) CDS		213	20.8	18.9	17.9	88.8	88.2	218.3
DVU3131	transcriptional regulator, putative (TIGR) CDS		948	21	22.5	21.8	292.8	297.6	340.7
DVU3132	glycerol-3-phosphate dehydrogenase, FAD-dependent (TIGR) (		1,641	20.8	31.2	26.3	237.2	249.8	224
DVU3133	glpF CDS	glpF	756	63	90.8	83.9	240.3	221.6	214.7
DVU3134	glpK CDS	glpK	1,494	66.5	115.5	99.5	205.7	207.4	156.7
DVU3135	mdaB CDS	mdaB	609	169.7	190.2	175.6	244.4	237.7	174.8
DVU3136	nitroreductase family protein (TIGR) CDS		657	146	148.8	142	179.2	178.9	192
DVU3137	fabG CDS	fabG	777	74.9	80.1	78.3	109.7	123.5	97.8
DVU3139	bacterial extracellular solute-binding protein, family 3 (TIGR) C		777	122.7	125	119.7	43.1	41	59.9
DVU3140	capsular polysaccharide transport protein, putative (TIGR) CDS		1,614	155.3	154.8	162.4	312.7	301.6	276.7
DVU3141	lipoprotein, putative (TIGR) CDS		381	223.1	255.4	245.7	476	422.4	508.7
DVU3142	sigma-54 dependent transcriptional regulator (TIGR) CDS		1,704	63.9	67.6	66.1	112.1	112.3	109.5
DVU3143	iron-sulfur cluster-binding protein (TIGR) CDS		1,590	20.8	20.4	17.8	44.3	33.5	34.3
DVU3144	cytochrome c family protein (TIGR) CDS		1,629	22	24.7	21.9	41.6	37	45.2
DVU3145	b1670 CDS	b1670	609	34.1	45.9	45.5	19	19	16.1
DVU3146	hypothetical protein (TIGR) CDS		774	209.1	214.3	201.3	711.4	675.1	729.8
DVU3147	6-phosphofructo-2-kinase/fructose-2,6- biphosphatase (TIGR)		1,263	74.2	74	66.3	67.1	68.7	52
DVU3148	malQ CDS	malQ	1,512	98.2	95.9	98	139.2	134.9	111.8
DVU3149	sppA CDS	sppA	891	308.5	348.9	337.7	661.2	648.7	781.6
DVU3150	rpsA CDS	rpsA	1,734	2262.4	2521.8	2320.6	1977.4	1826.7	3026.4
DVU3151	MiaB-like tRNA modifying enzyme YliG, TIGR01125 (TIGR) CDS		1,293	125.4	130.1	125.1	168.5	170.8	133.9
DVU3152	sensory box histidine kinase (TIGR) CDS		1,662	102	94.9	81.7	209.2	203.5	257.8
DVU3153	hypothetical protein (TIGR) CDS		120	79.3	94.3	64.7	112.7	91.7	148.5
DVU3154	HAM1 family protein (TIGR) CDS		624	91.7	87.8	71.2	88.5	80.1	87.4
DVU3155	dcrH CDS	dcrH	2,892	19.6	27.1	22.5	71.9	61.9	47.4
DVU3156	glmS CDS	glmS	1,824	317	347	300.8	308.3	313.3	310.3

DVU3157	conserved hypothetical protein (TIGR) CDS		1,443	100.4	106.5	99.5	114.6	124.2	94.9
DVU3158	vacJhomolog CDS	vacJhomolc	888	132.1	121.9	122.9	104.3	114.8	126.9
DVU3159	gpsA CDS	gpsA	993	120.7	116.5	111.6	89.5	99.7	67.2
DVU3161	ABC transporter, ATP-binding protein (TIGR) CDS		1,050	424.2	408.5	397.3	280.8	282.9	315
DVU3162	ABC transporter, periplasmic substrate-binding protein (TIGR)		1,296	829.7	817.4	688.1	240.3	217.3	210.5
DVU3163	ABC transporter, permease protein (TIGR) CDS		882	233.1	244.8	224.2	161.1	151	140
DVU3164	ABC transporter, permease protein (TIGR) CDS		834	249.6	277.7	263.6	138.8	137.9	117.1
DVU3165	conserved domain protein (TIGR) CDS		861	287.6	290	313.3	159.9	160.1	108.7
DVU3166	alanyl-tRNA synthetase family protein, putative (TIGR) CDS		657	134.8	158.5	158.8	71.6	79.3	69.3
DVU3167	heme biosynthesis protein, putative (TIGR) CDS		483	305.6	361.7	309.3	434.8	424.6	692.3
DVU3168	hemL CDS	hemL	1,272	442	440.1	410.2	297.6	300.1	297.4
DVU3169	cbiG CDS	cbiG	1,197	75.1	74.8	79	55.4	52.2	50.1
DVU3170	cobJ CDS	cobJ	855	73.6	77.5	70.1	52.7	64.4	32.6
DVU3171	cytochrome c3 (TIGR) CDS		390	2826.6	2927.1	2664.1	728.5	702	936.9
DVU3173	hypothetical protein (TIGR) CDS		177	657.4	687.8	650.3	539.5	517.9	602.9
DVU3174	ubiE CDS	ubiE	777	457.8	447.8	440.7	648.2	622.8	750.7
DVU3175	membrane protein, putative (TIGR) CDS		204	408.1	448.5	397	389.7	394.2	319.2
DVU3176	UDP-glucose/GDP-mannose dehydrogenase family protein (TI		1,323	354.5	366.2	361.3	463.3	458.8	556
DVU3177	hypothetical protein (TIGR) CDS		150	339.8	426	385.2	162.6	148.4	210.2
DVU3179	ispB CDS	ispB	966	199.9	236.6	206.4	206.9	197.1	196.9
DVU3180	GGDEF domain protein (TIGR) CDS		2,502	132.2	152.1	128.1	170.9	175.7	181.6
DVU3181	purL CDS	purL	2,982	308.1	321.8	280.2	265.1	271.8	228.7
DVU3182	dcrA CDS	dcrA	2,010	91.6	84.7	84.2	110	115.8	117.5
DVU3183	rbO CDS	rbO	381	2400.7	2785.6	2246.6	1995.3	1801.4	2633.8
DVU3184	rubredoxin (TIGR) CDS		159	2411.9	2726.1	2295.9	1862.2	1571.4	2878.4
DVU3185	roO CDS	roO	1,209	919	1054.2	878.5	564.5	555.3	668.2
DVU3186	hypothetical protein (TIGR) CDS		822	232.8	224.6	228.3	231.2	260	345.9
DVU3187	hup-4 CDS	hup-4	288	1329.6	1395.4	1204.3	1110.7	1076.1	1525.4
DVU3188	NLP/P60 family protein (TIGR) CDS		720	293.1	318.2	326.7	384.9	366.2	333.8
DVU3189	NOL1/NOP2/sun family protein (TIGR) CDS		1,296	58.3	67.3	68.3	65.3	70	47.5
DVU3190	hypothetical protein (TIGR) CDS		1,668	662.6	689.4	612.5	658.7	608.2	761.9
DVU3191	rluC CDS	rluC	1,173	152.6	167.5	155.1	131.2	131	132.6
DVU3192	glycosyl transferase, group 1 family protein (TIGR) CDS		1,161	128.4	128.6	127.7	128.4	134.3	86.4
DVU3194	engA CDS	engA	1,476	238.3	273.2	232.5	241.3	254.2	354.7
DVU3195	lipoprotein, putative (TIGR) CDS		1,389	87.5	94.6	89	251	243	211.9
DVU3197	ilvE CDS	ilvE	930	423.4	418.6	384.3	369.4	373.4	409.6
DVU3198	dnaZX CDS	dnaZX	1,851	354.8	360.5	333.4	202.6	222.1	237.7
DVU3199	conserved hypothetical protein TIGR00103 (TIGR) CDS		312	940.3	908.2	859.5	308	334	412.5
DVU3200	recR CDS	recR	606	766.5	768	731.5	424.2	416.9	406.4
DVU3201	hypothetical protein (TIGR) CDS		1,062	150.7	149.7	137.5	231.9	224.3	233.6
DVU3202	hydrolase, TatD family (TIGR) CDS		837	96.9	99.3	99.7	67.5	75.2	82.4
DVU3204	purA CDS	purA	1,281	721.9	766.1	731	942.8	889.5	1505
DVU3205	transglycosylase SLT domain protein (TIGR) CDS		1,446	165.4	205.9	207	109.4	111.8	83.7
DVU3207	RNB-like family protein (TIGR) CDS		2,097	260.1	290.7	267.8	271.1	269.7	307.7
DVU3208	membrane protein, putative (TIGR) CDS		984	285.1	288.2	268	209.4	199.9	193.3
DVU3212	nox CDS	nox	1,710	526.2	586.9	560.8	442.9	424.2	484.5
DVU3213	hypothetical protein (TIGR) CDS		285	122.2	111.1	113.3	296	296.3	319.2
DVU3214	phosphoenolpyruvate synthase-related protein (TIGR) CDS		2,655	133.4	116	114.1	139.2	137.8	119.4
DVU3215	drrA CDS	drrA	366	114.1	97.5	87.2	169.7	162.7	130.6
DVU3216	cckA CDS	cckA	1,698	130.5	119.5	114.5	176.1	167	174.6
DVU3217	hypothetical protein (TIGR) CDS		429	431.9	373.4	371	346.9	376.4	398.8
DVU3218	pncA CDS	pncA	621	176.5	171.8	165	118.5	133.5	76.6
DVU3219	hypothetical protein (TIGR) CDS		1,203	101.8	110.2	101.3	94.6	95.1	53.2
DVU3220	atoC CDS	atoC	1,380	238	245.2	230.1	402.9	425.8	366.9
DVU3221	sensor histidine kinase (TIGR) CDS		1,527	209.7	201.2	194.3	255.6	253.7	295
DVU3222	pgi CDS	pgi	1,344	214.3	217.9	206.4	415.5	398.5	456.5
DVU3223	aspB CDS	aspB	1,173	177.5	172.3	171.4	187.5	193.3	145.8
DVU3224	sfsA CDS	sfsA	729	123.2	133.3	120.1	155.9	175.9	159.2
DVU3225	hypothetical protein (TIGR) CDS		423	142.4	140.4	131.1	189.6	170.4	165.5
DVU3226	hypothetical protein (TIGR) CDS		330	229.7	262.2	224.4	253.4	287.6	339.9
DVU3227	flagellar basal body-associated protein, putative (TIGR) CDS		684	292.8	329.1	307.7	305.4	294.6	363.5
DVU3228	cheY-3 CDS	cheY-3	381	824.5	907	869.5	750.5	752.6	897.3
DVU3229	fliA CDS	fliA	798	311.5	317.5	286.3	569.3	538.1	652.8
DVU3230	flagellar synthesis regulator FleN (TIGR) CDS		828	274.1	258.9	237	466.9	482.5	494.1
DVU3231	flagellar biosynthesis protein FlhF, putative (TIGR) CDS		1,098	146	138.1	132.1	299.2	285.4	353.6
DVU3232	flhA CDS	flhA	2,112	67.4	73.6	65.6	171.4	169.1	176.7
DVU3233	flhB CDS	flhB	1,074	40.7	41.2	43.9	155.1	156.1	178.6

DVU3234	flagellar biosynthetic protein FliR (TIGR) CDS		792	72.3	72.8	62.4	211.8	199.1	192.5
DVU3235	purH CDS	purH	603	470.3	472.6	408.3	220.8	220.7	168
DVU3236	hflX CDS	hflX	1,644	123.3	126.3	117.9	82.8	82.8	72.6
DVU3238	response regulator (TIGR) CDS		405	206.8	212.7	205.4	240.5	258.1	244.4
DVU3239	PAP2 family protein (TIGR) CDS		666	167.1	173.1	159.3	88	101.4	61.7
DVU3241	conserved hypothetical protein (TIGR) CDS		747	56.4	54.3	56.3	33.9	39.6	25.6
DVU3242	rpoZ CDS	rpoZ	234	847.7	1068.4	946.6	750	705.7	890.1
DVU3243	dnaJ CDS	dnaJ	1,131	597.8	720.5	645.3	752.5	723.4	868.7
DVU3245	greA CDS	greA	492	607.1	664.3	598.2	532.6	540.6	534.7
DVU3246	RND efflux system, outer membrane protein, NodT family (TIG		1,626	18.4	28	21.9	63.6	58.4	43.2
DVU3247	efflux transporter, RND family, MFP subunit (TIGR) CDS		1,170	13.3	15.6	13.1	52.4	43.8	23
DVU3248	AcrB/AcrD/AcrF family protein (TIGR) CDS		3,144	13.2	16.5	14.4	37.2	34.6	21.3
DVU3249	lipoprotein, putative (TIGR) CDS		681	20.1	25.8	21.6	50.7	46.3	42.1
DVU3251	membrane protein, HPP family (TIGR) CDS		540	14.1	12.5	11.8	107.7	113	194.3
DVU3252	hypothetical protein (TIGR) CDS		252	9.5	14.3	9.1	23.5	22.6	22.6
DVU3253	phenylacetate-coenzyme A ligase, putative (TIGR) CDS		1,266	418.5	460.7	386.1	234.9	214.5	244
DVU3254	PDZ domain protein (TIGR) CDS		1,365	227	237.3	229.7	473.5	443.2	395.6
DVU3255	transcriptional regulator, CopG family (TIGR) CDS		399	191.4	217.3	194.5	152.9	146.9	119.8
DVU3256	mutM CDS	mutM	1,098	84.8	93.9	92.1	67.4	71.4	37.2
DVU3257	DNA internalization-related competence protein ComEC/Rec2		2,925	57.4	53.4	58.5	30.2	35	14.7
DVU3258	murA CDS	murA	1,254	190.9	193.3	187.6	203.6	221.1	183.9
DVU3259	xth CDS	xth	774	177.2	185.9	142.5	196	185.8	183.7
DVU3261	frdC CDS	frdC	651	161.2	138.3	136.2	228.2	220.4	194.5
DVU3262	fdrA CDS	fdrA	1,839	135.8	123.1	115.4	236.3	231.2	209.9
DVU3263	frdB CDS	frdB	744	135.4	140	120.1	226.9	223.1	223
DVU3264	tartrate dehydratase alpha subunit, putative (TIGR) CDS		840	136.6	137.2	124.8	193.1	206.7	190.7
DVU3265	tartrate dehydratase beta subunit, putative (TIGR) CDS		552	133.8	133.6	114.3	119.3	116.6	130.1
DVU3266	conserved hypothetical protein (TIGR) CDS		792	94.1	91.8	92.4	123.5	130.4	100.5
DVU3268	conserved hypothetical protein (TIGR) CDS		1,263	67	72.6	62.8	132.3	126.1	132.2
DVU3269	sensory box histidine kinase/response regulator (TIGR) CDS		2,520	75	67.3	63.3	134.2	133.3	133.5
DVU3270	cydB CDS	cydB	1,026	2570.4	2478.5	2058.7	1783.2	1619.6	2784
DVU3271	cydA CDS	cydA	1,302	2452.6	2460.1	1941.9	1553.3	1482	2125.1
DVU3272	TPR domain protein (TIGR) CDS		624	829	871.2	753.4	578.8	568.2	672.1
DVU3273	conserved hypothetical protein (TIGR) CDS		393	653.7	717.3	649.7	262.3	287.2	352.4
DVU3274	hypothetical protein (TIGR) CDS		669	550.6	602.6	553.1	429.6	397.4	382.4
DVU3275	hypothetical protein (TIGR) CDS		141	886.2	973.3	920.5	873.2	758.7	815.6
DVU3276	ferredoxin I (TIGR) CDS		189	6095.3	6713.7	5572.9	2571.5	2600.9	3265.2
DVU3277	hypothetical protein (TIGR) CDS		99	1234.4	1386.3	1145.2	812.1	840.5	1981.2
DVU3278	htrA CDS	htrA	1,557	133.5	142.9	136.6	153.1	161.1	134.9
DVU3279	cobT CDS	cobT	1,074	175.3	175.5	174	159.3	170.2	143.4
DVU3281	hypothetical protein (TIGR) CDS		501	295.5	308.5	287.9	215.4	216.3	235.2
DVU3282	ADP-ribosylglycohydrolase family protein (TIGR) CDS		900	263.6	261.3	256.5	370.6	363.8	465.1
DVU3283	hypothetical protein (TIGR) CDS		234	189.9	267	195	80.9	88.4	90.5
DVU3284	b2975 CDS	b2975	1,632	59.5	62.5	57.9	44.6	52.3	38
DVU3285	hypothetical protein (TIGR) CDS		177	37.7	76.2	50.3	25.5	41.5	32.1
DVU3289	hypothetical protein (TIGR) CDS		165	23.8	28.9	18.4	16.6	23.1	18.8
DVU3290	conserved domain protein (TIGR) CDS		1,056	23.2	27.8	25	13.9	19.6	7.1
DVU3291	glutamate synthase, iron-sulfur cluster-binding subunit, putati		1,635	27.9	30.1	26.1	24.2	30	12.2
DVU3292	pyridine nucleotide-disulfide oxidoreductase (TIGR) CDS		2,331	30.9	42.2	30.6	33.4	42.8	30.8
DVU3293	thiamine pyrophosphate-requiring enzyme (TIGR) CDS		1,644	146.2	142.8	114.5	302.2	283.6	397.4
DVU3294	areC CDS	areC	1,395	142.9	138.6	126	353.4	350.5	439.1
DVU3295	hemolysin III (TIGR) CDS		648	176.6	175.1	159.1	262.5	241.1	252.8
DVU3296	membrane protein, putative (TIGR) CDS		528	99.7	94.3	85.4	86.4	103.2	82.2
DVU3297	mtr CDS	mtr	1,260	87.9	89.2	78.7	77.8	80	68.1
DVU3298	hypothetical protein (TIGR) CDS		783	46.9	35.7	35.9	20.7	25.3	15.2
DVU3299	membrane protein, putative (TIGR) CDS		1,071	19	15.7	13.6	20.8	25.2	5.8
DVU3300	hypothetical protein (TIGR) CDS		294	5.8	5.4	6.4	10.7	10	8.8
DVU3301	hypothetical protein (TIGR) CDS		543	12.8	9	6	18.1	20.5	2.8
DVU3303	lon CDS	lon	2,109	27.4	31.9	34	27.7	31.3	29.7
DVU3305	atoC CDS	atoC	1,356	38.6	42.4	49.7	28.9	27.9	29.7
DVU3306	hypothetical protein (TIGR) CDS		165	91.1	83.5	95.2	73.7	66.1	87.7
DVU3307	ubiX CDS	ubiX	564	968.7	1057.8	943.4	601.6	610.6	708.4
DVU3308	metallo-beta-lactamase family protein (TIGR) CDS		720	717.9	754.6	647.5	482.6	482.8	674.1
DVU3309	endo/excinuclease amino terminal domain protein (TIGR) CDS		333	517.4	510.5	456	273.8	311.7	249.9
DVU3310	deaD CDS	deaD	1,599	398.9	442.6	364.6	194.6	179.2	198.1
DVU3311	hypothetical protein (TIGR) CDS		177	136.8	157.3	118.2	48.4	63.2	75.9
DVU3312	conserved hypothetical protein (TIGR) CDS		456	64.6	60.3	56.8	53.2	60	49.3

DVU3313	transcriptional regulator, LysR family (TIGR) CDS		891	50.9	54.1	50.7	62.2	69.9	48.4
DVU3314	peptidase, U32 family (TIGR) CDS		1,977	179.2	196.4	187.1	226.9	226.1	236.4
DVU3315	pyrK CDS	pyrK	819	421.5	481.4	400.7	383.6	376	419.4
DVU3316	pyrD CDS	pyrD	924	414.5	420.7	375	391.8	389.7	428.8
DVU3318	hypothetical protein (TIGR) CDS		171	11.7	20.1	15.5	8.5	14.2	18.1
DVU3319	putA CDS	putA	3,021	390.2	378.5	333.6	339	321.9	377.9
DVU3320	conserved domain protein (TIGR) CDS		381	120.1	111.5	104.9	106	84.5	77.3
DVU3322	conserved domain protein (TIGR) CDS		459	17.2	17.3	24.3	13.9	20.6	9
DVU3323	ABC transporter, permease protein (TIGR) CDS		1,467	22.8	21.3	21.4	13.2	15.2	8.4
DVU3324	ABC transporter, ATP-binding protein (TIGR) CDS		666	19.8	26.8	26.8	20.3	25.3	13.2
DVU3325	hypothetical protein (TIGR) CDS		57	43.9	36.2	44.9	47.4	28.3	18.1
DVU3326	multidrug resistance protein, Smr family (TIGR) CDS		321	62.9	47.2	65.6	54.3	49	47.5
DVU3327	multidrug resistance protein, Smr family (TIGR) CDS		384	52.6	46.1	46.3	24	34.9	34.3
DVU3329	hypothetical protein (TIGR) CDS		126	1.9	3.9	5.6	1.4	1.6	0
DVU3330	hypothetical iron-regulated P-type ATPase (Dmitry Rodionov)		276	83.2	68.5	86	29.1	35.9	61.8
DVU3331	hypothetical protein (TIGR) CDS		384	37.2	27.4	37.2	17	18.9	14.8
DVU3332	heavy metal translocating P-type ATPase (TIGR) CDS		1,821	30.8	28.7	28.2	17.4	17.5	15.7
DVU3333	hypothetical protein (TIGR) CDS		459	39	39.9	38.8	93.9	85.1	72.6
DVU3334	sigma-54 dependent DNA-binding response regulator (TIGR) C		1,350	40.5	47.6	41.1	45.8	44.2	51.5
DVU3335	sensory box histidine kinase (TIGR) CDS		1,782	29.1	34.4	28.8	47.1	49.2	49.2
DVU3336	kdpD CDS	kdpD	1,140	28.4	33.8	30.9	58	59.5	74.4
DVU3337	kdpC CDS	kdpC	558	12.4	12.4	8.2	22.5	18	9.3
DVU3338	kdpB CDS	kdpB	2,037	12.1	13.9	12.8	25.6	24.1	40.7
DVU3339	kdpA CDS	kdpA	1,710	10.5	12.7	12.1	39.1	39.1	47.7
DVU3339.1	kdpF CDS	kdpF	90	46.4	46.5	46.6	67.6	58.4	140.7
DVU3342	hypothetical protein (TIGR) CDS		417	47.7	51.8	46.1	65.9	70.3	66.9
DVU3343	hypothetical protein (TIGR) CDS		420	47.3	45.9	42.4	82.7	82	88.7
DVU3344	hypothetical protein (TIGR) CDS		1,170	40.6	41.5	39.3	75.1	69.6	75.5
DVU3347	pyruvate ferredoxin/flavodoxin oxidoreductase family protein		549	851.6	838.7	781.1	857.5	837.8	1013.5
DVU3348	pyruvate ferredoxin/flavodoxin oxidoreductase, beta subunit,		783	763.7	740.9	667.3	449.1	454.9	580.9
DVU3349	pyruvate flavodoxin/ferredoxin oxidoreductase, thiamine diP-l		1,074	813.2	764.6	718.8	496	490	611.2
DVU3350	oorD CDS	oorD	234	1000.2	880.4	857.8	725.2	754.6	948.7
DVU3351	queA CDS	queA	1,116	110.3	110.5	103.8	155.5	169.5	168.6
DVU3352	lipoprotein, putative (TIGR) CDS		570	526	515.4	468.8	302.3	295.7	392.2
DVU3353	coaBC CDS	coaBC	1,215	260.5	263.9	234.1	285.9	276	348.8
DVU3355	ebs CDS	ebs	756	111.7	109.4	79.9	158.7	140.4	207.2
DVU3356	NAD-dependent epimerase/dehydratase family protein (TIGR)		1,008	305.7	286.5	230	306.3	287.8	443.6
DVU3357	hypothetical protein (TIGR) CDS		198	92.4	77	92.7	21.4	22.8	15.6
DVU3358	parA CDS	parA	831	168.4	162.6	149	101.9	100.8	113.2
DVU3359	hypothetical protein (TIGR) CDS		420	319	307.8	313.4	523.1	495.8	513.2
DVU3360	parB CDS	parB	915	132.2	133.8	130.3	122.7	123.1	111.6
DVU3361	rfaE CDS	rfaE	1,026	114.8	100.5	106.2	113.8	114.3	75.3
DVU3362	conserved hypothetical protein (TIGR) CDS		381	159.1	150.1	168.9	83.5	84.9	75.9
DVU3363	sun CDS	sun	1,524	151.7	151.2	144.8	153.2	158.1	119.7
DVU3364	conserved hypothetical protein (TIGR) CDS		924	183	177.4	166.6	273.4	277.6	339.5
DVU3365	fmt CDS	fmt	993	256.5	274.5	250.1	339.3	327.8	389.8
DVU3366	def CDS	def	516	340.5	379.5	332	204.7	203.5	229.4
DVU3367	aspS CDS	aspS	1,833	375.7	416	391	255.9	249	281.3
DVU3368	hisS CDS	hisS	1,254	394.2	441.5	422.6	332	344.7	398.4
DVU3369	conserved domain protein (TIGR) CDS		789	68	70.4	58.7	177.1	187.8	153.2
DVU3371	metE CDS	metE	2,358	24.8	16.3	23.4	9.1	10.5	7
DVU3372	hypothetical protein (TIGR) CDS		132	3.1	2.2	5.4	2.8	5.1	0
DVU3373	ilvD CDS	ilvD	1,665	202.8	180.1	171.8	274.4	268.2	265.5
DVU3374	permease, putative (TIGR) CDS		834	159.3	127.4	135	204.2	208.1	183.4
DVU3375	ftsE CDS	ftsE	717	221.8	201.1	202.6	271.4	282.5	324
DVU3376	sulfatase family protein (TIGR) CDS		1,575	95.6	105.8	92	83.6	79.7	67.6
DVU3377	dgkA CDS	dgkA	375	134.8	121.7	114.1	69.4	72.8	35.8
DVU3378	YbaK/EbsC protein (TIGR) CDS		462	186.4	206.6	205.7	81.3	101.3	96.3
DVU3379	ribonucleoside-diphosphate reductase (TIGR) CDS		2,334	618.9	596	484.7	339.2	346.6	457.5
DVU3380	hypothetical protein (TIGR) CDS		123	38	39.2	31.6	21.3	24.6	33.6
DVU3381	ntrC CDS	ntrC	1,380	130	147.3	145.5	200.1	207.8	178.1
DVU3382	zraS CDS	zraS	2,040	101.1	99.3	94.3	225.3	256.3	265.4
DVU3384	zraP CDS	zraP	522	405.5	474.3	317.3	2966.4	2492.1	5245.7
DVU3386	permease, putative (TIGR) CDS		1,383	9.6	10.7	11.4	20.5	20.3	23.1
DVU3387	hypothetical protein (TIGR) CDS		1,014	155.1	149.1	156	504.6	511.2	545.3
DVU3388	lipoprotein, putative (TIGR) CDS		828	161.6	154.8	141.8	171	173.4	148.5
DVU3389	topA CDS	topA	2,283	301.5	336	304	448.8	444.5	552.2

DVU3392	glnA CDS	glnA	1,344	274.5	300.7	218.5	266.8	257.9	287.3
DVU3393	hypothetical protein (TIGR) CDS		225	46.2	34.1	33.7	7.6	9	9.2
DVU3394	hypothetical protein (TIGR) CDS		180	9.5	9.3	14.7	3.5	2.8	2.9
DVU3395	peptidase, M23/M37 family (TIGR) CDS		1,311	236.9	224	214.1	178.7	180.2	131.3
DVUA0001	hypothetical protein (TIGR) CDS		174	38.9	43.8	25.8	15	18	25.2
DVUA0002	soj CDS	soj	819	134.8	123.1	105.7	170.4	174.3	223.8
DVUA0003	hypothetical protein (TIGR) CDS		3,396	143.7	141.7	128.7	88.8	92.3	89.9
DVUA0004	DNA-binding protein HU, putative (TIGR) CDS		354	136.8	161.2	144.1	57.3	59.2	57
DVUA0005	universal stress protein family (TIGR) CDS		936	250.7	254	261.5	333.7	347.5	354
DVUA0006	mgtE CDS	mgtE	996	360.6	401.8	366.5	219.5	228	225.2
DVUA0007	nifB CDS	nifB	1,545	9.2	13.8	12.3	8.1	8.6	8
DVUA0008	nifN CDS	nifN	1,515	6.7	9.2	8.4	9.6	9.8	7.3
DVUA0009	nifE CDS	nifE	1,707	9.4	7.5	8.8	11.3	8.4	10.1
DVUA0010	ferredoxin, 2fe-2s (TIGR) CDS		303	6.3	8.5	5.3	5.6	2.2	3.4
DVUA0011	nifK CDS	nifK	1,386	4.8	7.6	4.8	4.2	4.5	3.8
DVUA0012	nifD CDS	nifD	1,629	6.8	9.4	8.2	13	10.8	8.2
DVUA0013	glnB-2 CDS	glnB-2	396	7.6	4.9	7.5	6.2	6.9	2.6
DVUA0014	glnB-3 CDS	glnB-3	327	4.9	5.3	7.3	7.7	5.6	3.1
DVUA0015	nifH CDS	nifH	834	10.1	10.9	9.3	13.3	14.9	15.5
DVUA0016	nifV CDS	nifV	1,155	6.5	6.8	7.1	39.7	44.1	29.6
DVUA0019	type II DNA modification methyltransferase, putative (TIGR) CI		1,659	252	280.7	254.2	100.7	103.9	101.6
DVUA0020	type II restriction endonuclease, putative (TIGR) CDS		741	248.2	264.3	252.4	60.9	70.5	57.2
DVUA0021	conserved hypothetical protein (TIGR) CDS		1,062	116.3	115.6	124.5	174.3	176.8	144.3
DVUA0022	ABC transporter, ATP-binding protein (TIGR) CDS		687	20.3	26.8	23.7	37.2	38.3	28.2
DVUA0023	ABC transporter, permease protein, putative (TIGR) CDS		1,131	34.2	32.5	30.4	71.6	75.9	51.7
DVUA0024	atoC CDS	atoC	1,140	10.8	12.2	10	24.2	24.4	21.8
DVUA0025	response regulator receiver domain protein (TIGR) CDS		462	18.1	24.2	15.2	56.7	56.7	58.1
DVUA0028	hypothetical protein (TIGR) CDS		411	65.9	44.2	46.4	116.7	100.1	106.9
DVUA0029	hypothetical protein (TIGR) CDS		681	6.6	10.7	7.3	29.6	33.5	23.5
DVUA0030	hypothetical protein (TIGR) CDS		702	22	24.1	24.1	52.7	54.1	45.6
DVUA0031	hypothetical protein (TIGR) CDS		867	10.4	13.4	12.2	41.4	40.8	47.1
DVUA0032	hypothetical protein (TIGR) CDS		861	13	13.8	14	26.8	22.6	17.4
DVUA0034	conserved domain protein (TIGR) CDS		2,970	6.8	9.8	8.3	12.8	15.9	14.8
DVUA0036	TPR domain protein (TIGR) CDS		2,748	17.7	17	17	20.3	22.8	22.2
DVUA0037	sugar transferase domain protein (TIGR) CDS		1,455	22.2	21.4	20.1	38.4	41.4	39.8
DVUA0038	b0983 CDS	b0983	807	6.2	5.7	6.4	5.6	4.6	6
DVUA0039	chain length determinant family protein (TIGR) CDS		1,503	4.8	4.8	4.3	4.8	3.7	2.9
DVUA0040	polysaccharide biosynthesis protein, putative (TIGR) CDS		1,119	6.8	7.1	7.7	8.2	8.4	11
DVUA0041	exeA CDS	exeA	1,320	3.9	5.3	3	6.6	6.6	6.3
DVUA0042	lipoprotein, putative (TIGR) CDS		1,323	9.6	9.8	8.2	12.3	12.2	7.8
DVUA0043	polysaccharide deacetylase family protein (TIGR) CDS		852	4.7	9	7.5	13.2	19.3	10.3
DVUA0044	conserved hypothetical protein (TIGR) CDS		978	9.1	8.6	9.8	7.3	7.1	5.8
DVUA0045	aminotransferase, DegT/DnrJ/EryC1/StrS family (TIGR) CDS		1,617	16.3	14.3	16.4	14.1	15.2	11.7
DVUA0046	glycosyl transferase, group 2 family protein (TIGR) CDS		1,449	7.6	8.8	9.4	15.6	13.1	14.8
DVUA0047	hypothetical protein (TIGR) CDS		1,317	5.1	4.7	5.7	7	10.5	7.1
DVUA0048	exopolysaccharide production protein, putative (TIGR) CDS		1,398	5.4	7.1	8.2	5.7	5.7	6.7
DVUA0049	polysaccharide biosynthesis family protein (TIGR) CDS		1,470	5.7	6.3	4.1	7.5	7.3	4.6
DVUA0050	conserved hypothetical protein (TIGR) CDS		1,257	5.1	5.5	4.8	4.7	5.2	3.3
DVUA0051	glycosyl transferase, group 1 family protein (TIGR) CDS		1,389	4.8	8	6.2	5.9	8.5	7.1
DVUA0052	conserved hypothetical protein (TIGR) CDS		669	5.7	8.8	9.6	7.7	4.5	7.7
DVUA0053	conserved hypothetical protein (TIGR) CDS		588	8.1	11.9	10.5	13.5	11	5.3
DVUA0054	glycosyl transferase, group 1 family protein (TIGR) CDS		1,401	10.2	12.1	12.8	13.5	16.1	14.8
DVUA0055	membrane protein, putative (TIGR) CDS		954	4.8	6	7.5	6.7	6.4	4.4
DVUA0056	hypothetical protein (TIGR) CDS		621	4.9	9.5	7.4	10.5	6.6	5
DVUA0057	atoC CDS	atoC	1,431	11	12	12.7	11.3	14.9	8.6
DVUA0058	BNR/Asp-box repeat protein (TIGR) CDS		2,736	13.9	15.3	15.4	16.4	19.1	13.4
DVUA0059	conserved hypothetical protein (TIGR) CDS		1,377	8.1	8.1	7.9	14	13.2	13.9
DVUA0060	membrane protein, putative (TIGR) CDS		1,386	7.4	11.2	8.5	9.3	10.4	5.9
DVUA0061	membrane protein, putative (TIGR) CDS		1,353	10.4	9.2	10	7.6	8.9	7.3
DVUA0062	conserved domain protein (TIGR) CDS		1,296	9.3	10.6	11.4	12.5	14.8	12
DVUA0063	Orn/DAP/Arg family decarboxylase (TIGR) CDS		1,557	5.2	7.5	6.3	6.5	6.2	3
DVUA0065	sensor histidine kinase (TIGR) CDS		2,037	5.8	7.9	7.2	6.2	7	6.4
DVUA0066	phospholipase, patatin family (TIGR) CDS		1,413	25.2	32	30.6	17	19.7	9.5
DVUA0067	membrane protein, putative (TIGR) CDS		1,125	66.7	76.2	68.1	18.6	21.1	11
DVUA0068	membrane protein, putative (TIGR) CDS		1,983	100.4	117.4	104.4	77.1	81.9	45.3
DVUA0069	GtrA family protein, selenocysteine-containing (TIGR) CDS		1,158	201	228	205.4	112.1	106.2	97.1
DVUA0070	conserved domain protein (TIGR) CDS		1,932	250.8	304.8	265.9	183.2	179.5	130

DVUA0071	glycosyl transferase, group 1/2 family protein (TIGR) CDS		2,157	290.9	335.8	285.3	255.9	252	206.3
DVUA0072	glycosyl transferase, group 1 family protein (TIGR) CDS		1,338	274.3	312.4	267	149.2	156.8	142.5
DVUA0073	asparagine synthase (glutamine-hydrolyzing), putative (TIGR) (		2,670	297.6	335.2	308.5	234.6	247.4	234.6
DVUA0074	sulfotransferase family protein (TIGR) CDS		690	358	416.6	359.7	196.1	194.3	192.5
DVUA0075	radical SAM domain protein (TIGR) CDS		1,407	421.4	440.8	413.7	308.7	308.2	318.7
DVUA0076	ABC transporter, ATP-binding protein (TIGR) CDS		1,395	459.9	473.8	446	429.9	430.8	419.2
DVUA0077	ABC transporter, permease protein (TIGR) CDS		885	451	470.5	435.9	543.1	529.2	642.4
DVUA0079	cysC CDS	cysC	687	282.9	297.4	281.6	307.4	319.1	275.3
DVUA0080	glycosyl transferase, group 2 family protein (TIGR) CDS		882	222.2	227.1	224.1	180.4	197.5	191.4
DVUA0081	glycosyl transferase, group 1/2 family protein (TIGR) CDS		2,115	108.1	97.9	100.8	133	137.7	103
DVUA0082	xerD CDS	xerD	1,032	85.3	82.7	88.7	87.3	82.9	63.1
DVUA0084	transcriptional regulator, AbrB family (TIGR) CDS		192	94.4	86	82.7	119.7	131.5	88.9
DVUA0085	conserved hypothetical protein (TIGR) CDS		3,531	51.7	60.7	54.7	36.9	43	24.9
DVUA0086	response regulator (TIGR) CDS		1,092	81.1	89.7	88.2	75	85.2	66.5
DVUA0087	sensory box histidine kinase (TIGR) CDS		3,114	71.2	75.1	64.9	95.2	93.8	84.9
DVUA0088	conserved hypothetical protein (TIGR) CDS		1,020	70.6	74.5	60.1	298.4	289.6	351.7
DVUA0089	hypothetical protein (TIGR) CDS		618	10	14.5	8.7	22.7	17.3	23.4
DVUA0090	membrane protein, putative (TIGR) CDS		873	34	37.8	36.8	37.8	43.2	33.8
DVUA0091	katA CDS	katA	1,458	96.7	92.7	71.7	137.7	127.4	148.5
DVUA0092	hypothetical protein (TIGR) CDS		480	196.9	191.7	184.5	226.9	227.7	152.9
DVUA0093	chromate transport family protein (TIGR) CDS		1,338	25.4	28.8	27.7	38.8	40.9	27.4
DVUA0094	chrB CDS	chrB	1,005	32.4	34.6	35.9	32	30.8	23.1
DVUA0096	major facilitator superfamily protein (TIGR) CDS		1,212	15.4	10.3	15.2	7.5	6.2	3.4
DVUA0097	radical SAM domain protein (TIGR) CDS		1,500	112.1	129.4	111.5	127.6	136.3	115.1
DVUA0098	dehydrogenase, putative (TIGR) CDS		1,050	81.8	80.7	83.4	143.4	147.9	115.6
DVUA0099	HAMP domain protein (TIGR) CDS		2,184	60.3	67.5	61.5	93.2	90.3	63.2
DVUA0100	flrC CDS	flrC	1,728	91.9	99.2	91.1	175.2	174.5	134.6
DVUA0101	flhB CDS	flhB	1,041	59.8	61.1	59.5	155.7	159	129.6
DVUA0102	escT CDS	escT	816	56.2	50.5	56	243.1	218.5	150.4
DVUA0103	invX CDS	invX	261	61.4	59.4	62.4	254.3	252	274.3
DVUA0104	sctV CDS	sctV	2,094	65.6	74.4	77	447.3	417.7	450.6
DVUA0105	conserved hypothetical protein (TIGR) CDS		375	69.2	74.7	77.7	1048.2	926.8	1215
DVUA0106	type III secretion target, YopN family (TIGR) CDS		1,125	111.8	123.1	129.6	610.1	583.7	791.4
DVUA0109	type III secretion system chaperone, LcrH/SycD family (TIGR) C		501	335.5	369.1	345.9	2289.4	1961	2971.1
DVUA0110	type III secretion system target, YopB family (TIGR) CDS		1,008	236	258.4	248.8	1458.3	1242.9	1737
DVUA0111	type III secretion system protein, IpaC family, putative (TIGR) (		897	278.6	311.2	300.9	982.2	867.2	1002.9
DVUA0112	type III secretion system protein, YscC family (TIGR) CDS		1,875	124.2	137	131.2	641.2	585.2	593.8
DVUA0113	type III secretion protein, YscD family (TIGR) CDS		1,809	134.2	158.5	161.2	737.3	670.9	899.4
DVUA0114	hypothetical protein (TIGR) CDS		210	310.7	361.4	331.3	918.1	856.6	1071.8
DVUA0115	type III secretion system protein, YscF family (TIGR) CDS		252	339.9	408.5	360.7	682.4	687.9	651.2
DVUA0116	conserved hypothetical protein (TIGR) CDS		366	281.8	349	310.3	816.4	766.1	652.4
DVUA0117	escJ CDS	escJ	816	161.4	197.2	170.8	534.1	492.2	533
DVUA0118	type III secretion protein, YopL family (TIGR) CDS		618	111.9	132.3	124.3	419.4	398.5	265.1
DVUA0119	sctN CDS	sctN	1,317	115.1	121.8	121.9	289.4	285.7	195.4
DVUA0120	type III secretion protein, putative (TIGR) CDS		693	144.7	135.1	149.9	299.8	277.8	186.5
DVUA0121	type III secretion system protein, YopQ family (TIGR) CDS		1,455	100	115.4	112.7	293.9	273	198.6
DVUA0122	yscR CDS	yscR	651	81	83.2	78	257	257	185.7
DVUA0123	anti-anti-sigma factor (TIGR) CDS		336	166	161.2	143.5	291.8	276.6	158.4
DVUA0124	sigma factor serine-protein kinase (TIGR) CDS		417	125.2	145.4	137.8	172.7	182.9	111.6
DVUA0125	slt CDS	slt	1,353	60.1	60.3	62.6	118.9	115.1	66.9
DVUA0126	conserved hypothetical protein (TIGR) CDS		468	107.1	114	94.7	911.4	820.5	1540.6
DVUA0129	cas3 CDS	cas3	2,109	66.5	81.5	75.7	32	34.5	33.1
DVUA0130	CRISPR-associated protein, CT1134 family (TIGR) CDS		684	125.8	147.9	143.7	33.6	42.4	29.1
DVUA0131	CRISPR-associated protein, CT1133 family (TIGR) CDS		1,839	154.8	195.4	181	35.9	37.5	34.2
DVUA0132	CRISPR-associated protein, TM1801 family (TIGR) CDS		873	234.8	299.6	304.9	39.4	39.9	24.9
DVUA0133	CRISPR-associated protein Cas4 (TIGR) CDS		639	147.1	188.6	180.6	80.2	75	59.9
DVUA0134	cas1 CDS	cas1	1,032	113.4	143.6	134.4	32	35.6	24.6
DVUA0135	CRISPR-associated protein Cas2 (TIGR) CDS		309	213.5	241.3	240.3	125.7	122.4	71.9
DVUA0136	zupT CDS	zupT	834	66.5	89.5	81	66.7	77.4	58.2
DVUA0137	response regulator (TIGR) CDS		648	53.2	51.3	60	33.4	37.6	27.1
DVUA0138	sensor histidine kinase (TIGR) CDS		2,085	56	60.7	59.1	45.9	45.2	31.3
DVUA0139	outer membrane autotransporter barrel domain protein (TIGR		1,980	41	47	42.1	57.3	55.6	30.8
DVUA0141	hypothetical protein (TIGR) CDS		237	8.5	24.4	14.9	3	9.9	13.1
DVUA0143	nifA-2 CDS	nifA-2	1,548	9.2	10.6	9.1	57.3	63.5	52.4
DVUA0144	hypothetical protein (TIGR) CDS		144	9.8	10.9	10.5	5.6	6	7.2
DVUA0145	conserved domain protein (TIGR) CDS		3,927	66	74.6	70.1	457.8	420.5	507.4
DVUA0146	hypothetical protein (TIGR) CDS		471	126.3	155.5	135	395.1	391.2	422.5

DVUA0147	conserved hypothetical protein (TIGR) CDS	1,242	89.8	96.8	81.8	201.6	192.4	227.4
DVUA0148	major facilitator superfamily protein (TIGR) CDS	3,018	124.6	124.6	129.6	174.9	175.7	127.3
DVUA0149	hypothetical protein (TIGR) CDS	1,785	77.6	80.6	73.1	73.4	80.8	52.7
DVUA0150	bacterial extracellular solute-binding protein, family 3 (TIGR) C	738	60.8	50.8	55.7	52.5	56	46.3
DVUA0151	DNA-binding protein, putative (TIGR) CDS	393	40.9	44.6	46.5	19.5	18.3	7.9
DVUA0152	conserved domain protein (TIGR) CDS	1,296	31.8	42	36.4	25.7	24	18.8

VITA

Samuel Ronald Fels was born in St. Louis, Missouri, on 29 September 1986, the son of Daniel Edgar Fels and Mary Julianne Rice Fels. After graduating from Parkway North High School, he enrolled at Truman State University in Kirksville, Missouri. There he received a Bachelor of Science degree in Biology in May 2009. In June 2009 he entered The Graduate School at The University of Missouri in the Molecular Microbiology and Veterinary Pathobiology Program (now the Molecular Pathogenesis and Therapeutics Program).