

# H-NOX-mediated nitric oxide sensing modulates symbiotic colonization by *Vibrio fischeri*

Yanling Wang<sup>a</sup>, Yann S. Dufour<sup>b</sup>, Hans K. Carlson<sup>c</sup>, Timothy J. Donohue<sup>b</sup>, Michael A. Marletta<sup>c,d,1</sup>, and Edward G. Ruby<sup>a,1</sup>

Departments of <sup>a</sup>Medical Microbiology and Immunology and <sup>b</sup>Bacteriology, University of Wisconsin, Madison, WI 53706; and Departments of <sup>c</sup>Chemistry and <sup>d</sup>Molecular and Cell Biology, University of California, Berkeley, CA 94720

Contributed by Michael A. Marletta, March 23, 2010 (sent for review February 14, 2010)

The bioluminescent bacterium *Vibrio fischeri* initiates a specific, persistent symbiosis in the light organ of the squid *Euprymna scolopes*. During the early stages of colonization, *V. fischeri* is exposed to host-derived nitric oxide (NO). Although NO can be both an antimicrobial component of innate immunity and a key signaling molecule in eukaryotes, potential roles in beneficial host-microbe associations have not been described. *V. fischeri* *hnoX* encodes a heme NO/oxygen-binding (H-NOX) protein, a member of a family of bacterial NO- and/or O<sub>2</sub>-binding proteins of unknown function. We hypothesized that H-NOX acts as a NO sensor that is involved in regulating symbiosis-related genes early in colonization. Whole-genome expression studies identified 20 genes that were repressed in an NO- and H-NOX-dependent fashion. Ten of these, including hemin-utilization genes, have a promoter with a putative ferric-uptake regulator (Fur) binding site. As predicted, in the presence of NO, wild-type *V. fischeri* grew more slowly on hemin than a *hnoX* deletion mutant. Host-colonization studies showed that the *hnoX* mutant was also 10-fold more efficient in initially colonizing the squid host than the wild type; similarly, in mixed inoculations, it outcompeted the wild-type strain by an average of 16-fold after 24 h. However, the presence of excess hemin or iron reversed this dominance. The advantage of the mutant in colonizing the iron-limited light-organ tissues is caused, at least in part, by its greater ability to acquire host-derived hemin. Our data suggest that *V. fischeri* normally senses a host-generated NO signal through H-NOX<sub>vf</sub> and modulates the expression of its iron uptake capacity during the early stages of the light-organ symbiosis.

symbiosis | iron uptake | transcriptional analysis | colonization

Small molecules have important signaling functions in microbe-microbe and microbe-host interactions (1). One such molecule, nitric oxide (NO), plays a key role in both cellular defense and signaling. When produced at high concentrations by activated macrophages and tissues, it is a powerful antimicrobial (2, 3). In contrast, when produced at low concentrations, NO can serve as a signaling molecule; for instance, in eukaryotic endothelial cells, it regulates activities such as vasodilation, and in bacteria that contain specific NO sensors, it facilitates responses to environmental conditions (4, 5). A family of putative sensor proteins widely distributed among bacteria binds O<sub>2</sub> and/or NO within a Fe(II)-heme domain that displays a high sequence identity to a domain of the eukaryotic soluble guanylate cyclase (sGC) (6). Thus, these putative sensors are collectively called heme NO/oxygen-binding (H-NOX) proteins. Several proteins in this family, such as those in *Vibrio cholerae* and *Thermoanaerobacter tengcongensis*, have been characterized both for structure (7, 8) and their ligand-discrimination properties (9). Nevertheless, the physiological role of H-NOX proteins has not been described in any bacterium. Members of the H-NOX family are either stand-alone proteins or are fused to other domains related to signaling functions. In addition, the *hnoX* gene is most often found in a predicted operon that includes a putative histidine kinase. This arrangement suggests that a H-NOX-mediated sensing mechanism may be involved in the bacterium's response to environments containing NO or O<sub>2</sub> (6, 10).

One such environment occurs in the mutualistic symbiotic association between the Hawaiian bobtail squid, *Euprymna scolopes*, and

the marine bioluminescent bacterium, *V. fischeri* (11). The bacterial symbionts are housed in the crypts of the host's light-emitting organ, and they grow as a monospecific culture along the apical surfaces of the crypt epithelia (12). After reaching a high cell density in the organ, the bacteria induce their *lux* operon, producing light that is used by the host in an antipredatory behavior called counterillumination. In exchange for this bioluminescence, the host squid supplies nutrients that support symbiont proliferation (13).

The nascent light organ of a newly hatched juvenile squid is free of symbionts. During the initiation of the symbiosis, *V. fischeri* present in the ambient seawater gather as an aggregate in the mucus shed by superficial epithelia on the nascent organ. The bacteria in the aggregate then migrate to and into pores on the organ surface, moving through ducts to the deep crypts where the symbiont population is established (12). During this transit, the migrating *V. fischeri* are exposed to host-derived NO produced both by vesicles embedded in the secreted mucus and later, by the epithelium lining of the ducts (2), where reactive oxygen species are also produced (14). Given its antimicrobial and signaling properties, the generation of this host-derived NO has been proposed to be involved in the early stages of the association not only as a specificity determinant but also as a symbiotic signal (2, 12).

Analysis of the *V. fischeri* genome sequence (15) revealed the presence of a gene (*VF\_A0071*) encoding a H-NOX homolog (H-NOX<sub>vf</sub>) that is located just upstream of a putative histidine kinase (HK; *VF\_A0072*). H-NOX regulation of a histidine kinase in *Shewanella oneidensis* has been reported (10). We hypothesized that H-NOX<sub>vf</sub> plays a role in NO sensing and subsequent regulation of symbiosis-related genes. In this study, we examined the role of H-NOX<sub>vf</sub> as a sensor for NO both in culture and in the symbiosis. In this paper, we show that H-NOX<sub>vf</sub> binds NO, but not O<sub>2</sub>, in vitro, and these are properties that are consistent with serving as an NO sensor. We also show that ~20 genes are negatively regulated in both a H-NOX<sub>vf</sub>- and NO-dependent manner and that H-NOX<sub>vf</sub>-mediated NO sensing modulates the effectiveness of symbiosis initiation.

## Results

**Ligand-Binding Properties of H-NOX<sub>vf</sub>.** Sequence alignments and homology models of the *V. fischeri* H-NOX with other proteins bearing H-NOX domains indicated that H-NOX<sub>vf</sub> lacks the distal-pocket tyrosine that stabilizes oxygen binding in the H-NOXs (16), which leads to the prediction that H-NOX<sub>vf</sub> will not form an O<sub>2</sub> complex. Indeed, the purified H-NOX<sub>vf</sub> protein formed stable Fe(II)-NO and Fe(II)-CO complexes (Fig. 1 and Table 1) but

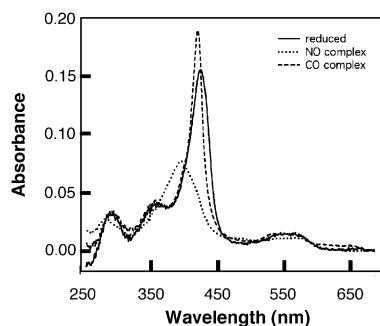
Author contributions: Y.W., Y.S.D., H.K.C., M.A.M., and E.G.R. designed research; Y.W., Y.S.D., and H.K.C. performed research; Y.W., Y.S.D., H.K.C., T.J.D., M.A.M., and E.G.R. analyzed data; and Y.W., Y.S.D., H.K.C., M.A.M., and E.G.R. wrote the paper.

The authors declare no conflict of interest.

Data deposition: The whole-genome transcriptional data reported in this paper have been deposited in the GenBank database (accession no. GSE15522).

<sup>1</sup>To whom correspondence may be addressed. E-mail: marletta@berkeley.edu or egruby@wisc.edu.

This article contains supporting information online at: [www.pnas.org/lookup/suppl/doi:10.1073/pnas.1003571107/-DCSupplemental](http://www.pnas.org/lookup/suppl/doi:10.1073/pnas.1003571107/-DCSupplemental).



**Fig. 1.** Electronic absorption spectra of protein complexes of the H-NOX protein from *V. fischeri*. Purified H-NOX<sub>Vf</sub>-Fe(II) (solid), -Fe(II)-CO (dotted), and -Fe(II)-NO (dashed) at concentrations of  $\sim 1 \mu\text{M}$  are shown.

showed no measurable affinity for O<sub>2</sub>. The Fe(II) unligated complex displayed no noticeable spectral change when exposed to air for over 30 min, attesting to the aerobic stability of this protein and its slow oxidation rate. Based on these results, it is unlikely that H-NOX<sub>Vf</sub> functions in vivo as a redox sensor, although this possibility cannot be completely ruled out. The H-NOX<sub>Vf</sub>  $k_{\text{off}}$  for NO is slow (Table 2), similar to the  $k_{\text{off}}$  of sGCs (17) and other bacterial H-NOX proteins (7), and assuming a  $k_{\text{on}}$  for NO like that seen for NO in other H-NOXs, the  $K_{\text{d}}$  for NO would be in the picomolar range. Taken together, these results indicate a possible role for H-NOX<sub>Vf</sub> as a high-affinity NO sensor.

**Certain Iron-Uptake Genes Are Repressed in a H-NOX<sub>Vf</sub><sup>-</sup> and NO-Dependent Manner.** Because *V. fischeri* encounters host-derived NO during its colonization of the squid light organ (2), we asked if H-NOX<sub>Vf</sub> might convey this information about the symbiotic environment to the bacterium, leading to changes in the symbiont's gene expression. To determine which *V. fischeri* genes might be regulated by NO only in the presence of H-NOX<sub>Vf</sub>, we compared the transcriptional profile of the *hnoX*-insertion mutant, YLW1 (Table S1; Fig. S1), with that of wild-type cells when the cultures were exposed to NO (diethylamine NONOate) for 30 min. To test if the *hnoX* insertion was not polar on the downstream HK gene, we used qRT-PCR analysis and showed that there was only a small (1.2- to 1.4-fold) difference between the NO-induced transcriptional response of the HK gene in the *hnoX* mutant and its parent.

Evidence that both the mutant and wild type produced a transcriptional response to NO treatment came from their elevated (>100-fold) expression of *VF\_2316*, the *V. fischeri* homolog of the *Escherichia coli* NO dioxygenase-encoding *hmp*, a gene previously shown to be induced by NO exposure (18). A four-way contrast analysis with the cutoff for a false-discovery rate set at 0.05 was

**Table 1.** UV-visible peak positions for Fe(II) complexes of H-NOX proteins (at 20 °C)

Protein	Soret	$\alpha$	$\beta$	Reference
<b>Fe(II) unligated</b>				
sGC	431	555	555	40
H-NOX <sub>Vc</sub>	429	568	568	7
H-NOX <sub>Vf</sub>	428	568	568	This study
<b>Fe(II)-CO</b>				
sGC	423	541	567	40
H-NOX <sub>Vc</sub>	423	541	566	7
H-NOX <sub>Vf</sub>	423	538	571	This study
<b>Fe(II)-NO</b>				
sGC	398	537	572	40
H-NOX <sub>Vc</sub>	398	540	573	7
H-NOX <sub>Vf</sub>	398	539	571	This study

**Table 2.** NO dissociation rates ( $\text{s}^{-1} \times 10^{-4}$ ) for H-NOX proteins

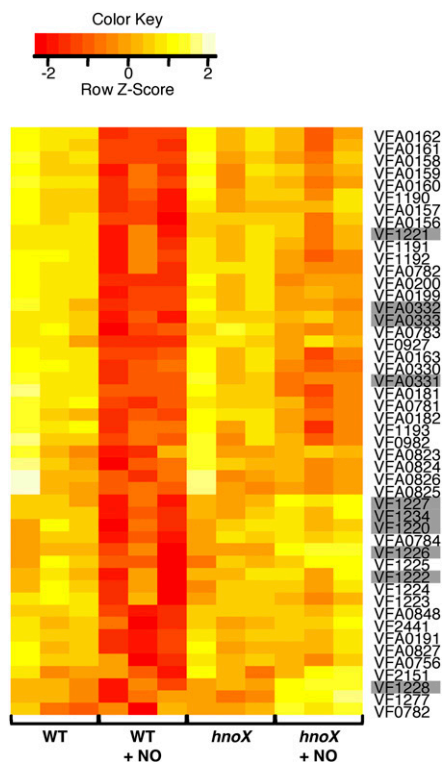
Protein	$k_{\text{m1}}$ ( $k_{\text{off}}$ )	$k_{\text{m2}}$	Reference
sGC	$3.6 \pm 0.8$	$166 \pm 44$	17
H-NOX <sub>Vf</sub>	$21 \pm 0.6$	$100 \pm 10$	this study

performed to identify those genes whose regulation required the presence of both NO and H-NOX<sub>Vf</sub> (Table S2). Although *V. fischeri* homologs of genes typically associated with NO detoxification were induced by the presence of NO, they were not differentially regulated between the wild-type and *hnoX*-insertion mutant (Table S2), suggesting that H-NOX<sub>Vf</sub> is not required for a typical bacterial defensive response to NO (Fig. S2).

In contrast, 40 other genes were differentially expressed in the wild-type strain on NO exposure, whereas their expression remained relatively unchanged in the *hnoX* mutant strain (Table S2). This group contains 20 genes that were up-regulated by NO treatment and another 20 genes that were down-regulated (Table S3). The promoter sequences of each of these two sets of genes were aligned to search for shared regulatory sequence elements, and a conserved palindromic motif was identified in 10 of 20 down-regulated genes (Fig. S3). This motif is similar to the binding site of the master iron-responsive regulator ferric-uptake regulator (Fur) of *E. coli* (19). Corroborating this observation, the annotation of these predicted targets indicated that 8 of 10 are in loci that have functions related to iron acquisition or use (Table S3). To determine if the effect of NO exposure on these putative Fur targets could be generalized to the entire Fur regulon, the genome sequence of *V. fischeri* ES114 was searched for additional putative Fur-binding sites using a position-specific weight-matrix model derived from the initial 10 targets. The expression patterns of the top 48 Fur targets from this analysis show a strong correlation with each other (Fig. 2), suggesting that the expression level of the entire Fur regulon is affected by the NO treatment in a H-NOX<sub>Vf</sub>-dependent manner. Thus, in response to nonlethal concentrations of NO, H-NOX<sub>Vf</sub> plays a role in down-regulating the expression of iron-use genes either directly or indirectly by modulating their repression by Fur.

**Exposure to NO Suppresses *V. fischeri* Growth on Hemin.** Among the genes shown to be down-regulated in NO-treated wild-type cells, but not the *hnoX*-insertion mutant, were those encoding putative TonB-dependent hemin receptors (*VF\_1234* and *VF\_A0331-A0333*), a hemin transporter (*VF\_1220-1222*), and hemin-degradation proteins (*VF\_1226-1228*) (Fig. 2 and Table S2). Thus, we predicted that, when exposed to NO, wild type would grow more slowly than the *hnoX* mutant in an iron-depleted minimal medium supplemented with hemin. To test this hypothesis using a nonpolar deletion of the *hnoX* gene, the mutant, YLW37 ( $\Delta hnoX$ ), was examined (Table S1). Both wild type and mutant were able to use hemin as the sole iron source, and the addition of NO initially delayed the growth of both cultures (Fig. 3A) (3). However, when growth resumed, the NO-treated wild-type cells grew at a significantly lower rate than the  $\Delta hnoX$  mutant cells (Fig. 3B). Taken together, these data suggest that (i) NO exerts a suppressive effect on hemin uptake and use by wild-type cells and (ii) this suppression requires the presence of H-NOX<sub>Vf</sub>. As predicted, the NO-dependent growth-rate phenotype of the  $\Delta hnoX$  mutant could be genetically complemented by introduction of the *hnoX* gene *in trans*, which decreased the rate of growth back to that of wild-type cells (Fig. 3B).

The *hnoX* mutant had the same low growth rate as wild type in a low iron medium lacking hemin, both in the presence and absence of NO (Fig. S4). This result is consistent with the observation that the regulation of putative nonheme ferric- and ferrous-iron transporter operons (*VF\_2149-2151* and *VF\_0833-*

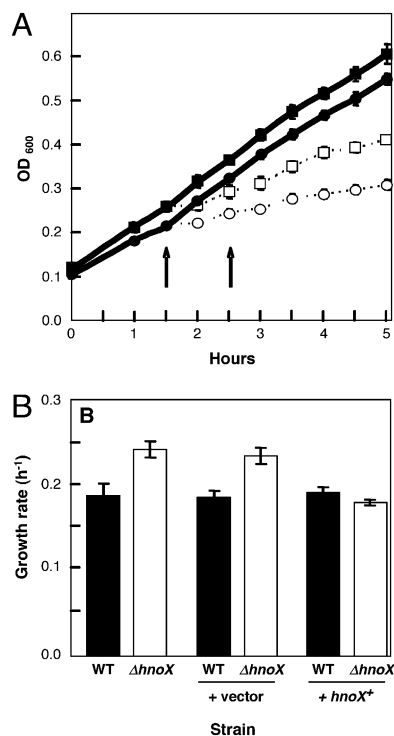


**Fig. 2.** Heat map summarizing the expression profile of all genes of *V. fischeri* E5114 whose promoter regions are predicted to contain a Fur-binding site. Genes are identified by their locus tags (rows), and experimental treatment triplicates are grouped in vertical columns. WT, wild-type cells; *hnoX*, *hnoX*-insertion mutant cells; NO, nitric-oxide treatment. The expression-level values were normalized to their Z scores for each row (red, low expression level; white, high expression level). The hemin-related genes are indicated by gray boxes.

0835) was neither under Fur control (Fig. 2) nor dependent on H-NOX<sub>Vf</sub> (Table S2).

**Deletion of the *hnoX* Gene Results in an Increased Symbiotic Competence.** We reasoned that, during the colonization process, H-NOX<sub>Vf</sub> serves as a sensor of host-derived NO for *V. fischeri*, and thus, loss of *hnoX* might give rise to symbiotic defects. However, the  $\Delta hnoX$  mutant was actually more proficient in the initiation of colonization, particularly at a low inoculum density. Specifically, juveniles infected with the  $\Delta hnoX$  mutant became luminescent sooner, reaching a higher maximum bioluminescence within 18 h, than did wild-type infected animals (Fig. 4A). Because the onset of luminescence is a good marker for colonization (20), the observation that the  $\Delta hnoX$  mutant produces the same level of luminescence per cell as wild type in culture (Fig. S5) indicated that the mutant was more effective at colonizing. This greater degree of infectivity was tested by determining the inoculum dose that resulted in colonization of 50% of the animals (ID<sub>50</sub>). In this assay, only about 125 cfu/mL of the  $\Delta hnoX$  mutant were required to colonize one-half of a juvenile cohort, whereas the ID<sub>50</sub> of the wild type was ~10-fold higher (Fig. 4B).

To better understand the nature of this increased efficiency, we performed competition experiments, which provided a direct measurement of the relative symbiotic proficiency of the wild-type and  $\Delta hnoX$  mutant. When juvenile squids were inoculated with a mixed culture containing the two strains at a 1:1 ratio, the mutant outcompeted the wild type by an average of 16-fold (Fig. 4C); that is, after 24 h, the population of *V. fischeri* in the light organ was ~94% mutant. The competitive advantage of the  $\Delta hnoX$  mutant

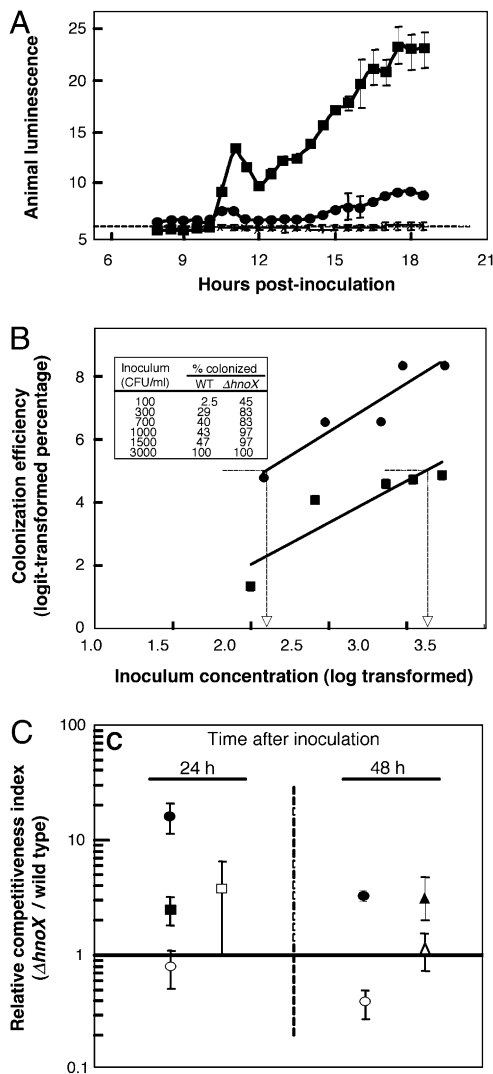


**Fig. 3.** Responses of wild-type *V. fischeri* and the  $\Delta hnoX$  mutant to the addition of NO during the growth on hemin. (A) An iron-depleted, minimal-salts medium containing hemin (10  $\mu$ M) as the sole iron source was inoculated with either the wild-type strain E5114 (circles) or the  $\Delta hnoX$ -insertion mutant (squares), and growth was monitored by optical density (OD<sub>600</sub>) at 28 °C with shaking. One-half of each culture (open symbols) was treated two times with the NO generator DEA-NONOate (arrows) as growth was monitored. Error bars indicate the SEM of triplicate cultures in a single experiment. Similar results were obtained in two other experiments. (B) The growth rates of the cultures in panel A were determined for the period between 2 and 5 h after inoculation in either the absence (solid bars) or presence (open bars) of DEA-NONOate. Growth rates were also determined for the wild type and  $\Delta hnoX$  mutant, carrying either the plasmid vector (pVS105) or the vector with an intact copy of the *hnoX* gene (pComhnoX; *hnoX*<sup>+</sup>). Plasmid carriage itself had no effect on the growth rates of either of the strains (Fig. S6). Error bars indicate the SEM of the mean growth rates calculated from three separate experiments; *t* test analysis indicated a significantly faster growth rate in the presence of NO for the  $\Delta hnoX$  and  $\Delta hnoX$  + vector.

diminished over the course of the next day, dropping to a 3-fold advantage (i.e., becoming 75% of the population) by 48 h post-inoculation. As predicted, the competitive advantage of the  $\Delta hnoX$  mutant was reversed by the introduction of an intact copy of the *hnoX* gene, decreasing the relative competitiveness index (RCI) value at 48 h from 3.1 to 1.1 (Fig. 4C).

This result suggested that *V. fischeri* cells have an increased competence in initiating symbiotic colonization in the absence of H-NOX<sub>Vf</sub>, the putative NO sensor. As described above, in the presence of NO, wild-type cells repress certain genes involved in iron acquisition, including those for hemin uptake and use. Thus, we reasoned that the competitive advantage of the  $\Delta hnoX$  mutant might be, at least in part, caused by its greater ability for iron accumulation, perhaps in the form of host-derived hemin. Such a capability would be predicted to support a faster growth rate in the iron-limited tissues of the light organ. This hypothesis was tested by supplementing the seawater containing newly hatched squids with an excess of hemin (0.2  $\mu$ M) or free iron (10  $\mu$ M), thereby offsetting the mutant's putative advantage in scavenging low levels of this nutrient. Under either of these conditions of iron surplus, there was no longer evidence of a competitive advantage for the  $\Delta hnoX$





**Fig. 4.** Colonization by the *V. fischeri*  $\Delta hnoX$  mutant. (A) Newly hatched juvenile squid ( $n = 22$ ) were inoculated with either wild-type (circles) or mutant (squares) bacteria, and the appearance of luminescence was monitored periodically. Uninoculated squid (X) did not produce light above background (dashed line). One luminescence unit is equivalent to  $\sim 4 \times 10^5$  quanta/sec. (B) Juvenile squid were exposed to different dosages (Inset) of either the wild-type (circles) or mutant (squares) bacteria. Colonization efficiency was determined by mathematically estimating the inoculation dosage at which 50% of the host animals became colonized (arrows) as indicated by the appearance of luminescence by 48 h (*Materials and Methods*). The  $r^2$  values of both regressions (solid lines) were  $> 0.8$ . (C) Juvenile squid ( $n = 30$ ) were exposed to a mixed inoculum ( $\sim 1:1$ ) of the wild type and mutant at a total concentration of 3,000 cfu/mL. The ratio of the two strains in the light-organ population (relative competitive index) (39) at 24 and 48 h postinoculation was measured with no additions (closed circles), 0.2  $\mu$ M hemin (closed square), 10  $\mu$ M FeCl<sub>3</sub> (open circles), or 100  $\mu$ M S-methyl-L-thiocitrulline (SMTC), an inhibitor of host NO synthase (2) (open squares) added at the time of inoculation. Open or closed triangles indicate carriage of either a complementing *hnoX*-encoding plasmid or the vector control, respectively.

mutant 24 h after inoculation (Fig. 4C). In fact, as time passed, the wild type had an advantage over the mutant in the presence of added iron; specifically, the RCI dropped significantly below 1 to a value of 0.4 by 48 h. To further test the hypothesis, we experimentally lowered the concentration of NO encountered by colonizing *V. fischeri* cells. S-methyl-L-thiocitrulline (SMTC) is a general NOS inhibitor, and therefore, the addition of SMTC during colonization would be expected to diminish the NO-induced suppression of hemin acqui-

sition in the wild type and thereby, strengthen its symbiotic proficiency. Indeed, the addition of SMTC to the seawater increased the relative colonization competence of the wild type by 4-fold (Fig. 4C). It is worth noting that supplementation with either hemin or the NOS inhibitor did not compromise the squid's capacity to support normal levels of *V. fischeri* growth in the light organ (Fig. S7). Taken together, these results support the hypothesis that, during the colonization process, H-NOX<sub>Vf</sub> senses host-derived NO, represses the bacterium's ability to acquire hemin, and suppresses rapid growth of the symbiont.

## Discussion

Although well-characterized in vitro (7, 8, 21), the biological functions of the widely distributed bacterial H-NOX proteins in general and the NO-binding domain that they share with sGC in particular have remained an open question. Using the symbiosis between *V. fischeri* and the bobtail squid, we have established a connection between H-NOX<sub>Vf</sub> and four bacterial activities: (i) sensing of environmental NO, (ii) transcriptional regulation of a set of genes, including those in the Fur regulon, (iii) suppression of the ability to use hemin, and (iv) modulation of the effectiveness of colonization. Thus, H-NOX<sub>Vf</sub> couples the presence of a host-generated signal (NO) with an essential symbiont activity (colonization).

**H-NOX<sub>Vf</sub> Senses NO and Regulates the Cell's Iron Metabolism.** H-NOX<sub>Vf</sub> is not involved in regulating the bacterium's NO-detoxification capacity; nevertheless, it does influence the expression of *V. fischeri* genes associated with specific iron-acquisition proteins. Expression of the genes associated with the uptake of free (ferrous or ferric) iron is unaffected by H-NOX<sub>Vf</sub>, suggesting that this is not the natural source of iron that limits growth in the light organ. Thus, it is not surprising that wild-type *V. fischeri* and an *hnoX* mutant grow equally well either in medium containing ferric iron as the source of iron or in the host when ferric iron is added in excess (Fig. 4C). In contrast, the transcription of genes encoding hemin transport is repressed in an NO- and H-NOX<sub>Vf</sub>-dependent manner (Fig. S8). Thus, when growing in culture with hemin as the major iron source but only in the presence of NO, the absence of H-NOX<sub>Vf</sub> regulation provides the  $\Delta hnoX$  mutant with an advantage (Fig. 3B).

The mechanism or pathway underlying regulation of iron metabolism by H-NOX<sub>Vf</sub> is unknown; nevertheless, because essentially all *V. fischeri* genes predicted to have a Fur box in their promoters are regulated by H-NOX<sub>Vf</sub>-NO (Fig. 2), it is possible that this complex somehow targets the same regulon as this iron-binding, Fe-uptake regulator. NO has been reported to directly nitrosylate Fur-bound iron in *E. coli*, thereby abolishing its ability to repress transcription under iron-replete conditions (22, 23). However, the presence of NO produces the opposite effect in *V. fischeri*: a H-NOX-dependent increase in the repression of iron-uptake genes. Thus, *V. fischeri*, and perhaps other H-NOX-encoding bacteria, regulate iron metabolism by a mechanism not found in *E. coli*. We propose that this mechanism is a signal transduction pathway involving H-NOX<sub>Vf</sub> and its associated HK, as well as an unknown response regulator (10), and it counters the effect of Fur nitrosylation.

## Why Does the *hnoX* Mutant Dominate During Initiation of Symbiosis?

The most striking finding in this study was the competitive advantage that a *V. fischeri*  $\Delta hnoX$  mutant exhibits early in the colonization of the juvenile squid light organ (Fig. 4C). How might the presence of H-NOX<sub>Vf</sub> provide an initial disadvantage to the symbiont but, eventually, prove advantageous?

During the onset of colonization by *V. fischeri*, the light organ is an iron-limited growth environment that requires the bacterium to scavenge this nutrient (24). However, although iron is essential for growth, a high concentration of free intracellular iron in the reducing environment of the cell can be toxic because of its role in generating hydroxyl radicals through the Fenton reaction. For this

reason, iron homeostasis is tightly regulated in bacteria (25). Fenton chemistry involves iron,  $H_2O_2$ , and a source of reducing equivalents. Evidence that *V. fischeri* encounters  $H_2O_2$  during initiation of colonization includes the presence of halide peroxidase activity in the tissues of the light organ (14) and the colonization defect of a *V. fischeri katG* mutant, which was deficient in a periplasmic catalase (26). Thus, the role of H-NOX<sub>Vf</sub>-NO may be to sense the light-organ environment, initially suppressing hemin accumulation (and growth rate) in the presence of host-generated oxidants. *V. fischeri* encounter NO even before they are exposed to host-derived oxidative stress in the ducts (12); hence, it is possible that these cells are primed for a subsequent exposure through the role of H-NOX<sub>Vf</sub> in NO sensing and down-regulation of iron accumulation. Then, 24–48 h later, when the presence of these oxidants has been reduced (2, 27), the symbionts would be depressed for hemin acquisition. In this way, whereas the  $\Delta hnoX$  mutant might have an initial colonization advantage because of its ready accumulation of hemin, these bacteria could experience a higher mutation rate that eventually results in a loss of fitness. Such a scenario may explain, at least in part, why the RCI of the mutant dropped from 16- to 3-fold after the first 24 h post-inoculation (Fig. 4C). In the context of this hypothesis, it is interesting that two genes involved with *V. fischeri* cystine transport are also down-regulated 3- to 5-fold by H-NOX<sub>Vf</sub> in an NO-dependent manner (Table S2). An increased level of cystine would result in the generation of cysteine, which potentiates oxidative DNA damage in *E. coli* (28). Free cysteine, if present, would provide the essential source of reducing equivalents to drive DNA-damaging Fenton chemistry. As similar mechanisms of DNA damage are likely to apply in *V. fischeri*, a successful symbiont would be expected to initially maintain its concentrations of both cellular iron and cystine/cysteine low. As noted above, light-organ symbionts are provided with an abundance of host-derived amino acids (13); therefore, it is intriguing that genes associated with nitrogen starvation are also up-regulated in a NO- and H-NOX-dependent fashion (Table S2). Further investigation into the *V. fischeri* /squid symbiosis, as well as discovery of H-NOX/NO-regulated genes in other bacteria, will provide additional clues to identify the diversity of biological functions performed by this family of proteins.

**Conclusion.** For bacteria to adapt to a symbiotic lifestyle, they must be able to correctly sense and successfully respond to the suite of host-derived signals that indicate they have arrived in their specific target tissue. *V. fischeri* apparently has adapted its homolog of the widely distributed family of NO-sensing H-NOX-domain proteins to such a role. Thus, the continued study of H-NOX<sub>Vf</sub> signaling in *V. fischeri* will provide a paradigm for both the regulatory mechanism of these proteins and their potential biological roles.

## Materials and Methods

**Bacterial Strains and Growth Conditions.** The *hnoX*-insertion mutant (YLW1) was constructed by plasmid integration (29), and the  $\Delta hnoX$  in-frame deletion mutant (YLW37) was constructed by allelic exchange (30) (Table S1).

- Shank EA, Kolter R (2009) New developments in microbial interspecies signaling. *Curr Opin Microbiol* 12:205–214.
- Davidson SK, Koropatnick TA, Kossmehl R, Sycuro L, McFall-Ngai MJ (2004) NO means 'yes' in the squid-vibrio symbiosis: Nitric oxide (NO) during the initial stages of a beneficial association. *Cell Microbiol* 6:1139–1151.
- Fang FC (2004) Antimicrobial reactive oxygen and nitrogen species: Concepts and controversies. *Nat Rev Microbiol* 2:820–832.
- Spiro S (2007) Regulators of bacterial responses to nitric oxide. *FEMS Microbiol Rev* 31:193–211.
- Spiro T (2008) A twist on heme signaling. *ACS Chem Biol* 3:673–675.
- Iyer LM, Anantharaman V, Aravind L (2003) Ancient conserved domains shared by animal soluble guanylyl cyclases and bacterial signaling proteins. *BMC Genomics* 4:5.
- Karow DS, et al. (2004) Spectroscopic characterization of the soluble guanylate cyclase-like heme domains from *Vibrio cholerae* and *Thermoanaerobacter tengcongensis*. *Biochemistry* 43:10203–10211.
- Pellucena P, Karow DS, Boon EM, Marletta MA, Kuriyan J (2004) Crystal structure of an oxygen-binding heme domain related to soluble guanylate cyclases. *Proc Natl Acad Sci USA* 101:12854–12859.
- Boon EM, Marletta MA (2005) Ligand discrimination in soluble guanylate cyclase and the H-NOX family of heme sensor proteins. *Curr Opin Chem Biol* 9:441–446.
- Price MS, Chao LY, Marletta MA (2007) *Shewanella oneidensis* MR-1 H-NOX regulation of a histidine kinase by nitric oxide. *Biochemistry* 46:13677–13683.
- Visick KL, Ruby EG (2006) *Vibrio fischeri* and its host: It takes two to tango. *Curr Opin Microbiol* 9:632–638.
- Nyholm SV, McFall-Ngai MJ (2004) The winnowing: Establishing the squid-vibrio symbiosis. *Nat Rev Microbiol* 2:632–642.
- Graf J, Ruby EG (1998) Host-derived amino acids support the proliferation of symbiotic bacteria. *Proc Natl Acad Sci USA* 95:1818–1822.
- Small AL, McFall-Ngai MJ (1999) Halide peroxidase in tissues that interact with bacteria in the host squid *Euprymna scolopes*. *J Cell Biochem* 72:445–457.

When exposed to NO, *V. fischeri* was grown in minimal salts (MS) medium, which contained (per liter) 500 mL 2× artificial seawater stock (31) supplemented with 1 mL 5.4%  $K_2HPO_4$ , 50 mL 1 M Tris-HCl buffer (pH 7.5), and 449 mL tap water. There was no significant loss in the viability of mutant or wild-type cultures when exposed up to 500  $\mu$ M of the NO generator DEA-NONOate (Cayman Chemical) (Fig. S2); 10 mM *N*-acetyl-D-glucosamine (MP Biomedicals) served as the carbon and nitrogen source, and when desired, the iron in the medium was depleted by the addition of 50  $\mu$ M of the deferrated iron chelator EDDHA (24).

**Spectroscopic Characterization of H-NOX<sub>Vf</sub>.** Protein complexes were prepared as described previously (7, 16, 32, 33). Purified protein was desalted into the spectral buffer [50 mM triethanolamine (10), 50 mM NaCl at pH 7.5] using a PD10 desalting column (GE Healthcare) in an anaerobic glove bag. The protein was then oxidized with 20-fold molar excess of  $K_3Fe(CN)_6$  and desalted to give the oxidized protein. Oxidized protein was reduced with a 50-fold excess of  $Na_2S_2O_4$  and desalted to give the reduced complex. NO was added by providing a 10-fold excess of DEA-NONOate to the reduced-protein preparation, and the protein was desalted to give the ferrous-NO complex. The H-NOX<sub>Vf</sub> spectra were recorded at 20 °C on a Cary 3E spectrophotometer.

**Expression Studies and Data Analysis.** The wild type and *hnoX* mutant were freshly grown in LB-salt medium at 28 °C with an OD<sub>600</sub> of 1.0. The precultures were diluted 1:100 and grown in MS medium to the early exponential phase (OD<sub>600</sub> 0.2–0.3). One-half of each culture was exposed to DEA-NONOate (80  $\mu$ M), which has a half-life of 16 min at 23 °C, and the other one-half of each culture was left untreated as control. After 30 min, cells from all of the cultures were fixed with RNeasy Protect Bacteria Reagent (Qiagen). Total RNA was isolated and purified using the RNeasy Mini Kit (Qiagen) according to the manufacturer's instructions. Procedures for total RNA labeling and hybridization to the *V. fischeri* Affymetrix chip (34) were performed based on the protocols from *E. coli* Genome Project at the University of Wisconsin at Madison. Three independent experiments were carried out on separate days.

The microarray data were normalized using the RMAExpress version 1.0 software (<http://rmaexpress.bmbolstad.com/>) with background adjustment, quantile normalization (35), and the Probe Level Model summarization method (36). Genes differentially expressed between experimental treatments were detected with a false discovery rate of 0.05 using the *limma* package (37) in the R statistical environment (38). Data were deposited to GenBank under accession number GSE115522.

**Growth Under Low Iron Conditions.** *V. fischeri* were grown in MS medium supplemented with 50  $\mu$ M deferrated ethylenediamine-N,N'-bis(2-hydroxyphenylacetic acid) and 10  $\mu$ M hemin (Sigma-Aldrich). Cultures were continuously exposed to NO by supplementation with two dosages of 80  $\mu$ M DEA-NONOate. Culture OD<sub>600</sub> was recorded until stationary phase, and then, growth rates were calculated for the period between 2 and 5 h after NO exposure.

**ACKNOWLEDGMENTS.** We thank A. Dunn for helpful suggestions, W. Davis and S. Splinter BonDurant for help in performing the microarray experiments, and M. Altura for confocal microscopy analyses. We are also indebted to M. J. McFall-Ngai and A. Richardson for insightful discussions. The authors also thank M. J. McFall-Ngai for animal facilities support through National Science Foundation Integrated Organismal Systems Grant 0517007. Y.S.D. is a fellow in the Department of Energy-funded Bringing Advanced Computational Techniques to Energy Research program (DE-FG02-04ER25627). This work was supported by National Institutes of Health Grant RR12294 (to E.G.R. and M.J.M.), National Institutes of Health Grant GM070671 (to M.A.M.), and National Institutes of Health Grant GM075273 (to T.J.D.).

15. Ruby EG, et al. (2005) Complete genome sequence of *Vibrio fischeri*: A symbiotic bacterium with pathogenic congeners. *Proc Natl Acad Sci USA* 102:3004–3009.
16. Boon EM, et al. (2006) Nitric oxide binding to prokaryotic homologs of the soluble guanylate cyclase beta1 H-NOX domain. *J Biol Chem* 281:21892–21902.
17. Winger JA, Derbyshire ER, Marletta MA (2007) Dissociation of nitric oxide from soluble guanylate cyclase and heme-nitric oxide/oxygen binding domain constructs. *J Biol Chem* 282:897–907.
18. Stevanin TM, Read RC, Poole RK (2007) The hmp gene encoding the NO-inducible flavohaemoglobin in *Escherichia coli* confers a protective advantage in resisting killing within macrophages, but not *in vitro*: Links with swarming motility. *Gene* 398: 62–68.
19. Chen Z, et al. (2007) Discovery of Fur binding site clusters in *Escherichia coli* by information theory models. *Nucleic Acids Res* 35:6762–6777.
20. Ruby EG, Asato LM (1993) Growth and flagellation of *Vibrio fischeri* during initiation of the sepiolid squid light organ symbiosis. *Arch Microbiol* 159:160–167.
21. Capece L, Estrin DA, Marti MA (2008) Dynamical characterization of the heme NO oxygen binding (HNOX) domain. Insight into soluble guanylate cyclase allosteric transition. *Biochemistry* 47:9416–9427.
22. D'Autréaux B, et al. (2004) Spectroscopic description of the two nitrosyl-iron complexes responsible for fur inhibition by nitric oxide. *J Am Chem Soc* 126:6005–6016.
23. D'Autréaux B, Touati D, Bersch B, Latour JM, Michaud-Soret I (2002) Direct inhibition by nitric oxide of the transcriptional ferric uptake regulation protein via nitrosylation of the iron. *Proc Natl Acad Sci USA* 99:16619–16624.
24. Graf J, Ruby EG (2000) Novel effects of a transposon insertion in the *Vibrio fischeri* *glnD* gene: Defects in iron uptake and symbiotic persistence in addition to nitrogen utilization. *Mol Microbiol* 37:168–179.
25. Semsey S, et al. (2006) Genetic regulation of fluxes: Iron homeostasis of *Escherichia coli*. *Nucleic Acids Res* 34:4960–4967.
26. Visick KL, Ruby EG (1998) The periplasmic, group III catalase of *Vibrio fischeri* is required for normal symbiotic competence and is induced both by oxidative stress and by approach to stationary phase. *J Bacteriol* 180:2087–2092.
27. Small-Howard AL (2004) *Biological Sciences* (University of Southern California, Los Angeles), p 393.
28. Park S, Imlay JA (2003) High levels of intracellular cysteine promote oxidative DNA damage by driving the fenton reaction. *J Bacteriol* 185:1942–1950.
29. Hussa EA, O'Shea TM, Darnell CL, Ruby EG, Visick KL (2007) Two-component response regulators of *Vibrio fischeri*: Identification, mutagenesis, and characterization. *J Bacteriol* 189:5825–5838.
30. Dunn AK, Stabb EV (2008) Genetic analysis of trimethylamine *N*-oxide reductases in the light organ symbiont *Vibrio fischeri* ES114. *J Bacteriol* 190:5814–5823.
31. Boettcher KJ, Ruby EG (1990) Depressed light emission by symbiotic *Vibrio fischeri* of the sepiolid squid *Euprymna scolopes*. *J Bacteriol* 172:3701–3706.
32. Boon EM, Huang SH, Marletta MA (2005) A molecular basis for NO selectivity in soluble guanylate cyclase. *Nat Chem Biol* 1:53–59.
33. Karow DS, et al. (2005) Characterization of functional heme domains from soluble guanylate cyclase. *Biochemistry* 44:16266–16274.
34. Antunes LC, et al. (2007) Transcriptome analysis of the *Vibrio fischeri* LuxR-LuxI regulon. *J Bacteriol* 189:8387–8391.
35. Bolstad BM, Irizarry RA, Astrand M, Speed TP (2003) A comparison of normalization methods for high density oligonucleotide array data based on variance and bias. *Bioinformatics* 19:185–193.
36. Bolstad BM (2004) *Biostatistics* (University of California, Berkeley, CA), p 156.
37. Smyth GK (2004) *Statistical Applications in Genetics and Molecular Biology* (Berkeley Electronic Press, Berkeley, CA), Vol 3.
38. R Development Core Team (2005) *R: A language and environment for statistical computing*. (R Foundation for Statistical Computing, Vienna, Austria.) Available at: <http://www.R-project.org>.
39. Stabb EV, Ruby EG (2003) Contribution of *pilA* to competitive colonization of the squid *Euprymna scolopes* by *Vibrio fischeri*. *Appl Environ Microbiol* 69:820–826.
40. Stone JR, Marletta MA (1994) Soluble guanylate cyclase from bovine lung: Activation with nitric oxide and carbon monoxide and spectral characterization of the ferrous and ferric states. *Biochemistry* 33:5636–5640.

## Supporting Information

### Supporting Materials and Methods

*Expression and purification of H-NOX<sub>Vf</sub>.* As described previously (1, 2), upstream and downstream primers (Table S1) containing NdeI and XhoI sites, were used to clone a PCR product containing *hnoX<sub>Vf</sub>* into the Ni-affinity, protein expression construct, pET-20b (Invitrogen Inc.). *E. coli* strain BL21DE3(pLysS) was transformed with the H-NOX<sub>Vf</sub> expression construct, and grown in a phosphate-buffered yeast extract broth with shaking at 37 °C to an OD<sub>600</sub> of 0.6-0.9. Expression was induced with the addition of 50 µM IPTG, and cultures were supplemented with 1mM aminolevulinic acid (Sigma-Aldrich). Shaking was continued and the temperature was lowered to 25 °C for another 16-18 h. Bacterial cells were harvested by centrifugation, and resuspended in buffer A (50 mM Na<sub>2</sub>H<sub>2</sub>PO<sub>4</sub>, 300 mM NaCl, 5% glycerol, pH 7.9) containing 20 mM imidazole. Cells were lysed by high-pressure homogenization (Avestin), and the lysate centrifuged for 1 h at 42,000 rpm. The clarified supernatant was passed over a Ni-NTA column (Qiagen) equilibrated with buffer A. The column was then washed with 12 column volumes of buffer A, and the H-NOX<sub>Vf</sub> protein was eluted with 5 column volumes of buffer A containing 250 mM imidazole. H-NOX<sub>Vf</sub> was further purified by gel filtration using a Sephacryl S-200 26/60 column equilibrated in a buffer containing 50 mM TEA, 50 mM NaCl, 5% glycerol and 5 mM DTT, at pH 7.5. Fractions containing the H-NOX<sub>Vf</sub> at >95% purity (as judged by Coomassie staining of protein gels) were pooled for spectral studies. As purified, the protein was a mixture of oxidized and reduced species.

*NO dissociation rate of H-NOX<sub>Vf</sub>.* To determine dissociation kinetics, anaerobic cuvettes were filled with 5 µM H-NOX<sub>Vf</sub> ferrous-NO complexes in spectral buffer and rapidly mixed 1:1 with anaerobic buffer containing 60 mM Na<sub>2</sub>SO<sub>4</sub> and saturated CO (3, 4). Binding of CO is not rate limiting in these experiments. The concentration of dithionite was varied between 3 and 300 mM with no observable effect on the rate. The dissociation of NO from the heme was monitored

at 423 nm as the formation of the Fe(II)-CO complex. Difference spectra were obtained by subtracting the first scan from each subsequent scan, and the increase in absorbance was plotted against time. Two parallel exponentials of the form  $f(x) = A X (1 - e^{-kx})$  were fitted to the plot. The experiment was performed seven times and the resulting rates averaged.

*Growth conditions.* Cultures of *E. coli* were incubated at 37 °C in either LB (5) or BHI (Difco) media. When needed, chloramphenicol (Cam) and kanamycin (Kan) were added to LB at 20 and 50 µg/mL respectively. Erythromycin (Erm) was added to BHI medium at 150 µg/mL.

Cultures of *V. fischeri* were grown at 28 °C in LBS (6) medium, solidified with 1.5% (w/v) Bacto-Agar (Difco Laboratories) as required. Cam, Erm and Kan were added to LBS at 5, 5, and 100 µg/mL, respectively.

*Resistance to NO exposure.* *V. fischeri* strains were grown aerobically in minimal-salts (MS) medium (see text) for approximately 4.5 h (OD<sub>600</sub> between 0.2 and 0.3). The cultures were split, and one half was challenged with the NO generator DEA-NONOate (500 µM); the other half was untreated. One hour after the challenge, 0.1 ml from each culture was serially diluted and plated onto LBS agar to determine the viable colony-forming units (CFUs). The percentage of viable cells was calculated by dividing the number of CFUs/mL in the NO-treated culture by that in the untreated culture (Fig. S2). The anaerobic experiments were performed similarly, except that all the cultures were grown under N<sub>2</sub>, and treated with only 40 µM DEA-NONOate.

*Determination of consensus promoter region.* Conserved sequence motifs (Fig. S3) were discovered using the MEME algorithm (7) on a set of candidate promoter sequences consisting of the 300 base-pairs upstream of predicted start codons. To identify additional occurrences of



candidate motifs in the genome, a library of promoter sequences was scanned with candidate motifs using the MAST algorithm (8).

*Animal colonization experiments.* The minimal infection dosage (MID) experiment and competitive colonization assay were carried out as previously described (9, 10). To calculate the efficiency of infection ( $ID_{50}$ ), we determined the percentage of animals that became colonized as a function of the inoculum dose. In these calculations we assumed that the log inoculum is paired with the logit of percent of animals colonized, and applied the log-logistic model to estimate the  $ID_{50}$  values of the wild type and  $\Delta hnoX$  (11). Wild-type and mutant strains were marked with a stable plasmid carrying either the *gfp* (pVSV102) or *rfp* (pVSV208) gene. The ratio of CFUs could be easily enumerated by their color. The relative competitiveness index (RCI) was calculated by dividing the ratio of mutant to wild-type CFUs in each light organ by the ratio of these strains in the initial inoculum. Because these plasmid markers are incompatible with the *hnoX*+ complementing plasmid vector, pVSV105 (Cam<sup>R</sup>), DM135, an Erm<sup>R</sup>-marked derivative of ES114 (12), served as the parent strain containing a wild-type *hnoX*. One hundred colonies were patched onto LBS agar containing Cam and Erm to determine the ratio of the  $\Delta hnoX$ -*hnoX*+ strain (Cam<sup>R</sup>Erm<sup>S</sup>) to DM135 (Cam<sup>R</sup>Erm<sup>R</sup>). Competition with chemical supplementation was performed similarly, except that 10  $\mu$ M FeCl<sub>3</sub> or 100  $\mu$ M NOS inhibitor, SMTC (S-methyl-L-thiocitrulline; Sigma-Aldrich), was provided in the seawater throughout the experiment period.

**Table S1.** Strains, plasmids and primers used in this study

Strain, plasmid or primer sequence	Relevant characteristics*	Source or reference
<u>Bacterial strains</u>		
<i>Escherichia coli</i>		
DH5α λpir	DH5α lysogenized with λpir	(12)
DH5α-T1 <sup>R</sup>	F- φ80 <i>lacZ</i> ΔM15 Δ( <i>lacZYA-argF</i> )U169 <i>recA1 endA1 hsdR17</i> (rk-, mk+) <i>phoA supE44 thi-1 gyrA96 relA1 tonA</i> (confers resistance to phage T1)	Invitrogen Inc.
BL21DE3(pLysS)	Protein overexpression strain (for H-NOX <sub>Vf</sub> )	Invitrogen Inc.
<i>Vibrio fischeri</i>		
ES114	Wild-type isolate from <i>E. scolopes</i> light organ	(13)
DM135	ES114 miniTn7- <i>gfp</i> , Erm <sup>R</sup>	(12)
YLW1	ES114::pYLW20, insertion mutant of <i>hnoX</i> , Erm <sup>R</sup>	this study
YLW8	ES114 carrying pVSV208, Cam <sup>R</sup>	this study
YLW9	ES114 carrying pVSV102, Kan <sup>R</sup>	this study
YLW25	ES114 carrying pVSV105, Cam <sup>R</sup>	this study
YLW37	ES114Δ <i>hnoX</i> (allelic exchange from pYLW26 into ES114), in-frame deletion mutant of <i>hnoX</i>	this study
YLW43	ES114 carrying pComhnoX, Cam <sup>R</sup>	this study
YLW66	ES114Δ <i>hnoX</i> carrying pVSV102, Kan <sup>R</sup>	this study
YLW67	ES114Δ <i>hnoX</i> carrying pVSV208, Cam <sup>R</sup>	this study
YLW69	ES114Δ <i>hnoX</i> carrying pVSV105, Cam <sup>R</sup>	this study

YLW70	ES114 $\Delta hnoX$ carrying pComhnoX, Cam <sup>R</sup>	this study
YLW109	DM135 carrying pVSV105, Erm <sup>R</sup> , Cam <sup>R</sup>	this study
YLW110	DM135 carrying pComhnoX, Erm <sup>R</sup> , Cam <sup>R</sup>	this study

### Plasmids

pCR-BluntII TOPO	TOPO PCR-cloning vector, Kan <sup>R</sup>	Invitrogen Inc.
pEVS104	<i>oriV</i> <sub>R6KY</sub> , <i>oriT</i> <sub>RP4</sub> , RP4-derived conjugative helper plasmid, Kan <sup>R</sup>	(12)
pEVS122	<i>oriV</i> <sub>R6KY</sub> , <i>oriT</i> <sub>RP4</sub> , <i>lacZ</i> $\alpha$ , Erm <sup>R</sup>	(12)
pVSV105	<i>oriV</i> <sub>R6KY</sub> , <i>oriT</i> <sub>RP4</sub> , <i>oriV</i> <sub>pES213</sub> , complementation vector, Cam <sup>R</sup>	(14)
pVSV208	<i>oriV</i> <sub>R6KY</sub> , <i>oriT</i> <sub>RP4</sub> , <i>oriV</i> <sub>pES213</sub> , <i>rfp</i> -tagged, Cam <sup>R</sup> ,	(14)
pET-20b	Overexpression plasmid (for H-NOX <sub>vf</sub> )	Invitrogen Inc.
pYLW20	~200 bp internal <i>hnoX</i> fragment (PCR product, primers ylw1 and ylw2) cloned into PstI/BamHI-digested pEVS122, Erm <sup>R</sup>	this study
pYLW24	~1.5 kb fragment upstream of <i>hnoX</i> start codon (PCR product, primers ylw3 and ylw4) cloned into pCR-BluntII TOPO, Kan <sup>R</sup>	this study
pYLW25	~1.5 kb fragment downstream of <i>hnoX</i> stop codon (PCR product, primers ylw5 and ylw6) cloned into SmaI-cut pEVS122, Erm <sup>R</sup>	this study
pYLW26	pYLW24 NheI-digested fused to NheI-digested pYLW25; <i>oriV</i> <sub>coIE1</sub> <i>oriV</i> <sub>R6KY</sub> , <i>oriT</i> <sub>RP4</sub> , $\Delta hnoX$ allele,	this study

	Kan <sup>R</sup> , Erm <sup>R</sup>	
pYLW30	pComhnoX, <i>hnoX</i> + complementing fragment (PCR product; primers ylw7 and ylw8) cloned into Sall/NdeI-digested pVSV105, Cam <sup>R</sup>	this study
<u>Primers</u> <sup>†</sup>		
ylw1	5'-AGG <i>ctg cag</i> GGC TTA CAC CGC TGT TGG TAC TTA-3'	this study
ylw2	5'-CGC <i>gga tcc</i> GAG GGT TCG CTT CAG CGT ATA ACT-3'	this study
ylw3	5'-CGA TCG TTG CTG ATG AAC-3'	this study
ylw4	5'-ATC <i>gct agc</i> AAT CCC TTT CAT AAA CAC TCC-3'	this study
ylw5	5'-ATC <i>gct agc</i> TAA ACG ATT AAG GCG GGA TAA-3'	this study
ylw6	5'-CTT CAA CCG CGA GAA TAG-3'	this study
ylw7	5'-AGT CTC GA <i>g tgc acT</i> GGG ATT CAG GAC TAC AG-3'	this study
ylw8	5'-TAC GCT AG <i>c ata tgc</i> ATC CAT TTA TCC CGC CT-3'	this study
hkc1	5'-GGA ATT <i>cat atg</i> AAA GGG ATT ATT TTT TCA-3'	this study
hkc2	5'-CCG <i>ctc gag</i> TTA TGA TTT AGT TAA GGT AAA-3'	this study

---

\*Abbreviations used: Cam<sup>R</sup>, chloramphenicol resistance; Erm<sup>R</sup>, erythromycin resistance; Kan<sup>R</sup>, kanamycin resistance; kb, kilobase; *gfp*, green fluorescent protein gene; *rfp*, red fluorescent protein gene.

<sup>†</sup>Sequences in italics indicate the restriction enzyme recognition sites introduced into primers (PstI: CTGCA/G; BamHI: G/GATCC; NheI: G/CTAGC; Sall: G/TCGAC; NdeI: CA/TATG).





VF0646	9.5	9.8	9.6	9.6	8.9	9.0	9.1	9.0	-1.5	9.5	10.0	9.9	9.8	9.1	9.3	9.1	9.1	-1.6	Thiol/disulfide interchange protein DsBa	
VF0656	7.7	7.6	7.3	7.7	6.5	6.1	6.7	6.4	-2.1	7.5	7.2	7.3	7.3	6.0	6.6	6.0	6.2	-2.2	endonuclease	
VF0670	6.2	5.9	5.8	5.9	4.9	5.5	5.4	5.3	-1.6	6.2	5.5	5.7	5.8	5.1	5.0	5.2	5.1	-1.6	urease accessory protein UreG	
VF0671	5.9	5.7	5.6	5.7	4.7	5.2	5.0	5.0	-1.6	5.7	5.1	5.2	5.4	4.8	4.4	4.8	4.7	-1.6	urease accessory protein UreF	
VF0683	6.5	6.1	6.1	6.2	5.5	5.6	5.7	5.6	-1.6	6.2	5.8	6.0	6.0	5.6	5.4	5.6	5.5	-1.4	putative transcriptional regulator	
VF0686	9.3	9.1	8.9	9.1	8.2	8.7	8.5	8.5	-1.5	9.1	8.9	8.9	9.0	8.3	8.5	8.5	8.4	-1.5	methionine transport ATP-binding protein	
VF0705	7.0	6.7	6.7	6.8	5.6	6.7	6.9	6.7	-2.1	6.8	6.2	6.6	6.5	6.7	6.5	6.0	5.9	-1.5	thiamine-mono-phosphate kinase	
VF0712	7.9	7.6	7.5	7.7	6.5	6.9	6.8	6.7	-2.0	7.9	7.3	7.5	7.5	6.9	6.6	6.9	6.8	-1.6	dimethylallyltransferase	
VF0713	8.1	7.9	7.6	7.9	6.6	7.1	6.8	6.9	-2.0	8.0	7.7	7.9	7.9	7.2	7.3	7.4	7.3	-1.5	exodeoxyribonuclease VII small subunit	
VF0719	6.9	6.0	5.8	6.2	4.7	4.5	5.3	4.8	-2.6	6.5	5.7	5.7	6.0	5.6	4.8	4.5	4.6	-2.6	putative sugar hydrolase	
VF0720	7.2	6.4	6.6	6.7	5.8	5.9	6.1	6.0	-1.7	7.0	6.0	6.5	6.5	4.4	5.3	5.6	5.4	-2.1	AmpG protein	
VF0727	10.2	10.0	10.3	10.1	9.2	9.6	9.5	9.5	-1.6	10.1	9.6	10.0	9.9	9.9	9.5	8.7	9.3	9.2	-1.7	Na(+)-translocating NADH-quinone reductase subunit C
VF0729	10.3	9.9	10.2	10.1	9.1	9.6	9.6	9.5	-1.6	10.1	9.7	9.9	9.9	9.2	8.5	8.9	8.9	-2.0	Na(+)-translocating NADH-quinone reductase subunit E	
VF0730	10.4	10.2	10.5	10.4	9.5	9.9	9.8	9.7	-1.6	10.3	9.9	10.2	10.1	9.5	8.8	9.4	9.2	-1.9	Na(+)-translocating NADH-quinone reductase subunit E	
VF0731	9.9	9.5	9.8	9.7	8.8	9.1	9.3	9.1	-1.6	9.7	9.3	9.6	9.6	8.8	8.1	8.5	8.5	-2.1	Na(+)-translocating NADH-quinone reductase subunit F	
VF0736	9.0	9.2	9.1	9.1	10.3	10.3	10.4	10.3	2.4	9.0	8.9	9.1	9.0	10.2	10.0	10.3	10.2	2.3	aminocacyl-histidine dipeptidase	
VF0736to737	5.1	4.4	3.7	4.4	6.7	6.2	6.7	6.5	4.4	4.7	4.3	4.0	4.3	5.8	5.5	5.1	5.5	2.2	aminocacyl-histidine dipeptidase	
VF0740	9.7	9.5	9.6	9.6	8.7	9.0	8.8	8.8	-1.7	9.7	9.4	9.4	9.5	8.7	8.7	8.9	8.8	-1.6	gamma-glutamyl kinase	
VF0741	8.8	8.3	8.3	8.4	7.3	7.6	7.5	7.5	-2.0	8.6	8.1	8.1	8.3	7.4	7.2	7.4	7.3	-1.9	gamma-glutamyl phosphate reductase	
VF0759	8.6	8.1	8.4	8.4	7.2	7.4	7.4	7.3	-2.1	8.5	7.9	8.3	8.2	7.5	6.8	7.5	7.2	-2.0	tRNA 2-methylthioadenosine synthase	
VF0762	9.1	8.7	9.0	8.9	8.3	8.2	8.4	8.3	-1.6	9.0	8.5	8.8	8.8	8.1	7.8	7.9	7.9	-1.8	hypothetical protein	
VF0763	9.1	8.8	8.9	8.9	8.2	8.4	8.5	8.4	-1.5	8.9	8.7	8.7	8.8	8.2	7.9	8.0	8.0	-1.6	peptidyl-tRNA hydrolase	
VF0772	8.2	7.6	7.9	7.9	7.2	7.1	7.6	7.3	-1.6	8.1	7.6	7.6	7.8	6.9	6.8	7.1	6.9	-1.8	2-dehydro-3-deoxyphosphoconate aldolase	
VF0778	8.7	8.3	8.4	8.5	7.4	7.4	7.7	7.5	-1.9	8.8	8.2	8.4	8.5	7.9	8.0	7.9	7.9	-1.4	UDP-sugar diphosphatase	
VF0795	10.3	9.8	10.1	10.1	9.1	9.4	9.3	9.3	-1.7	10.2	9.6	10.0	9.9	9.4	8.9	9.4	9.2	-1.6	trigger factor	
VF0799	8.5	8.0	7.9	8.2	7.2	7.5	7.5	7.4	-1.7	8.4	7.8	7.8	8.0	7.1	7.3	7.3	7.2	-1.7	DNA-binding protein HU	
VF0802	10.2	9.8	10.3	10.2	9.2	9.8	9.8	9.7	-1.6	10.2	9.8	10.3	10.2	9.2	8.7	9.2	9.2	-1.7	Trp-peptide transporter	
VF0818	8.6	8.3	8.3	8.4	6.8	7.3	7.5	7.2	-2.3	8.6	8.0	8.2	8.3	7.5	7.5	7.6	7.5	-1.7	citrate synthase	
VF0826	9.7	10.0	9.8	9.8	8.4	9.2	9.0	8.9	-1.9	9.7	9.6	9.8	9.7	8.9	8.7	8.7	8.8	-1.9	succinyl-CoA synthetase alpha subunit	
VF0832to833	5.9	5.7	5.6	5.7	4.8	5.1	5.3	5.1	-1.6	5.6	5.3	5.5	5.5	5.0	4.7	4.6	4.8	-1.6	hypothetical protein	
VF0836	10.1	9.6	9.8	9.8	8.8	8.7	9.1	8.8	-2.0	9.9	9.3	9.6	9.6	8.7	7.9	8.7	8.4	-2.3	phosphate acetyltransferase	
VF0851	5.3	5.7	5.9	5.9	5.0	5.2	5.2	5.0	-1.7	5.7	5.2	5.2	5.2	4.8	4.8	4.8	4.8	-2.0	transporter	
VF0857	6.9	6.2	6.3	6.5	5.7	5.4	6.0	5.7	-1.7	6.5	6.0	6.2	6.2	5.0	4.7	5.0	4.9	-2.5	3-oxoacyl-(acyl carrier protein) synthase	
VF0858	7.9	7.7	7.7	7.8	6.8	7.0	7.3	7.0	-1.6	7.7	7.4	7.7	7.6	6.9	6.7	6.7	6.8	-1.8	putative beta-hydroxydecanoyl-ACP dehydrase	
VF0859	7.7	7.6	7.5	7.6	6.8	6.8	7.1	6.9	-1.6	7.6	7.3	7.5	7.5	6.7	6.8	6.6	6.7	-1.7	3-ketoacyl-(acyl carrier protein) reductase	
VF0860	7.4	6.8	7.0	7.1	6.3	6.2	6.5	6.3	-1.7	7.3	6.7	6.9	7.0	5.9	6.0	6.1	6.0	-1.9	3-oxoacyl-(acyl carrier protein) synthase	
VF0862	10.9	10.5	11.2	10.9	10.1	9.5	10.9	9.9	-2.0	10.9	10.5	11.1	10.8	9.9	9.9	9.9	9.9	-1.9	50S ribosomal protein L25	
VF0878	4.9	4.7	4.7	4.7	6.5	6.0	6.4	6.3	3.0	4.7	4.5	4.5	4.5	5.5	5.3	5.5	5.4	1.9	multidrug resistance protein A	
VF0903	6.4	6.2	6.5	6.4	11.6	10.5	11.7	11.3	30.3	6.6	6.1	6.4	6.3	12.0	11.8	12.1	12.0	49.4	alanine dehydrogenase	
VF0911	7.3	7.1	7.2	7.2	6.2	5.9	6.8	6.4	-1.7	7.0	7.0	7.2	7.1	6.6	6.1	6.3	6.3	-1.7	inosine-guanosine kinase	
VF0922	8.6	7.9	7.9	8.2	9.2	8.7	9.2	9.1	1.9	8.6	7.8	7.9	8.1	8.9	9.0	9.2	9.0	1.9	glutaredoxin	
VF0946	7.7	7.6	7.3	7.5	6.6	6.9	6.8	6.8	-1.7	7.7	7.1	7.4	7.4	6.9	6.8	6.9	6.9	-1.4	ATP-dependent Zn protease	
VF0953	10.0	9.6	9.8	9.8	10.4	10.7	10.5	10.5	1.6	9.8	9.5	9.7	9.6	10.1	10.0	10.6	10.2	1.5	cytochrome d ubiquinol oxidase subunit I	
VF0954	9.6	9.2	9.4	9.4	10.0	10.1	10.2	10.1	1.6	9.5	9.1	9.2	9.2	9.7	9.6	10.0	9.8	1.4	cytochrome d ubiquinol oxidase subunit II	
VF0964	10.4	10.4	10.1	10.3	9.7	9.6	9.7	9.7	1.7	10.3	10.1	10.2	10.2	9.6	9.1	9.3	9.3	-1.9	ToI system periplasmic component YbgF	
VF0967	3.6	3.2	3.1	3.3	8.5	6.9	8.9	8.1	28.7	3.6	3.0	3.2	3.3	7.4	7.2	7.4	7.4	17.4	hypothetical protein	
VF0990	6.7	6.1	6.0	6.3	5.2	5.3	5.6	5.4	-1.9	6.7	5.7	5.9	6.1	5.2	5.2	5.1	5.2	-1.9	transporter, MFS superfamily	
VF0986	9.0	9.3	9.1	9.1	7.7	7.2	7.8	7.6	-2.9	8.9	9.0	9.1	9.0	6.7	7.1	6.6	6.8	-4.6	chitinase precursor	
VF0991	4.9	4.3	4.1	4.4	3.6	3.5	4.0	3.7	-1.6	4.4	3.8	4.2	4.1	3.3	3.2	3.2	3.3	-1.8	protein phosphatase 2C	
VF0994	5.0	4.3	4.0	4.4	3.5	3.6	3.9	3.7	-1.7	4.3	3.9	3.9	4.0	3.1	3.2	3.0	3.1	-1.9	hypothetical membrane associated protein	
VF0995	5.4	5.3	4.8	5.2	4.4	4.6	4.8	4.6	-1.5	5.2	4.9	4.9	5.0	4.1	4.1	4.1	4.1	-1.9	hypothetical protein	
VF1003	6.9	6.3	6.1	6.4	3.9	3.8	4.3	3.9	-2.9	6.1	4.0	4.7	5.0	3.4	3.6	3.4	3.4	-3.4	hypothetical protein	
VF1004	5.9	4.4	4.6	4.9	2.8	2.8	3.4	3.0	-3.8	5.6	3.4	4.0	4.3	2.7	2.7	2.5	2.7	-3.2	hypothetical cytosolic protein	
VF1006	6.1	5.8	5.2	5.7	4.4	5.0	4.4	4.6	-2.2	5.9	5.2	5.5	5.5	4.9	4.7	4.9	4.8	-1.7	hypothetical protein	
VF1010	11.4	11.1	11.5	11.3	9.0	9.5	9.6	9.3	-4.0	11.4	10.7	11.3	11.1	10.0	9.6	10.1	9.9	-2.3	hypothetical protein	
VF1010to1011	6.6	6.1	5.7	6.1	4.8	4.7	5.2	4.9	-2.3	6.1	5.7	5.9	5.9	4.5	4.8	4.6	4.6	-2.4	hypothetical protein	
VF1011	11.8	11.3	11.1	11.4	9.4	9.9	9.7	9.7	-3.3	11.9	10.9	11.2	11.3	9.9	10.1	10.0	10.0	-2.5	hypothetical protein	
VF1020	6.8	6.6	6.6	6.7	5.5	5.8	5.7	5.7	-2.0	6.5	6.3	6.6	6.5	5.7	5.1	5.4	5.4	-2.1	tRNA pseudouridine synthase A	
VF1026	6.1	5.2	5.0	5.4	6.3	6.4	6.5	6.4	-2.0	5.8	5.1	5.2	5.4	6.7	6.0	6.5	6.4	2.1	proton glutamate symport protein	
VF1039	6.7	6.2	6.0	6.3	5.3	5.5	5.7	5.5	-1.7	6.4	5.9	6.3	6.2	5.5	5.4	5.6	5.5	-1.6	short chain dehydrogenase	
VF1059	6.9	6.7	6.2	6.6	5.1	4.7	5.6	5.1	-2.8	6.4	5.9	6.4	6.2	4.3	4.9	4.7	4.7	-3.0	basic endochitinase	
VF1066	6.8	6.3	6.1	6.4	5.1	5.5	5.5	5.4	-2.1	6.6	6.2	6.3	6.4	5.8	5.4	5.3	5.5	-1.3	hypothetical protein	
VF1087	5.7	5.0	4.8	5.2	4.1	4.1	4.6	4.2	-1.9	5.4	4.6	4.9	5.0	3.9	3.8	4.1	3.9	-2.1	hypothetical protein	
VF1129	5.7	5.5	5.1	5.4	4.2	4.3	4.5	4.3	-2.2	5.5	5.0	5.3	5.3	4.7	4.4	4.7	4.6	-1.6	hypothetical protein	
VF1144	7.4	7.2	7.2	7.3	6.0	6.5	6.5	6.3	-1.9	7.3	6.7	7.1	7.0	6.5	5.9	6.5	6.3	-1.6	putative ATP-dependent RNA helicase RhlE	
VF1145	6.4	6.3	6.1	6.3	4.9	5.6	5.5	5.3	-1.9	6.4	5.9	6.0	6.1	5.6	5.0	5.5	5.3	-1.7	hypothetical protein	
VF1151	8.9	9.9	9.6	9.5	7.9	8.3	8.0	8.0	-2.7	9.1	10.4	10.0	9.8	7.9	7.7	7.6	7.8	-4.2	hypothetical protein	
VF1153	8.0	7.6	7.3	7.6	6.8	7.1	7.0	7.0	-1.5	7.9	7.4	7.4	7.6	6.9	6.9	7.1	7.0	-1.6	hypothetical protein	
VF1155	5.1	4.9	4.7	4.9	5.7	5.9	6.4	6.0	2.1	5.0	4.8	4.6	4.8	6.7	7.1	6.7	6.8	4.1	proton glutamate symport protein	
VF1173	9.7	10.1	9.9	9.9	11.3	11.7	11.8	11.6	3.3	10.0	10.2	10.0	10.0	10.3	11.0	10.7	10.7	1.6	hypothetical protein	
VF1176	6.1	5.7	6.0	5.9	5.1	5.1	5.5	5.2	-1.6	6.0	5.5	5.6	5.7	5.2	5.1	5.1	5.1	-1.5	L-serine dehydratase	
VF1187	8.2	8.0																		

VF1380	7.3	7.0	7.0	7.1	6.9	6.2	6.9	6.4	-1.6	7.1	7.0	7.0	7.0	6.4	6.3	6.0	6.3	-1.7	penicillin-binding protein
VF1390	8.0	7.4	7.8	7.5	6.2	7.4	7.4	7.4	-1.7	7.6	7.3	7.3	7.4	6.7	6.2	5.9	6.1	-2.5	carbohydrate binding domain protein
VF1399to1400	8.5	9.0	8.6	8.7	9.6	9.5	9.4	9.5	1.7	8.2	9.1	8.8	8.7	9.2	9.9	9.4	9.5	1.8	glycosyltransferase involved in cell wall biogenesis
VF1409	6.3	5.8	5.8	6.0	4.9	5.0	5.4	5.1	-1.9	5.9	5.5	5.8	5.8	5.0	4.2	5.1	4.8	-2.0	hypothetical cytosolic protein
VF1420	6.9	6.4	6.2	6.5	5.4	5.4	5.6	5.5	-2.0	6.6	6.4	6.3	6.4	4.9	4.9	4.6	4.4	-3.1	hypothetical protein
VF1421	6.4	6.1	5.9	6.1	5.3	5.2	5.2	5.2	-2.0	6.1	5.8	5.8	5.9	4.5	4.6	4.1	4.8	-2.8	transporter
VF1422	6.9	6.7	6.5	6.7	6.0	6.0	6.0	6.0	-1.6	6.2	6.0	6.0	6.0	6.5	6.5	6.4	5.0	-2.7	hypothetical protein
VF1451	6.3	6.0	6.1	6.1	4.8	4.8	5.1	4.9	-2.4	5.9	5.4	5.6	5.6	5.0	5.0	4.9	5.0	-1.6	nuclease
VF1471	5.6	6.0	4.9	5.5	7.4	8.4	8.2	8.0	5.7	5.4	5.6	5.0	5.3	5.8	6.5	6.5	6.3	2.0	hypothetical protein
VF1503	6.4	5.5	5.6	5.8	3.9	4.5	4.6	4.3	-2.8	6.1	5.1	5.4	5.6	4.4	4.0	3.8	4.0	-2.9	methyl-accepting chemotaxis protein
VF1541	7.2	7.1	7.0	7.1	6.3	6.6	6.6	6.5	-1.5	7.1	6.8	7.0	7.0	6.6	6.1	6.5	6.4	-1.5	phosphohydrolase (MutT/nudix family protein)
VF1542	7.5	7.2	7.3	7.3	6.2	6.4	6.3	6.3	-2.1	7.2	6.9	7.2	7.1	6.7	6.7	6.3	6.6	-1.5	acetyltransferase
VF1564	4.8	4.0	3.7	4.2	3.4	3.1	3.5	3.4	-1.8	4.1	3.7	3.5	3.7	2.7	3.1	3.0	2.9	-1.8	hypothetical protein
VF1565	7.0	6.4	6.4	6.6	5.6	5.7	6.0	5.8	-1.7	6.7	6.1	6.4	6.4	5.0	4.5	4.7	4.7	-3.2	cobalt transport ATP-binding protein CbiO
VF1566	7.4	6.5	6.5	6.8	5.7	5.6	6.0	5.8	-2.1	7.0	6.0	6.6	6.5	5.5	4.5	5.1	5.0	-2.9	hypothetical protein
VF1569	8.1	8.4	7.8	8.1	7.3	7.8	7.5	7.6	-1.5	8.2	8.1	8.1	8.1	7.5	7.5	7.4	7.4	-1.6	hypothetical protein
VF1587	10.9	10.8	10.8	10.8	11.2	11.6	11.5	11.4	1.5	11.0	10.8	10.7	10.8	11.6	11.6	11.6	11.6	1.7	lysine-arginine-ornithine-binding protein
VF1598	9.8	9.4	9.4	9.5	7.5	7.2	7.7	7.5	-4.2	9.7	8.7	9.4	9.3	7.2	7.4	7.0	7.2	-4.2	exochitinase
VF1615	7.5	7.2	6.9	7.2	8.0	7.9	8.3	8.1	1.8	7.3	7.5	6.9	7.2	8.6	8.5	8.6	8.6	2.5	hypothetical protein
VF1638	6.0	5.3	5.1	5.5	4.6	4.6	4.8	4.7	-1.8	5.7	5.1	5.1	5.3	4.7	4.5	4.7	4.6	-1.6	tRNA-dihydrouridine synthase
VF1640	6.6	6.3	6.1	6.3	5.1	5.4	5.4	5.3	-2.0	6.4	6.2	6.5	6.4	5.8	5.6	5.6	5.7	-1.6	hypothetical protein
VF1659	5.5	4.8	4.6	5.0	4.0	3.9	4.3	4.1	-1.9	5.3	4.2	4.6	4.7	3.9	3.5	4.2	3.9	-1.8	hypothetical protein
VF1660	6.6	6.2	5.9	6.2	5.2	5.0	5.1	5.1	-2.2	6.4	5.8	6.0	6.1	5.2	4.9	5.3	5.1	-1.9	hypothetical protein
VF1662	5.7	5.3	4.8	5.2	4.3	3.3	4.5	4.1	-2.3	5.5	5.0	4.8	5.1	4.0	4.4	3.9	4.1	-2.0	hypothetical DNA binding protein
VF1667	6.8	6.1	5.9	6.3	4.7	4.9	5.2	4.9	-2.5	6.5	5.5	6.0	6.0	5.0	4.9	5.0	5.1	-1.9	O-succinylbenzoate synthase
VF1668	6.8	6.0	6.1	6.3	4.8	4.9	5.2	5.0	-2.5	6.6	5.4	5.9	6.0	5.4	4.4	5.1	4.8	-2.2	naphthoate synthase
VF1669	6.5	6.2	6.0	6.0	5.2	5.7	6.0	6.0	-2.5	6.0	5.7	6.0	6.0	6.8	6.9	6.1	6.1	-2.2	hypothetical protein
VF1670	7.6	7.0	7.1	7.2	5.7	6.0	6.3	6.0	-2.3	7.3	6.6	7.0	7.0	6.3	5.4	6.2	6.0	-2.0	hypothetical protein
VF1673	9.1	8.4	8.5	8.7	6.0	6.9	6.4	6.4	-4.8	8.9	8.1	8.3	8.4	6.2	6.1	6.2	6.2	-4.9	aspartate aminotransferase
VF1721	12.2	12.0	11.9	12.0	8.1	8.6	8.9	8.5	-1.2	12.1	11.5	11.9	11.9	9.3	9.6	9.2	9.3	-5.7	5-methyltetrahydropteroylglutamate-- homocysteine methyltransferase
VF1722	7.6	7.1	6.9	7.2	5.5	6.1	6.1	5.9	-2.5	7.4	6.6	6.8	6.9	5.5	5.8	5.4	5.6	-2.6	transcriptional activator protein MetR
VF1726	8.8	8.5	8.4	8.6	7.7	8.0	7.7	7.8	-1.7	8.8	8.1	8.4	8.4	7.9	7.5	7.9	7.8	-1.6	hypothetical protein
VF1732	8.9	8.3	8.6	8.6	7.1	6.4	7.4	6.9	-3.1	8.7	8.3	8.5	8.5	7.0	7.0	6.9	7.0	-2.9	PTS system, glucose-specific IIBC component
VF1740	11.2	11.0	10.9	11.0	10.1	10.2	10.2	10.2	-1.7	11.2	10.7	11.0	10.9	10.1	9.4	9.4	9.6	-2.5	3-ketoacyl-(acyl-carrier-protein) reductase
VF1743	9.5	9.3	9.3	9.4	8.8	8.5	8.6	8.6	-1.7	9.4	9.0	9.2	9.2	8.7	8.0	8.4	8.4	-1.8	fatty acid phospholipid synthesis protein
VF1746	9.5	9.1	9.1	9.2	7.9	7.9	8.0	7.9	-2.5	9.4	8.9	9.0	9.1	8.9	8.1	8.5	8.1	-2.2	LSU ribosomal protein L32P
VF1745	11.8	11.5	11.5	11.6	10.4	10.4	10.6	10.5	-2.2	11.7	11.4	11.4	11.5	10.4	10.1	10.3	10.3	-2.3	hypothetical protein
VF1768	8.1	7.8	7.7	7.9	7.3	7.4	7.3	7.3	-1.5	7.9	7.5	7.8	7.7	7.3	7.0	7.2	7.2	-1.4	hypothetical protein
VF1775	10.7	10.6	10.7	10.7	9.7	10.3	10.0	10.0	-1.6	10.6	10.4	10.6	10.5	10.1	9.9	10.1	10.0	-1.4	isocitrate dehydrogenase [NADP]
VF1812	9.1	8.8	8.6	8.9	7.7	8.0	8.0	7.9	-2.0	9.1	8.6	8.8	8.8	8.3	8.4	8.2	8.3	-1.5	long-chain fatty acid transport protein precursor
VF1817	8.0	7.7	7.8	7.8	7.0	7.4	7.4	7.3	-1.5	7.9	7.5	7.7	7.7	7.4	7.2	7.0	7.0	-1.6	cytochrome c-type biogenesis protein CcmH
VF1825	8.8	8.4	8.5	8.5	7.9	7.8	7.9	7.9	-1.6	8.8	8.3	8.7	8.6	7.8	7.8	7.8	7.8	-1.7	hypothetical protein
VF1826	9.9	9.7	9.7	9.7	9.2	8.8	9.2	9.0	-1.6	9.9	9.5	9.8	9.7	8.9	8.9	8.8	8.9	-1.8	chemotaxis protein CheW
VF1827	8.4	8.4	8.3	8.3	7.8	7.7	7.8	7.8	-1.5	8.2	8.0	8.3	8.2	7.1	7.2	7.1	7.1	-2.1	CheW-like domain
VF1828	8.6	8.6	8.7	8.6	8.2	7.8	8.2	8.1	-1.4	8.4	8.1	8.6	8.4	7.4	7.1	7.4	7.3	-2.1	hypothetical protein
VF1894	11.3	11.2	11.1	11.2	10.3	10.5	10.3	10.4	-1.8	11.2	10.9	11.0	11.0	10.5	10.4	10.7	10.5	-1.4	phosphocarrier protein HPr
VF1895	11.0	10.8	10.8	10.9	9.8	10.2	10.0	10.0	-1.8	10.9	10.4	10.7	10.7	10.1	9.7	10.1	10.0	-1.6	phosphoenolpyruvate-protein phosphotransferase
VF1896	10.9	10.6	10.7	10.8	9.4	9.8	9.7	9.6	-2.2	10.9	10.0	10.6	10.5	9.9	9.1	9.8	9.6	-1.9	phosphoenolpyruvate-protein phosphotransferase
VF1899	6.1	5.6	5.5	5.7	4.8	4.9	5.3	5.0	-1.7	5.8	5.3	5.6	5.6	5.0	4.9	4.9	4.9	-1.6	hypothetical protein
VF1939	6.8	6.4	6.4	6.5	5.5	5.9	5.7	5.7	-1.8	6.6	6.1	6.2	6.3	5.8	5.6	5.7	5.7	-1.5	membrane-bound lytic murein transglycosylase D precursor
VF1966	8.6	8.8	8.5	9.1	8.2	8.3	8.4	8.3	-1.7	8.7	8.3	8.5	8.5	7.9	8.5	7.9	8.4	-1.4	protein export protein SecE
VF1967	8.9	8.3	8.7	8.6	7.6	7.9	7.7	7.7	-1.9	8.7	8.1	8.5	8.5	7.8	7.0	7.7	7.5	-1.9	protein export protein SecD
VF1968	9.0	8.4	8.6	8.7	7.6	7.9	7.8	7.7	-1.9	8.8	8.1	8.5	8.5	7.6	7.2	7.7	7.5	-1.9	preprotein translocase subunit YajC
VF1969	8.9	8.6	8.7	8.7	7.8	8.1	8.2	8.0	-1.6	8.8	8.4	8.7	8.7	8.1	7.5	7.9	7.8	-1.8	queuine tRNA-ribosyltransferase
VF1970	7.7	7.3	7.4	7.5	6.1	6.7	6.4	6.4	-2.1	7.6	6.7	7.2	7.2	6.3	5.6	6.2	6.0	-2.2	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
VF1990	8.6	8.1	8.4	8.4	6.7	7.1	7.0	7.0	-2.6	8.5	7.7	8.3	8.2	7.3	6.4	7.1	6.9	-2.4	peptidase family U32
VF1991	5.9	5.0	5.3	5.4	3.8	3.8	4.4	4.0	-2.6	5.5	4.4	5.0	5.0	4.2	3.5	4.0	3.9	-2.4	ferredoxin
VF2059	9.3	8.3	8.3	8.6	6.9	7.0	7.0	7.0	-3.2	9.2	7.7	8.2	8.3	6.9	5.9	6.9	6.6	-3.1	Na(+)-linked D-alanine glycine permease
VF2067	11.5	11.5	11.6	11.5	12.4	12.1	12.4	12.3	1.7	11.4	11.7	11.4	11.5	12.1	12.1	12.3	12.2	1.6	RNA polymerase sigma factor RpoS
VF2089	9.8	9.4	9.8	9.6	9.0	8.8	9.1	9.0	-1.6	9.7	9.2	9.6	9.5	9.0	8.4	8.9	8.7	-1.7	GTP-binding protein LepA
VF2110	7.5	7.2	7.4	7.4	6.0	6.5	6.4	6.3	-2.1	7.2	7.0	7.3	7.2	6.7	5.5	6.5	6.2	-2.0	Na(+)-linked D-alanine glycine permease
VF2149	7.6	6.8	7.1	7.1	6.2	6.0	6.5	6.2	-1.9	7.4	6.5	6.8	6.9	6.1	5.4	6.0	5.8	-2.0	ABC transporter ATP-binding protein
VF2150	7.8	7.2	7.5	7.5	6.5	6.3	6.5	6.4	-2.1	7.5	6.7	7.2	7.1	6.5	5.7	6.4	6.2	-2.1	iron(III)-transport system permease protein StuD
VF2170	7.6	7.1	7.4	7.4	6.3	6.5	6.7	6.5	-1.8	7.4	6.7	7.4	7.2	6.4	5.3	6.2	6.0	-2.3	pantoate-beta-alanine ligase
VF2221	10.5	9.9	10.3	10.2	9.1	8.9	9.4	9.1	-2.2	10.4	9.7	10.0	10.0	9.1	8.3	8.8	8.7	-2.5	30S ribosomal protein S9
VF2222	12.2	11.8	12.2	12.1	12.0	11.2	11.3	11.2	-1.6	12.1	11.6	12.2	12.0	11.5	10.4	11.3	11.0	-1.9	50S ribosomal protein L13
VF2227	8.5	8.2	8.3	8.3	7.4	7.6	7.9	7.7	-1.6	8.4	7.8	8.2	8.1	7.7	7.1	7.6	7.5	-1.6	DNA topoisomerase IV subunit A
VF2240	8.9	8.5	8.8	8.7	8.2	7.8	8.2	8.1	-1.6	8.8	8.3	8.5	8.5	7.8	7.2	7.7	7.6	-1.9	low-affinity inorganic phosphate transporter
VF2250	10.1	9.4	9.6	9.7	8.9	8.7	9.1	8.9	-1.7	9.9	9.2	9.4	9.5	8.9	8.0	8.4	8.7	-1.8	30S ribosomal protein S21
VF2251	11.3	10.9	11.0	11.1	10.3	10.2	10.4	10.3	-1.7	11.2	10.7	11.0	11.0	10.5	10.0	10.4	10.3	-1.6	GaII/YqeY domain protein
VF2289	7.0	6.6	6.6	6.7	5.9	5.9	6.1	6.0	-1.7	6.8	6.2	6.6	6.5	6.1	5.5	5.8	5.8	-1.7	DNA adenine methylase
VF2310																			

VF2528	10.6	10.1	10.0	10.2	12.9	13.2	13.1	13.0	7.1	10.5	10.4	10.0	10.3	12.6	12.7	12.5	12.6	5.0	keto-acid reductoisomerase
VF2529	5.6	4.7	4.5	4.8	5.5	4.7	6.0	5.7	1.9	5.2	4.1	4.1	4.6	4.8	6.7	6.0	6.0	6.0	transcriptional activator protein IrvY
VF2565	11.3	11.0	11.3	11.2	10.5	10.3	10.8	10.5	-1.6	11.2	10.7	11.1	11.0	9.8	9.3	9.7	9.6	-2.6	ATP synthase subunit C
VF2567	11.9	11.8	11.8	11.8	11.3	11.3	11.5	11.4	-1.4	11.8	11.6	11.8	11.7	11.2	11.0	11.1	11.1	-1.5	ATP synthase subunit B
VF2568	11.2	11.0	11.1	11.1	10.6	10.4	10.7	10.6	-1.4	11.1	10.6	10.9	10.9	10.3	10.1	10.2	10.2	-1.6	ABC transporter ATP-binding protein
VFA0015	6.6	6.3	6.4	6.5	5.3	5.8	5.6	5.6	-1.9	6.5	5.9	6.6	6.3	5.4	4.7	5.2	5.1	-2.4	hypothetical cytosolic protein
VFA0051	6.6	6.1	6.0	6.3	5.3	6.4	5.6	5.4	-1.8	6.6	6.1	6.2	6.3	5.4	5.5	5.4	5.6	-1.7	MshQ
VFA0075	5.9	5.7	5.2	5.6	4.8	4.7	5.3	4.9	-1.6	5.6	5.5	5.3	5.5	4.9	4.9	4.9	4.9	-1.5	MshD
VFA0078	5.4	4.9	4.8	5.0	3.9	4.0	4.2	4.1	-2.0	4.9	4.7	4.5	4.7	4.1	4.1	4.0	4.1	-1.5	gamma-glutamyltranspeptidase
VFA0086	6.9	6.5	6.4	6.6	4.9	5.1	5.3	5.1	-2.8	6.6	6.0	6.4	6.3	5.6	5.5	5.6	5.6	-1.7	PTS system, IIB component
VFA0128	4.5	4.3	3.4	4.1	3.0	2.8	3.5	3.1	-1.9	4.3	4.0	4.0	4.1	3.1	3.2	3.0	3.1	-2.0	ascorbate-specific PTS system enzyme IIC
VFA0129	5.3	4.8	4.6	4.9	3.9	4.0	4.5	4.1	-1.7	5.1	4.6	4.9	4.9	4.1	4.0	4.1	4.1	-1.7	N(6)-hydroxylysine O-acetyltransferase
VFA0162	12.1	11.9	11.8	11.9	10.2	10.4	10.4	10.4	-3.0	12.1	11.5	11.9	11.8	11.5	10.7	11.3	11.2	-1.6	siderophore biosynthesis lucC protein
VFA0163	11.6	11.3	11.3	11.4	9.5	9.6	9.9	9.7	-3.4	11.5	10.7	11.2	11.1	10.5	9.6	10.2	10.1	-2.1	L-lysine 6-monooxygenase
VFA0164	12.4	12.2	12.1	12.2	11.1	10.9	11.4	11.1	-2.1	12.2	11.7	12.1	12.0	10.8	10.4	10.7	10.6	-2.6	ferric aerobactin receptor precursor
VFA0165	12.2	12.1	12.0	12.1	10.9	10.8	11.0	10.9	-2.4	12.2	11.6	12.0	11.9	10.4	9.9	10.2	10.2	-3.4	hypothetical protein
VFA0166	10.1	9.9	9.8	9.9	9.3	9.2	9.5	9.3	-1.5	9.9	9.6	9.7	9.8	9.3	9.3	9.4	9.3	-1.4	methyl-accepting chemotaxis protein
VFA0168	6.2	5.7	5.5	5.8	4.6	5.1	5.3	5.0	-1.8	5.9	5.5	5.4	5.6	4.7	4.1	4.9	4.6	-2.1	hypothetical protein
VFA0172	5.4	4.6	4.3	4.8	11.9	11.8	12.1	11.9	142.6	5.1	4.6	4.5	4.7	12.2	12.2	12.2	12.2	176.6	3-hydroxyisobutyrate dehydrogenase and related proteins
VFA0173	8.0	7.7	7.6	7.8	7.0	6.9	7.1	7.0	-2.7	7.9	7.7	7.6	7.7	6.6	7.1	6.8	6.8	-1.9	probable transcriptional regulator SyrB
VFA0181	7.0	6.6	6.6	6.8	5.7	5.8	5.8	5.8	-1.0	6.7	6.5	6.4	6.5	5.9	5.7	6.0	5.8	-1.6	two component system histidine kinase
VFA0182	6.4	6.0	5.9	6.1	5.0	5.3	5.3	5.2	-1.8	6.2	6.1	6.1	6.1	5.8	5.4	5.6	5.6	-1.5	transporter, MFS superfamily
VFA0206	8.8	9.2	9.3	9.1	9.7	10.1	10.0	9.9	1.8	8.9	9.3	9.2	9.1	9.8	9.7	9.7	9.7	1.5	choloyglycine hydrolase
VFA0241	7.7	7.2	7.3	7.4	6.1	6.5	6.6	6.4	-2.0	7.6	6.7	7.3	7.2	6.5	6.7	6.6	6.3	-1.8	amino-acid abc transporter binding protein
VFA0285	8.9	8.9	8.5	8.8	9.5	9.5	9.6	9.5	1.7	8.7	9.1	8.5	8.8	9.5	9.6	9.6	9.3	1.7	hypothetical protein
VFA0304	6.4	6.3	6.2	6.3	5.8	5.6	6.0	5.8	-1.4	6.1	6.3	6.4	6.3	5.5	5.2	5.3	5.5	-1.9	3-oxo membrane protein
VFA0329	7.1	7.0	6.6	6.9	4.4	5.0	4.9	4.8	-4.4	4.8	4.6	4.8	4.6	4.1	3.5	3.9	3.9	-2.9	hypothetical protein
VFA0330	7.8	7.6	7.3	7.5	4.2	5.1	5.2	4.8	-6.5	7.6	6.6	7.3	7.2	5.7	5.0	5.4	5.4	-4.0	hypothetical protein
VFA0331	6.0	5.4	5.2	5.5	3.0	3.4	3.4	3.3	-4.6	5.8	4.6	5.1	5.2	3.9	4.0	4.1	4.0	-2.3	osmotically inducible protein C
VFA0335	7.8	7.3	7.1	7.4	8.5	8.7	8.9	8.7	-2.4	7.5	7.6	7.2	7.4	9.2	9.8	9.4	9.5	4.1	hypothetical membrane spanning protein
VFA0345	5.1	5.2	5.0	5.1	6.6	6.7	6.6	6.7	-1.8	6.6	6.7	6.6	6.6	6.2	6.7	6.4	6.4	-1.7	ATP-dependent RNA helicase
VFA0384	8.6	8.7	9.0	8.7	7.7	7.8	7.7	7.8	-2.0	8.5	8.2	8.8	8.5	8.2	6.9	7.8	7.6	-1.9	amino acid ABC transporter permease protein
VFA0390	7.3	7.3	7.2	7.3	6.6	6.8	6.8	6.7	-1.5	7.2	7.0	7.0	7.1	6.4	5.8	6.4	6.2	-1.8	hypothetical protein
VFA0438	5.1	5.0	4.9	5.0	6.3	5.6	6.6	6.2	4.2	5.0	5.0	4.8	4.9	5.6	6.1	5.6	5.8	1.8	asparagine synthetase [glutamine-hydrolyzing]
VFA0439	5.3	4.7	4.5	4.8	10.5	10.3	10.5	10.4	27.9	5.0	4.8	4.5	4.8	10.6	10.7	10.6	10.6	58.6	copper/silver resistance outer membrane protein
VFA0443	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	-3.6	7.3	7.3	7.3	7.3	7.3	7.3	7.3	7.3	-2.0	copper/silver resistance periplasmic protein
VFA0444	9.4	9.0	9.0	9.1	6.8	7.6	7.4	7.3	-3.6	9.2	8.7	8.8	8.9	8.0	7.6	8.0	7.9	-2.0	copper/silver resistance inner membrane protein
VFA0445	8.8	8.4	8.3	8.5	6.4	7.3	7.1	6.9	-3.0	8.6	8.0	8.2	8.3	7.4	6.9	7.4	7.2	-2.1	histidine ammonia-lyase
VFA0450	6.0	6.1	6.0	6.0	5.3	5.5	5.6	5.5	-1.5	5.7	5.8	5.8	5.7	4.7	5.2	4.7	4.9	-1.8	Sensory box/GDEF family protein
VFA0475	3.9	3.1	3.0	3.4	2.5	2.6	2.9	2.7	-1.6	3.4	3.2	3.2	3.3	2.5	2.6	2.7	2.6	-1.6	3D-hypothetical protein
VFA0479	5.3	5.8	5.6	5.9	3.0	2.3	3.5	3.2	-1.5	3.7	3.7	3.6	3.7	3.0	2.8	2.9	2.9	-1.7	rod shape-determining protein RodA
VFA0483	6.8	6.1	6.2	6.4	5.4	5.3	5.3	5.3	-2.0	6.4	5.8	6.1	6.1	5.7	4.6	5.2	5.2	-2.0	methyl-accepting chemotaxis protein
VFA0527	6.6	5.2	4.7	5.5	3.2	3.5	3.8	3.5	-4.1	6.3	3.6	4.3	4.7	2.9	3.0	2.8	2.9	-3.6	superfamily I DNA helicases and helicase subunits
VFA0542	7.3	7.0	7.0	7.1	6.5	6.3	6.8	6.5	-1.6	7.0	6.6	7.0	6.9	6.0	6.0	5.9	6.0	-1.9	hypothetical protein
VFA0544	7.1	6.5	6.6	6.8	6.0	6.0	6.4	6.1	-1.6	6.6	6.3	6.5	6.4	5.2	5.4	5.7	5.5	-2.0	hypothetical cytosolic protein
VFA0545	7.9	7.9	7.9	7.9	7.5	7.5	7.4	7.5	-1.4	7.9	7.7	7.8	7.8	7.0	7.2	7.1	7.1	-1.6	hypothetical protein
VFA0546	7.3	6.9	7.0	7.1	6.5	6.4	6.6	6.5	-1.5	6.9	6.8	6.8	6.9	6.2	6.0	6.0	6.0	-1.8	hypothetical protein
VFA0547	7.9	7.7	7.7	7.8	7.2	7.3	7.5	7.4	-1.4	7.8	7.6	7.7	7.7	7.1	6.9	7.1	7.0	-1.6	D-alanylalanine synthetase
VFA0570	8.8	8.6	8.4	8.6	7.8	8.0	7.7	7.8	-1.7	8.6	8.2	8.4	8.4	8.0	7.5	8.0	7.8	-1.5	transcriptional activator HlyU
VFA0587	6.9	6.6	6.6	6.7	6.0	6.2	6.3	6.2	-1.4	6.5	6.3	6.3	6.4	6.0	5.9	5.9	6.0	-1.3	3D-hypothetical protein
VFA0616	7.9	7.7	7.8	7.9	3.6	3.9	4.4	4.0	-2.1	4.8	5.0	5.1	5.3	3.8	3.7	3.3	3.6	-2.2	hypothetical protein
VFA0618	7.9	7.7	8.0	7.9	8.6	9.1	9.4	9.0	2.2	7.7	7.5	7.9	7.7	8.6	8.0	8.5	8.4	1.6	hypothetical protein
VFA0619	6.8	6.1	5.8	6.2	5.1	4.8	5.2	5.0	-2.3	6.7	5.6	6.0	6.1	5.1	4.8	4.7	4.9	-2.4	methyl-accepting chemotaxis protein
VFA0677	6.9	6.6	6.7	6.7	6.1	6.3	6.3	6.2	-1.4	6.6	6.3	6.4	6.4	6.0	5.8	5.7	5.8	-1.5	transporter
VFA0682	6.3	5.6	5.6	5.8	4.5	5.2	5.3	5.0	-1.8	6.0	5.4	5.6	5.6	4.6	4.7	4.6	4.6	-2.0	transaldolase
VFA0685	7.6	7.8	7.8	7.7	6.5	6.5	6.7	6.6	-2.2	7.6	7.9	7.8	7.8	6.9	6.9	7.2	7.0	-1.7	transketolase
VFA0686	7.0	7.1	6.9	7.0	5.2	5.4	5.7	5.4	-3.0	7.0	7.0	7.1	7.0	5.8	5.8	5.7	5.8	-2.4	mannose-6-phosphate isomerase
VFA0710	7.1	6.8	6.9	6.9	5.9	6.2	6.1	6.1	-1.9	6.8	6.4	6.8	6.7	6.2	6.0	6.2	6.1	-1.4	serine protease
VFA0714to07	4.1	4.3	3.8	4.1	3.2	3.5	3.5	3.4	-1.6	4.0	4.1	4.1	4.1	3.6	3.4	3.4	3.5	-1.5	chitin-dextrinase precursor
VFA0715	7.2	7.3	7.4	7.3	5.7	6.0	6.1	5.9	-2.6	7.0	6.8	7.2	7.0	6.0	5.5	6.0	5.9	-2.2	hypothetical protein
VFA0752	9.2	9.7	9.0	9.3	11.4	12.1	11.8	11.7	5.4	9.2	9.6	9.1	9.3	11.0	11.4	10.5	10.7	2.6	deoxyribodipyrimidine photolyase
VFA0753	8.4	8.9	8.2	8.5	10.5	11.2	10.7	10.8	4.9	8.3	8.7	8.3	8.4	9.3	10.3	9.6	9.7	2.5	hypothetical membrane protein
VFA0757	7.6	8.1	7.3	7.7	9.8	10.5	10.3	10.2	5.7	7.7	8.0	7.4	7.7	8.3	9.1	8.8	8.8	2.1	hypothetical membrane protein
VFA0758	8.9	9.4	8.9	9.1	11.1	11.7	11.5	11.4	5.2	9.1	9.4	8.9	9.1	8.8	10.5	10.2	10.2	2.1	hypothetical membrane protein
VFA0759	7.9	8.3	8.0	8.1	9.8	10.3	10.2	10.1	4.0	7.9	8.4	7.9	8.1	8.5	9.3	8.8	8.9	1.7	cydopropene-fatty-acyl-phospholipid synthase
VFA0760	9.7	10.2	9.7	9.9	11.5	12.0	11.7	11.7	3.5	9.9	10.2	9.7	9.8	10.2	11.0	10.7	10.6	1.6	transcriptional activator ChrR
VFA0765	9.2	9.9	9.0	9.4	11.1	12.0	11.6	11.6	4.6	9.5	9.7	9.1	9.4	10.0	10.6	10.3	10.3	1.8	cysteine desulfhydrase
VFA0768	7.2	7.1	7.2	7.2	8.6	8.1	8.6	8.4	2.3	6.9	7.2	7.1	7.1	8.8	8.5	9.0	8.8	3.8	agglutination protein
VFA0769	8.2	8.4	8.4	8.3	9.8	9.3	9.9	9.7	2.6	8.1	8.5	8.4	8.3	10.1	10.0	10.4	10.2	3.5	ToIR protein
VFA0777	7.5	7.4	7.4	7.4	6.5	7.1	6.9	6.8	-1.5	7.3	7.4	7.4	7.4	7.0	6.7	6.9	6.9	-1.4	hypothetical protein
VFA0780	7.3	7.3	7.3	7.2	5.9	6.5	6.4	6.3	-1.9	7.1	6.9	7.2	7.1	6.7	6.3	6.6	6.5	-1.6	ferrichrome-binding protein
VFA0782	6.3	6.2	6.3																



VFA1074	6.5	6.2	5.7	6.1	5.2	4.7	5.9	5.2	-1.9	6.1	5.9	5.7	5.9	4.2	4.0	4.1	4.1	-3.5	acC-like gene
VFA1095	6.8	6.5	6.5	6.5	5.6	5.5	6.2	5.7	-1.7	6.5	6.5	6.3	6.4	4.9	5.4	5.0	5.1	-2.4	HuvK, haloarabin
VFA1098	6.9	7.0	6.9	6.9	6.0	6.3	6.5	6.3	-1.6	6.7	7.0	6.8	6.9	5.4	5.6	5.4	5.4	-2.7	hypothetical protein
VFA1106	5.6	5.3	5.4	5.4	5.9	6.0	6.3	6.1	1.6	5.0	5.7	5.5	5.4	6.9	7.5	7.1	7.2	3.3	hypothetical protein
VFA1112	6.5	5.6	5.9	6.0	4.2	4.1	4.5	4.3	-3.3	6.2	5.8	5.9	5.9	4.8	5.3	4.4	4.8	-2.2	transporter, LyseE family
VFA1114	8.1	7.9	8.1	8.0	8.7	8.7	8.8	8.7	-1.6	8.0	7.9	8.0	8.0	9.3	9.1	9.2	9.2	2.4	cobalt-zinc-cadmium resistance protein CzcD
VFA1118	4.1	3.6	3.7	3.8	4.7	4.7	5.3	4.9	3.2	5.3	3.9	3.6	3.8	4.6	4.5	4.7	4.6	1.8	hypothetical protein
VFA1158	7.0	6.6	6.3	6.6	5.4	5.5	5.8	5.6	-2.1	6.8	6.2	6.3	6.4	5.6	5.9	5.7	5.7	1.7	hypothetical cytosolic protein
VFB04	9.0	9.2	9.1	9.1	9.3	9.7	9.7	9.6	1.4	8.8	9.2	9.1	9.0	9.6	9.5	9.7	9.6	1.5	hypothetical protein
VFB07	8.4	8.8	8.9	8.7	9.1	9.6	9.3	9.3	1.6	8.2	8.9	8.7	8.6	9.6	9.3	9.6	9.5	1.9	DNA repair protein RadC
VFB13	8.8	8.9	8.5	8.7	9.4	9.6	9.6	9.5	1.7	8.8	9.3	8.8	9.0	10.0	10.1	10.1	10.1	2.1	hypothetical protein
VFB40	6.4	6.7	6.6	6.6	5.6	6.1	6.0	5.9	-1.6	6.0	6.3	6.2	6.2	4.8	4.7	4.7	4.7	-2.9	channel protein VirB6
VFB42	6.4	6.7	6.8	6.7	5.8	6.4	5.9	6.0	-1.6	6.2	6.5	6.5	6.4	5.1	5.1	5.4	5.2	-2.2	channel protein VirB10
VFB43	6.6	6.9	6.7	6.7	5.9	6.3	6.0	6.1	-1.6	6.2	6.5	6.4	6.4	5.6	5.2	5.5	5.4	-1.9	VirB11 ATPase
VFB44	6.5	6.9	6.9	6.8	5.9	6.3	6.0	6.1	-1.6	6.2	6.7	6.6	6.5	5.1	5.1	5.1	5.1	-2.6	protein VirD4
VFB45	6.7	7.1	6.8	6.9	5.9	6.3	6.1	6.1	-1.7	6.4	6.9	6.5	6.6	5.2	5.7	5.3	5.4	-2.3	single-strand DNA binding protein
VFB46	6.5	7.0	6.8	6.8	5.7	6.3	5.8	5.9	-1.8	6.2	6.5	6.5	6.4	4.8	5.3	5.3	5.2	-2.4	DNA topoisomerase III
VFB47	6.2	6.7	6.8	6.6	5.0	5.8	5.3	5.3	-2.3	5.8	6.4	6.2	6.2	4.2	4.5	4.1	4.2	-3.8	outer membrane protein
VFB48	5.5	5.8	5.7	5.7	4.2	4.9	4.2	4.4	-2.4	4.9	5.5	5.3	5.2	3.3	3.5	3.2	3.3	-3.7	hypothetical protein
VFB49	4.1	4.7	4.5	4.4	3.2	4.0	3.0	3.4	-2.0	3.6	4.5	3.6	3.9	2.2	2.3	2.1	2.2	-3.3	hypothetical protein
VFB50	6.4	7.2	6.9	6.8	6.0	6.4	5.8	6.0	-1.7	6.2	6.7	6.6	6.5	5.4	5.7	5.3	5.5	-2.0	relaxase
VFB51	6.2	6.5	6.2	6.3	5.3	5.6	5.8	5.6	-1.7	5.7	6.3	6.1	6.1	4.9	5.0	4.7	4.9	-2.3	hypothetical protein
VFB52	7.4	7.6	7.6	7.5	6.8	7.0	7.2	7.0	-1.5	7.2	7.5	7.5	7.4	6.6	6.5	6.6	6.6	-1.8	hypothetical protein
VFB53	6.4	6.4	6.4	6.4	5.6	5.4	6.1	5.7	-1.6	6.1	6.2	6.2	6.1	5.2	4.9	5.0	5.1	-2.1	hypothetical protein
VFB54	5.6	5.7	5.7	5.7	4.2	4.3	4.5	4.3	-2.6	5.4	5.6	5.3	5.4	4.3	4.1	3.8	4.1	-2.5	attachment mediating protein VirB5 homolog
<b>40 genes*</b>																			
VF0006	9.2	8.8	8.8	8.9	5.5	6.5	6.3	6.1	-7.1	9.0	9.3	8.9	9.1	9.5	9.7	9.4	9.5	1.4	cystine transport ATP-binding protein
VF0007	8.7	8.0	8.4	8.4	4.9	5.8	5.9	5.5	-7.3	8.3	8.8	8.4	8.5	9.3	9.1	9.1	9.2	1.6	cystine transport system permease protein
VF0095	6.8	6.5	6.5	6.6	8.7	7.7	8.5	8.3	-3.3	6.5	6.2	6.4	6.4	6.2	6.1	6.2	6.2	-1.1	nitrogen regulation protein NR(I)
VF0098	11.6	11.8	11.8	11.7	13.1	12.8	12.9	12.9	2.3	11.5	11.5	11.7	11.6	11.3	11.3	11.3	11.3	-1.2	nitrogen regulation protein NR(B)
VF0407	10.5	10.1	10.0	10.2	10.9	11.5	11.9	11.9	2.3	10.5	10.2	9.8	10.2	9.8	9.1	9.4	9.4	-1.7	glutamine synthetase
VF0616	10.6	10.4	10.6	10.5	9.7	9.8	10.0	9.8	-1.7	10.6	10.5	10.5	10.5	10.7	10.9	11.0	10.9	1.3	ornithine carbamoyltransferase
VF0637	9.6	9.3	9.4	9.4	7.5	8.1	7.9	7.8	-3.0	9.6	8.6	9.4	9.2	9.5	9.3	9.5	9.4	1.2	RifZ family protein
VF0789	9.7	9.8	9.4	9.6	9.4	9.3	9.7	9.5	-1.8	9.7	9.8	9.3	9.7	9.3	9.3	9.5	9.3	-1.3	inositol-S-monophosphate dehydrogenase
VF0808	10.5	10.1	10.3	10.3	7.9	8.0	8.5	8.1	-4.5	10.4	9.9	10.2	10.2	9.5	9.9	9.9	9.8	-1.3	cell division inhibitor
VF0927	9.3	9.3	8.8	9.1	7.8	7.6	7.7	7.7	-2.6	9.2	9.4	9.0	9.2	8.7	9.4	8.9	9.0	-1.2	hypothetical protein
VF0970	7.0	7.1	6.7	6.9	7.7	8.4	8.3	8.1	-2.3	6.9	7.0	6.8	6.9	6.7	6.9	6.9	6.8	-1.1	C factor cell-cell signaling protein
VF1227	11.0	11.0	10.9	11.0	10.3	10.7	10.3	10.4	1.5	10.9	10.9	11.0	10.9	11.2	11.2	11.3	11.2	1.2	hypothetical protein
VF1234	10.1	10.3	10.2	10.2	7.9	8.9	8.1	8.3	-3.7	8.1	9.7	10.3	10.0	10.6	10.0	10.7	10.4	1.0	hemin receptor
VF1363	4.1	4.0	4.1	4.0	4.5	4.8	5.2	4.8	1.7	3.5	3.5	4.3	3.8	3.1	3.3	3.2	3.2	1.5	formate hydrogenase subunit 6
VF1472	6.1	6.5	5.5	6.0	8.2	9.1	8.9	8.7	6.4	6.2	6.5	5.7	6.1	6.6	7.3	7.1	7.0	-1.8	zinc finger protein
VF1512	8.3	8.0	8.0	8.1	7.2	7.3	7.6	7.4	-1.6	8.3	8.0	8.2	8.2	8.5	8.2	8.4	8.4	1.2	thiopurine S-methyltransferase
VF2151to2151	5.7	5.7	5.7	5.7	8.8	6.9	7.9	7.9	4.5	5.5	5.6	5.5	5.5	5.2	5.0	4.9	5.0	-1.4	iron(III)-binding protein
VF2152	5.3	5.2	5.3	5.3	9.2	7.1	8.6	8.3	-1.8	5.1	5.0	5.2	5.1	4.2	4.2	4.2	4.2	-1.2	ammonium transporter
VF2153	4.0	3.9	4.1	4.0	9.3	7.4	8.9	8.5	22.9	3.9	4.0	3.9	3.9	3.4	3.2	3.4	3.3	-1.5	nitrogen regulatory protein GlnK
VF2440	8.5	8.5	8.6	8.5	7.9	7.8	7.9	7.9	-1.6	8.5	8.4	8.5	8.5	8.6	8.6	8.6	8.6	1.1	Na(+)-driven multidrug efflux pump
VFA0157	7.9	7.6	7.5	7.6	6.4	6.5	6.3	6.4	-2.3	7.7	7.2	7.3	7.4	7.4	7.4	7.6	7.5	1.0	permease
VFA0171	1.8	1.9	2.0	1.9	2.8	2.7	2.9	2.8	-1.9	2.1	1.9	2.0	2.0	2.1	2.1	1.6	1.9	-1.0	hypothetical protein
VFA0191	9.3	9.1	9.0	9.1	7.0	7.0	7.3	7.1	-4.0	9.3	8.6	8.9	8.9	9.1	8.7	9.2	9.0	1.0	FliuE receptor precursor
VFA0192	8.2	8.0	7.7	8.0	6.0	6.4	6.5	6.3	-3.2	8.1	7.7	7.8	7.8	7.8	7.6	7.8	7.7	-1.1	hypothetical protein
VFA0193	8.0	7.8	7.7	7.8	6.0	6.6	6.5	6.4	-2.8	8.0	7.4	7.6	7.7	7.7	7.2	7.8	7.6	-1.1	ToIQ protein
VFA0199	8.7	8.5	8.5	8.6	6.9	7.1	7.1	7.0	-2.9	8.5	8.2	8.5	8.4	7.9	8.2	7.9	8.0	-1.3	oligosaccharide transport ATP-binding protein
VFA0333	7.1	7.1	6.7	7.0	4.1	5.1	4.3	4.5	-2.8	7.1	6.6	6.9	6.9	6.5	6.6	6.1	6.4	-1.4	protease II
VFA0695	8.3	7.6	7.9	7.9	9.4	9.3	9.4	9.4	2.7	8.1	8.0	7.6	7.9	7.8	7.2	7.9	7.7	-1.2	guanosine S'-monophosphate oxidoreductase
VFA0702	9.9	9.7	9.7	9.8	8.3	9.0	8.9	8.7	-2.1	9.7	9.4	9.8	9.6	9.6	9.7	9.9	9.8	1.1	glycine cleavage system protein H
VFA0762	10.1	10.3	10.1	10.2	11.4	11.6	11.5	11.5	2.6	10.0	10.3	10.0	10.1	10.0	10.7	10.4	10.4	1.2	putative dehydrogenase
VFA0763	9.4	9.8	9.4	9.5	11.0	11.4	11.2	11.2	3.2	9.4	9.8	9.4	9.5	9.7	10.2	10.0	10.0	1.0	short chain dehydrogenase
VFA0784	9.5	10.0	9.5	9.7	11.2	11.6	11.5	11.4	3.3	9.6	10.0	9.6	9.7	9.9	10.4	10.2	10.2	1.4	hypothetical transcriptional regulatory protein
VFA0784	8.0	8.2	8.2	8.1	7.1	7.5	7.1	7.2	-1.8	7.9	8.3	8.2	8.2	8.3	8.3	8.4	8.3	1.1	ferrichrome-iron receptor
VFA0827	8.0	7.6	7.7	7.8	6.6	6.4	6.8	6.6	-2.3	8.0	7.4	7.6	7.6	7.5	7.6	7.8	7.6	1.0	Ferric angucabactin-binding protein
VFA0842	6.0	5.8	5.3	5.7	7.0	7.4	7.7	7.4	-3.1	6.1	5.9	5.2	5.8	5.6	6.0	5.6	5.7	-1.0	outer membrane lipoprotein Blc
VFA0848	11.3	11.3	11.4	11.3	10.4	10.0	10.1	10.2	-2.2	11.2	11.3	11.3	11.3	11.2	11.2	11.5	11.3	1.0	hypothetical protein
VFA0849	9.7	9.9	9.5	9.7	10.7	10.4	10.9	10.7	-1.9	9.6	10.4	9.9	10.0	9.1	9.8	9.1	9.3	-1.6	glutathione S-transferase
VFA0851	6.1	6.0	5.7	6.0	6.8	6.6	7.0	6.8	1.8	6.1	6.1	6.1	6.1	5.9	6.0	6.0	6.0	-1.1	transcriptional regulatory protein
VFA0853	8.1	7.5	7.6	7.7	9.7	9.2	9.4	9.4	3.3	7.7	7.7	7.3	7.6	7.7	7.				

VF0536	9.4	9.4	9.4	9.4	8.6	9.1	8.8	8.8	-1.5	9.5	9.1	9.4	9.3	9.4	9.2	9.3	9.3	-1.0	alanyl-tRNA synthetase
VF0560	7.0	6.6	6.5	6.7	5.9	6.0	6.4	6.1	-1.5	6.6	6.3	6.6	6.6	6.5	6.3	6.4	6.4	-1.1	cysteine desulfhydrase
VF0614	8.4	7.9	8.7	8.4	6.9	7.1	6.9	7.0	-2.6	8.4	7.6	8.6	8.2	8.3	7.1	8.1	7.8	-1.3	myo-inositol-1(or 4)-monophosphatase
VF0619	10.5	10.2	10.3	10.3	9.5	9.9	9.7	9.7	-1.5	10.4	10.3	10.2	10.3	10.4	10.5	10.5	10.5	1.1	HesB protein family
VF0620	9.7	9.3	9.4	9.5	8.3	8.9	8.5	8.5	-1.9	9.6	9.2	9.3	9.4	9.2	9.0	9.2	9.1	-0.2	co-chaperone HscB
VF0621	9.2	8.7	9.0	9.0	7.9	8.3	8.3	8.2	-1.7	9.1	8.6	8.8	8.8	8.9	8.2	8.8	8.6	-1.2	chaperone protein HscA
VF0636	7.5	6.8	6.8	6.9	5.9	6.6	6.0	5.6	-2.2	7.4	6.5	6.9	6.9	6.6	6.0	6.5	6.4	-1.0	exocytobionuclease VII large subunit
VF0638	8.3	7.7	7.9	8.0	6.0	6.5	6.8	6.4	-2.9	8.3	7.0	7.8	7.7	7.8	7.5	7.7	7.7	-1.0	bifunctional GMP synthase/glutamine amidotransferase protein
VF0645to646	6.2	6.2	6.1	6.2	4.8	5.5	5.4	5.3	-1.9	6.1	6.4	6.3	6.3	6.1	6.5	6.1	6.2	-1.0	glutathione-dependent formaldehyde dehydrogenase
VF0651	7.6	7.4	7.3	7.4	6.4	6.8	6.8	6.7	-1.7	7.4	6.8	7.3	7.2	6.9	6.2	6.7	6.6	-1.5	amino-acid abc transporter binding protein
VF0654	6.6	6.7	6.5	6.6	5.5	5.9	5.6	5.7	-1.9	6.6	6.3	6.5	6.5	6.2	6.1	5.9	6.1	-1.3	hypothetical protein
VF0655	8.9	8.5	8.7	8.7	7.9	8.2	8.2	8.1	-1.5	8.7	8.4	8.4	8.5	8.1	8.0	8.1	8.0	-1.4	methionine transport system permease protein
VF0688	7.0	6.8	7.3	7.0	6.3	6.5	6.6	6.5	-1.5	6.8	6.7	6.7	6.7	6.9	7.0	7.1	7.0	1.2	oligopeptide transport system permease protein OppB
VF0689	7.3	7.3	7.5	7.4	6.6	6.9	7.0	6.8	-1.4	7.3	7.1	7.3	7.2	7.4	7.5	7.4	7.4	1.1	oligopeptide transport system permease protein OppC
VF0702	9.9	9.7	9.9	9.8	9.1	9.5	9.4	9.4	-1.4	9.7	9.7	9.7	9.7	9.9	9.7	10.0	9.9	1.1	3,4-dihydroxy-2-butanone-4-phosphate synthase
VF0703	10.1	9.9	9.9	10.0	9.2	9.4	9.4	9.3	-1.6	10.0	9.7	9.9	9.9	9.6	9.3	10.6	9.5	-1.3	riboflavin synthase subunit beta
VF0704	8.8	8.2	8.5	8.5	7.7	7.6	7.9	7.7	-1.7	8.7	7.9	8.3	8.3	7.9	7.5	7.9	7.7	-1.5	transcription antitermination protein NusB
VF0753	9.4	9.2	9.3	9.3	8.3	8.7	8.7	8.6	-1.6	9.3	8.9	9.1	9.1	8.9	8.6	9.0	8.8	-1.2	leucyl-tRNA synthetase
VF0764	9.9	9.8	10.0	9.9	9.0	9.4	9.1	9.1	-1.7	9.8	9.6	9.9	9.8	10.0	9.7	10.2	10.0	1.1	ribose-phosphate pyrophosphokinase
VF0768	8.2	8.0	8.3	8.1	7.3	7.6	7.6	7.5	-1.5	8.1	7.8	8.2	8.0	7.9	7.4	7.9	7.7	-1.2	peptide chain release factor 1
VF0776	5.6	4.5	4.9	5.0	6.1	5.5	6.4	6.0	2.1	5.5	4.8	4.5	4.9	5.0	4.7	4.9	4.8	-1.1	nitrite reductase [NAD(P)H] large subunit
VF0906	9.1	8.8	9.0	9.0	7.9	8.0	8.2	8.0	-1.9	8.9	8.5	8.7	8.7	8.6	8.4	8.7	8.6	-1.1	N-acetylglucosamine repressor
VF0907	10.8	10.7	10.7	10.7	9.8	10.0	10.1	9.9	-1.7	10.8	10.6	10.8	10.7	10.6	10.6	10.7	10.6	-1.1	N-acetylglucosamine-6-phosphate deacetylase
VF0916	9.0	8.7	9.0	8.9	8.0	8.5	8.3	8.3	-1.6	8.9	8.4	8.8	8.7	8.7	8.2	8.8	8.5	-1.1	phosphoglucumutase
VF0917	7.0	6.2	6.5	6.6	5.4	5.8	5.9	5.7	-1.8	6.7	5.9	6.4	6.4	6.3	5.5	6.1	6.0	-1.3	NIF3-related protein
VF0919	7.6	6.8	7.1	7.2	5.9	6.1	6.6	6.2	-2.0	7.4	6.5	6.8	6.9	6.6	6.3	6.7	6.5	-1.3	succinate dehydrogenase cytochrome b556 large membrane subunit
VF0920	7.9	7.6	7.8	7.4	5.7	6.9	6.7	6.2	-2.1	7.3	6.5	6.7	6.7	6.5	6.6	6.4	6.2	-1.4	succinate dehydrogenase anchor subunit
VF0921	8.1	7.8	8.1	8.0	6.8	7.4	7.3	7.2	-1.8	8.1	7.5	7.9	7.8	7.8	7.4	7.8	7.6	-1.1	succinate dehydrogenase catalytic subunit
VF0923	9.1	8.8	8.9	8.9	7.8	8.4	8.3	8.1	-1.7	9.0	8.4	8.7	8.7	8.5	8.2	8.4	8.3	-1.3	2-oxoglutarate dehydrogenase E1 component
VF0924	9.8	9.8	9.8	9.8	8.5	9.4	9.1	9.0	-2.1	9.6	9.5	9.9	9.7	9.3	9.2	9.2	9.3	-1.3	dihydropyrimidine acetyltransferase
VF0925	9.7	10.0	10.0	9.9	8.4	9.4	8.8	8.9	-1.7	9.7	9.5	9.9	9.7	9.0	9.0	9.0	9.1	-1.5	succinyl-CoA synthetase subunit beta
VF0978	6.5	6.2	6.2	6.3	6.3	6.3	6.3	6.2	-1.8	6.2	6.2	6.2	6.2	6.2	6.2	6.2	6.2	-1.4	acyl drug resistance protein B
VF0985	6.4	6.0	6.1	6.2	5.3	5.6	5.5	5.5	-1.6	6.3	5.8	5.9	6.0	6.2	5.7	6.4	6.1	-1.1	ABC transporter permease protein
VF0989	7.6	7.3	7.3	7.4	6.4	6.8	6.5	6.6	-1.8	7.4	6.9	7.3	7.2	7.3	6.7	7.5	7.2	-1.0	hypothetical protein
VF0992	8.5	8.4	8.4	8.4	7.4	8.0	7.7	7.7	-1.7	8.4	8.2	8.4	8.3	8.2	8.2	8.2	8.2	-1.1	glutamate decarboxylase
VF0996	7.9	7.9	7.7	7.8	6.3	6.9	7.0	6.7	-2.2	7.9	8.1	7.6	7.9	7.1	7.8	7.4	7.4	-1.4	DNA transformation protein TfoX
VF0997	7.7	7.9	7.8	7.8	7.0	7.3	7.8	7.7	-1.6	7.9	7.6	7.8	7.7	7.1	7.1	7.5	7.4	-1.1	transport ATP-binding protein TfoC
VF0933	8.0	8.0	7.8	7.9	7.1	7.3	7.1	7.1	-1.7	7.9	7.7	7.9	7.8	7.6	7.2	7.5	7.5	-1.3	electron transport complex protein RnfC
VF0934	7.8	7.5	7.4	7.6	6.8	7.2	7.0	7.0	-1.5	7.8	7.3	7.4	7.5	7.5	7.1	7.2	7.3	-1.2	electron transport complex protein RnfB
VF0947	7.0	6.6	6.4	6.7	5.7	6.1	6.0	5.9	-1.7	6.7	6.4	6.3	6.5	6.3	6.2	6.3	6.3	-1.1	methylytransferase
VF0948	7.3	7.0	7.1	7.1	6.5	6.5	6.7	6.6	-1.5	7.1	6.8	7.0	7.0	7.1	6.7	7.1	7.0	-1.0	hypothetical protein
VF0968	7.7	7.9	7.6	7.7	6.7	7.3	7.2	7.2	-1.5	7.6	7.9	7.5	7.7	7.6	8.1	7.9	7.9	-1.1	transporter, drug/metabolite exporter family
VF0982	7.7	7.0	7.0	7.2	6.0	6.3	6.2	6.2	-2.0	7.6	6.6	7.2	7.1	6.9	6.2	6.6	6.5	-1.5	hypothetical protein
VF0988	7.8	7.5	7.6	7.6	7.0	7.1	7.2	7.1	-1.4	7.7	7.6	7.6	7.6	7.2	7.5	7.0	7.2	-1.3	hypothetical protein
VF0999	5.0	4.2	4.2	4.5	3.5	3.7	3.8	3.7	-1.7	4.5	4.0	3.8	4.1	3.6	3.3	3.3	3.4	-1.6	ATP-dependent protease subunit
VF1007	7.5	7.5	7.2	7.4	6.4	6.9	6.6	6.6	-1.7	7.3	7.1	7.1	7.2	6.9	6.7	6.9	6.8	-1.3	primosomal replication protein N'
VF1008	7.3	7.1	6.9	7.1	6.7	6.5	6.7	6.7	-1.4	7.2	6.9	7.1	7.0	7.0	6.8	7.1	7.0	-1.2	acyl-CoA hydrolase
VF1027	7.5	7.6	7.3	7.5	6.8	7.0	7.1	6.9	-1.4	7.3	6.9	7.1	7.1	6.8	6.6	6.9	6.8	-1.3	tryptophan synthase subunit alpha
VF1028	8.7	9.0	8.8	8.8	7.9	8.3	8.4	8.2	-1.5	8.5	8.3	8.7	8.5	8.5	8.1	8.6	8.4	-1.1	tryptophan synthase subunit beta
VF1033	7.2	7.8	7.4	7.5	6.3	6.9	6.9	6.7	-1.7	7.1	6.7	7.1	7.0	7.2	7.3	8.0	7.5	-1.0	anthranilate synthase component I
VF1085	9.2	9.0	9.1	9.1	7.7	8.4	8.0	8.1	-2.1	9.0	8.9	9.1	9.0	9.2	8.7	9.1	9.0	-1.0	hypothetical protein
VF1089	4.9	5.4	4.9	5.4	4.3	4.7	4.8	4.5	-1.8	5.5	5.0	5.1	5.2	4.7	4.2	4.7	4.5	-1.2	beta-lactamase
VF1108	8.3	8.3	8.2	8.3	7.6	7.7	7.7	7.6	-1.5	8.2	8.1	8.3	8.2	8.0	8.1	8.2	8.1	-1.1	chaperone protein DnaJ
VF1109	6.7	6.5	6.5	6.6	5.7	5.8	6.1	5.9	-1.6	6.4	6.1	6.4	6.3	6.0	6.0	6.3	6.1	-1.2	hypothetical protein
VF1122	8.6	8.6	8.6	8.6	8.1	8.2	8.3	8.2	-1.3	8.5	8.6	8.6	8.6	8.7	8.8	9.0	8.8	1.2	prolyl endopeptidase
VF1130	6.8	6.0	6.0	6.3	5.4	5.3	5.4	5.4	-1.9	6.6	5.7	6.1	6.1	5.8	5.6	5.7	5.7	-1.4	23S rRNA methyltransferase
VF1133	5.4	5.2	4.6	5.1	3.9	4.5	4.2	4.2	-1.8	5.0	5.2	4.8	5.0	4.2	4.7	4.4	4.5	-1.4	methyl-accepting chemotaxis protein
VF1147	9.1	8.2	8.2	8.5	6.3	6.0	6.3	6.9	-3.1	9.2	8.4	8.3	8.6	8.4	9.1	8.8	8.8	1.1	carbon starvation protein A
VF1174	10.3	10.7	10.4	10.5	11.6	11.6	11.8	11.7	-2.0	10.5	11.0	10.5	10.7	10.6	11.5	10.9	11.0	1.2	hypothetical protein
VF1179	6.3	6.1	6.0	6.1	5.3	5.6	5.5	5.5	-1.6	6.0	5.9	6.1	6.0	6.0	6.0	6.0	6.0	1.0	para-aminobenzoate synthase component I
VF1180	8.1	8.1	8.2	8.1	7.6	7.7	7.7	7.7	-1.4	8.0	8.2	8.1	8.1	8.0	8.0	8.2	8.0	-1.1	lumarate hydratase
VF1190	11.6	11.3	11.2	11.4	10.2	10.6	10.1	10.3	-2.1	11.5	11.0	11.3	11.3	11.3	10.9	11.4	11.2	-1.2	hypothetical protein
VF1191	9.1	9.1	9.0	9.0	7.4	8.2	7.6	7.8	-2.5	9.1	8.7	9.1	9.0	8.7	8.1	8.6	8.5	-1.4	hypothetical protein
VF1193	9.2	9.0	9.2	9.1	7.7	8.2	8.2	8.1	-2.1	9.1	8.4	9.0	8.8	8.5	7.7	8.3	8.2	-1.6	hypothetical protein
VF1194	9.5	9.4	9.6	9.5	8.8	9.0	9.0	8.9	-1.5	9.4	9.1	9.4	9.3	9.0	8.7	9.1	8.9	-1.3	hydroxycyglutathione hydrolase
VF1210	8.3	7.9	8.1	8.1	7.4	7.4	7.6	7.5	-1.5	8.1	8.1	8.0	8.1	8.0	7.9	8.0	8.0	-1.1	sporulation-control protein
VF1220	10.3	10.7	10.5	10.5	9.3	10.0	9.5	9.6	-1.9	10.2	10.5	10.6	10.4	10.6	10.3	10.5	10.5	1.0	hemin transport system ATP-binding protein HmuV
VF1221	10.0	10.1	10.1	10.0	8.8	9.5	8.8	9.1	-2.0	9.9	9.7	10.0	9.9	9.9	9.3	9.8	9.7	-1.1	hemin transport system permease protein HmuU
VF1222	10.8	11.0	10.9	10.9	9.9	10.7	9.9	10.2	-1.7	10.7	10.8	11.0	10.8	11.0	10.7	11.1	11.0	1.1	hemin-binding periplasmic protein HmuT precursor
VF1223	10.4	10.6	10.4	10.5	9.6	10.2	9.4	9.7	-1.7	10.2	10.3	10.3	10.3	10.2	10.4	10.2	10.2	-1.1	ToIR protein
VF1224	10.4	10.7	10.5	10.6	9.9	10.4	9.7	10.0	-1.5	10.3	10.5	10.5	10.5	10.5	10.0	10.6	10.5	1.0	ToIC protein
VF1225	1																		

VF1644	6.3	5.9	6.0	6.1	5.2	5.3	5.2	5.2	-1.8	6.1	5.7	5.9	5.9	5.5	5.5	5.5	5.5	-1.3	cytoplasmic asparaginase I
VF1651	6.1	6.7	4.9	5.6	4.2	4.5	4.8	4.8	-2.1	6.0	5.4	5.4	5.6	4.6	5.1	4.9	4.9	-1.6	A-type carbonic anhydrase
VF1666	6.2	5.7	5.3	5.7	4.8	4.9	5.2	5.0	-1.7	5.9	5.1	5.4	5.4	4.9	4.7	4.9	4.8	-1.5	O-succinylbenzoic acid-CoA ligase
VF1685	6.9	6.1	6.4	6.5	5.5	5.6	6.0	5.7	-1.7	6.4	5.8	6.1	6.1	5.7	5.3	5.5	5.5	-1.5	recombination protein RecR
VF1687	8.2	8.0	8.0	8.1	7.3	7.8	7.6	7.6	-1.4	8.1	7.8	8.0	8.0	7.6	7.3	7.5	7.5	-1.4	DNA polymerase III subunits gamma and tau
VF1754	9.5	9.5	9.4	9.4	8.7	9.2	8.9	8.9	-1.4	9.5	9.2	9.4	9.4	9.2	9.1	9.3	9.2	-1.1	methionyl-tRNA synthetase
VF1764	9.4	9.1	8.7	9.1	8.3	8.5	8.4	8.4	-1.6	9.4	9.2	9.1	9.2	9.0	9.0	9.0	9.0	-1.2	transition initiation factor IF-1
VF1765	10.5	10.7	10.7	10.6	11.5	11.0	11.5	11.3	1.6	10.6	10.9	10.6	10.7	10.2	10.7	10.3	10.4	-1.2	ATP-dependent Clp protease ATP-binding subunit ClpA
VF1784	9.5	9.4	9.5	9.5	8.6	9.1	8.9	8.8	-1.5	9.5	9.3	9.5	9.4	9.5	9.4	9.6	9.5	-1.0	tRNA (5-methylaminoethyl-2-thiouridylyl)-methyltransferase
VF1785	9.2	9.0	9.1	9.1	8.1	8.7	8.2	8.3	-1.7	9.0	8.6	8.8	8.8	8.8	8.6	9.0	8.8	1.0	hypothetical protein
VF1787	7.1	7.0	6.7	6.9	6.1	6.2	6.5	6.3	-1.6	6.9	6.7	6.9	6.8	6.7	6.7	6.8	6.7	-1.1	transcriptional regulator, AraC family
VF1820	8.5	8.3	8.5	8.4	7.6	8.1	8.0	7.9	-1.5	8.4	8.0	8.4	8.3	8.1	7.8	8.0	8.0	-1.3	cytochrome c-type biogenesis heme chaperone
VF1835	9.5	9.3	9.4	9.4	9.8	10.6	10.0	10.1	1.6	9.6	9.2	9.5	9.4	9.4	8.8	9.3	9.2	-1.2	flagellar biosynthesis regulator FlcN
VF1836	8.2	8.0	7.9	8.0	8.4	9.3	8.7	8.8	1.7	8.3	7.7	8.0	8.0	8.2	7.5	8.2	8.0	-1.2	flagellar biosynthesis protein
VF1837	7.0	6.8	6.8	6.9	7.2	7.9	7.4	7.5	1.5	6.9	6.7	6.7	6.8	6.9	6.5	6.8	6.7	-1.0	flagellar biosynthesis protein
VF1862	8.8	8.8	9.1	8.9	8.2	8.3	8.4	8.3	-1.6	8.8	8.6	8.8	8.7	8.6	8.9	8.7	8.7	-1.0	flagellin
VF1881	9.2	9.0	9.2	9.2	9.7	9.5	9.9	9.7	1.5	9.2	9.3	9.0	9.2	9.0	9.3	9.2	9.2	1.0	negative regulator of flagellin synthesis FlgM
VF1882	8.3	8.4	8.3	8.4	9.0	8.9	9.0	9.0	1.5	8.3	8.7	8.4	8.5	8.3	8.5	8.6	8.5	1.0	FlgN
VF1887	9.3	8.9	8.9	9.0	8.2	8.4	8.3	8.3	-1.6	9.3	8.7	8.8	8.9	8.9	8.6	8.9	8.8	-1.1	glutamyl-tRNA synthetase
VF1889to189t	3.5	3.3	3.2	3.3	2.7	2.6	2.9	2.8	-1.5	3.6	3.3	3.3	3.4	2.9	3.1	2.8	2.9	-1.4	outer membrane porin protein precursor
VF1897	10.6	10.2	10.5	10.4	9.7	9.6	9.8	9.7	-1.6	10.6	10.0	10.3	10.3	9.9	9.7	10.1	9.9	-1.3	glucose-specific PTS system enzyme IIA component
VF1900	6.4	5.9	5.8	6.0	4.9	5.0	5.4	5.1	-1.9	6.2	5.5	5.7	5.8	5.2	5.1	5.3	5.2	-1.5	COME operon protein 3
VF1940	5.8	5.1	5.0	5.3	4.3	4.4	4.8	4.5	-1.8	5.4	4.9	4.9	5.1	4.7	4.7	4.5	4.6	-1.4	hypothetical protein
VF1943	5.8	5.3	5.4	5.5	6.3	6.4	7.1	6.6	2.2	5.5	5.3	5.0	5.3	4.8	5.4	5.3	5.1	-1.1	cytochrome c-554(548)
VF1944	7.6	7.7	7.6	7.6	8.4	9.0	9.1	8.8	2.3	7.6	7.5	7.4	7.5	7.6	8.1	7.8	7.8	1.3	cell cycle protein MesJ
VF1961	9.8	9.4	10.0	9.7	8.7	8.6	8.8	8.7	-1.5	9.7	9.3	9.7	9.6	9.3	8.5	9.3	9.0	-1.5	elongation factor Ts
VF1962	12.0	12.1	11.7	11.8	11.2	11.6	11.6	11.6	-1.5	12.0	11.6	11.6	11.9	11.7	11.5	11.8	11.7	-1.5	110S ribosomal protein S2
VF1964	8.3	8.3	8.4	8.3	8.0	7.8	7.9	7.9	-1.4	8.1	8.0	8.1	8.1	8.4	8.2	8.5	8.3	1.2	PII uridylyl-transferase
VF1965	7.7	8.2	7.7	7.9	7.2	7.0	7.4	7.2	-1.6	7.6	8.2	7.9	7.9	8.0	8.1	8.0	8.0	1.1	putative structural protein
VF2075	11.9	11.4	11.5	11.6	11.0	10.8	11.1	11.0	-1.5	11.9	11.3	11.4	11.5	11.1	10.8	11.1	11.0	-1.4	phosphopyruvate hydratase
VF2082	6.6	5.8	5.9	6.1	5.2	5.1	5.5	5.3	-1.8	6.4	5.6	5.8	5.9	5.6	5.4	5.3	5.4	-1.4	sensor protein BarA
VF2085	8.6	7.5	7.7	7.8	6.5	7.0	7.8	7.8	-1.4	7.1	7.7	7.5	7.7	7.6	7.3	7.7	7.6	-1.1	ribose-5-phosphate isomerase A
VF2115	8.2	7.8	7.2	7.7	9.0	8.7	9.5	9.0	2.5	8.1	7.8	7.5	7.8	7.8	8.5	8.0	8.1	1.2	formate acetyltransferase
VF2129	6.5	5.8	5.6	6.0	4.7	4.9	5.2	4.9	-2.1	6.2	5.1	5.5	5.6	5.4	4.7	5.4	5.2	-1.3	adenosylcobinamide-phosphate synthase
VF2131	7.1	6.7	6.6	6.8	5.9	6.2	6.3	6.1	-2.0	6.9	6.4	6.8	6.7	6.7	6.7	6.7	6.7	-1.0	cell wall endopeptidase, family M23/M37
VF2138	6.6	6.0	5.8	6.1	4.7	5.2	5.5	5.1	-1.6	6.4	5.8	5.9	6.0	5.4	5.5	5.3	5.4	-1.5	two-component sensor histidine kinase
VF2139	6.5	6.0	5.9	6.1	6.0	6.2	5.8	5.6	-1.6	6.5	6.7	5.9	6.0	5.6	5.2	5.3	5.3	-1.5	chitinoglycosaccharinase-binding protein
VF2189	8.3	8.2	8.2	8.3	9.3	8.4	9.5	9.0	1.7	8.2	8.6	8.2	8.3	7.8	7.9	7.7	7.8	-1.4	dephospho-CoA kinase
VF2228	8.4	7.9	8.1	8.1	7.3	7.5	7.5	7.5	-1.6	8.2	7.5	8.0	7.9	7.5	6.9	7.5	7.3	-1.5	DNA topoisomerase IV subunit B
VF2246	7.8	7.4	7.3	7.5	6.5	7.0	6.9	6.8	-1.6	7.7	7.1	7.2	7.3	7.0	6.8	7.1	7.0	-1.3	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase
VF2247	7.7	7.6	7.4	7.6	7.0	7.1	7.0	7.0	-1.4	7.7	7.5	7.4	7.5	7.3	7.5	7.4	7.4	-1.1	dihydroneopterin aldolase
VF2260	6.9	6.4	6.5	6.2	8.3	7.0	8.4	7.9	-1.6	6.6	6.7	5.9	6.4	6.7	6.1	6.0	6.5	-1.1	hypothetical protein
VF2265	8.3	7.9	7.8	8.0	7.1	7.5	7.5	7.4	-1.5	8.2	7.6	7.9	7.9	7.5	7.4	7.4	7.4	-1.4	probable activator protein in leuABCD operon
VF2276	6.2	6.1	5.7	6.0	5.1	5.2	5.6	5.3	-1.6	6.1	5.7	5.7	5.8	5.1	5.7	5.4	5.4	-1.3	cell division protein FtsN
VF2280	9.5	9.1	8.3	9.0	7.6	7.8	8.0	7.8	-2.2	9.5	8.9	8.7	9.0	8.2	9.0	8.2	8.6	-1.5	catabolite gene activator Vfr
VF2288	8.3	7.7	8.0	8.0	7.0	7.1	7.4	7.2	-1.8	8.2	7.3	7.9	7.8	7.7	7.2	7.8	7.6	-1.2	ribose-phosphate 3-epimerase
VF2308	10.6	10.2	10.4	10.4	9.9	9.7	10.4	10.4	-1.4	10.5	10.3	10.2	10.4	10.3	10.1	10.1	10.1	-1.2	5,10-methylenetetrahydrofolate reductase
VF2326	7.6	7.5	7.4	7.5	6.9	7.1	7.1	7.0	-1.4	7.5	7.3	7.4	7.4	7.3	7.2	7.3	7.3	-1.1	N-acetylmuramoyl-L-alanine amidase
VF2349	8.9	8.1	8.2	8.4	7.2	7.5	7.6	7.4	-2.0	8.7	7.7	8.2	8.2	7.6	7.1	7.7	7.5	-1.7	export protein SecB
VF2350	9.6	9.1	9.1	9.3	8.2	8.5	8.5	8.4	-1.8	9.5	8.8	9.1	9.1	8.7	8.4	8.6	8.6	-1.5	rhodanese-related sulfurtransferase
VF2397	9.2	9.0	8.2	8.8	8.0	7.8	8.1	8.0	-1.8	9.3	8.6	8.7	8.9	8.0	8.4	8.2	8.2	-1.6	DNA-binding protein HU
VF2401	7.1	7.1	7.0	7.1	8.4	7.1	7.4	7.4	-1.7	7.0	7.3	7.1	7.2	7.3	7.5	7.1	7.3	-1.1	protein TngI
VF2424	7.5	7.0	6.8	7.1	6.3	6.2	6.6	6.4	-1.7	7.4	6.7	6.9	7.0	6.5	6.5	6.6	6.5	-1.4	pantothenate kinase
VF2439	6.6	6.1	5.7	6.1	5.0	5.2	5.7	5.3	-1.8	6.4	5.7	5.9	6.0	5.4	5.5	5.3	5.4	-1.5	soluble pyridine nucleotide transhydrogenase
VF2441	10.9	10.7	10.8	10.8	10.4	9.9	10.0	10.1	-1.7	10.8	10.6	10.7	10.7	10.8	10.8	11.0	10.9	1.1	hypothetical protein
VF2457to245t	4.6	5.0	4.2	4.6	5.3	5.1	5.6	5.3	-1.6	4.7	5.1	4.8	4.9	5.0	5.2	4.8	5.0	1.1	hypothetical protein
VF2561	10.6	10.0	10.3	10.3	9.5	9.4	9.4	9.4	-1.6	10.7	9.6	10.2	10.2	10.0	9.2	9.7	9.6	-1.4	cold shock protein
VFA0003	4.8	4.7	4.5	4.6	3.9	4.3	4.2	4.1	-1.4	4.4	4.2	4.4	4.3	4.3	4.1	4.3	4.2	-1.1	hypothetical protein
VFA0008	6.3	6.1	6.2	6.2	5.3	5.5	6.0	5.6	-1.5	6.2	6.4	6.2	6.3	6.2	6.6	6.1	6.3	1.0	phospholipase
VFA0018	6.5	5.7	5.8	6.0	4.9	5.1	5.6	5.2	-1.8	6.4	5.7	5.9	6.0	5.4	5.5	5.7	5.6	-1.4	ribosome-associated GTPase
VFA0034	7.3	7.1	7.0	7.1	7.7	7.4	7.6	7.6	1.3	7.2	7.2	7.1	7.2	6.9	6.9	6.8	6.9	-1.2	transcriptional regulators, LysR family
VFA0049	7.6	7.6	7.5	7.5	6.5	7.1	7.1	6.8	-1.6	7.4	7.3	7.5	7.4	7.2	6.9	7.2	7.3	-1.2	hypothetical protein
VFA0074	7.7	7.5	7.5	7.6	6.7	6.9	7.1	6.9	-1.6	7.7	7.2	7.5	7.5	7.2	7.0	7.3	7.2	-1.3	hypothetical protein
VFA0076	5.7	5.0	4.5	5.0	3.1	4.0	4.2	3.8	-2.4	5.4	5.0	5.0	5.1	4.3	4.5	4.2	4.3	-1.7	MshP
VFA0077	5.3	4.7	4.4	4.8	3.0	3.4	4.1	3.5	-2.4	5.0	4.1	4.3	4.5	5.0	3.6	3.8	3.7	-1.8	MshO
VFA0079	6.0	5.4	5.3	5.6	4.3	4.4	5.0	4.6	-2.0	5.6	5.4	5.6	5.5	5.7	5.2	4.5	4.7	-1.6	hypothetical protein
VFA0091	8.7	8.6	8.7	8.7	8.0	8.0	8.3	8.1	-1.5	8.5	8.5	8.5	8.5	8.6	8.5	8.7	8.6	1.0	peptidase family M3
VFA0108	7.6	7.1	7.2	7.3	5.8	5.8	6.6	6.1	-2.3	7.4	7.5	7.3	7.4	6.7	7.3	6.8	6.9	-1.4	hypothetical protein
VFA0131	6.5	5.5	5.4	5.8	4.0	4.7	4.9	4.5	-2.5	6.2	5.1	5.4	5.6	5.1	4.4	4.7	4.8	-1.8	CAAX amino terminal protease family
VFA0149	9.3	9.3	9.1	9.2	8.3	8.7	8.5	8.5	-1.6	9.2	9.3	9.4	9.3	9.2	9.2	9.2	9.2	-1.1	hypothetical protein
VFA0150	9.7	9.5	9.3	9.5	8.7	9.0	8.8	8.8	-1.6	9.7	9.4	9.5	9.5	9.3	9.4	9.3	9.3	-1.1	hypothetical protein
VFA0156	8.9	8.7	8.8	8.8	8.2	8.2	8.0												

VFA0541	7.5	7.3	7.1	7.3	6.5	6.8	6.9	6.8	-1.5	7.2	6.9	7.2	7.1	6.8	6.5	6.7	6.7	-1.4	hypothetical protein	
VFA0555	5.2	4.8	4.5	4.9	3.7	7.9	4.4	4.9	-1.9	5.1	4.4	4.5	4.7	4.1	4.7	4.0	4.1	-1.5	phosphate-binding protein	
VFA0582	7.7	7.7	7.3	7.6	8.5	8.3	9.1	8.6	2.1	7.5	8.5	7.7	7.9	8.2	8.8	8.5	8.5	1.5	cryptic phage CTXphi transcriptional repressor rstR	
VFA0637	6.0	5.7	5.5	5.7	5.0	5.2	5.2	5.1	-1.5	5.6	5.9	5.4	5.6	5.1	5.3	5.4	5.3	-1.3	hypothetical protein	
VFA0669	7.2	6.8	6.7	6.9	6.4	6.1	6.5	6.3	-1.5	7.2	6.8	6.8	6.9	7.1	6.9	7.1	7.0	1.1	hypothetical protein	
VFA0671	8.2	8.2	8.6	8.4	7.4	7.8	7.7	7.6	-1.6	7.7	8.3	8.2	8.0	7.9	7.6	8.2	7.9	-1.1	hypothetical protein	
VFA0671to065	8.8	9.3	9.5	9.2	7.9	8.6	7.9	8.1	-2.1	8.3	9.3	9.2	8.9	8.9	8.8	9.2	9.0	1.0	hypothetical protein	
VFA0671to065	6.4	6.8	7.1	6.8	4.7	5.8	4.4	5.0	-3.5	5.5	6.4	6.7	6.2	6.3	5.5	6.2	6.0	-1.2	hypothetical protein	
VFA0672	10.1	10.5	10.8	10.4	9.0	9.6	8.7	9.1	-2.6	9.5	10.3	10.4	10.1	9.7	9.5	10.1	9.8	-1.2	outer membrane heme receptor	
VFA0673	9.4	9.7	10.3	9.8	8.1	8.9	7.9	8.3	-2.8	8.7	9.7	9.9	9.4	9.5	9.2	9.9	9.5	1.1	SbmA protein	
VFA0674	9.0	9.0	9.6	9.2	7.7	8.3	7.4	7.8	-2.7	8.3	9.0	9.0	8.8	8.7	8.6	9.2	8.8	1.0	hypothetical protein	
VFA0674to065	7.3	7.5	7.4	7.4	6.5	7.0	6.4	6.6	-1.7	6.8	7.4	7.4	7.2	6.9	7.4	7.4	7.2	1.0	hypothetical protein	
VFA0683	7.3	7.0	6.9	7.1	5.8	6.2	6.2	6.1	-2.0	6.9	6.7	7.0	6.9	6.4	6.5	6.5	6.4	-1.4	hypothetical protein	
VFA0700	8.4	7.9	8.0	8.1	7.1	7.4	7.6	7.4	-1.7	8.3	7.7	7.9	8.0	7.7	7.7	7.8	7.7	-1.2	aminomethyltransferase	
VFA0701	7.6	7.3	7.0	7.3	6.2	6.6	6.7	6.5	-1.7	7.3	7.0	7.2	7.2	6.8	7.2	6.9	7.0	-1.1	transcriptional regulator	
VFA0703	9.3	8.9	9.0	9.1	7.5	8.1	8.1	7.9	-2.2	9.1	8.4	8.9	8.8	8.8	8.8	8.9	8.8	-1.0	glycine dehydrogenase	
VFA0708	5.6	5.4	5.3	5.4	4.4	4.7	5.0	4.7	-1.6	5.4	5.5	5.0	5.3	4.7	5.0	4.8	4.8	-1.4	transcriptional regulator, AraC family	
VFA0722	7.5	6.5	6.2	6.7	7.7	9.0	9.5	8.7	3.9	7.5	6.4	6.4	6.8	7.2	5.9	6.6	6.6	-1.1	Na(+)/H(+) antiporter	
VFA0726	8.7	8.7	8.6	8.7	7.9	8.3	8.1	8.1	-1.5	8.6	8.4	8.6	8.5	8.4	8.4	8.8	8.6	-1.1	NAD-dependent oxidoreductase	
VFA0727	9.3	9.1	9.2	9.2	8.5	8.8	8.7	8.7	-1.4	9.0	8.9	9.2	9.0	9.2	8.9	9.3	9.1	1.1	hypothetical cytosolic protein	
VFA0745	7.8	7.1	7.1	7.3	6.2	6.7	6.8	6.6	-1.7	7.5	6.8	7.0	7.1	6.6	6.2	6.4	6.4	-1.6	dithiolotin synthetase	
VFA0746	8.4	7.9	8.0	8.1	7.1	7.4	7.5	7.4	-1.7	8.3	7.5	8.0	7.9	7.5	7.1	7.5	7.4	-1.5	biotin synthesis protein BiotC	
VFA0747	9.7	9.5	9.6	9.6	8.8	9.2	9.0	9.0	-1.5	9.6	9.1	9.6	9.4	9.2	8.9	9.2	9.1	-1.2	8-amino-7-oxononanoate synthase	
VFA0747to071	6.1	6.4	6.3	6.3	5.4	6.1	5.3	5.6	-1.6	6.0	5.8	6.3	6.0	6.2	5.8	5.9	6.0	-1.0	8-amino-7-oxononanoate synthase	
VFA0747to071	10.1	10.1	10.0	10.1	9.4	9.7	9.4	9.5	-1.4	10.1	9.7	10.1	10.0	9.8	9.7	9.9	9.8	-1.1	8-amino-7-oxononanoate synthase	
VFA0756	10.2	10.1	10.0	10.1	9.8	9.1	9.4	9.4	-1.6	10.1	10.0	10.0	10.0	10.0	9.7	10.0	9.9	-1.1	putative lipoprotein	
VFA0759	9.2	9.6	9.3	9.4	10.5	10.8	10.6	10.6	2.4	9.1	9.5	9.3	9.3	9.2	10.0	9.5	9.6	1.2	plasmid partition ParA protein	
VFA0779	7.4	7.5	7.4	7.4	6.4	7.0	6.8	6.7	-1.6	7.3	7.3	7.5	7.4	7.1	6.8	6.9	6.9	-1.4	ToIQ protein	
VFA0781	6.3	6.1	6.2	6.2	5.5	5.4	5.6	5.5	-1.7	6.2	6.1	6.1	6.1	6.0	5.6	5.7	5.8	-1.3	ferrichrome transport system permease protein FhuB	
VFA0783	6.8	6.9	6.7	6.8	5.7	6.1	6.1	6.0	-1.8	6.7	7.0	6.8	6.9	6.5	6.4	6.5	6.5	-1.3	ferrichrome transport ATP-binding protein FhuC	
VFA0787	9.0	8.7	8.9	8.9	8.0	8.2	8.3	8.2	-1.6	9.0	8.4	8.8	8.8	8.5	7.9	8.5	8.3	-1.4	ABC transporter ATP-binding protein	
VFA0812	7.0	6.7	6.5	6.6	6.4	6.9	6.7	6.6	-1.7	6.8	6.8	6.8	6.6	6.1	6.1	6.3	6.2	-1.3	5-membered membrane protein	
VFA0824	5.9	5.2	4.8	5.3	3.3	4.2	4.3	3.9	-2.6	5.7	5.1	4.9	5.2	4.9	4.5	4.8	4.7	-1.4	ferric anguibacillin transport ATP-binding protein	
VFA0826	5.2	4.4	4.4	4.6	3.9	3.6	4.0	3.8	-1.7	5.1	4.1	4.3	4.5	4.3	4.2	4.3	4.3	-1.2	ferric anguibacillin transport system permease protein FatD	
VFA0841	5.4	5.0	5.1	5.2	4.4	4.6	4.5	4.5	-1.6	5.1	4.9	5.1	5.0	4.9	5.0	5.2	5.1	1.0	3-hydroxy-3-methylglutaryl-coenzyme A reductase	
VFA0852	6.5	4.8	5.3	5.5	8.9	8.7	8.7	8.8	9.8	6.0	4.7	5.2	5.3	6.8	5.8	6.9	6.5	2.3	transcriptional regulatory protein	
VFA0922	8.6	9.3	9.3	9.4	7.4	7.3	8.4	8.4	-1.7	8.4	9.0	8.3	8.2	7.6	7.4	7.7	7.6	-1.7	LuxD, acyl transferase	
VFA0984	4.6	4.4	4.3	4.4	2.8	3.7	3.0	3.2	-2.4	3.9	2.8	4.0	3.6	3.7	2.5	4.0	3.4	-1.1	amino-acid ABC transporter binding protein	
VFA0985	4.7	4.9	4.0	4.5	2.4	2.7	2.7	2.6	-3.8	3.5	3.2	4.2	3.6	4.0	2.1	4.1	3.4	-1.1	hypothetical protein	
VFA0992	5.9	5.6	5.8	5.7	4.5	5.4	5.2	5.0	-1.9	5.5	5.3	5.6	5.5	5.2	5.2	4.9	5.1	-1.3	arylsulfatase	
VFA0998	5.7	5.1	5.0	5.3	4.2	4.1	4.8	4.3	-1.6	5.5	4.9	4.7	5.0	4.7	4.1	4.3	4.4	-1.6	5-keto-4-deoxyuronate isomerase	
VFA1039	7.8	7.5	7.5	7.6	6.9	7.1	7.2	7.1	-1.4	7.7	7.3	7.5	7.5	7.1	7.2	7.3	7.3	-1.2	hypothetical protein	
VFA1043	7.8	7.6	7.7	7.7	7.9	8.6	8.5	8.3	1.6	7.8	7.4	7.5	7.6	7.6	7.6	7.8	7.7	1.1	ABC transporter ATP-binding protein	
VFA1072	4.7	4.9	4.1	4.6	3.7	3.6	4.1	3.8	-1.7	4.5	4.1	4.0	4.2	3.8	3.7	3.9	3.8	-1.3	methyl-accepting chemotaxis protein	
VFA1081	3.6	3.1	2.8	3.2	1.8	2.0	2.2	2.0	-2.2	2.9	2.6	2.5	2.7	2.9	2.0	2.2	2.1	-1.4	hypothetical protein	
VFA1084	4.2	4.1	3.0	3.7	2.6	2.8	3.0	2.8	-1.9	3.8	3.4	3.0	3.4	2.9	2.7	2.8	2.8	-1.5	methyl-accepting chemotaxis protein	
VFA1144	6.7	6.6	6.3	6.5	5.5	5.9	5.6	5.6	-1.8	6.6	6.3	6.1	6.3	5.7	5.7	5.9	5.8	-1.4	hypothetical cytosolic protein	
VFIRNAtc243	6.5	6.6	6.5	6.5	5.4	6.0	5.7	5.7	-1.8	6.5	6.2	6.6	6.4	6.4	5.4	5.6	5.8	-1.5	rRNA	
<b>47 genes*</b>																				
VF0203to24C	5.6	5.5	5.4	5.5	5.5	5.8	5.5	5.6	1.0	5.6	5.0	5.3	5.3	4.3	4.0	3.3	3.9	-2.6	Alcohol dehydrogenase	
VF0086	8.5	8.5	8.7	8.6	9.8	8.4	9.5	9.2	1.6	8.4	8.7	8.6	8.6	7.4	7.3	7.3	7.3	-2.3	NAD(FAD)-utilizing dehydrogenase	
VF0171	8.9	8.4	8.4	8.6	8.2	8.1	8.9	8.4	-1.1	8.4	8.0	8.4	8.3	6.1	5.1	5.5	5.5	-6.8	hypothetical protein	
VF0172	9.4	9.0	8.9	9.1	8.8	8.3	8.9	8.7	-1.3	9.2	8.7	9.0	9.0	6.4	5.9	6.0	6.1	-7.1	O-acetyltransferase	
VF0173	8.7	8.0	8.3	8.3	7.6	7.4	8.2	7.8	-1.5	8.3	7.5	8.2	8.0	5.1	4.0	4.7	4.6	-10.5	hypothetical protein	
VF0173to174	8.0	7.2	7.8	7.7	6.9	6.5	7.2	6.9	-1.4	7.6	6.6	7.5	7.2	6.0	5.0	2.6	3.7	3.4	-13.8	hypothetical protein
VF0174	8.9	8.0	8.3	8.4	7.9	7.0	7.7	7.5	-1.8	8.4	7.4	8.1	8.0	4.8	3.8	4.6	4.4	-12.0	beta-D-GlcNAc beta-1,3-galactosyltransferase	
VF0240	12.7	12.7	12.7	12.7	12.2	12.0	12.3	12.2	-1.5	12.7	12.5	12.6	12.6	11.0	9.5	10.6	10.4	-4.7	30S ribosomal protein S19	
VF0242	12.6	12.6	12.6	12.6	12.1	11.8	12.0	12.0	-1.5	12.6	12.3	12.5	12.5	10.7	9.2	10.4	10.1	-5.1	30S ribosomal protein S3	
VF0243	12.7	12.7	12.6	12.7	12.2	12.0	12.2	12.2	-1.4	12.7	12.5	12.7	12.6	11.1	9.8	10.8	10.6	-4.1	50S ribosomal protein L16	
VF0244	12.9	13.0	12.8	12.9	12.4	12.4	12.4	12.4	-1.4	12.9	12.8	12.9	12.9	11.5	10.5	11.3	11.1	-3.4	50S ribosomal protein L29	
VF0312	9.7	9.6	10.3	9.8	7.4	9.8	8.1	8.4	-2.6	9.4	10.7	10.1	10.1	12.6	12.5	12.7	12.6	5.6	phosphoadenosine phosphosulfate reductase	
VF0323	10.0	9.9	10.3	10.1	6.9	10.2	7.8	8.3	-3.4	9.6	10.9	10.2	10.2	12.5	12.4	12.6	12.5	4.8	adenylsulfate kinase	
VF0329	8.8	8.5	8.0	8.4	8.5	7.7	8.5	8.2	-1.1	8.7	8.4	8.1	8.4	7.1	6.2	6.2	6.5	-3.8	protein YtfJ precursor	
VF0406	9.3	9.7	9.6	9.6	9.5	9.3	9.9	9.6	-1.0	9.2	9.5	9.6	9.4	10.6	10.5	10.8	10.6	2.3	aspartate carbamoyltransferase catalytic subunit	
VF0595	9.8	9.7	9.7	9.7	10.2	9.7	10.2	10.0	1.3	9.8	9.7	9.6	9.7	9.0	9.1	8.9	9.0	-1.6	hypothetical protein	
VF0644	7.6	7.5	7.3	7.5	7.8	7.0	7.9	7.6	1.1	7.5	7.6	7.1	7.4	6.1	6.3	6.1	6.2	-2.4	S-formylglutathione hydrolase	
VF0657	9.1	8.8	9.0	9.0	9.3	8.4	9.2	9.0	-1.0	9.0	9.0	8.9	9.0	7.3	7.7	7.1	7.4	-3.1	succinylglutamate desuccinylase/aspartoacylase family protein	
VF0658	8.9	8.9	8.7	8.8	9.6	8.6	9.4	9.2	1.3	8.8	9.2	8.9	8.9	7.6	7.9	7.3	7.6	-2.5	ribosomal protein S6 modification protein	
VF0659	8.3	8.1	8.0	8.1	9.1	7.8	9.1	8.7	1.5	8.1	8.3	7.8	8.1	6.6	6.9	6.2	6.6	-2.8	ribosomal protein S6 modification protein	
VF0733	7.1	6.7	6.5	6.7	6.1	5.9	6.6	6.2	-1.4	7.0	7.2	6.6	7.0	8.4	9.2	8.6	8.7	3.4	uroporphyrin-III C-methyltransferase	
VF0902	9.4	9.2	9.2	9.3	9.6	9.3	9.6	9.5	1.2	9.3	9.6	9.3	9.4	10.6	10.8	10.7	10.7	2.5	thioredoxin reductase	
VF1037	6.9	7.0	6.5	6.8	6.5	5.4	6.5	6.1	-1.6	6.8	7.0									



VFA1159	4.9	4.1	3.9	4.3	3.7	4.4	4.5	4.2	-1.0	4.5	4.3	3.9	4.3	7.4	6.2	7.1	6.9	6.3	bicyclomycin resistance protein
VFA1162-2	9.4	9.5	9.4	9.4	9.5	9.3	9.6	9.5	1.0	9.3	9.5	9.4	9.4	8.6	8.5	8.2	8.4	8.4	iron-regulated protein Frc
VFB38	6.3	6.3	6.4	6.3	5.7	6.2	5.8	5.9	-1.3	6.0	6.0	5.9	6.0	4.4	4.7	4.3	4.5	-2.8	attachment mediating protein VirB2 homolog
<b>80S_genes:</b>																			
VFO001	7.3	6.8	6.4	6.8	6.4	6.1	6.5	6.3	-1.4	7.3	6.3	6.5	6.7	5.8	5.8	5.9	5.8	-1.8	flavodoxin
VFO013	6.5	6.0	5.9	6.1	6.6	6.9	6.9	6.8	1.6	6.0	6.2	6.0	6.1	6.5	7.4	6.9	6.9	1.8	small heat shock protein
VFO024	5.0	4.7	4.4	4.7	5.0	5.1	5.4	5.2	1.4	4.3	4.9	4.1	4.5	5.1	9.5	8.4	7.7	9.2	acetyl-CoA acetyltransferase
VFO025	5.1	5.4	5.2	5.2	5.9	5.7	6.1	5.9	1.6	4.9	5.6	5.2	5.2	6.4	10.7	9.3	8.8	11.6	3-hydroxyacyl-CoA dehydrogenase
VFO031	7.6	7.2	7.2	7.3	7.7	6.5	7.9	7.4	1.0	7.4	7.6	7.0	7.3	8.4	8.6	8.5	8.5	2.3	chloride channel protein
VFO037	5.3	4.6	4.2	4.7	4.2	3.8	4.2	4.1	-1.5	5.0	4.3	4.6	4.6	4.6	3.8	3.7	3.7	-1.8	hypothetical protein
VFO048	9.0	8.9	8.9	8.9	9.2	8.6	9.2	9.0	1.1	9.0	8.9	8.9	8.9	8.5	8.4	8.4	8.4	-1.4	putative ubiquinone biosynthesis protein UbiB
VFO051	9.1	8.4	8.7	8.7	8.4	7.8	8.6	8.2	-1.4	9.0	8.3	8.5	8.6	7.9	7.4	7.9	7.7	-1.8	Sec-independent protein translocase protein TatC
VFO063	7.6	7.2	6.9	7.2	7.5	6.8	7.7	7.3	1.3	7.4	7.2	7.1	7.2	6.3	6.2	6.1	6.2	-2.0	HemY protein
VFO067	9.7	9.5	9.7	9.6	10.1	10.1	10.0	10.0	1.1	9.6	9.3	9.6	9.5	10.2	9.7	10.2	10.1	1.5	adenylate cyclase
VFO073to74	9.1	8.9	8.5	8.8	8.5	8.1	8.2	8.3	-1.5	9.2	8.8	8.7	8.9	8.2	8.4	8.3	8.3	-1.5	transporter
VFO078	9.1	8.9	8.9	9.0	8.6	8.1	8.7	8.4	-1.4	9.0	8.7	9.0	8.9	8.1	7.7	8.0	7.9	-2.0	hypothetical protein
VFO079	8.5	8.2	8.1	8.2	7.8	7.4	8.1	7.8	-1.4	8.3	7.9	8.1	8.1	7.3	6.9	7.0	7.1	-2.1	putative coproporphyrinogen III oxidase
VFO080	7.3	6.7	6.9	6.9	6.6	6.2	6.9	6.6	-1.3	7.2	6.6	6.6	6.8	5.8	5.5	5.5	5.6	-2.3	coproporphyrinogen III oxidase
VFO087	7.0	6.7	6.3	6.7	7.0	6.0	7.0	6.7	-1.0	6.7	6.9	6.5	6.7	5.5	5.6	5.4	5.5	-2.3	sensory transduction protein kinase
VFO088	6.5	6.0	5.8	6.1	5.7	5.1	5.9	5.6	-1.4	6.3	5.3	5.8	5.8	5.0	4.8	5.1	5.0	-1.9	hypothetical cytosolic protein
VFO103	6.3	5.7	5.8	5.9	5.6	5.2	5.7	5.5	-1.3	6.2	5.5	5.7	5.8	5.0	5.0	5.0	5.0	-1.8	tRNA (guanosine-2'-O-)-methyltransferase
VFO106	9.8	9.7	9.8	9.7	9.3	9.3	9.5	9.3	-1.3	9.7	9.6	9.8	9.7	9.4	9.1	9.3	9.3	-1.3	guanylate kinase
VFO107	6.4	5.7	5.7	5.9	6.1	5.2	6.1	5.8	-1.1	6.1	5.7	5.8	5.9	5.0	4.9	5.0	5.0	-1.7	hypothetical protein
VFO108	6.7	6.2	6.0	6.3	5.9	5.7	6.3	6.0	-1.2	6.6	6.3	6.3	6.4	5.8	5.9	5.2	5.7	-1.7	hypothetical protein
VFO109	5.7	5.1	5.2	5.4	5.1	4.3	5.3	5.2	-1.3	5.6	5.2	5.4	5.4	4.6	4.1	4.1	4.3	-2.2	transporter, drug/metabolite exporter family
VFO115	6.1	5.9	5.8	5.9	5.5	5.5	5.9	5.7	-1.2	6.1	5.7	5.8	5.9	5.3	5.4	5.0	5.2	-1.6	osmolarity sensor protein
VFO116	7.4	6.6	6.7	6.9	5.5	6.1	6.0	5.9	-2.0	7.3	5.5	6.8	6.5	4.4	4.0	4.9	4.5	-4.1	xanthine permease
VFO121	7.8	7.4	7.2	7.5	6.9	6.7	7.0	6.9	-1.5	7.7	7.1	7.3	7.4	6.7	6.5	6.7	6.6	-1.7	transcription elongation factor GreB
VFO122	7.7	7.3	7.2	7.4	7.0	6.8	7.2	7.0	-1.3	7.5	7.2	7.2	7.3	6.7	6.5	6.7	6.6	-1.6	lipid A biosynthesis lauryl acyltransferase
VFO123	7.9	6.4	6.1	6.8	6.1	6.4	6.8	6.2	-1.4	6.7	6.5	6.2	6.2	6.4	5.5	6.3	6.4	-1.8	Tkx protein
VFO127	11.5	11.1	11.1	11.2	10.9	10.5	10.8	10.7	-1.4	11.4	11.0	11.0	11.2	10.3	10.0	10.2	10.2	-2.0	LSU ribosomal protein L28P
VFO148	10.3	10.1	10.0	10.2	10.1	9.9	10.2	10.1	-1.1	10.2	10.0	10.0	10.1	9.7	9.6	9.6	9.6	-1.3	flagellin modification protein A
VFO149	8.8	8.3	8.2	8.5	8.2	7.8	8.5	8.2	-1.2	8.7	8.1	8.0	8.3	7.4	7.0	7.2	7.2	-2.2	glycosyltransferase
VFO150	7.2	6.3	6.1	6.5	5.6	5.1	5.7	5.5	-2.1	7.1	6.0	6.2	6.4	5.8	4.8	5.0	5.2	-2.3	hypothetical protein
VFO157	6.6	5.1	5.4	5.7	3.0	2.9	5.0	4.2	-2.9	6.1	4.0	5.4	5.2	3.3	2.9	3.3	3.2	-4.0	30S ribosomal protein L3P
VFO158	6.6	5.7	5.6	6.0	4.4	4.4	5.1	4.7	-2.5	6.4	4.7	5.5	5.5	4.7	3.4	3.7	3.9	-3.0	hypothetical protein
VFO160	7.3	6.4	6.5	6.7	5.7	5.8	5.8	5.7	-1.9	6.9	5.7	6.5	6.4	5.5	4.4	5.5	5.1	-2.3	WbdD protein
VFO161	8.6	8.6	8.1	8.4	8.5	8.0	8.3	8.2	-1.3	8.5	8.4	8.3	8.4	7.7	7.9	7.7	7.8	-1.5	hypothetical protein
VFO166	8.6	8.3	8.3	8.4	7.9	7.9	8.2	8.0	-1.1	8.4	7.7	8.3	8.2	7.8	6.9	7.7	7.4	-1.7	tUDP-glucose 4,6-dehydratase
VFO167	9.3	8.9	8.9	9.0	8.6	8.6	8.9	8.7	-1.3	9.0	8.2	8.8	8.7	8.2	7.1	8.1	7.8	-1.9	Glucose-1-phosphate thymidyltransferase
VFO168	9.2	8.7	8.8	8.9	8.4	8.3	8.6	8.4	-1.4	8.9	8.1	8.7	8.6	8.0	6.9	7.9	7.6	-2.0	tUDP-4-dehydrohamnose 3,5-epimerase
VFO169	9.0	8.7	8.6	8.8	8.6	8.4	8.8	8.6	-1.4	8.8	8.4	8.6	8.6	8.0	7.1	7.5	7.5	-2.1	hypothetical protein
VFO170	8.3	7.9	8.0	8.1	7.6	7.3	7.9	7.6	-1.4	8.1	7.3	7.9	7.8	6.6	4.9	5.8	5.7	-4.1	flippase
VFO192	9.3	9.1	9.1	9.2	9.3	9.0	9.3	9.2	1.0	9.2	9.0	9.0	9.1	8.5	8.7	8.3	8.5	-1.5	UDP-2-acetamido-2,6-dideoxy-beta-L-talose 4-dehydrogenase
VFO193	9.1	8.8	8.7	8.9	8.9	8.7	8.8	8.5	-1.1	9.0	8.6	8.8	8.8	8.1	8.1	8.2	8.2	-1.6	UDP-2-acetamido-2,6-dideoxy-beta-L-talose 2-epimerase
VFO212	8.4	8.1	8.2	8.3	8.2	8.0	8.2	8.1	-1.1	8.3	8.1	8.1	8.2	7.8	7.5	7.8	7.7	-1.4	1,4-dihydroxy-2-naphthoate octaprenyltransferase,
VFO230	12.6	12.4	12.5	12.5	12.2	12.1	12.3	12.2	-1.2	12.7	12.4	12.5	12.5	11.8	11.2	11.6	11.5	-1.6	30S ribosomal protein S12
VFO231	10.3	9.7	10.2	10.0	9.3	9.1	9.3	9.2	-1.7	10.1	9.5	9.9	9.8	8.7	7.6	8.6	8.3	-2.9	30S ribosomal protein S7
VFO234	12.6	12.4	12.5	12.5	12.2	12.1	12.4	12.2	-1.2	12.5	12.3	12.4	12.4	11.2	9.5	10.7	10.5	-3.7	30S ribosomal protein S10
VFO235	12.6	12.7	12.8	12.8	12.4	12.3	12.6	12.4	-1.3	12.7	12.5	12.7	12.6	11.6	9.9	11.2	10.9	-3.4	LSU ribosomal protein L3P
VFO236	13.0	13.0	13.0	13.0	12.6	12.6	12.6	12.6	-1.3	12.9	12.8	13.0	12.9	11.9	10.1	11.5	11.1	-3.4	LSU ribosomal protein L3P
VFO237	12.9	12.9	12.9	12.9	12.5	12.4	12.5	12.5	-1.3	12.8	12.7	12.9	12.8	11.6	9.9	11.2	10.9	-3.4	50S ribosomal protein L4
VFO238	12.5	12.5	12.6	12.5	11.9	12.1	12.0	12.0	-1.4	12.3	12.3	12.5	12.4	11.2	9.5	10.7	10.5	-3.9	50S ribosomal protein L23
VFO239	12.9	13.0	13.0	13.0	12.5	12.5	12.6	12.5	-1.4	12.9	12.8	12.9	12.9	11.6	10.0	11.1	10.9	-3.9	50S ribosomal protein L2
VFO241	12.9	13.0	13.0	12.9	12.4	12.4	12.5	12.4	-1.4	12.8	12.6	12.9	12.8	11.4	10.0	11.0	10.8	-4.2	50S ribosomal protein L22
VFO245	12.5	12.5	12.3	12.4	12.1	12.0	12.1	12.1	-1.3	12.5	12.4	12.4	12.4	11.6	11.5	11.6	11.6	-1.8	30S ribosomal protein S17
VFO251	12.3	12.2	12.2	12.2	11.8	11.8	12.0	11.9	-1.3	12.2	12.0	12.1	12.1	11.8	11.5	11.8	11.7	-1.3	30S ribosomal protein S8
VFO252	11.7	11.5	11.7	11.6	11.1	11.0	11.3	11.2	-1.4	11.6	11.2	11.5	11.4	11.0	10.3	10.9	10.7	-1.6	50S ribosomal protein L6
VFO253	11.8	11.7	11.9	11.8	11.2	11.1	11.4	11.3	-1.4	11.7	11.4	11.7	11.6	11.2	10.5	11.0	10.9	-1.6	50S ribosomal protein L16
VFO254	12.5	12.4	12.6	12.5	12.0	12.0	12.2	12.1	-1.3	12.4	12.2	12.4	12.3	11.9	11.3	11.8	11.7	-1.6	SSU ribosomal protein SSP
VFO255	12.5	12.3	12.5	12.4	12.0	11.9	12.1	12.0	-1.3	12.4	12.1	12.4	12.3	11.9	11.2	11.7	11.6	-1.6	50S ribosomal protein L30
VFO256	12.2	12.0	12.3	12.2	11.8	11.6	11.8	11.7	-1.3	12.2	11.8	12.2	12.1	11.7	10.9	11.5	11.4	-1.6	LSU ribosomal protein L16P
VFO257	12.5	12.3	12.6	12.5	12.1	12.0	12.2	12.1	-1.3	12.5	12.2	12.4	12.4	11.8	11.2	11.8	11.6	-1.6	preprotein translocase SecY
VFO258	12.0	11.9	11.9	11.9	11.4	11.5	11.5	11.5	-1.4	11.9	11.6	11.8	11.8	10.9	10.3	10.7	10.6	-2.2	50S ribosomal protein L36
VFO264	8.9	8.8	8.5	8.7	9.0	8.1	9.2	8.8	1.0	8.8	9.0	8.6	8.8	7.3	7.8	7.3	7.4	-2.6	fructose-1,6-bisphosphatase
VFO270	8.7	8.6	8.5	8.6	9.0	8.2	9.2	8.8	1.1	8.6	8.7	8.5	8.6	7.9	7.8	7.7	7.8	-1.7	ATP-dependent helicase HepA
VFO271	7.9	7.8	7.6	7.8	8.3	7.4	8.3	8.0	1.2	7.7	8.0	7.6	7.8	6.9	7.2	6.8	6.9	-1.8	ribosomal large subunit pseudouridine synthase A
VFO272	7.5	7.0	6.9	7.1	6.8	6.0	7.1	6.6	-1.4	7.3	6.7	6.8	6.9	5.7	5.3	5.5	5.5	-2.6	universal stress protein family
VFO273	8.4	8.0	8.0	8.1	7.7	7.3	7.9	7.6	-1.4	8.3	7.6	8.0	8.0	7.2	6.5	7.0	6.9	-2.1	transporter
VFO280	8.4	8.0	8.3	8.3	8.6	7.7	8.6	8.3	1.0	8.4	8.2	8.1	8.2	7.5	7.6	7.5	7.5	-1.6	GTP-binding protein CgtA
VFO300	6.0	5.6	5.2	5.6	5.4	5.0	5.5	5.3	-1.2	5.8	5.4	5.5	5.6	4.8	5.2	5.0	5.0	-	

VF0363	6.8	6.5	6.5	6.6	6.2	6.1	6.5	6.3	-1.3	6.7	6.3	6.4	6.4	6.1	5.3	5.8	5.7	-1.6	general secretion pathway protein F	
VF0364	6.0	6.0	6.0	6.2	5.5	6.0	6.0	5.8	-1.3	6.3	5.8	5.8	5.8	4.9	4.5	4.7	4.7	-1.3	hypothetical protein	
VF0365	7.3	6.9	7.0	7.1	6.7	6.6	6.9	6.7	-1.3	7.3	6.7	6.9	7.0	6.3	6.4	6.6	6.4	-1.4	hypothetical protein	
VF0366	7.3	6.8	6.8	7.0	6.7	6.4	6.8	6.6	-1.3	7.3	6.9	6.6	6.9	6.1	6.3	6.2	6.2	-1.6	MshA, mannose-sensitive haemagglutinin	
VF0377	7.8	7.4	7.5	7.6	7.1	6.9	7.3	7.1	-1.4	7.8	7.1	7.6	7.5	7.0	6.6	6.9	6.8	-1.6	hypothetical protein	
VF0378	9.0	8.8	8.7	8.8	8.8	8.2	8.9	8.7	-1.1	9.0	8.8	8.8	8.9	8.2	8.2	8.2	8.2	-1.6	beta-ureidopropionase	
VF0383	5.4	4.6	4.5	4.8	4.3	3.8	4.3	4.1	-1.6	5.2	4.3	4.4	4.6	3.4	3.5	3.4	3.4	-2.4	phosphocarrier protein HPr	
VF0384	7.6	7.1	7.0	7.2	6.8	6.3	6.7	6.6	-1.6	7.4	6.6	7.0	7.0	5.7	5.2	5.4	5.4	-3.0	hypothetical protein	
VF0385	8.2	7.8	7.8	7.9	8.0	7.3	7.9	7.7	-1.2	8.0	7.5	7.5	7.7	6.6	6.3	6.4	6.5	-2.3	nitrogen regulatory IIA protein	
VF0386	11.0	10.9	10.6	10.9	11.1	10.5	11.1	10.9	1.0	10.9	11.1	10.8	10.9	9.9	10.2	9.9	10.0	-1.9	ribosome-associated factor Y	
VF0387	9.7	9.7	9.5	9.6	9.9	9.5	9.9	9.8	1.0	9.7	9.7	9.5	9.7	9.1	9.0	8.9	9.0	-1.6	DNA-directed RNA polymerase subunit N	
VF0388	9.1	8.8	8.7	8.9	9.0	8.9	9.3	9.1	1.1	9.0	8.8	8.9	8.9	8.4	8.2	8.3	8.3	-1.5	ABC transporter ATP-binding protein	
VF0389	9.3	9.3	9.0	9.2	9.4	9.2	9.4	9.3	1.1	9.3	9.3	9.3	9.3	8.8	8.7	8.6	8.7	-1.5	hypothetical protein	
VF0390	9.2	9.3	9.0	9.2	9.4	9.2	9.5	9.3	1.1	9.1	9.4	9.2	9.2	8.8	8.8	8.7	8.8	-1.4	probable exported protein [imported]	
VF0400	9.5	9.2	9.1	9.3	9.1	8.8	9.2	9.1	-1.2	9.5	9.2	9.2	9.2	8.7	8.6	8.7	8.7	-1.5	toluene tolerance protein TTG2F	
VF0401	9.4	9.0	9.2	9.2	8.9	8.6	8.9	8.8	-1.3	9.4	8.9	9.2	9.2	8.7	8.3	8.7	8.6	-1.6	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	
VF0402	6.9	6.0	6.2	6.4	6.0	6.0	6.2	6.1	-1.3	6.8	6.0	6.0	6.2	5.5	5.2	5.3	5.3	-1.9	1-acyl-sn-glycerol-3-phosphate acyltransferase	
VF0405	8.6	8.8	8.7	8.7	8.9	8.4	9.3	8.9	1.1	8.4	8.7	8.8	8.6	9.9	9.9	10.1	10.0	2.5	aspartate carbamoyltransferase regulatory subunit	
VF0417	6.4	5.2	5.4	5.7	4.9	4.1	5.2	4.7	-1.9	6.0	5.0	4.8	5.3	3.8	4.1	3.4	3.7	-2.9	hypothetical protein	
VF0422to423t	8.0	7.4	7.4	7.6	7.6	7.0	7.8	7.5	-1.1	7.9	7.3	7.5	7.6	6.5	6.3	6.3	6.4	-2.3	A/G-specific adenine DNA glycosylase	
VF0423	6.8	6.2	6.3	6.4	6.4	5.7	6.7	6.3	-1.1	6.7	6.4	6.2	6.4	5.5	5.2	5.6	5.4	-2.0	glutaminase	
VF0433	7.1	6.6	6.4	6.7	6.8	6.2	7.1	6.7	-1.0	6.8	6.6	6.1	6.5	5.6	6.0	5.4	5.7	-1.8	Holliday junction resolvase-like protein	
VF0450	6.9	6.1	6.4	6.5	6.0	5.3	6.1	5.8	-1.6	6.7	5.7	6.1	6.2	5.5	5.1	5.3	5.3	-1.9	single-stranded-DNA-specific exonuclease RecJ	
VF0461	5.2	4.2	4.2	4.5	3.9	3.7	4.4	4.0	-1.4	5.1	4.2	4.0	4.4	3.5	3.5	3.4	3.5	-1.8	sodium-dependent phosphate transporter	
VF0464	10.1	9.7	9.5	9.8	9.4	9.0	9.4	9.3	-1.4	10.0	9.7	9.5	9.7	8.9	9.3	9.1	9.1	-1.5	SSU ribosomal protein S20P	
VF0471to472	5.7	5.9	5.9	5.8	5.5	5.6	5.7	5.6	-1.2	5.2	5.3	5.5	5.3	6.3	5.5	6.6	6.1	1.7	dihydrodipicolinate reductase	
VF0484	6.2	5.4	5.6	6.0	6.0	5.9	6.0	5.9	-1.4	10.9	9.2	9.0	9.8	9.2	8.3	8.9	9.2	9.1	-1.9	hypothetical protein
VF0486	9.7	9.5	9.8	9.7	9.1	9.1	9.3	9.1	-1.4	9.7	9.2	9.7	9.5	8.9	8.6	9.0	8.9	-1.6	translation initiation factor IF-2	
VF0487	8.4	7.7	8.1	8.1	7.9	7.3	8.5	7.9	-1.1	8.2	7.7	7.9	8.0	6.7	6.4	6.3	6.5	-2.8	ribosome-binding factor A	
VF0488	7.5	6.5	7.3	7.1	6.9	6.3	7.0	7.2	6.8	7.4	6.7	7.0	7.2	5.9	5.4	5.6	5.6	-2.6	tRNA pseudouridine synthase B	
VF0489	9.8	9.4	9.1	9.4	9.2	8.7	9.2	9.0	-1.3	9.9	9.6	9.3	9.6	8.6	8.5	8.6	8.6	-2.0	30S ribosomal protein S15	
VF0494	6.2	5.4	5.6	6.0	6.0	5.9	6.0	5.9	-1.1	7.0	6.8	6.7	6.8	5.8	5.8	6.2	6.1	-1.6	sensory transduction protein kinase	
VF0505	7.2	7.2	7.2	7.2	6.9	6.7	7.1	6.9	-1.2	7.2	7.2	7.1	7.1	6.7	6.7	6.8	6.7	-1.3	thymidine phosphorylase	
VF0522	5.6	5.3	5.2	5.4	4.8	4.9	5.2	5.0	-1.2	5.4	5.2	5.4	5.3	4.9	4.7	4.7	4.8	-1.5	TadG-like protein	
VF0524	5.7	5.5	4.8	5.3	4.7	4.6	5.2	4.8	-1.4	5.4	5.5	5.1	5.4	4.4	4.6	4.6	4.5	-1.8	sensor protein PhoQ	
VF0529	11.0	10.5	10.7	10.7	10.6	9.9	10.6	10.4	-1.3	10.9	10.6	10.5	10.7	10.0	9.6	9.9	9.8	-1.7	elongation factor EF-2	
VF0532to533	5.6	5.4	5.6	5.5	5.9	5.3	5.7	5.9	1.3	5.4	5.6	5.6	5.5	6.2	6.0	6.1	6.1	-1.1	cytosine permease	
VF0539	10.7	10.2	10.4	10.5	10.0	10.5	10.3	10.3	-1.1	10.6	10.1	10.3	10.3	9.9	9.5	9.8	9.7	-1.5	oxaloacetate decarboxylase	
VF0540	9.4	9.0	9.1	9.2	8.6	9.1	9.0	8.9	-1.2	9.2	8.8	8.8	9.0	8.4	8.0	8.3	8.2	-1.7	oxaloacetate decarboxylase beta chain	
VF0541	7.8	7.4	7.4	7.5	7.1	7.1	7.5	7.3	-1.2	7.6	7.2	7.4	7.4	7.0	6.9	6.8	6.9	-1.4	hypothetical protein	
VF0542	9.1	8.9	9.0	9.0	8.6	8.6	9.0	8.8	-1.2	9.1	8.7	9.0	9.0	8.5	8.4	8.5	8.5	-1.4	peptidase family M16	
VF0556	9.0	7.8	7.8	7.8	7.4	7.7	7.9	7.6	-1.1	7.9	7.9	7.9	7.9	7.3	7.3	7.2	7.3	-1.2	hypothetical protein	
VF0584	6.0	5.2	5.4	5.6	5.2	5.2	5.2	5.2	-1.3	5.7	5.3	5.1	5.4	4.4	4.0	4.0	4.1	-2.4	quaternary ammonium compound-resistance protein	
VF0600	6.9	6.3	6.3	6.5	5.7	6.0	5.9	5.8	-1.6	6.7	6.1	6.3	6.4	6.0	5.5	5.7	5.7	-1.5	hypothetical protein	
VF0604	5.0	4.4	4.4	4.6	4.1	4.2	4.8	4.4	-1.2	4.6	4.4	4.4	4.4	3.6	4.1	3.6	3.8	-1.4	hypothetical protein	
VF0606	6.1	6.1	5.9	6.0	5.4	5.6	5.8	5.6	-1.3	5.9	5.8	6.1	6.0	5.4	5.3	5.5	5.4	-1.5	glucokinase	
VF0611	5.4	4.5	4.7	4.7	3.9	4.7	4.5	4.1	-1.6	4.5	4.4	3.9	4.4	3.7	3.3	3.5	3.4	-2.0	FTS system, diacetylchitinase-specific IIA component	
VF0629	9.3	9.0	9.0	9.1	8.7	8.9	8.9	8.8	-1.2	9.2	8.8	8.9	9.0	8.6	8.2	8.6	8.5	-1.4	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	
VF0631	9.2	9.0	9.1	9.1	8.7	8.9	9.0	8.9	-1.1	9.1	8.8	8.8	8.9	8.5	8.2	8.4	8.4	-1.4	hypothetical protein	
VF0632	8.7	8.2	8.4	8.4	8.2	8.3	8.3	8.3	-1.0	8.5	8.0	8.3	8.3	7.9	7.4	7.7	7.7	-1.5	hypothetical protein	
VF0633	8.2	7.6	7.6	7.8	7.8	7.5	8.0	7.8	-1.0	8.1	7.5	7.5	7.7	6.8	6.4	6.8	6.6	-2.1	GTP-binding protein EngA	
VF0634	5.4	5.4	5.4	5.5	5.2	5.4	5.5	5.3	-1.3	5.9	5.0	4.8	5.2	4.0	3.9	3.8	3.9	-2.8	hypothetical protein	
VF0645_s	9.8	9.6	9.5	9.6	9.9	8.8	9.8	9.5	-1.1	9.7	9.7	9.4	9.6	8.2	8.4	8.1	8.2	-2.6	glutathione-dependent formaldehyde dehydrogenase	
VF0647	5.7	4.9	4.8	5.1	4.9	4.4	5.3	4.9	-1.2	5.4	5.1	5.1	5.2	4.6	4.3	4.4	4.4	-1.8	proton/sodium-glutamate symport protein	
VF0674	5.0	3.7	3.8	4.2	3.0	3.1	3.9	3.4	-1.7	4.7	3.7	3.7	4.0	2.8	2.7	2.9	2.8	-3.4	urease beta subunit	
VF0684	10.6	10.5	10.4	10.5	10.2	10.2	10.5	10.3	-1.1	10.5	10.8	10.3	10.5	9.9	10.1	10.1	10.0	-1.4	methionine-binding protein	
VF0693	6.4	6.2	5.9	6.1	6.5	5.7	6.5	6.1	-1.1	6.4	6.3	6.1	6.2	5.4	5.6	5.1	6.4	-1.6	hypothetical protein	
VF0707	6.0	5.4	5.1	5.5	4.8	4.7	5.4	5.0	-1.5	5.9	5.2	5.2	5.4	4.6	4.4	4.8	4.6	-1.8	LuxP protein precursor	
VF0711	7.7	7.4	7.4	7.5	7.3	6.8	7.5	7.2	-1.2	7.6	7.3	7.3	7.4	6.8	6.7	6.7	6.7	-1.6	1-deoxy-D-xylulose-5-phosphate synthase	
VF0728	10.3	9.9	10.2	10.2	9.3	9.7	9.8	9.6	-1.5	10.2	9.7	10.0	10.0	9.4	8.8	9.1	9.1	-1.8	NADH-ubiquinone oxidoreductase	
VF0732	7.9	7.6	7.6	7.7	7.4	6.9	7.4	7.2	-1.4	7.7	7.4	7.5	7.5	6.3	6.4	6.3	6.3	-2.3	iron-sulfur cluster assembly/repair protein ApbE	
VF0747	6.9	6.4	6.4	6.6	6.7	5.9	6.3	6.0	-1.5	6.7	6.1	6.5	6.5	5.9	5.6	5.8	5.8	-1.6	rod shape-determining protein rodA	
VF0748	6.6	6.4	6.3	6.4	6.0	5.7	6.0	5.9	-1.4	6.6	6.1	6.3	6.3	5.9	5.6	5.6	5.7	-1.5	cell elongation specific D,D-transpeptidase	
VF0761	7.8	7.1	7.0	7.3	6.7	6.3	7.0	6.7	-1.6	7.6	6.6	6.9	7.1	6.0	5.8	6.0	5.9	-2.2	GTP-binding protein	
VF0771	8.6	8.4	8.5	8.5	7.7	8.0	8.2	8.0	-1.4	8.5	8.3	8.5	8.4	8.0	7.6	7.9	7.8	-1.5	transcriptional regulator	
VF0777	7.1	6.9	6.8	6.9	6.4	6.5	6.7	6.5	-1.3	7.0	6.7	6.8	6.8	6.2	6.4	6.2	6.3	-1.5	methyl-accepting chemotaxis protein	
VF0786	5.5	5.2	5.4	5.4	5.2	5.5	5.3	5.3	-1.0	5.1	4.9	4.9	5.0	5.8	5.3	5.6	5.6	1.5	glycine betaine/L-proline transport system permease protein ProW	
VF0787	5.3	4.9	4.7	5.0	4.9	5.5	5.0	5.1	-1.1	4.9	4.6	4.8	4.8	6.2	5.0	5.6	5.6	-1.8	glycine betaine/L-proline transport ATP-binding protein ProV	
VF0793	9.2	8.3	8.3	8.6	7.8	7.7	8.2	7.9	-1.6	9.1	8.2	8.3	8.5	7.7	7.4	7.7	7.6	-1.9	adenylate kinase	
VF0811	6.1	5.6	5.3	5.7	5.7	6.0	6.4	6.0	1.3	5.6	5.8	5.4	5.6	6.2	5.3	5.3	6.0	5.0	hypothetical protein	
VF0851	7.2	6.7	6.7	6.8	6.2	6.2	6.7	6.4	-1.4	7.1	6.5	6.5	6.7	6.3	9.8	8.9	8.0	-1.6	hypothetical protein	
VF0852	8.3	7.9	8.1	8.1	7.5	7.7	7.9	7.7	-1.3	8.1	7.8									

VF1013	8.6	8.2	8.4	8.4	7.9	8.6	8.6	8.3	-1.0	8.9	8.2	8.5	8.5	9.2	9.8	9.6	9.5	2.0	histidinol dehydrogenase
VF1014	8.6	8.2	8.4	8.4	7.9	8.6	8.6	8.4	-1.0	9.0	8.2	8.5	8.5	9.2	9.8	9.6	9.5	2.2	histidinol phosphate aminotransferase
VF1015	8.6	8.0	8.4	8.3	8.0	8.7	8.8	8.5	1.1	8.9	8.2	8.4	8.5	9.2	10.3	9.9	9.8	2.5	imidazole glycerol-phosphate dehydratase/histidinol phosphatase
VF1016	7.5	6.9	7.2	7.2	6.7	7.4	7.7	7.2	1.0	7.7	6.7	7.2	7.2	7.7	8.6	8.6	8.4	2.2	imidazole glycerol phosphate synthase subunit HisH
VF1017	8.5	8.0	8.5	8.3	7.9	8.5	8.9	8.5	1.1	8.8	8.1	8.6	8.5	9.2	9.5	9.7	9.5	2.0	1-(5-phosphoribosyl)-5-[(S- phosphoribosylamino)methylideneamino] imidaz
VF1021	6.9	6.8	6.8	6.8	6.3	6.2	6.5	6.3	-1.4	7.0	6.6	7.0	6.8	6.2	5.7	6.2	6.0	-1.7	methyltransferase
VF1043	7.8	7.5	7.4	7.6	7.6	7.3	7.9	7.6	-1.0	7.9	7.5	7.4	7.5	7.9	6.9	7.0	7.0	-1.6	hypothetical protein
VF1043	6.1	5.8	5.4	5.7	5.0	5.4	5.4	5.3	-1.4	5.9	5.8	5.5	5.7	5.0	5.1	5.1	5.1	-1.6	hypothetical protein
VF1045	5.7	4.6	4.6	5.0	4.0	4.1	4.7	4.3	-1.6	5.3	4.6	4.8	4.9	3.5	3.1	3.7	3.4	-2.8	hypothetical protein
VF1047to1048	6.1	6.0	5.6	5.9	5.8	5.9	6.1	6.0	1.0	6.2	6.1	5.7	6.0	5.6	5.6	5.3	5.5	-1.5	hypothetical protein
VF1048to1051	5.4	4.9	4.4	4.9	4.5	4.5	4.9	4.6	-1.2	5.1	4.5	4.9	4.8	3.9	4.2	4.0	4.0	-1.8	putative DNA methylase
VF1050_s	8.6	8.3	7.7	8.2	8.0	7.8	8.2	8.0	-1.2	8.5	8.1	8.0	8.2	7.6	7.5	7.2	7.5	-1.7	Protein CytN
VF1051	9.1	8.9	9.0	9.0	8.8	8.5	8.9	8.7	-1.2	9.1	8.7	9.0	8.9	8.5	8.3	8.5	8.5	-1.4	DNA topoisomerase I
VF1055	9.1	9.2	9.1	9.2	9.2	9.4	9.5	9.4	-1.2	9.1	9.3	9.1	9.2	9.6	9.7	9.8	9.7	1.4	D-lactate dehydrogenase
VF1064	11.6	11.0	11.1	11.2	11.4	10.8	11.5	11.2	-1.0	11.4	10.8	11.0	11.0	10.1	9.6	10.3	10.0	-2.1	glutamate decarboxylase
VF1065	10.8	10.4	10.3	10.5	10.3	9.8	10.4	10.2	-1.2	10.6	9.9	10.3	10.3	9.3	8.5	9.3	9.0	-2.4	integral membrane protein with TrkA domains
VF1072	6.5	6.2	6.0	6.2	7.0	6.2	7.1	6.8	1.5	6.2	6.5	6.0	6.2	5.7	5.3	5.2	5.4	-1.7	transcriptional regulators, LysR family
VF1080	6.0	5.5	5.5	5.6	5.1	4.9	5.5	5.2	-1.4	5.5	5.3	5.3	5.4	4.6	4.6	4.8	4.7	-1.7	hypothetical protein
VF1106	6.3	6.1	5.7	6.0	5.8	5.3	6.2	5.8	-1.2	6.2	6.0	5.9	6.0	4.8	5.5	5.1	5.1	-1.9	hypothetical protein
VF1117	5.3	4.7	4.2	4.7	4.5	4.5	5.1	4.7	-1.0	4.8	4.7	4.4	4.6	3.8	4.0	3.5	3.8	-1.8	toxin coregulated pilus biosynthesis protein I
VF1120	7.2	7.3	7.1	7.2	7.6	7.0	7.8	7.5	-1.2	7.0	7.7	7.2	7.3	6.4	6.6	6.4	6.5	-1.7	acetyltransferase
VF1121	5.7	5.4	5.3	5.4	4.9	5.1	5.1	5.0	-1.3	5.4	5.4	5.5	5.4	5.1	5.0	4.8	5.0	-1.3	BCC1 family transporter
VF1125	6.6	6.5	6.4	6.2	5.9	5.1	6.2	5.8	-1.4	6.3	6.4	6.0	6.2	4.0	4.5	4.2	4.2	-4.0	hypothetical protein
VF1125to1126	7.0	6.7	6.4	6.7	6.6	6.3	6.9	6.6	-1.1	6.7	7.0	6.5	6.8	5.9	6.4	5.9	6.1	-1.6	hypothetical protein
VF1136	10.9	11.1	11.1	11.0	10.7	10.7	10.8	10.7	-1.2	10.8	11.0	10.9	10.9	10.5	10.4	10.5	10.5	-1.3	hypothetical protein
VF1137	10.7	10.8	10.7	10.7	10.4	10.4	10.4	10.4	-1.2	10.7	10.8	10.6	10.7	10.2	10.1	10.3	10.2	-1.4	putative lipoprotein
VF1152	7.5	7.4	7.7	7.7	7.1	7.1	7.1	7.1	-1.1	7.5	7.7	7.2	7.3	7.2	7.2	7.2	7.2	-1.4	7.8 shock protein HtpX
VF1160	6.6	5.7	5.4	5.9	5.8	5.0	6.0	5.6	-1.2	6.5	5.8	5.3	5.9	4.8	4.6	4.4	4.6	-2.3	quosine biosynthesis protein QueD
VF1161	6.5	6.0	5.9	6.2	5.4	5.4	5.8	5.5	-1.6	6.4	5.8	6.2	6.1	5.3	5.5	5.5	5.4	-1.6	periplasmic component of efflux system
VF1172	5.0	4.9	4.7	4.9	4.3	4.9	4.8	4.7	-1.1	5.0	4.9	4.8	4.9	4.3	4.3	4.1	4.2	-1.6	tyrosine-specific transport protein
VF1202	8.6	7.3	7.5	7.8	6.7	6.2	6.9	6.6	-2.2	8.5	6.9	7.4	7.6	6.3	6.2	6.3	6.3	-2.5	ribonucleotide-diphosphate reductase alpha subunit
VF1211	10.2	10.1	9.9	10.2	10.0	10.0	10.0	10.0	-1.2	10.2	10.0	10.0	10.2	10.0	10.0	10.0	10.0	-4.1	hypothetical protein
VF1217	12.8	12.8	12.7	12.8	12.6	12.6	12.7	12.6	-1.2	12.8	12.8	12.7	12.8	12.4	12.3	12.3	12.3	-1.3	50S ribosomal protein L35
VF1218	11.1	10.7	10.4	10.7	10.6	10.1	10.7	10.4	-1.1	10.8	10.5	10.1	10.5	9.4	9.6	9.5	9.5	-1.9	50S ribosomal protein L20
VF1246	6.6	6.4	6.0	6.4	6.3	5.5	6.4	6.1	-1.2	6.4	6.6	6.2	6.4	5.4	5.6	5.1	5.4	-2.1	putative omptin family serine protease
VF1251	7.0	6.9	6.4	6.8	6.2	6.3	6.8	6.5	-1.2	6.6	6.8	6.7	6.7	6.2	6.1	6.0	6.1	-1.5	hypothetical protein
VF1270	5.7	5.6	5.5	5.6	5.2	5.4	5.5	5.4	-1.2	5.5	5.6	5.7	5.5	5.3	5.3	5.3	5.3	-1.8	hydroxyadenyl dehydratase precursor
VF1292	9.4	9.3	9.4	9.4	8.9	8.7	8.8	8.8	-1.5	9.4	9.5	9.6	9.5	9.0	8.9	8.1	8.0	-2.8	3-hydroxydecanoyl-ACP dehydratase
VF1308	9.5	9.5	9.8	9.6	9.3	9.6	9.5	9.5	-1.1	9.5	9.6	9.8	9.7	10.1	10.1	10.4	10.2	1.5	transcriptional regulatory protein, Fnr
VF1312	7.4	7.2	6.9	7.1	6.8	6.6	7.0	6.8	-1.3	7.2	7.2	6.9	7.1	6.2	6.4	6.2	6.2	-1.8	hypothetical protein
VF1315	8.3	8.1	7.9	8.2	8.0	7.7	8.1	7.9	-1.1	8.1	7.9	7.8	7.9	7.3	7.0	7.3	7.3	-1.7	putrescine/spermidine ABC transporter ATPase
VF1316	8.4	8.4	8.2	8.3	8.0	8.1	8.2	8.1	-1.2	8.2	8.2	8.3	8.2	8.1	8.2	8.3	7.5	-1.7	spermidine/putrescine ABC transporter membrane component
VF1317	8.2	7.6	7.4	7.7	7.8	7.3	8.0	7.7	-1.0	7.9	7.5	7.4	7.6	6.8	6.6	6.5	6.7	-2.0	spermidine/putrescine ABC transporter membrane component
VF1318	8.1	7.7	7.5	7.8	7.3	6.9	7.5	7.2	-1.4	7.8	7.6	7.6	7.7	6.7	6.6	6.4	6.6	-2.2	spermidine/putrescine-binding protein
VF1323	6.3	6.0	5.3	5.9	5.7	5.3	6.1	5.7	-1.1	6.2	6.0	5.6	5.9	4.8	5.3	5.0	5.0	-1.9	lipoprotein
VF1324	7.7	7.8	7.6	7.7	7.6	7.2	7.8	7.5	-1.1	7.6	8.0	7.7	7.8	7.0	7.2	7.0	7.1	-1.6	hypothetical protein
VF1325	8.2	8.5	8.0	8.2	8.1	7.8	8.5	8.1	-1.1	8.5	8.7	8.0	8.2	7.2	7.8	7.3	7.4	-1.7	hypothetical protein
VF1327	7.2	7.1	7.0	7.1	7.1	6.5	7.3	6.9	-1.1	7.0	7.4	7.0	7.1	6.0	6.1	6.1	6.1	-2.0	transporter
VF1328	7.7	7.4	7.4	7.5	7.5	6.7	7.7	7.3	-1.1	7.4	7.4	7.3	7.4	6.0	6.0	5.9	6.0	-2.7	ferrichrome-binding protein
VF1329	8.2	8.1	8.0	8.1	8.5	7.5	8.5	8.2	-1.1	8.0	8.4	7.9	8.1	7.1	7.0	6.8	7.0	-2.2	soluble lytic murein transglycosylase
VF1335	6.7	6.0	6.0	6.2	5.4	5.1	5.9	5.5	-1.7	6.5	6.0	5.7	6.1	4.1	4.3	4.3	4.3	-3.5	metal-dependent phosphohydrolase
VF1348	7.2	6.7	7.0	7.0	6.6	6.7	6.7	6.7	-1.2	7.0	6.8	6.9	6.8	6.7	6.5	6.1	6.4	-1.5	hypothetical cytosolic protein
VF1349	8.6	8.6	8.4	8.5	8.5	8.0	8.5	8.3	-1.1	8.6	8.5	8.4	8.5	7.9	8.0	7.9	7.9	-1.5	hypothetical protein
VF1357	4.2	3.8	3.6	3.9	3.6	3.4	3.9	3.6	-1.2	3.7	3.9	3.6	3.7	3.1	3.1	2.6	2.9	-1.8	formate dehydrogenase, cytochrome B556 subunit
VF1361	5.0	5.3	5.1	5.2	4.8	5.1	5.7	5.2	1.0	4.8	5.3	5.7	5.3	4.3	4.5	4.2	4.3	-1.9	hypothetical protein
VF1362	5.3	5.6	5.2	5.4	5.2	5.4	5.9	5.5	1.1	4.9	5.1	5.6	5.2	4.5	4.7	4.1	4.4	-1.7	hypothetical protein
VF1370	7.3	7.0	6.9	7.0	6.3	6.8	6.8	6.6	-1.3	7.2	6.7	7.0	6.9	6.3	5.9	6.0	6.1	-1.8	methylidene-carboxylate peptidase
VF1371	7.2	6.6	6.7	6.9	6.2	6.5	6.7	6.5	-1.3	7.0	6.2	6.5	6.6	5.9	5.4	5.8	5.7	-1.9	permease
VF1372	7.1	6.5	6.5	6.7	5.8	6.3	6.5	6.2	-1.4	7.0	6.1	6.3	6.5	5.6	5.4	5.4	5.5	-2.0	permease
VF1384	6.3	5.8	5.6	5.9	5.2	5.0	5.7	5.3	-1.5	6.0	5.7	5.6	5.8	5.0	5.2	4.9	5.0	-1.6	stringent starvation protein A
VF1392	5.2	4.7	4.1	4.6	4.6	4.0	5.2	4.6	-1.0	5.1	4.8	4.4	4.8	3.5	3.6	3.6	3.6	-2.3	hypothetical protein
VF1395to1401	4.5	4.6	4.2	4.5	4.4	4.3	4.2	4.3	-1.2	4.5	4.5	4.4	4.5	4.0	4.1	3.9	4.0	-1.4	glycosyltransferase involved in cell wall biogenesis
VF1403	5.7	5.1	5.0	5.3	5.1	5.2	5.4	5.3	-1.0	5.2	4.8	5.0	5.0	4.1	3.9	4.4	4.1	-1.8	molybdenum transport system permease protein ModB
VF1404	7.0	6.7	6.6	6.8	6.8	6.6	7.2	6.9	-1.1	6.8	6.6	6.6	6.6	6.1	6.2	5.9	6.1	-1.5	molybdenum transport ATP-binding protein ModC
VF1410	5.3	4.9	5.1	5.1	5.3	5.3	5.5	5.4	1.2	5.2	4.7	4.8	4.9	6.0	5.6	6.6	6.0	-2.2	putative efflux pump component MtrF
VF1411	6.4	6.0	5.7	6.0	6.4	5.7	6.5	6.2	1.1	6.2	6.3	5.7	6.1	5.4	5.2	5.3	5.3	-1.7	probable lipoprotein NipC precursor
VF1413	7.4	7.5	7.0	7.3	8.0	6.7	8.2	7.6	1.2	7.2	7.9	7.2	7.4	6.1	7.0	6.1	6.4	-2.1	phosphatidylserine decarboxylase
VF1415	5.5	5.0	5.2	5.2	4.6	4.6	4.8	4.7	-1.5	5.4	4.9	4.9	5.1	4.4	4.2	4.4	4.3	-1.7	multidrug efflux protein NorA
VF1419	6.6	6.1	5.9	6.2	5.7	5.2	6.1	5.7	-1.4	6.5	6.1	6.0	6.2	5.3	5.4	5.4	5.3	-1.8	transcriptional regulators, LysR family
VF1426	6.7	6.5	6.0	6.4	6.5	5.9	6.8	6.4	-1.0	6.6	6.8	6.3	6.6	5.0	5.7	4.9	5.2	-2.8	tetratricopeptide repeat family protein
VF1427	12.1	12.3	12.1	12.2	12.2	11.3	12.1	11.9	-1.3	12.2	12.8	12.3	12.4	10.2	11.2	9.9	10.4	-4.0	sulfitase family protein
VF1438	6.8																		

VF1654	5.8	5.3	4.7	5.3	5.4	4.5	5.9	5.2	-1.0	5.6	5.1	5.1	5.3	3.8	4.3	4.3	4.1	-2.3	IAA acetyltransferase
VF1661	6.9	6.1	6.3	4.4	3.7	4.1	4.0	3.8	-1.6	4.6	3.9	3.8	4.1	4.0	3.8	3.1	3.2	-1.1	Nsi(+)/Hh(+)-antiprotein NhaC
VF1671	6.9	6.2	6.3	6.5	5.7	5.7	6.1	5.8	-1.6	6.7	6.1	6.4	6.4	6.0	4.8	5.7	5.5	-2.3	2-oxoglutarate decarboxylase
VF1680	6.1	4.9	5.1	5.4	4.4	4.5	5.0	4.6	-1.7	5.6	4.8	4.9	5.1	4.0	3.8	3.9	3.9	-1.9	transporter, drug/metabolite exporter family
VF1683	5.7	5.4	5.1	5.4	4.8	5.1	5.2	5.0	-1.3	5.3	5.1	4.9	5.1	4.2	4.4	4.5	4.4	-1.7	hypothetical cytosolic protein
VF1686	7.6	7.4	7.1	7.4	6.7	7.1	6.9	6.9	-1.4	7.5	7.3	7.2	7.3	6.7	7.0	6.9	6.9	-1.4	hypothetical protein
VF1688	8.4	8.1	8.2	8.3	8.0	7.9	7.9	7.8	-1.2	8.3	8.1	8.1	8.2	7.6	7.3	7.7	7.6	-1.3	adenine phosphoribosyltransferase
VF1688to1685	7.8	8.0	8.0	7.9	8.5	8.0	8.5	8.4	1.3	7.5	8.3	7.9	7.9	7.2	7.4	6.9	7.2	-1.7	adenine phosphoribosyltransferase
VF1695	10.0	9.7	9.9	9.9	9.8	9.5	9.8	9.7	-1.1	10.0	9.7	9.7	9.8	9.5	8.3	8.8	8.9	-1.9	acetyl-CoA carboxylase beta subunit
VF1700	10.2	9.9	10.0	10.0	9.9	9.5	9.8	9.8	-1.2	10.2	9.8	10.0	10.0	9.8	8.1	8.7	8.9	-2.2	3-oxoacyl-[acyl-carrier-protein] synthase
VF1708	7.5	7.0	7.1	7.2	6.8	7.0	7.1	7.0	-1.2	7.3	7.0	7.1	7.1	6.7	6.5	6.7	6.6	-1.4	acyl-CoA synthase
VF1718	5.5	5.1	4.8	5.1	4.5	4.0	4.8	4.4	-1.6	5.4	4.7	5.0	5.0	4.1	4.3	3.9	4.1	-1.9	MatI protein regulator
VF1719	4.7	4.2	4.2	4.4	3.9	4.0	4.0	4.0	-1.4	4.6	4.1	4.0	4.3	3.7	3.5	3.7	3.6	-1.6	PTS system, glucose-specific IiAB component
VF1734	7.7	7.4	7.3	7.5	7.4	7.4	7.6	7.5	-1.0	7.5	7.2	7.3	7.3	6.9	6.9	6.9	6.9	-1.4	DNA polymerase III, delta' subunit
VF1736	7.5	7.5	7.3	7.4	6.9	7.2	7.1	7.1	-1.3	7.3	7.2	7.3	7.3	6.9	6.8	6.8	6.8	-1.4	hypothetical protein
VF1737	7.1	6.7	6.6	6.8	6.3	6.4	6.8	6.5	-1.2	6.8	6.9	6.6	6.8	6.2	6.3	6.3	6.3	-1.4	4-amino-4-deoxychorismate lyase
VF1738	10.1	9.5	9.9	9.8	9.1	8.9	8.8	8.9	-1.9	9.9	9.3	9.5	9.6	8.7	6.9	7.7	7.8	-3.5	3-oxoacyl-[acyl carrier protein] synthase
VF1739	12.0	12.0	11.7	11.9	11.6	11.5	11.4	11.5	-1.3	12.1	12.0	12.0	12.0	11.6	10.7	11.0	11.1	-1.9	acyl carrier protein
VF1741	10.7	10.4	10.4	10.5	9.8	9.8	9.9	9.9	-1.6	10.6	10.2	10.4	10.4	9.5	8.3	8.7	8.9	-2.9	acyl carrier protein S-malonyltransferase
VF1742	10.2	9.9	10.1	10.1	9.6	9.3	9.6	9.5	-1.5	10.1	9.7	10.1	10.0	9.4	7.9	8.6	8.6	-2.6	3-oxoacyl-[acyl carrier protein] synthase
VF1755	7.5	7.4	7.2	7.3	7.4	7.7	7.3	7.4	-1.1	7.3	7.0	6.9	7.1	7.6	7.5	7.8	7.6	1.5	orotidine 5-phosphate decarboxylase
VF1771	10.0	10.5	10.2	10.2	11.3	10.1	11.2	10.9	1.5	9.8	10.9	10.1	10.3	8.9	9.7	8.7	9.1	-2.3	sensor protein kinase
VF1772	10.8	11.2	10.9	11.0	12.0	10.8	11.8	11.5	1.5	10.6	11.5	10.9	11.0	9.4	10.5	9.3	9.7	-2.4	hypothetical protein
VF1773	9.4	9.8	9.6	9.6	10.6	9.5	10.4	10.2	1.5	9.2	10.2	9.6	9.6	8.0	9.0	7.8	8.3	-2.6	hypothetical protein
VF1774	9.3	9.6	9.3	9.4	10.4	9.2	10.1	9.9	1.4	9.0	10.1	9.4	9.5	7.6	8.9	7.5	8.0	-2.8	stage V sporulation protein R
VF1779	6.8	6.6	6.2	6.5	7.0	6.6	7.3	7.0	1.4	6.5	6.8	6.2	6.5	7.0	8.0	7.4	7.5	2.0	telurite resistance protein TehB
VF1780	6.6	6.2	6.3	6.5	7.0	6.9	7.0	7.0	-1.2	6.7	7.0	6.9	7.0	6.4	6.4	6.4	6.4	1.9	ferredoxin-NADP reductase
VF1796	6.6	5.4	5.3	5.7	5.2	4.4	5.8	5.1	-1.5	6.2	5.4	5.4	5.7	4.3	4.5	3.7	4.2	-2.9	23S rRNA m(1G 745 methyltransferase
VF1798	5.9	5.7	5.8	5.8	5.9	5.7	5.9	5.8	-1.0	5.6	5.7	5.6	5.7	6.2	6.3	6.3	6.3	1.5	chloride channel protein
VF1809	7.2	7.3	7.1	7.2	7.4	6.9	7.5	7.2	1.0	7.0	7.3	7.2	7.2	6.4	6.5	6.5	6.5	-1.6	insulin-degrading enzyme
VF1810	5.6	5.0	5.1	5.2	4.8	5.3	5.5	5.2	-1.0	5.5	5.0	5.1	5.2	5.8	8.3	7.5	7.2	4.0	3-hydroxyacyl-CoA dehydrogenase
VF1811	6.4	5.5	5.1	5.4	5.4	5.1	5.4	5.4	-1.4	5.3	5.2	5.3	5.3	4.7	4.7	4.7	4.0	-1.6	acetyl-CoA acetyltransferase
VF1816	7.6	7.1	7.4	7.4	6.6	6.8	7.0	6.8	-1.5	7.5	6.9	7.2	7.2	6.6	6.3	6.7	6.5	-1.6	cytochrome c-type biogenesis protein CcmI
VF1818	8.2	7.7	7.8	7.9	7.4	7.5	7.9	7.6	-1.2	8.0	7.5	7.7	7.7	7.3	6.9	7.2	7.1	-1.5	thiol:disulfide interchange protein TlpA
VF1819	8.2	7.8	8.0	8.0	7.1	7.4	7.5	7.3	-1.3	8.1	7.3	7.7	7.7	7.2	6.6	7.1	7.0	-1.7	heme chaperone-apocytochrome heme-lyase
VF1829	8.8	8.6	8.9	8.8	8.5	8.2	8.6	8.4	-1.6	8.7	8.3	8.8	8.6	7.7	7.2	7.7	7.5	-2.0	chromosome partitioning protein ParA
VF1830	9.5	9.4	9.8	9.6	9.4	9.2	9.4	9.2	-1.2	9.4	9.2	9.6	9.4	8.6	8.3	8.3	8.3	-1.8	chemotaxis-specific methyltransferase
VF1831	9.3	9.2	9.4	9.3	9.3	9.5	9.3	9.4	1.1	9.3	8.8	9.3	9.1	8.5	8.2	8.5	8.4	-1.7	chemotaxis protein CheA
VF1848	6.1	5.8	5.4	5.8	5.4	5.8	5.9	5.7	-1.1	5.8	5.4	5.7	5.7	5.1	5.1	4.9	5.1	-1.5	flagellar protein
VF1875	9.1	9.1	9.3	9.2	9.3	9.4	9.4	9.3	1.1	9.1	9.1	9.2	9.1	8.7	8.6	8.9	8.7	-1.3	flagellar basal body rod modification protein
VF1889	6.9	6.8	6.7	6.8	6.4	6.1	6.7	6.4	-1.3	6.8	6.8	6.4	6.7	6.3	6.1	5.9	6.1	-1.5	outer membrane porin protein precursor
VF1900	6.9	6.6	6.4	6.6	6.1	6.2	6.4	6.3	-1.3	6.8	6.3	6.6	6.6	6.0	5.7	5.8	5.8	-1.7	DNA ligase
VF1908	6.8	6.5	6.0	6.4	6.3	5.8	6.5	6.2	-1.2	6.7	6.4	6.2	6.5	6.0	5.8	5.5	5.7	-1.6	nitrate/nitrite sensor protein NarQ
VF1911	7.0	6.7	6.4	6.7	7.4	6.3	7.3	7.0	-1.2	6.8	6.8	6.4	6.7	5.7	5.9	5.6	5.7	-1.9	hypothetical protein
VF1932	8.5	8.7	8.9	8.7	8.5	8.7	8.6	8.6	-1.0	8.3	8.6	8.6	8.5	8.0	9.8	9.8	9.8	2.3	acyl-CoA dehydrogenase
VF1933	7.1	7.3	7.5	7.3	7.2	7.5	7.2	7.3	-1.0	7.0	7.6	7.3	7.3	7.5	11.0	9.6	9.4	4.3	acyl-CoA dehydrogenase
VF1941	6.4	5.7	5.9	5.8	5.2	4.9	5.7	5.3	-1.4	6.1	5.3	5.3	5.5	4.7	4.2	4.6	4.5	-1.6	hypothetical protein
VF1946	8.8	8.3	8.4	8.5	7.8	7.7	8.1	7.8	-1.6	8.7	8.2	8.3	8.4	7.7	6.4	7.1	7.1	-2.5	acetyl-CoA carboxylase alpha subunit
VF1950	10.2	10.0	10.1	10.1	9.7	9.6	9.8	9.7	-1.3	10.2	9.9	10.1	10.0	9.6	9.1	9.3	9.3	-1.7	UDP-N-acetylglucosamine acyltransferase
VF1951	10.4	10.1	10.2	10.2	9.9	9.7	10.0	9.9	-1.3	10.3	10.0	10.2	10.2	9.7	9.3	9.6	9.5	-1.6	(3R)-hydroxymyristoyl ACP dehydratase
VF1956	6.2	5.5	5.8	5.9	5.3	5.1	5.4	5.3	-1.5	6.0	5.2	5.6	5.6	5.3	4.5	4.7	4.8	-1.7	1-deoxy-D-xylulose 5-phosphate reductoisomerase
VF1960	9.1	8.6	8.4	8.8	8.1	8.2	8.4	8.2	-1.5	8.4	8.2	8.3	8.4	7.4	7.4	7.9	7.9	-1.7	uridylyl kinase
VF1972	6.3	6.8	6.4	6.5	6.0	6.0	6.5	6.2	-1.2	6.1	6.6	6.3	6.3	5.6	5.7	5.5	5.6	-1.7	isocitrate lyase
VF1973	4.8	4.7	4.6	4.7	4.4	4.3	5.0	4.6	-1.1	4.3	4.9	4.5	4.6	3.8	4.1	3.9	3.9	-1.6	malate synthase
VF1981	11.0	10.8	10.4	10.7	11.4	10.3	11.3	11.0	1.2	11.0	11.0	10.3	10.8	9.2	10.0	9.2	9.5	-2.4	hypothetical protein
VF1984	7.0	6.9	6.6	6.8	6.4	6.5	6.7	6.5	-1.2	6.9	6.5	6.8	6.8	6.3	6.0	6.2	6.2	-1.5	phosphate transport system permease protein PstA
VF1995	7.2	6.9	6.7	7.0	6.8	6.9	7.0	6.6	-1.3	6.9	6.9	6.7	6.9	6.7	5.8	5.7	5.8	-2.2	hypothetical protein
VF2003to2004	4.2	4.1	3.6	4.0	3.9	3.8	3.9	3.9	-1.1	3.9	3.9	3.6	3.8	3.2	3.5	2.7	3.1	-1.6	hypothetical protein
VF2007	6.3	5.8	5.4	5.8	5.7	5.5	5.9	5.7	-1.1	6.1	5.5	5.5	5.7	5.0	4.8	5.1	5.0	-1.6	hypothetical protein
VF2027to2028	4.8	4.2	4.1	4.4	4.0	4.1	4.3	4.1	-1.2	4.4	4.1	4.2	4.2	3.6	3.5	3.4	3.5	-1.7	hypothetical protein
VF2033	5.2	4.8	4.7	4.9	4.8	4.7	4.5	4.7	-1.2	4.9	4.6	4.6	4.7	4.2	4.1	4.3	4.2	-1.4	hypothetical bacteriophage protein
VF2035	5.5	5.0	5.0	5.2	5.1	4.4	5.0	4.8	-1.3	5.0	4.4	4.5	4.6	3.7	3.8	3.9	3.8	-1.8	hypothetical protein
VF2036	5.9	5.6	5.5	5.7	4.9	5.1	5.2	5.1	-1.5	5.3	4.8	5.4	5.2	4.5	3.9	4.5	4.3	-1.8	possible phage regulatory protein (CII)
VF2037	10.3	10.3	10.3	10.3	10.6	10.8	10.6	10.7	1.3	10.1	10.3	10.3	10.2	10.8	10.7	10.8	10.7	1.4	transcriptional regulator, Cro/CII family
VF2038	10.7	10.9	10.8	10.8	11.0	11.2	10.9	11.0	1.3	10.6	10.9	10.7	10.7	11.1	11.1	11.3	11.2	1.3	hypothetical protein
VF2041	6.6	6.5	6.3	6.4	5.8	6.2	6.1	6.1	-1.2	6.5	6.0	6.2	6.2	5.9	5.3	5.7	5.6	-1.5	DNA integration/recombination/inversion protein
VF2048	5.1	4.6	4.3	4.6	4.2	4.1	4.6	4.3	-1.3	4.9	4.5	4.7	4.7	4.0	3.8	3.9	3.9	-1.7	amylc-1-6-glucosidase
VF2049	5.7	5.4	5.2	5.4	5.1	4.9	5.4	5.1	-1.2	5.6	5.3	5.5	5.4	4.8	4.4	4.6	4.6	-1.8	cyclomaltodextrinase
VF2060	6.4	6.2	6.3	6.3	6.0	6.3	6.3	6.2	-1.1	6.2	6.3	6.2	6.2	6.6	6.9	6.9	6.8	1.5	transcriptional activator CadC
VF2061	4.5	3.9	3.2	3.9	5.3	4.0	4.6	4.6	-1.7	4.3	3.6	3.4	3.7	4.1	5.8	7.0	5.7	3.7	hypothetical protein
VF2062	5.8	4.4	4.4	4.8	7.0	5.2	5.7	6.0	2.2	5.5	4.5	4.3	5.8	5.2	7.2	8.6	7.0	4.7	hypothetical protein



VF2198	8.9	8.6	8.6	8.7	8.5	8.4	8.8	8.6	-1.1	8.8	8.5	8.4	8.6	7.9	8.0	8.0	7.9	-1.5	cell division protein FtsO
VF2199	10.0	9.8	9.9	9.9	9.9	9.6	10.0	9.8	-1.0	9.9	9.9	9.6	9.8	9.4	9.3	9.4	9.4	-1.3	cell division protein FtsO
VF2215	10.0	9.4	9.6	9.7	9.0	9.4	9.2	9.2	-1.4	9.9	9.2	9.4	9.5	9.0	8.7	9.0	8.9	-1.6	stringent starvation protein B
VF2220	8.5	8.4	8.7	8.5	8.4	8.6	8.7	8.6	-1.0	8.5	8.2	8.3	8.3	8.7	8.7	9.0	8.8	-1.3	ubiquinol-cytochrome c reductase iron-sulfur subunit
VF2233	9.6	9.4	9.2	9.4	9.4	9.1	9.5	9.3	-1.0	9.5	9.3	9.2	9.3	8.8	8.9	8.8	8.8	-1.4	outer membrane channel precursor protein
VF2239	9.5	8.9	9.0	9.1	8.9	8.4	9.0	8.7	-1.3	9.3	8.8	9.0	9.0	8.8	8.0	8.1	8.1	-1.9	hypothetical protein
VF2241	9.2	8.7	8.5	8.8	8.6	8.4	8.7	8.4	-1.3	8.6	8.7	8.6	8.6	8.9	8.2	7.9	8.0	-1.8	arabinosyltransferase
VF2248	8.3	7.8	8.0	8.1	8.0	7.6	8.1	7.9	-1.1	8.2	8.0	8.0	8.1	7.8	5.7	6.6	6.7	-2.6	hypothetical protein
VF2253	8.3	8.2	8.1	8.2	8.2	8.0	8.4	8.2	-1.0	8.2	8.2	8.1	8.2	7.6	7.5	7.4	7.5	-1.6	DNA primase
VF2254	10.4	10.1	10.3	10.2	10.0	10.0	10.2	10.1	-1.1	10.3	10.1	10.3	10.2	9.9	9.4	9.9	9.7	-1.4	RNA polymerase sigma factor
VF2268	7.6	7.1	6.5	7.1	6.9	6.6	7.3	6.9	-1.1	7.4	7.0	6.7	7.1	6.0	6.4	5.9	6.1	-2.0	transcriptional repressor protein MetJ
VF2273	9.4	8.9	8.5	8.9	8.5	7.9	8.5	8.3	-1.6	9.5	8.9	8.7	9.0	7.9	7.8	7.7	7.8	-2.4	50S ribosomal protein L31
VF2290	9.0	8.9	9.0	9.0	8.3	8.5	8.5	8.4	-1.4	8.9	8.5	8.9	8.8	8.4	7.8	8.3	8.2	-1.5	hypothetical protein
VF2292	10.0	9.5	9.8	9.8	9.4	9.3	9.5	9.4	-1.3	10.0	9.3	9.5	9.6	9.0	8.6	9.0	8.9	-1.6	shikimate kinase I
VF2294	5.5	5.0	4.7	5.1	4.4	4.6	4.6	4.5	-1.5	5.1	4.7	4.6	4.8	4.1	4.5	3.9	4.2	-1.7	pilus expression protein
VF2306	10.8	10.3	10.4	10.5	10.5	11.7	11.7	11.3	-1.8	10.9	10.3	10.3	10.5	10.1	8.8	9.3	9.4	-2.1	N-acetyl-gamma-glutamyl-phosphate reductase
VF2311	12.2	11.9	12.0	12.0	11.6	11.4	11.8	11.6	-1.3	12.1	11.9	11.8	11.9	10.8	10.3	10.7	10.6	-2.5	30S ribosomal protein S18
VF2312	12.2	12.0	12.2	12.1	11.7	11.5	11.7	11.6	-1.4	12.1	11.9	12.1	12.0	11.2	10.6	11.1	11.0	-2.1	30S ribosomal protein S6
VF2317	6.6	6.4	6.3	6.4	6.3	6.4	6.5	6.4	-1.1	6.5	6.6	6.3	6.5	5.8	6.0	5.8	5.9	-1.5	sodium-type polar flagellar protein MotX
VF2320	10.1	9.5	9.5	9.7	9.4	9.1	9.7	9.4	-1.2	10.0	9.3	9.4	9.6	9.0	8.6	8.8	8.8	-1.7	protease activity modulator HflC
VF2321	10.5	10.3	10.4	10.4	9.9	9.9	10.1	10.0	-1.3	10.5	10.1	10.3	10.3	9.9	9.6	9.9	9.8	-1.4	protease activity modulator HflK
VF2322	10.3	10.0	10.2	10.2	10.0	9.7	10.1	9.9	-1.2	10.3	9.8	9.9	10.0	9.5	9.3	9.6	9.5	-1.5	GTP-binding protein HflX
VF2330	9.1	9.0	9.0	9.0	9.3	8.8	9.3	9.2	1.1	8.9	9.0	8.9	9.0	8.5	8.4	8.6	8.5	-1.4	ribosome-associated GTPase
VF2342	9.2	9.6	9.1	9.3	9.1	8.8	9.1	9.0	-1.2	9.2	9.6	9.3	9.4	8.7	9.0	8.7	8.8	-1.5	periplasmic protein CpxP
VF2358	7.0	6.4	6.6	6.7	6.5	6.2	6.7	6.4	-1.2	6.7	6.6	6.5	6.6	5.9	5.9	6.0	5.9	-1.6	transporter, MFS superfamily
VF2362	8.4	8.3	8.1	8.3	8.6	7.8	8.9	8.4	-1.1	8.3	8.6	8.2	8.4	7.5	8.0	7.3	7.6	-1.7	GDDEF family protein
VF2377	4.1	4.6	4.5	4.5	4.1	4.6	4.5	4.1	-1.3	4.3	4.6	4.5	4.3	4.5	3.8	4.2	4.1	-1.7	hypothetical protein
VF2378_s	5.3	4.8	5.1	5.1	5.0	4.5	5.1	4.9	-1.1	4.9	5.1	5.1	5.1	4.1	4.4	4.2	4.2	-1.8	sodium:olute symporter family protein
VF2385	10.2	9.6	9.8	9.9	9.6	8.9	9.7	9.4	-1.3	10.0	9.3	9.7	9.7	8.6	6.2	7.1	7.3	-5.2	3-dehydroquinate dehydratase
VF2386	10.7	10.3	10.4	10.5	10.2	9.6	10.2	10.0	-1.4	10.6	9.9	10.3	10.3	9.2	7.0	7.8	8.0	-4.9	acetyl-CoA carboxylase
VF2387	10.5	10.1	10.2	10.3	9.8	9.3	9.5	9.5	-1.7	10.5	9.7	10.2	10.1	9.0	7.2	7.6	7.9	-4.7	acetyl-CoA carboxylase
VF2388	8.7	7.8	7.3	8.0	7.5	7.4	7.8	7.4	-1.6	8.7	7.9	7.4	7.4	7.1	6.4	6.8	7.2	-1.1	72S ribosomal protein L11 methyltransferase
VF2398	7.5	7.1	7.2	7.2	6.5	7.1	6.7	6.8	-1.4	7.2	7.0	7.1	7.1	6.5	6.2	6.6	6.5	-1.6	CBS-domain containing protein
VF2405	7.0	6.9	6.7	6.8	6.9	6.5	7.0	6.8	-1.0	6.9	7.0	6.8	6.9	6.3	6.4	6.0	6.2	-1.6	curli production assembly/transport component CsgG precursor
VF2406	6.2	5.5	5.5	5.7	5.5	4.6	6.5	5.5	-1.3	5.8	5.8	5.4	5.7	4.3	4.4	3.2	4.0	-3.2	curli production assembly/transport component CsgF precursor
VF2407	6.1	5.9	5.6	5.9	5.6	4.8	6.2	5.5	-1.1	5.8	6.1	5.8	5.9	4.0	4.2	3.6	3.9	-3.9	CsgE-like protein
VF2410	5.5	5.2	4.9	5.2	5.2	4.8	5.2	5.1	-1.1	5.4	5.4	5.2	5.3	4.6	4.0	4.7	4.8	-1.7	CsgE-like protein
VF2411	11.1	11.1	11.1	11.1	10.8	10.4	10.6	10.6	-1.4	11.0	10.8	11.0	10.9	10.2	9.7	10.2	10.0	-1.9	DNA-directed RNA polymerase beta' chain
VF2412	11.4	11.4	11.5	11.5	11.1	10.7	11.1	11.0	-1.4	11.4	11.2	11.4	11.3	10.6	10.3	10.6	10.5	-1.9	DNA-directed RNA polymerase beta' chain
VF2413	11.4	11.1	11.4	11.3	10.8	10.4	11.1	10.8	-1.5	11.3	10.9	11.2	11.1	10.4	9.8	10.4	10.2	-1.9	DNA-directed RNA polymerase beta chain
VF2414	11.9	11.9	12.0	11.9	11.5	11.4	11.6	11.5	-1.3	11.8	11.7	11.9	11.8	11.6	10.8	11.4	11.3	-1.5	DNA-directed RNA polymerase beta chain
VF2415	11.5	11.0	11.3	11.3	11.3	10.6	11.1	10.9	-1.3	11.4	10.9	11.1	11.1	10.7	10.1	10.6	10.5	-1.6	110S ribosomal protein L7/L12
VF2417	12.2	12.1	12.2	12.2	11.6	11.7	11.8	11.7	-1.4	12.2	12.0	12.1	12.1	11.4	10.5	11.1	11.0	-2.2	50S ribosomal protein L1
VF2418	11.8	11.7	11.8	11.8	11.2	11.3	11.3	11.3	-1.4	11.8	11.6	11.8	11.7	11.0	10.2	10.8	10.7	-2.0	LSU ribosomal protein L1P
VF2419	12.4	12.4	12.4	12.4	12.1	12.2	12.2	12.2	-1.2	12.5	12.4	12.5	12.5	12.0	11.5	11.9	11.7	-1.6	50S ribosomal protein L11
VF2422	10.5	10.2	10.5	10.4	10.2	9.9	10.2	10.1	-1.2	10.4	10.1	10.3	10.3	9.9	9.5	9.9	9.7	-1.4	translocase
VF2426	9.0	8.4	8.9	8.6	8.1	8.0	8.2	8.1	-1.4	8.9	8.0	8.3	8.4	7.6	7.3	7.8	7.6	-1.7	phosphatidylserine synthase
VF2446	5.6	5.2	4.6	5.1	5.3	4.4	5.3	5.0	-1.1	5.3	5.2	4.9	5.1	3.7	4.3	3.7	3.9	-2.3	flagellar basal body-associated protein
VF2464	7.9	7.5	7.4	7.6	7.2	6.8	7.5	7.2	-1.3	7.8	7.4	7.4	7.5	7.0	6.9	6.7	6.8	-1.6	general secretion pathway protein N
VF2465	8.0	7.6	7.7	7.7	7.1	7.0	7.6	7.2	-1.4	7.8	7.4	7.6	7.6	7.0	6.8	6.8	6.9	-1.6	general secretion pathway protein M
VF2466	7.7	7.4	7.5	7.5	7.1	6.8	7.2	7.0	-1.4	7.6	7.1	7.5	7.4	6.8	6.5	6.9	6.7	-1.6	general secretion pathway protein L
VF2467	7.1	6.7	6.8	6.9	6.3	6.0	6.5	6.3	-1.5	6.9	6.4	6.8	6.7	6.0	6.2	6.3	6.0	-1.8	general secretion pathway protein F
VF2468	6.3	5.6	5.7	5.9	5.7	4.8	5.7	5.4	-1.4	5.9	5.4	5.6	5.7	5.2	4.4	4.6	4.7	-1.9	general secretion pathway protein J
VF2469	6.5	6.1	6.1	6.2	5.7	5.2	5.8	5.6	-1.6	6.4	5.6	5.8	5.9	5.8	4.9	4.9	4.9	-1.9	general secretion pathway protein I
VF2470	6.0	5.4	5.5	5.6	5.4	5.1	5.5	5.3	-1.2	5.7	5.4	5.3	5.5	4.9	4.8	4.7	4.8	-1.6	general secretion pathway protein H
VF2472	7.5	7.2	7.3	7.3	7.1	6.8	7.2	7.0	-1.3	7.2	6.8	7.3	7.1	6.4	6.4	6.5	6.4	-1.6	general secretion pathway protein F
VF2510	4.7	4.1	4.1	4.3	3.7	3.6	4.0	3.8	-1.5	4.2	4.1	3.7	4.0	3.4	3.3	3.4	3.4	-1.5	general secretion pathway protein E
VF2474	7.7	7.4	7.5	7.5	7.5	7.1	7.7	7.4	-1.1	7.6	7.1	7.4	7.4	6.9	6.5	6.7	6.7	-1.6	general secretion pathway protein D
VF2492	5.7	5.2	4.8	5.2	4.7	4.0	4.9	4.5	-1.6	5.2	4.8	4.7	4.9	4.1	4.1	4.1	4.1	-1.8	copper sensitivity protein ScaC
VF2495	7.3	6.8	6.5	6.9	7.5	6.4	7.9	7.2	-1.3	7.2	6.9	6.6	6.9	6.1	5.8	5.6	5.8	-2.1	hypothetical protein
VF2508	5.8	5.1	4.9	5.3	5.2	4.4	5.7	5.1	-1.1	5.4	4.8	5.0	5.1	3.6	4.1	3.9	3.9	-2.3	L-seryl-RNA selenium transferase family
VF2510	4.7	4.1	4.1	4.3	3.7	3.6	4.0	3.8	-1.5	4.2	4.1	3.7	4.0	3.4	3.3	3.4	3.4	-1.5	PTS system, mannitol (cryptic)-specific IIA component
VF2513	8.4	8.0	7.9	8.1	8.9	7.8	8.9	8.5	1.3	8.3	8.0	8.0	8.1	7.2	7.3	7.0	7.1	-1.9	cyclic nucleotide binding protein/2 CBS domains
VF2514	7.8	7.5	7.1	7.5	8.1	6.9	8.0	7.7	1.2	7.7	7.5	7.3	7.5	6.4	6.3	6.0	6.2	-2.5	DNA polymerase III subunit epsilon
VF2520	8.2	8.0	8.0	8.1	7.9	8.0	8.2	8.0	-1.0	8.2	7.8	8.0	8.0	8.4	8.5	8.6	8.5	1.4	cytochrome c5
VF2522	9.2	9.3	9.1	9.2	9.5	8.8	9.6	9.3	-1.1	9.0	9.4	9.0	9.1	8.4	8.6	8.4	8.5	-1.6	transcriptional regulator, TetR family
VF2523	9.2	9.0	9.1	9.1	9.3	8.4	9.4	9.0	-1.0	9.1	9.2	9.0	9.1	8.2	8.2	8.1	8.2	-1.9	PTS system, mannitol-specific IIB component
VF2524	8.8	8.8	8.8	8.8	8.7	8.2	8.8	8.6	-1.2	8.7	8.8	8.6	8.7	7.7	7.6	7.5	7.6	-2.1	acriflavin resistance plasma membrane protein
VF2545	8.0	7.5	7.5	7.7	7.3	7.1	7.4	7.3	-1.3	8.0	7.1	7.4	7.5	6.8	6.3	6.7	6.6	-1.8	16S rRNA m(5)C 967 methyltransferase
VF2546	7.9	7.3	7.5	7.6	7.0	6.9	7.1	7.0	-1.5	7.8	7.0	7.3	7.4	6.6	6.2	6.3	6.4	-2.0	potassium transporter peripheral membrane component
VF2547	6.5	5.8	5.9	6.1	5.1	5.4	5.7	5.4	-1.6	6.3	5.5	5.8	5.9	5.1	4.7	4			

VFA0105	8.1	8.1	7.9	8.0	8.7	8.0	8.7	8.5	1.3	7.9	8.5	8.0	8.1	7.4	7.7	7.3	7.5	-1.6	transcriptional regulator
VFA0123	7.3	7.3	7.9	7.5	7.4	7.8	7.8	7.7	-1.2	6.8	7.7	7.7	7.3	7.9	7.0	8.2	8.0	1.7	di-tripeptide transporter
VFA0151	5.5	4.9	4.6	5.0	4.3	4.0	4.4	4.2	-1.7	5.2	4.4	4.9	4.8	4.3	3.7	4.1	4.0	-1.7	ATP-dependent RNA helicase
VFA0167	9.6	9.2	9.1	9.3	8.8	8.3	8.9	8.7	-1.5	9.4	9.0	9.0	9.1	8.5	8.5	8.6	8.5	-1.5	hypothetical protein
VFA0169	5.3	5.0	4.7	5.0	4.6	4.8	5.2	4.8	-1.1	5.1	4.9	4.9	5.0	4.6	4.0	4.4	4.3	-1.5	methyl-accepting chemotaxis protein
VFA0174	6.6	6.4	6.3	6.4	6.7	5.7	7.3	6.6	-1.1	6.3	6.8	6.3	6.5	5.4	5.5	5.2	5.4	-2.2	hypothetical protein
VFA0178	6.6	6.8	6.5	6.5	6.4	6.8	6.7	6.2	-1.3	6.5	6.7	6.4	6.5	6.2	5.8	5.8	6.5	-2.0	sensor protein IiS
VFA0185	4.7	4.4	3.8	4.3	4.6	4.3	5.1	4.7	1.3	4.8	4.6	4.2	4.5	3.7	3.7	3.4	3.6	-1.9	hypothetical protein
VFA0201	6.7	6.4	6.0	6.3	6.4	6.1	6.6	6.4	1.0	6.5	6.3	6.2	6.3	5.7	5.6	5.9	5.7	-1.5	hypothetical protein
VFA0236	6.6	6.7	6.6	6.6	6.6	6.1	6.7	6.5	-1.1	6.5	6.9	6.7	6.7	6.1	5.9	5.7	5.9	-1.7	glycerol kinase
VFA0237	5.4	5.7	5.0	5.3	5.2	4.7	5.4	5.1	-1.2	5.3	5.5	5.2	5.4	4.4	4.1	4.1	4.2	-2.3	RscS, sensor kinase protein
VFA0239	4.7	4.7	4.6	4.7	4.1	4.2	4.4	4.2	-1.4	4.6	5.3	4.5	4.8	3.5	3.6	3.3	3.5	-2.5	glycerol-3-phosphate dehydrogenase
VFA0257	4.3	4.3	3.8	4.1	5.0	4.6	5.7	5.1	2.0	4.2	4.7	4.0	4.3	5.0	6.6	5.9	5.8	2.9	malate synthase
VFA0258	6.6	6.7	6.4	6.5	7.0	6.8	7.2	7.0	1.4	6.3	7.1	6.5	6.7	7.2	8.6	8.2	8.0	2.5	transcriptional regulator, MerR family
VFA0259	6.6	6.7	6.1	6.4	5.4	5.8	6.7	6.0	-1.4	6.9	6.6	6.4	6.6	5.3	6.1	5.4	5.6	-2.1	hypothetical transcriptional regulatory protein
VFA0280	7.5	7.3	7.2	7.4	7.0	7.0	7.3	7.1	-1.2	7.3	7.0	7.2	7.2	6.8	6.5	6.6	6.6	-1.5	glutathione-regulated potassium-efflux system protein KefC
VFA0282	3.2	2.6	2.6	2.8	2.3	2.5	2.8	2.6	-1.2	2.8	2.6	2.6	2.7	2.2	1.9	2.0	2.0	-1.5	quaternary ammonium compound-resistance protein
VFA0268	6.9	6.6	6.4	6.6	6.5	6.5	7.0	6.6	1.0	6.9	6.6	6.4	6.7	6.0	6.2	6.1	6.1	-1.5	hypothetical membrane spanning protein
VFA0277	7.5	7.2	6.9	7.2	7.4	6.4	7.4	7.1	-1.0	7.2	7.2	7.2	7.2	6.5	6.2	6.3	6.4	-1.8	hypothetical protein
VFA0279	6.6	6.8	6.3	6.6	6.7	6.2	7.0	6.6	1.0	6.5	7.0	6.7	6.7	5.9	6.3	5.7	6.0	-1.7	hypothetical protein
VFA0298	8.7	8.8	8.9	8.8	9.0	8.5	9.0	8.8	1.0	8.6	8.9	8.7	8.7	8.0	7.9	7.9	7.9	-1.7	cytochrome c-type protein TorC
VFA0299	9.3	9.1	9.5	9.3	9.2	8.6	9.4	9.1	-1.2	9.2	9.2	9.3	9.3	8.2	8.0	8.1	8.1	-2.2	trimethylamine-N-oxide reductase
VFA0305	7.8	7.7	7.7	7.7	7.4	7.3	7.7	7.5	-1.2	7.6	7.6	7.7	7.6	7.0	6.9	6.9	6.9	-1.6	peptide transport system ATP-binding protein SapF
VFA0306	8.4	8.4	8.3	8.4	8.1	8.2	8.2	8.2	-1.2	8.2	8.4	8.3	8.3	7.8	7.5	7.5	7.6	-1.6	peptide transport system ATP-binding protein SapD
VFA0307	7.6	7.3	7.4	7.4	7.0	7.1	7.4	7.2	1.4	7.3	7.3	7.4	7.3	6.9	6.4	6.6	6.6	-1.6	peptide transport system permease protein SapC
VFA0308	7.4	7.2	7.0	7.2	7.2	7.2	7.6	7.3	-1.1	7.2	7.2	7.1	7.2	6.8	6.6	6.6	6.7	-1.4	peptide transport system permease protein SapB
VFA0309	6.4	6.4	6.5	6.5	6.7	6.0	6.5	6.0	-1.0	6.8	6.2	6.2	6.4	6.5	5.8	5.8	5.9	-1.9	peptide transport protein SapA
VFA0320	6.1	5.8	5.7	5.9	5.2	5.6	5.9	5.6	-1.3	6.2	5.8	5.9	6.0	5.4	5.1	5.6	5.4	-1.5	transcriptional activator TenA
VFA0321	6.6	6.4	6.2	6.4	6.0	6.1	6.2	6.1	-1.2	6.3	6.3	6.0	6.2	5.7	5.6	5.8	5.7	-1.4	hydroxyethylthiazole kinase
VFA0360	6.8	6.7	6.5	6.7	6.4	5.4	6.7	6.2	-1.4	6.6	6.7	6.4	6.6	5.1	5.4	4.9	5.2	-2.7	senescence induction protein kinase
VFA0376	7.3	7.1	7.2	7.2	6.5	7.0	6.8	6.8	-1.3	7.0	7.3	7.2	7.2	6.7	6.5	6.6	6.6	-1.4	hypothetical protein
VFA0377	7.2	6.8	6.4	6.7	6.8	6.6	6.7	6.7	-1.2	7.0	6.7	6.7	6.9	6.1	6.2	6.2	6.0	-1.9	hypothetical protein
VFA0386	5.1	4.7	4.5	4.8	4.3	4.5	4.9	4.6	-1.2	4.7	4.4	4.3	4.5	3.6	3.6	3.9	3.7	-1.7	formate/nitrite transporter family protein
VFA0387	7.5	7.5	7.4	7.5	7.6	7.8	7.9	7.7	-1.2	7.5	7.4	7.5	7.5	8.1	7.8	8.1	8.0	-1.4	transcriptional regulators, LysR family
VFA0391	9.5	9.4	9.4	9.4	8.8	9.0	9.1	9.0	-1.3	9.3	9.2	9.1	9.2	8.5	8.3	8.5	8.5	-1.7	ABC transporter amino acid-binding protein
VFA0392	6.8	6.3	6.0	6.4	5.8	6.0	6.1	6.0	-1.3	6.5	6.0	6.1	6.2	5.6	5.1	5.3	5.4	-1.8	amino acid ABC transporter permease protein
VFA0403	9.5	9.1	9.4	9.4	8.9	8.1	9.0	8.6	-1.1	9.3	8.7	8.4	8.5	7.7	7.9	7.6	7.9	-1.7	potassium uptake protein KtrA
VFA0404	7.2	7.0	6.9	7.1	7.2	6.6	7.2	7.0	-1.0	7.0	7.2	7.1	7.1	6.2	6.2	6.3	6.2	-1.8	potassium uptake protein KtrB
VFA0415	9.2	9.5	9.4	9.3	9.5	9.9	9.6	9.6	-1.2	9.1	9.8	9.4	9.4	9.9	10.0	10.1	10.0	-1.5	hypothetical protein
VFA0418	6.1	5.5	5.7	5.8	5.0	5.1	5.4	5.1	-1.6	5.9	5.2	5.4	5.5	4.9	4.7	4.8	4.8	-1.7	2-amino-3-ketobutyrate coenzyme A ligase
VFA0451	6.8	6.9	6.6	6.8	6.7	6.5	6.7	6.6	-1.1	6.6	6.6	6.8	6.6	6.0	5.8	6.0	5.9	-1.7	urocanate hydratase
VFA0480	3.2	2.5	2.0	2.6	1.9	2.0	2.6	2.0	-1.4	2.9	2.7	2.9	2.8	1.7	1.7	1.5	1.6	-2.2	hypothetical protein
VFA0481	5.2	4.7	4.6	4.9	4.2	4.4	4.7	4.4	-1.4	4.9	5.1	4.7	4.9	3.8	4.0	3.6	3.8	-2.1	methyl-accepting chemotaxis protein
VFA0482	6.4	5.8	5.7	6.0	5.3	5.3	5.5	5.3	-1.5	6.0	5.2	5.6	5.6	4.7	4.2	4.7	4.6	-2.1	sodium/glutamate symport carrier protein
VFA0525	6.8	5.4	5.5	5.9	4.7	4.6	5.4	4.9	-2.0	6.5	4.6	5.3	5.5	4.2	3.9	4.1	4.1	-2.7	transcriptional regulator, AraC family
VFA0526	6.8	5.1	5.3	5.7	4.2	3.8	4.8	4.3	-2.7	6.4	4.1	5.2	5.2	3.8	2.9	3.5	3.4	-3.5	senescence box/GDEF family protein
VFA0529	6.9	6.6	6.4	6.9	6.2	6.3	6.2	6.1	-1.5	6.9	4.8	5.4	5.7	4.1	3.7	3.8	3.8	-3.6	methyl-accepting chemotaxis protein
VFA0528to05	5.5	4.7	4.6	4.9	4.2	4.7	5.0	4.6	-1.2	5.1	4.4	4.7	4.8	4.2	3.8	4.0	4.0	-1.7	methyl-accepting chemotaxis protein
VFA0529	6.7	6.2	6.2	6.4	6.0	6.0	6.4	6.1	-1.2	6.5	6.2	6.2	6.3	5.9	5.5	5.7	5.7	-1.5	N-ribosylnicotinamide transporter
VFA0531	6.2	5.8	5.6	5.9	5.6	5.5	5.8	5.6	-1.2	5.9	5.9	5.7	5.8	5.3	4.9	5.3	5.2	-1.5	hypothetical cyclic nucleotide-binding domain protein
VFA0543	7.1	6.8	6.9	6.9	6.5	6.5	6.6	6.3	-1.5	6.8	6.5	6.7	6.7	5.3	5.7	6.1	5.9	-1.7	hypothetical protein
VFA0558	6.4	6.5	5.9	6.3	6.1	5.5	6.6	6.1	-1.1	6.2	6.2	6.4	6.3	5.2	5.2	5.9	5.1	-1.9	acetyltransferase family
VFA0572	4.7	4.0	3.4	4.0	3.4	3.1	3.9	3.5	-1.5	4.6	4.6	3.6	4.3	5.1	6.3	5.4	5.6	2.5	minor tail protein
VFA0576	5.0	4.9	4.3	4.7	4.9	4.7	5.3	5.0	-1.2	4.6	5.1	4.6	4.7	4.1	4.2	4.0	4.1	-1.6	zona occludens toxin
VFA0588	5.8	6.0	5.4	5.7	5.1	5.4	5.5	5.3	-1.3	5.9	5.8	5.7	5.8	5.0	5.4	5.2	5.2	-1.5	hypothetical protein
VFA0589	6.1	5.7	5.5	5.8	5.5	5.2	5.6	5.5	-1.2	5.9	5.6	5.5	5.6	5.1	4.7	4.5	4.8	-1.8	integral membrane protein
VFA0590	6.2	5.8	5.5	5.9	5.8	5.5	6.2	5.8	-1.0	5.9	6.0	6.6	5.8	5.1	5.2	5.0	5.1	-1.7	daurorubicin resistance transmembrane protein
VFA0598	7.7	7.2	7.2	7.4	6.6	6.7	6.6	6.6	-1.7	7.6	6.9	7.2	7.2	7.1	4.3	5.9	5.7	-2.8	hypothetical protein
VFA0609	7.6	7.2	7.0	7.3	6.0	6.2	6.9	6.4	-1.9	7.9	7.0	6.9	7.3	5.6	5.2	5.6	5.5	-3.5	hypothetical protein
VFA0610	7.3	6.5	6.5	6.7	5.6	5.9	6.0	5.8	-1.9	7.3	6.1	6.6	6.7	6.0	5.4	5.8	5.7	-1.9	hypothetical protein
VFA0613	7.0	6.9	6.3	6.7	6.7	6.6	7.0	6.8	-1.0	6.7	6.8	6.5	6.7	6.0	6.1	6.0	6.0	-1.6	hypothetical protein
VFA0620	7.9	8.0	7.8	7.9	7.7	7.1	7.9	7.6	-1.3	7.9	8.4	8.0	8.1	6.6	7.3	6.7	6.9	-2.3	hypothetical protein
VFA0623to06	3.7	3.6	3.7	3.7	3.2	3.2	3.5	3.3	-1.3	3.4	3.6	3.2	3.4	3.2	2.7	2.6	2.8	-1.5	hypothetical protein
VFA0645	5.7	5.4	5.2	5.4	5.4	5.3	5.6	5.4	-1.0	5.4	5.8	5.0	5.4	4.9	4.6	4.5	4.7	-1.7	acetyltransferase
VFA0663	6.2	5.0	4.1	5.1	3.9	3.1	4.2	3.7	-2.5	6.0	4.3	4.6	4.9	3.4	3.0	2.8	3.1	-3.7	integrase/recombinase (XerC/CodV family)
VFA0681	6.3	5.6	5.5	5.8	5.0	5.0	5.2	5.1	-1.7	6.1	5.2	5.7	5.7	4.9	5.2	4.5	4.9	-1.7	hypothetical membrane spanning protein
VFA0688	5.4	4.7	4.3	4.8	4.1	4.2	5.1	4.5	-1.2	5.1	5.3	4.4	5.0	6.4	6.6	6.8	6.6	3.1	hypothetical protein
VFA0767	4.4	4.3	4.1	4.2	5.0	4.6	4.7	4.8	-1.4	4.1	4.1	4.0	4.1	5.5	4.9	5.1	5.2	2.2	cytochrome c-554(548)
VFA0775	6.9	6.9	6.6	6.8	6.2	6.4	6.5	6.4	-1.3	6.7	7.0	6.6	6.8	6.0	6.4	6.2	6.2	-1.5	short chain dehydrogenase
VFA0778	6.4	6.1	6.0	6.2	5.2	5.6	5.9	5.6	-1.5	6.2	5.8	5.8	5.9	5.3	5.3	5.3	5.3	-1.6	ToIQ protein
VFA0790	4.2	3.8	3.5	3.8	3.3	3.3	3.7	3.5	-1.3	3.9	3.8	3.6	3.8	3.0	3.2	3.1	3.1	-1.6	chloramphenicol acetyltransferase
VFA0801	7.2	6.1	5.9	6.4	6.1	5.8	6.3	6.1	-1.1	7.0	6.2	6.2	6.4	5.1	5.2	5.5	5.2	-2.3	isomylase
VFA0804	6.6	6.4	5.9	6.3	5.7	5.7	6.												

VFA0932	7.5	7.2	7.0	7.2	7.4	7.6	8.1	7.7	1.4	7.4	7.1	7.3	7.2	8.2	8.2	8.4	8.3	2.1	putative phospholipid-binding protein	
VFA0939	6.3	5.4	5.3	5.6	5.1	4.9	5.4	5.1	-1.4	6.0	5.2	5.2	5.5	4.5	4.3	4.5	4.4	-2.1	hypothetical protein	
VFA0941	6.2	6.1	5.6	6.0	5.8	5.1	6.2	5.7	-1.2	5.9	6.2	5.8	6.0	4.3	4.9	3.5	4.2	-3.3	1-phosphofructokinase	
VFA0942	6.1	6.0	5.7	5.9	5.8	5.1	6.4	5.8	-1.1	6.0	6.1	5.6	5.9	4.3	4.8	4.2	4.5	-2.7	PTS system, fructose-specific IIA/FPR component	
VFA0946_x	4.4	4.4	3.8	4.2	4.0	4.0	4.5	4.2	-1.0	4.2	4.4	4.1	4.2	3.4	3.7	3.5	3.5	-1.7	hypothetical protein	
VFA0958	4.2	3.6	3.2	3.7	3.0	2.8	3.3	3.0	-1.5	3.9	3.4	3.3	3.5	2.5	2.6	2.8	2.6	-1.9	glycerophosphoryl diester phosphodiesterase	
VFA0959	6.0	5.4	5.0	5.5	4.6	4.7	5.0	4.7	-1.7	6.0	5.3	5.6	5.6	4.8	4.0	4.4	4.4	-2.4	GAD6F protein	
VFA0968	5.6	5.1	4.8	5.2	5.1	4.6	5.2	5.0	-1.2	5.3	5.2	5.0	5.2	4.3	4.0	4.0	4.1	-2.2	purine nucleoside phosphorylase	
VFA0980	8.2	9.1	8.6	8.6	9.0	9.3	8.9	9.1	1.4	8.0	8.8	8.9	8.6	9.8	10.7	10.2	10.2	3.2	hypothetical protein	
VFA0991	5.6	5.3	5.3	5.4	4.9	5.2	5.4	5.2	-1.2	5.4	5.4	5.3	5.4	5.0	5.0	4.5	4.8	-1.8	hypothetical protein	
VFA0995	10.8	11.0	11.0	10.9	11.5	11.6	11.2	11.4	1.5	10.6	11.3	11.1	11.0	12.0	12.3	12.1	12.1	2.2	high-affinity iron permease	
VFA0996	6.3	5.9	6.1	6.1	5.5	5.4	5.9	5.6	-1.4	5.9	5.8	6.0	5.9	5.6	5.4	5.0	5.3	-1.5	hypothetical protein	
VFA0999	4.6	4.4	4.3	4.4	3.8	3.7	4.3	3.9	-1.4	4.3	4.0	4.2	4.2	3.5	3.4	3.6	3.5	-1.6	N-acetylglucosamine-6-phosphate deacetylase	
VFA1000	4.2	3.8	3.8	3.9	3.6	3.4	3.6	3.5	-1.3	3.7	3.9	3.6	3.7	3.2	3.2	2.9	3.1	-1.5	PTS system, N-acetylglucosamine-specific IIA component	
VFA1009	4.3	4.4	3.8	4.2	4.4	3.8	4.9	4.4	-1.2	4.1	4.4	4.2	4.2	3.4	3.7	3.0	3.4	-1.8	hypothetical protein	
VFA1012	7.8	7.7	7.6	7.7	7.4	6.9	7.6	7.3	-1.3	7.6	7.9	7.8	7.8	7.1	7.1	7.0	7.1	-1.6	two component response regulator	
VFA1014	8.3	8.5	8.0	8.3	7.7	6.7	7.9	7.4	-1.8	8.1	8.4	8.1	8.2	6.5	6.5	6.3	6.5	-3.4	hypothetical protein	
VFA1015	9.6	9.6	9.3	9.5	9.1	8.2	9.5	8.9	-1.5	9.5	9.6	9.3	9.5	7.9	8.0	7.8	7.9	-3.0	RpoS-like sigma factor	
VFA1016	8.7	8.8	8.2	8.6	8.8	7.5	8.9	8.4	-1.1	8.6	8.9	8.6	8.7	6.8	7.4	6.3	6.8	-3.6	sensory transduction protein kinase	
VFA1017	9.0	9.1	8.5	8.9	8.9	7.5	8.8	8.4	-1.4	8.9	9.1	8.8	8.9	6.7	7.6	6.3	6.8	-4.3	two component response regulator	
VFA1038	8.0	7.6	7.6	7.7	7.4	7.3	7.7	7.5	-1.2	7.9	7.7	7.7	7.8	7.3	7.4	7.2	7.3	-1.4	sensory box/GGDEF family protein	
VFA1051	7.3	7.1	7.0	7.1	7.3	7.0	7.5	7.3	1.1	7.1	7.4	7.1	7.2	6.6	6.7	6.5	6.6	-1.5	universal stress protein family	
VFA1066	6.0	5.3	5.1	5.5	5.2	5.2	5.8	5.4	-1.1	5.6	5.4	5.0	5.3	4.3	4.4	4.2	4.3	-2.0	transcriptional regulator, LysR family	
VFA1073	4.1	3.4	2.4	3.3	2.3	2.3	2.3	2.3	-2.0	3.6	2.7	3.0	3.1	2.3	2.0	1.8	2.0	-2.1	methyl-accepting chemotaxis protein	
VFA1077	6.4	6.2	6.0	6.2	6.3	5.7	6.5	6.2	-1.1	6.2	6.5	6.0	6.2	5.5	5.6	5.7	5.6	-1.5	RI01 protein	
VFA1079	7.1	6.8	6.8	6.9	6.8	6.5	7.1	6.8	-1.1	7.0	6.8	6.5	6.8	6.3	6.0	6.3	6.2	-1.5	hypothetical membrane spanning protein	
VFA1080	6.4	6.0	6.2	6.2	5.7	5.2	5.7	5.2	-1.2	5.2	5.2	5.3	5.2	4.9	4.3	4.6	4.6	-1.9	transporter, drug/metabolite exporter family	
VFA1094_x	6.3	5.6	5.5	5.8	4.7	5.3	5.0	5.0	-1.8	6.0	4.9	5.3	5.4	4.8	4.2	4.4	4.5	-1.8	cold shock protein	
VFA1099	4.1	3.8	3.5	3.8	3.8	4.1	4.0	4.0	-1.0	4.1	3.9	3.7	3.9	3.1	3.5	3.5	3.4	-1.4	hypothetical protein	
VFA1105	5.7	5.7	5.2	5.5	5.5	5.2	5.7	5.5	-1.0	5.5	5.5	5.5	5.5	4.9	4.6	4.8	4.8	-1.6	HvnC; halovibrin	
VFA1127	5.4	4.8	3.7	4.6	4.2	4.1	5.1	4.5	-1.1	4.8	4.8	4.4	4.7	3.2	3.7	3.4	3.4	-2.4	hypothetical protein	
VFA1136	6.3	6.0	6.2	6.2	5.4	5.1	5.8	5.4	-1.4	5.4	5.1	5.4	5.4	4.9	4.9	4.9	5.0	-1.7	anaerobic glycerol-3-phosphate dehydrogenase subunit C	
VFB01	5.2	4.4	4.1	4.6	4.9	4.4	5.7	5.0	1.4	4.9	4.3	4.1	4.5	6.3	5.7	6.5	6.2	3.3	hypothetical protein	
VFB05	8.7	9.0	8.9	8.9	9.1	9.6	9.2	9.3	1.3	8.7	9.0	9.0	8.9	9.6	9.1	9.6	9.4	1.5	hypothetical protein	
VFB06	8.9	9.2	9.3	9.1	9.4	9.9	9.7	9.7	1.5	8.7	9.3	9.2	9.1	10.0	9.5	9.9	9.8	1.7	hypothetical protein	
VFB12	7.9	7.7	7.3	7.6	8.1	8.1	8.3	8.1	1.4	7.5	7.9	7.6	7.7	8.3	8.3	8.6	8.4	1.7	hypothetical protein	
VFB31	7.1	7.5	7.9	7.5	6.7	7.2	6.7	6.7	-1.7	6.7	7.4	7.3	7.2	6.7	6.2	6.2	6.2	-1.4	hypothetical protein	
VFB32	7.8	8.8	8.8	8.5	7.4	8.3	7.5	7.7	-1.7	7.5	8.5	8.2	8.1	6.8	7.3	6.6	6.9	-2.2	transporter	
VFB37	5.2	5.5	5.5	5.4	4.6	5.5	5.2	5.1	-1.2	4.6	5.3	4.8	4.9	4.1	4.3	3.8	4.1	-1.8	hypothetical protein	
VFB39	6.6	6.5	6.6	6.6	5.9	6.5	6.3	6.2	-1.3	6.2	6.3	6.4	6.3	5.0	5.4	5.4	5.3	-2.1	VirB4 ATPase	
VFB41	6.0	6.3	6.2	6.2	5.1	6.0	5.5	5.5	-1.6	5.4	6.0	6.1	5.8	4.5	4.6	4.0	4.4	-2.7	channel protein VirB9	
<b>2897 genes*</b>																				
VF0002	7.2	6.6	6.8	6.9	6.8	6.6	7.0	6.8	-1.1	7.1	6.6	6.7	6.8	6.6	6.5	6.5	6.5	-1.2	rRNA modification GTPase	
VF0009	8.5	8.0	8.1	8.2	8.2	8.1	8.3	8.2	-1.0	8.4	7.7	7.9	8.0	7.6	7.2	7.7	7.5	-1.4	chromosomal replication initiation protein	
VF0010	9.5	9.1	9.3	9.3	9.1	9.2	9.2	9.2	-1.1	9.4	9.0	9.2	9.2	9.1	8.7	9.2	9.0	-1.2	DNA polymerase III subunit beta	
VF0011	9.4	9.1	9.2	9.2	8.6	8.7	8.8	8.7	-1.4	9.4	8.8	9.1	9.1	8.8	8.3	8.8	8.6	-1.4	recombination protein F	
VF0012	8.8	8.1	8.5	8.5	7.7	7.7	8.2	7.9	-1.5	8.7	7.9	8.3	8.3	7.8	7.2	7.8	7.6	-1.6	DNA gyrase subunit B	
VF0014	8.1	7.8	7.9	7.9	7.8	7.9	8.0	7.9	-1.0	7.9	7.8	7.7	7.8	7.9	8.0	8.1	8.0	1.1	valine-pyruvate transaminase	
VF0015	9.5	9.0	9.2	9.2	8.8	8.9	9.0	8.9	-1.3	9.4	8.6	9.0	9.0	8.8	8.3	8.8	8.6	-1.3	glycyl-tRNA synthetase alpha subunit	
VF0016	8.4	8.0	8.2	8.2	7.5	7.9	8.0	7.7	-1.3	7.9	8.0	8.2	8.0	7.7	7.0	7.6	7.4	-1.4	glycyl-tRNA synthetase beta subunit	
VF0017	7.9	7.7	7.6	7.7	7.7	7.5	8.0	7.7	-1.0	7.7	7.6	7.5	7.6	7.3	7.4	7.5	7.4	-1.2	alpha-amylase	
VF0018	6.6	6.0	5.5	6.0	6.0	5.4	6.6	6.0	-1.0	6.7	6.4	5.8	6.3	5.8	6.5	6.1	6.1	-1.1	NADH dehydrogenase subunit II-related protein	
VF0019	5.8	5.3	4.3	5.1	4.5	4.4	4.6	4.5	-1.6	5.3	4.9	5.1	5.1	4.3	4.5	4.2	4.3	-1.7	hypothetical transcriptional regulatory protein	
VF0021	6.8	6.1	6.2	6.3	6.1	6.1	6.6	6.3	-1.1	6.6	6.0	5.9	6.1	6.2	6.0	6.1	6.1	-1.0	transcriptional regulators, LysR family	
VF0022	6.5	5.8	5.7	6.0	5.8	5.6	6.2	5.9	-1.2	6.4	5.7	5.6	5.9	5.5	5.5	5.4	5.4	-1.4	hypothetical protein	
VF0023	8.6	8.1	8.1	8.2	8.5	7.4	8.7	8.2	-1.0	8.5	8.2	8.1	8.3	7.5	7.6	7.5	7.5	-1.7	Alcohol dehydrogenase	
VF0023to24	4.2	3.7	3.2	3.7	3.6	3.4	4.1	3.7	-1.0	4.0	3.7	3.3	3.7	3.1	5.3	4.2	4.2	-1.4	Alcohol dehydrogenase	
VF0026	6.3	5.8	5.5	5.9	6.0	5.5	6.2	5.9	-1.0	6.0	5.6	5.5	5.7	5.3	5.2	5.5	5.3	-1.3	hypothetical protein	
VF0027	6.5	6.0	6.1	6.2	5.9	5.5	6.2	5.9	-1.2	6.4	5.8	5.9	6.0	5.9	5.5	5.9	5.8	-1.2	Trk system potassium uptake protein TrkH	
VF0028	6.7	5.4	5.2	5.8	5.5	5.2	6.0	5.5	-1.2	6.4	5.3	5.3	5.6	5.1	4.9	5.1	5.1	-1.5	protoporphyrinogen oxidase	
VF0029	8.9	8.3	8.2	8.4	7.9	7.9	8.3	8.0	-1.4	8.9	7.8	8.1	8.3	7.9	7.6	7.9	7.8	-1.4	zinc protease	
VF0030	6.5	6.1	5.9	6.2	6.1	5.9	6.1	6.0	-1.1	6.5	6.0	6.0	6.2	6.0	6.0	6.1	6.0	-1.4	hypothetical protein	
VF0031to32	6.4	5.8	5.5	5.9	6.0	5.2	6.2	5.8	-1.0	6.1	6.2	5.8	6.0	6.3	6.2	6.3	6.3	-1.2	chloride channel protein	
VF0031to32C	3.4	2.9	2.6	3.0	2.8	2.5	3.4	2.9	-1.0	3.0	2.9	2.6	2.8	2.6	3.1	2.6	2.7	1.1	channel protein	
VF0032	5.2	4.2	4.2	4.5	4.7	4.4	4.5	4.6	1.0	4.7	4.4	4.1	4.4	4.7	4.4	4.5	4.5	-1.1	thiamine biosynthesis protein ThiC	
VF0033	4.6	4.0	3.9	4.2	4.0	3.8	4.2	4.0	-1.1	4.1	4.0	3.9	4.0	4.1	3.9	4.1	4.1	1.0	thiamin-phosphate pyrophosphorylase	
VF0034	4.7	4.0	4.0	4.3	4.1	4.0	4.5	4.2	-1.0	4.3	3.9	4.1	4.1	4.1	3.8	3.7	3.9	-1.2	molybdopterin biosynthesis MoeB protein	
VF0035	4.9	3.8	4.0	4.2	4.0	3.8	4.8	4.2	-1.0	4.3	3.9	3.8	4.0	3.5	3.4	3.8	3.6	-1.3	thiazole synthase	
VF0036	5.8	5.0	4.8	5.2	5.3	5.1	5.4	5.3	1.1	5.4	5.1	5.1	5.2	4.9	5.0	4.9	4.9	-1.2	thiamine biosynthesis protein ThiH	
VF0038	8.6	8.1	8.1	8.3	7.8	7.9	8.2	8.0	-1.2	8.6	7.8	8.1	8.2	8.2	7.9	7.6	8.0	7.9	-1.1	Xaa-Pro aminopeptidase
VF0039	6.7	6.0	5.7	6.1	6.7	5.9	7.0	6.5	1.3	6.3	5.7	5.7	5.9	5.4	5.1	5.2	5.3	-1.6	virulence genes transcriptional regulator PhcA	
VF0040	6.4	5.4	5.3	5.7	6.3	5.4	6.7	6.2	1.4	6.0	5.3	5.6	5.6	5.3	4.8	5.3	5.1	-1.4	transcriptional regulatory protein	
VF0041	5.9	5.2	5.0	5.4	5.3	5.1	5.5	5.3	-1.1	5.7	4.9	5.0	5.2	5.0	4.7					

VF0064	8.1	7.8	7.8	7.9	8.1	7.6	8.4	8.0	1.1	7.9	7.7	7.8	7.8	7.4	7.0	7.2	7.2	-1.5	uroporphyrin-III C-methyltransferase
VF0065	8.1	7.9	7.3	7.9	8.4	7.7	8.5	8.0	-1.2	8.0	7.8	7.9	7.9	7.7	7.6	7.4	7.5	-1.3	uroporphyrinogen-III synthase
VF0066	7.8	7.1	7.0	7.3	7.0	6.8	7.4	7.0	-1.2	7.7	6.6	7.0	7.1	7.0	6.8	7.1	7.0	-1.1	porphobilinogen deaminase
VF0068	7.1	6.9	7.0	7.0	6.7	6.9	7.0	6.9	-1.1	7.0	6.6	6.9	6.8	6.9	6.8	6.8	6.9	1.0	DNA helicase II
VF0069	5.6	4.9	5.1	5.2	4.8	4.4	5.2	4.8	-1.3	5.4	4.6	4.8	4.9	4.4	4.4	4.4	4.4	-1.5	chloramphenicol-sensitive protein RadD
VF0070	7.3	6.8	7.0	7.0	6.1	6.3	6.5	6.3	-1.6	7.1	6.4	6.9	6.8	6.4	5.5	6.4	6.1	-1.6	ATP-dependent DNA helicase RecQ
VF0072	5.1	4.4	3.9	4.5	4.2	4.2	4.5	4.3	-1.1	4.2	4.3	4.7	4.5	4.1	3.9	4.1	4.1	-1.4	glycero-3-phosphate transporter
VF0073	7.8	6.1	6.6	6.9	6.4	5.7	6.7	6.3	-1.5	7.5	5.9	6.5	6.7	6.1	4.9	6.1	5.7	-2.0	transporter
VF0074	8.1	7.6	7.7	7.8	7.3	7.4	7.7	7.5	-1.2	8.0	7.2	7.5	7.6	7.3	7.1	7.3	7.3	-1.2	DNA polymerase I
VF0074to75	4.5	4.0	3.5	4.0	4.7	4.4	4.8	4.7	1.6	4.5	3.8	3.9	4.1	3.9	4.1	3.7	3.9	-1.1	DNA polymerase I
VF0074to75C	4.0	3.7	3.7	3.8	3.6	3.3	3.6	3.5	-1.3	3.9	3.7	3.8	3.8	3.8	3.6	3.4	3.6	-1.2	DNA polymerase I
VF0075	7.8	7.3	7.4	7.5	7.3	7.1	7.5	7.3	-1.2	7.8	7.0	7.3	7.4	7.3	7.1	7.3	7.2	-1.1	GTP-binding protein
VF0076	9.2	9.4	9.4	9.4	9.0	9.2	9.0	9.0	-1.2	9.2	9.2	9.3	9.3	9.4	9.2	9.4	9.3	1.1	cytochrome c4
VF0081	7.3	7.1	7.0	7.1	7.0	7.0	7.2	7.1	-1.1	7.2	6.7	6.8	6.9	6.5	6.9	6.7	6.7	-1.2	transcriptional regulator, AsnC family
VF0082	7.0	6.6	6.9	6.8	6.7	6.5	7.0	6.7	-1.1	6.9	6.4	6.6	6.6	6.7	6.5	6.7	6.6	1.0	SAM-dependent methyltransferase
VF0083	7.4	7.0	6.8	7.1	7.1	6.0	7.6	6.9	-1.1	7.2	7.2	6.9	7.1	6.4	7.3	6.8	6.9	-1.2	universal stress protein A
VF0084	9.8	9.9	9.7	9.8	11.1	9.9	11.0	10.6	1.8	9.7	10.2	9.6	9.8	9.2	9.7	9.0	9.3	-1.5	ferritin
VF0089	7.2	7.0	6.8	7.0	6.9	6.3	6.9	6.7	-1.2	7.0	6.9	7.0	7.0	6.7	6.6	6.5	6.6	-1.3	hypothetical outer membrane protein
VF0090	7.1	6.4	6.6	6.7	6.4	6.2	6.7	6.4	-1.2	6.9	6.2	6.6	6.5	6.6	6.4	6.7	6.6	-1.0	2-dehydro-3-deoxyphosphogluconate aldolase
VF0091	4.1	3.5	3.2	3.6	3.2	3.4	3.7	3.4	-1.1	3.6	3.3	3.5	3.4	3.2	3.1	3.2	3.2	-1.2	sensory box/GGDEF family protein
VF0092	8.1	7.7	7.6	7.8	8.1	7.7	8.4	8.1	-1.2	7.9	7.7	7.5	7.7	7.2	7.5	7.6	7.6	-1.1	adenosine deaminase
VF0093	7.9	7.1	7.4	7.4	7.8	7.1	8.2	7.7	1.2	7.7	7.0	7.1	7.3	7.2	7.0	7.3	7.2	-1.1	adenosine deaminase
VF0094	4.9	4.7	4.1	4.6	4.7	4.3	5.2	4.7	1.1	4.6	4.1	4.1	4.2	3.5	3.8	3.4	3.6	-1.6	sensory box/GGDEF family protein
VF0097	5.9	4.8	4.7	5.1	6.1	5.0	6.1	5.7	1.5	5.6	4.5	4.9	5.0	3.9	4.6	4.0	4.2	-1.8	hypothetical protein
VF0098to99	7.1	6.8	6.9	6.9	7.1	6.9	7.1	7.0	1.1	6.8	6.5	6.6	6.6	6.3	6.3	6.3	6.3	-1.3	glutamine synthetase
VF0098to99C	6.3	6.0	5.8	6.0	6.0	5.7	6.5	6.1	1.0	6.0	5.7	5.7	5.8	5.7	5.6	5.3	5.5	-1.2	glutamine synthetase
VF0099	10.4	10.0	10.3	10.4	10.4	10.0	10.3	10.3	-1.1	10.4	10.2	10.3	10.3	10.3	10.3	10.3	10.3	-1.0	GTP-binding protein TypA/BpA
VF0100	8.3	8.1	8.1	8.2	7.8	8.1	7.9	7.9	-1.2	8.3	7.8	7.9	8.0	7.8	7.7	7.9	7.8	-1.1	ribonuclease BN
VF0101	8.7	8.3	8.4	8.5	8.0	8.0	8.2	8.1	-1.3	8.6	8.0	8.3	8.3	8.0	7.8	7.9	7.9	-1.3	D-tyrosyl-tRNA deacylase
VF0101to102	7.8	7.4	7.5	7.5	7.2	7.1	7.4	7.2	1.0	7.6	7.1	7.3	7.3	7.0	7.0	6.9	7.0	-1.2	D-tyrosyl-tRNA deacylase
VF0101to102A	4.2	4.3	3.4	4.0	3.5	3.5	3.2	3.4	-1.5	3.9	3.6	3.3	3.6	3.2	2.9	2.7	2.9	-1.6	D-tyrosyl-tRNA deacylase
VF0102	8.5	8.1	8.3	8.4	8.0	8.0	8.3	8.0	-1.3	8.0	8.0	8.3	8.2	8.0	7.9	8.3	8.1	-1.1	acylttransferase
VF0104	8.6	8.2	8.4	8.4	8.1	7.7	8.2	8.0	-1.3	8.4	8.0	8.3	8.2	8.1	8.1	8.3	8.2	-1.1	GTP pyrophosphokinase
VF0105	10.7	10.7	10.6	10.7	10.8	10.5	10.7	10.7	-1.0	10.8	10.8	10.7	10.8	10.8	10.9	10.8	10.8	1.0	DNA-directed RNA polymerase omega subunit
VF0110	8.6	8.0	8.4	8.3	7.8	7.6	7.8	7.8	-1.5	8.5	7.8	8.2	8.2	8.2	7.8	8.3	8.1	-1.1	protein YicC
VF0111	7.8	7.5	7.4	7.5	7.5	7.0	7.6	7.4	-1.1	7.7	7.3	7.3	7.4	7.1	6.8	7.2	7.0	-1.3	ribonuclease PH
VF0112	6.9	6.5	6.5	6.8	6.6	6.3	6.6	6.3	-1.3	6.7	6.3	6.5	6.5	6.7	5.9	6.6	6.4	-1.6	crotonate phosphoribosyltransferase
VF0113	3.7	3.6	3.3	3.5	3.9	3.9	4.3	4.0	1.4	3.6	3.9	3.3	3.6	3.7	3.8	3.7	3.7	-1.1	chromosome partitioning protein ParA
VF0114	8.2	7.9	8.1	8.1	8.3	7.9	8.4	8.2	1.1	8.1	8.1	7.9	8.0	7.8	8.0	8.0	8.0	-1.0	osmolarity response regulator
VF0117	3.6	3.1	3.2	3.3	3.1	2.8	3.2	3.0	-1.2	3.0	3.1	2.9	3.0	2.7	2.8	2.8	2.7	-1.2	competence protein F
VF0118	7.8	7.3	7.3	7.5	7.2	7.1	7.6	7.3	-1.1	7.6	7.1	7.3	7.3	7.1	7.1	7.2	7.1	-1.1	BioH protein
VF0119	7.4	7.0	7.3	7.2	7.0	6.8	7.2	7.0	-1.1	7.3	6.9	7.1	7.1	7.1	6.8	7.0	7.0	-1.1	hypothetical protein
VF0124	7.7	7.1	7.1	7.3	6.9	6.7	7.1	6.9	-1.3	7.5	7.0	7.2	7.2	6.8	6.8	6.9	6.8	-1.3	Tk protein
VF0125	8.3	7.9	7.7	8.0	7.5	7.7	7.7	7.6	-1.3	8.1	7.6	7.9	7.9	7.7	7.5	7.8	7.7	-1.1	phosphopantothencysteine synthase/decarboxylase
VF0126	4.8	4.4	4.4	4.5	4.1	4.0	4.3	4.1	-1.3	4.6	4.2	4.1	4.3	4.0	4.1	4.1	4.1	-1.2	DNA repair protein RadC
VF0129	7.8	7.6	7.6	7.7	7.5	7.5	7.8	7.6	-1.0	7.7	7.5	7.6	7.6	7.6	7.7	7.7	7.7	1.1	hypothetical protein
VF0130	8.9	8.8	8.9	8.8	8.4	8.6	8.6	8.3	-1.3	8.8	8.5	8.6	8.7	8.4	8.7	8.7	8.6	-1.1	formamylglymidine-DNA glycosylase
VF0131	7.2	7.1	6.9	7.1	6.7	7.2	7.1	7.0	-1.0	7.1	6.8	7.0	7.0	6.9	6.9	6.9	6.9	-1.1	phosphoglycerol transferase MdoB and related proteins, alkaline phosphatase
VF0132	6.7	5.8	6.1	6.2	5.6	5.4	6.0	5.7	-1.5	6.3	5.5	5.8	5.8	5.4	5.0	5.2	5.2	-1.5	phosphopantetheine adenylyltransferase
VF0133	7.9	7.4	7.4	7.6	6.8	7.0	7.3	7.0	-1.4	7.6	7.1	7.3	7.3	7.1	6.7	6.9	6.9	-1.4	glycosyltransferase
VF0134	8.2	7.7	8.0	7.9	7.4	7.3	7.6	7.4	-1.4	8.0	7.4	7.8	7.7	7.6	7.1	7.6	7.5	-1.2	alpha-L-glycero-D-manno-heptose beta-1,4-glycosyltransferase
VF0135	8.9	8.8	8.9	8.8	8.4	8.6	8.6	8.3	-1.3	8.8	8.5	8.6	8.7	8.4	8.7	8.7	8.6	-1.1	ADP-heptose-LPS heptosyltransferase III
VF0136	7.8	7.7	7.6	7.7	7.7	7.5	7.8	7.7	-1.0	7.7	7.5	7.5	7.6	7.5	7.8	7.5	7.6	-1.0	3-deoxy-D-manno-octulosonic-acid kinase
VF0137	7.9	7.6	7.5	7.7	7.4	7.4	7.5	7.4	-1.2	7.8	7.4	7.5	7.6	7.4	7.2	7.3	7.3	-1.2	phosphoglycerol transferase MdoB and related proteins, alkaline phosphatase
VF0138	8.2	7.9	8.0	8.0	7.4	7.5	7.5	7.5	-1.5	8.0	7.5	8.0	7.8	7.7	7.1	7.6	7.4	-1.3	3-deoxy-D-manno-octulosonic-acid transferase
VF0139	8.5	8.1	8.4	8.3	8.1	7.9	8.5	8.2	-1.1	8.5	8.0	8.3	8.2	8.1	7.6	8.1	7.9	-1.3	ADP-heptose-LPS heptosyltransferase II
VF0140	10.4	10.0	10.1	10.2	10.3	10.1	10.5	10.3	1.1	10.3	10.2	10.1	10.1	10.1	10.1	10.2	10.1	1.0	UDP-N-acetylglucosamine 4,6-dehydratase
VF0141	9.7	9.4	9.5	9.6	9.6	9.6	9.8	9.7	1.1	9.6	9.4	9.5	9.5	9.6	9.4	9.5	9.5	-1.0	UDP-bacillosamine synthetase
VF0142	10.3	10.2	10.2	10.3	10.3	10.3	10.3	10.3	1.0	10.3	10.2	10.2	10.2	10.1	10.1	10.3	10.1	-1.1	UDP-N-acetylglucosamine 2-epimerase (N-acetylmannosamine-forming)
VF0143	10.1	9.8	9.8	9.9	10.0	10.0	10.0	10.0	1.1	10.0	9.7	9.8	9.8	9.7	9.6	9.8	9.7	-1.1	N-acetylneuraminate synthase
VF0144	9.7	9.4	9.3	9.4	9.4	9.5	9.6	9.5	1.0	9.5	9.2	9.2	9.3	9.2	8.9	9.3	9.1	-1.1	sialic acid biosynthesis protein NeuD
VF0145	9.9	9.7	9.7	9.8	9.6	9.7	9.8	9.7	-1.0	9.8	9.4	9.5	9.6	9.4	9.0	9.4	9.3	-1.2	mannose-1-phosphate guanylyltransferase
VF0146	9.7	9.5	9.4	9.5	9.5	9.4	9.6	9.5	-1.0	9.6	9.3	9.4	9.4	9.3	8.9	9.2	9.1	-1.2	oxidoreductase
VF0147	9.8	9.5	9.6	9.6	9.5	9.3	9.7	9.5	-1.1	9.7	9.2	9.4	9.5	9.3	8.8	9.2	9.1	-1.3	aclyneuraminate cytidylyltransferase
VF0152	9.1	8.6	8.8	8.8	9.2	8.5	9.2	9.0	-1.1	9.0	8.6	8.8	8.8	8.9	8.7	8.7	8.9	1.1	ADP-L-glycero-D-manno-heptose-6-epimerase
VF0152to53	3.5	3.6	3.0	3.4	3.3	3.3	3.5	3.4	-1.0	3.6	3.5	3.1	3.4	2.9	3.3	2.8	2.9	-1.4	ADP-L-glycero-D-manno-heptose-6-epimerase
VF0152to53C	7.5	7.5	7.2	7.4	7.9	7.2	8.0	7.7	1.2	7.3	7.6	7.4	7.4	7.0	7.3	7.1	7.1	-1.2	ADP-L-glycero-D-manno-heptose-6-epimerase
VF0153	6.5	6.3	6.1	6.3	6.6	5.9	6.6	6.4	1.0	6.0	6.2	6.1	6.1	5.7	6.1	5.8	5.8	-1.2	cleavage and polyadenylation
VF0154	5.0	4.0	3.6	4.2	4.5	3.6	4.8	4.3	1.1	4.3	3.8	3.4	3.8	3.1	3.4	3.6	3.4	-1.4	hypothetical protein
VF0155	8.2	7.9	7.8	8.0	8.1	7.9	8.2	8.1	-1.1	8.0	7.9	7.8	7.9	7.9	8.3	8.0	8.1	1.1	transcriptional regulator, TetR family
VF0173to174	2.5	2.2	2.0	2.2	2.3	1.9	2.1	2.1	-1.1	2.4	1.9	2.1	2.1	1.9	2.0	1.8	1.9	-1.2	

VF0205	10.0	9.4	9.6	9.7	9.0	9.5	9.5	9.3	-1.2	9.7	9.4	9.5	9.5	9.1	9.0	9.3	9.1	-1.3	chaperonin GroEL
VF0206	10.2	9.3	9.6	9.7	9.6	9.8	9.3	9.3	-1.3	10.1	9.3	9.4	9.6	9.3	9.1	9.4	9.3	-1.2	triosephosphate isomerase
VF0207	6.2	5.4	5.3	5.6	4.8	4.5	5.4	4.9	-1.7	5.9	5.0	5.2	5.4	4.9	5.0	5.0	5.0	-1.3	5-carboxymethyl-2-hydroxyruconate delta-isomerase
VF0208	6.9	6.5	5.7	6.4	7.6	6.2	8.1	7.3	2.0	6.6	7.2	6.1	6.7	5.0	6.2	4.6	5.3	-2.6	hypothetical protein
VF0208to209	3.6	3.5	3.6	3.6	3.8	3.8	3.6	3.7	-1.1	3.6	3.5	3.6	3.6	3.6	3.9	3.6	3.7	-1.1	hypothetical protein
VF0208to209	4.0	3.6	3.4	3.7	3.5	3.3	4.0	3.6	-1.1	3.8	3.5	3.4	3.6	3.4	3.6	3.4	3.5	-1.1	hypothetical protein
VF0209	8.6	8.1	8.3	8.3	8.0	8.2	7.9	8.1	-1.2	8.5	7.7	8.1	8.1	8.0	8.5	8.2	8.7	-1.3	fructose 1,5-bisphosphatase II
VF0210	6.6	6.4	5.8	6.3	5.9	5.5	5.7	5.7	-1.5	6.6	6.1	6.2	6.3	5.7	6.1	5.8	5.9	-1.3	transcriptional regulator
VF0211	8.0	7.5	7.5	7.6	7.4	7.2	7.6	7.4	-1.2	7.9	7.3	7.5	7.5	7.1	6.9	7.2	7.1	-1.4	ribonuclease activity regulator protein RraA
VF0213	8.4	7.8	8.0	8.1	7.3	7.6	7.7	7.5	-1.4	8.3	7.4	7.9	7.9	7.7	7.5	7.8	7.7	-1.1	phosphoribulokinase
VF0214	8.6	8.1	8.2	8.3	7.6	7.7	7.9	7.7	-1.5	8.5	7.8	8.1	8.1	8.1	7.9	8.2	8.0	-1.1	phosphoribulokinase
VF0215	5.3	4.8	4.3	4.8	5.3	12.2	5.9	5.5	1.6	5.1	4.8	4.6	4.8	4.5	5.0	4.7	4.7	-1.0	hypothetical protein
VF0217	5.2	4.1	3.6	4.3	4.1	4.1	4.6	4.3	-1.0	4.8	3.8	3.8	4.1	3.2	3.5	3.3	3.3	-1.7	hypothetical protein
VF0218	7.5	6.8	6.8	7.0	6.1	6.4	6.6	6.4	-1.6	7.4	6.5	6.9	6.9	6.4	6.1	6.6	6.4	-1.5	ABC transporter ATP-binding protein
VF0219	9.1	9.1	9.2	9.1	8.9	9.2	9.2	9.1	-1.0	9.1	9.0	9.2	9.1	9.1	9.0	9.1	9.1	-1.0	glutathione-regulated potassium-efflux system ancillary protein
VF0220	7.4	6.9	7.0	7.1	6.8	6.8	7.2	6.9	-1.1	7.3	6.6	6.5	6.8	6.6	6.2	6.6	6.5	-1.2	glutathione-regulated potassium-efflux system protein KefB
VF0221	8.3	8.0	8.2	8.2	7.9	8.1	8.2	8.0	-1.1	8.2	7.9	8.1	8.1	7.9	7.8	7.9	7.9	-1.1	glutathione-regulated potassium-efflux system protein KefB
VF0222	9.2	8.9	9.1	9.1	8.6	8.6	8.8	8.7	-1.3	9.1	8.9	9.1	9.0	8.8	8.7	9.0	8.8	-1.1	hypothetical protein
VF0223	8.3	7.9	8.0	8.1	7.7	7.5	7.8	7.7	-1.3	8.2	7.8	8.0	8.0	8.0	7.9	8.0	7.9	-1.1	peptidyl-prolyl cis-trans isomerase
VF0224	6.3	5.9	5.4	5.9	5.6	5.1	6.0	5.6	-1.2	6.0	5.5	5.5	5.7	5.2	5.5	5.3	5.3	-1.3	hypothetical protein
VF0225	6.8	6.4	6.7	6.6	6.8	6.6	7.1	6.8	-1.1	6.5	6.3	6.4	6.4	6.4	6.5	6.3	6.4	-1.0	vegetable incompatibility protein HET-E-1
VF0226	10.3	10.1	9.9	10.1	9.5	9.6	9.5	9.5	-1.5	10.3	9.4	10.7	9.9	9.8	9.2	9.7	9.5	-1.3	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA
VF0227	7.4	6.6	6.4	6.8	6.9	6.3	7.1	6.8	-1.0	7.2	6.4	6.4	6.7	6.1	6.1	6.5	6.2	-1.4	MukF protein
VF0228	7.0	6.4	6.3	6.6	6.5	6.0	6.8	6.4	-1.1	6.7	6.3	6.2	6.4	6.0	5.8	6.1	6.0	-1.4	hypothetical protein
VF0229	6.4	5.8	5.8	6.0	5.8	5.2	6.1	5.7	-1.2	6.2	5.5	5.6	5.8	5.2	5.0	5.4	5.2	-1.5	intracellular sulfur oxidation protein dsrF
VF0233_s	13.0	12.8	12.9	12.9	12.6	12.5	12.7	12.6	-1.2	13.0	12.8	12.9	12.9	12.6	12.4	12.6	12.6	-1.2	elongation factor Tu
VF0234	12.3	12.3	12.6	12.6	12.5	12.6	12.6	12.5	-1.1	12.5	12.6	12.6	12.6	12.4	12.5	12.5	12.5	-1.2	LSU ribosomal protein L14P
VF0247	12.0	11.8	11.9	11.9	11.5	11.6	11.8	11.6	-1.2	11.9	11.8	11.9	11.9	11.8	11.5	11.7	11.7	-1.1	LSU ribosomal protein L14P
VF0248	12.5	12.4	12.5	12.5	12.2	12.2	12.3	12.3	-1.2	12.4	12.3	12.4	12.4	12.3	12.1	12.3	12.3	-1.1	50S ribosomal protein L24
VF0249	12.5	12.2	12.4	12.3	12.1	11.9	12.2	12.0	-1.2	12.4	12.0	12.2	12.2	12.0	11.6	11.9	11.8	-1.3	50S ribosomal protein L54
VF0250	12.4	12.3	12.4	12.4	12.1	12.0	12.3	12.1	-1.2	12.4	12.2	12.3	12.3	12.1	11.7	12.0	11.9	-1.3	30S ribosomal protein S14
VF0259	12.2	12.3	12.4	12.4	12.2	12.2	12.4	12.2	-1.2	12.2	12.2	12.4	12.2	12.2	11.9	12.3	12.3	-1.3	30S ribosomal protein S13
VF0260	12.4	12.2	12.5	12.3	12.0	12.0	12.1	12.0	-1.2	12.4	12.0	12.4	12.3	12.2	11.8	12.2	12.0	-1.2	30S ribosomal protein S11
VF0261	12.6	12.5	12.8	12.6	12.1	12.4	12.2	12.3	-1.3	12.5	12.4	12.6	12.5	12.5	12.1	12.5	12.4	-1.1	30S ribosomal protein S4
VF0262	12.3	12.2	12.6	12.4	11.8	11.9	11.8	11.8	-1.4	12.4	12.0	12.4	12.3	12.2	11.5	12.2	12.0	-1.3	DNA-directed RNA polymerase alpha subunit
VF0265	8.2	7.6	7.7	7.8	7.8	7.6	8.1	7.9	-1.0	8.1	7.4	7.6	7.7	7.7	7.5	7.7	7.6	-1.1	UDP-N-acetylmuramate L-alanyl-gamma-D-glutamyl- meso-diaminopimelate
VF0267	6.6	6.7	6.4	6.9	5.9	6.1	6.9	6.1	-1.2	6.6	6.1	5.7	5.8	5.5	4.9	5.5	5.4	-1.4	thiamine-binding protein
VF0268	5.1	4.5	4.2	4.6	4.7	4.2	4.9	4.6	-1.0	5.0	4.1	4.1	4.4	4.1	4.1	4.2	4.1	-1.2	thiamine ABC transporter membrane component
VF0269	6.0	5.0	4.9	5.3	5.0	4.8	5.7	5.1	-1.1	5.6	4.8	4.7	5.0	4.6	4.6	4.6	4.6	-1.3	thiamine transport ATP-binding protein ThiQ
VF0274	10.8	10.6	10.6	10.7	10.7	10.4	10.9	10.6	-1.0	10.9	10.4	10.7	10.6	10.6	10.5	10.6	10.6	-1.0	immunogenic protein
VF0275	8.0	7.6	7.7	7.8	7.8	7.7	8.0	7.8	-1.1	7.9	7.5	7.7	7.7	7.6	7.4	7.7	7.6	-1.1	arginine repressor
VF0277	8.5	8.4	8.5	8.5	8.5	12.4	8.9	8.6	-1.1	8.5	8.3	8.4	8.4	8.6	8.7	8.7	8.7	-1.2	arneseyl cyclophosphatase synthetase
VF0278	12.7	12.7	12.6	12.7	12.3	12.4	12.2	12.3	-1.3	12.7	12.7	12.7	12.7	12.4	12.3	12.4	12.4	-1.2	50S ribosomal protein L21
VF0281	5.5	5.0	4.9	5.1	4.5	4.4	5.0	4.6	-1.4	5.0	4.5	4.8	4.8	4.6	4.3	4.7	4.6	-1.2	hypothetical protein
VF0282	5.2	4.7	4.3	4.7	4.2	4.1	4.5	4.3	-1.3	5.0	4.2	3.9	4.4	4.4	4.0	4.3	4.2	-1.4	hypothetical protein
VF0283	5.9	5.0	4.7	5.2	4.7	4.7	5.4	4.9	-1.2	5.5	4.4	4.5	4.8	4.4	4.6	4.5	4.5	-1.2	hypothetical protein
VF0284	6.6	5.9	5.9	6.1	6.0	5.7	6.5	6.1	-1.0	6.5	5.9	5.9	6.0	5.9	5.7	6.0	5.9	-1.1	6-hydroxylate reductase
VF0285	5.2	4.2	4.3	4.6	3.9	3.7	4.2	3.9	-1.6	4.9	3.8	4.0	4.2	4.1	3.3	3.7	3.7	-1.5	diadenosinetriphosphatase
VF0286	8.4	8.1	7.9	8.1	8.3	8.0	8.5	8.3	-1.1	8.2	8.0	7.9	8.0	7.9	7.9	7.8	7.8	-1.2	dimethyladenosine transferase
VF0287	8.4	8.0	8.1	8.2	7.8	8.1	8.2	8.0	-1.1	8.1	7.8	8.0	8.0	8.1	7.8	8.0	8.0	-1.0	4-hydroxythreonine-4-phosphate dehydrogenase
VF0288	8.2	8.2	8.0	8.1	7.7	8.3	7.8	7.9	-1.2	8.1	7.9	8.0	8.0	8.1	8.0	7.9	8.0	-1.0	peptidyl-prolyl cis-trans isomerase
VF0289	8.2	8.2	8.0	8.2	8.3	8.2	8.2	8.0	-1.0	8.3	7.9	8.1	8.1	8.1	8.2	8.2	8.2	-1.1	organic solvent tolerance protein precursor
VF0290	8.2	8.3	8.1	8.2	8.0	8.0	8.1	8.0	-1.1	8.2	8.1	8.3	8.2	8.0	7.9	8.0	8.0	-1.1	Dna-J like membrane chaperone protein
VF0292	9.6	9.7	9.4	9.6	9.0	11.1	9.1	9.7	-1.1	9.6	9.0	9.5	9.4	8.5	8.9	8.4	8.6	-1.1	isopropylmalate isomerase small subunit
VF0293	10.0	9.9	9.8	9.9	9.3	11.2	9.7	10.1	-1.1	9.8	9.4	9.8	9.7	9.0	9.2	8.9	9.0	-1.6	isopropylmalate isomerase large subunit
VF0294	10.6	10.5	10.4	10.5	10.0	11.6	10.6	10.7	-1.2	10.6	10.1	10.5	10.4	9.7	9.7	9.7	9.7	-1.6	3-isopropylmalate dehydrogenase
VF0295	10.3	10.3	9.9	10.2	9.8	11.2	10.7	10.6	-1.3	10.2	10.0	10.1	10.2	9.4	9.5	9.5	9.5	-1.7	2-isopropylmalate synthase
VF0299	5.2	4.6	4.5	4.8	4.4	4.3	4.9	4.5	-1.2	4.9	4.6	4.5	4.7	4.1	4.1	4.0	4.1	-1.5	outer membrane protein
VF0301	8.5	8.1	8.4	8.3	7.9	7.8	8.2	8.0	-1.3	8.4	7.9	8.2	8.2	8.0	7.7	8.0	7.9	-1.2	replicative DNA helicase
VF0302	7.2	6.4	6.5	6.7	6.2	6.0	6.6	6.3	-1.3	7.0	6.0	6.4	6.5	5.8	5.6	6.1	5.8	-1.5	alanine racemase
VF0303	5.8	5.3	5.2	5.4	4.7	4.6	5.2	4.8	-1.5	5.7	5.0	4.9	5.2	4.9	5.0	5.1	5.0	-1.2	hypothetical protein
VF0305	8.0	7.6	8.0	7.9	7.3	7.2	7.3	7.3	-1.5	7.9	7.4	7.8	7.7	7.9	7.1	7.7	7.6	-1.1	possible inhibitor of MCP methylation
VF0306	8.6	8.4	8.4	8.5	8.0	8.1	8.0	8.0	-1.3	8.5	8.0	8.3	8.3	8.3	7.9	8.2	8.1	-1.1	zinc uptake regulation protein
VF0307	9.1	9.0	9.1	9.0	8.8	9.0	9.0	8.9	-1.1	9.0	8.8	9.0	8.9	9.0	8.7	9.1	8.9	-1.0	NIFR3-like protein
VF0308	7.5	7.2	7.2	7.3	7.1	7.1	7.4	7.2	-1.7	7.5	6.9	6.9	7.1	7.0	7.1	7.0	7.0	-1.1	hypothetical protein
VF0309	6.9	7.1	6.8	6.9	8.0	7.0	8.1	7.7	-1.1	6.7	7.6	6.9	7.1	6.7	7.1	6.4	6.7	-1.3	hypothetical protein
VF0315	7.4	7.3	7.0	7.2	7.5	7.3	7.8	7.5	-1.2	7.3	7.2	7.0	7.2	6.9	7.3	6.9	7.0	-1.1	opacly associated proteins OpaA
VF0316	5.5	4.7	4.8	5.0	4.2	4.0	4.5	4.2	-1.5	4.9	4.1	4.5	4.5	4.1	3.7	3.8	3.8	-1.6	transporter, drug/metabolite exporter family
VF0317	5.8	5.1	4.8	5.3	4.6	4.4	4.9	4.6	-1.7	5.5	4.4	4.9	4.9	4.4	4.2	4.4	4.4	-1.5	acetyltransferase
VF0318	5.0	3.9	3.6	4.1	4.1	3.7	4.5	4.1	-1.7	4.6	3.9	3.6	4.1	3.4	3.7	3.5	3.5	-1.9	transcription regulator, Crp family
VF0330	9.4	9.1	8.4	9.0	10.0	9.0	10.2	9.7											

VF0391	8.1	8.0	8.0	8.1	8.0	8.2	8.1	8.1	1.0	8.2	7.8	8.1	8.0	8.2	8.2	8.3	8.2	1.1	PmbA protein
VF0392	7.6	7.5	7.5	7.5	7.7	7.4	7.9	7.7	-1.1	7.2	7.5	7.5	7.4	7.5	7.4	7.5	7.4	-1.1	Mg(2+) transporter MgtE
VF0391	8.7	8.6	8.6	8.6	8.9	8.6	9.0	8.8	1.2	8.6	8.6	8.5	8.6	8.3	8.2	8.3	8.3	-1.0	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
VF0392	8.3	7.8	7.8	8.0	8.0	8.4	8.3	8.2	1.2	8.2	7.6	7.6	7.8	7.9	7.7	8.0	7.9	-1.2	arabinose-5-phosphate isomerase
VF0393	8.1	7.6	7.7	7.8	7.3	7.7	7.7	7.6	-1.2	8.0	7.4	7.6	7.7	7.5	7.3	7.5	7.4	-1.2	sodium-calcium exchanger
VF0394	7.0	6.6	6.7	6.8	7.2	6.5	7.5	7.1	-1.3	6.9	6.7	6.5	6.7	6.5	6.3	6.4	6.4	-1.2	toluene tolerance protein TTG2A
VF0395	6.2	5.4	5.4	5.6	6.0	5.2	6.3	5.6	-1.1	5.9	5.3	5.1	5.4	5.1	4.8	4.7	4.9	-1.5	toluene tolerance protein TTG2B
VF0396	7.7	7.4	7.4	7.5	7.7	7.4	7.8	7.6	-1.1	7.5	7.4	7.5	7.5	7.3	7.2	7.3	7.2	-1.2	toluene tolerance protein TTG2C
VF0397	8.5	8.4	8.2	8.4	8.2	8.3	8.6	8.4	-1.0	8.3	8.4	8.5	8.4	8.3	8.2	8.3	8.3	-1.2	toluene tolerance protein TTG2D
VF0398	8.1	7.8	7.7	7.8	7.7	7.8	8.1	7.9	-1.0	7.8	7.7	7.6	7.7	7.5	7.4	7.5	7.5	-1.2	toluene tolerance protein TTG2D
VF0399	8.4	8.2	7.9	8.2	7.9	8.0	8.2	8.0	-1.1	8.1	8.1	8.1	8.1	7.8	7.7	7.8	7.7	-1.3	YrB protein
VF0403	4.2	3.1	3.0	3.4	3.3	2.7	3.5	3.2	-1.2	3.7	2.8	3.2	3.3	2.8	3.0	3.1	2.9	-1.2	isopentenyl-diphosphate delta-isomerase
VF0404	9.5	9.0	8.7	9.1	8.4	8.2	8.6	8.4	-1.6	9.6	8.8	8.8	9.1	8.7	8.6	8.7	8.7	-1.3	translation initiation inhibitor
VF0408	7.6	7.3	7.2	7.4	7.1	7.3	7.2	7.2	-1.1	7.5	6.9	7.0	7.1	7.3	7.2	7.5	7.3	-1.2	arginine deiminase
VF0409	8.8	8.3	8.2	8.4	8.6	8.0	8.7	8.5	1.0	8.8	8.4	8.3	8.5	8.2	8.4	8.3	8.3	-1.1	hypothetical cytosolic protein
VF0410	7.1	6.6	6.5	6.7	6.9	6.2	7.2	6.8	1.0	6.9	6.4	6.5	6.6	6.3	5.9	6.2	6.2	-1.3	hypothetical protein
VF0411	9.3	9.1	9.2	9.2	8.6	8.8	8.8	8.7	-1.4	9.3	8.9	9.2	9.1	9.0	8.8	9.1	9.0	-1.1	valyl-tRNA synthetase
VF0412	8.0	7.6	7.7	7.7	7.3	7.5	7.8	7.5	-1.1	7.8	7.5	7.7	7.7	7.8	7.7	7.8	7.8	1.1	DNA polymerase III subunit chi
VF0413	9.0	8.6	8.8	8.8	8.1	8.4	8.4	8.3	-1.4	8.9	8.4	8.5	8.6	8.4	8.2	8.4	8.4	-1.2	leucyl aminopeptidase
VF0414	7.8	7.6	7.7	7.7	7.4	7.5	7.6	7.5	-1.1	7.7	7.3	7.6	7.5	7.5	7.3	7.6	7.5	-1.0	hypothetical membrane spanning protein
VF0415	8.1	8.2	8.1	8.1	7.8	8.3	8.1	8.1	-1.0	8.2	8.0	8.2	8.1	8.3	8.2	8.2	8.2	1.1	hypothetical membrane spanning protein
VF0416	7.5	6.7	6.7	7.0	6.4	6.0	6.6	6.4	-1.5	7.5	6.5	6.7	6.9	6.5	6.4	6.5	6.5	-1.3	proline-rich antigen
VF0420	6.9	6.3	6.1	6.4	5.5	5.5	5.8	5.6	-1.7	6.5	5.5	5.9	5.9	5.8	5.1	5.7	5.5	-1.3	membrane-bound lytic murein transglycosylase C precursor
VF0421	7.7	6.9	6.8	7.1	6.6	6.2	6.6	6.5	-1.6	7.4	6.5	6.8	6.9	6.5	6.5	6.8	6.6	-1.2	hypothetical protein
VF0422	7.3	6.8	6.8	7.0	6.6	6.6	6.7	6.6	-1.3	7.2	6.5	6.8	6.8	6.6	6.6	6.8	6.7	-1.1	A/G-specific adenine DNA glycosylase
VF0422to423	4.5	4.4	4.1	4.3	4.5	3.6	4.4	4.2	-1.1	4.2	4.2	3.8	4.1	3.9	3.9	3.4	3.7	-1.3	A/G-specific adenine DNA glycosylase
VF0425	2.2	2.1	1.8	2.0	2.1	2.2	2.4	2.2	-1.4	2.4	2.2	2.4	2.4	2.5	2.5	2.5	2.0	-1.3	putative deoxyribonucleotide triphosphate pyrophosphatase
VF0427	7.3	7.0	7.1	7.1	6.5	6.8	6.7	6.7	-1.4	7.2	6.7	7.0	6.9	7.0	6.7	7.0	6.9	-1.0	hypothetical protein
VF0428	7.5	7.0	7.1	7.2	6.6	6.8	7.0	6.8	-1.3	7.4	6.8	6.9	7.1	6.8	6.6	6.9	6.8	-1.2	integral membrane protein
VF0429	7.7	7.4	7.4	7.5	6.8	7.4	7.3	7.2	-1.3	7.6	7.2	7.3	7.4	7.2	7.2	7.2	7.2	-1.2	pyroline-5-carboxylate reductase
VF0430	7.9	7.8	7.8	7.8	7.5	7.7	7.7	7.7	-1.1	7.9	7.7	7.9	7.8	7.9	8.0	7.9	7.9	1.1	hypothetical protein
VF0431	6.5	6.0	6.2	6.3	6.0	6.0	6.3	6.0	-1.2	6.3	6.0	6.2	6.0	6.0	5.7	6.0	5.7	-1.2	pili retraction protein PiliT
VF0432	6.5	6.3	6.2	6.3	5.9	6.0	6.3	6.1	-1.2	6.4	6.2	6.3	6.3	6.1	6.0	6.1	6.1	-1.2	pili retraction protein PiliU
VF0434	8.4	8.1	8.0	8.1	8.3	7.8	8.6	8.2	-1.1	8.1	8.2	8.0	8.1	7.4	7.9	7.5	7.6	-1.4	hypothetical protein
VF0435	9.5	9.3	9.3	9.4	9.4	9.2	9.7	9.4	1.1	9.3	9.4	9.3	9.3	9.0	9.3	9.0	9.1	-1.2	glutathione synthetase
VF0436	8.1	7.7	7.6	7.8	7.8	7.5	8.2	7.8	1.0	7.9	7.7	7.5	7.7	7.3	7.5	7.5	7.4	-1.2	hypothetical protein
VF0437	5.6	5.7	5.4	5.6	5.4	5.6	5.6	5.5	-1.0	5.3	5.6	5.6	5.6	6.1	6.1	6.1	6.1	-1.2	endonuclease I
VF0438	6.1	5.5	5.2	5.6	4.8	5.0	5.1	5.0	-1.6	5.8	4.8	4.7	5.1	4.5	4.1	4.4	4.3	-1.7	hypothetical protein
VF0441	7.9	7.2	7.5	7.5	7.2	7.1	7.6	7.3	-1.2	7.6	7.0	7.3	7.3	7.2	6.9	7.4	7.2	-1.1	D-erythrose 4-phosphate dehydrogenase
VF0442	11.1	10.4	10.6	10.7	10.3	10.3	10.4	10.3	-1.3	10.8	10.2	10.5	10.5	10.1	9.6	10.2	10.0	-1.4	phosphoglycerate kinase
VF0443	11.1	10.5	10.4	10.7	10.5	10.4	10.6	10.5	-1.1	11.0	10.3	10.3	10.5	10.2	10.3	10.4	10.3	-1.2	fructose-bisphosphate aldolase
VF0444	8.3	7.9	8.1	8.1	7.7	7.8	7.9	7.6	-1.3	8.2	7.6	7.9	7.9	7.7	7.3	7.7	7.6	-1.3	ATP-dependent RNA helicase SrmB
VF0445	6.5	6.2	6.0	6.2	6.4	6.3	6.8	6.5	1.2	6.2	6.1	6.1	6.1	6.1	6.6	6.4	6.4	1.2	methyltransferase
VF0446	8.6	7.5	8.1	8.1	9.1	9.1	9.3	9.2	2.1	8.5	6.7	7.9	7.7	8.7	8.3	8.7	8.6	1.8	branched chain amino acid transport system II carrier protein
VF0447	7.2	6.6	6.5	6.6	6.7	6.7	6.2	6.9	-1.1	7.1	6.6	6.5	6.7	6.7	6.6	6.6	6.7	-1.0	flavodoxin
VF0448	6.8	6.6	6.5	6.8	6.2	6.5	6.6	6.4	-1.1	6.6	6.4	6.4	6.5	6.4	6.3	6.6	6.4	-1.0	tyrosine recombinase
VF0449	8.4	8.1	8.0	8.2	8.0	8.0	8.1	8.1	-1.1	8.3	7.9	8.0	8.0	8.1	7.9	8.0	8.0	-1.2	3-oxoisoleiute interchange protein DsbC
VF0451	1.8	1.9	1.7	1.8	1.7	2.0	1.6	1.7	-1.0	2.2	1.8	1.8	1.9	2.0	1.9	1.8	1.9	-1.0	hypothetical protein
VF0452	9.9	9.7	9.7	9.8	9.1	9.6	9.4	9.4	-1.1	9.8	9.4	9.6	9.6	9.6	9.3	9.6	9.5	-1.1	bacterial peptide chain release factor 2 (RF-2)
VF0453	10.4	10.1	10.1	10.2	9.5	9.9	9.8	9.7	-1.4	10.3	9.8	10.0	10.1	10.0	9.5	9.9	9.8	-1.2	lysyl-tRNA synthetase
VF0455	6.9	6.8	6.7	6.8	7.0	6.8	7.0	6.9	-1.1	6.7	6.8	6.7	6.7	6.9	7.0	7.1	7.0	1.2	DNA mismatch repair protein
VF0455to456	2.0	2.0	1.7	2.0	1.8	2.0	2.1	2.0	-1.1	2.1	2.2	2.1	2.1	2.1	2.1	2.1	2.0	-1.1	DNA mismatch repair protein
VF0455to456t	4.9	4.4	4.4	4.6	4.2	4.3	4.7	4.4	-1.1	4.3	4.1	4.2	4.2	4.0	3.5	4.0	3.8	-1.3	DNA mismatch repair protein
VF0456	9.3	9.2	9.3	9.3	9.1	9.2	9.1	9.2	-1.1	9.3	9.1	9.2	9.2	9.3	9.4	9.5	9.4	1.1	dinucleoside polyphosphate hydrolase
VF0457	8.9	8.8	8.8	8.8	8.5	8.8	8.7	8.7	-1.1	8.8	8.6	8.8	8.7	8.9	8.6	8.9	8.8	1.0	phosphoenolpyruvate-protein phosphotransferase
VF0458	7.9	7.6	7.8	7.8	7.5	7.6	7.9	7.7	-1.1	7.8	7.5	7.7	7.7	7.9	7.3	7.9	7.7	1.0	hypothetical protein
VF0459	8.2	7.9	8.0	8.0	7.5	7.9	7.8	7.9	-1.2	8.0	7.7	7.9	7.9	7.4	7.4	7.7	7.7	-1.1	prolipoprotein diacylglycerol transferase
VF0460	7.4	7.1	6.9	7.1	6.9	6.8	7.0	6.9	-1.2	7.3	6.8	7.0	7.0	7.0	6.9	6.9	6.9	-1.1	thymidylate synthase
VF0462	7.2	6.6	6.6	6.8	6.6	6.6	7.2	6.8	-1.0	7.0	6.7	6.6	6.7	6.8	7.0	6.8	6.9	-1.1	transcriptional activator protein NhaR
VF0463	6.7	6.2	5.8	6.2	6.7	6.3	6.8	6.6	-1.3	6.4	6.2	5.8	6.2	5.9	6.9	7.2	6.7	-1.4	transcriptional activator HlyU
VF0465	8.0	7.8	8.0	7.9	7.3	7.8	7.5	7.6	-1.3	7.9	7.5	7.8	7.7	7.8	7.5	7.9	7.7	-1.0	virulence factor MvN
VF0466	9.3	9.0	9.2	9.2	8.7	8.9	8.9	8.8	-1.3	9.1	8.8	9.0	9.0	8.9	8.5	8.9	8.8	-1.2	hypothetical protein
VF0467	10.1	9.9	10.1	10.0	9.4	9.7	9.6	9.6	-1.4	10.1	9.7	10.0	9.9	9.9	9.4	9.8	9.7	-1.2	isoleucyl-tRNA synthetase
VF0468	9.4	8.9	9.3	9.2	8.6	8.6	8.9	8.7	-1.4	9.3	8.7	9.2	9.0	8.9	8.1	8.7	8.6	-1.4	signal peptidase II
VF0469	8.5	8.1	8.5	8.4	7.6	7.8	8.0	7.8	-1.5	8.3	7.8	8.2	8.1	8.0	7.5	8.0	7.8	-1.2	peptidyl-prolyl cis-trans isomerase
VF0471	9.2	9.1	9.1	9.1	8.8	9.1	9.1	9.0	-1.0	9.2	9.1	9.2	9.2	9.0	9.0	9.1	9.0	-1.1	dihydrodipicolinate reductase
VF0471to472t	2.0	2.0	1.7	1.9	1.8	2.0	2.1	2.0	-1.0	2.1	2.1	1.7	2.0	1.7	1.9	1.9	1.9	-1.1	dihydrodipicolinate reductase
VF0472	9.9	10.0	10.0	9.9	9.8	10.4	10.2	10.1	1.1	9.7	9.8	9.9	9.8	10.2	9.5	10.3	10.0	1.2	carbamoyl-phosphate synthase small subunit
VF0473	10.4	10.6	10.7	10.6	10.5	10.6	10.9	10.7	1.1	10.3	10.3	10.5	10.4	10.7	10.2	10.8	10.6	1.1	carbamoyl-phosphate synthase large subunit
VF0474	4.5	3.9	3.2	3.9	3.3	3.3	3.5	3.3	-1.5	4.4	3.3	3.5	3.7	3.2	3.1	3.1	3.2	-1.5	D-alanyl-meso-diaminopimelate endopeptidase
VF0475to476t	5.6	5.0	5.0	5.2	4.5	4.5	4.8	4.6	-1.5	5.3	4.6	4.9	4.9	4.8	4.3	4.4	4.5	-1.3	OmpU, outer membrane protein
VF0476	9.8	9.7	9.7	9.7	9.4	9.3	9.5</												



VF0515	5.5	4.7	4.6	4.9	4.5	4.6	4.9	4.7	-1.2	5.1	4.5	4.6	4.7	4.4	4.3	4.2	4.3	-1.3	ATPase involved in chromosome partitioning
VF0516	5.1	6.9	4.7	6.0	4.6	4.9	5.3	4.9	-1.1	5.2	4.8	4.8	4.9	4.4	4.8	4.8	4.8	-1.1	putative type IV secretion NTPase similar to TadA
VF0517	4.9	4.5	4.2	4.5	4.5	4.2	4.8	4.5	-1.0	4.8	4.5	4.4	4.6	4.3	4.3	4.4	4.4	-1.2	TadB-like protein involved in pilus formation and/or protein secretion
VF0518	4.8	4.4	4.2	4.5	4.2	4.0	4.4	4.2	-1.2	4.4	4.3	4.2	4.3	4.2	3.6	3.7	3.8	-1.4	bipartite nuclear localization signal containing protein, similar to TadC
VF0519	4.9	4.0	3.3	4.1	3.3	3.9	4.7	4.0	-1.1	4.2	4.1	3.4	3.9	3.2	3.8	3.9	3.6	-1.2	secretory protein containing TPR-repeats, similar to TadD
VF0520	4.3	3.4	3.5	3.7	3.3	3.6	3.7	3.5	-1.1	3.9	3.7	3.2	3.6	3.2	3.0	3.1	3.1	-1.4	TadE-like protein
VF0521	4.0	3.5	3.3	3.6	3.4	3.2	4.0	3.5	-1.0	3.9	3.4	3.4	3.5	3.4	3.0	3.2	3.2	-1.2	ATP/GTP-binding site motif A (P-loop) surface protein involved in fimbriae
VF0523	6.7	6.6	6.2	6.5	6.4	6.1	6.6	6.3	-1.1	6.6	6.5	6.3	6.5	6.0	6.2	5.8	6.0	-1.4	outer membrane protein
VF0525	6.1	5.8	5.0	5.6	5.4	5.3	5.6	5.4	-1.1	5.6	5.6	5.2	5.5	5.1	5.2	5.0	5.1	-1.3	sensor protein PhoQ
VF0526	6.9	6.3	6.1	6.4	6.3	6.0	6.7	6.3	-1.2	6.5	6.2	6.0	6.2	5.9	6.0	6.0	6.0	-1.2	transcriptional regulator
VF0527	7.4	7.0	6.9	7.1	6.8	6.7	7.2	6.9	-1.1	7.3	6.9	6.8	7.0	6.7	6.8	6.6	6.7	-1.3	hypothetical protein
VF0528	8.0	7.8	7.9	7.9	7.6	7.8	7.8	7.7	-1.1	7.9	7.6	7.7	7.8	7.9	7.6	7.9	7.8	-1.0	DNA repair protein RadA
VF0530	5.5	5.3	4.3	5.0	5.9	5.1	5.7	5.6	1.5	5.4	5.2	4.8	5.1	5.0	5.5	5.1	5.2	1.0	hypothetical protein
VF0531	7.4	6.9	7.0	7.1	6.7	7.1	6.9	6.9	-1.1	7.2	6.7	6.9	6.9	7.3	6.8	7.3	7.1	1.1	cytosine deaminase
VF0532	6.0	5.2	5.4	5.5	5.6	6.1	5.5	5.7	1.2	5.6	5.0	5.3	5.3	5.9	5.3	6.0	5.7	1.4	cytosine permease
VF0532to533	4.6	4.4	3.6	4.2	4.7	4.5	5.2	4.8	1.5	4.5	4.5	4.0	4.3	3.7	4.5	4.0	4.1	-1.2	cytosine permease
VF0532to533t	4.7	3.8	3.7	4.1	4.3	4.3	4.9	4.5	1.4	4.6	3.6	3.9	4.0	4.2	4.1	4.2	4.2	1.1	hypothetical protein
VF0532to533t	4.5	4.1	3.4	4.0	4.0	3.9	4.3	4.1	1.1	4.3	3.6	3.7	3.8	4.0	3.8	4.0	3.9	1.0	cytosine permease
VF0535	9.6	9.4	9.6	9.5	9.1	9.4	9.3	9.3	-1.2	9.5	9.3	9.4	9.4	9.3	9.1	9.4	9.3	-1.1	recombinase A
VF0537	9.0	8.9	8.9	8.9	8.4	8.8	8.7	8.6	-1.2	9.0	8.7	8.8	8.8	8.6	8.6	8.7	8.7	-1.1	aspartate kinase
VF0538	10.5	10.3	10.5	10.4	10.0	10.0	10.1	10.0	-1.3	10.5	10.1	10.3	10.3	10.2	10.0	10.4	10.2	-1.1	carbon storage regulator
VF0543	8.4	8.0	8.0	8.1	7.9	7.7	8.0	7.9	-1.2	8.4	7.6	7.9	8.0	7.8	7.7	7.8	7.8	-1.1	glutamate-cysteine ligase
VF0544	7.1	6.8	6.6	6.9	6.4	6.6	6.5	6.5	-1.3	7.0	6.3	6.6	6.6	6.3	5.9	6.5	6.3	-1.3	hypothetical protein
VF0545	9.1	8.8	8.8	8.9	8.6	9.1	9.0	8.9	1.0	9.2	8.9	8.7	8.9	8.9	9.2	9.1	9.1	1.1	S-ribosylhomocysteine
VF0546	7.3	6.9	6.7	7.0	6.4	6.3	6.4	6.4	-1.5	7.1	6.4	6.5	6.7	6.4	6.2	6.4	6.4	-1.2	magnesium and cobalt efflux protein CorB
VF0547	7.9	7.5	7.6	7.7	7.6	7.7	8.0	7.8	-1.0	7.8	7.5	7.5	7.6	7.4	7.7	7.8	7.7	1.1	CsaA-related protein
VF0548	9.5	9.5	9.4	9.5	9.4	9.4	9.5	9.5	-1.5	9.5	9.5	9.5	9.5	9.5	9.4	9.4	9.4	-1.1	signal recognition particle, subunit FFH/SRP54
VF0557	9.1	8.9	9.1	9.0	8.6	8.5	8.8	8.6	-1.3	9.1	8.7	9.0	8.9	8.6	8.3	8.7	8.5	-1.3	ABC transporter ATP-binding protein
VF0558	7.7	7.4	7.2	7.5	7.2	7.3	7.5	7.4	-1.1	7.7	7.2	7.4	7.4	7.2	7.2	7.4	7.3	-1.3	soluble lytic murein transglycosylase
VF0559	6.4	5.9	5.7	6.0	5.9	5.9	6.2	6.0	1.0	6.5	5.9	5.8	6.1	5.9	5.9	5.9	5.8	-1.2	Trp operon repressor
VF0560	8.9	8.7	8.6	8.7	8.4	8.6	8.6	8.5	-1.2	8.8	8.5	8.6	8.6	8.5	8.5	8.5	8.5	-1.1	hypothetical protein
VF0561	9.7	9.5	9.4	9.5	9.3	9.5	9.3	9.3	-1.1	9.5	9.4	9.4	9.4	9.0	9.0	9.0	9.1	-1.2	hypothetical protein
VF0562	9.2	9.3	8.8	9.1	8.7	8.1	8.9	8.6	-1.5	9.4	9.7	9.3	9.5	8.8	10.5	9.5	9.6	1.1	ribosome-associated factor Y
VF0563	8.4	8.0	8.0	8.1	7.8	7.9	8.1	7.9	-1.1	8.4	7.9	7.9	8.1	7.8	7.7	7.8	7.7	-1.3	Lipoprotein, ComL family
VF0564	8.7	8.3	8.6	8.5	8.2	8.3	8.5	8.4	-1.2	8.6	8.2	8.4	8.4	8.5	8.3	8.6	8.5	-1.1	ribosomal large subunit pseudouridine synthase D
VF0565	8.0	7.7	7.8	7.8	7.5	7.5	7.7	7.5	-1.2	7.9	7.5	7.6	7.7	7.6	7.5	7.6	7.5	-1.1	hypothetical protein
VF0566	8.7	8.3	8.2	8.4	8.3	8.2	8.9	8.7	-1.3	8.9	8.4	8.3	8.3	8.2	8.3	8.5	8.3	-1.0	ClaB protein
VF0568	4.4	3.7	2.9	3.7	3.4	3.2	4.2	3.6	-1.0	3.8	3.6	3.4	3.6	3.0	3.3	2.9	3.1	-1.4	hypothetical protein
VF0569	4.3	3.3	3.1	3.6	3.5	3.0	4.0	3.5	-1.0	3.8	3.5	3.2	3.5	2.8	3.4	3.0	3.1	-1.3	hypothetical protein
VF0570	3.0	2.7	2.1	2.6	2.8	2.5	2.8	2.7	1.1	3.0	2.5	2.5	2.7	2.0	2.3	2.1	2.1	-1.4	hypothetical protein
VF0571	3.7	3.7	3.4	3.6	3.7	3.4	3.8	3.7	1.0	3.5	3.6	3.4	3.5	3.5	3.6	3.0	3.4	-1.1	pili retraction protein PilT
VF0572	5.7	5.3	4.5	5.1	4.8	5.0	5.3	5.0	-1.1	5.3	4.3	4.6	5.1	4.6	5.1	4.5	4.7	-1.3	pili subunit PIA
VF0573	5.4	4.2	4.0	4.5	4.5	4.6	4.9	4.7	1.1	4.7	4.0	4.1	4.3	4.1	4.2	4.0	4.1	-1.1	chromate transport protein
VF0574	5.9	5.1	5.0	5.3	4.9	4.8	5.2	5.0	-1.3	5.7	5.1	5.1	5.3	4.7	4.9	4.9	4.8	-1.3	transcriptional regulators, LysR family
VF0575	4.7	3.6	3.2	3.8	3.4	3.3	4.3	3.7	-1.1	4.1	3.3	3.9	3.8	3.1	3.6	3.0	3.2	-1.5	hypothetical protein
VF0576	9.2	8.6	8.9	8.9	8.3	8.5	8.4	8.4	-1.4	9.1	8.1	8.5	8.6	8.5	8.2	8.6	8.4	-1.1	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
VF0577	5.5	4.8	4.2	4.8	4.9	4.5	5.1	4.5	-1.0	5.5	4.7	4.7	5.0	5.3	5.0	4.9	5.0	-1.1	hypothetical protein
VF0581	7.0	6.3	6.5	6.6	6.4	6.6	6.8	6.6	-1.0	6.9	6.0	6.3	6.4	6.7	6.4	6.8	6.6	-1.2	exodeoxyribonuclease V gamma chain
VF0582	7.2	6.9	6.9	7.0	6.7	7.2	7.0	7.0	-1.0	7.1	6.6	6.8	6.8	7.0	6.7	6.9	6.9	1.1	exodeoxyribonuclease V beta chain
VF0583	7.1	6.7	6.6	6.8	6.7	6.8	7.1	6.9	-1.0	6.9	6.5	6.7	6.7	6.9	6.7	6.5	6.5	-1.1	exodeoxyribonuclease V alpha chain
VF0585	9.2	8.8	9.0	9.0	8.9	10.1	10.1	9.7	1.6	9.0	9.0	8.9	9.0	8.9	8.7	8.3	8.2	-1.6	N-acetylglutamate synthase
VF0586	6.2	4.6	4.4	4.7	4.3	4.0	4.7	4.3	-1.4	4.8	4.2	4.3	4.4	4.3	4.3	4.3	4.3	-1.3	hypothetical protein
VF0587	6.0	5.1	5.3	5.4	4.8	4.9	4.9	4.9	-1.5	5.8	4.9	5.4	5.4	5.2	4.6	5.0	4.9	-1.4	membrane-bound lytic murein transglycosylase A
VF0589	6.6	6.0	5.9	6.2	5.8	5.9	6.5	6.0	-1.1	6.2	5.9	5.7	6.0	5.8	5.8	5.9	5.8	-1.1	SuE protein
VF0591	7.1	6.6	6.6	6.8	6.4	6.5	6.7	6.5	-1.2	6.8	6.4	6.5	6.6	6.7	6.5	6.7	6.6	1.0	glycine cleavage system transcriptional activator
VF0592	7.7	6.9	7.0	7.2	6.8	6.8	7.3	6.9	-1.2	7.5	6.8	6.9	7.1	6.8	6.6	6.9	6.8	-1.2	hypothetical protein
VF0593	8.4	8.0	8.1	8.1	7.7	7.7	7.8	7.8	-1.3	8.3	7.9	8.0	8.1	7.8	7.6	7.9	7.8	-1.2	methytransferase
VF0594	7.9	7.7	7.7	7.8	7.4	7.6	7.8	7.6	-1.2	7.7	7.8	7.7	7.7	7.9	8.0	8.0	8.0	1.2	exonuclease IX
VF0596	6.6	6.4	6.2	6.4	5.8	6.4	6.3	6.2	-1.1	6.4	6.4	6.3	6.4	6.4	6.6	6.5	6.5	1.1	diguanylate cyclase/phosphodiesterase domain 1 (GGDEF)
VF0597	6.8	6.8	6.4	6.7	6.2	6.5	6.2	6.3	-1.3	6.8	6.6	6.6	6.7	6.3	6.8	6.6	6.5	-1.1	hypothetical protein
VF0598	7.3	7.0	7.0	7.1	6.9	6.8	7.1	6.9	-1.1	7.2	6.9	7.2	7.1	7.2	7.2	7.2	7.2	1.1	hypothetical protein
VF0599	7.2	6.7	6.6	6.8	6.2	6.4	6.6	6.4	-1.4	7.2	6.5	6.6	6.8	6.4	6.2	6.3	6.3	-1.4	SecY interacting protein Syd
VF0601	7.2	6.9	6.9	7.0	6.6	6.8	6.9	6.8	-1.2	7.1	6.7	6.8	6.9	7.0	7.1	7.0	7.1	1.1	hypothetical protein
VF0602	7.2	7.0	6.7	7.0	6.9	6.8	6.9	6.8	-1.1	7.0	6.9	6.9	6.9	7.0	7.2	7.2	7.1	1.1	hypothetical protein
VF0602to603	5.4	6.0	6.0	5.8	5.4	5.8	5.4	5.5	-1.2	5.4	5.9	6.0	5.8	6.1	6.2	6.1	6.1	1.3	hypothetical protein
VF0602to603t	10.0	10.1	9.9	10.0	10.0	10.0	10.0	10.0	-1.0	9.9	10.1	10.0	10.0	10.0	10.1	10.1	10.1	1.1	hypothetical protein
VF0603	4.5	3.8	4.2	4.1	4.0	4.3	4.8	4.4	1.2	4.1	4.2	4.0	4.1	4.3	4.0	4.1	4.1	1.0	FTS system, cellulose-specific IIC component
VF0605	6.3	6.0	5.9	6.1	6.0	5.7	6.2	6.0	-1.1	6.1	5.9	5.8	6.0	5.6	5.5	5.4	5.5	-1.4	6-phospho-beta-glucosidase
VF0608	6.0	5.1	4.7	5.3	5.1	4.8	5.5	5.1	-1.1	5.9	4.8	4.8	5.2	4.6	4.6	4.8	4.7	-1.4	transcriptional regulator, LacI family
VF0610	6.7	6.0	5.5	6.1	5.3	5.5	5.9	5.5	-1.4	6.4	5.3	5.5	5.8	4.9	5.0	5.3	5.1	-1.6	hypothetical protein
VF0611	7.9	7.3	7.4	7.5	7.1	7.2	7.5	7.2	-1.2	7.7	6.9	7.3	7.3	7.2	7.0	7.4	7.2	-1.1	hypothetical protein
VF0612	7.6	7.3	7.2	7.3	7.1	7.2	7.5	7.3	-1.1	7.4	7.1	7.3	7.2	7.1	7.2	7.1	7.2	-1.1	hypothetical protein

VF0662	7.1	6.5	5.8	6.5	6.5	6.1	6.8	6.5	1.0	7.0	6.4	5.8	6.4	5.8	6.4	5.9	6.1	-1.3	hypothetical protein
VF0663	6.5	6.4	4.1	4.5	4.1	4.4	4.7	4.8	-1.2	4.1	4.1	4.2	4.3	4.1	4.0	4.1	4.1	-1.2	N-4-acetylaminopyridase
VF0664	7.1	6.6	6.6	6.8	6.5	6.4	6.8	6.6	-1.1	7.0	6.6	6.4	6.7	6.3	6.6	6.5	6.5	-1.2	transcriptional regulator, RpiR family
VF0665	7.5	7.3	7.1	7.3	6.8	7.0	7.2	7.0	-1.2	7.3	7.3	7.1	7.2	7.4	7.4	7.3	7.3	1.1	N-acetylglucosamine-6-phosphate deacetylase
VF0666	3.5	3.2	3.2	3.3	3.5	3.3	3.3	3.3	1.0	3.8	3.2	3.1	3.4	3.1	3.1	3.1	3.1	-1.2	N-acetylmannosamine-6-phosphate 2-epimerase
VF0667	3.4	3.1	3.3	3.3	3.0	3.3	3.3	3.2	1.0	3.1	3.3	3.3	3.2	3.5	3.2	3.2	3.3	1.0	N-acetylmannosamine kinase
VF0668	4.1	3.3	3.4	3.6	3.3	3.4	3.6	3.4	-1.1	3.4	3.4	3.4	3.4	3.1	2.9	3.1	3.0	-1.1	sodium-glucose/galactose cotransporter
VF0669	4.2	3.7	3.6	3.8	3.4	3.6	3.7	3.6	-1.2	4.1	3.7	3.6	3.8	3.6	3.5	3.5	3.5	-1.2	hypothetical cytosolic protein
VF0672	5.5	4.5	4.6	4.9	4.1	4.2	4.3	4.2	-1.6	5.0	4.2	4.4	4.5	4.2	4.0	3.9	4.1	-1.4	urease accessory protein UreE
VF0673	5.3	4.8	4.5	4.9	4.0	4.4	4.7	4.4	-1.4	5.0	4.2	4.5	4.6	4.3	3.6	3.8	3.9	-1.6	urease alpha subunit
VF0675	5.0	3.4	3.6	4.0	3.5	3.5	4.2	3.7	-1.2	4.7	3.6	3.8	4.0	3.5	3.4	3.4	3.4	-1.5	urease gamma subunit
VF0676	4.0	3.3	3.3	3.6	2.9	3.2	3.2	3.1	-1.4	3.7	3.2	3.2	3.4	2.9	3.1	2.8	2.9	-1.3	urease accessory protein UreD
VF0677	3.7	3.1	2.5	3.1	3.0	2.8	3.3	3.1	-1.0	3.2	3.0	2.5	2.9	2.6	2.4	2.6	2.6	-1.2	putative dipeptide ABC transporter
VF0678	5.9	5.6	5.5	5.7	5.2	5.5	5.6	5.5	-1.1	5.5	5.4	5.5	5.5	5.4	5.4	5.4	5.4	-1.0	oligopeptide transport ATP-binding protein OppD
VF0679	4.2	3.9	3.3	3.8	3.5	3.3	4.1	3.6	-1.1	3.9	3.6	3.8	3.8	3.2	3.5	3.9	3.6	-1.1	oligopeptide transport system permease protein OppC
VF0680	4.0	3.2	3.2	3.5	3.4	3.2	3.5	3.3	-1.1	3.7	3.3	3.2	3.4	3.0	3.1	3.4	3.1	-1.2	oligopeptide transport system permease protein OppB
VF0681	3.2	3.2	3.2	3.2	3.1	3.0	3.2	3.1	-1.1	3.3	3.2	3.1	3.2	3.2	2.6	2.9	2.9	-1.2	oligopeptide-binding protein OppA
VF0682	9.3	9.1	9.2	9.2	8.8	9.0	8.9	8.9	-1.2	9.2	9.0	9.1	9.1	9.0	8.9	9.1	9.0	-1.1	prolyl-tRNA synthetase
VF0687	7.7	7.5	7.3	7.5	7.2	7.2	7.3	7.2	-1.2	7.7	7.3	7.2	7.4	7.2	7.2	7.3	7.2	-1.1	hypothetical protein
VF0687to688	6.0	5.7	5.5	5.8	5.5	5.4	5.6	5.5	-1.2	5.9	5.7	5.5	5.7	5.4	5.6	5.2	5.4	-1.3	hypothetical protein
VF0687to688	2.5	2.2	2.3	2.3	2.2	2.0	2.4	2.2	-1.1	2.3	2.4	2.1	2.3	2.1	2.3	2.1	2.1	-1.1	hypothetical protein
VF0690	8.3	8.3	8.4	8.4	8.1	8.3	8.4	8.3	-1.1	8.3	8.3	8.3	8.3	8.5	8.5	8.4	8.5	1.2	oligopeptide-binding protein OppA
VF0691	8.0	7.9	8.1	8.0	7.7	8.0	8.1	7.9	-1.0	7.8	7.9	7.9	7.9	8.0	7.8	7.7	7.8	-1.0	oligopeptide transport ATP-binding protein OppD
VF0692	6.6	6.4	6.4	6.5	6.1	6.2	6.9	6.4	-1.0	6.4	6.3	6.2	6.3	6.0	5.8	5.4	5.8	-1.5	oligopeptide transport ATP-binding protein OppF
VF0694	4.6	3.5	3.8	4.0	4.1	3.9	4.2	4.1	-1.1	4.4	3.8	3.3	3.8	3.8	4.1	4.0	4.0	-1.3	hypothetical membrane spanning protein
VF0695	12.2	12.0	11.8	12.0	11.7	12.0	11.9	11.9	-1.1	12.2	11.8	11.9	12.0	12.2	12.5	12.3	12.3	1.3	serine hydroxymethyltransferase
VF0696	6.5	6.0	6.2	6.5	6.1	6.2	6.5	6.1	-1.3	6.3	6.1	6.2	6.3	6.2	6.2	6.2	6.0	-1.2	accessory colonization factor AcfD-like protein
VF0697	10.0	9.8	9.2	9.6	10.2	9.6	10.2	10.0	1.3	10.1	10.0	9.6	9.9	9.7	10.2	9.7	9.9	-1.0	hypothetical protein
VF0698	5.4	5.2	4.9	5.2	4.8	4.9	5.2	5.0	-1.1	5.2	5.2	5.0	5.1	4.6	4.9	4.7	4.8	-1.3	methyl-accepting chemotaxis protein
VF0699	8.9	8.8	8.9	8.9	8.6	8.8	9.0	8.8	-1.1	8.8	8.8	8.9	8.8	9.1	9.1	9.1	9.1	1.2	hypothetical protein
VF0700	8.7	8.8	8.6	8.7	8.3	8.6	8.4	8.4	-1.2	8.5	8.6	8.7	8.6	8.7	8.8	8.9	8.7	1.1	5-amino-6-(5-phosphoribosylamino)uracil reductase
VF0701	8.4	8.4	8.4	8.4	8.4	8.4	8.4	8.4	-1.3	8.4	8.4	8.4	8.4	8.6	8.6	8.6	8.6	1.7	riboflavin synthase subunit alpha
VF0706	6.8	6.2	6.2	6.4	5.8	5.7	6.4	6.0	-1.4	6.7	6.1	6.0	6.3	5.7	5.9	5.9	5.8	-1.4	phosphatidylglycerophosphatase A
VF0708	5.3	4.6	4.2	4.7	4.1	4.2	4.6	4.3	-1.4	4.8	4.1	4.0	4.3	3.8	3.6	3.8	3.7	-1.5	sensor protein LuxQ
VF0709	6.6	6.2	5.3	6.0	6.1	5.8	6.7	6.2	1.1	6.4	6.3	5.7	6.1	5.8	6.2	5.9	5.9	-1.1	hypothetical protein
VF0710	7.1	6.2	5.9	6.4	6.2	6.6	6.7	6.5	1.1	7.0	6.3	6.1	6.5	6.2	6.2	6.1	6.2	-1.2	hypothetical protein
VF0714	3.3	6.9	7.1	7.1	6.8	7.7	7.2	7.2	-1.2	6.9	7.1	6.9	7.2	7.1	6.7	7.0	6.9	-1.2	flagellar motor protein
VF0715	6.6	6.5	6.5	6.5	6.4	6.9	6.5	6.6	1.1	6.5	6.4	6.4	6.4	6.4	6.1	6.3	6.3	-1.1	flagellar motor protein
VF0716	8.4	8.2	8.3	8.3	7.7	7.9	7.9	7.8	-1.4	8.3	8.2	8.2	8.2	7.9	7.3	8.0	7.7	-1.4	thiamine biosynthesis protein ThiI
VF0717	8.2	7.9	7.5	7.8	7.9	7.2	8.3	7.8	-1.7	8.1	7.9	7.7	7.9	7.3	7.2	7.1	7.2	-1.6	4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis enzyme
VF0718	6.6	6.1	5.7	6.2	5.2	5.3	5.7	5.4	-1.0	6.5	5.5	5.8	5.9	5.6	5.3	5.6	5.5	-1.4	2-dehydroantoinic acid 2-reductase
VF0721	8.5	8.5	8.1	8.4	7.9	8.1	8.0	8.1	-1.3	8.5	8.5	8.1	8.4	7.8	8.0	7.9	7.9	-1.4	peptidyl-prolyl cis-trans isomerase
VF0722	8.8	8.4	8.4	8.5	7.9	8.1	8.3	8.1	-1.3	8.7	8.1	8.2	8.3	8.1	7.9	8.1	8.0	-1.2	putative lipoprotein
VF0723	7.5	7.2	7.2	7.3	6.7	7.0	7.1	6.9	-1.3	7.4	7.0	7.1	7.2	7.0	6.9	7.2	7.0	-1.1	16S rRNA m(2)G 966 methyltransferase
VF0724	8.3	7.8	7.9	8.0	7.5	7.4	7.8	7.6	-1.3	8.1	7.5	7.7	7.7	7.3	7.0	7.4	7.2	-1.4	BoIa protein
VF0725	10.7	10.5	10.8	10.7	10.2	10.4	10.4	10.3	-1.3	10.7	10.4	10.7	10.6	10.5	9.9	10.5	10.3	-1.3	Na(+)-translocating NADH-quinone reductase subunit A
VF0726	9.3	9.9	9.7	10.2	9.5	9.7	9.7	9.7	-1.1	9.3	9.7	10.2	9.9	9.8	9.7	9.7	9.7	-1.5	Na(+)-translocating NADH-quinone reductase subunit B
VF0733	6.6	6.4	6.6	6.6	7.1	5.9	7.0	6.7	1.1	6.4	6.6	6.3	6.4	5.8	5.8	5.9	5.8	-1.5	putative periplasmic protein
VF0734	6.5	6.6	6.7	6.6	6.2	6.5	6.5	6.4	-1.1	6.1	6.3	6.3	6.2	6.5	6.2	6.5	6.4	1.1	DNA polymerase IV
VF0735	7.3	7.1	7.3	7.2	7.0	6.9	7.3	7.1	-1.2	7.1	7.0	7.2	7.1	7.2	6.9	7.2	7.1	-1.0	alanine racemase
VF0735to737	4.6	4.0	3.6	4.1	3.9	3.6	3.8	3.8	-1.2	4.2	3.8	3.6	3.9	3.5	3.8	3.8	3.7	-1.1	aminocacyl-histidine dipeptidase
VF0737	8.5	9.0	9.2	9.2	8.6	9.3	8.9	8.9	-1.3	9.4	8.5	9.0	9.0	9.5	9.0	9.5	9.3	-1.4	guanine-hypoxanthine permease
VF0738	9.6	9.2	9.3	9.3	9.0	9.2	9.2	9.1	-1.2	9.5	9.0	9.2	9.3	9.4	9.1	9.4	9.3	1.0	xanthine phosphoribosyltransferase
VF0739	7.7	7.1	7.3	7.3	7.2	6.9	7.5	7.2	-1.1	7.6	6.8	7.0	7.1	6.9	7.0	7.0	6.9	-1.1	hypothetical protein
VF0742	7.8	7.8	7.5	7.7	7.4	7.7	7.5	7.5	-1.1	7.7	7.5	7.7	7.6	7.8	7.9	7.9	7.9	1.2	lipoyl synthase
VF0743	9.4	9.3	9.2	9.3	9.1	9.3	9.3	9.2	-1.1	9.4	9.0	9.2	9.2	9.4	9.3	9.5	9.4	1.1	lipoyltransferase
VF0744	8.3	7.8	7.5	7.9	7.7	7.0	7.9	7.5	-1.3	7.8	7.7	7.7	7.8	7.4	7.5	7.5	7.5	-1.2	hypothetical protein
VF0745	9.3	9.1	9.2	9.2	8.6	9.0	8.9	8.8	-1.3	9.2	8.9	9.1	9.1	9.1	9.0	9.1	9.1	-1.0	D-alanyl-D-alanine serine-type carboxypeptidase
VF0746	7.0	6.8	6.4	6.7	6.0	6.4	6.2	6.2	-1.4	6.8	6.4	6.5	6.6	6.2	6.4	6.2	6.3	-1.3	lipoprotein
VF0749	7.5	7.1	6.8	7.1	6.7	6.4	6.9	6.7	-1.4	7.2	6.7	6.8	6.9	6.4	6.3	6.5	6.4	-1.4	hypothetical protein
VF0750	8.1	7.7	7.4	7.7	7.4	7.4	7.9	7.5	-1.1	7.9	7.5	7.6	7.7	7.3	7.0	7.5	7.2	-1.3	iojap protein family
VF0751	8.0	7.8	7.4	7.8	7.0	7.6	7.4	7.3	-1.3	7.8	7.7	7.7	7.8	7.4	7.5	7.5	7.5	-1.2	DNA polymerase III subunit delta
VF0752	8.4	8.4	8.1	8.3	7.6	8.1	7.9	7.9	-1.4	8.3	8.3	8.3	8.3	8.1	8.1	8.1	8.1	-1.1	rare lipoprotein B precursor
VF0754	8.2	8.2	8.1	8.1	8.4	7.8	8.8	8.3	-1.1	7.9	8.7	8.3	8.3	7.9	8.6	7.9	8.1	-1.1	hypothetical protein
VF0755	6.4	6.0	5.8	6.0	4.9	5.3	5.6	5.3	-1.7	6.1	5.4	5.6	5.7	5.5	4.6	5.1	5.1	-1.5	apolipoprotein N-acyltransferase
VF0756	9.5	9.2	9.1	9.2	9.0	9.1	9.1	9.1	-1.1	9.3	8.9	9.2	9.1	9.2	9.0	9.2	9.1	1.0	magnesium and cobalt efflux protein CorC
VF0757	8.5	8.2	8.1	8.3	7.9	8.0	8.3	8.0	-1.2	8.3	8.1	8.0	8.2	7.9	8.1	7.8	7.9	-1.4	hypothetical protein
VF0758	8.0	7.5	7.2	7.6	7.2	7.7	7.8	7.6	-1.0	7.6	7.4	7.3	7.5	7.0	7.2	7.1	7.1	-1.3	PhoH-like protein
VF0760	6.8	6.5	6.2	6.5	6.1	6.4	6.8	6.4	-1.1	6.5	6.3	6.4	6.4	6.2	6.5	6.4	6.3	-1.0	2-oxaprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase
VF0765	9.0	9.0	8.9	9.0	8.9	8.5	8.8	8.7	-1.2	9.0	9.0	8.9	9.0	8.8	8.7	8.9	8.8	-1.1	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase
VF0766	7.6	7.7	7.2	7.5	7.9	7.3	7.8	7.7	-1.1	7.4	7.8	7.4	7.5	7.3	7.4	7.4	7.4	-1.1	outer membrane lipoprotein LoIB precursor
VF0767	8.7	8.4	8.7	8.6	8.0														

VF0810	9.4	9.3	8.7	9.2	9.1	9.1	9.4	9.2	1.0	9.6	9.4	9.1	9.4	9.2	9.7	9.2	9.3	-1.0	ferric uptake regulator
VF0812	8.9	8.3	8.5	8.5	8.2	8.0	8.4	8.2	-1.3	9.0	8.2	8.3	8.5	8.2	8.1	8.3	8.2	-1.2	flavodoxin
VF0813	9.4	8.8	9.0	9.1	8.7	8.6	9.0	8.8	-1.2	9.1	8.8	8.9	8.9	9.0	8.7	9.0	8.9	-1.0	hypothetical protein
VF0814	7.8	7.8	7.6	7.7	7.8	7.6	8.1	7.8	1.1	7.5	7.9	7.7	7.7	7.3	7.3	7.4	7.3	-1.3	esterase/lipase
VF0815	9.3	9.1	9.4	9.3	8.7	9.0	8.8	8.8	-1.4	9.2	8.8	9.2	9.1	9.2	8.8	9.3	9.1	1.0	SeqA protein
VF0822	8.3	7.9	7.9	8.1	7.1	7.5	7.7	7.4	-1.5	8.2	7.5	7.8	7.8	7.6	7.6	7.6	7.6	-1.2	succinate dehydrogenase catalytic subunit
VF0827	5.9	5.7	5.3	5.6	5.1	5.6	5.7	5.4	-1.1	5.7	5.6	5.7	5.6	5.4	5.6	5.6	5.6	-1.0	methyl-accepting chemotaxis protein
VF0828	5.7	4.7	4.7	5.0	4.6	4.2	4.8	4.6	-1.4	5.5	4.3	4.5	4.7	4.6	3.5	4.3	4.1	-1.5	high-affinity zinc uptake system membrane protein ZnuB
VF0829	6.2	5.6	5.6	5.8	5.2	5.4	5.7	5.4	-1.3	6.0	5.1	5.3	5.4	5.6	5.1	5.5	5.4	-1.0	high-affinity zinc uptake system ATP-binding protein ZnuC
VF0830	8.2	7.9	7.8	7.9	7.6	7.7	7.8	7.7	-1.2	8.1	7.7	7.8	7.9	7.6	7.5	7.6	7.6	-1.2	high-affinity zinc uptake system protein ZnuA precursor
VF0831	7.3	7.1	7.0	7.1	6.6	7.1	6.7	6.8	-1.2	7.2	7.1	7.0	7.1	6.8	6.6	6.8	6.7	-1.3	cell wall endopeptidase, family M23/M37
VF0832	7.5	7.2	7.1	7.3	6.7	7.0	7.0	6.9	-1.3	7.4	7.0	7.1	7.2	6.9	6.8	7.0	6.9	-1.2	hypothetical protein
VF0832to833t	5.3	5.4	4.6	5.1	4.8	5.2	5.4	5.1	1.0	5.1	5.9	5.2	5.4	5.0	5.9	4.9	5.3	-1.1	hypothetical protein
VF0833	8.1	7.8	7.8	7.9	8.0	7.6	8.2	7.9	1.0	7.9	7.9	7.8	7.9	7.5	7.7	7.6	7.6	-1.2	ferrous iron transport protein A
VF0834	8.4	8.2	8.3	8.3	8.0	8.0	8.1	8.0	-1.2	8.3	8.1	8.2	8.2	7.9	7.9	7.9	7.9	-1.2	ferrous iron transport protein B
VF0835	5.7	5.7	4.7	5.4	4.9	5.0	5.1	5.0	-1.3	5.5	5.5	5.1	5.4	4.3	4.9	4.7	4.6	-1.7	hypothetical protein
VF0837	9.8	9.4	9.6	9.6	9.4	9.0	9.8	9.3	-1.2	9.6	9.2	9.3	9.4	9.0	8.6	9.1	8.9	-1.4	acetylacetylphosphate kinase
VF0838	8.8	8.8	8.9	8.8	9.3	8.7	9.5	9.2	1.3	8.8	9.1	8.7	8.8	8.6	8.8	8.6	8.7	-1.1	hypothetical protein
VF0839	8.7	8.5	8.7	8.6	8.2	8.4	8.3	8.3	-1.2	8.6	8.4	8.6	8.5	8.6	8.2	8.6	8.5	-1.1	arginyl-tRNA synthetase
VF0840	7.4	7.2	7.0	7.2	6.8	6.9	7.1	6.9	-1.2	7.3	7.0	7.0	7.1	7.0	7.0	7.0	7.0	-1.1	protein YecM
VF0841	5.6	4.9	4.9	5.1	4.3	4.1	4.9	4.4	-1.6	5.4	4.4	4.3	4.7	4.0	3.8	3.8	3.9	-1.8	dehydrogenase
VF0842	7.5	6.9	6.9	7.1	6.5	6.7	6.7	6.6	-1.4	7.3	6.7	6.9	7.0	6.6	6.3	6.6	6.5	-1.4	putative O-methyltransferase
VF0843	8.0	7.8	7.5	7.8	7.3	7.5	7.4	7.4	-1.3	7.8	7.5	7.6	7.6	7.6	7.6	7.6	7.6	-1.0	hypothetical protein
VF0844	8.1	7.7	7.7	7.8	7.7	7.7	7.9	7.8	-1.0	7.9	7.6	7.6	7.7	7.7	7.7	7.8	7.7	-1.0	hypothetical protein
VF0845	7.9	7.6	7.5	7.6	7.3	7.4	7.5	7.4	-1.2	7.7	7.5	7.5	7.6	7.3	7.2	7.3	7.3	-1.2	1-acyl-sn-glycerol-3-phosphate acyltransferase
VF0846	8.9	8.6	8.3	8.6	8.3	8.4	8.7	8.5	-1.1	8.9	8.6	8.5	8.6	8.5	8.3	8.5	8.5	-1.1	acyl carrier protein
VF0847	8.4	7.4	7.1	7.3	8.2	7.3	8.3	7.9	-1.2	7.2	6.9	7.2	7.2	7.0	6.8	7.1	7.0	-1.1	acyl carrier protein
VF0848	7.7	7.1	7.1	7.3	6.9	7.1	7.2	7.1	-1.2	7.6	6.9	6.9	7.1	6.8	6.5	6.8	6.7	-1.3	DNA gyrase subunit B
VF0849	6.7	6.3	6.2	6.4	5.9	6.1	6.1	6.0	-1.3	6.4	5.8	6.3	6.2	6.0	5.2	5.8	5.7	-1.4	AMP-(fatty)acid ligase
VF0850	7.5	6.7	6.9	7.0	6.7	6.3	7.1	6.7	-1.3	7.2	6.7	6.7	6.8	6.5	5.9	6.4	6.2	-1.5	AMP-(fatty)acid ligase
VF0854to855t	3.0	2.9	3.0	2.9	2.7	2.5	2.5	2.6	-1.3	2.8	2.6	2.6	2.7	2.5	2.6	2.3	2.5	-1.1	hypothetical protein
VF0855	10.2	9.3	9.6	9.6	10.2	9.3	10.3	9.2	-1.3	9.6	9.5	9.7	9.7	9.2	9.1	9.2	9.2	-1.4	heat shock protein Hsc70
VF0864	6.3	6.3	6.2	6.2	5.7	5.9	6.0	5.9	-1.3	6.2	6.0	6.2	6.1	6.2	5.6	6.1	6.0	-1.1	hypothetical protein
VF0864to886t	3.5	3.1	2.9	3.2	3.5	3.6	3.7	3.6	1.3	3.2	3.3	3.3	3.2	2.9	3.2	2.8	2.9	-1.2	hypothetical protein
VF0864to886t	3.9	3.1	2.7	3.2	3.0	3.1	3.6	3.2	1.0	3.1	3.4	3.2	3.2	2.8	2.8	2.4	2.7	-1.5	hypothetical protein
VF0865	7.2	7.2	7.0	7.1	7.5	7.2	7.5	7.4	1.2	7.0	7.2	6.9	7.0	6.9	6.9	6.9	6.9	-1.1	cardiolipin synthetase
VF0866	3.5	3.5	3.3	3.4	3.1	3.1	3.1	3.1	-1.3	3.3	3.2	3.2	3.1	3.1	3.1	2.9	3.0	-1.1	hypothetical protein
VF0867	3.8	3.5	3.2	3.5	3.4	3.3	3.5	3.4	-1.1	3.5	3.5	3.3	3.4	3.3	3.2	3.2	3.2	-1.2	hypothetical protein
VF0868	6.8	6.2	6.5	6.5	6.2	6.2	6.6	6.3	-1.1	6.6	6.0	6.1	6.3	6.3	6.2	6.2	6.2	-1.2	hypothetical protein
VF0869	3.0	2.6	1.9	2.5	2.0	2.2	2.4	2.2	-1.2	2.4	2.1	2.3	2.3	1.9	2.1	2.2	2.0	-1.2	hypothetical protein
VF0870	3.0	2.7	2.5	2.7	2.7	2.5	2.8	2.7	-1.0	2.6	2.7	2.5	2.6	2.6	2.6	2.3	2.5	-1.1	hypothetical protein
VF0871	5.1	4.3	3.6	4.3	4.1	4.3	4.3	4.1	-1.2	4.9	3.9	3.7	4.2	3.5	3.7	3.3	3.5	-1.6	transcriptional regulator, TetR family
VF0872	4.3	3.7	3.1	3.7	3.6	3.4	3.6	3.5	-1.1	3.8	3.3	3.4	3.5	3.4	3.4	3.6	3.5	-1.0	methyl-accepting chemotaxis protein
VF0873	7.5	6.7	6.5	6.9	6.4	6.4	6.7	6.5	-1.4	7.4	6.3	6.6	6.8	6.1	5.5	6.2	5.9	-1.8	hypothetical protein
VF0874	3.8	2.9	2.8	3.2	2.9	3.2	3.5	3.2	-1.0	3.4	3.2	2.8	3.1	3.1	2.6	2.7	2.8	-1.3	protein translocase subunit SecF
VF0875	3.8	3.6	4.0	3.8	4.0	3.9	4.0	4.0	-1.1	3.9	3.8	3.6	3.8	4.0	3.9	3.9	3.9	-1.1	protein translocase subunit SecD
VF0876	6.7	6.0	5.6	6.1	5.2	5.3	5.7	5.4	-1.7	6.6	5.5	5.7	5.9	5.2	5.6	5.5	5.4	-1.4	hypothetical protein
VF0877	6.3	5.8	5.6	5.9	6.5	5.5	6.8	6.3	1.3	6.0	6.2	5.6	5.9	5.2	5.7	5.2	5.4	-1.5	transcriptional regulators, LysR family
VF0880	7.2	7.1	7.0	7.1	6.8	6.9	6.9	6.8	-1.0	7.2	7.0	7.0	7.0	7.0	6.6	7.1	6.9	-1.1	ribosomal small subunit pseudouridine synthase A
VF0881	6.0	5.3	5.6	5.6	5.0	4.9	5.5	5.2	-1.5	5.5	4.9	5.1	5.2	5.0	4.8	5.6	5.2	-1.0	bicyclomycin resistance protein
VF0882	6.1	5.3	5.3	5.6	5.2	5.1	5.7	5.4	-1.2	5.9	5.2	5.1	5.4	5.2	5.0	5.0	5.1	-1.3	hypothetical protein
VF0883	8.3	7.4	7.1	7.3	8.2	7.3	8.3	7.9	-1.3	8.3	7.6	7.2	7.4	7.7	7.1	6.6	6.8	-1.1	nucleoside-diphosphate-sugar epimerase
VF0884	8.1	7.8	7.8	7.9	7.4	7.7	7.4	7.5	-1.3	7.9	7.7	7.8	7.8	8.2	8.0	8.4	8.2	1.3	ABC transporter ATP-binding protein
VF0886	6.7	6.4	6.3	6.4	5.7	6.0	6.1	5.9	-1.4	6.6	6.0	6.5	6.4	6.6	6.1	6.5	6.4	1.0	hypothetical secreted protein
VF0887	7.2	6.6	6.9	6.9	6.4	6.0	6.7	6.4	-1.4	7.1	6.5	6.4	6.6	6.4	5.9	6.2	6.2	-1.4	Na <sup>+</sup> /H <sup>+</sup> antiporter NhaA
VF0887to888t	4.7	4.6	3.7	4.3	4.2	4.6	4.6	4.5	-1.4	4.1	4.6	4.1	4.3	4.8	5.1	3.9	4.6	1.2	Na <sup>+</sup> /H <sup>+</sup> antiporter NhaA
VF0890	8.4	7.8	7.3	7.8	8.2	7.9	8.3	8.1	-1.1	8.3	7.8	7.5	7.8	7.4	7.8	7.7	7.6	-1.2	glutaredoxin
VF0891	7.3	6.7	6.4	6.8	7.1	6.6	7.5	7.1	-1.2	7.0	6.4	6.2	6.5	5.8	6.2	5.9	6.0	-1.5	transcriptional regulator, RpiR family
VF0893	7.3	6.7	6.3	6.8	5.7	6.0	6.3	6.0	-1.7	7.2	6.4	6.5	6.7	6.0	6.2	6.1	6.1	-1.5	hypothetical protein
VF0894	7.1	6.4	6.5	6.7	5.9	6.0	6.3	6.1	-1.5	6.9	6.2	6.4	6.5	6.1	5.9	6.3	6.1	-1.3	putative surface protein
VF0895	7.3	6.8	6.6	6.9	6.6	6.3	6.7	6.6	-1.3	7.2	6.4	6.5	6.7	6.4	6.7	6.7	6.6	-1.1	hypothetical protein
VF0897	8.7	8.0	8.2	8.3	8.4	9.1	8.7	8.7	1.4	8.9	7.7	8.1	8.2	8.4	7.8	8.4	8.2	-1.0	hypothetical protein
VF0898	8.2	8.0	8.0	8.1	7.7	8.0	7.9	7.9	-1.2	8.3	7.8	8.0	8.0	8.0	7.9	8.0	8.0	-1.0	hypothetical protein
VF0899	10.0	9.5	9.8	9.8	9.1	9.4	9.4	9.3	-1.4	10.0	9.3	9.6	9.7	9.5	9.1	9.5	9.4	-1.2	phosphoserine aminotransferase
VF0900	7.1	6.6	6.6	6.8	5.8	6.1	6.4	6.1	-1.6	6.9	6.2	6.5	6.5	6.0	6.0	6.0	6.0	-1.4	transport ATP-binding protein CydC
VF0904	9.3	9.0	9.0	9.1	8.9	9.5	9.1	9.2	-1.1	9.4	8.9	8.8	9.0	8.3	8.8	8.4	8.5	-1.4	leucine-responsive regulatory protein
VF0905	7.8	7.7	7.7	7.7	7.3	7.7	7.5	7.5	-1.2	7.6	7.5	7.7	7.6	7.4	7.2	7.3	7.3	-1.2	cell division protein FtsK
VF0906	8.5	8.4	8.2	8.3	7.8	8.3	8.1	8.1	-1.2	8.5	8.2	8.2	8.3	8.2	7.9	8.0	8.0	-1.2	outer-membrane lipoproteins carrier protein
VF0907	7.8	7.3	7.4	7.5	7.2	7.4	7.5	7.4	-1.1	7.7	7.1	7.4	7.4	7.1	6.9	7.0	7.0	-1.2	ATPase, AAA family
VF0908	8.8	8.4	8.7	8.6	8.2	8.2	8.4	8.3	-1.3	8.8	8.5	8.6	8.6	8.6	8.4	8.6	8.5	-1.1	seryl-tRNA synthetase
VF0909	7.9	7.2	7.1	7.4	7.2	7.3	7.7	7.4	-1.0	7.6	7.2	7.2	7.3	6.8	7.1	7.0	7.0	-1.3	thioredoxin
VF0910	8.1	8.1	7.9	8.0	8.2	8.0	8.2	8.1	1.1	8.2	8.3	7.8	8.1	7.9	8.4	8.0	8.1	-1.0	hypothetical protein
VF0912	7.9	7.4	7.3																

VF0940	10.1	10.2	10.1	10.1	10.2	10.2	10.1	10.2	1.1	10.0	10.4	10.0	10.1	10.1	10.5	10.1	10.2	1.1	molybdenum cofactor biosynthesis protein A
VF0941	9.9	9.7	9.9	9.8	9.9	9.7	9.7	9.8	-1.0	9.8	9.9	9.7	9.8	9.6	9.7	9.6	9.8	-1.2	molybdenum cofactor biosynthesis protein C
VF0942	9.3	8.7	8.8	8.9	8.9	8.7	9.0	8.9	-1.0	9.1	9.1	8.7	8.9	8.5	8.4	8.6	8.5	-1.4	molybdopterin converting factor, small subunit
VF0949	9.0	8.8	8.9	8.9	8.5	8.8	8.8	8.7	-1.1	8.9	8.7	8.8	8.8	8.9	8.8	8.9	8.9	-1.1	aspartyl-tRNA synthetase
VF0950	6.7	6.8	6.8	6.8	6.8	6.7	7.0	6.8	-1.0	6.5	6.7	6.7	6.6	6.6	6.3	6.5	6.5	-1.1	Holliday junction resolvase
VF0951	8.2	8.4	8.5	8.4	8.3	8.4	8.4	8.4	-1.0	8.2	8.3	8.4	8.3	8.4	8.1	8.4	8.3	1.0	Holliday junction DNA helicase motor protein
VF0952	7.6	7.5	7.8	7.6	7.5	7.6	7.6	7.5	-1.0	7.5	7.4	7.5	7.5	7.4	7.3	7.4	7.3	-1.1	Holliday junction DNA helicase RuvB
VF0955	9.5	8.6	8.9	9.0	9.7	9.2	10.0	9.6	1.6	9.3	8.6	8.7	8.9	9.2	9.0	9.4	9.2	1.2	protein YbgT
VF0956	9.2	8.1	8.1	8.5	9.4	8.9	9.6	9.3	1.8	9.0	8.2	8.2	8.5	8.5	8.6	8.7	8.6	1.1	hypothetical protein
VF0957	8.3	8.0	8.0	8.1	7.9	8.0	8.3	8.1	-1.0	8.3	7.9	8.0	8.1	8.2	7.9	8.2	8.1	-1.0	short chain acyl-CoA thioesterase YbgC
VF0958	8.2	8.1	8.2	8.2	7.8	7.9	8.1	7.9	-1.2	8.1	7.8	8.0	8.0	7.9	8.0	8.0	7.8	-1.1	ToIQ protein
VF0959	8.2	8.1	8.0	8.1	7.7	8.0	7.8	7.8	-1.3	8.0	7.9	8.0	8.0	8.0	7.7	7.9	7.8	-1.1	ToIR protein
VF0960	3.1	3.1	3.0	3.1	2.9	2.8	2.9	2.9	-1.2	3.2	3.0	3.1	3.1	2.9	2.4	2.9	2.7	-1.3	ToIA protein
VF0960_s	7.7	7.7	7.6	7.7	7.1	7.6	7.5	7.4	-1.2	7.6	7.5	7.6	7.6	7.4	7.3	7.4	7.4	-1.1	ToIA protein
VF0960to961	2.4	2.6	2.5	2.5	2.4	2.6	2.5	2.5	-1.0	2.8	2.4	2.6	2.6	2.4	2.3	2.4	2.4	-1.2	ToIA protein
VF0960to961t	2.5	2.4	2.3	2.4	2.4	2.5	2.5	2.5	-1.0	2.5	2.4	2.3	2.4	2.3	2.4	2.4	2.4	-1.0	ToIA protein
VF0961	7.9	8.2	8.0	8.0	8.2	8.0	8.1	8.1	1.1	7.8	8.3	8.0	8.1	7.7	8.0	7.8	7.8	-1.2	ToIA protein
VF0962	10.3	10.3	10.3	10.3	10.4	10.3	10.4	10.4	-1.0	10.3	10.4	10.2	10.3	10.0	10.0	10.1	10.1	-1.2	translocation protein TolB precursor
VF0965	7.5	7.4	7.4	7.4	6.9	7.1	7.1	7.0	-1.3	7.4	7.0	7.3	7.2	7.2	6.9	7.3	7.1	-1.1	quinolinate synthetase
VF0966	8.1	7.3	7.4	7.6	7.6	7.5	7.8	7.7	1.0	8.1	7.1	7.5	7.6	7.9	7.3	7.7	7.6	1.1	hypothetical protein
VF0971	7.0	6.8	6.8	6.9	6.6	6.9	6.8	6.8	-1.0	6.9	6.4	6.6	6.6	6.3	6.6	6.5	6.5	-1.1	GTP-binding protein HtlX
VF0972	7.4	7.0	7.0	7.1	7.1	7.0	7.2	7.1	-1.0	7.5	7.0	7.1	7.2	7.0	7.4	7.1	7.2	-1.0	RNA polymerase sigma-70 factor
VF0973	5.4	5.3	5.0	5.2	5.3	5.3	5.6	5.4	1.1	5.2	5.2	5.2	5.2	5.1	4.8	5.0	5.0	-1.2	glutamate-cysteine ligase
VF0974	6.6	6.7	6.6	6.6	6.4	6.6	6.5	6.5	-1.1	6.4	6.5	6.5	6.5	6.3	5.8	6.4	6.2	-1.2	multidrug resistance ABC transporter ATP-binding and permease protein
VF0975	6.8	7.1	7.0	7.0	6.7	6.8	6.7	6.7	-1.2	6.8	6.8	6.9	6.8	6.8	6.7	6.8	6.8	-1.0	multidrug resistance ABC transporter ATP-binding and permease protein
VF0976	7.1	6.9	7.1	7.1	6.5	6.8	7.0	6.8	-1.2	7.2	7.2	7.3	7.2	7.0	6.7	6.7	6.8	-1.3	glutathione synthetase
VF0977	5.9	6.2	6.4	6.4	6.2	6.8	6.4	6.4	-1.4	6.2	6.8	6.4	6.2	6.4	6.1	6.2	6.0	-1.2	acetyltransferase
VF0979	5.9	5.3	4.9	5.4	4.6	4.4	4.9	4.6	-1.6	5.8	5.1	5.0	5.3	4.8	4.4	4.7	4.6	-1.6	hypothetical protein
VF0983	8.2	8.3	7.6	8.0	7.9	7.9	8.1	8.0	-1.0	8.2	8.3	7.7	8.1	7.4	8.0	7.3	7.6	-1.4	hypothetical protein
VF0984	8.5	8.6	8.2	8.5	8.0	8.2	8.4	8.2	-1.2	8.5	8.5	8.4	8.5	8.1	8.4	8.0	8.1	-1.2	hypothetical protein
VF0986to987	2.2	2.1	1.9	2.0	2.0	2.0	2.0	2.0	-1.0	2.2	2.0	1.9	2.0	2.0	1.9	1.9	1.9	-1.1	chitinase precursor
VF0986to987t	2.5	2.7	2.8	3.1	2.5	2.7	2.8	2.8	-1.0	1.7	1.6	1.8	1.7	1.8	1.7	1.6	1.6	-1.6	chitinase precursor
VF0987	5.9	6.1	5.7	5.9	5.6	5.7	6.0	5.8	-1.1	5.7	6.0	5.6	5.8	5.5	5.7	5.3	5.5	-1.2	methyl-accepting chemotaxis protein
VF0989	4.6	4.0	3.9	4.2	3.7	3.4	4.2	3.8	-1.3	4.4	4.1	3.8	4.1	3.4	3.7	3.5	3.5	-1.5	sensory box/GGDEF family protein
VF0990	5.4	5.3	4.8	5.2	5.0	4.5	4.9	4.8	-1.5	5.1	5.2	4.9	5.1	4.7	4.9	4.7	4.7	-1.4	serine/threonine protein kinase
VF0998	4.6	3.5	3.4	3.8	3.2	3.1	3.6	3.3	-1.3	4.0	3.3	3.4	3.6	3.1	3.1	3.1	3.1	-1.4	transcriptional regulator
VF1000	3.5	3.0	2.8	3.1	2.5	2.7	2.8	2.8	-1.4	3.1	2.7	2.8	2.9	2.4	2.5	2.4	2.4	-1.5	quinolinate dehydrogenase
VF1001	3.9	3.4	2.9	3.4	2.8	2.9	2.9	2.9	-1.4	3.5	3.0	3.0	3.2	2.8	2.5	2.4	2.6	-1.5	hypothetical protein
VF1002	4.2	3.1	2.9	3.4	2.6	2.7	3.0	2.8	-1.5	3.7	2.8	2.8	3.1	2.2	2.8	2.5	2.5	-1.5	hypothetical protein
VF1005	3.2	2.5	2.6	2.7	2.5	2.4	2.3	2.4	-1.3	3.4	2.4	3.0	2.9	2.2	2.4	2.0	2.2	-1.6	Flagellar L-ring protein FliH
VF1008	7.1	6.5	6.6	6.7	5.9	6.3	6.4	6.2	-1.5	6.8	6.5	6.6	6.6	6.4	6.1	6.4	6.3	-1.3	hypothetical membrane spanning protein
VF1009	8.1	8.0	8.9	8.0	8.3	8.8	8.7	8.6	-1.3	8.9	8.4	8.9	8.7	8.7	8.5	8.7	8.7	-1.1	ATP-dependent helicase, DinG family
VF1010to1011	3.2	3.1	2.5	3.0	2.9	2.7	3.5	3.0	1.1	3.0	3.3	2.5	2.9	2.2	2.9	2.4	2.5	-1.3	hypothetical protein
VF1018	9.0	8.7	8.9	8.9	8.4	9.1	9.6	9.0	1.1	9.3	8.9	9.1	9.1	9.2	9.4	9.8	9.6	1.5	imidazole glycerol phosphate synthase subunit HisF
VF1019	7.8	7.5	7.3	7.5	7.3	7.8	8.9	8.0	1.4	8.2	7.7	7.6	7.8	7.9	8.0	7.7	7.9	-1.3	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase
VF1022	7.0	6.3	5.9	6.4	5.9	6.0	6.5	6.1	-1.2	6.8	6.1	6.0	6.3	5.9	6.1	5.9	6.0	-1.3	hypothetical protein
VF1023	7.1	6.5	6.3	6.6	6.5	6.2	7.0	6.6	-1.0	7.0	6.8	6.2	6.6	6.2	6.3	6.1	6.2	-1.3	putative intracellular septation protein
VF1025	7.6	7.1	7.0	7.2	7.0	6.8	7.1	7.0	-1.2	7.4	6.7	6.8	7.0	6.8	6.6	6.9	6.8	-1.2	bifunctional indole-3-glycerol phosphate synthase/phosphoribosylanthranilate synthase
VF1029	8.2	8.6	8.4	8.4	7.6	8.0	7.9	7.8	-1.5	8.0	7.7	8.2	8.0	8.3	7.8	8.8	8.3	1.3	anthranilate phosphoribosyltransferase
VF1030	7.7	8.0	7.8	7.8	7.1	7.4	7.5	7.3	-1.4	7.4	7.1	7.6	7.4	7.8	7.4	8.4	7.9	-1.4	anthranilate phosphoribosyltransferase
VF1031	7.6	8.0	7.8	7.8	7.0	7.4	7.6	7.3	-1.4	7.4	7.2	7.6	7.4	7.7	7.5	8.5	7.9	-1.4	anthranilate phosphoribosyltransferase
VF1032	6.3	6.4	6.2	6.3	6.5	6.9	7.0	6.8	-1.5	7.0	6.6	7.1	6.9	7.0	7.1	8.0	7.5	-1.0	anthranilate synthase component II
VF1033to1034	6.3	6.4	6.2	6.3	5.2	5.2	5.9	5.4	-1.8	6.0	5.0	5.7	5.6	5.8	5.4	6.6	5.9	1.3	anthranilate synthase component I
VF1033to1034t	4.4	3.8	3.6	3.9	3.8	3.8	4.0	3.9	-1.1	4.0	3.6	3.5	3.7	3.6	3.3	3.4	3.4	-1.3	anthranilate synthase component I
VF1034	8.7	8.8	8.7	8.7	8.5	8.6	8.7	8.6	-1.0	8.6	8.3	8.7	8.5	8.6	8.5	8.6	8.5	-1.0	PHP domain containing protein (TRPH)
VF1035	8.5	8.3	8.1	8.3	8.2	8.3	8.6	8.4	-1.1	8.5	8.2	8.1	8.3	8.0	8.1	8.1	8.1	-1.1	Sua5/YcoY/YrdC/YwcC family protein
VF1036	5.8	5.4	4.8	5.3	4.5	4.1	5.2	4.6	-1.7	5.4	5.5	4.9	5.3	4.5	4.6	4.6	4.5	-1.7	autoinducer regulatory protein AinR
VF1038	9.5	9.6	9.9	9.7	9.1	9.4	9.2	9.2	-1.4	9.4	9.5	9.7	9.6	9.6	9.5	9.8	9.6	-1.1	ribosomal large subunit pseudouridine synthase B
VF1040	7.7	7.5	7.3	7.5	6.8	7.4	7.2	7.2	-1.3	7.7	7.2	7.2	7.4	7.2	7.2	7.2	7.2	-1.1	possible protease SohB
VF1041	5.8	5.2	5.3	5.4	5.6	4.8	5.8	5.4	-1.0	5.5	5.3	5.1	5.3	4.7	4.6	4.9	4.7	-1.5	hypothetical protein
VF1044	6.8	6.4	6.0	6.4	6.1	6.0	6.4	6.2	-1.2	6.6	6.3	6.3	6.4	5.8	6.0	5.7	5.8	-1.5	RNA-directed DNA polymerase
VF1046	7.4	7.0	7.0	7.1	6.7	6.9	7.1	6.9	-1.2	7.1	7.2	6.9	7.1	6.9	6.8	7.1	7.0	-1.1	hypothetical protein
VF1047	7.5	7.3	7.0	7.3	6.9	7.2	7.3	7.1	-1.1	7.5	7.4	7.0	7.3	6.9	7.3	7.2	7.1	-1.1	hypothetical protein
VF1047to1048	5.2	5.4	4.8	5.1	4.9	4.9	5.2	5.0	-1.1	5.2	5.7	5.2	5.4	4.7	5.1	4.6	4.8	-1.5	hypothetical protein
VF1048	5.6	5.4	5.2	5.4	5.0	5.1	5.7	5.3	-1.0	5.3	5.2	5.1	5.2	5.0	4.5	4.5	4.7	-1.5	hypothetical protein
VF1049	4.0	3.3	3.6	3.6	3.6	3.4	3.8	3.6	-1.1	3.5	3.6	3.5	3.5	3.2	3.5	3.4	3.4	-1.1	putative DNA methylase
VF1049to1050	3.7	3.7	3.2	3.5	3.4	3.2	3.4	3.3	-1.2	3.4	3.7	3.5	3.5	3.0	3.2	3.2	3.1	-1.3	putative DNA methylase
VF1052	3.9	3.9	3.4	3.7	3.9	3.7	4.2	3.9	-1.1	3.9	3.8	3.9	3.9	3.3	3.9	3.7	3.6	-1.2	transporter, divalent anion/sodium symporter family
VF1053	5.8	5.6	5.5	5.6	5.6	5.4	5.8	5.6	-1.0	5.5	5.7	5.3	5.5	5.3	5.4	5.1	5.3	-1.2	sensory transduction protein kinase
VF1054	7.1	6.9	6.7	6.9	6.7	6.5	7.1	6.7	-1.1	6.9	7.0	6.7	6.9	6.5	6.7	6.6	6.6	-1.2	hypothetical protein
VF1056	8.9	8.9	8.9	8.9	9.1	8.8	9.3	9.1	-1.1	8.9	9.1	8.9	9.0	8.5	8.6	8.6	8.6	-1.3	phosphoglucomutase
VF1057	4.4	3.6	3.5	3.8	3.3	3.7	3.7	3.6	-1.2	3.6	3.7	3.6	3.6	3.5	3.5				

VF1092	6.7	6.6	6.1	6.5	5.9	6.5	6.2	6.2	-1.2	6.4	6.5	6.3	6.4	6.5	6.7	6.6	6.6	1.1	toxin coregulated pilus biosynthesis protein I
VF1093	7.1	6.6	6.4	6.0	9.3	6.2	6.4	6.4	1.9	7.6	6.4	6.0	6.0	7.2	7.6	7.2	7.4	1.2	glutamate-gated potassium channel
VF1094	7.6	7.8	7.6	7.7	8.7	7.7	8.7	8.4	1.6	7.4	8.0	7.5	7.6	6.9	7.2	6.8	6.9	-1.6	SAM-dependent methyltransferase
VF1096	4.9	4.4	4.8	4.7	4.6	4.5	4.9	4.6	-1.0	4.5	4.7	4.6	4.6	4.7	4.4	4.1	4.4	-1.1	nucleoside permease NupC
VF1097	4.9	3.6	3.4	4.0	2.8	3.1	3.6	3.2	-1.7	4.0	3.5	3.6	3.7	2.8	3.0	2.9	2.9	-1.7	BAX protein
VF1098	5.9	5.1	4.3	5.1	4.0	4.4	4.7	4.4	-1.6	5.6	4.4	4.8	4.9	4.2	4.1	3.7	4.0	-1.9	peptidyl-prolyl cis-trans isomerase
VF1100	7.1	7.2	7.0	7.1	6.5	7.0	6.7	6.7	-1.3	7.0	6.9	7.1	7.0	7.1	7.1	7.1	7.1	1.1	D-cysteine desulfhydrase homolog
VF1101	7.8	7.8	7.7	7.8	7.3	7.7	7.6	7.6	-1.2	7.7	7.6	7.7	7.7	8.0	7.9	8.0	7.9	1.2	hypothetical protein
VF1102	6.0	5.4	5.3	5.6	5.0	5.3	5.5	5.3	-1.2	5.7	5.7	5.3	5.5	5.1	5.5	5.3	5.3	1.2	hypothetical protein
VF1103	8.2	8.0	8.2	8.1	9.0	8.2	9.0	8.7	1.5	7.9	8.3	8.1	8.1	7.8	7.7	7.7	7.7	-1.3	hypothetical protein
VF1104	6.9	7.2	7.1	7.1	7.4	7.0	7.5	7.3	1.2	6.8	7.2	7.1	7.0	6.7	6.9	6.5	6.7	-1.2	hypothetical protein
VF1105	5.3	5.3	4.7	5.1	4.9	4.1	5.1	4.7	-1.3	5.1	5.2	4.9	5.0	4.3	4.6	4.4	4.4	-1.5	transporter
VF1107	7.4	7.4	7.0	7.2	6.9	6.6	7.2	6.9	-1.3	7.1	7.4	7.1	7.2	6.4	7.1	6.5	6.6	-1.5	ABC transporter ATP-binding protein
VF1110	3.4	3.1	2.9	3.1	3.2	2.8	3.4	3.1	1.0	3.4	3.3	3.0	3.2	2.9	3.1	2.9	3.0	1.0	hypothetical protein
VF1111	6.6	6.4	6.1	6.3	6.3	6.4	6.6	6.4	1.1	6.2	6.2	6.2	6.2	6.1	6.2	6.2	6.2	-1.0	transcriptional regulators, LysR family
VF1112	8.3	8.7	8.3	8.5	8.3	8.0	8.6	8.3	1.1	8.1	8.8	8.5	8.5	7.8	8.2	7.8	7.9	-1.5	nonspecific acid phosphatase precursor
VF1113	6.0	5.4	5.2	5.5	4.3	4.7	5.3	4.8	-1.7	5.5	5.6	5.2	5.4	4.5	4.9	5.0	4.8	-1.6	transcriptional regulator, RpiR family
VF1114	5.4	4.9	5.0	5.1	4.6	4.5	5.0	4.7	-1.4	5.3	5.0	4.8	5.1	5.1	4.8	5.1	5.0	-1.1	hypothetical protein
VF1115	5.0	4.4	4.2	4.5	3.9	4.0	4.4	4.1	-1.3	5.0	4.2	4.3	4.5	4.0	3.8	4.2	4.0	-1.4	PTS system, sucrose-specific IIBC component
VF1115to1116	2.4	2.0	2.0	2.1	1.7	1.8	2.0	1.9	-1.2	2.1	1.9	1.9	2.0	1.8	1.7	1.8	1.8	-1.1	PTS system, sucrose-specific IIBC component
VF1116to1116	1.8	1.7	1.8	1.8	1.9	1.8	1.8	1.8	-1.1	1.8	1.8	1.7	1.8	1.8	1.9	1.7	1.8	1.0	PTS system, sucrose-specific IIBC component
VF1116	4.1	3.7	2.8	3.5	3.5	3.0	3.5	3.3	-1.1	3.7	3.3	3.2	3.4	3.0	3.0	2.6	2.9	-1.5	hypothetical protein
VF1118	4.0	3.6	3.6	3.7	3.5	3.2	3.5	3.4	-1.3	3.9	3.3	3.4	3.5	3.3	3.3	3.3	3.3	-1.2	cellulose synthase operon C protein
VF1119	5.2	4.3	4.1	4.5	4.1	3.8	4.3	4.1	-1.4	4.9	4.5	4.4	4.6	4.1	3.7	4.0	3.9	-1.5	hypothetical protein
VF1123	5.6	5.4	5.2	5.4	4.7	4.9	5.0	4.9	-1.4	5.4	5.1	5.1	5.2	4.4	5.0	4.7	4.7	-1.4	hypothetical protein
VF1124	3.5	3.4	3.2	3.4	3.6	3.2	3.8	3.5	1.1	3.3	3.5	3.2	3.3	3.0	3.0	3.5	3.2	-1.1	di-/tripeptide transporter
VF1125to1126	8.0	7.9	8.0	8.2	7.6	7.9	7.7	7.7	-1.1	8.2	7.9	7.9	8.1	7.8	7.8	7.8	7.8	-1.1	hypothetical protein
VF1126	7.9	7.9	7.8	7.8	7.4	7.9	7.7	7.7	-1.1	7.8	7.9	7.6	7.7	7.5	7.7	7.6	7.6	1.1	hypothetical protein
VF1127	7.8	7.8	7.7	7.8	7.4	7.7	7.7	7.7	-1.1	7.7	7.8	7.6	7.7	7.8	7.7	7.8	7.8	1.1	hypothetical protein
VF1128	8.0	8.0	7.8	8.0	7.5	7.7	7.9	7.7	-1.2	7.9	8.1	7.9	8.0	7.9	8.1	8.0	7.9	-1.1	hypothetical protein
VF1131	7.3	6.8	7.0	7.0	6.7	6.6	7.0	6.8	-1.2	7.1	6.7	6.8	6.9	6.6	6.5	6.7	6.6	-1.2	hypothetical protein
VF1132	6.1	5.2	6.0	6.4	6.6	7.8	6.0	6.4	-1.2	6.3	6.0	6.5	6.2	6.1	6.7	6.1	6.1	-2.1	alpha-amylase
VF1134	9.2	8.8	9.0	9.0	9.1	8.8	9.4	9.1	1.1	9.1	9.0	8.8	9.0	8.9	9.1	9.0	9.0	1.0	HIT family hydrolase
VF1135	9.7	10.1	10.0	9.9	9.4	9.7	9.5	9.5	-1.3	9.6	10.0	10.0	9.9	9.7	9.7	9.7	9.7	-1.1	hypothetical protein
VF1138	3.9	3.3	3.4	3.6	3.4	3.4	4.0	3.6	1.0	3.8	3.6	3.0	3.5	3.1	3.1	2.6	2.9	-1.4	TcpI, toxin-coregulated pilus biosynthesis gene
VF1139	6.2	5.4	5.2	5.6	5.4	4.7	5.5	5.2	-1.4	6.1	5.3	5.4	5.6	5.1	5.0	5.2	5.1	-1.4	hypothetical protein
VF1140	3.0	2.9	2.8	2.9	2.8	2.7	2.9	2.8	-1.1	2.9	2.9	2.9	2.9	2.7	2.7	3.0	2.9	-1.9	methyltransferase
VF1141	5.7	4.9	4.9	5.2	4.9	4.8	5.2	5.0	-1.1	5.5	5.0	4.9	5.1	5.1	4.8	5.1	5.0	-1.1	beta-glucosidase
VF1142	7.1	6.5	6.5	6.7	6.0	6.0	6.4	6.1	-1.5	6.9	6.5	6.5	6.6	6.2	6.3	6.4	6.3	-1.3	hypothetical protein
VF1143	9.8	9.5	9.5	9.6	9.5	9.6	9.7	9.6	-1.0	9.8	9.5	9.5	9.6	9.6	9.7	9.8	9.7	1.1	NADH dehydrogenase
VF1146	5.9	5.8	5.6	5.8	5.5	5.4	5.6	5.5	-1.2	5.8	5.1	5.4	5.4	5.2	5.1	5.2	5.2	-1.2	chitinase precursor
VF1148	7.1	6.7	6.4	6.7	6.5	6.2	6.7	6.5	-1.2	6.8	6.9	6.5	6.6	6.2	6.2	6.3	6.1	-1.3	two-component response regulator
VF1149	6.2	6.0	5.4	5.9	5.6	5.4	6.0	5.7	-1.1	6.1	5.9	5.8	5.9	5.2	5.6	5.6	5.5	-1.3	hypothetical protein
VF1150	7.2	5.8	5.9	6.3	5.6	5.3	5.7	5.5	-1.7	6.9	5.5	6.1	6.2	5.7	4.7	5.7	5.4	-1.7	transcriptional regulator
VF1154	6.7	6.0	6.2	6.3	5.8	5.4	5.6	5.6	-1.6	6.5	5.7	6.0	6.1	6.3	5.5	6.2	6.0	-1.0	hypothetical protein
VF1156	5.5	5.1	4.9	5.2	4.7	4.7	5.0	4.8	-1.3	5.1	5.0	4.9	5.0	4.9	4.9	4.9	5.0	-1.0	chlorohydroxylase/oxaminase family protein
VF1157	6.3	6.5	6.5	6.4	7.8	6.3	7.8	7.3	-1.9	6.7	7.2	6.3	6.6	7.8	6.7	6.5	6.5	-1.6	cell wall degradation protein
VF1158	7.8	8.2	8.3	8.1	7.6	8.0	7.6	7.7	-1.3	7.5	8.5	8.2	8.1	8.1	8.3	8.4	8.3	1.2	hypothetical membrane associated protein
VF1159	9.9	9.6	9.6	9.7	9.1	9.3	9.3	9.3	-1.3	9.8	9.2	9.5	9.5	9.1	8.8	9.3	9.1	-1.2	asparaginyl-tRNA synthetase
VF1162	7.4	7.1	7.0	7.2	6.5	6.8	6.9	6.8	-1.3	7.3	7.1	7.1	7.1	6.8	6.8	6.8	6.8	-1.3	outer membrane protein TolC
VF1163	7.8	7.8	7.8	7.8	7.6	7.5	7.8	7.6	-1.1	7.7	7.9	7.7	7.8	7.5	7.3	7.5	7.4	-1.2	export ABC transporter permease protein
VF1164	8.0	7.9	8.0	8.0	7.6	7.9	8.0	7.9	-1.2	7.9	8.0	7.9	7.9	7.6	7.4	7.7	7.6	-1.1	export ABC transporter permease protein
VF1165	7.8	7.8	7.5	7.7	7.3	7.6	7.6	7.5	-1.1	7.7	7.7	7.6	7.7	7.5	7.3	7.3	7.4	-1.2	ABC transporter ATP-binding protein
VF1166	5.9	5.6	5.1	5.5	5.4	5.3	5.7	5.5	-1.0	5.5	5.4	5.2	5.4	5.1	5.1	4.9	5.0	-1.3	hypothetical protein
VF1167	6.8	6.5	6.4	6.5	6.0	6.3	6.5	6.3	-1.2	6.5	6.1	6.3	6.3	6.3	6.1	6.3	6.2	-1.1	exonuclease SbcD
VF1168	7.1	7.0	7.0	7.1	6.5	7.1	6.9	6.8	-1.2	7.1	6.8	7.1	7.0	7.2	7.1	7.4	7.2	1.2	exonuclease SbcC
VF1169	7.7	7.8	7.5	7.7	7.3	7.8	7.6	7.5	-1.1	7.6	7.7	7.8	7.7	7.6	7.9	7.8	7.9	1.1	acyl-CoA hydrolase
VF1170	6.1	5.7	5.5	5.7	5.3	5.3	5.8	5.5	-1.2	5.7	5.6	5.4	5.5	5.4	5.7	4.9	5.3	-1.1	hypothetical protein
VF1171	4.6	4.0	3.7	4.1	3.7	3.6	4.4	3.9	-1.1	4.2	3.5	3.6	3.8	3.3	3.4	3.1	3.3	-1.4	tyrosine-specific transport protein
VF1175	8.0	8.5	8.0	8.2	9.0	8.3	9.1	8.8	1.6	7.9	9.1	8.3	8.4	8.0	8.9	8.1	8.3	-1.1	hypothetical protein
VF1177	5.4	4.7	4.5	4.9	4.6	4.3	4.7	4.6	-1.2	4.9	4.7	4.4	4.7	4.4	4.3	4.0	4.2	-1.4	serine transporter
VF1178	6.2	6.1	5.8	6.1	6.7	5.7	6.6	6.3	1.2	5.8	6.1	5.9	5.9	5.9	6.1	6.0	6.0	1.1	COA pyrophosphatase
VF1181	8.1	8.0	7.7	7.9	8.2	8.1	8.3	8.2	1.2	8.0	8.1	7.9	8.0	8.1	8.4	8.3	8.3	1.2	hypothetical protein
VF1182	8.8	8.7	8.6	8.7	9.3	8.9	9.5	9.2	1.4	8.6	8.9	8.6	8.7	8.9	9.3	8.9	9.0	1.3	acriflavin resistance periplasmic protein
VF1183	8.5	8.6	8.2	8.4	8.9	8.6	9.1	8.9	1.4	8.3	8.7	8.3	8.4	8.4	8.9	8.5	8.6	1.1	acriflavin resistance periplasmic protein
VF1184	8.5	8.3	8.5	8.4	8.7	8.5	8.9	8.7	1.2	8.3	8.4	8.3	8.3	8.3	8.4	8.3	8.3	1.0	acriflavin resistance plasma membrane protein
VF1185	7.0	6.7	6.4	6.7	6.6	6.4	6.8	6.6	-1.1	7.0	6.7	6.5	6.8	6.6	6.8	6.8	6.8	1.0	hypothetical protein
VF1186	9.4	9.3	9.2	9.3	9.0	9.3	9.1	9.1	-1.2	9.4	8.9	9.2	9.2	9.2	9.0	9.2	9.2	-1.0	cystathionine beta-lyase
VF1188	6.4	6.4	6.3	6.4	5.7	6.0	6.2	5.9	-1.3	6.1	6.4	6.2	6.2	5.9	6.1	5.9	6.0	-1.2	alcohol dehydrogenase II
VF1189	7.6	7.5	7.2	7.4	7.4	8.0	7.8	7.7	1.2	7.6	7.3	7.2	7.4	7.4	7.5	7.5	7.4	1.1	GTP cyclohydrolase II protein
VF1196	8.2	8.0	7.8	8.0	7.6	7.7	7.8	7.7	-1.2	8.1	7.7	7.7	7.9	7.7	7.6	8.0	7.8	-1.0	hypothetical protein
VF1198	8.6	8.7	8.5	8.6	8.8	8.8	8.9	8.8	1.1	8.6	8.8	8.6	8.7	8.7	8.9	8.7	8.8	1.1	putative competence-damage protein
VF1199	8.2	8.5	8.0	8.2	8.5	8.3	8.5	8.5	-1.2	8.1	8.								

VF1237	10.3	10.6	9.7	10.2	10.8	10.3	10.7	10.6	1.3	10.4	10.8	10.0	10.4	9.6	10.2	9.6	9.8	-1.5	integration host factor alpha subunit
VF1238	6.4	6.5	6.3	6.5	6.6	6.5	6.1	6.7	-1.2	6.4	6.3	6.3	6.4	6.7	6.7	6.9	6.7	1.3	succinylglutamate succinylase
VF1239	7.7	7.5	7.3	7.5	6.9	7.1	7.3	7.1	-1.3	7.4	7.1	7.4	7.3	7.4	7.3	7.6	7.4	1.1	oligoendopeptidase F
VF1240	8.4	7.8	8.2	8.1	7.9	7.6	8.0	7.8	-1.2	8.3	7.8	8.1	8.1	8.4	7.9	8.5	8.2	1.1	hypothetical protein
VF1241	8.8	8.5	8.6	8.6	8.4	8.5	8.6	8.5	-1.1	8.8	8.4	8.3	8.5	8.5	8.7	8.8	8.7	1.1	3-deoxy-7-phosphoheptulonase synthase
VF1242	7.6	7.3	7.2	7.4	7.3	7.4	7.4	7.4	-1.0	7.6	7.2	7.1	7.3	7.6	7.4	7.4	7.4	1.0	phosphoenolpyruvate synthase
VF1243	7.5	7.1	7.0	7.2	6.9	6.8	7.2	7.0	-1.2	7.3	6.9	7.0	7.0	7.0	6.8	7.1	7.0	-1.0	hypothetical protein
VF1244	8.3	8.2	8.2	8.2	8.0	8.1	8.2	8.1	-1.1	8.1	8.1	8.2	8.2	8.4	8.4	8.6	8.5	1.2	hypothetical protein
VF1245	7.3	7.3	7.2	7.3	6.9	7.1	7.0	7.0	-1.2	7.2	7.2	7.3	7.2	7.4	7.3	7.5	7.4	1.1	hypothetical protein
VF1247	6.6	6.6	6.0	6.4	6.0	6.1	6.4	6.2	-1.1	6.7	6.7	6.1	6.5	6.0	6.8	6.4	6.4	-1.1	hypothetical protein
VF1248_x	2.6	1.9	2.0	2.2	2.1	1.8	2.2	2.0	-1.1	2.2	2.3	2.0	2.2	1.9	2.1	1.7	1.9	-1.2	hypothetical protein
VF1248to1248	2.1	2.3	2.1	2.2	2.0	2.3	2.5	2.3	1.1	2.4	2.1	2.1	2.2	2.0	2.0	2.1	2.1	-1.1	hypothetical protein
VF1248to1248	2.2	2.2	1.8	2.0	1.7	1.9	2.1	1.9	-1.1	2.1	2.3	1.9	2.1	1.9	2.1	1.8	1.9	-1.1	hypothetical protein
VF1249	4.5	4.3	3.8	4.2	3.8	4.0	4.2	4.0	-1.2	4.3	3.7	3.9	4.0	3.6	3.6	3.5	3.6	-1.3	phosphoenolpyruvate phosphomutase
VF1250	4.7	4.4	3.9	4.3	4.0	4.1	4.8	4.3	-1.0	4.4	4.2	4.1	4.2	4.1	3.6	3.6	3.8	-1.4	hypothetical protein
VF1252	6.7	6.6	6.0	6.5	6.0	6.3	6.5	6.2	-1.2	6.5	6.5	6.2	6.4	6.0	6.1	5.9	6.0	-1.3	L-sulfolactate dehydrogenase
VF1253	3.7	3.7	3.6	3.7	2.8	3.3	3.8	3.2	-1.4	3.8	3.5	3.7	3.8	4.0	3.5	3.3	3.6	1.0	cystathionine beta-lyase
VF1254	3.5	3.2	3.1	3.3	3.5	3.1	3.3	3.3	1.0	3.6	3.5	3.3	3.4	3.3	3.2	3.2	3.2	1.2	Na(+)/H(+) antiporter NhaC
VF1256	6.9	6.5	6.7	6.7	6.4	6.8	6.8	6.7	-1.0	6.8	6.5	6.6	6.6	6.8	6.6	6.7	6.7	-1.0	3'-5'-cyclic-nucleotide phosphodiesterase
VF1257	6.4	6.3	5.5	6.0	5.5	5.6	6.2	5.8	-1.2	6.3	5.9	5.8	6.0	5.7	5.7	5.9	5.8	-1.2	hypothetical protein
VF1264	5.4	5.1	4.7	5.1	5.1	5.1	5.3	5.1	-1.1	5.1	4.9	4.8	5.0	5.1	5.0	5.2	5.1	1.1	chlorohydrolase/deaminase family protein
VF1265	4.4	3.8	3.1	3.7	3.5	3.6	4.1	3.8	1.1	4.0	3.3	3.5	3.6	3.5	3.9	3.3	3.5	-1.0	hypothetical protein
VF1266	3.8	3.4	3.2	3.4	3.1	3.0	3.4	3.2	-1.2	3.6	3.2	3.1	3.3	3.1	2.8	2.7	2.9	-1.3	Na(+)-driven multidrug efflux pump
VF1267	3.7	3.5	3.2	3.5	3.1	3.4	3.5	3.3	-1.1	3.4	3.4	3.5	3.5	3.5	3.7	3.1	3.4	-1.0	hypothetical protein
VF1268	4.2	3.8	3.6	3.9	3.7	3.1	4.0	3.6	-1.2	3.9	3.8	3.1	3.6	3.2	3.1	2.9	3.1	1.1	hypothetical protein
VF1269	6.1	5.7	5.9	5.9	5.6	5.3	5.8	5.6	-1.3	5.8	5.6	5.8	5.7	5.7	5.1	5.1	5.3	-1.3	DNA polymerase V subunit
VF1271	6.5	6.3	6.1	6.2	6.1	6.3	6.3	6.2	-1.4	6.5	6.3	6.2	6.3	6.3	6.3	6.3	6.3	-1.0	hypothetical membrane spanning protein
VF1272	9.0	8.4	8.2	8.5	7.8	7.7	8.1	7.9	-1.6	8.9	7.9	8.3	8.4	8.0	7.7	8.0	7.9	-1.4	elongation factor P
VF1275	7.9	7.7	7.6	7.7	7.6	7.3	7.7	7.5	-1.6	7.9	7.5	7.6	7.7	7.4	7.1	7.2	7.2	-1.4	paraquat-inducible protein B
VF1276	6.6	6.2	6.1	6.3	6.5	5.9	6.5	6.3	-1.0	6.3	6.4	6.1	6.3	5.9	5.8	5.3	5.7	-1.5	paraquat-inducible protein A
VF1277	7.4	7.4	7.3	7.4	7.0	7.2	7.3	7.2	-1.1	7.3	7.3	7.3	7.3	7.5	7.5	7.6	7.6	1.2	transporter
VF1278	9.2	9.3	9.6	9.7	9.4	9.4	9.5	9.4	-1.1	9.4	9.4	9.4	9.4	9.1	9.1	9.4	9.4	-1.1	GtaF domain-containing proteins
VF1279	10.6	10.3	10.4	10.4	10.2	10.2	10.3	10.2	-1.1	10.5	10.1	10.4	10.3	10.2	10.2	10.3	10.3	-1.1	putative solute/DNA competence effector
VF1280	10.0	9.8	9.7	9.8	9.2	9.4	9.4	9.4	-1.4	10.0	9.5	9.6	9.7	9.3	9.2	9.4	9.3	-1.3	carboxy-terminal processing protease precursor
VF1282	9.2	9.2	9.3	9.2	9.2	9.2	9.3	9.2	1.0	9.1	9.1	9.1	9.1	9.2	9.1	9.3	9.2	1.1	membrane alanine aminopeptidase
VF1283	6.3	5.7	5.4	5.8	5.7	5.4	6.1	5.7	-1.1	5.9	5.8	5.4	5.7	5.1	5.9	5.4	5.5	-1.2	hypothetical protein
VF1284	8.7	8.9	8.9	8.8	9.2	8.8	9.0	9.2	-1.3	9.4	8.9	8.9	8.8	8.5	8.7	8.5	8.6	-1.2	NAD-specific glutamate dehydrogenase
VF1285	8.4	7.9	7.7	8.0	7.3	7.5	7.3	7.3	-1.6	8.4	7.5	7.8	7.9	8.0	7.7	8.1	7.9	-1.0	dihydroorotate dehydrogenase
VF1286	5.5	5.1	4.3	5.0	4.7	4.3	5.3	4.8	-1.2	5.4	4.8	4.6	4.9	4.5	4.5	4.5	4.5	-1.4	hypothetical protein
VF1286to1287	2.5	2.6	2.5	2.6	2.5	2.4	2.4	2.4	-1.1	2.7	2.7	2.3	2.5	2.6	2.9	2.6	2.7	1.1	hypothetical protein
VF1286to1287	2.6	2.5	2.4	2.5	2.5	2.5	2.5	2.5	-1.0	2.6	2.6	2.4	2.5	2.6	2.5	2.3	2.5	-1.0	hypothetical protein
VF1288	8.4	8.3	8.3	8.3	7.8	8.1	7.9	7.9	-1.4	8.3	8.1	8.3	8.2	8.3	8.0	8.3	8.2	-1.3	ABC transporter ATP-binding protein Uup
VF1290	9.2	9.4	9.4	9.3	8.8	9.3	9.0	9.0	-1.2	9.1	9.3	9.5	9.3	9.5	9.2	9.4	9.4	1.1	hypothetical protein
VF1291	11.1	11.7	10.8	11.2	11.0	10.4	10.7	10.7	-1.4	11.0	11.8	11.1	11.3	10.6	11.6	10.9	11.0	-1.2	ribosome modulation factor
VF1293	8.3	8.2	8.3	8.2	7.7	8.0	7.8	7.7	-1.3	8.2	7.9	8.2	8.1	8.3	8.0	8.3	8.2	1.0	ATP-dependent protease La
VF1294	8.1	8.5	8.0	8.2	7.5	7.7	7.9	7.8	-1.4	8.2	8.7	8.1	8.3	8.0	8.7	8.3	8.3	1.0	hypothetical protein
VF1295	6.0	5.7	5.8	5.8	5.5	5.9	6.0	5.9	-1.0	5.9	5.7	5.9	5.7	5.9	5.9	6.0	5.9	-1.0	hypothetical protein
VF1295to1296	2.0	2.0	2.0	2.0	2.0	1.9	2.0	2.0	-1.0	2.1	2.0	1.9	2.0	1.8	2.0	2.0	1.9	-1.0	hypothetical protein
VF1295to1296	2.7	3.0	2.4	2.7	2.7	2.7	2.9	2.7	-1.0	2.5	3.4	2.3	2.7	2.2	3.1	2.4	2.6	-1.1	hypothetical protein
VF1296	6.2	5.8	5.6	5.9	5.3	5.7	5.8	5.6	-1.2	5.9	5.5	5.5	5.6	5.3	5.8	5.3	5.1	-1.4	sensor protein LuxQ
VF1297	6.2	5.9	5.7	5.9	5.6	5.7	6.0	5.8	-1.1	6.0	5.8	5.5	5.8	5.5	5.9	5.7	5.7	-1.1	hypothetical protein
VF1298	7.0	6.7	6.5	6.7	6.8	6.7	7.0	6.7	-1.0	7.0	6.7	6.4	6.7	6.4	6.4	6.5	6.6	-1.5	hypothetical protein
VF1299	8.5	8.6	8.8	8.7	7.8	8.6	8.2	8.2	-1.4	8.6	8.3	8.5	8.5	8.9	8.7	8.9	8.8	1.3	cytochrome c oxidase polypeptide I
VF1300	8.0	8.0	8.3	8.1	7.2	8.0	7.9	7.9	-1.3	7.9	7.7	7.9	7.8	8.2	8.0	8.3	8.1	1.2	cytochrome c oxidase, monoheme subunit, membrane-bound
VF1301	8.3	8.1	8.4	8.2	7.5	8.2	8.1	7.9	-1.3	8.2	8.0	8.2	8.1	8.3	8.2	8.5	8.3	1.2	hypothetical protein
VF1302	7.8	7.9	7.9	7.9	7.3	7.8	7.5	7.6	-1.2	7.6	7.6	7.6	7.6	7.8	7.8	7.7	7.8	1.1	hypothetical protein
VF1303	6.9	6.8	6.4	6.7	5.8	6.5	6.2	6.2	-1.5	6.7	6.6	6.6	6.6	6.6	6.8	6.6	6.7	1.0	hypothetical protein
VF1304	5.4	4.8	4.4	4.9	3.9	4.2	4.4	4.2	-1.6	5.2	4.4	4.5	4.7	3.8	4.4	3.7	4.0	-1.7	copper-exporting ATPase
VF1305	5.0	4.2	4.2	4.5	3.7	3.8	4.1	3.9	-1.5	4.8	4.0	4.0	4.3	3.5	3.8	3.6	3.6	-1.6	copper-exporting ATPase
VF1306	5.6	4.8	4.4	4.9	4.4	4.5	5.0	4.7	-1.2	5.2	4.8	4.5	4.8	4.4	4.3	4.3	4.3	-1.4	nitrogen fixation protein FixS
VF1307	5.4	4.6	4.7	4.9	4.5	4.5	4.9	4.6	-1.2	5.1	4.7	4.5	4.8	4.4	4.4	4.5	4.4	-1.3	integral membrane protein
VF1308	8.5	8.2	8.4	8.4	8.0	8.4	8.3	8.2	-1.1	8.4	8.3	8.1	8.3	8.5	8.7	8.7	8.7	1.3	transcriptional regulator
VF1310	9.5	9.8	9.6	9.6	10.2	9.3	10.4	9.9	1.3	9.4	10.2	9.7	9.8	9.3	10.1	9.3	9.6	-1.2	universal stress protein family
VF1320	7.2	7.5	7.7	7.5	6.6	7.0	7.0	6.8	-1.6	7.0	8.0	7.3	7.4	6.8	6.8	6.9	6.8	-1.5	NAD-dependent deacetylase
VF1321	6.2	5.4	5.2	5.6	5.3	4.9	5.7	5.3	-1.3	5.7	4.9	5.1	5.2	5.2	5.3	5.3	5.3	1.0	transcriptional regulators, LysR family
VF1322	4.5	4.5	4.2	4.4	4.3	4.1	4.5	4.3	-1.1	4.5	4.1	4.3	4.3	4.0	3.9	3.9	3.9	-1.3	nucleoside permease NupC
VF1325	8.1	8.3	8.1	8.1	8.3	7.9	8.4	8.2	1.0	7.9	8.5	8.0	8.1	8.4	7.8	7.5	7.6	-1.4	putative acetyltransferase in HXT11-HXT8 intergenic region
VF1331	6.6	6.2	6.0	6.2	5.5	5.5	6.0	5.7	-1.5	6.4	6.1	6.1	6.2	5.6	5.9	6.2	5.9	-1.2	hypothetical protein
VF1332	5.1	4.6	4.6	4.8	4.1	4.3	4.5	4.3	-1.4	4.6	4.3	4.7	4.6	4.3	4.2	4.2	4.2	-1.2	Na(+)-driven multidrug efflux pump
VF1339	4.9	4.2	3.8	4.3	4.0	3.5	4.3	4.0	-1.3	5.0	4.0	4.3	4.4	4.1	3.8	3.9	3.9	-1.4	hypothetical protein
VF1340	5.0	4.1	3.7	4.3	4.0	3.8	4.5	4.1	-1.1	4.7	3.9	3.4	4.0	3.8	3.9	4.1	3.9	-1.1	hypothetical protein
VF1341	6.4	6.1	5.8	6.1	5.3	5.5	6.0	5.6	-1.5	6.3	6.1	5.8	6.1	5.7	6.0	5.7	5.8	-1.2	cellulose phosphotransferase system CelC

VF1379	7.8	7.6	7.5	7.6	7.0	7.2	7.4	7.2	-1.3	7.6	7.5	7.4	7.5	7.2	7.2	7.3	7.3	-1.2	hypothetical protein
VF1381	7.6	7.6	7.6	7.6	8.5	8.5	8.4	8.1	-1.4	7.6	7.5	7.4	7.5	7.2	7.2	6.9	6.7	-1.6	hypothetical protein
VF1382	8.4	8.8	8.5	8.6	9.6	8.7	9.7	9.3	1.7	8.3	9.2	8.6	8.7	8.2	8.8	8.2	8.4	-1.3	ribosomal-protein-alanine acetyltransferase
VF1385	8.7	9.0	8.7	8.8	9.6	8.9	9.8	9.4	1.5	8.5	9.3	8.8	8.9	8.7	8.8	8.6	8.7	-1.1	hypothetical protein
VF1386	8.7	8.5	8.7	8.6	8.1	8.4	8.3	8.3	-1.3	8.5	8.4	8.6	8.5	8.5	8.3	8.7	8.5	1.0	acetyltransferase, GNAT family
VF1387	8.5	8.4	8.4	8.5	8.1	8.4	8.3	8.3	-1.2	8.4	8.4	8.4	8.4	8.4	8.3	8.6	8.4	1.0	3-mercaptopyruvate sulfurtransferase
VF1388	7.8	7.4	7.5	7.6	7.1	7.4	7.5	7.3	-1.2	7.6	7.2	7.2	7.4	7.0	7.0	7.3	7.1	-1.2	7-TDP-glucose 4,6-dehydratase
VF1389	8.0	7.8	7.9	7.9	7.1	7.7	7.6	7.5	-1.3	7.9	7.6	7.7	7.7	7.5	7.4	7.7	7.5	-1.2	ribosomal-protein-alanine acetyltransferase
VF1391	4.7	4.0	3.5	4.1	4.0	3.9	4.6	4.2	1.1	4.2	4.1	3.7	4.0	3.7	3.9	3.9	3.9	-1.1	hypothetical protein
VF1392to1393	6.0	5.3	5.0	5.4	4.9	5.1	5.6	5.2	-1.2	5.7	5.2	5.1	5.3	5.2	4.6	5.0	4.9	-1.3	hypothetical protein
VF1392to1393	3.1	2.6	2.5	2.8	2.8	2.8	3.1	2.9	-1.1	3.2	2.9	2.6	2.9	2.9	3.3	2.8	3.0	1.1	hypothetical protein
VF1394	4.9	4.4	5.0	4.8	5.2	4.7	5.2	5.0	1.2	5.0	3.7	4.6	4.4	5.0	3.6	5.1	4.5	1.1	glycine betaine transporter
VF1395	7.9	7.8	7.5	7.8	7.6	7.6	8.0	7.7	-1.0	7.8	7.8	7.8	7.8	7.6	8.0	7.6	7.7	-1.1	hypothetical protein
VF1396	6.8	6.4	6.1	6.4	6.5	6.2	6.7	6.4	-1.0	6.5	6.5	6.3	6.4	6.3	6.5	6.4	6.4	-1.0	transcriptional regulator
VF1397	6.3	6.2	5.9	6.1	5.6	5.5	5.8	5.6	-1.4	6.0	5.8	5.7	5.9	5.2	5.4	5.6	5.4	-1.4	sensor protein PhoQ
VF1398	5.6	5.4	5.5	5.5	5.2	5.0	5.7	5.3	-1.2	5.5	5.3	5.5	5.5	5.3	5.2	5.4	5.3	-1.1	hypothetical protein
VF1399	5.9	5.4	5.8	5.7	5.8	5.4	6.1	5.8	1.0	5.7	5.7	5.7	5.7	5.9	5.3	5.6	5.6	-1.1	glycosyltransferase involved in cell wall biogenesis
VF1400	6.1	6.3	5.8	6.1	5.6	6.2	5.8	5.9	-1.1	6.0	6.3	6.1	6.1	6.2	6.3	6.2	6.2	1.1	C4-dicarboxylate transport sensor protein DcbB
VF1401	6.9	7.0	6.9	6.9	6.6	7.0	7.0	6.9	-1.0	6.7	7.0	6.7	6.8	6.9	7.3	7.2	7.2	1.3	C4-dicarboxylate transport transcriptional regulatory protein DctD
VF1402	6.8	6.7	6.8	6.8	6.6	7.2	7.1	7.0	1.2	6.6	6.7	6.8	6.7	6.3	6.3	6.3	6.3	-1.3	molybdate-binding protein
VF1405	7.2	6.7	6.7	6.9	6.6	6.3	6.9	6.6	-1.2	6.8	6.5	6.6	6.6	6.2	6.0	6.4	6.2	-1.3	molybdopterin-guanine dinucleotide biosynthesis protein A
VF1406	7.5	7.3	7.3	7.4	7.0	6.9	7.2	7.0	-1.3	7.2	7.1	7.2	7.2	6.8	6.6	6.9	6.8	-1.3	molybdopterin biosynthesis MoeA protein
VF1407	6.4	5.6	4.7	5.6	5.2	4.9	5.7	5.2	-1.3	6.1	5.4	5.2	5.6	4.8	5.5	4.9	5.0	-1.5	hypothetical protein
VF1408	7.2	6.1	6.2	6.5	6.0	5.9	6.4	6.1	-1.3	7.1	5.8	6.0	6.3	5.7	5.5	5.8	5.7	-1.6	glucokinase
VF1409to1411	3.1	3.2	2.8	3.0	3.6	3.0	3.9	3.5	1.3	3.3	3.1	2.9	3.1	2.8	3.0	2.8	2.9	-1.2	hypothetical cytosolic protein
VF1409to1411	7.3	7.1	7.1	7.1	6.6	6.7	6.7	6.6	-1.4	7.1	6.6	7.0	6.9	6.7	6.5	6.9	6.7	-1.2	hypothetical cytosolic protein
VF1412	7.5	7.3	7.6	7.6	7.1	7.7	7.9	7.6	-1.1	7.7	7.9	7.8	7.8	7.7	7.6	8.0	7.8	-1.0	hypothetical protein
VF1414	8.1	7.7	7.9	7.9	7.9	8.0	8.3	8.1	-1.1	8.0	7.8	7.7	7.8	7.9	7.9	8.1	8.0	-1.1	riboflavin synthase subunit alpha
VF1416	5.4	4.9	4.3	4.8	4.6	4.5	5.1	4.7	-1.1	5.2	4.9	4.8	5.0	4.4	5.1	4.9	4.8	-1.1	tetratricopeptide repeat family protein
VF1417	5.5	4.9	4.4	4.9	4.6	4.7	4.9	4.7	-1.2	5.5	4.8	4.6	5.0	4.4	4.9	5.0	4.8	-1.2	arylsulfatase regulator (Fe-S oxidoreductase)
VF1418	4.8	4.4	4.1	4.4	4.7	4.6	4.9	4.7	-1.2	4.6	4.9	4.1	4.5	4.1	4.5	4.5	4.3	-1.2	hypothetical protein
VF1420	5.9	5.6	5.4	5.7	5.5	5.5	5.8	5.4	-1.2	5.3	5.3	5.2	5.3	5.4	5.4	5.3	5.4	-1.3	sulfatase family protein
VF1429	3.6	3.3	2.8	3.2	3.0	2.9	3.4	3.1	-1.1	3.2	3.3	3.2	3.2	2.9	3.1	2.7	2.9	-1.2	hypothetical protein
VF1430	6.2	6.2	6.1	6.2	5.9	6.0	6.1	6.0	-1.1	6.2	6.1	6.2	6.2	6.1	6.0	6.0	6.0	-1.1	sulfatase family protein
VF1431	6.9	6.4	6.0	6.4	5.7	5.6	6.4	5.9	-1.4	6.9	6.2	6.4	6.5	6.2	6.2	6.3	6.2	-1.2	hypothetical protein
VF1432	7.3	7.1	6.4	6.9	7.0	6.6	7.3	7.0	-1.0	7.0	7.0	6.7	6.9	6.7	6.6	6.5	6.6	-1.2	hypothetical protein
VF1433	6.9	6.8	6.4	6.7	6.5	6.5	6.8	6.5	-1.2	6.9	6.7	6.4	6.6	6.5	6.2	6.1	6.2	-1.1	hypothetical protein
VF1434	5.6	4.9	4.3	4.9	5.0	4.6	5.3	5.0	1.1	5.3	5.1	4.7	5.0	4.5	4.6	4.6	4.6	-1.4	putative periplasmic protein
VF1435	7.1	6.9	6.8	6.9	6.8	6.9	7.1	6.9	1.0	6.7	6.8	6.7	6.8	6.7	6.8	6.7	6.8	-1.0	hypothetical protein
VF1436	8.2	7.9	7.9	8.0	8.0	8.0	8.2	8.0	-1.0	8.0	7.9	7.8	7.9	8.0	7.9	8.1	8.0	1.1	hypothetical protein
VF1437	8.1	7.8	7.6	7.8	7.2	7.2	7.5	7.3	-1.4	8.0	7.6	7.6	7.7	7.4	7.1	7.2	7.2	-1.4	hypothetical protein
VF1439	7.6	7.3	7.6	7.5	7.1	7.2	7.1	7.1	-1.3	7.6	7.0	7.3	7.3	7.1	6.7	7.0	6.9	-1.3	putative ATP-dependent RNA helicase RhlE
VF1440	5.8	5.8	5.6	5.7	5.7	5.7	5.8	5.7	-1.0	5.6	5.8	5.6	5.7	5.6	5.6	5.8	5.7	-1.0	hypothetical protein
VF1441	4.5	3.9	3.6	4.0	3.6	3.8	4.1	3.9	-1.0	4.1	3.8	3.7	3.9	3.3	3.4	3.1	3.3	-1.5	hypothetical protein
VF1442	6.5	6.7	6.0	6.2	7.0	6.2	7.0	6.7	1.3	6.4	6.9	6.3	6.5	6.0	6.2	5.9	6.0	-1.4	hypothetical protein
VF1443	5.3	5.6	4.8	5.4	5.4	5.5	5.6	5.5	1.2	5.3	5.6	5.1	5.3	5.6	6.0	5.9	5.8	1.4	virulence gene repressor RsaL
VF1444	2.5	2.4	2.2	2.4	2.3	2.9	2.5	2.7	-1.3	2.4	2.2	2.3	2.5	2.2	2.6	2.4	2.4	-1.0	high affinity ribose transport protein RbsD
VF1445	3.2	3.1	3.1	3.1	3.0	2.9	3.1	3.0	-1.1	2.8	3.2	3.0	3.0	3.0	3.2	3.1	3.1	1.1	ribose transport ATP-binding protein RbsA
VF1446	4.5	4.0	3.9	4.1	4.1	4.5	4.5	4.4	-1.2	4.4	4.1	3.9	4.1	4.0	4.1	4.2	4.1	1.0	ribose high-affinity ABC transporter permease component
VF1447	5.4	5.2	5.0	5.2	4.6	4.9	5.0	4.8	-1.0	5.1	5.1	5.1	5.1	4.8	4.9	4.6	4.8	-1.2	D-ribose-binding protein
VF1448	6.2	6.2	6.1	6.2	5.8	5.8	6.1	5.9	-1.3	6.1	6.1	6.1	6.1	6.1	6.0	6.1	6.1	-1.0	ribokinase
VF1449	5.9	5.6	5.4	5.7	6.1	6.5	6.4	6.6	-1.1	5.8	5.5	5.4	5.6	5.5	5.7	5.5	5.5	-1.0	transcriptional regulator, LacI family
VF1450	5.9	5.8	5.7	5.8	5.6	5.7	5.8	5.7	-1.1	5.7	5.5	5.8	5.7	5.8	5.8	5.6	5.7	1.0	DNA ligase
VF1452	7.4	7.5	7.4	7.4	7.9	7.1	7.9	7.6	-1.1	7.3	7.4	7.3	7.3	6.9	6.8	6.8	6.8	-1.4	Na(+)-driven multidrug efflux pump
VF1453	7.9	7.9	7.7	7.8	8.0	7.9	8.1	7.9	1.1	7.9	8.0	8.0	8.0	7.9	7.9	7.9	7.9	-1.0	hypothetical protein
VF1453to1454	3.8	3.8	3.3	3.6	3.6	3.9	3.5	3.6	1.0	3.6	3.9	3.7	3.7	3.4	4.2	3.7	3.8	1.0	hypothetical protein
VF1454	6.7	7.0	7.4	7.0	6.0	6.8	6.1	6.3	-1.7	6.6	7.1	7.1	6.9	6.8	7.1	7.0	6.9	-1.0	Na(+)-linked D-alanine glycine permease
VF1455	7.1	7.1	6.8	7.0	6.8	6.8	6.8	6.8	-1.2	6.8	6.9	6.7	6.8	6.7	6.9	7.0	6.9	-1.0	mechanosensitive ion channel
VF1456	8.4	8.2	8.2	8.3	7.8	7.8	8.1	7.9	-1.0	8.3	7.9	8.2	8.1	8.0	7.6	8.1	7.9	-1.2	homoserine/homoserine lactone efflux protein
VF1456to1457	3.1	2.4	2.0	2.5	2.2	2.1	2.6	2.3	-1.1	2.8	2.2	2.2	2.4	2.0	2.2	2.0	2.1	-1.3	homoserine/homoserine lactone efflux protein
VF1456to1457	2.6	2.4	2.2	2.4	2.1	2.2	2.3	2.2	-1.1	2.7	2.5	2.4	2.5	2.3	2.6	2.5	2.5	-1.1	homoserine/homoserine lactone efflux protein
VF1458	3.4	3.0	2.8	3.1	3.0	2.9	3.2	3.0	-1.1	3.0	2.7	2.6	2.8	3.0	2.5	2.9	2.8	1.0	threonine synthase
VF1459	3.0	2.8	2.3	2.7	2.6	2.9	3.2	2.9	1.1	3.0	2.6	2.7	2.8	2.4	2.8	2.6	2.6	-1.0	translation initiation inhibitor
VF1460	5.9	5.5	5.2	5.5	5.2	5.3	5.8	5.4	-1.1	5.6	5.2	5.2	5.4	5.5	5.3	5.3	5.4	1.0	transcriptional regulators, LysR family
VF1461	7.8	8.0	7.8	7.9	7.1	7.7	7.4	7.4	-1.4	7.8	8.0	7.8	7.9	7.9	8.1	7.9	8.0	1.1	hypothetical protein
VF1463	7.1	6.9	6.6	6.9	6.3	6.5	6.5	6.4	-1.4	7.1	7.0	6.6	6.9	6.9	6.7	6.7	6.6	-1.2	hypothetical protein
VF1464	3.4	3.0	2.9	3.1	3.1	2.9	2.9	2.9	-1.1	3.7	3.1	2.9	3.2	2.8	2.9	3.1	2.9	-1.2	superfamily I DNA and RNA helicases
VF1465	3.9	3.6	2.9	3.5	3.3	3.1	3.8	3.4	-1.0	3.6	3.6	3.3	3.5	3.1	3.0	2.9	3.0	-1.4	superfamily I DNA and RNA helicases
VF1466	6.2	5.8	6.1	6.0	5.7	6.5	6.0	6.1	-1.0	5.5	5.9	5.8	5.7	5.6	6.0	5.7	5.8	1.0	small heat shock protein
VF1467	6.0	6.1	5.9	6.0	5.6	6.5	6.1	6.1	-1.0	5.8	5.9	5.9	5.9	6.1	6.1	5.8	6.0	1.1	molecular chaperone DnaK
VF1468	7.1	6.7	6.5	6.8	6.2	6.2	6.5	6.3	-1.4	7.0	6.4	6.6	6.7	6.4	6.0	6.3	6.2	-1.4	hypothetical protein
VF1469	4.5	5.2	4.4	5.1	5.3	5.6	6.1	5.7	1.5	5.5	5.2	4.6	5.1	4.7	5.2	4.7	4.9	-1.2	transcriptional regulator, MerR family
VF1470	6.1	5																	



VF1504	3.3	2.7	2.8	2.9	2.7	3.1	3.1	3.0	1.0	2.8	2.9	3.0	2.9	2.5	2.9	2.7	2.7	-1.1	methyl-accepting chemotaxis protein
VF1506-1	9.9	10.0	9.9	9.8	10.1	10.0	10.2	10.1	-1.2	9.8	10.1	9.8	9.9	9.5	9.7	9.5	9.6	-1.2	iron-regulated protein FrpC
VF1507	7.9	7.9	7.1	7.6	7.4	7.2	7.4	7.4	-1.2	7.9	7.9	7.3	7.7	7.3	7.8	7.3	7.5	-1.2	hypothetical protein
VF1508	6.0	5.8	5.6	5.8	5.6	5.6	6.1	5.8	-1.0	5.7	5.8	5.6	5.7	5.4	5.5	5.4	5.4	-1.2	anaerobic C4-dicarboxylate transporter
VF1509	5.0	4.6	4.3	4.6	3.8	4.3	4.8	4.3	-1.3	4.4	4.6	4.4	4.5	4.3	4.1	4.4	4.3	-1.2	isoaspartyl dipeptidase
VF1510	4.0	3.0	3.2	3.4	3.1	2.9	3.7	3.2	-1.1	3.4	3.1	3.1	3.2	2.9	2.8	3.0	2.9	-1.2	transcriptional regulator
VF1511	6.0	5.8	5.4	5.8	5.3	5.4	5.8	5.4	-1.2	5.8	5.6	5.4	5.6	5.4	5.6	5.4	5.5	-1.1	Z'-3'-cyclic-nucleotide 2'-phosphodiesterase
VF1514	6.5	6.2	5.9	6.2	5.9	6.0	6.2	6.0	-1.1	6.1	6.2	6.0	6.1	5.9	5.8	6.1	5.9	-1.1	Exonuclease KapD
VF1515	6.5	6.4	6.1	6.3	6.2	6.0	6.7	6.3	-1.0	6.3	6.5	6.0	6.3	6.0	6.1	6.0	6.1	-1.1	hypothetical protein
VF1516	8.2	7.5	7.6	7.8	7.8	7.5	8.0	7.8	-1.0	7.9	7.4	7.6	7.6	7.3	7.0	7.5	7.3	-1.3	hypothetical protein
VF1517	8.3	8.0	8.1	8.1	7.9	8.1	8.1	8.0	-1.1	8.1	7.8	8.0	8.0	8.0	7.4	7.8	7.7	-1.2	heat shock protein 70
VF1518to1515	7.5	7.7	7.7	7.6	7.6	7.7	7.7	7.7	1.0	7.7	7.7	7.7	7.7	7.4	7.7	7.5	7.6	1.0	heat shock protein 70
VF1518to1515	3.3	2.8	2.8	3.0	2.5	2.7	2.7	2.6	-1.2	2.8	2.7	2.8	2.8	2.6	2.5	2.5	2.5	-1.2	heat shock protein 70
VF1519	8.4	8.1	7.8	8.1	8.0	8.1	8.5	8.2	-1.1	8.3	8.3	7.9	8.2	8.1	8.2	7.9	8.1	-1.1	hypothetical protein
VF1520	8.3	7.8	7.9	8.0	7.9	8.3	8.5	8.2	-1.2	8.1	7.8	7.8	7.9	7.7	7.5	7.7	7.6	-1.2	hypothetical protein
VF1522	8.5	8.7	8.8	8.7	8.5	9.2	8.5	8.7	1.1	8.4	9.1	8.7	8.7	9.1	9.5	8.7	9.1	1.3	lead, cadmium, zinc and mercury transporting ATPase
VF1523	10.0	10.2	9.5	9.9	11.3	10.2	11.3	10.9	2.0	10.0	10.8	9.8	10.2	9.0	10.2	8.9	9.4	-1.8	CDS domain containing protein
VF1524	7.7	7.8	7.6	7.7	7.5	7.7	7.8	7.7	-1.0	7.6	7.9	7.8	7.7	8.0	7.8	7.9	7.9	1.1	hypothetical protein
VF1525	7.7	7.8	7.8	7.8	7.5	8.0	7.7	7.7	-1.1	7.7	7.6	7.7	7.6	7.9	7.9	8.0	7.9	1.2	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VF1526	7.0	6.3	6.2	6.5	6.2	6.9	6.9	6.7	-1.1	7.1	6.2	6.2	6.5	6.0	5.4	5.8	5.7	-1.7	hypothetical protein
VF1527	5.6	5.2	4.9	5.2	5.2	4.8	5.5	5.1	-1.1	5.4	5.3	4.9	5.2	4.1	4.7	4.8	4.5	-1.5	L-asparaginase
VF1530	7.1	6.6	6.6	6.8	6.6	7.0	7.0	6.9	1.1	7.0	6.5	6.5	6.7	6.9	6.8	6.9	6.9	1.2	transcriptional regulator, GntR family
VF1532	7.8	8.5	8.1	8.1	8.0	8.8	8.2	8.3	1.2	7.6	9.1	7.8	8.2	7.3	8.0	7.4	7.6	-1.5	general L-amino acid-binding protein
VF1533	4.8	4.8	4.7	4.8	4.4	5.2	4.9	4.8	1.0	4.4	5.0	4.5	4.6	4.6	4.8	4.1	4.5	-1.1	general L-amino acid transport system permease protein AapQ
VF1534	5.2	5.3	5.1	5.2	4.9	5.4	5.2	5.2	-1.0	4.7	5.7	4.6	5.0	4.6	5.1	4.9	4.8	-1.1	general L-amino acid transport system permease protein AapM
VF1536	9.9	9.5	9.7	9.7	10.0	9.6	10.2	9.9	1.2	9.9	9.6	9.6	9.7	9.6	9.6	9.7	9.6	-1.0	SecY stabilizing membrane protein
VF1537	6.1	5.7	5.7	6.4	6.3	6.0	6.3	6.1	-1.3	6.1	6.0	6.1	6.3	6.0	6.0	6.1	6.0	-1.1	hypothetical protein
VF1540	8.4	8.1	7.8	8.1	7.9	8.1	8.3	8.1	1.0	8.4	7.9	7.9	8.1	8.0	8.0	8.1	8.0	-1.0	suppressor/enhancer of lin-12
VF1543	5.6	5.5	5.1	5.4	5.3	5.3	5.5	5.4	1.0	5.5	5.4	5.3	5.4	5.2	5.5	5.2	5.3	-1.1	long-chain fatty acid transport protein precursor
VF1544	6.9	6.7	6.9	6.8	6.7	7.0	7.0	6.9	-1.1	6.6	6.4	6.9	6.6	7.0	6.0	6.7	6.6	-1.1	phosphatidylglycerophosphatase B homolog
VF1545	5.0	4.6	4.8	4.8	4.1	4.1	4.7	4.3	-1.4	4.8	4.6	4.8	4.7	4.3	4.6	4.3	4.4	-1.3	transcriptional regulator
VF1546	3.2	3.0	3.0	3.0	3.2	3.0	3.2	3.0	1.2	3.2	3.0	3.2	3.0	3.1	3.1	3.0	3.1	-1.1	anaerobic C4-dicarboxylate transporter
VF1547	3.0	3.0	2.9	3.0	2.7	2.7	3.0	2.8	-1.1	3.1	3.0	2.5	2.9	2.6	3.3	2.7	2.9	-1.0	aspartate racemase
VF1548	6.3	5.9	5.6	5.9	5.5	5.7	6.0	5.7	-1.1	6.0	5.7	5.7	5.8	5.3	5.3	5.6	5.4	-1.3	cytochrome c-type biogenesis protein CcmH
VF1549	6.8	6.7	6.5	6.7	6.0	6.4	6.7	6.4	-1.3	6.6	6.7	6.4	6.6	6.3	6.5	6.3	6.4	-1.1	thiol:disulfide interchange protein TlpA
VF1550	5.5	5.4	5.2	5.4	5.0	5.0	5.4	5.2	-1.4	5.3	5.5	5.4	5.4	5.2	5.2	5.1	5.2	-1.2	heme chaparonone-apocytochrome heme-lyase
VF1551	4.7	4.2	4.3	4.4	4.1	4.1	4.7	4.3	-1.1	4.3	4.0	4.0	4.1	3.9	3.7	4.0	4.1	-1.1	NrD protein
VF1552	6.0	5.9	6.1	6.0	5.6	5.9	6.0	5.8	-1.1	5.8	5.9	6.0	5.9	5.8	6.0	6.0	5.9	-1.0	thiosulfate reductase electron transport subunit
VF1553	6.0	5.7	5.9	5.9	5.4	5.8	6.1	5.8	-1.1	5.7	5.7	5.6	5.6	5.8	5.8	5.7	5.8	1.1	cytochrome c-type protein NrB
VF1554	4.8	5.1	4.6	4.8	5.3	4.9	5.3	5.2	-1.4	4.5	5.2	4.6	4.7	4.7	5.1	5.2	5.0	-1.2	cytochrome c552
VF1556	7.0	6.2	6.2	6.5	6.8	7.8	7.3	7.3	1.8	7.1	5.8	6.2	6.4	7.0	6.0	7.0	6.7	1.2	phospholipase A1
VF1557	6.1	5.6	5.3	5.7	5.5	5.3	5.7	5.5	-1.1	6.0	5.4	5.6	5.6	5.2	5.0	5.2	5.1	-1.4	ATP-dependent helicase HrpA
VF1559	5.1	4.5	4.4	4.7	4.5	4.5	5.1	4.7	-1.0	4.7	4.1	4.4	4.4	4.5	4.0	4.3	4.3	-1.1	hypothetical protein
VF1560	6.3	5.7	5.2	5.8	5.5	5.4	6.0	5.6	-1.1	6.1	5.5	5.5	5.7	5.3	5.6	5.4	5.4	-1.4	SanA protein
VF1561	7.5	7.2	7.1	7.3	6.8	7.1	7.3	7.1	-1.1	7.5	7.2	6.9	7.2	7.1	7.1	7.1	7.1	-1.5	sensory box/GGDEF family protein
VF1562	6.0	5.8	5.6	5.8	6.5	5.4	6.6	6.2	1.3	5.8	6.0	5.5	5.8	5.2	5.2	5.0	5.2	-1.0	hypothetical protein
VF1563	5.4	4.9	4.9	4.9	4.9	4.7	5.2	4.9	-1.0	5.2	4.9	4.5	4.8	5.0	4.9	4.8	4.9	-1.4	hypothetical protein
VF1567	5.4	5.3	4.9	5.2	5.0	5.1	5.5	5.2	-1.0	5.2	5.6	5.3	5.4	5.2	5.1	5.2	5.2	-1.2	hypothetical protein
VF1570	8.0	7.6	7.6	7.8	8.3	7.6	8.5	8.1	1.3	8.1	7.9	7.5	7.8	7.6	7.7	7.7	7.7	-1.1	TorCAD operon transcriptional regulatory protein TorR
VF1571	7.7	7.4	7.3	7.5	7.2	7.2	7.5	7.3	-1.4	7.7	7.2	7.4	7.4	7.3	7.2	7.4	7.3	-1.1	chaperone protein TorD
VF1574	7.3	7.2	7.4	7.3	8.0	7.4	8.2	7.8	1.5	7.3	7.6	7.3	7.4	6.9	7.0	6.8	6.9	-1.4	hypothetical protein
VF1575	6.1	5.7	5.7	5.7	5.4	5.3	5.6	5.4	-1.2	6.0	5.8	5.4	5.7	5.6	6.0	5.5	5.6	-1.1	O6-methylguanine-DNA methyltransferase
VF1577	7.6	7.4	7.3	7.4	7.5	7.4	7.7	7.5	-1.1	7.6	7.4	7.4	7.5	7.5	7.5	7.5	7.5	-1.0	acyl-CoA thioesterase II
VF1578	4.4	3.7	3.2	3.8	4.3	3.2	4.7	4.1	1.2	4.2	3.6	3.1	3.6	3.2	2.9	3.1	3.1	-1.5	transcriptional regulator, AsnC family
VF1579	4.3	4.1	4.1	4.2	4.6	4.6	4.5	4.6	-1.3	4.2	4.2	3.9	4.1	4.3	3.9	4.1	4.1	-1.1	cysteine synthase
VF1580	6.1	5.3	5.4	5.6	5.4	5.1	5.9	5.5	1.3	5.9	5.1	5.4	5.5	5.6	5.4	5.7	5.6	1.1	queuosine biosynthesis protein QueC
VF1581	6.5	6.3	6.3	6.4	6.0	6.2	6.2	6.1	-1.2	6.4	6.1	6.2	6.2	6.3	6.1	6.4	6.3	1.0	acriflavine resistance plasma membrane protein
VF1582	6.7	6.4	6.6	6.6	6.3	6.4	6.5	6.4	-1.1	6.6	6.3	6.6	6.5	6.3	6.4	6.7	6.4	-1.0	periplasmic component of efflux system
VF1583	8.1	7.6	7.5	7.7	7.4	7.4	7.7	7.5	-1.2	7.8	7.6	7.4	7.6	7.3	7.5	7.4	7.4	-1.1	exodeoxyribonuclease III
VF1584	8.0	7.6	7.6	7.7	7.3	7.0	7.5	7.3	-1.4	7.8	7.4	7.5	7.6	7.1	7.0	7.3	7.1	-1.3	glutaredoxin 2
VF1588to1587	5.1	4.8	4.4	4.8	4.9	4.7	5.2	4.9	-1.1	4.8	4.5	4.5	4.6	4.6	4.5	4.1	4.4	-1.2	histidine transport ATP-binding protein HisP
VF1588to1587	6.0	5.8	5.6	5.8	5.8	5.6	6.3	5.9	1.1	5.7	5.8	5.6	5.7	5.8	5.3	5.3	5.4	-1.2	histidine transport ATP-binding protein HisP
VF1589	7.7	7.3	7.3	7.4	7.5	7.3	7.5	7.4	-1.0	7.5	7.1	7.1	7.2	7.0	6.7	6.9	6.9	-1.3	hypothetical protein
VF1590	11.4	11.0	11.0	11.1	11.0	10.8	11.2	11.0	1.0	11.4	10.9	11.0	11.1	11.1	11.0	11.1	11.1	-1.0	formate acetyltransferase
VF1591	8.0	7.8	7.7	7.8	7.8	7.7	8.1	7.9	-1.0	7.9	7.8	7.6	7.8	7.7	7.8	7.7	7.7	-1.7	pyruvate formate-lyase activating enzyme
VF1593	7.0	6.0	6.3	6.4	5.7	5.9	6.4	6.0	-1.3	6.8	5.6	6.2	6.2	5.6	5.3	5.5	5.5	-1.7	oligopeptide transport ATP-binding protein OppF
VF1594	8.2	7.4	7.7	7.8	6.9	7.7	7.6	7.3	-1.4	8.2	7.0	7.7	7.6	7.4	6.8	7.0	7.0	-1.5	oligopeptide transporter ATP-binding component
VF1595	7.7	6.7	7.0	7.1	6.1	6.6	6.9	6.5	-1.5	7.5	6.1	7.1	6.9	6.8	6.3	6.6	6.6	-1.3	oligopeptide transport system permease protein OppC
VF1596	7.4	6.6	7.0	7.0	5.6	6.4	6.3	6.1	-1.9	7.3	5.9	7.0	6.7	6.7	6.2	6.6	6.5	-1.2	oligopeptide permease ABC transporter membrane component
VF1597	10.5	10.3	10.4	10.4	9.8	10.3	10.2	10.1	-1.2	10.5	9.8	10.4	10.3	10.2	10.4	10.6	10.5	-1.2	oligopeptide-binding protein OppA
VF1597to1597	7.2	7.0	7.0	7.1	7.7	7.1	8.0	7.6	-1.4	7.0	7.1	6.9	7.0	7.2	7.0	7.3	7.2	1.1	oligopeptide-binding protein OppA
VF1597to1597	3.7	3.4	3.5	3.5	3.6	3.3	3.8	3.6	1.0										

VF1625	7.2	6.6	6.7	6.9	6.7	6.4	6.9	6.7	-1.1	7.1	6.7	6.3	6.7	6.1	6.0	6.4	6.2	-1.4	CDP-diacylglycerol-glycerol-3-phosphate 3-phosphatidytransferase
VF1626	6.9	6.6	6.6	6.6	8.5	8.5	8.5	8.5	-1.1	8.5	8.6	8.5	8.6	8.6	8.6	8.7	8.8	1.1	response regulator
VF1629	7.7	7.5	7.4	7.5	7.3	7.3	7.3	7.3	-1.1	7.6	7.2	7.4	7.4	7.3	7.1	7.6	7.3	-1.1	hypothetical protein
VF1630	8.9	8.5	8.6	8.7	7.7	8.4	7.9	8.0	-1.6	8.8	8.3	8.4	8.5	8.3	7.7	8.4	8.1	-1.3	Na(+)/H(+) antiporter
VF1631	8.3	8.6	7.6	8.2	8.0	8.3	8.1	8.1	-1.0	8.4	8.5	8.0	8.3	7.9	8.4	7.9	8.1	-1.2	DNA-binding protein H-NS
VF1632	5.0	4.3	3.5	4.3	3.6	3.7	4.2	3.8	-1.3	4.6	3.9	3.5	4.0	3.8	3.5	3.4	3.6	-1.3	hypothetical outer membrane protein
VF1634	6.6	6.1	6.3	6.3	5.7	6.0	5.9	6.0	-1.4	6.6	6.0	6.0	6.1	5.9	5.4	5.7	5.7	-1.4	Na(+)/H(+) antiporter NhaB
VF1635	6.6	6.0	6.1	6.2	5.8	5.7	6.1	5.9	-1.3	6.3	5.6	5.9	5.9	5.7	5.6	5.4	5.6	-1.3	disulfide bond formation protein B
VF1636	7.0	6.5	6.5	6.7	6.3	5.9	6.2	6.1	-1.4	6.9	6.3	6.5	6.6	6.3	6.1	6.3	6.2	-1.3	preprotein translocase subunit-like protein
VF1637	5.5	4.6	4.5	4.9	3.9	4.0	4.7	4.2	-1.6	4.9	4.1	4.2	4.4	3.9	4.0	4.2	4.0	-1.3	hypothetical protein
VF1639	7.2	7.2	7.1	7.2	6.7	7.0	6.8	6.8	-1.3	7.0	6.9	7.0	7.0	6.8	6.2	6.7	6.6	-1.3	hypothetical protein
VF1641	6.9	6.9	6.9	6.9	6.5	6.7	6.6	6.6	-1.2	6.8	6.8	6.8	6.8	6.8	7.0	7.0	6.9	1.1	DNA topoisomerase III
VF1642	5.5	5.3	4.7	5.2	5.1	4.9	5.2	5.1	-1.1	5.2	5.1	5.0	5.1	5.0	7.6	6.4	6.3	2.3	2,4-dienoyl-CoA reductase [NADPH]
VF1643	8.6	8.4	8.5	8.5	8.2	8.3	8.5	8.3	-1.1	8.4	8.1	8.3	8.3	8.4	8.4	8.6	8.4	1.1	signal peptide peptidase SppA
VF1645	12.2	12.3	12.2	12.2	12.0	12.3	12.2	12.2	-1.0	12.2	12.4	12.4	12.4	12.5	12.7	12.4	12.5	1.1	aspartate-semialdehyde dehydrogenase
VF1646	5.3	4.2	4.0	4.5	4.0	4.0	4.4	4.1	-1.3	4.7	4.0	3.7	4.1	4.4	3.8	3.9	4.0	-1.1	malate-2H+/lactate-NA+ antiporter
VF1646to1647	2.1	2.0	1.6	1.9	1.8	1.8	2.0	1.9	-1.0	2.1	1.9	1.9	2.0	1.7	1.9	1.7	1.8	-1.2	malate-2H+/lactate-NA+ antiporter
VF1646to1647	5.5	5.0	5.0	5.2	4.4	5.0	5.0	4.8	-1.3	5.2	4.9	5.1	5.0	5.0	4.6	4.5	4.7	-1.3	malate-2H+/lactate-NA+ antiporter
VF1648	8.3	7.9	7.9	8.0	7.7	7.9	8.1	7.9	-1.1	8.2	7.4	7.9	7.8	7.9	7.4	8.0	7.8	-1.0	nucleoid-associated protein NdpA
VF1649	9.1	9.1	9.0	9.1	9.1	9.0	9.3	9.2	1.1	9.0	9.2	9.0	9.0	8.9	9.0	9.0	8.9	-1.1	hypothetical protein
VF1650	8.3	8.3	8.1	8.2	8.0	8.0	8.0	8.0	-1.2	8.3	8.1	8.1	8.2	7.8	7.9	8.0	7.9	-1.2	phosphoglycerol transferase MdoB and related proteins, alkaline phosphatase
VF1652	3.2	2.9	2.9	3.0	3.4	3.1	3.2	3.2	1.1	3.1	3.2	2.8	3.0	3.0	3.2	3.0	3.1	1.0	hypothetical protein
VF1653	5.7	5.1	5.0	5.3	5.1	4.9	5.6	5.2	-1.1	5.6	5.1	5.1	5.2	4.6	4.8	4.4	4.6	-1.6	hypothetical protein
VF1655	3.6	3.2	2.8	3.2	3.1	3.1	3.5	3.3	1.0	3.2	3.2	2.9	3.1	2.9	2.8	2.8	2.8	2.8	hypothetical protein
VF1656	4.4	3.9	3.5	3.9	3.6	3.4	3.9	3.6	-1.2	3.8	3.8	3.7	3.8	3.1	3.3	3.6	3.3	-1.3	hypothetical protein
VF1657	6.5	6.1	6.2	6.3	5.8	5.9	6.1	5.9	-1.3	6.4	5.9	6.0	6.1	5.9	5.8	5.7	5.8	-1.2	oxidoreductase
VF1658	7.5	6.7	6.6	6.8	6.5	6.6	6.7	6.6	-1.0	6.7	6.6	6.6	6.7	6.6	6.5	6.5	6.6	-1.2	short chain dehydrogenase
VF1663	8.6	8.1	8.3	8.3	8.1	7.7	8.2	8.0	-1.3	8.5	8.0	8.1	8.2	8.0	7.8	8.0	7.9	-1.2	hypothetical protein
VF1664	6.7	6.6	6.3	6.5	6.5	6.4	6.8	6.6	1.0	6.5	6.7	6.2	6.5	6.4	6.3	6.2	6.3	-1.1	transcriptional regulator, TetR family
VF1665	5.7	5.5	4.9	5.4	5.2	4.9	5.3	5.1	-1.2	5.6	5.4	5.2	5.4	4.9	4.9	5.0	4.9	-1.4	1-acyl-sn-glycerol-3-phosphate acyltransferase
VF1672	7.8	7.4	7.4	7.5	7.2	6.9	7.3	7.1	-1.3	7.6	7.1	7.1	7.3	6.8	6.4	6.9	6.7	-1.5	menaquinone-specific isochorismate synthase
VF1673	5.9	5.3	5.3	5.5	5.4	5.4	5.5	5.4	-1.0	5.3	5.2	5.2	5.3	4.9	4.6	4.9	4.8	-1.0	oligopeptide-binding protein OppA
VF1675	4.7	4.2	4.5	4.5	4.4	4.2	4.8	4.5	1.0	4.8	4.5	4.2	4.5	3.7	3.8	4.2	3.9	-1.5	pyrimidine reductase
VF1676	5.5	5.0	4.4	5.0	5.1	5.1	5.7	5.3	1.2	5.3	5.1	4.7	5.0	5.2	4.8	5.1	5.0	-1.0	hypothetical protein
VF1677	6.3	6.4	6.3	6.4	6.6	6.7	6.8	6.7	1.3	6.3	6.6	6.3	6.4	6.6	6.6	6.9	6.7	1.2	transcriptional regulator, AraC family
VF1678	7.0	7.2	6.9	7.0	7.2	7.2	7.7	7.4	1.3	6.8	7.9	7.0	7.2	6.9	7.4	6.9	7.1	-1.1	NADH-dependent butanol dehydrogenase B
VF1679	6.5	6.3	6.9	6.2	6.4	6.3	6.4	6.3	-1.1	6.3	6.4	6.1	6.3	5.1	5.4	5.0	5.2	-1.0	hypothetical protein
VF1681	6.6	6.3	6.2	6.4	5.8	6.3	6.3	6.1	-1.2	6.4	6.2	6.2	6.3	6.5	6.3	6.3	6.4	1.1	coniferyl aldehyde dehydrogenase
VF1682	7.7	7.2	7.1	7.4	7.3	7.4	7.7	7.5	1.0	7.5	7.0	7.1	7.2	7.0	7.1	6.9	7.0	-1.1	deoxyguanosinetriphosphate triphosphohydrolase-like protein
VF1684	7.0	7.0	6.8	6.9	6.7	6.8	6.9	6.8	-1.1	6.9	6.9	6.8	6.8	6.9	7.1	6.9	7.0	1.1	integral membrane protein (rhomboid family)
VF1688to1689	4.5	4.2	3.8	4.1	3.7	3.7	4.0	3.8	-1.3	4.1	4.1	3.6	3.9	3.5	4.1	3.7	3.7	-1.1	adenine phosphoribosyltransferase
VF1690	9.9	10.6	10.4	10.3	11.4	10.7	11.3	11.1	-1.1	9.9	11.0	10.7	10.4	9.9	9.9	10.5	10.8	-1.1	Hmr protein
VF1690	7.9	7.9	7.8	7.9	7.9	7.9	8.0	7.9	1.0	7.8	8.0	7.9	7.9	7.9	7.9	8.0	7.9	1.0	transcriptional regulators, LysR family
VF1691	8.5	7.9	7.9	8.1	7.6	8.1	7.9	7.9	-1.1	8.4	7.4	7.8	7.9	8.2	8.0	8.4	8.2	1.3	amidophosphoribosyltransferase
VF1692	8.4	7.5	7.7	7.9	7.7	7.6	7.5	7.5	-1.3	8.1	7.0	7.7	7.6	7.8	7.4	7.9	7.7	1.1	colicin V production protein
VF1693	8.3	7.9	8.2	8.1	7.3	7.5	7.8	7.7	-1.3	8.1	7.8	8.0	8.0	7.9	7.7	7.9	7.8	-1.1	DeoD protein
VF1694	7.4	7.2	7.3	7.3	8.7	7.9	8.6	8.3	-1.3	7.4	7.2	7.3	7.2	7.2	7.0	6.8	6.9	-1.2	dihydrofolate synthase
VF1696	8.4	8.2	8.0	8.2	8.3	8.0	8.5	8.2	1.0	8.3	8.2	8.1	8.2	8.0	8.3	8.0	8.1	-1.1	tRNA pseudouridine synthase A
VF1697	8.4	8.4	8.2	8.3	7.9	8.2	8.1	8.1	-1.2	8.3	8.2	8.4	8.3	8.0	8.1	8.2	8.1	-1.1	latent nuclear antigen
VF1698	8.3	7.7	7.9	8.0	7.4	7.8	7.8	7.7	-1.2	8.3	7.8	7.7	7.9	7.6	7.7	7.8	7.7	-1.2	aspartate-semialdehyde dehydrogenase
VF1699	7.5	7.2	7.3	7.3	6.8	6.8	7.1	6.9	-1.4	7.4	6.9	7.2	7.2	6.9	6.9	7.0	6.9	-1.2	erythronate-4-phosphate dehydrogenase
VF1701	8.5	8.1	8.9	8.2	8.0	8.3	8.4	8.3	-1.0	8.3	8.0	8.1	8.4	8.3	8.5	8.5	8.4	-1.2	hypothetical protein
VF1702	8.6	8.5	8.5	8.5	8.0	8.2	8.2	8.1	-1.3	8.6	8.2	8.3	8.4	8.3	8.1	8.4	8.2	-1.1	membrane-bound lytic murein transglycosylase B
VF1703	8.2	8.0	7.9	8.1	7.5	7.6	7.8	7.8	-1.4	8.1	7.8	7.9	8.0	7.8	7.8	7.8	7.8	-1.1	protein YcgL
VF1704	9.1	8.8	9.0	9.0	8.6	8.7	8.9	8.8	-1.2	9.0	8.7	8.8	8.9	8.8	8.8	9.0	8.9	1.0	septum formation inhibitor
VF1705	8.9	8.3	8.3	8.5	8.3	8.2	8.5	8.3	-1.1	8.9	8.2	8.1	8.4	8.1	8.1	8.1	8.1	-1.2	cell division inhibitor MinD
VF1706	7.3	6.7	6.0	6.7	6.3	6.7	6.8	6.6	-1.0	7.3	6.7	6.1	6.7	6.1	6.6	6.1	6.3	-1.4	cell division topological specificity factor MinE
VF1707	6.7	6.3	6.3	6.4	6.0	6.0	6.0	6.0	-1.3	6.7	5.9	6.3	6.3	5.9	5.7	5.9	5.8	-1.4	ribonuclease D
VF1709	6.8	6.4	6.4	6.5	6.4	6.5	6.8	6.6	-1.0	6.6	6.2	6.3	6.3	6.3	6.0	6.1	6.2	-1.1	hydrolase
VF1710	7.8	7.5	7.9	7.7	7.5	7.7	7.8	7.7	-1.0	7.6	7.4	7.7	7.6	7.8	7.5	7.9	7.7	-1.1	outer membrane protein Slp precursor
VF1711	6.9	6.6	6.6	6.7	6.4	6.5	6.4	6.4	-1.2	6.6	6.4	6.5	6.5	6.4	6.2	6.5	6.4	-1.1	hypothetical protein
VF1712	7.4	7.5	7.5	7.5	7.0	7.4	7.1	7.2	-1.2	7.3	7.2	7.3	7.3	7.4	7.2	7.6	7.4	1.1	glycoprotease protein family
VF1713	8.1	7.8	7.9	7.9	7.3	7.6	7.6	7.5	-1.3	7.9	7.5	7.9	7.7	7.8	7.5	7.8	7.7	-1.0	ATP-dependent helicase, DinG family
VF1714	9.3	9.0	9.0	9.1	9.0	9.3	9.3	9.2	-1.1	9.2	8.9	9.1	9.1	9.2	9.2	9.3	9.2	1.1	formyltetrahydrofolate deformylase
VF1715	7.7	7.4	7.3	7.4	7.4	7.0	7.5	7.3	-1.0	7.7	7.2	7.0	7.3	7.0	6.9	7.1	7.0	-1.2	tetranaectin resistance protein
VF1716	6.1	5.9	5.6	5.9	5.7	5.8	5.9	5.8	-1.1	5.8	5.7	5.7	5.7	5.6	5.6	5.5	5.6	-1.1	transcriptional regulator, AraC family
VF1717	5.5	5.6	5.0	5.4	6.1	5.5	6.1	5.9	1.4	5.1	5.8	5.1	5.4	4.7	5.2	4.5	4.8	-1.5	transporter, drug/metabolite exporter family
VF1720	6.4	6.2	5.8	6.2	5.7	5.9	6.1	5.9	-1.2	6.3	5.8	5.8	6.0	5.7	5.4	5.6	5.6	-1.3	maltose regulon regulatory protein Mall
VF1723	8.2	7.6	7.7	7.8	7.3	7.3	7.6	7.4	-1.4	8.1	7.5	7.7	7.8	7.6	7.1	7.4	7.4	-1.3	hypothetical protein
VF1724	6.1	5.3	5.2	5.6	5.0	5.2	5.5	5.2	-1.2	5.6	5.2	5.3	5.4	5.1	5.2	5.1	5.1	-1.2	anaerobic C4-dicarboxylate transporter
VF1725	5.6	4.7	4.6	5.0	4.8	4.1	4.7	4.5	-1.4	5.6	4.6	4.8	5.0	4.7	4.3	4.4	4.5	-1.4	secretory (tripeptidyl) aminopeptidase
VF1726	6.8	6.2	5.5	6.2	5.4	6.1	6.3	5.9	-1.2	6.2	6.3	5.							

VF1770	8.5	8.0	8.2	8.3	8.2	8.6	8.5	8.4	1.1	8.5	7.6	8.0	8.0	8.4	8.3	8.7	8.5	1.4	methylene tetrahydrofolate cyclohydrolase
VF1772	6.1	6.6	6.6	6.7	6.3	6.6	6.5	6.6	-1.1	6.6	6.6	6.5	6.6	6.7	6.6	6.6	6.6	1.0	ribosomal large subunit pseudouridine synthase E
VF1776to1777	2.4	2.5	2.5	2.5	2.7	2.5	2.6	2.6	1.1	2.7	2.5	2.8	2.7	2.5	2.6	2.4	2.5	-1.1	ribosomal large subunit pseudouridine synthase E
VF1776to1777	2.6	2.4	2.4	2.4	2.5	2.6	2.5	2.5	1.1	2.8	2.5	2.7	2.7	2.6	2.5	2.5	2.5	-1.1	ribosomal large subunit pseudouridine synthase E
VF1777	6.0	5.9	5.0	5.6	5.2	4.8	5.2	5.1	-1.5	6.0	5.5	5.4	5.6	5.1	5.9	5.3	5.4	-1.2	hypothetical protein
VF1778	4.6	4.0	3.6	4.1	3.8	3.8	4.3	4.0	-1.1	4.1	4.1	3.7	4.0	3.4	3.8	3.3	3.5	-1.4	methyl-accepting chemotaxis protein
VF1783	6.1	5.7	5.4	5.7	5.9	5.9	6.4	6.0	1.2	5.8	5.8	5.6	5.7	5.7	5.8	5.7	5.7	1.0	anaerobic nitric oxide reductase transcription regulator
VF1786	9.0	8.4	8.1	8.5	7.4	8.2	7.8	7.8	-1.6	8.8	7.7	8.1	8.2	8.2	7.7	8.3	8.1	-1.1	adenylosuccinate lyase
VF1788	7.5	7.5	7.1	7.4	7.5	7.3	7.7	7.5	-1.1	7.6	7.7	7.4	7.5	7.2	7.4	7.2	7.3	-1.2	hypothetical protein
VF1789	4.8	4.2	4.0	4.3	3.9	3.9	4.4	4.1	-1.2	4.5	4.0	4.1	4.2	3.6	3.8	3.5	3.6	-1.5	methyl-accepting chemotaxis protein
VF1790	7.4	7.0	6.7	7.1	6.7	6.7	6.9	6.8	-1.2	7.4	6.9	6.9	7.1	6.7	6.7	6.7	6.7	-1.3	ATP-dependent RNA helicase
VF1791	8.1	7.9	7.8	7.9	7.6	7.7	8.0	7.8	-1.1	8.1	7.8	7.8	7.9	7.8	7.8	7.8	7.8	-1.1	serine protease
VF1792	7.5	7.3	7.2	7.4	7.1	7.0	7.3	7.1	-1.2	7.4	7.1	7.2	7.2	7.1	6.9	7.1	7.1	-1.1	regulatory protein
VF1792to1793	5.4	5.1	5.0	5.2	5.1	4.9	5.5	5.2	1.0	5.1	4.9	5.2	5.1	5.0	5.1	5.2	5.1	1.0	regulatory protein
VF1792to1793	2.9	2.8	2.2	2.6	3.0	2.5	2.7	2.7	1.1	2.5	2.8	2.3	2.5	2.2	2.3	2.1	2.2	-1.3	regulatory protein
VF1793	7.1	6.6	6.7	6.8	6.1	6.6	6.4	6.4	-1.3	6.8	6.6	6.6	6.6	6.8	6.7	6.9	6.8	1.1	formate-tetrahydrofolate ligase
VF1794	7.6	7.0	6.7	7.1	6.8	6.8	7.3	7.0	-1.1	7.4	7.3	7.0	7.2	6.8	7.2	6.7	6.9	-1.3	hypothetical protein
VF1795	5.5	4.5	4.4	4.8	4.3	4.4	4.6	4.4	-1.3	4.9	4.2	4.2	4.4	4.1	4.1	4.2	4.1	-1.2	Outer membrane protein C
VF1797	5.9	6.1	5.9	6.0	6.6	6.0	6.9	6.5	1.5	5.6	6.6	5.7	6.0	5.2	5.6	4.6	5.1	-1.2	hypothetical protein
VF1799	7.7	7.5	7.4	7.5	7.4	7.6	7.6	7.5	1.0	7.7	7.4	7.6	7.5	7.5	7.4	7.6	7.5	-1.0	lipid A biosynthesis lauroyl acyltransferase
VF1800	7.1	6.6	6.5	6.7	6.6	6.5	7.0	6.7	-1.0	6.9	6.4	6.5	6.6	6.6	6.6	6.5	6.6	-1.0	HIT family hydrolase
VF1801	7.4	7.1	6.7	7.0	6.8	6.6	7.0	6.8	-1.2	7.2	7.0	6.7	7.0	6.6	7.0	6.7	6.8	-1.1	hypothetical protein
VF1802	7.5	7.2	7.1	7.3	6.8	6.9	7.0	6.9	-1.3	7.4	7.0	7.2	7.2	7.0	6.8	7.1	7.0	-1.1	hypothetical protein
VF1803	4.5	4.0	3.6	4.1	3.6	3.2	3.6	3.5	-1.5	4.4	3.7	3.6	3.9	3.8	3.5	3.4	3.6	-1.2	Mg(2+) transport ATPase protein C
VF1804	4.2	3.3	3.5	3.7	3.5	3.1	3.8	3.5	-1.1	4.0	3.5	3.7	3.7	3.4	3.4	3.2	3.3	-1.4	hypothetical membrane spanning protein
VF1805	9.4	9.1	9.1	9.2	8.6	8.8	8.8	8.7	-1.4	9.3	8.8	9.0	9.0	8.7	8.8	8.9	8.8	-1.2	chorismate synthase
VF1805to1807	7.5	7.0	6.9	7.1	7.0	6.7	7.4	7.3	-1.1	5.0	4.6	4.7	4.8	4.6	4.6	4.7	4.7	-1.1	chorismate synthase
VF1805to1807	4.8	4.8	4.6	4.7	4.9	5.0	5.1	5.0	1.2	4.7	4.9	4.5	4.7	5.0	5.4	5.0	5.1	1.3	chorismate synthase
VF1806	9.0	8.7	9.0	8.9	8.4	8.6	8.6	8.5	-1.0	9.0	8.5	8.9	8.8	8.9	8.5	8.9	8.8	-1.0	ribosomal protein L3P methyltransferase
VF1807	7.3	7.4	6.9	7.2	7.5	7.3	7.6	7.5	1.0	7.2	7.4	7.0	7.2	7.4	7.0	7.2	7.2	1.0	hypothetical protein
VF1808	7.0	6.5	6.1	6.5	6.7	6.0	6.9	6.5	1.2	7.0	6.6	6.1	6.6	6.1	6.7	6.0	6.2	-1.3	phosphohistidine phosphatase SixA
VF1811to1813	8.0	7.4	7.7	8.4	8.3	8.4	8.3	8.0	-1.0	3.8	3.4	3.4	3.4	3.8	3.2	3.4	3.4	-1.3	acetyl-CoA acetyltransferase
VF1811to1813	3.4	3.2	2.6	3.1	3.2	3.1	3.6	3.3	1.2	3.2	2.9	2.7	2.9	2.9	5.6	4.1	4.2	2.4	acetyl-CoA acetyltransferase
VF1813	4.0	3.6	3.6	3.7	3.1	3.3	3.5	3.3	-1.4	3.6	3.6	3.5	3.6	3.4	3.5	3.3	3.4	-1.1	long-chain fatty acid transport protein precursor
VF1814	6.4	5.6	5.3	5.8	6.1	5.0	6.5	5.9	1.1	6.1	5.5	5.5	5.7	5.2	4.9	4.8	5.0	-1.7	hypothetical membrane spanning protein
VF1815	6.8	6.4	6.1	6.5	6.7	6.0	7.0	6.6	1.1	6.5	6.3	6.2	6.3	6.1	6.1	5.9	6.0	-1.2	lipoprotein
VF1821	8.2	7.5	7.7	7.7	7.0	7.3	7.4	7.3	-1.4	7.8	7.4	7.7	7.6	7.4	6.9	7.3	7.2	-1.2	heme exporter protein D
VF1822	8.2	8.0	8.3	8.2	7.7	7.8	7.9	7.8	-1.3	8.2	7.8	8.2	8.1	8.0	7.6	8.0	7.9	-1.2	heme chaperone heme-lyase
VF1823	7.1	6.6	6.9	6.9	6.6	6.5	6.8	6.6	-1.2	6.9	6.7	6.7	6.8	6.7	6.7	6.8	6.7	-1.0	heme exporter protein B
VF1824	8.0	7.7	7.8	7.8	7.6	7.6	7.7	7.6	-1.2	7.9	7.7	7.7	7.8	7.9	7.9	8.1	8.0	1.1	heme exporter protein A
VF1832	10.1	10.1	10.2	10.1	10.2	10.9	10.2	10.4	-1.2	10.1	9.7	10.2	10.0	9.6	9.1	9.4	9.4	-1.5	chemotaxis protein CheZ
VF1833	9.7	9.8	9.6	9.7	9.9	10.7	10.1	10.2	1.4	9.7	9.4	9.7	9.7	9.3	9.3	9.1	9.1	-1.3	chemotaxis protein CheY
VF1834	9.2	9.1	9.1	9.1	9.4	10.2	9.5	9.7	1.5	9.2	8.8	9.0	9.0	8.7	8.1	8.6	8.5	-1.4	flagellar biosynthesis sigma factor FliA
VF1838	6.9	6.5	6.2	6.6	6.1	5.9	6.4	6.1	-1.3	6.8	6.1	6.5	6.5	6.1	5.7	6.1	6.0	-1.4	hypothetical protein
VF1839	5.6	5.1	4.9	5.2	5.0	5.2	5.3	5.1	-1.1	5.2	4.3	4.5	4.7	4.6	4.4	4.4	4.5	-1.2	flagellar biosynthesis protein
VF1840	5.5	4.0	4.4	4.6	4.3	4.1	4.9	4.4	-1.0	4.8	3.7	4.1	4.2	3.4	3.4	3.5	3.3	-1.8	flagellar biosynthesis protein
VF1841	6.6	5.8	5.7	6.0	6.1	6.4	6.5	6.4	-1.2	6.5	5.8	5.4	5.7	5.1	4.7	5.1	5.0	-1.7	flagellar biosynthesis protein
VF1842	6.9	6.4	6.6	6.6	6.3	7.1	6.7	6.7	1.1	6.8	5.8	6.6	6.4	6.0	5.2	5.5	5.6	-1.8	flagellar biosynthesis protein
VF1843	6.5	5.6	5.7	5.9	5.6	6.6	6.1	6.1	1.1	6.2	4.8	5.5	5.5	5.1	4.0	4.8	4.6	-1.8	flagellar protein FliO
VF1844	7.4	6.8	7.0	7.1	7.0	8.2	7.6	7.6	1.4	7.6	6.3	6.9	7.0	6.6	5.8	6.6	6.4	-1.5	flagellar motor switch protein
VF1845	8.0	7.7	7.8	7.8	7.7	9.2	8.1	8.4	1.5	8.2	7.3	7.8	7.7	7.9	6.9	6.9	7.6	-1.1	flagellar motor switch protein
VF1846	7.3	7.0	6.8	7.1	7.0	8.8	7.6	7.6	1.6	7.7	6.6	6.9	7.4	7.2	6.5	7.2	7.0	-1.2	flagellar basal-body-associated protein
VF1847	7.0	6.9	6.6	6.8	7.0	8.4	7.2	7.5	1.6	7.3	6.5	6.9	6.9	7.5	6.9	7.4	7.3	1.3	flagellar hook-length control protein
VF1849	7.2	6.9	7.0	7.0	6.9	6.9	7.2	7.0	1.0	6.9	6.5	6.8	6.7	6.5	6.4	6.7	6.5	-1.2	flagellum-specific ATP synthase
VF1850	7.7	7.6	7.6	7.7	7.9	8.0	8.1	8.0	1.3	7.6	7.6	7.5	7.6	7.4	7.4	7.3	7.4	-1.1	flagellar assembly protein
VF1851	7.9	7.5	7.9	7.8	7.8	8.9	8.2	8.3	1.5	7.9	6.7	7.8	7.5	7.8	6.7	7.6	7.4	-1.1	flagellar motor protein
VF1852	7.8	7.4	7.6	7.6	7.5	9.1	8.0	8.2	1.6	7.7	6.6	7.5	7.3	7.7	6.8	7.7	7.4	-1.0	flagellar M-ring protein
VF1853	7.9	7.6	7.7	7.8	8.1	9.5	8.5	8.7	1.9	8.1	7.1	7.7	7.6	8.2	7.6	8.3	8.0	1.3	flagellar hook-basal body protein
VF1854	7.9	7.6	7.8	7.8	8.0	9.5	8.4	8.7	1.9	7.9	7.0	7.8	7.6	8.2	7.1	8.1	7.8	1.2	FliC; two-component response regulator
VF1855	8.0	7.7	7.9	7.9	8.2	9.9	8.6	8.9	2.0	8.1	7.2	7.9	7.7	8.6	7.5	8.5	8.2	1.4	FliB; two-component sensor kinase
VF1856	9.1	9.0	9.1	9.1	9.0	8.6	8.8	8.8	-1.2	9.0	8.9	8.8	8.9	8.7	8.5	8.7	8.6	-1.2	FliA; sigma-54-dependent transcriptional activator
VF1856to1857	2.5	2.4	2.4	2.4	2.3	2.3	2.4	2.3	-1.1	2.3	2.1	2.3	2.2	2.6	2.3	2.5	2.5	1.2	FliA; sigma-54-dependent transcriptional activator
VF1856to1857	2.4	2.4	2.5	2.4	2.3	2.3	2.3	2.3	-1.0	2.6	2.3	2.2	2.4	2.4	2.6	2.3	2.4	1.0	FliA; sigma-54-dependent transcriptional activator
VF1857_s	9.6	9.4	9.3	9.4	9.5	9.0	9.6	9.4	-1.1	9.5	9.4	9.2	9.4	9.1	8.9	9.1	9.0	-1.3	transcriptional regulatory protein
VF1858	7.9	7.6	7.4	7.6	7.8	9.2	8.1	8.4	1.7	8.1	7.2	7.6	7.6	8.1	7.6	8.0	7.9	-1.2	flagellar protein FliS
VF1859	7.5	7.4	7.1	7.3	7.3	8.7	7.7	7.9	1.5	7.7	7.0	7.4	7.4	7.7	7.3	7.6	7.6	1.1	FliI
VF1860	6.6	6.1	6.2	6.3	6.3	6.7	6.5	6.5	1.2	6.4	5.9	6.2	6.2	6.0	5.8	6.1	6.0	-1.2	flagellar hook-associated protein
VF1861	6.8	6.5	6.6	6.7	6.2	6.9	6.6	6.6	-1.1	6.5	6.2	6.5	6.4	6.2	6.3	6.5	6.3	-1.1	flagellar protein FliG
VF1863	7.7	7.6	7.6	7.6	7.0	7.5	7.4	7.3	-1.2	7.6	7.4	7.4	7.5	6.8	7.3	7.1	7.0	-1.4	flagellin
VF1864	7.6	7.1	7.3	7.3	6.4	6.6	6.9	6.6	-1.6	7.6	6.8	7.1	7.2	6.3	7.1	6.6	6.6	-1.5	flagellin
VF1865	5.9	5.8	5.5	5.8	5.7	5.6	5.8	5.7	-1.0	5.8	5.6	5.6	5.7	5.4	5.8	5.4	5.5	-1.1	flagellin
VF1866	7.0	6.2	6.7	6.6	6.8	7.1	7.1	7.0	1.3	6.8	6.8	6.4	6.3	6.2	6.0	6.5	6.2	-1.0	flagellin
VF1866to1867	5.9																		

VF1698	7.9	7.2	7.2	7.4	7.2	6.9	7.5	7.2	-1.2	7.7	6.9	7.1	7.2	7.1	6.8	7.0	7.0	-1.2	melanin biosynthesis protein TyrA
VF1901	6.7	6.6	5.9	6.4	5.9	6.0	6.2	6.0	-1.3	6.5	6.6	6.5	6.5	6.9	6.7	6.2	6.2	-1.2	hypothetical protein
VF1902	4.2	3.7	3.3	3.7	4.0	3.6	4.0	3.9	1.1	3.9	3.7	3.3	3.6	3.3	3.2	3.3	3.3	-1.3	hypothetical protein
VF1903	8.2	8.0	8.1	8.1	8.4	7.8	8.5	8.2	1.1	8.2	8.2	8.1	8.2	7.7	7.6	7.7	7.7	-1.4	cytochrome c-type protein NapC
VF1904	8.2	7.7	7.9	7.9	8.2	7.6	8.6	8.1	1.2	8.0	7.7	7.7	7.8	7.5	7.3	7.3	7.4	-1.3	cytochrome c-type protein NapB
VF1905	9.0	9.1	9.2	9.1	9.4	9.2	9.5	9.4	1.2	9.0	9.3	9.1	9.1	9.1	9.0	9.0	9.0	-1.1	nitrate reductase
VF1906	9.4	9.4	9.4	9.4	9.9	9.3	10.0	9.7	1.2	10.0	9.4	9.4	9.3	9.2	9.4	9.5	9.5	-1.1	NapD protein
VF1907	8.3	8.2	8.3	8.3	8.8	8.1	8.9	8.6	1.2	8.1	8.3	8.1	8.2	8.2	8.2	8.2	8.2	1.0	ferredoxin-type protein NapF
VF1909	8.5	8.5	8.4	8.5	8.6	8.2	8.8	8.6	1.1	8.4	8.7	8.4	8.5	8.1	8.4	8.1	8.2	1.0	nitrate/nitrite response regulator protein NarP
VF1910	7.5	8.1	7.4	7.6	7.9	7.6	8.0	7.8	1.1	7.4	8.3	7.4	7.7	6.9	7.7	7.1	7.2	-1.4	ubiquinone biosynthesis protein AarF
VF1912	6.8	6.3	6.3	6.5	6.0	6.0	6.3	6.1	-1.3	6.5	6.1	6.1	6.2	5.8	5.7	5.8	5.8	-1.3	hypothetical protein
VF1913	9.3	9.1	8.8	9.1	8.7	8.8	8.9	8.8	-1.2	9.2	8.9	9.1	9.0	8.8	8.8	8.8	8.8	-1.2	arsenate reductase
VF1914	8.9	8.6	8.5	8.7	8.3	8.4	8.6	8.4	-1.2	8.8	8.3	8.5	8.6	8.5	8.4	8.4	8.4	-1.1	succinyl-D-aminopimelate desuccinylase
VF1915	7.2	7.0	6.8	7.0	6.8	7.0	7.1	6.9	-1.0	7.0	7.0	7.0	7.0	6.9	7.0	7.0	7.0	-1.1	D-alanyl-D-alanine carboxypeptidase
VF1916	6.9	6.9	6.7	6.8	6.9	6.7	7.3	7.0	1.1	6.7	7.1	6.7	6.8	6.8	7.2	7.0	7.0	-1.1	hypothetical protein
VF1917	9.4	9.1	9.3	9.3	8.8	9.1	9.0	9.0	-1.2	9.4	8.9	9.3	9.2	9.2	9.0	9.1	9.1	-1.1	lipoprotein-34 precursor
VF1918	9.9	9.6	9.8	9.7	9.4	9.7	9.6	9.6	-1.1	10.0	9.4	9.8	9.7	9.8	9.5	9.7	9.7	-1.0	dihydrodipicolinate synthase
VF1919	8.2	8.1	7.9	8.1	7.9	8.1	8.0	8.0	-1.0	8.1	7.8	7.9	8.0	7.9	8.1	8.1	8.0	1.0	glycine cleavage system transcriptional repressor
VF1920	8.9	8.3	7.9	8.4	8.1	8.3	8.6	8.3	-1.0	8.8	8.0	7.9	8.2	8.0	7.9	7.9	7.9	-1.2	bacterioferritin comigratory protein
VF1921	7.2	6.9	6.8	7.0	7.1	6.7	7.4	7.1	-1.1	7.1	6.8	6.7	6.8	6.5	6.3	6.5	6.5	-1.3	transporter
VF1922	7.8	7.5	7.3	7.5	7.2	7.4	7.6	7.4	1.1	7.6	7.2	7.2	7.3	7.3	7.3	7.3	7.3	-1.0	zinc metalloprotease
VF1923	9.4	9.4	9.1	9.3	8.6	9.5	9.1	9.1	-1.2	9.3	9.3	9.3	9.3	9.3	9.5	9.4	9.4	1.1	arsenate reductase family protein
VF1924	8.4	7.9	7.7	8.0	7.4	8.1	7.9	7.8	-1.1	8.2	7.9	7.8	8.0	7.9	7.9	7.8	7.9	-1.1	hypothetical protein
VF1925	7.7	7.6	7.5	7.6	7.4	7.5	7.5	7.4	-1.1	7.6	7.5	7.5	7.5	7.6	7.4	7.5	7.5	-1.0	hypothetical protein
VF1926	6.4	6.0	5.7	6.0	5.4	5.4	5.6	5.5	-1.5	6.1	5.6	5.6	5.7	5.7	5.5	5.6	5.6	-1.1	uracil permease
VF1927	8.2	7.7	7.6	7.8	8.4	8.0	8.4	8.2	1.3	8.1	7.7	7.4	7.7	7.7	7.7	7.8	7.7	-1.0	uracil phosphoribosyltransferase
VF1928	9.5	9.2	9.5	9.4	9.2	9.3	9.4	9.3	-1.2	9.5	9.2	9.3	9.2	9.1	9.2	9.2	9.2	-1.2	phosphoribosylamidoimidazole synthetase
VF1929	7.7	6.9	7.0	7.2	6.8	6.7	6.9	6.8	-1.4	7.5	6.4	6.9	6.9	6.7	6.6	7.0	6.8	-1.1	phosphoribosylglycinamide formyltransferase
VF1930	7.8	7.4	7.4	7.5	7.2	7.2	7.3	7.2	-1.2	7.7	7.3	7.3	7.4	7.3	7.4	7.4	7.3	-1.1	glutamine amidotransferase class-II
VF1931	9.1	8.4	8.8	8.7	8.5	8.5	8.8	8.6	-1.1	9.0	8.4	8.5	8.6	8.5	8.5	8.6	8.6	-1.0	phosphoheptose isomerase
VF1934	7.3	7.1	6.9	7.1	6.5	6.7	6.8	6.7	-1.3	7.2	6.9	6.9	7.0	6.7	6.8	6.8	6.7	-1.2	ferredoxin-dependent glutamate synthase
VF1935	7.5	6.7	7.1	7.2	7.1	6.8	7.1	7.1	-1.1	7.3	7.2	7.0	7.0	7.0	6.7	7.1	6.9	-1.1	DNA polymerase III subunit epsilon
VF1936	6.7	6.4	6.1	6.4	6.1	5.8	6.3	6.1	-1.3	6.6	6.1	6.5	6.4	5.9	6.2	6.2	6.1	-1.2	ribonuclease H
VF1937	7.7	7.4	7.3	7.5	8.0	7.2	8.2	7.8	-1.3	7.6	7.6	7.4	7.5	7.1	7.3	7.0	7.1	-1.2	methyltransferase
VF1938	7.8	7.4	7.3	7.5	7.3	7.5	7.7	7.5	-1.0	7.6	7.4	7.3	7.4	7.3	7.4	7.3	7.3	-1.1	hydroxyacylglutathione hydrolase
VF1942	8.9	8.4	7.9	8.4	8.5	8.2	8.6	8.4	-1.0	8.9	8.4	8.2	8.5	8.1	8.4	8.2	8.2	-1.2	nitrogen regulatory protein GlnK
VF1945	7.6	7.3	7.4	7.4	7.0	7.3	7.5	7.1	-1.1	7.4	7.1	7.3	7.3	7.1	7.0	7.2	7.1	-1.1	cell cycle protein MiesJ
VF1947	8.2	8.0	8.1	8.1	7.4	7.8	7.6	7.6	-1.4	8.1	7.7	8.0	7.9	7.7	7.3	7.6	7.6	-1.3	DNA polymerase III subunit alpha
VF1948	7.7	7.3	7.1	7.4	7.0	7.0	7.2	7.1	-1.0	7.6	6.9	7.0	7.2	6.7	6.7	6.9	6.8	-1.3	ribonuclease HII
VF1949	8.3	8.0	8.0	8.1	7.5	7.7	7.8	7.6	-1.4	8.2	7.7	8.0	7.9	7.7	7.3	7.6	7.6	-1.3	lipid A-disaccharide synthase
VF1952	9.6	9.5	9.7	9.6	9.2	9.3	9.4	9.3	-1.2	9.6	9.3	9.5	9.5	9.2	9.0	9.2	9.1	-1.2	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
VF1953	9.6	9.2	9.5	9.4	9.2	9.3	9.4	9.3	-1.1	9.5	9.2	9.3	9.3	9.1	9.2	9.2	9.2	-1.1	outer membrane protein OmpH
VF1954	8.2	8.1	8.3	8.2	7.7	8.0	8.0	7.9	-1.2	8.1	7.9	8.2	8.1	7.8	7.6	7.8	7.7	-1.3	protective surface antigen
VF1955	7.4	6.8	6.9	7.0	6.5	6.5	6.8	6.6	-1.4	7.2	6.3	6.7	6.7	6.6	6.2	6.4	6.4	-1.3	membrane metalloprotease
VF1957	8.0	7.4	7.8	7.7	7.3	7.4	7.4	7.4	-1.3	7.8	7.2	7.5	7.5	7.5	6.9	7.5	7.3	-1.1	phosphatidate cytidyltransferase
VF1958	8.9	8.4	8.6	8.6	8.3	8.3	8.4	8.3	-1.2	8.9	8.2	8.5	8.5	8.5	8.1	8.5	8.4	-1.1	undecaprenyl pyrophosphate synthetase
VF1959	9.4	8.7	9.2	9.1	8.5	8.4	8.9	8.6	-1.4	9.3	8.7	9.1	8.9	8.7	8.1	8.7	8.5	-1.3	ribosome releasing factor
VF1963	9.4	9.0	9.0	9.1	9.0	8.9	9.1	9.0	-1.1	9.3	9.0	9.1	9.2	9.3	9.4	9.2	9.3	-1.1	methionine aminopeptidase
VF1971	6.4	6.2	5.3	6.0	6.7	5.8	7.3	6.6	1.6	6.2	6.6	5.6	6.1	4.6	6.1	4.8	5.2	-1.9	acetoin utilization AcuB protein
VF1973to1974	2.8	2.6	2.4	2.6	2.6	2.3	3.1	2.7	1.1	2.7	2.6	2.4	2.6	2.6	2.5	2.3	2.5	-1.1	malate synthase
VF1973to1974	3.3	3.4	2.9	3.2	2.9	3.1	3.5	3.2	-1.0	2.9	3.4	3.1	3.1	2.7	3.3	2.9	2.9	-1.1	malate synthase
VF1974	7.4	6.7	7.1	7.1	6.9	6.8	7.3	7.0	-1.0	7.3	6.9	7.0	7.0	7.3	6.7	7.2	7.1	-1.1	hydrogen peroxide-inducible genes activator
VF1975	11.7	11.1	11.3	11.4	11.6	11.1	11.6	11.4	-1.0	11.7	11.1	11.3	11.3	11.1	10.9	11.2	11.1	-1.2	alkyl hydroperoxide reductase C22 protein
VF1976	5.5	4.4	4.3	4.8	4.2	4.0	4.6	4.3	-1.4	5.0	4.6	4.6	4.7	4.3	4.3	3.9	4.1	-1.5	copper homeostasis protein CutC
VF1977	5.6	4.9	5.3	5.3	5.3	4.7	5.5	5.2	-1.1	5.4	4.9	5.3	5.2	5.0	4.6	4.9	4.8	-1.3	Protein YgiW precursor
VF1978	5.0	4.2	4.1	4.4	4.1	3.6	4.8	4.1	-1.2	4.6	4.1	4.1	4.3	3.9	3.2	3.5	3.5	-1.7	accessory colonization factor AcfA-like protein
VF1979	7.4	7.0	6.6	7.0	6.9	7.0	7.4	7.1	-1.1	7.2	6.8	6.6	6.9	6.6	6.6	6.6	6.6	-1.2	transcriptional regulators, LysR family
VF1979to1980	2.4	2.5	1.9	2.3	2.2	2.3	2.1	2.2	-1.0	2.4	2.3	1.9	2.2	2.1	2.2	2.0	2.1	-1.1	transcriptional regulators, LysR family
VF1979to1980	3.5	2.9	2.5	3.0	3.0	2.4	3.2	2.9	-1.1	3.0	2.5	2.7	2.8	2.5	2.3	2.3	2.4	-1.1	transcriptional regulators, LysR family
VF1980	3.7	3.7	3.0	3.5	3.2	2.9	3.2	3.1	-1.3	3.3	3.1	3.0	3.1	2.9	2.7	2.6	2.7	-1.3	hypothetical protein
VF1982	7.3	7.0	6.7	7.0	6.7	6.6	7.1	6.8	-1.1	7.2	6.8	6.5	6.8	6.5	6.5	6.5	6.5	-1.3	phosphate transport system protein PhoU
VF1983	8.3	8.2	8.2	8.2	7.9	8.2	8.3	8.1	-1.1	8.2	8.3	8.3	8.3	8.1	8.1	8.0	8.0	-1.2	phosphate transport-ATP-binding protein PstB
VF1985	6.8	6.6	6.4	6.6	6.3	6.2	6.4	6.3	-1.2	6.7	6.5	6.5	6.6	6.3	6.2	6.0	6.2	-1.3	phosphate transport system permease protein PstC
VF1986	6.6	6.6	6.3	6.5	6.1	6.2	6.4	6.2	-1.2	6.4	6.5	6.4	6.4	6.0	6.1	6.2	6.1	-1.3	phosphate-binding protein
VF1987	8.4	8.5	8.4	8.4	8.3	8.4	8.5	8.4	-1.0	8.3	8.5	8.4	8.4	8.3	8.3	8.4	8.3	-1.1	phosphate regulon sensor protein PhoR
VF1988	8.4	8.0	8.0	8.1	8.3	7.7	8.6	8.2	-1.0	8.2	8.0	8.0	8.1	7.7	7.8	7.9	7.8	-1.2	phosphate regulon transcriptional regulatory protein PhoB
VF1989	7.6	7.3	7.2	7.4	6.9	7.0	7.1	7.0	-1.3	7.5	7.2	7.3	7.4	7.1	7.5	7.4	7.3	-1.0	recombination associated protein
VF1992	6.2	5.9	5.8	6.0	5.7	5.9	6.0	5.8	-1.1	6.1	5.9	5.8	5.9	5.8	5.9	5.7	5.8	-1.1	hypothetical protein
VF1993	8.3	7.7	8.1	8.0	7.9	7.8	8.1	7.9	-1.1	7.9	7.7	7.9	7.8	7.6	7.4	7.8	7.6	-1.1	chaperone protein DnaJ
VF1994	10.7	10.4	10.4	10.5	10.1	10.5	10.4	10.3	-1.1	10.5	10.4	10.5	10.5	10.2	10.2	10.5	10.3	-1.1	molecular chaperone DnaK
VF1996	8.8	8.5	8.3	8.5	8.0	8.2	8.2	8.2	-1.3	8.6	8.6	8.4	8.5	8.2	8.4	8.3	8.3	-1.2	GrpE protein
VF1997	7.3	7.0	7.0	7.1	6.7	6.8	7.0	6.8	-1.2	7.2	6.8	7.0	7.0						

VF2019	6.0	5.6	5.2	5.6	5.5	5.1	5.8	5.5	-1.1	5.8	5.6	5.3	5.6	4.9	5.1	5.1	5.0	-1.4	hypothetical protein
VF2020	6.4	6.6	6.5	6.6	6.6	6.2	6.2	6.5	-1.1	6.8	6.6	6.6	6.6	6.5	6.4	6.5	6.5	-1.1	putative phage tail protein
VF2021	4.8	3.7	3.7	4.1	3.2	3.6	4.4	3.7	-1.3	4.2	3.9	3.6	3.9	3.3	3.3	3.1	3.2	-1.6	hypothetical protein
VF2022	5.5	4.7	4.7	5.0	4.7	4.6	5.3	4.9	-1.1	5.1	4.7	4.6	4.8	4.6	4.6	4.3	4.5	-1.6	phage protein
VF2023	5.0	4.3	3.9	4.4	4.2	3.8	4.5	4.2	-1.2	4.5	4.3	4.1	4.3	4.3	3.4	3.9	3.9	-1.4	phage protein
VF2024	4.7	3.9	3.7	4.1	3.8	3.4	4.3	3.9	-1.2	4.2	3.6	3.9	3.9	3.2	3.5	3.3	3.3	-1.5	hypothetical protein
VF2025	4.8	4.3	3.9	4.3	3.8	4.1	4.3	4.0	-1.2	4.3	4.2	3.9	4.1	4.3	4.0	3.8	3.7	-1.3	putative phage baseplate assembly protein
VF2026	4.7	3.9	4.0	4.2	4.3	4.2	4.6	4.4	1.1	4.3	4.2	3.7	4.1	3.7	3.6	3.9	3.7	-1.2	putative phage tail protein
VF2027	5.1	4.7	5.0	4.9	5.2	4.7	5.2	5.0	1.1	5.0	4.4	4.7	4.7	4.6	4.3	4.5	4.5	-1.1	hypothetical protein
VF2027to2028	2.2	2.1	2.2	2.2	2.2	2.0	2.2	2.2	-1.0	2.2	1.9	2.2	2.1	2.1	2.0	2.3	2.1	1.0	hypothetical protein
VF2028	6.6	6.0	5.8	6.1	5.7	5.1	6.2	5.7	-1.4	6.4	5.8	6.0	6.1	5.8	5.1	5.6	5.5	-1.5	hypothetical protein
VF2029	6.3	6.1	5.7	6.0	5.3	5.3	6.0	5.5	-1.4	6.1	5.8	5.8	5.9	6.0	5.5	5.3	5.2	-1.5	hypothetical protein
VF2030	6.5	6.0	5.9	6.1	5.7	5.0	6.1	5.6	-1.4	6.2	5.8	5.9	6.0	5.6	5.2	5.7	5.5	-1.4	exodeoxyribonuclease VIII
VF2031	5.2	5.0	5.0	5.1	4.6	4.7	5.0	4.7	-1.3	4.8	4.5	5.0	4.8	4.7	4.9	4.8	4.8	-1.0	hypothetical protein
VF2032	7.6	6.9	6.9	7.1	6.8	6.6	7.0	6.8	-1.3	7.3	6.7	6.8	6.9	6.6	6.4	6.6	6.6	-1.3	hypothetical protein
VF2034	5.7	5.0	5.4	5.4	5.1	4.6	5.1	4.9	-1.4	5.4	4.7	4.8	5.0	4.4	4.2	4.4	4.4	-1.5	hypothetical protein
VF2038to2033	6.3	5.8	5.7	5.9	5.4	5.3	5.5	5.4	-1.5	5.8	4.8	4.9	5.2	4.6	4.0	4.7	4.4	-1.7	possible phage regulatory protein (CI)
VF2038to2033	5.3	4.9	4.7	5.0	4.4	4.4	4.8	4.5	-1.4	4.6	4.5	4.2	4.5	4.2	4.4	4.5	4.4	-1.1	possible phage regulatory protein (CII)
VF2039	10.2	10.2	10.1	10.2	10.2	10.4	10.1	10.2	-1.0	10.1	10.0	10.2	10.1	10.4	9.9	10.4	10.2	1.1	hypothetical protein
VF2040	9.5	9.3	9.4	9.4	9.4	9.6	9.5	9.5	1.1	9.2	9.3	9.4	9.3	9.5	9.1	9.6	9.4	1.1	hypothetical protein
VF2040to2041	8.1	8.2	8.1	8.1	7.8	8.2	8.0	8.0	-1.1	8.0	7.9	7.9	8.0	8.0	7.5	7.9	7.8	-1.1	hypothetical protein
VF2040to2041	4.0	3.7	3.3	3.7	3.1	3.0	3.2	3.1	-1.5	3.6	3.4	3.0	3.3	3.1	3.1	3.0	3.1	-1.2	hypothetical protein
VF2042	4.2	3.7	3.6	3.9	3.9	4.0	4.1	4.0	1.1	4.1	4.0	3.9	4.0	3.7	4.2	3.6	3.9	-1.1	methyl-accepting chemotaxis protein
VF2043	4.8	4.2	3.8	4.2	3.8	3.6	3.7	3.7	-1.5	4.3	3.9	3.8	4.0	3.7	3.8	3.7	3.7	-1.2	maltose/maltodextrin-binding protein
VF2044	4.5	4.2	3.5	4.1	3.6	3.7	3.4	3.6	-1.4	4.0	3.9	3.6	3.8	3.9	3.4	3.5	3.6	-1.2	maltose transport system permease protein MalF
VF2045	3.8	3.2	2.9	3.3	3.0	2.8	2.9	2.9	-1.3	3.5	2.8	3.0	3.1	2.8	3.0	3.1	3.0	-1.1	maltose transport system permease protein MalG
VF2046	5.4	4.4	3.9	4.6	4.9	4.4	4.9	4.5	-1.5	4.9	4.3	4.8	4.9	4.0	3.8	4.0	3.9	-1.2	maltose/maltodextrin transport ATP-binding protein MalK
VF2047	3.9	3.4	2.8	3.4	2.7	2.6	3.1	2.8	-1.5	3.3	3.0	2.8	3.0	2.7	2.9	2.6	2.7	-1.2	hypothetical protein
VF2050	5.3	4.8	5.0	5.0	4.6	4.4	5.1	4.7	-1.3	5.0	4.9	5.0	5.0	4.8	4.2	4.4	4.5	-1.4	putative cyclomaltodextrinase
VF2051	4.7	3.7	3.3	3.9	3.5	3.7	4.0	3.8	-1.1	4.2	3.9	3.8	4.0	3.9	3.7	3.5	3.5	-1.4	transcriptional regulators, LysR family
VF2052	3.4	3.1	3.1	3.2	3.6	3.2	3.1	3.3	-1.1	3.3	3.0	3.1	3.1	2.9	3.0	3.0	2.9	-1.1	Mg(2+) transporter MgIE
VF2053	4.0	3.8	4.1	3.4	3.5	3.2	3.1	3.4	-1.3	3.8	3.2	3.0	3.2	3.3	2.8	2.8	2.7	-1.4	hypothetical protein
VF2054	4.7	3.9	3.2	3.9	3.9	3.4	4.1	3.8	-1.1	4.3	3.9	3.4	3.9	3.6	3.8	3.2	3.5	-1.3	hypothetical protein
VF2055	5.1	5.1	4.7	4.9	4.8	4.8	5.1	4.9	-1.0	4.7	4.7	4.8	4.7	4.5	4.6	4.6	4.6	-1.1	cytochrome c peroxidase
VF2056	5.7	4.8	4.9	5.2	4.6	4.9	5.1	4.9	-1.2	5.5	4.7	4.6	4.9	4.7	4.5	4.7	4.6	-1.2	pyridoxine kinase
VF2057	4.4	4.2	4.0	4.2	4.5	4.3	4.5	4.4	-1.2	4.0	4.3	4.2	4.2	4.1	4.1	3.7	4.0	-1.1	lysine decarboxylase
VF2058	4.0	3.8	4.1	4.0	3.5	3.6	4.1	3.7	-1.2	3.9	3.8	3.6	3.7	4.1	3.7	3.6	3.6	-1.1	cadaverine/lysine antiporter
VF2058to2055	2.8	2.4	2.0	2.4	2.4	2.3	2.3	2.3	-1.0	2.5	2.4	2.2	2.4	2.1	2.3	2.2	2.2	-1.1	cadaverine/lysine antiporter
VF2058to2055	4.4	4.3	3.7	4.2	3.8	3.7	4.0	3.9	-1.2	4.4	4.0	4.1	4.2	3.5	3.7	3.7	3.6	-1.4	cadaverine/lysine antiporter
VF2060to2061	4.4	3.8	3.8	4.0	3.8	4.1	4.2	4.0	1.1	4.1	3.9	3.7	3.9	4.1	4.2	4.2	4.2	1.2	transcriptional activator CadC
VF2060to2061	1.8	1.7	1.5	1.7	1.8	1.7	1.9	1.8	1.0	1.7	1.8	1.6	1.7	1.6	1.8	1.5	1.6	-1.1	transcriptional activator CadC
VF2064	4.4	4.1	3.5	4.0	4.1	3.9	4.2	4.1	-1.1	4.1	4.1	3.5	3.9	3.6	3.7	3.7	3.7	-1.2	anaerobic Co-dicarboxylate transporter
VF2065	4.1	3.5	4.0	3.9	3.1	3.3	3.5	3.3	-1.4	4.0	3.3	3.5	3.6	3.2	3.1	3.3	3.2	-1.3	nucleoside permease NupC
VF2066	6.4	5.9	5.7	6.0	7.2	5.8	7.4	6.8	-1.8	6.1	6.2	5.5	5.9	5.4	5.9	5.5	5.6	-1.2	hypothetical protein
VF2068	8.9	9.1	9.1	9.0	9.3	9.4	9.3	9.3	-1.1	8.7	9.2	8.9	9.0	9.3	9.4	9.5	9.4	-1.4	lipoprotein NlpD
VF2069	7.5	7.0	7.1	7.2	6.9	7.0	7.2	7.0	-1.2	7.4	6.8	7.0	7.0	7.1	6.8	7.0	6.9	-1.1	protein-L-isocaspate O-methyltransferase
VF2070	8.0	7.9	7.9	7.9	7.6	8.0	7.7	7.6	-1.1	8.0	7.7	7.6	7.8	7.6	7.8	7.8	7.8	-1.0	acid phosphatase
VF2071	8.4	8.2	8.1	8.2	7.9	8.2	8.2	8.1	-1.1	8.4	8.1	8.1	8.2	8.2	8.1	8.3	8.2	-1.0	tRNA pseudouridine synthase D
VF2072	7.7	7.2	7.3	7.4	6.8	6.9	7.3	7.0	-1.3	7.5	7.0	7.0	7.2	7.0	6.7	7.3	7.0	-1.1	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
VF2073	7.6	7.3	7.5	7.5	7.0	7.3	7.3	7.2	-1.2	7.5	7.1	7.1	7.2	7.2	7.0	7.1	7.1	-1.1	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase
VF2074	7.2	6.6	6.7	6.9	6.2	6.5	6.9	6.5	-1.2	7.1	6.3	6.7	6.7	6.8	6.4	6.7	6.7	-1.0	cell division protein FtsB
VF2075	10.4	10.0	10.0	10.2	9.9	9.8	10.3	9.9	-1.2	10.2	9.8	10.0	10.0	9.9	9.6	9.9	9.8	-1.2	CTP synthetase
VF2077	8.5	8.3	8.0	8.3	8.3	7.3	8.5	8.0	-1.2	8.3	8.5	8.3	8.3	7.6	7.9	7.5	7.7	-1.6	hypothetical protein
VF2078	7.3	6.9	6.8	7.0	6.5	6.5	6.9	6.6	-1.3	7.2	6.7	6.8	6.9	6.6	6.6	6.8	6.7	-1.2	putative beta-lactamase regulatory protein
VF2079	6.2	5.7	5.4	5.8	5.5	5.5	5.9	5.6	-1.1	5.8	5.6	5.5	5.6	4.9	5.7	5.0	5.2	-1.3	flagellin
VF2080	8.8	8.5	8.7	8.7	8.6	8.3	8.8	8.6	-1.1	8.7	8.6	8.7	8.7	8.7	8.4	8.6	8.6	-1.1	GTP pyrophosphokinase
VF2081	7.8	7.4	7.4	7.5	7.4	7.2	7.8	7.5	-1.0	7.8	7.3	7.5	7.5	7.4	7.5	7.4	7.4	-1.1	23S rRNA (uracil 5-)methyltransferase
VF2083	8.3	7.8	7.8	8.0	7.5	7.6	7.8	7.6	-1.3	8.3	7.8	7.8	8.0	7.8	7.8	7.7	7.8	-1.2	4'-phosphopantetheinyl transferase
VF2084	9.5	9.2	9.2	9.3	8.7	9.0	9.0	8.9	-1.3	9.5	9.1	9.2	9.3	9.1	9.2	9.2	9.1	-1.1	pyridoxal phosphate biosynthetic protein
VF2090	8.0	7.6	7.6	7.8	7.6	7.3	7.8	7.6	-1.2	7.8	7.3	7.4	7.5	7.2	6.8	7.0	7.0	-1.4	putative sigma-E factor regulatory protein
VF2091	7.9	7.5	7.7	7.7	7.5	7.4	7.4	7.4	-1.1	7.8	7.1	7.5	7.5	7.4	7.1	7.4	7.3	-1.1	periplasmic negative regulator of sigmaE
VF2092	9.3	9.0	9.5	9.3	9.7	9.3	9.7	9.5	1.2	9.3	8.9	9.2	9.1	9.5	9.2	9.5	9.4	1.2	sigma-E factor negative regulatory protein
VF2095	3.8	3.4	3.0	3.4	3.0	2.9	3.2	3.0	-1.3	3.5	3.2	3.0	3.2	3.3	3.0	2.7	3.0	-1.2	hypothetical protein
VF2096	6.3	5.8	5.5	5.9	5.6	5.3	5.6	5.5	-1.3	6.3	5.8	5.7	5.9	5.3	5.6	5.5	5.5	-1.3	hypothetical protein
VF2097	8.0	7.5	7.7	7.7	7.5	7.4	7.7	7.5	-1.2	7.8	7.2	7.7	7.6	7.7	7.3	7.7	7.6	-1.4	aminomethyltransferase homolog
VF2098	6.7	6.2	6.1	6.3	5.8	5.9	5.9	5.9	-1.4	6.4	5.6	5.9	6.0	5.7	5.4	5.4	5.5	-1.4	regulatory protein
VF2098	4.8	4.4	3.9	4.4	4.4	4.1	4.3	4.3	-1.4	4.7	4.7	3.9	4.4	3.9	4.6	4.0	4.2	-1.2	hypothetical protein
VF2100	7.0	6.5	6.5	6.7	6.0	6.2	6.3	6.2	-1.4	6.9	6.1	6.6	6.6	6.1	5.8	6.2	6.1	-1.4	hypothetical protein
VF2101	7.6	6.9	7.0	7.2	6.8	6.6	7.1	6.8	-1.2	7.3	6.7	6.8	6.9	6.7	6.6	6.9	6.7	-1.2	2-octaprenyl-6-methoxyphenyl hydroxylase
VF2102	8.4	8.0	8.0	8.2	7.9	7.8	8.2	8.0	-1.1	8.4	8.0	8.0	8.0	7.9	7.6	7.8	7.8	-1.2	hypothetical protein
VF2103	7.4	7.0	6.4	6.9	6.9	6.5	7.1	6.8	-1.1	7.3	7.2	6.6	7.0	6.7	7.3	7.0	7.0	-1.0	hypothetical protein
VF2104	6.3	5.5	4.9	5.6	4.6	4.7	5.1	4.8	-1.7	5.8	4.6	4.9	5.1	4.5	4.3	4.1	4.3	-1.9	

VF2134	9.1	8.8	8.6	8.8	8.7	8.5	8.9	8.7	-1.1	9.1	8.9	8.7	8.9	9.0	9.4	9.1	9.2	1.2	HesB protein family
VF2135	7.9	7.6	7.7	7.7	7.3	7.2	7.6	7.4	-1.3	7.8	7.7	7.5	7.5	7.6	7.4	7.9	7.6	1.1	glutamate-1-semialdehyde aminotransferase
VF2136	8.0	7.6	7.6	7.7	7.2	7.3	7.4	7.3	-1.3	7.9	7.3	7.6	7.6	7.6	7.2	7.7	7.5	-1.1	hypothetical membrane spanning protein
VF2137	7.0	6.3	6.1	6.5	5.7	5.7	6.2	5.8	-1.6	6.8	5.7	6.0	6.2	5.9	5.8	5.9	5.8	-1.3	16S rRNA m(2)G 1207 methyltransferase
VF2138to2138	5.7	5.7	5.1	5.5	5.4	5.4	5.7	5.5	1.0	5.6	5.8	5.2	5.6	5.2	5.8	5.3	5.4	-1.1	two-component sensor histidine kinase
VF2138to2138	3.0	3.0	2.8	2.9	3.1	2.7	3.2	3.0	1.1	3.0	2.9	2.6	2.8	2.7	2.6	2.5	2.5	-1.2	two-component sensor histidine kinase
VF2140	3.5	2.6	2.4	2.9	2.1	2.3	2.6	2.3	-1.4	3.1	2.6	2.4	2.7	2.5	2.5	2.4	2.5	-1.2	chito oligosaccharide transport system permease protein
VF2142	4.9	4.1	3.8	4.3	3.6	3.4	4.2	3.8	-1.4	4.4	3.8	3.7	4.0	2.9	3.1	3.4	3.1	-1.8	oligosaccharide transport ATP-binding protein
VF2143	5.6	5.2	5.2	5.3	5.0	4.9	5.4	5.1	-1.2	5.4	4.9	5.0	5.1	4.8	4.7	4.8	4.8	-1.3	chito oligosaccharide transport ATP-binding protein
VF2144	5.0	4.0	4.2	4.4	3.8	4.1	4.3	4.0	-1.3	4.4	4.1	4.3	4.3	3.7	3.6	3.6	3.6	-1.6	endothelinase
VF2145	5.2	4.9	4.5	4.9	4.7	4.7	4.8	4.7	-1.1	5.2	4.6	4.7	4.9	4.4	4.1	4.6	4.4	-1.4	N-acetylglucosamine kinase
VF2151	11.7	11.6	11.6	11.6	11.6	11.5	11.4	11.5	-1.1	11.7	11.7	11.5	11.6	11.6	11.7	11.8	11.7	1.0	iron(III)-binding protein
VF2151to2151	3.7	3.7	3.3	3.6	4.6	3.8	3.9	4.1	1.4	3.5	3.7	3.5	3.6	3.1	3.7	3.1	3.3	-1.2	iron(III)-binding protein
VF2154	5.4	4.7	4.5	4.9	5.2	4.5	5.5	5.0	1.1	5.2	5.1	4.8	5.0	4.3	4.8	4.5	4.5	-1.4	hypothetical protein
VF2155	4.1	3.1	2.7	3.3	3.0	2.9	3.2	3.1	-1.2	3.8	3.5	2.9	3.4	2.4	3.0	2.8	2.7	-1.6	carbohydrate diacid regulator
VF2156	4.9	4.7	4.7	4.8	4.6	4.3	4.6	4.5	-1.2	4.5	4.4	4.6	4.5	4.3	4.4	4.3	4.3	-1.1	glucuronate permease
VF2158	9.3	9.2	9.4	9.3	9.1	9.3	9.3	9.2	-1.1	9.3	9.1	9.3	9.2	9.3	9.5	9.4	9.5	1.2	acetonate hydratase
VF2159	8.2	8.0	8.0	8.1	7.8	7.9	8.0	7.9	-1.1	8.0	7.7	8.0	7.9	8.0	7.8	8.2	8.0	-1.1	serine protease
VF2161	6.3	6.1	6.0	6.1	5.9	6.2	6.4	6.1	1.0	6.1	5.7	5.8	5.9	5.8	5.8	5.6	5.7	-1.1	methyl-accepting chemotaxis protein
VF2162	7.3	7.1	7.3	7.2	7.0	7.1	7.3	7.1	-1.1	7.1	7.3	7.2	7.2	6.9	6.8	7.0	6.9	-1.2	multimodular transpeptidase-transglycosylase PBP 1B
VF2163	6.7	6.4	6.5	6.6	6.4	6.6	6.7	6.6	-1.0	6.7	6.4	6.5	6.5	6.8	6.4	6.7	6.6	1.1	ATP-dependent helicase HrpB
VF2164	7.9	7.7	7.6	7.8	7.6	7.4	7.8	7.6	-1.1	7.8	7.8	7.8	7.8	7.5	7.8	7.5	7.6	-1.2	sugar fermentation stimulation protein A
VF2165to2165	5.5	4.6	4.2	4.8	4.8	4.2	4.8	4.6	-1.1	4.9	4.4	4.4	4.6	4.3	4.0	4.1	4.1	-1.3	DnaK suppressor protein
VF2165to2165	4.4	4.6	4.1	4.4	4.0	4.3	4.5	4.2	-1.1	3.9	4.3	4.2	4.2	4.3	4.0	3.6	3.7	-1.4	DnaK suppressor protein
VF2171	6.6	5.8	5.7	6.0	5.7	6.0	6.1	5.9	-1.1	6.3	5.7	5.4	5.8	5.7	5.9	6.1	5.9	-1.1	ABC transporter permease protein
VF2172	7.3	6.9	6.9	7.1	6.9	7.1	7.1	7.0	-1.0	7.1	6.9	6.8	7.0	7.2	7.3	7.4	7.3	1.3	ABC transporter ATP-binding protein
VF2176	8.6	7.6	7.3	7.7	8.1	7.6	7.3	7.5	-1.1	8.4	7.5	7.4	7.7	7.5	7.4	7.5	7.4	-1.2	7-oxoxanthine-guanine phosphoribosyltransferase
VF2177	11.9	11.9	11.7	11.9	12.2	12.2	12.2	12.2	1.3	11.9	12.0	11.8	11.9	12.0	12.3	12.1	12.1	1.2	LIR, transcriptional regulator
VF2178	10.2	9.6	9.7	9.9	9.7	9.7	10.1	9.8	-1.0	10.2	9.5	9.7	9.8	9.6	9.1	9.6	9.4	-1.3	dihydrolipamide dehydrogenase
VF2179	10.9	10.4	10.5	10.6	10.7	10.6	11.1	10.8	1.0	10.9	10.2	10.4	10.5	10.8	10.3	10.7	10.6	1.1	dihydrolipamide acetyltransferase
VF2180	10.0	9.5	9.6	9.7	9.7	9.9	10.2	9.9	1.2	9.9	9.4	9.4	9.6	10.0	9.5	9.9	9.8	1.2	pyruvate dehydrogenase E1 component
VF2180to2181	3.8	3.8	3.8	3.8	3.8	3.8	3.8	3.8	1.2	4.1	4.2	4.2	4.2	4.1	3.8	4.0	4.0	-1.0	pyruvate dehydrogenase E1 component
VF2180to2181	2.6	2.7	2.6	2.6	2.4	2.8	2.6	2.6	-1.0	2.8	2.5	2.7	2.7	2.7	2.4	2.7	2.6	-1.1	pyruvate dehydrogenase E1 component
VF2181	11.0	10.6	10.6	10.7	10.8	10.9	10.9	10.9	1.0	11.0	10.4	10.5	10.6	11.0	10.5	11.1	10.9	1.2	pyruvate dehydrogenase E1 component
VF2182	9.9	9.5	9.5	9.6	9.9	9.9	10.0	9.9	1.2	9.9	9.3	9.4	9.5	9.8	9.7	9.8	9.7	1.2	transcriptional regulator of pyruvate dehydrogenase complex
VF2183	6.6	6.1	5.7	6.1	6.0	5.7	6.4	6.0	-1.1	6.5	5.8	5.7	6.0	5.7	5.8	5.8	5.7	-1.2	anhydro-N-acetylmuramoyl-tripeptide amidase
VF2184	7.0	6.8	6.6	6.8	6.8	6.5	6.8	6.8	-1.1	7.1	6.5	6.8	6.9	6.8	6.9	6.8	6.8	-1.1	nicotinate-nucleotide pyrophosphorylase
VF2185	4.3	3.5	3.4	3.8	3.4	3.2	3.6	3.4	-1.3	4.0	3.4	3.2	3.5	3.6	3.2	3.2	3.3	-1.1	pilin subunit PilA
VF2186	3.7	3.6	3.2	3.5	3.4	3.4	3.5	3.4	-1.1	3.6	3.1	3.5	3.4	3.5	3.2	3.4	3.4	-1.0	plus assembly protein PilB
VF2187	3.1	2.6	2.9	2.8	2.6	2.8	2.8	2.7	-1.1	2.8	2.5	2.9	2.7	2.8	2.7	2.8	2.8	1.0	plus assembly protein PilC
VF2188	7.4	7.0	7.1	7.2	7.7	7.2	7.9	7.6	-1.4	7.2	7.2	7.0	7.1	6.9	7.0	7.0	6.9	-1.1	type 4 prepilin peptidase
VF2190	8.3	8.1	7.9	8.1	8.4	8.3	8.3	8.1	-1.1	8.5	8.0	7.9	8.0	7.7	7.8	7.7	7.7	-1.2	hypothetical protein
VF2191	6.2	5.5	4.8	5.5	5.4	4.9	5.5	5.3	-1.2	5.5	5.2	4.9	5.2	4.3	4.8	4.6	4.5	-1.6	zinc-binding protein
VF2192	4.8	3.9	3.4	4.0	3.0	3.6	3.6	3.4	-1.5	4.3	3.8	3.6	3.9	3.2	3.3	3.2	3.2	-1.6	mutator MutT protein (7,8-dihydro-8-oxoguanine-triphosphatase)
VF2193	8.9	8.7	8.8	8.8	8.5	9.0	8.8	8.8	-1.1	8.8	8.6	8.8	8.7	8.6	8.5	8.7	8.6	-1.1	translocase
VF2194	6.2	5.6	5.3	5.7	6.1	5.5	6.5	6.0	-1.2	6.0	5.6	5.4	5.7	5.0	5.6	5.2	5.3	-1.3	hypothetical protein
VF2195	10.6	10.3	10.7	10.5	10.5	10.3	10.4	10.4	-1.0	10.5	10.2	10.5	10.4	10.5	10.8	10.5	10.8	1.2	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase
VF2200	8.4	7.9	8.1	8.1	7.7	7.7	7.9	7.7	-1.3	8.3	7.7	7.8	7.9	7.6	7.0	7.5	7.3	-1.5	UDP-N-acetylmuramate-L-alanine ligase
VF2201	7.7	7.3	7.4	7.5	6.8	6.8	7.0	6.8	-1.5	7.6	6.9	7.4	7.3	6.9	6.2	6.8	6.6	-1.5	N-acetylglucosaminyl transferase
VF2202	7.0	6.5	6.6	6.7	6.1	6.0	6.4	6.1	-1.5	6.7	6.2	6.4	6.4	6.1	5.6	6.2	6.0	-1.4	cell division protein FtsW
VF2203	7.9	7.4	7.3	7.5	7.0	6.9	7.5	7.1	-1.3	7.7	7.0	7.2	7.3	7.0	6.7	6.9	6.9	-1.4	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase
VF2204	8.3	7.8	7.7	7.3	6.4	6.7	7.1	6.7	-1.5	7.5	6.9	7.1	7.2	6.7	6.7	6.3	6.5	-1.4	UDP-N-acetylmuramoyl-pentapeptide-transferase
VF2205	8.1	7.7	7.7	7.9	7.2	7.4	7.6	7.4	-1.4	7.9	7.5	7.7	7.7	7.6	7.1	7.5	7.4	-1.3	UDP-N-acetylmuramoyl-L-D-glutamyl-2, 6-diaminopimelate-D-alanyl-D
VF2206	8.3	8.0	8.0	8.1	7.3	7.7	7.8	7.6	-1.4	8.2	7.7	7.9	7.9	7.7	7.3	7.6	7.5	-1.3	UDP-N-acetylmuramoyl-L-D-glutamate-2, 6-diaminopimelate ligase
VF2207	7.4	7.0	7.2	7.2	6.5	6.7	6.7	6.7	-1.4	7.3	6.9	7.0	7.1	6.9	6.3	6.8	6.7	-1.3	cell division protein FtsI
VF2208	6.3	5.2	4.8	5.4	4.9	4.6	5.6	5.0	-1.3	5.9	5.0	4.8	5.2	4.9	4.6	4.8	4.8	-1.4	cell division protein FtsL
VF2209	7.9	7.5	7.4	7.6	7.4	7.3	7.6	7.4	-1.1	7.8	7.2	7.5	7.5	7.4	7.4	7.4	7.5	-1.0	S-adenosyl-methyltransferase
VF2209to2210	13.0	13.3	13.1	13.1	13.5	13.4	13.4	13.4	1.2	13.2	13.4	13.1	13.2	13.3	13.5	13.4	13.4	1.1	S-adenosyl-methyltransferase
VF2209to2210	7.4	8.5	8.2	8.0	8.1	8.6	7.8	8.1	1.1	7.3	8.3	7.8	7.8	8.0	8.6	8.1	8.3	1.4	S-adenosyl-methyltransferase
VF2210	9.0	9.1	9.1	9.1	8.9	8.9	9.0	8.9	-1.1	8.8	8.9	9.0	8.9	9.0	9.0	9.1	9.1	1.1	corrin/porphyrin methyltransferase
VF2211	9.1	9.2	9.0	9.1	8.9	9.0	9.0	9.0	-1.1	9.0	9.0	9.1	9.0	9.0	8.9	9.0	9.0	-1.0	G56 antigen
VF2212	8.2	8.1	8.0	8.1	7.7	8.0	8.0	7.9	-1.0	8.1	7.9	7.9	8.0	7.8	7.9	8.0	7.9	-1.0	hypothetical protein
VF2213	8.2	8.0	8.0	8.0	7.6	8.0	7.8	7.8	-1.2	8.0	7.9	8.0	7.9	7.9	8.0	7.9	7.9	-1.0	phosphohepse isomerase
VF2214	7.7	7.5	7.2	7.5	6.9	7.2	7.2	7.1	-1.3	7.6	7.5	7.3	7.5	7.1	7.5	7.2	7.2	-1.2	21 kDa hemolysin precursor
VF2216	10.8	10.4	10.6	10.6	10.2	10.4	10.3	10.3	-1.2	10.8	10.3	10.5	10.6	10.4	10.0	10.3	10.2	-1.3	stringent starvation protein A
VF2217	8.6	8.3	8.5	8.5	8.3	8.7	8.7	8.5	-1.1	8.5	8.3	8.2	8.3	8.5	8.3	8.5	8.4	-1.1	cytochrome c1
VF2218	8.9	8.5	8.7	8.7	8.5	9.0	8.9	8.8	-1.1	8.8	8.5	8.5	8.6	8.9	8.8	8.9	8.9	-1.2	cytochrome b
VF2219	7.5	7.1	7.2	7.2	7.2	7.5	7.7	7.5	-1.2	7.3	7.1	7.0	7.1	7.4	7.4	7.4	7.4	1.2	ubiquinol-cytochrome c reductase iron-sulfur subunit
VF2219_x	7.6	7.2	7.2	7.4	7.3	7.7	7.8	7.6	-1.2	7.4	7.3	7.2	7.3	7.6	7.7	7.6	7.7	1.2	ubiquinol-cytochrome c reductase iron-sulfur subunit
VF2223	6.4	5.6	5.6	5.9	5.8	5.3	6.2	5.8	-1.1	6.0	5.6	5.5	5.7	5.0	4.9	5.1	5.0	-1.6	ATPase
VF2224	8.4	7.9	7.5	7.9	7.3	7.6</													

VF2263	10.5	10.4	10.5	10.5	10.4	11.2	10.7	10.8	1.2	10.5	10.3	10.4	10.4	10.6	10.7	10.8	10.7	1.2	acetolactate synthase III large subunit
VF2264	9.3	7.8	8.7	7.9	7.3	7.6	7.6	7.5	-1.3	7.3	7.9	7.9	7.9	7.9	8.0	8.0	8.0	7.9	7-long-chain-fatty-acid-CoA ligase
VF2266	8.0	7.4	7.7	7.7	7.6	7.7	8.0	7.7	1.0	8.0	7.2	7.5	7.6	7.2	6.8	7.3	7.1	-1.4	bifunctional aspartate kinase II/homoserine dehydrogenase II
VF2267	8.6	8.2	8.3	8.3	8.2	8.4	8.7	8.4	1.1	8.5	8.0	8.2	8.2	8.0	7.9	8.1	8.0	-1.2	cystathionine gamma-synthase
VF2269	8.8	7.2	6.6	7.5	7.0	7.1	7.0	7.0	-1.4	8.7	6.2	6.6	7.2	5.6	5.4	5.5	5.5	-3.2	glycosidase
VF2270	6.6	4.9	4.9	5.5	4.8	5.0	5.1	5.0	-1.4	6.4	4.7	4.9	5.3	4.3	4.5	4.1	4.3	-2.0	hypothetical protein
VF2271	7.1	6.6	6.5	6.7	6.4	6.7	6.6	6.7	-1.1	6.9	6.6	6.7	6.7	6.6	6.7	6.6	6.8	6.8	multimeric operon periplasmic protein precursor
VF2272	9.3	9.1	9.1	9.2	9.3	8.9	9.2	9.1	-1.0	9.2	9.0	8.7	9.0	8.7	8.3	8.4	8.5	-1.4	NADP-dependent malic enzyme
VF2274	7.7	7.3	7.3	7.5	7.1	7.1	7.3	7.2	-1.2	7.6	7.0	7.4	7.4	7.2	6.9	7.1	7.1	-1.2	primosome assembly protein PriA
VF2275	8.4	8.2	8.0	8.2	7.5	7.7	7.9	7.7	-1.4	8.3	7.9	8.1	8.1	8.1	8.2	8.1	8.1	1.0	transcriptional repressor CytR
VF2277	8.4	7.6	7.6	7.9	7.6	8.1	8.2	8.0	-1.1	8.0	7.6	7.7	7.8	7.4	7.4	7.5	7.4	-1.3	ATP-dependent protease peptidase subunit
VF2278	7.9	7.1	7.2	7.4	7.1	7.6	7.8	7.5	1.1	7.6	7.1	7.1	7.3	7.0	6.8	7.0	6.9	-1.2	ATP-dependent protease ATP-binding subunit
VF2279	6.4	5.7	5.4	5.8	5.8	5.7	6.2	5.9	1.1	6.1	5.8	5.4	5.8	5.3	6.2	5.7	5.8	-1.0	OsmC-like protein
VF2281	7.8	7.8	7.7	7.8	8.0	7.6	8.4	8.0	1.2	7.6	7.8	7.6	7.7	7.5	7.7	7.5	7.6	-1.1	hypothetical protein
VF2282	8.8	8.7	8.8	8.8	8.8	8.5	8.9	8.7	-1.0	8.5	8.5	8.6	8.5	8.7	8.6	8.8	8.7	1.1	succinylglutamic semialdehyde dehydrogenase
VF2283	8.9	8.8	8.8	8.8	8.6	8.7	8.8	8.7	-1.1	8.5	8.5	8.7	8.6	8.6	8.6	8.6	8.6	-1.0	arginine N-succinyltransferase, beta chain
VF2284	9.2	9.0	9.0	9.0	8.9	9.1	9.2	9.1	1.0	9.1	8.8	8.9	8.9	8.9	9.1	9.1	9.0	1.1	bifunctional N-succinylaminoimidate-amino-transferase/acetylornithine tra
VF2285	4.2	3.1	3.4	3.6	3.0	2.6	2.9	2.8	-1.7	4.2	2.9	3.1	3.4	2.7	2.5	3.0	2.7	-1.6	para-aminobenzoate synthase component II
VF2286	9.4	8.9	9.3	9.2	8.4	8.5	8.7	8.5	-1.6	9.3	8.4	9.3	9.0	9.0	8.2	9.2	8.8	-1.1	tryptophanyl-tRNA synthetase
VF2287	7.4	6.4	6.5	6.8	5.9	5.8	6.2	6.0	-1.7	7.2	6.1	6.4	6.5	6.2	5.5	6.3	6.0	-1.5	phosphoglycolate phosphatase
VF2291	8.9	8.3	8.7	8.6	8.1	7.9	8.3	8.1	-1.5	8.8	7.9	8.4	8.3	7.9	7.0	7.8	7.6	-1.7	3-dehydroquinase synthase
VF2293	5.3	4.6	4.3	4.7	3.7	4.1	4.5	4.1	-1.5	4.9	4.2	4.5	4.5	4.4	3.8	4.2	4.2	-1.3	pili secretion protein PilQ
VF2295	4.4	3.4	3.4	3.7	2.8	3.1	3.8	3.2	-1.4	4.1	3.5	3.4	3.7	3.0	3.2	3.1	3.1	-1.5	pili assembly protein PilO
VF2296	5.0	3.7	3.5	4.0	3.4	3.2	4.0	3.5	-1.4	4.4	3.9	3.3	3.9	2.9	3.2	3.1	3.0	-1.8	pili assembly protein PilM
VF2297	4.2	3.6	3.4	3.7	3.0	3.3	3.5	3.3	-1.4	3.8	3.2	3.4	3.5	3.1	3.0	2.9	3.0	-1.4	pili assembly protein PilN
VF2298	9.1	9.1	9.1	9.1	8.8	9.0	8.9	8.9	-1.2	9.1	8.9	9.1	9.0	8.9	8.8	8.9	8.9	-1.1	multimodular transpeptidase-transglycosylase PBP 1A
VF2299	5.8	5.8	5.8	5.8	5.8	5.8	5.8	5.8	-1.2	6.2	5.9	6.2	6.2	6.1	5.9	6.0	6.1	-1.1	hydrogen peroxide-inducible genes activator
VF2300	7.2	7.1	7.0	7.1	6.6	6.8	7.1	6.8	-1.2	6.9	6.8	7.0	6.9	6.9	7.6	7.2	7.2	1.2	glutaredoxin
VF2301	5.9	5.8	5.8	5.8	5.7	5.6	6.0	5.8	-1.0	5.6	5.7	5.6	5.6	5.8	6.0	5.6	5.8	1.1	dihydropolipamide dehydrogenase
VF2302	4.4	3.5	3.1	3.7	2.8	2.6	2.9	2.8	-1.8	4.2	3.3	3.4	3.6	3.2	2.7	2.8	2.9	-1.7	hypothetical protein
VF2304	11.0	10.2	10.5	10.6	11.9	10.2	12.1	11.4	-1.8	10.9	10.2	10.3	10.4	9.8	10.6	10.7	10.4	-1.0	RNA delta(2)-isopentenylpyrophosphate transferase
VF2305	9.2	8.9	9.2	9.0	8.7	9.2	9.0	9.0	-1.0	9.2	8.9	9.0	9.0	8.9	9.0	8.9	8.9	1.1	8-ethylornithine desuccinylase
VF2308	10.0	9.3	9.5	9.6	10.2	10.2	10.2	10.2	1.5	9.9	9.0	9.3	9.4	9.6	9.3	9.6	9.5	-1.1	phosphoenolpyruvate carboxylase
VF2319	6.1	5.6	5.5	5.7	5.2	5.1	5.7	5.3	-1.3	5.8	5.4	5.6	5.6	5.2	4.9	5.5	5.2	-1.4	hypothetical protein
VF2323	10.6	10.4	10.5	10.5	10.4	10.2	10.5	10.4	-1.1	10.5	10.3	10.4	10.4	10.1	10.2	10.1	10.1	-1.2	RNA-binding protein Hfq
VF2324	10.8	11.0	10.9	10.9	10.9	10.9	10.9	10.9	-1.0	10.8	10.9	10.9	10.9	10.9	11.0	10.9	10.9	1.0	RNA delta(2)-isopentenylpyrophosphate transferase
VF2325	7.9	7.7	7.5	7.7	7.0	7.1	7.4	7.2	-1.4	7.9	7.4	7.5	7.5	7.5	7.5	7.4	7.4	-1.1	DNA mismatch repair protein
VF2327	8.6	8.3	8.3	8.4	8.0	8.1	8.3	8.1	-1.2	8.5	8.2	8.2	8.3	8.1	8.1	8.1	8.1	-1.1	ATP/GTP hydrolase
VF2328	6.8	6.2	6.2	6.4	6.6	6.0	6.8	6.5	-1.1	6.6	6.2	6.1	6.3	6.1	6.0	6.3	6.1	-1.1	iron-sulfur cluster-binding protein
VF2328toIRN	4.0	3.2	2.6	3.2	3.2	2.6	3.5	3.1	-1.2	3.7	2.8	2.4	2.9	2.6	2.8	2.4	2.6	-1.3	iron-sulfur cluster-binding protein
VF2328toIRN	2.4	2.1	1.9	2.1	1.9	1.8	2.0	1.9	-1.1	2.3	1.9	1.9	2.0	1.9	1.8	1.8	1.8	-1.2	iron-sulfur cluster-binding protein
VF2329	9.3	9.0	8.7	9.0	8.4	8.5	8.5	8.5	-1.4	9.3	8.9	8.9	9.0	8.7	8.7	8.7	8.7	-1.2	elastobinuclease
VF2331	9.5	9.1	9.1	9.2	9.1	8.8	9.2	9.1	-1.1	9.5	9.0	8.9	9.1	8.9	8.7	8.8	8.8	-1.3	phosphatidylserine decarboxylase
VF2332	4.7	3.7	3.9	4.1	3.8	3.5	3.9	3.7	-1.3	4.4	3.5	3.2	3.7	3.0	3.5	3.5	3.3	-1.3	transporter, drug/metabolite exporter family
VF2333	6.9	6.0	5.9	6.2	6.2	6.0	6.4	6.2	-1.0	6.6	5.6	5.8	6.0	6.0	5.8	6.0	5.9	-1.0	lysyl-tRNA synthetase
VF2334	6.0	5.4	5.6	5.7	5.4	5.3	5.7	5.5	-1.2	5.8	5.4	5.7	5.6	5.4	5.2	5.1	5.2	-1.3	fumarate reductase
VF2335	6.5	5.8	6.1	6.2	5.7	5.6	6.3	5.8	-1.2	6.2	5.7	6.0	6.1	6.0	5.7	5.4	5.8	-1.3	succinate dehydrogenase
VF2336	6.8	5.8	6.1	6.2	6.0	5.6	6.6	6.1	-1.1	6.4	5.9	5.9	6.1	5.7	5.5	5.6	5.6	-1.4	fumarate reductase subunit C
VF2337	6.3	5.7	5.7	5.9	5.7	5.7	6.3	5.9	-1.0	6.2	5.7	5.8	5.9	5.4	5.2	5.6	5.4	-1.4	fumarate reductase subunit D
VF2338	8.1	7.3	7.5	7.6	7.4	6.8	7.6	7.3	-1.3	8.0	7.3	7.3	7.6	7.0	7.1	7.1	7.1	-1.4	elongation factor P
VF2339	6.8	6.4	6.4	6.5	6.2	6.2	6.7	6.4	-1.1	6.5	6.1	6.1	6.3	6.0	6.0	6.1	6.0	-1.2	lysine 2,3-aminomutase
VF2340	9.3	9.0	9.4	9.5	9.8	9.1	9.3	9.5	-1.0	9.9	9.3	9.3	9.5	9.0	9.0	9.2	9.1	-1.1	6-phosphofructokinase
VF2341	8.2	7.7	7.8	7.9	7.8	7.6	8.0	7.8	-1.1	8.0	7.6	7.7	7.8	7.9	8.0	8.0	8.0	1.2	ferrous iron efflux protein F
VF2343	7.6	7.2	7.0	7.3	7.3	7.1	7.8	7.4	-1.1	7.2	7.2	7.2	7.2	6.9	7.1	7.1	7.0	-1.1	transcriptional regulatory protein CpxR
VF2344	7.3	7.1	6.9	7.1	6.9	6.9	7.1	7.0	-1.1	7.0	7.0	6.9	7.0	6.7	6.7	6.8	6.7	-1.2	two-component sensor protein
VF2345	6.5	6.1	6.0	6.2	6.0	6.1	6.1	6.1	-1.1	6.4	6.0	6.1	6.2	6.1	6.0	5.9	6.0	-1.1	23S rRNA methyltransferase
VF2346	7.2	6.3	6.3	6.6	6.6	6.1	6.7	6.5	-1.1	7.1	6.1	6.2	6.5	6.8	6.0	6.0	6.0	-1.4	serine acetyltransferase
VF2347	7.5	6.9	7.1	7.2	6.8	6.7	7.2	6.9	-1.2	7.4	6.6	6.8	6.9	6.5	6.4	6.6	6.5	-1.3	serine acetyltransferase
VF2348	8.1	7.5	7.7	7.8	7.6	7.2	7.8	7.5	-1.4	7.9	7.3	7.6	7.6	7.2	7.0	7.3	7.1	-1.4	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase
VF2351	5.9	5.2	5.2	5.4	4.7	4.9	5.1	4.9	-1.5	5.9	5.0	5.2	5.4	4.9	4.9	5.0	5.0	-1.3	cell wall endopeptidase, family M23/M37
VF2352	6.4	5.5	5.5	5.8	6.1	5.5	6.4	6.0	-1.2	6.2	5.8	5.4	5.8	4.9	4.3	5.2	5.1	-1.6	FxA protein
VF2353	7.8	7.6	7.3	7.6	7.3	7.1	7.7	7.3	-1.2	7.7	7.6	7.3	7.5	7.1	7.6	7.4	7.4	-1.1	aspartate ammonia-lyase
VF2354	6.1	5.7	5.6	5.8	5.4	5.1	5.6	5.3	-1.4	6.0	5.6	5.6	5.8	5.4	5.2	5.1	5.2	-1.4	anaerobic C4-dicarboxylate transporter
VF2355	6.9	6.2	5.8	6.3	6.1	5.0	6.9	6.0	-1.2	6.5	6.4	5.7	6.2	5.6	7.1	5.8	6.2	-1.0	universal stress protein A
VF2357	10.2	9.7	9.6	9.8	9.2	9.2	9.5	9.3	-1.4	10.2	9.6	9.6	9.8	9.4	9.6	9.6	9.6	-1.2	glucosamine-6-phosphate deaminase
VF2359	8.0	7.9	7.9	7.9	8.0	7.9	8.2	8.0	-1.0	7.8	8.2	7.8	8.0	7.6	8.0	7.8	7.8	-1.1	protein tyrosine phosphatase
VF2360	7.9	7.9	8.0	7.9	7.7	7.9	7.9	7.8	-1.0	7.7	8.1	7.7	7.8	7.8	8.1	7.9	7.9	1.1	glyceraldehyde-3-phosphate dehydrogenase
VF2361	7.2	6.8	6.8	6.9	7.2	6.9	7.4	7.1	-1.1	6.9	7.0	6.6	6.9	6.8	6.9	6.7	6.8	-1.1	transcriptional regulator, ArsR family
VF2363	8.2	8.1	8.0	8.1	9.0	8.0	9.0	8.6	1.4	8.1	8.3	8.0	8.1	7.5	7.7	7.5	7.6	-1.5	glyceraldehyde-3-phosphate dehydrogenase
VF2364	4.7	4.2	4.2	4.4	4.4	3.7	4.6	4.2	-1.1	4.4	4.2	3.9	4.2	4.1	3.9	3.4	3.8	-1.3	NADH dehydrogenase
VF2365	4.5	3.8	3.3	3.9	4.4	3.7	4.3	4.1	-1.2	4.3	3.9	3.5	3.9	3.6	3.6	3.3	3.5	-1.3	high-affinity zinc uptake system protein ZnuA precursor
VF2366	4.8	4.4																	



VF2409	2.6	2.9	2.2	2.6	1.9	2.4	2.9	2.4	-1.1	2.3	2.9	2.6	2.6	2.0	2.1	2.0	2.1	-1.4	minor curlin subunit CsgB
VF2415	12.2	12.2	12.4	6.4	12.2	12.1	12.3	12.2	-1.2	12.5	12.2	12.4	12.4	12.1	11.7	12.0	11.9	-1.4	LSU ribosomal protein L10P
VF2421	10.5	10.0	10.3	10.2	9.9	9.6	10.1	9.9	-1.3	10.3	9.8	10.0	10.0	9.7	9.3	9.6	9.5	-1.4	transcription antitermination protein NusG
VF2425	7.2	6.5	6.6	6.8	6.7	6.7	7.1	6.8	-1.0	7.1	6.4	6.4	6.6	6.5	6.5	6.6	6.5	-1.1	biotin operon repressor
VF2426	8.2	7.6	7.8	7.9	7.7	7.6	8.0	7.8	-1.0	8.0	7.3	7.8	7.7	7.8	7.4	7.7	7.7	-1.4	UDP-N-acetylglucosamine 6-phosphate 4-epimerase
VF2427	6.6	5.5	5.3	5.8	5.3	5.1	5.7	5.4	-1.3	6.1	4.9	5.5	5.5	5.1	4.8	5.0	5.0	-1.4	hypothetical protein
VF2432	9.0	8.4	8.7	8.7	8.1	7.8	8.3	8.1	-1.6	8.3	8.2	8.5	8.6	8.2	8.2	8.2	8.1	-1.4	hypothetical protein
VF2433	7.5	7.1	7.2	7.3	7.0	7.0	7.3	7.1	-1.1	7.3	6.8	7.2	7.1	7.2	6.8	7.3	7.1	-1.0	glutamate racemase
VF2434	5.8	5.1	4.8	5.2	4.3	4.1	4.8	4.4	-1.8	5.5	4.6	4.8	4.9	4.6	4.3	4.5	4.5	-1.4	hypothetical protein
VF2436	7.8	7.6	7.5	7.7	8.4	7.5	8.5	8.1	1.4	7.6	7.8	7.6	7.7	7.1	7.2	6.9	7.1	-1.5	tRNA (uracil-5)-methyltransferase
VF2437	7.6	6.9	7.1	7.2	7.0	7.1	7.6	7.2	1.0	7.7	7.1	7.1	7.3	7.0	6.9	7.2	7.0	-1.2	Acetyl-coenzyme A synthetase
VF2438	7.6	7.2	7.4	7.4	7.0	7.1	7.4	7.2	-1.2	7.5	7.0	7.2	7.2	7.2	7.0	6.8	7.2	-1.2	transcriptional repressor of FabB
VF2442	8.6	8.7	8.8	8.7	8.9	8.8	8.9	8.9	1.2	8.6	8.7	8.7	8.7	9.1	8.9	8.9	8.9	1.2	LexA repressor
VF2443	7.2	6.6	6.5	6.8	7.1	6.4	7.3	6.9	1.1	7.0	6.4	6.2	6.5	6.1	6.9	6.6	6.5	1.0	glycerol-3-phosphate acyltransferase
VF2444	6.3	5.6	5.7	5.9	5.5	5.5	5.8	5.6	-1.2	6.2	5.5	5.7	5.8	5.5	5.2	5.6	5.5	-1.3	4-hydroxybenzoate polyphenyltransferase
VF2445	7.2	6.6	6.4	6.8	6.8	6.5	7.2	6.9	-1.1	7.1	6.7	6.5	6.7	6.6	6.6	6.5	6.6	-1.1	chorismate-pyruvate lyase
VF2447	8.3	7.8	7.8	8.0	7.8	7.8	7.9	7.9	-1.1	8.2	7.6	7.7	7.8	7.8	7.6	7.8	7.7	-1.1	integral membrane protein (thomboid family)
VF2448	8.9	8.3	8.2	8.5	8.4	8.2	8.8	8.5	1.0	8.7	8.0	8.3	8.3	8.3	8.3	8.3	8.3	-1.0	thiosulfate sulfurtransferase
VF2449	8.9	8.5	9.1	8.9	9.0	8.7	9.0	8.9	1.0	8.9	8.5	8.9	8.8	8.8	8.4	8.8	8.7	-1.1	RNA polymerase sigma-32 factor
VF2450	10.2	9.8	10.4	10.1	10.4	10.0	10.4	10.3	1.1	10.2	9.9	10.3	10.1	10.2	9.7	10.2	10.0	-1.1	RNA polymerase sigma-32 factor
VF2451	8.2	8.0	8.1	8.1	7.9	8.1	8.1	8.0	-1.1	8.2	7.9	8.0	8.0	8.0	7.8	8.0	7.9	-1.1	cell division protein FtsX
VF2452	8.8	8.5	8.6	8.6	8.4	8.5	8.6	8.5	-1.1	8.7	8.3	8.5	8.5	8.5	8.3	8.6	8.5	-1.0	cell division ATP-binding protein FtsE
VF2453	8.4	8.3	8.3	8.3	8.0	8.1	8.0	8.0	-1.2	8.3	8.1	8.3	8.2	8.2	8.2	8.3	8.2	-1.0	cell division protein FtsY
VF2454	7.7	7.4	7.7	7.6	7.5	7.1	7.7	7.4	-1.2	7.6	7.3	7.3	7.4	6.9	7.0	7.1	7.0	-1.0	hypothetical protein
VF2455	7.5	6.6	6.2	6.8	6.9	6.1	7.1	6.7	-1.1	7.2	6.6	6.3	6.7	5.8	6.2	6.0	6.0	-1.6	hypothetical protein
VF2456	5.2	4.3	4.1	4.5	4.9	5.0	5.6	5.2	-1.6	5.0	4.2	4.2	4.5	5.0	4.8	4.8	4.9	1.3	multiple antibiotic resistance protein MarC
VF2457	6.7	6.3	6.2	6.4	6.5	6.4	6.5	6.4	-1.5	7.3	6.4	6.5	6.5	6.4	6.5	6.5	6.5	-1.0	hypothetical protein
VF2457to2458	2.2	2.3	2.1	2.2	2.3	2.1	2.4	2.3	1.1	2.1	2.3	2.0	2.1	2.2	2.2	2.0	2.1	-1.0	hypothetical protein
VF2458	6.0	5.4	4.3	5.2	5.2	5.0	6.0	5.4	1.1	6.0	5.5	4.8	5.4	4.8	5.5	4.8	5.0	-1.0	hypothetical protein
VF2459	6.3	5.7	5.3	5.8	5.5	5.2	6.1	5.6	-1.1	6.0	5.5	5.6	5.7	5.4	5.8	5.6	5.6	-1.1	hypothetical protein
VF2460	6.2	5.9	5.6	5.9	5.6	5.6	5.8	5.7	-1.2	6.0	5.4	5.5	5.6	5.5	5.4	5.7	5.5	-1.1	ATP-dependent DNA helicase RecG
VF2461	9.7	9.2	9.7	9.2	9.2	9.0	9.2	9.2	-1.1	9.4	9.0	9.4	9.4	9.4	9.2	9.6	9.4	-1.0	thiostrepton
VF2462	8.0	7.3	7.5	7.6	7.3	6.9	7.6	7.3	-1.3	7.8	7.1	7.3	7.4	6.9	6.9	6.9	6.9	-1.4	3'(2',5')-bisposphate nucleotidase
VF2463	9.3	8.7	8.7	8.9	8.6	8.4	8.9	8.7	-1.2	9.2	8.5	8.8	8.8	8.5	8.5	8.5	8.5	-1.3	ADP-ribose pyrophosphatase
VF2475	7.5	7.2	7.0	7.2	7.5	6.6	7.7	7.3	1.0	7.2	7.0	7.0	7.1	6.7	6.7	6.5	6.6	-1.4	general secretion pathway protein C
VF2476	7.3	6.5	6.5	6.8	6.1	6.3	6.5	6.3	-1.4	7.0	6.5	6.7	6.7	6.3	6.4	6.6	6.4	-1.2	heat shock protein 15
VF2477	8.5	8.0	7.9	8.1	8.5	7.7	8.6	8.3	-1.1	8.6	8.1	8.6	8.2	7.6	7.5	7.6	7.6	-1.1	Hsp35-like chaperonin
VF2478	8.2	8.7	8.8	8.6	7.9	8.3	8.1	8.1	-1.4	8.2	8.7	8.6	8.5	8.6	9.0	8.8	8.8	-1.2	phosphoenolpyruvate carboxykinase
VF2479	6.0	5.4	5.2	5.5	5.1	5.0	5.5	5.2	-1.3	6.0	4.9	5.3	5.4	4.9	4.9	5.0	4.9	-1.4	hypothetical protein
VF2480	7.0	6.4	6.4	6.6	6.0	6.1	6.2	6.1	-1.1	6.9	6.1	6.4	6.5	6.0	5.8	6.2	6.0	-1.4	sensory box/GGDEF family protein
VF2481	6.6	6.0	6.0	6.2	6.0	5.7	6.6	6.1	-1.4	6.4	5.7	5.8	6.0	5.7	5.7	5.5	5.6	-1.3	lysophospholipase L2
VF2482	7.0	6.3	6.4	6.6	6.1	6.5	6.6	6.4	-1.1	6.7	6.1	6.4	6.4	6.2	6.2	6.0	6.3	-1.2	hydrolase (HAD superfamily)
VF2483	7.5	6.9	7.1	7.2	6.6	6.7	6.7	6.7	-1.4	7.2	6.3	6.9	6.8	6.7	6.2	6.7	6.5	-1.2	tyrosine recombinase
VF2483to2484	9.0	8.5	8.6	8.7	8.3	8.5	8.7	8.5	-1.2	8.9	8.2	8.6	8.5	8.7	8.2	8.4	8.4	-1.1	tyrosine recombinase
VF2483to2484	4.9	4.9	4.3	4.7	3.6	4.6	4.0	4.1	-1.6	4.5	4.0	3.3	3.9	3.9	3.9	3.3	3.7	-1.2	tyrosine recombinase
VF2484	9.3	8.8	9.0	9.0	8.6	8.6	8.8	8.7	-1.3	9.2	8.3	9.0	8.8	8.8	8.2	8.7	8.6	-1.2	diaminopimelate epimerase
VF2485	6.6	5.9	5.9	6.3	6.2	6.3	6.3	6.3	-1.3	6.9	6.4	6.3	6.3	6.7	6.7	6.7	6.7	-1.4	diaminopimelate decarboxylase
VF2486	6.2	5.3	5.0	5.5	5.2	4.6	5.8	5.2	-1.2	5.8	5.0	5.3	5.4	5.0	5.2	4.8	5.0	-1.4	frataxin-like protein
VF2487	8.9	8.5	8.6	8.7	8.4	8.4	8.8	8.5	-1.1	8.7	8.4	8.5	8.5	8.3	8.2	8.4	8.3	-1.1	oligopeptidase A
VF2488	7.4	7.0	7.0	7.1	6.7	6.6	7.0	6.8	-1.3	7.2	6.5	6.9	6.9	6.8	6.7	6.9	6.8	-1.1	protein involved in external DNA uptake
VF2489	10.0	9.6	9.9	9.9	9.6	9.5	9.8	9.7	-1.1	9.8	9.6	9.8	9.8	9.8	9.8	10.0	9.9	-1.1	glutathione reductase
VF2490	5.6	5.2	4.8	5.2	5.0	5.0	5.3	5.1	-1.2	6.2	5.7	5.9	6.0	5.7	5.8	5.8	5.8	-1.1	hypothetical protein
VF2491	4.6	4.5	3.9	4.3	4.7	4.3	4.8	4.6	-1.2	4.6	4.6	4.3	4.5	4.4	4.4	4.2	4.3	-1.1	hypothetical protein
VF2493	4.4	3.4	3.0	3.6	2.9	3.3	3.6	3.3	-1.2	3.8	3.0	3.0	3.2	3.0	2.9	3.1	3.0	-1.2	thiol:disulfide interchange protein TlpA
VF2494	4.6	3.6	3.9	4.0	3.6	3.5	4.1	3.7	-1.2	4.3	3.4	3.4	3.7	3.4	3.6	3.8	3.6	-1.1	thiol:disulfide interchange protein DsbD
VF2494to2495	5.7	4.6	4.2	4.8	4.6	3.9	5.2	4.6	-1.2	5.3	4.2	4.1	4.5	3.9	3.7	3.2	3.6	-1.9	thiol:disulfide interchange protein DsbD
VF2494to2495	2.7	2.4	2.3	2.5	2.7	2.4	2.8	2.6	-1.4	2.6	2.4	2.4	2.4	2.4	2.5	2.4	2.4	-1.1	serine/threonine protein kinase
VF2496	5.1	4.0	3.5	4.2	3.2	3.5	3.6	3.4	-1.7	4.7	3.6	3.5	3.9	3.2	3.5	3.1	3.3	-1.6	hypothetical protein
VF2497	4.4	3.3	2.7	3.5	3.0	3.2	3.5	3.2	-1.2	4.0	3.2	3.5	3.6	2.8	3.1	2.7	2.8	-1.6	hypothetical protein
VF2498	5.3	4.2	3.8	4.4	3.3	3.4	4.3	3.6	-1.7	4.9	3.7	3.9	4.1	3.3	3.2	2.7	3.1	-2.1	DNA-directed RNA polymerase specialized sigma subunit
VF2499	5.2	4.0	4.1	4.4	4.0	4.0	4.5	4.2	-1.2	4.8	4.0	4.0	4.3	3.9	3.5	2.7	3.7	-1.5	hypothetical protein
VF2500	5.6	5.2	4.8	5.2	5.0	5.0	5.3	5.1	-1.1	5.2	5.2	5.1	5.2	4.7	5.3	5.1	5.0	-1.1	hypothetical protein
VF2501	5.5	5.2	5.0	5.2	5.1	5.0	5.1	5.1	-1.1	5.4	5.3	5.1	5.3	4.9	4.8	4.9	4.8	-1.3	hypothetical protein
VF2502	2.3	2.1	1.7	2.1	2.0	2.0	2.3	2.1	-1.2	2.3	2.1	2.1	2.2	2.0	1.9	1.8	1.9	-1.2	transcriptional regulator
VF2503	3.7	3.6	3.3	3.5	3.4	3.4	3.4	3.4	-1.2	3.7	3.2	3.3	3.4	3.4	3.5	3.2	3.4	-1.0	transcriptional regulator
VF2504	2.6	2.1	1.9	2.2	1.9	1.9	1.9	1.9	-1.1	2.2	1.9	1.8	2.0	1.5	1.7	1.7	1.7	-1.2	hypothetical cytosolic protein
VF2505	4.0	3.4	3.5	3.6	3.4	3.6	3.6	3.5	-1.1	3.8	3.4	3.6	3.6	3.3	3.2	3.4	3.3	-1.2	permease
VF2506	4.4	3.7	3.7	3.9	3.6	3.7	4.0	3.8	-1.1	4.2	3.4	4.0	3.9	3.7	3.4	3.6	3.6	-1.2	hypothetical protein
VF2507	4.8	4.2	3.9	4.3	4.3	3.9	4.7	4.3	-1.0	4.4	4.0	4.3	4.2	3.6	3.7	3.5	3.6	-1.6	dihydroorotase
VF2509	5.8	4.9	4.5	5.0	5.3	4.5	5.7	5.1	1.1	5.1	5.0	5.0	5.1	4.5	4.1	3.9	4.2	-1.8	2-dehydro-3-deoxyphosphogluconate aldolase
VF2511	6.1	5.5	4.8	5.5	6.0	5.3	6.4	5.9	1.4	5.9	5.7	5.0	5.5	5.2	5.9	5.1	5.4	-1.1	hypothetical protein
VF2512	6.4	5.8	5.5	5.9	6.7	5.5	7.1	6.4	1.4	6.0	6.1	5.5	5.8	5.4	5.5	5.2			

VF2554	7.7	7.3	7.5	7.5	7.5	7.0	7.6	7.4	-1.1	7.6	7.2	7.4	7.4	7.2	6.6	6.8	6.9	-1.5	1-acyl-sn-glycerol-3-phosphate acyltransferase
VF2560	10.7	9.8	9.8	9.9	10.0	10.4	10.5	10.3	1.3	10.0	9.3	9.7	9.7	10.2	10.0	9.8	10.0	1.3	threonine dehydratase
VF2570	11.8	11.6	11.8	11.8	11.4	11.3	11.5	11.4	-1.3	11.7	11.5	11.7	11.6	11.3	10.9	11.4	11.2	-1.3	ATP synthase subunit A
VF2571	11.4	11.1	11.1	11.2	11.0	10.7	11.2	11.0	-1.2	11.3	10.9	11.0	11.1	10.7	10.5	10.7	10.6	-1.4	ATP synthase subunit I
VF2572	8.8	8.6	8.7	8.7	8.2	8.6	8.6	8.5	-1.2	8.7	8.3	8.6	8.6	8.4	8.2	8.4	8.3	-1.2	chromosome partitioning protein ParB
VF2573	9.0	8.7	9.0	8.9	8.4	8.6	8.9	8.6	-1.2	8.9	8.4	8.8	8.7	8.6	8.2	8.7	8.5	-1.1	chromosome partitioning protein ParA
VF2574	9.0	8.7	8.9	8.9	8.3	8.6	8.8	8.6	-1.2	8.9	8.4	8.7	8.7	8.5	7.9	8.4	8.2	-1.4	glucose-inhibited division protein B
VF2575	9.5	9.3	9.3	9.4	8.9	9.2	9.1	9.1	-1.2	9.4	9.1	9.2	9.2	9.0	8.6	9.1	8.9	-1.3	glucose-inhibited division protein A
VFA0001	9.1	9.0	9.2	9.1	8.8	9.1	9.0	9.0	-1.1	9.0	9.0	9.1	9.0	9.2	9.0	9.2	9.1	-1.1	hypothetical protein
VFA0002	5.6	5.2	4.5	5.1	4.7	4.9	5.1	4.9	-1.1	5.4	5.2	4.7	5.1	4.9	5.3	5.2	5.1	1.0	translation initiation inhibitor
VFA0007	4.2	4.1	3.8	4.0	3.5	3.6	3.9	3.7	-1.3	3.8	4.2	3.9	4.0	3.9	3.8	3.3	3.7	-1.2	glutathione-dependent formaldehyde-activating enzyme
VFA0009	8.2	7.8	8.0	8.0	7.5	7.6	8.1	7.7	-1.2	8.0	8.2	8.0	8.1	7.7	8.4	7.8	8.0	-1.1	KaIA, catalase
VFA0011	3.9	3.1	2.8	3.3	2.9	2.9	3.1	3.0	-1.2	3.0	2.8	2.6	2.8	2.9	3.0	2.7	2.9	1.1	hypothetical protein
VFA0012	1.8	1.8	1.5	1.7	1.7	1.6	1.7	1.6	-1.0	1.7	1.7	1.6	1.7	1.6	1.6	1.5	1.6	1.1	hypothetical protein
VFA0014	6.5	6.7	6.2	6.5	7.3	6.6	7.1	7.0	1.5	6.4	7.1	6.2	6.6	6.2	6.6	6.1	6.3	-1.2	hypothetical protein
VFA0016	5.1	4.0	3.8	4.3	4.0	3.5	4.2	3.9	-1.3	4.4	3.8	4.2	4.1	3.7	3.3	3.6	3.5	-1.5	DNA polymerase III epsilon subunit (3'-5' exonuclease)
VFA0017to001	4.1	3.9	3.8	3.9	4.0	3.7	4.2	4.0	-1.0	4.2	4.0	4.0	4.1	3.7	3.6	3.9	3.6	-1.3	hypothetical protein
VFA017to001	4.2	3.2	2.9	3.4	2.9	2.6	3.3	2.9	-1.4	3.1	2.8	3.1	3.0	2.9	2.8	2.6	2.8	-1.2	hypothetical protein
VFA020	7.2	6.6	6.8	6.9	6.8	6.3	7.1	6.7	-1.1	7.1	6.8	7.0	7.0	6.5	6.4	6.3	6.4	-1.4	hypothetical protein
VFA020to001	4.3	4.1	3.7	4.1	3.9	3.9	4.2	4.0	-1.0	4.1	4.2	4.0	4.1	3.8	4.2	3.7	3.9	-1.2	hypothetical protein
VFA020to001	3.1	2.8	2.6	2.9	3.1	2.8	3.1	3.0	-1.1	3.2	3.0	2.6	2.9	2.9	2.9	2.5	2.8	-1.1	hypothetical protein
VFA021	3.9	3.1	2.9	3.3	2.9	3.0	3.9	3.3	-1.0	2.9	3.2	3.3	3.1	2.9	3.0	3.0	3.0	-1.1	di-tripeptide transporter
VFA022	3.6	2.9	2.9	3.2	3.3	3.2	3.7	3.4	1.2	3.4	3.2	3.0	3.2	3.1	3.3	2.9	3.1	-1.1	hypothetical protein
VFA023	4.6	4.3	3.8	4.2	4.4	4.0	4.5	4.3	1.0	4.6	4.1	4.1	4.2	3.7	4.1	4.0	3.9	-1.3	enoyl-CoA hydratase
VFA024	5.2	4.5	4.4	4.7	5.2	5.0	5.7	5.3	1.5	4.8	4.5	4.3	4.5	4.7	4.6	5.0	4.8	-1.2	transcriptional regulators, LysR family
VFA025	5.7	5.3	4.7	5.2	4.9	5.2	5.4	5.2	-1.0	5.4	5.2	4.9	5.2	4.9	4.9	4.8	4.9	-1.2	transcriptional regulator, MarR family
VFA026	4.6	4.1	3.9	4.2	4.0	4.1	4.3	4.2	-1.1	4.2	4.1	4.3	4.2	4.1	3.9	4.2	3.7	-1.2	4-oxalyl efflux transporter A
VFA029	6.8	6.3	6.2	6.4	6.9	6.0	7.2	6.7	1.2	6.6	6.7	6.1	6.4	5.9	6.1	6.0	6.0	-1.4	transcriptional regulator, AraC family
VFA030	6.4	6.1	6.1	6.2	5.9	5.8	6.2	6.0	-1.2	6.2	6.2	6.1	6.2	6.1	5.9	6.2	6.1	-1.1	transporter, drug/metabolite exporter family
VFA031	4.9	4.3	3.8	4.3	4.1	4.1	4.7	4.3	-1.0	4.8	4.2	4.1	4.4	4.2	4.1	4.1	4.0	-1.1	transcriptional regulators, LysR family
VFA032	4.4	3.6	3.5	3.8	3.7	2.9	4.4	3.6	-1.1	4.0	3.6	3.3	3.6	3.2	3.4	3.1	3.3	-1.3	thioredoxin peroxidase
VFA033	5.5	5.4	5.6	5.6	5.4	5.4	5.6	5.4	-1.0	5.7	5.6	5.3	5.4	5.3	5.3	5.3	5.3	-1.2	alkyl sulfatase
VFA036	5.8	5.2	4.9	5.3	5.1	5.1	5.1	5.1	-1.1	5.4	5.2	5.1	5.2	5.2	5.1	4.7	5.0	-1.2	hypothetical protein
VFA037	6.2	5.5	5.3	5.7	5.3	5.3	5.8	5.5	-1.2	6.0	5.4	5.4	5.6	5.3	5.1	5.5	5.3	-1.2	hypothetical protein
VFA038	6.9	6.3	6.5	6.6	6.0	6.0	6.5	6.2	-1.3	6.8	6.4	6.4	6.5	6.3	6.4	6.6	6.4	-1.0	transcriptional regulators, LysR family
VFA039	4.8	4.4	4.3	4.5	4.3	4.2	4.2	4.2	-1.2	4.3	4.3	4.3	4.3	4.0	3.9	4.0	4.0	-1.2	regulatory protein UhpC
VFA040	3.9	3.6	3.1	3.5	3.3	3.4	3.3	3.3	-1.1	3.5	3.5	3.3	3.4	3.3	3.4	3.2	3.4	-1.2	sensor protein UhpB
VFA041	5.3	4.7	4.8	4.9	4.5	4.8	4.9	4.7	-1.1	5.0	4.8	4.6	4.8	4.7	4.8	4.6	4.7	-1.1	two component response regulator UhpA
VFA042	4.0	4.0	3.7	3.9	3.7	3.5	3.9	3.7	-1.2	4.0	3.6	3.7	3.7	3.7	3.7	3.8	3.7	-1.1	hexose phosphate transport protein
VFA043	6.9	6.6	6.4	6.6	6.3	6.6	6.6	6.5	-1.3	6.7	6.6	6.3	6.6	6.3	6.8	6.4	6.5	-1.0	transcriptional regulator, TetR family
VFA044	3.8	3.7	3.7	3.7	4.0	4.0	3.9	4.0	-1.2	3.7	3.9	3.9	3.8	3.8	4.1	3.7	3.9	1.0	acriflavine resistance periplasmic protein
VFA045	4.6	4.1	3.9	4.2	3.9	4.2	4.6	4.2	-1.0	4.2	4.0	4.2	4.1	4.2	4.0	4.0	3.8	-1.1	hypothetical protein
VFA046	4.0	3.3	3.6	3.6	3.6	3.6	3.9	3.7	-1.1	3.5	3.7	3.5	3.6	3.8	3.5	3.4	3.6	-1.0	transporter
VFA047	5.2	4.6	4.8	4.9	4.7	4.7	5.1	4.9	-1.0	4.9	5.0	4.3	4.7	4.7	4.6	4.5	4.6	-1.1	acriflavine resistance plasma membrane protein
VFA048	6.9	6.7	6.5	6.7	6.1	6.3	6.6	6.3	-1.3	6.9	6.7	6.7	6.8	6.3	6.2	6.5	6.3	-1.4	hypothetical protein
VFA050	5.2	5.0	5.1	5.1	4.7	5.0	5.1	4.9	-1.1	5.0	4.9	4.8	4.9	5.2	4.9	4.6	4.9	1.0	transporter
VFA053	5.4	4.7	4.9	4.9	4.9	4.8	5.1	4.9	-1.1	5.2	4.6	4.5	4.8	4.3	4.2	4.5	4.3	-1.4	transcriptional regulators, LysR family
VFA054	6.0	5.3	5.0	5.4	4.9	5.3	5.3	5.2	-1.2	5.6	5.3	4.9	5.3	5.0	5.1	5.0	5.0	-1.2	transcriptional regulator, Cro/Cli family
VFA055	6.4	6.2	5.9	6.2	5.5	6.2	5.9	5.9	-1.2	6.1	6.2	5.9	6.1	6.2	6.2	6.2	6.2	1.1	hypothetical protein
VFA057	3.9	3.3	2.9	3.3	3.3	3.2	3.5	3.3	-1.0	3.4	3.2	3.1	3.2	2.8	3.0	2.5	2.8	-1.3	sensor protein
VFA058	4.3	4.3	3.9	4.1	4.6	3.9	4.6	4.4	-1.2	4.0	4.3	4.0	4.1	3.6	4.0	3.5	3.7	-1.3	hypothetical protein
VFA059	3.5	3.1	3.1	3.2	3.0	2.8	3.3	3.0	-1.2	2.9	3.2	2.9	3.0	2.9	2.6	2.9	2.8	-1.2	3-oxo-dependent outer membrane receptor
VFA059to001	2.1	1.8	1.8	1.9	2.1	1.9	2.0	2.0	-1.1	2.3	2.0	1.9	2.1	1.9	1.9	1.9	1.9	-1.1	TonB-dependent outer membrane receptor
VFA060	3.3	3.0	2.4	2.9	2.8	2.6	3.3	2.9	-1.0	3.1	3.1	2.8	3.0	2.5	2.7	2.3	2.5	-1.4	PTS system, mannitol-specific IIA component
VFA063	6.8	6.4	6.4	6.6	5.9	6.2	6.5	6.2	-1.3	6.7	6.5	6.4	6.5	6.2	6.3	6.2	6.3	-1.2	transcriptional regulator
VFA064	6.3	5.8	5.7	5.9	5.5	5.5	6.0	5.7	-1.2	6.1	5.9	5.6	5.9	5.2	5.4	5.3	5.3	-1.5	hypothetical protein
VFA065	6.7	6.3	6.0	6.3	6.0	5.8	6.4	6.1	-1.2	6.6	6.4	6.0	6.3	6.2	5.7	5.9	5.8	-1.4	hypothetical protein
VFA066	1.6	1.5	1.3	1.5	1.4	1.5	1.4	1.4	-1.1	1.5	1.4	1.2	1.4	1.4	1.4	1.3	1.4	-1.0	hypothetical protein
VFA067	3.6	3.3	3.1	3.3	3.0	3.4	3.3	3.2	-1.1	3.2	3.4	3.1	3.2	2.9	2.9	3.3	3.1	-1.1	oxalate/formate antiporter
VFA068	2.6	2.4	2.1	2.4	2.1	2.1	2.2	2.1	-1.2	2.5	2.2	2.2	2.3	2.2	2.4	2.1	2.2	-1.1	hypothetical protein
VFA069	5.1	4.8	4.5	4.8	4.6	4.4	5.0	4.7	-1.1	4.9	4.8	4.2	4.6	4.2	4.2	4.2	4.1	-1.4	hypothetical protein
VFA071	9.6	9.8	9.5	9.6	10.8	9.8	9.2	9.9	-1.3	9.5	9.2	9.3	9.3	8.2	8.3	8.7	8.4	-1.9	hypothetical protein
VFA072	9.2	9.5	9.4	9.4	10.4	9.5	7.2	9.0	-1.3	8.7	8.0	8.2	8.3	7.2	7.5	8.2	7.6	-1.6	sensor protein LuxQ
VFA073	5.1	4.7	4.7	4.8	5.0	4.6	4.2	4.6	-1.0	4.8	4.3	4.1	4.4	4.1	3.9	4.2	4.1	-1.3	di-tripeptide transporter
VFA080	4.3	4.1	3.8	4.1	3.8	4.3	4.6	4.2	-1.1	4.1	4.3	3.6	4.0	3.4	3.9	3.8	3.7	-1.2	anaerobic dimethyl sulfoxide reductase chain C
VFA081	3.8	3.9	3.4	3.7	3.6	3.6	4.0	3.7	-1.0	3.8	3.4	3.4	3.5	3.4	3.3	3.3	3.3	-1.2	anaerobic dimethyl sulfoxide reductase chain B
VFA082	4.2	4.1	4.1	4.1	4.2	3.8	4.3	4.1	-1.0	4.0	4.2	3.8	4.0	3.8	3.5	3.6	3.6	-1.3	anaerobic dimethyl sulfoxide reductase chain A
VFA083	3.0	3.1	2.8	3.0	2.9	3.1	3.1	3.0	-1.0	3.0	3.1	3.0	3.0	2.9	3.1	2.7	2.9	-1.1	anaerobic dimethyl sulfoxide reductase chain YnfI
VFA084	3.8	3.8	3.4	3.7	3.9	3.8	3.8	3.9	-1.0	3.9	4.0	3.6	3.8	3.8	3.9	3.7	3.8	-1.0	ferredoxin-type protein NapF
VFA087	5.7	5.2	4.7	5.2	5.3	5.0	5.6	5.3	-1.1	5.2	5.2	5.1	5.2	4.7	5.0	4.9	4.9	-1.2	outer membrane protein RomA
VFA088	7.5	7.4	7.4	7.4	7.5	7.6	7.7	7.6	1.1	7.3	7.4	7.3	7.3	7.6	7.6	7.8	7.7	1.3	transcriptional regulator
VFA089	6.0	5.9	5.6	5.8	5.9	5.6	6.1	5.9	-1.0	5.8	5.7	5.7	5.7	5.2	5.8	5.5	6.5	-1.1	hypothetical hydrolase/lipase
VFA090	4.2	3.2	2.9	3.4	3.5	3.2	3												

VFA0116	5.4	4.5	4.2	4.7	4.3	4.3	5.0	4.5	-1.1	5.0	4.4	4.4	4.2	4.2	4.3	-1.3	acetyltransferase	
VFA0116	7.2	6.9	7.0	7.1	6.6	6.6	6.8	6.7	-1.3	7.2	6.8	6.8	6.6	6.7	6.8	-1.1	virulence factor MvM	
VFA0117	4.9	4.4	4.3	4.5	4.2	4.3	4.5	4.3	-1.4	4.8	4.2	3.9	4.0	3.9	4.2	4.1	transporter, drug/metabolite exporter family	
VFA0118	6.4	6.6	6.6	6.5	6.8	6.8	7.3	7.0	-1.4	6.3	7.1	6.7	6.7	6.9	7.6	7.1	morphinone reductase	
VFA0119	6.3	6.4	6.4	6.4	6.6	6.7	7.1	6.8	1.3	6.0	6.8	6.2	6.3	6.6	7.1	6.7	lactoylglutathione lyase	
VFA0120	6.3	6.5	6.5	6.4	6.2	6.0	7.4	6.5	1.1	6.5	6.7	6.9	6.7	7.0	6.7	5.7	hypothetical cytosolic protein	
VFA0121	5.3	5.1	4.9	5.1	5.2	5.1	6.2	5.5	1.3	5.1	5.7	5.2	5.4	5.1	5.2	4.1	hypothetical protein	
VFA0122	4.1	4.2	3.8	4.0	4.1	3.5	4.1	3.9	-1.1	4.0	4.1	3.8	4.0	3.7	3.9	3.9	hypothetical protein	
VFA0124	10.5	10.2	10.4	10.4	10.6	10.7	10.8	10.7	1.3	10.4	10.1	10.3	10.3	10.7	10.6	10.8	10.7	di-/tripeptide transporter
VFA0125	6.5	6.5	6.4	6.5	6.6	6.7	6.7	6.8	1.2	6.5	6.4	6.4	6.5	6.6	6.6	6.6	6.6	rhodanese-related sulfurtransferase
VFA0126	6.6	6.0	5.6	6.1	5.9	5.8	6.3	6.0	-1.1	6.6	6.1	5.9	6.2	5.6	5.9	5.7	5.7	DNA-3-methyladenine glycosylase
VFA0127	6.5	6.4	5.9	6.3	6.7	6.2	6.8	6.5	1.2	6.4	6.7	6.4	6.5	6.1	6.7	6.2	6.3	hypothetical protein
VFA0130	5.8	5.5	4.6	5.3	4.8	4.8	5.3	5.0	-1.3	5.6	5.4	5.0	5.3	4.3	5.0	4.2	4.5	PTS system, 3-keto-L-gulonate specific IIA component
VFA0132	6.6	6.3	5.2	6.0	5.7	5.3	5.7	5.6	-1.4	6.5	5.9	6.0	6.1	5.2	5.6	5.4	5.4	hypothetical protein
VFA0133	6.1	5.4	5.1	5.6	5.7	4.8	6.0	5.5	-1.0	5.8	5.5	5.2	5.5	5.2	4.8	5.1	5.0	hypothetical protein
VFA0134	3.5	3.5	3.5	3.5	3.4	3.2	3.3	3.3	-1.2	3.6	3.5	3.2	3.4	3.7	3.4	3.4	3.5	hypothetical protein
VFA0135	4.7	4.4	3.7	4.3	4.1	3.9	4.4	4.1	-1.1	4.3	4.7	4.0	4.3	3.9	4.5	3.6	4.0	DNA helicase II
VFA0136	6.8	6.3	6.4	6.5	6.1	6.1	6.4	6.2	-1.2	6.7	6.3	6.4	6.5	6.2	6.3	6.0	6.2	hypothetical protein
VFA0137	6.5	6.1	5.7	6.1	5.6	5.9	5.7	5.7	-1.2	6.2	5.7	5.9	6.0	5.8	5.6	5.8	5.8	Type II restriction-modification system methylation subunit
VFA0138	6.7	6.2	5.5	6.1	5.6	5.8	6.1	5.8	-1.2	6.4	6.2	6.1	6.2	6.0	6.2	6.1	6.1	hypothetical protein
VFA0139	4.1	3.6	3.8	3.8	3.4	3.2	3.7	3.4	-1.3	3.4	3.7	3.7	3.6	3.6	3.4	3.7	3.5	hypothetical protein
VFA0139to01	3.4	3.3	2.5	3.1	3.1	2.8	3.3	3.1	1.0	3.1	3.1	2.8	3.0	2.7	2.8	2.8	2.8	hypothetical protein
VFA0139to01	4.1	3.8	3.6	3.8	3.6	3.4	3.8	3.6	-1.2	4.2	3.7	3.9	3.9	3.7	3.8	3.5	3.7	hypothetical protein
VFA0140	5.8	5.2	5.0	5.3	4.9	4.7	5.2	4.9	-1.3	5.8	5.1	5.1	5.3	4.8	5.2	4.8	4.9	hypothetical protein
VFA0141	4.0	3.8	3.6	3.8	3.8	3.7	4.0	3.8	1.0	3.8	3.9	3.1	3.6	3.5	3.6	3.5	3.5	transporter, divalent anion:sodium symporter family
VFA0141to01	4.2	4.1	3.9	4.1	3.6	3.5	3.9	3.6	-1.3	4.1	3.7	3.9	3.9	3.7	3.5	3.7	3.7	transporter, divalent anion:sodium symporter family
VFA0141to01	3.4	3.2	3.2	3.3	3.2	3.2	3.3	3.0	1.0	3.2	3.2	3.2	3.2	3.1	3.2	3.1	3.1	transporter, divalent anion:sodium symporter family
VFA0142	5.0	4.5	4.4	4.6	4.5	4.5	4.6	4.5	-1.1	4.7	4.2	4.3	4.4	4.4	4.1	3.9	4.1	formate acetyltransferase
VFA0142to01	3.5	3.1	2.5	3.0	3.1	2.8	3.3	3.0	-1.1	2.7	3.2	2.7	2.9	2.8	2.9	2.5	2.7	formate acetyltransferase
VFA0142to01	2.9	2.6	2.2	2.6	2.5	2.3	2.5	2.5	-1.1	2.4	2.6	2.4	2.5	2.2	2.4	2.1	2.3	formate acetyltransferase
VFA0143	3.9	3.8	3.7	3.8	3.5	3.9	3.7	3.7	-1.0	3.7	3.7	3.6	3.7	3.9	3.5	3.4	3.6	chitin binding protein
VFA0144	4.1	3.6	2.4	3.4	3.6	2.4	2.4	2.5	-1.0	4.0	3.7	4.0	3.8	3.5	3.6	3.1	3.4	3-oxo-halobutrin
VFA0145	6.9	6.6	6.3	6.6	6.4	6.1	6.7	6.4	-1.1	6.9	6.5	6.5	6.6	6.6	6.4	6.5	6.5	hypothetical protein
VFA0146	5.5	5.1	4.6	5.0	4.8	4.9	5.3	5.0	-1.0	4.8	5.0	4.9	4.9	4.9	5.2	4.9	5.0	hypothetical protein
VFA0147	8.0	8.3	7.6	8.0	7.9	6.7	7.9	7.5	-1.4	8.1	9.4	8.2	8.6	7.9	9.6	8.3	8.6	hypothetical protein
VFA0148	4.2	4.0	3.5	3.9	3.5	3.7	4.1	3.8	-1.1	4.2	4.6	3.5	4.1	3.1	4.5	3.5	3.7	PIA-like type-IV pilus protein
VFA0152	4.8	4.1	3.8	4.2	3.8	4.2	3.8	4.5	-1.2	4.3	4.2	3.8	4.1	4.3	3.9	4.0	4.1	hypothetical protein
VFA0153	4.6	4.1	4.0	4.2	4.1	3.9	4.4	4.1	-1.1	4.1	4.3	4.3	4.2	4.4	4.1	4.0	4.2	multidrug resistance protein D
VFA0154	7.6	6.9	6.9	7.1	6.5	6.6	6.8	6.6	-1.4	7.4	6.8	6.7	7.0	6.5	6.5	6.6	6.5	ATP-dependent RNA helicase DbpA
VFA0155	5.2	4.6	4.2	4.7	4.1	4.4	4.8	4.4	-1.2	4.9	4.6	4.4	4.6	4.0	4.5	3.9	4.1	sensor box/GGDEF family protein
VFA0175	5.0	4.6	4.5	4.7	4.4	4.3	4.7	4.5	-1.2	4.6	4.6	4.4	4.5	4.4	3.8	4.0	4.1	hypothetical membrane spanning protein
VFA0176	6.7	6.4	5.9	6.4	6.4	6.5	6.6	6.4	-1.1	6.5	6.0	6.2	6.2	6.6	6.3	6.6	6.5	transcriptional regulator, ArsR family
VFA0177	7.0	6.6	6.4	6.6	6.5	6.8	6.8	6.7	-1.0	6.7	6.4	6.4	6.5	6.6	6.7	6.6	6.6	OS-methylguanine-DNA methyltransferase
VFA0179	8.2	8.4	7.9	8.1	8.3	7.6	8.4	8.1	-1.0	8.1	8.6	8.1	8.2	7.5	7.9	7.3	7.6	transcriptional activator protein ItrR
VFA0180	6.5	6.5	5.8	6.3	5.9	5.8	6.3	6.0	-1.2	6.3	6.5	6.3	6.4	5.9	6.2	5.9	6.0	hypothetical protein
VFA0183	3.8	3.9	3.7	3.8	3.7	3.8	4.3	3.9	-1.1	3.8	3.7	3.3	3.6	3.6	3.7	3.5	3.6	hypothetical protein
VFA0184	3.4	2.9	2.5	2.9	3.1	2.9	3.4	3.4	-1.4	2.9	3.2	2.4	2.9	2.4	2.5	2.4	2.4	hypothetical protein
VFA0186	5.3	5.1	4.7	5.0	5.1	4.9	5.4	5.1	1.1	5.0	5.3	4.9	5.1	4.4	4.9	4.1	4.5	chemotaxis MotA protein
VFA0187	4.3	4.1	3.8	4.1	4.1	4.0	4.5	4.2	-1.1	4.2	4.4	4.1	4.2	4.3	4.4	3.8	4.1	chemotaxis MotB protein
VFA0188	6.0	5.8	5.9	5.9	5.2	5.6	5.6	5.5	-1.3	5.8	5.7	5.8	5.8	5.6	5.4	5.2	5.4	biotin sulfoxide reductase
VFA0189	4.6	4.1	3.9	4.2	3.5	3.5	3.8	3.6	-1.5	4.0	3.7	3.6	3.8	3.3	3.4	3.7	3.5	cytochrome c-type protein TorC
VFA0190	5.1	5.6	5.4	5.4	5.4	5.4	5.4	5.4	-1.9	5.4	5.4	5.4	5.4	5.4	5.4	5.4	5.4	hypothetical protein
VFA0198	9.3	9.6	9.2	9.4	9.3	8.8	9.5	9.2	-1.1	9.3	9.7	9.4	9.4	8.8	9.3	8.7	8.9	transcriptional repressor
VFA0202	3.7	3.4	3.1	3.4	3.1	3.2	3.7	3.3	-1.0	3.3	3.4	3.2	3.3	3.1	3.3	3.0	3.1	hypothetical protein
VFA0203	2.3	2.1	1.7	2.0	2.0	2.0	2.1	2.0	-1.0	2.1	2.1	1.8	1.9	1.9	2.1	1.8	1.9	hypothetical protein
VFA0204	5.7	5.0	5.1	5.3	5.4	5.7	5.8	5.6	-1.3	5.0	4.6	5.1	4.9	5.5	5.0	5.7	5.4	hypothetical protein
VFA0207	6.4	6.4	6.0	6.3	7.4	6.4	7.6	7.1	-1.8	6.2	6.7	6.0	6.3	5.4	5.8	5.5	6.6	hypothetical protein
VFA0208	6.1	6.2	6.0	6.1	6.0	6.0	5.9	6.0	-1.1	6.0	5.9	5.9	5.9	6.3	6.1	6.0	6.2	arylsulfatase regulator (Fe-S oxidoreductase)
VFA0209	4.4	4.2	3.9	4.2	3.8	3.8	4.4	4.0	-1.1	4.3	4.1	3.8	4.1	3.6	3.7	3.9	3.7	phosphatidylserine decarboxylase
VFA0211	6.8	6.5	6.3	6.5	6.4	6.6	6.7	6.6	-1.0	6.6	6.3	6.3	6.4	6.5	6.6	6.4	6.5	transcriptional regulator
VFA0212	6.4	6.1	6.0	6.2	5.7	5.8	5.9	5.8	-1.3	6.2	5.8	5.8	5.9	5.9	5.5	5.6	5.7	two component sensor kinase
VFA0213	3.8	3.7	3.6	3.7	3.8	3.5	3.7	3.7	-1.0	3.7	3.3	4.0	3.7	3.2	3.8	3.6	3.5	sulfatase family protein
VFA0214	4.5	3.8	3.4	3.9	2.8	3.3	3.9	3.3	-1.5	4.0	3.4	3.3	3.6	2.8	3.3	3.2	3.1	probable transcriptional regulator SyrB
VFA0215	2.9	2.4	2.5	2.6	2.4	2.5	2.4	2.4	-1.1	2.6	2.5	2.5	2.5	2.3	2.5	2.5	2.4	hypothetical protein
VFA0216	3.8	3.0	2.8	3.2	2.6	2.6	3.3	2.8	-1.3	3.3	2.9	3.1	3.1	2.8	2.8	2.7	2.8	hypothetical protein
VFA0217	3.3	2.6	2.4	2.8	2.7	2.4	3.4	2.8	-1.0	3.2	2.8	2.3	2.8	2.3	2.6	2.4	2.4	hypothetical protein
VFA0218	3.9	3.1	3.1	3.3	2.5	2.5	3.0	2.7	-1.6	3.8	2.7	2.9	3.1	2.5	2.6	2.4	2.5	fimbrial protein precursor Flp1
VFA0219	2.3	2.2	2.2	2.2	2.2	2.3	2.4	2.3	1.1	2.2	2.2	2.3	2.2	2.2	2.2	2.2	2.2	tungstate-binding protein precursor
VFA0220	3.8	3.7	3.3	3.6	3.6	3.6	4.0	3.7	-1.1	3.6	3.3	3.0	3.3	3.1	3.2	3.2	3.2	general secretion pathway protein D
VFA0221	4.8	4.7	4.1	4.6	3.7	4.2	4.6	4.2	-1.3	4.6	4.4	4.3	4.5	3.9	4.1	3.8	3.9	hypothetical protein
VFA0222	4.9	4.5	4.2	4.5	4.0	4.5	4.6	4.4	-1.1	4.3	4.5	4.5	4.4	3.9	4.1	4.1	4.1	ATPase involved in chromosome partitioning
VFA0223	5.2	4.8	4.3	4.8	4.2	4.9	5.0	4.7	-1.0	4.8	4.7	4.5	4.7	4.2	4.4	4.2	4.3	putative type IV secretion NTPase similar to Tada
VFA0224	3.2	3.4	3.1	3.2	3.4	3.4	3.5	3.4	1.1	3.4	3.6	3.3	3.4	3.6	3.5	3.4	3.5	TadB-like protein involved in pilus formation and/or protein secretion
VFA0225	1.9	1.8	1.8	1.8	1.9	1.9	1.9	1.9	1.1	1.9	2.0	2.0	2.0	2.0	2.0	2.0	2.1	bipartite nuclear localization signal containing protein, similar to TadC
VFA0226	2.3	2.2	2.3	2.3	2.4	2.3	2.4	2.4	1.1	2.2	2.4	2.2	2.3	2.3	2.3	2.4	2.3	secretory protein containing TPR-repeats, similar to TadD
VFA0227	1.9	1.7	1.9	1.8	2.1	2.1	1.9	2.0	1.1	1.9	2.0	2.0	2.0	2.1	2.0	1.9	2.0	TadE-like protein
VFA0228	1.8	1																

VFA0250	3.5	3.3	3.8	3.5	3.6	3.6	3.6	3.6	1.0	3.8	3.6	3.7	3.7	3.4	3.5	3.6	3.5	-1.1	anaerobic glycerol-3-phosphate dehydrogenase subunit A	
VFA0251	6.1	5.2	6.1	6.1	5.6	5.2	6.2	6.4	-1.0	5.9	5.3	5.9	5.9	6.2	6.1	6.3	6.2	1.2	NAD(+)-dependent formate dehydrogenase alpha subunit	
VFA0252	5.4	5.3	5.1	5.3	4.8	5.3	5.3	5.1	-1.1	5.0	5.3	5.3	5.2	5.4	5.3	5.2	5.3	1.1	NADP-dependent formate dehydrogenase alpha subunit	
VFA0253	4.6	4.1	3.9	4.2	3.6	3.7	3.8	3.7	-1.4	4.4	3.9	4.2	4.2	3.9	4.2	3.6	3.9	-1.2	peptidase T	
VFA0254	2.9	2.4	2.2	2.5	2.2	2.3	2.3	2.2	-1.2	2.8	2.4	2.5	2.5	2.3	2.5	2.1	2.3	-1.2	hypothetical protein	
VFA0254a002	1.8	1.8	1.4	1.6	1.5	1.6	1.6	1.6	-1.0	1.6	1.6	1.6	1.6	1.5	1.6	1.4	1.5	-1.0	hypothetical protein	
VFA0254a002	2.0	1.9	1.7	1.9	1.9	1.9	2.1	2.0	1.1	1.9	1.9	1.7	1.8	1.9	1.8	1.9	1.6	-1.0	hypothetical protein	
VFA0255	7.5	7.2	7.2	7.3	6.9	7.4	7.5	7.3	-1.0	7.5	7.2	7.1	7.2	7.3	7.4	7.4	7.4	1.1	transcriptional regulator, AraC family	
VFA0256	6.2	5.9	5.8	6.0	5.9	5.9	6.5	6.1	-1.1	6.0	6.1	5.8	6.0	5.9	5.7	6.1	5.9	-1.0	hypothetical protein	
VFA0261	8.0	7.7	7.8	7.8	7.6	7.3	8.1	7.7	-1.1	7.9	7.6	7.7	7.7	7.4	6.9	7.4	7.2	-1.4	modulator of glutathione-dependent potassium efflux system	
VFA0263	6.9	6.7	6.2	6.6	6.3	6.3	6.2	6.3	-1.3	6.7	6.6	6.6	6.6	6.2	6.8	6.3	6.4	-1.2	hypothetical protein	
VFA0264	7.5	7.4	7.4	7.4	6.7	7.2	7.0	7.0	-1.4	7.3	7.2	7.4	7.3	7.3	7.2	7.4	7.3	-1.0	oxidoreductase (iron-sulfur cluster biosynthesis)	
VFA0265	6.4	6.1	5.7	6.1	5.5	5.9	5.8	5.8	-1.3	6.1	6.0	5.9	6.0	5.7	5.8	5.7	5.7	-1.2	hypothetical protein	
VFA0266	7.0	6.7	6.4	6.7	6.1	6.5	6.5	6.4	-1.3	6.8	6.6	6.6	6.7	6.7	6.6	6.6	6.6	-1.2	transcriptional regulator	
VFA0267	5.5	5.0	4.6	5.0	4.8	4.7	5.2	4.9	-1.1	5.3	5.3	4.7	5.1	5.1	4.9	4.8	4.9	-1.1	hypothetical protein	
VFA0269	7.9	8.0	7.8	7.9	8.7	7.5	8.8	8.3	-1.3	7.6	8.6	8.1	8.1	7.3	7.5	6.9	7.2	-1.8	hypothetical protein	
VFA0270	6.9	6.6	6.5	6.7	7.3	6.1	7.5	6.9	1.2	6.7	6.8	6.4	6.6	6.1	6.1	5.8	6.0	-1.5	transcriptional regulator	
VFA0271	6.2	5.8	5.5	5.9	6.2	5.6	6.4	6.0	1.1	5.8	6.1	5.5	5.8	5.1	5.3	5.1	5.2	-1.6	transcriptional regulators, LysR family	
VFA0272	8.6	8.3	8.5	8.5	8.5	8.4	8.8	8.5	1.0	8.6	8.4	8.5	8.5	8.6	8.4	8.5	8.5	-1.0	integral membrane protein	
VFA0274	9.3	9.6	9.7	9.5	8.7	9.4	9.0	9.1	-1.4	9.0	9.8	9.8	9.5	9.7	9.9	10.0	9.9	1.3	acyl-CoA desaturase	
VFA0275	6.5	6.5	5.9	6.3	6.3	6.2	6.4	6.3	-1.0	6.3	6.5	6.3	6.4	6.3	6.9	6.5	6.6	1.2	hypothetical protein	
VFA0276	6.9	6.6	6.4	6.6	6.6	6.6	6.9	6.7	1.1	6.8	6.7	6.5	6.7	6.7	6.9	6.8	6.8	1.1	sensory transduction/ GGDEF family protein	
VFA0278	5.3	4.6	4.6	4.8	4.4	4.1	5.0	4.5	-1.3	5.1	4.3	4.6	4.7	4.1	4.1	3.9	4.0	-1.6	tellurium resistance protein TerC	
VFA0280	6.0	5.9	5.3	5.8	5.2	5.7	5.7	5.5	-1.2	5.7	6.0	5.8	5.8	5.4	5.9	5.5	5.6	-1.2	hypothetical protein	
VFA0281	4.1	3.9	3.7	3.9	3.6	3.5	4.1	3.7	-1.1	4.0	3.8	3.7	3.8	4.1	3.7	3.6	3.8	-1.0	anaerobic ribonucleoside triphosphate reductase	
VFA0282	3.5	2.9	2.7	3.0	3.1	3.1	3.2	3.1	-1.1	3.1	2.9	2.9	3.0	3.1	3.2	2.6	2.9	-1.0	anaerobic ribonucleoside-triphosphate reductase activating protein	
VFA0283	6.1	6.6	6.6	6.7	6.6	6.6	6.8	6.7	-1.0	6.6	6.6	6.6	6.6	6.6	6.6	6.5	6.9	8.7	10.9	aspartate aminotransferase
VFA0284	9.9	9.8	9.4	9.7	10.0	9.6	9.9	9.8	1.1	9.9	9.8	9.4	9.7	9.1	9.5	9.3	9.3	-1.3	ATP-dependent Zn protease	
VFA0286	4.3	3.8	3.6	3.9	3.7	3.6	4.0	3.8	-1.1	3.8	4.1	3.6	3.9	4.0	3.8	3.1	3.6	-1.2	amino-acid abc transporter binding protein	
VFA0287	4.8	4.2	3.6	4.2	4.6	4.9	5.1	4.8	1.5	4.9	4.0	3.9	4.3	4.9	3.9	3.9	3.9	-1.0	hypothetical protein	
VFA0288	5.7	5.4	5.0	5.4	5.7	5.1	6.1	5.6	1.2	5.3	5.7	5.4	5.5	4.9	5.5	4.9	5.1	-1.3	protein YgiW precursor	
VFA0289	6.9	6.6	6.3	6.6	6.6	6.6	6.6	6.6	-1.0	6.6	6.6	6.6	6.6	6.6	6.6	6.6	6.6	-1.1	cybatic acid synthase	
VFA0290	7.3	7.1	7.1	7.2	6.7	7.3	7.2	7.1	-1.1	7.1	7.0	6.9	7.0	7.1	6.9	7.2	7.1	1.0	molybdate-binding protein	
VFA0291	7.1	6.9	6.9	7.0	6.7	6.9	6.7	6.8	-1.1	7.0	6.7	6.7	6.8	6.6	6.3	6.7	6.5	-1.2	molybdate transport permease protein	
VFA0292	6.9	6.4	6.5	6.6	5.7	6.4	6.1	6.1	-1.4	6.6	6.3	6.4	6.4	6.2	5.7	6.3	6.1	-1.3	molybdenum transport ATP-binding protein ModC	
VFA0293	6.3	6.0	6.0	6.1	5.8	5.9	5.8	5.8	-1.2	6.2	6.1	5.9	6.1	6.0	6.2	6.1	6.1	-1.0	nucleotidase	
VFA0294	7.6	7.7	7.3	7.5	7.1	7.5	7.1	7.2	-1.2	7.1	7.5	7.5	7.6	7.3	7.7	7.5	7.5	-1.0	hypothetical protein	
VFA0295	8.2	8.3	7.9	8.1	7.7	8.0	7.7	7.8	-1.3	8.2	8.0	8.1	8.1	8.0	8.2	8.2	8.1	1.0	nucleo/protein/poly/nucleotide-associated enzyme	
VFA0296	5.7	4.9	5.0	5.2	4.5	4.6	4.9	4.7	-1.4	5.3	5.0	4.9	5.1	4.9	4.9	4.8	4.9	-1.1	hypothetical protein	
VFA0297	8.7	8.8	9.0	8.8	9.3	8.4	9.2	9.0	1.0	8.6	9.0	8.9	8.8	8.4	8.2	8.2	8.3	-1.5	TorE protein	
VFA0300	5.4	5.2	5.0	5.2	5.0	5.3	5.5	5.3	1.2	5.1	5.3	5.1	5.2	5.0	5.2	4.9	5.0	-1.1	methyl-accepting chemotaxis protein	
VFA0301	7.3	7.2	7.1	7.2	6.6	7.0	7.0	6.9	-1.2	7.2	7.3	7.0	7.1	7.0	7.4	7.3	7.3	1.1	alpha-galactosidase	
VFA0302	5.0	5.0	4.8	4.9	4.6	4.9	5.0	4.8	-1.1	4.9	5.0	5.0	4.9	4.7	4.6	4.3	4.5	-1.4	methyl-accepting chemotaxis protein	
VFA0303	3.3	3.5	2.8	3.2	2.8	2.9	2.9	2.8	-1.3	3.3	3.3	2.9	3.2	2.8	2.9	2.4	2.7	-1.4	hypothetical protein	
VFA0310	5.9	5.1	4.9	5.3	5.3	5.3	5.6	5.4	1.0	5.6	5.1	4.9	5.2	5.0	4.8	5.1	5.2	-1.0	psp operon transcriptional activator	
VFA0311	6.9	6.5	6.4	6.6	6.5	6.7	7.4	6.9	1.2	6.7	6.7	6.4	6.6	6.6	6.7	6.7	6.6	1.0	phage shock protein A	
VFA0312	7.0	6.7	6.7	6.8	6.8	6.7	7.3	6.9	1.1	6.7	6.7	6.7	6.8	6.9	6.5	6.8	6.7	-1.8	phage shock protein B	
VFA0313	7.3	6.8	6.8	6.9	7.0	6.8	7.3	7.0	1.1	7.1	7.0	6.8	7.0	6.7	6.8	6.9	6.8	-1.1	stress-responsive transcriptional regulator PspC	
VFA0314	6.8	6.1	6.2	6.4	5.9	6.1	6.6	6.2	-1.1	6.5	6.2	6.3	6.3	6.0	6.0	6.1	6.0	-1.1	amino acid regulated cytosolic protein	
VFA0315	6.5	6.3	6.0	6.3	6.0	6.1	6.2	6.1	-1.1	6.4	6.1	6.2	6.3	6.3	6.2	6.1	6.2	-1.0	hypothetical protein	
VFA0316	4.5	3.3	3.4	3.7	3.3	3.0	3.6	3.3	-1.3	4.2	3.2	3.2	3.5	3.2	3.0	3.1	3.1	-1.3	phosphomethylpyrimidine kinase	
VFA0317	7.7	7.4	7.3	7.3	3.9	4.0	4.3	4.0	-1.2	4.6	4.3	4.0	4.3	4.1	4.1	4.1	4.1	-1.1	hydroxymethylpyrimidine transport ATP-binding protein	
VFA0318	4.6	4.2	3.8	4.2	3.6	4.0	4.4	4.0	-1.2	4.4	3.8	4.0	4.1	3.9	3.7	3.5	3.7	-1.3	hydroxymethylpyrimidine transport system permease protein	
VFA0319	5.7	5.0	5.0	5.3	4.5	4.4	5.2	4.7	-1.4	5.2	5.1	5.1	5.1	4.8	4.2	4.4	4.4	-1.6	hydroxymethylpyrimidine-binding protein	
VFA0322	6.4	6.2	6.2	6.3	5.9	6.1	6.2	6.1	-1.2	6.3	6.2	6.2	6.2	5.9	6.0	6.1	6.0	-1.2	thiamine-phosphate diphosphorylase	
VFA0323	6.0	5.4	5.2	5.5	5.0	5.1	5.5	5.2	-1.2	5.9	5.3	5.0	5.4	5.4	5.2	5.4	5.3	-1.0	sensory box/GGDEF family protein	
VFA0324	6.1	5.2	4.6	5.3	4.5	4.3	4.6	4.5	-1.8	5.8	4.7	5.2	5.2	4.6	4.1	4.3	4.3	-1.9	thiol disulfide interchange protein DsbD	
VFA0325	6.2	5.6	5.6	5.8	5.5	6.2	5.9	5.9	1.1	6.1	5.3	5.8	5.7	5.3	4.8	5.2	5.1	-1.6	methyl-accepting chemotaxis protein	
VFA0326	3.3	3.0	2.7	3.0	2.8	2.7	3.1	2.9	-1.1	3.3	2.9	2.7	3.0	2.8	2.7	2.6	2.7	-1.2	hypothetical protein	
VFA0327	4.7	4.5	4.1	4.4	4.2	4.1	4.3	4.2	-1.2	4.8	4.3	4.4	4.5	3.8	4.1	4.4	4.1	-1.3	hypothetical protein	
VFA0334	6.1	5.3	4.6	5.3	5.0	5.6	5.6	5.4	-1.0	5.6	5.0	4.8	5.1	5.6	5.7	5.2	5.5	1.3	DNA polymerase III, epsilon chain	
VFA0337	4.8	4.5	4.3	4.5	4.4	4.4	4.7	4.5	-1.0	4.8	4.6	4.3	4.6	4.3	4.5	3.9	4.2	-1.3	putative glucosyl hydrolase precursor	
VFA0338	3.2	3.2	2.6	3.0	2.5	2.9	2.8	2.7	-1.2	2.7	2.7	2.4	2.6	2.5	2.6	2.7	2.6	1.0	putative glucosyl hydrolase precursor	
VFA0339	3.5	3.4	3.2	3.4	3.3	3.1	3.6	3.3	-1.0	3.0	3.2	2.8	3.0	2.9	3.2	3.1	3.1	1.0	probable transcriptional regulator SsrB	
VFA0340	4.3	3.9	3.8	4.0	3.8	3.8	4.0	3.9	-1.1	3.9	4.1	4.0	4.0	3.9	3.6	4.1	3.9	-1.1	amino acid permease	
VFA0340a003	1.7	1.7	1.4	1.6	1.7	1.6	1.6	1.7	-1.1	1.7	1.6	1.4	1.6	1.5	1.6	1.5	1.5	-1.0	amino acid permease	
VFA0340b003	2.5	2.1	1.8	2.1	2.2	1.8	2.2	2.1	-1.0	2.5	2.3	2.2	2.3	2.1	2.2	1.9	2.1	-1.2	amino acid permease	
VFA0341	1.6	1.6	1.5	1.6	1.8	1.5	1.6	1.6	1.0	1.5	1.6	1.5	1.6	1.5	1.5	1.5	1.5	-1.0	hypothetical protein	
VFA0342	2.4	2.4	2.4	2.4	2.5	2.3	2.5	2.4	1.0	2.9	2.5	2.4	2.6	2.4	2.3	2.3	2.3	-1.0	sensory transduction protein kinase	
VFA0343	2.7	2.7	2.3	2.6	2.5	2.4	2.8	2.6	-1.0	2.9	2.3	2.3	2.5	2.2	2.5	2.3	2.4	-1.1	sensory transduction protein kinase	
VFA0344	5.4	5.2	4.8	5.1	4.9	5.0	5.4	5.1	-1.0	5.2	5.2	4.9	5.1	5.2	5.0	5.0	5.0	-1.0	sensory transduction protein kinase	
VFA0345	3.7	3.4	3.0	3.4	3.0	2.8	3.6	3.1	-1.2	3.5	3.3	2.8	3.2	3.2	2.7	2.9	2.8	-1.3	amino acid permease	
VFA0346																				

VFA0371	6.3	5.9	5.8	6.0	6.4	6.0	6.7	6.4	1.3	6.1	6.3	5.8	6.0	6.1	6.5	6.4	6.3	1.2	hypothetical protein
VFA0372	6.4	6.3	6.5	6.6	6.5	6.0	7.0	6.5	-1.0	6.6	6.4	6.2	6.4	6.1	6.0	6.3	6.1	-1.2	mechanosensitive ion channel
VFA0373	5.7	5.4	4.7	5.2	4.8	4.7	5.0	4.9	-1.3	5.1	5.1	4.6	5.0	4.4	4.2	4.3	4.3	-1.6	mechanosensitive ion channel
VFA0374	5.9	5.4	5.4	5.6	4.8	4.9	5.1	4.9	-1.5	5.7	5.2	5.5	5.5	4.8	4.9	5.4	5.0	-1.3	ATP-dependent RNA helicase
VFA0375	8.1	8.2	8.3	8.2	8.0	8.3	8.0	8.1	-1.0	8.0	8.3	8.1	8.1	7.9	7.8	8.0	7.9	-1.2	hypothetical protein
VFA0378	8.9	8.9	8.8	8.9	8.5	9.0	8.6	8.7	-1.1	8.9	8.8	8.9	8.9	9.2	9.2	9.4	9.2	1.3	glycine betaine transporter
VFA0379	8.5	8.3	8.1	8.3	8.5	8.2	8.9	8.5	1.2	8.6	8.3	8.1	8.2	8.2	8.3	8.3	8.3	1.0	fusaric acid resistance protein fusE
VFA0380	8.6	8.5	8.5	8.5	8.5	8.5	8.8	8.6	1.1	8.4	8.4	8.5	8.4	8.5	8.5	8.6	8.5	1.1	hypothetical protein
VFA0381	6.8	6.8	6.6	6.7	6.7	6.9	6.7	6.8	1.0	6.8	6.9	6.8	6.8	7.0	6.9	6.9	7.0	1.1	sensory transduction protein kinase
VFA0382	6.3	6.3	5.8	6.1	6.1	5.8	6.6	6.1	1.0	6.3	6.3	6.0	6.2	5.5	5.8	5.7	5.7	-1.4	hypothetical protein
VFA0383	8.6	8.6	8.5	8.6	8.1	8.5	8.2	8.3	-1.2	8.6	8.4	8.6	8.5	8.8	8.6	8.8	8.7	1.1	exoribonuclease II
VFA0385	7.5	7.3	6.8	7.2	6.8	7.0	7.2	7.0	-1.1	7.4	7.2	7.0	7.2	6.9	7.4	7.0	7.1	-1.0	spermidine N1-acetyltransferase
VFA0388	8.9	8.5	8.6	8.7	8.7	8.6	8.9	8.7	1.0	8.8	8.8	8.6	8.7	9.0	9.0	9.1	9.0	1.2	hypothetical membrane spanning protein
VFA0389	7.0	7.1	7.0	7.1	6.4	6.9	6.8	6.7	-1.3	6.9	7.5	7.1	7.1	7.0	7.6	7.1	7.2	1.1	methyl-accepting chemotaxis protein
VFA0393	6.5	6.0	5.7	6.1	5.7	6.1	6.1	6.0	-1.1	6.2	5.6	5.4	5.7	5.7	5.8	5.8	5.7	-1.0	amino acid transport ATP-binding protein
VFA0394	9.6	9.5	9.6	9.6	9.3	9.4	9.4	9.4	-1.1	9.6	9.3	9.6	9.5	9.6	9.4	9.5	9.5	1.0	3-deoxy-7-phosphoheptulonate synthase
VFA0395	6.2	5.7	5.3	5.7	5.9	5.1	6.4	5.8	1.0	5.7	6.0	5.7	5.8	5.4	5.9	5.6	5.6	-1.1	hypothetical protein
VFA0396	7.5	7.4	7.5	7.5	7.2	7.5	7.5	7.4	-1.1	7.4	7.4	7.4	7.4	7.6	7.2	7.5	7.5	1.0	5'-nucleotidase
VFA0397	4.2	3.1	2.7	3.3	3.0	3.0	4.2	3.4	1.1	4.2	3.1	2.7	3.4	2.2	2.9	2.5	2.5	-1.8	hypothetical protein
VFA0398	4.8	4.5	4.2	4.5	3.6	3.9	4.1	3.9	-1.5	4.5	4.5	4.1	4.4	3.7	4.3	3.6	3.9	-1.4	putative two component response regulator
VFA0399	4.7	4.0	3.4	4.0	3.7	3.8	3.6	3.7	-1.2	4.2	3.9	3.6	3.9	3.5	3.7	3.7	3.6	-1.2	hypothetical protein
VFA0400	6.5	6.4	6.3	6.4	6.1	6.4	6.3	6.3	-1.1	6.5	6.4	6.4	6.4	6.5	6.5	6.5	6.5	1.0	FTS system, mannitol-specific IIBC component
VFA0401	6.9	6.6	6.4	6.7	6.1	6.5	6.3	6.3	-1.3	6.6	6.6	6.3	6.5	6.6	6.4	6.4	6.5	-1.0	hypothetical protein
VFA0402	8.5	8.1	8.3	8.3	8.1	8.0	8.4	8.2	-1.1	8.3	8.4	8.2	8.3	8.2	8.1	8.3	8.2	-1.1	purine nucleoside phosphorylase
VFA0405	7.0	6.5	6.4	6.7	5.9	6.2	6.4	6.2	-1.4	6.8	6.1	6.4	6.4	6.1	5.8	6.1	6.0	-1.4	mechanosensitive ion channel
VFA0406	7.3	6.7	6.8	6.9	6.8	6.7	7.3	6.9	-1.0	7.1	6.6	6.7	6.8	6.7	6.4	6.7	6.6	-1.2	possible hydrogenase cytochrome b-type
VFA0407	8.3	8.3	8.2	8.3	8.2	8.3	8.2	8.1	-1.1	8.2	8.3	8.2	8.1	8.2	8.3	8.2	8.4	1.1	cytochrome c'
VFA0408	8.0	7.7	7.7	7.8	7.5	7.7	7.8	7.7	-1.1	7.9	7.6	7.6	7.7	7.7	7.5	7.6	7.6	-1.1	phosphohydrolase (MutT/nudix family protein)
VFA0409	7.1	6.5	6.7	6.8	6.5	6.6	7.0	6.7	-1.1	6.8	6.5	6.5	6.6	6.7	6.5	6.7	6.6	1.0	hypothetical protein
VFA0410	6.6	6.5	5.8	6.3	5.7	6.1	6.1	6.0	-1.1	6.4	6.7	6.3	6.5	6.2	6.5	6.2	6.3	-1.1	hypothetical protein
VFA0412	8.4	8.2	8.2	8.3	7.8	8.5	8.2	8.2	-1.3	8.3	8.1	8.3	8.2	8.4	7.9	8.5	8.3	1.1	dihydroorotase
VFA0413	7.8	7.9	8.2	8.3	8.1	8.2	8.3	8.2	-1.3	8.1	8.2	8.3	8.2	8.3	8.3	8.3	8.3	1.1	hypothetical protein
VFA0414	7.6	7.8	7.5	7.6	7.8	7.2	7.9	7.6	1.0	7.4	7.9	7.7	7.7	7.1	7.6	7.2	7.3	-1.3	ATP-dependent protease La
VFA0416	8.3	8.5	7.9	8.3	8.8	8.1	8.8	8.6	1.2	8.1	9.0	8.3	8.5	7.9	8.2	7.7	8.0	-1.4	DOPA 4,5-dioxygenase
VFA0417	6.0	5.6	5.3	5.6	5.4	4.9	5.5	5.3	-1.3	6.0	5.5	5.2	5.6	5.0	5.0	4.8	4.9	-1.6	L-threonine 3-dehydrogenase
VFA0419	6.6	6.1	6.1	6.3	5.8	5.9	6.3	6.0	-1.2	6.3	5.7	6.1	6.0	6.1	5.7	6.0	5.9	-1.1	transcriptional regulators, LysR family
VFA0420	7.7	7.7	7.5	7.6	7.3	7.4	7.4	7.3	-1.3	7.4	7.6	7.5	7.5	7.4	7.6	7.7	7.6	1.1	hypothetical protein
VFA0421	8.9	8.7	8.9	8.8	8.2	8.7	8.4	8.4	-1.3	9.0	8.6	8.9	8.8	9.0	8.7	9.0	8.9	1.0	putative manganese-dependent inorganic pyrophosphatase
VFA0422	8.1	8.1	8.0	8.1	8.1	8.0	8.3	8.2	-1.1	8.1	8.2	8.1	8.1	8.0	7.9	8.0	8.0	-1.1	flagellar biosynthesis protein FlhF
VFA0423	4.5	4.2	4.3	4.3	3.9	3.6	4.4	4.0	-1.3	3.9	4.1	4.0	4.0	3.9	4.0	3.7	3.9	-1.1	DNA translocation competence protein ComA
VFA0424	8.2	8.1	8.4	8.2	8.2	8.2	8.3	8.2	1.0	8.1	7.9	8.2	8.1	8.3	8.1	8.4	8.3	1.1	phospholipid-lipoplysaccharide ABC transporter
VFA0425	8.3	8.4	8.5	8.4	8.2	8.4	8.3	8.3	-1.1	8.2	8.4	8.4	8.3	8.5	8.3	8.5	8.4	-1.1	tetracycline-saccharide 4'-kinase
VFA0426	8.4	8.0	8.0	8.1	7.9	8.0	8.0	8.0	1.0	8.1	8.0	8.0	8.0	7.9	7.8	7.9	7.9	-1.1	conserved cytosolic protein
VFA0427	8.3	8.1	7.9	8.1	8.0	8.2	7.9	8.0	-1.1	8.3	8.1	8.0	8.1	7.8	7.9	7.9	7.9	-1.1	3-deoxy-manno-octulosonate cytidyltransferase
VFA0428	7.0	6.8	6.7	6.8	6.7	7.7	6.9	7.1	-1.2	6.8	6.6	6.8	6.7	7.1	6.9	7.1	7.0	1.1	integral membrane protein
VFA0429	7.6	7.5	7.3	7.5	6.8	7.2	7.2	7.1	-1.4	7.5	7.0	7.3	7.3	7.1	7.1	7.2	7.1	-1.2	SAM methyltransferase SmtA
VFA0431	7.8	7.2	7.3	7.5	6.4	6.9	6.7	6.5	-1.7	7.6	6.9	7.3	7.2	7.1	6.6	7.1	6.9	-1.2	condensin subunit E'
VFA0432	8.3	8.2	8.3	8.3	7.1	8.0	7.6	7.6	-1.6	8.3	7.9	8.3	8.2	8.1	7.6	8.0	7.9	-1.2	condensin subunit B
VFA0433	7.9	7.7	7.9	7.8	6.8	7.4	7.4	7.2	-1.7	7.7	7.4	7.9	7.7	7.6	7.0	7.5	7.4	-1.2	cell division protein MukB
VFA0434	5.4	4.8	4.5	4.9	5.0	6.4	5.6	5.7	-1.7	5.4	4.4	4.9	4.9	5.0	4.5	4.8	4.8	-1.1	molecular chaperones (DnaJ family)
VFA0437	3.5	3.1	2.9	3.2	2.7	2.7	3.0	2.8	-1.3	3.0	3.1	3.2	3.1	2.9	3.1	2.8	2.9	-1.1	hypothetical protein
VFA0440	7.8	7.8	7.8	7.8	7.7	8.0	7.7	7.8	-1.1	7.8	7.8	7.8	7.7	8.1	8.0	8.2	8.1	-1.1	esterase/lipase
VFA0441	3.4	2.9	2.7	3.0	2.8	2.7	3.3	2.9	-1.0	2.9	2.8	2.6	2.8	3.1	2.9	2.6	2.9	1.1	hypothetical membrane spanning protein
VFA0446	11.1	11.3	10.9	11.1	11.4	10.9	11.0	11.1	-1.0	11.0	11.4	10.9	11.1	10.6	11.0	10.9	10.8	-1.2	copper-binding protein
VFA0447	6.1	5.8	5.6	5.8	5.6	5.5	5.9	5.7	-1.2	5.6	5.7	5.4	5.6	5.4	5.1	5.1	5.2	-1.3	methyl-accepting chemotaxis protein
VFA0448	8.3	8.5	8.5	8.5	8.7	8.9	8.7	8.8	-1.1	8.2	8.3	8.2	8.2	8.6	8.4	8.8	8.6	1.3	hypothetical protein
VFA0449	6.4	6.1	5.5	6.0	5.8	5.5	6.2	5.9	-1.1	6.2	6.0	5.9	6.0	5.9	5.9	5.9	5.9	-1.2	hypothetical protein
VFA0452	5.3	5.0	4.4	4.9	5.4	4.8	5.4	5.2	1.2	4.7	4.7	4.8	4.7	4.1	4.1	4.3	4.1	-1.5	formimidoylglutamate
VFA0453	4.6	4.0	3.3	4.0	4.5	3.7	5.0	4.4	-1.2	3.6	3.7	4.1	3.8	3.3	3.2	3.2	3.2	-1.5	imidazolonepropionase
VFA0454	5.4	4.9	4.4	4.9	5.3	5.1	5.7	5.4	-1.3	5.2	4.8	4.8	4.9	4.4	4.4	4.6	4.5	-1.4	histidine utilization repressor
VFA0455	5.7	5.5	5.0	5.4	5.1	5.2	5.5	5.3	-1.1	5.5	5.2	5.4	5.4	5.5	5.7	5.6	5.6	1.1	hypothetical protein
VFA0456	6.8	6.6	6.1	6.5	6.2	6.3	6.4	6.3	-1.2	6.7	6.5	6.1	6.5	6.0	6.4	6.1	6.2	-1.2	peptidyl-prolyl cis-trans isomerase
VFA0457	7.9	7.6	7.3	7.6	7.0	7.3	7.4	7.2	-1.3	7.8	7.4	7.5	7.6	7.5	7.4	7.4	7.4	-1.1	hypothetical protein
VFA0458	8.9	8.8	8.8	8.8	8.6	8.7	8.7	8.6	-1.1	8.9	8.8	8.9	8.8	8.7	8.8	8.8	8.8	-1.1	hypothetical protein
VFA0459	8.2	8.3	8.2	8.2	7.9	7.9	8.2	8.0	-1.2	8.1	8.0	8.1	8.1	7.9	7.5	7.8	7.7	-1.3	transcription-repair coupling factor
VFA0460	8.4	8.2	8.2	8.3	8.3	7.9	8.2	8.2	-1.1	8.2	8.0	8.1	8.1	7.9	7.5	7.8	7.7	-1.3	transcription-repair coupling factor
VFA0461	8.6	8.5	8.2	8.4	8.9	8.3	9.1	8.3	-1.3	8.5	8.4	8.2	8.3	8.0	8.2	7.9	8.0	-1.2	hypothetical protein
VFA0462	7.3	7.2	7.3	7.3	7.0	7.2	7.3	7.2	-1.1	7.2	7.1	7.3	7.2	7.3	7.2	7.3	7.3	1.1	lipoprotein releasing system transmembrane protein LolE
VFA0463	7.8	7.8	8.0	7.9	7.8	7.9	8.0	7.9	-1.0	7.8	7.7	7.9	7.8	7.9	7.8	8.0	7.9	1.1	Lipoprotein releasing system ATP-binding protein LolD
VFA0464	5.9	5.8	5.8	5.8	5.8	5.7	5.9	5.8	-1.0	5.9	5.6	5.6	5.7	5.9	5.5	5.7	5.7	1.0	Lipoprotein releasing system transmembrane protein LolE
VFA0466	5.8	6.4	6.0	6.1	7.5	6.5	7.3	7.1	-2.1	5.6	7.2	6.1	6.3	5.9	6.4	5.6	5.9	-1.3	N-acetylglucosaminyltransferase
VFA0467	5.5	5.2	5.2	5.3	5.9	5.5	6.2	5.9	1.5	5.3	6.3	5.2	5.6	4.9	5.2	4.6	4.9	-1.6	hypothetical protein
VFA0468	6.8	6.4	6.3	6.5															

VFA0500	7.1	6.5	6.4	6.6	5.9	6.1	6.3	6.1	-1.5	6.8	6.2	6.2	6.4	5.9	5.9	6.0	5.9	-1.4	hypothetical protein
VFA0501	8.6	8.1	8.0	8.3	7.8	7.6	7.9	7.7	-1.5	8.5	7.7	7.9	8.0	8.0	7.7	7.5	7.7	-1.3	hypothetical protein
VFA0502	5.3	5.1	5.0	5.1	5.6	5.1	5.6	5.4	1.2	4.8	5.5	4.8	5.0	4.2	5.2	4.2	4.5	-1.4	outer membrane protein
VFA0503	9.0	8.8	8.5	8.8	9.0	8.5	9.3	8.9	1.1	8.9	8.9	8.6	8.8	9.0	9.1	8.9	9.0	1.1	CreA protein
VFA0504	9.5	9.4	9.3	9.4	9.8	9.2	9.7	9.6	1.2	9.4	9.4	9.1	9.3	9.4	9.5	9.5	9.5	1.1	hypothetical protein
VFA0505	8.3	8.1	8.4	8.2	8.4	7.9	8.3	8.2	-1.0	7.9	8.1	8.1	8.0	8.6	8.1	8.7	8.5	1.3	hypothetical protein
VFA0506	6.2	6.2	5.7	6.1	5.7	5.4	5.9	5.6	-1.3	5.8	6.0	5.9	5.9	5.8	5.8	5.7	5.7	-1.1	two component response regulator
VFA0507	7.8	7.6	7.6	7.7	8.8	7.3	8.7	8.3	1.5	7.4	7.7	7.3	7.5	6.8	6.7	6.7	6.7	-1.7	sodium/glutamate symport carrier protein
VFA0508	6.6	6.1	5.5	6.0	6.2	6.0	6.6	6.3	1.2	6.2	6.2	5.5	6.0	5.6	5.6	5.3	5.5	-1.4	hypothetical protein
VFA0509	7.9	7.7	7.8	7.8	7.4	8.0	7.8	7.7	-1.2	7.7	7.7	7.6	7.7	7.7	7.7	8.0	7.8	1.1	multidrug resistance ABC transporter ATP-binding and permease protein
VFA0510	7.6	7.5	7.5	7.5	7.1	7.3	7.4	7.3	-1.2	7.6	7.3	7.3	7.4	7.4	7.2	7.4	7.3	-1.1	low-affinity zinc transport protein
VFA0511	8.2	8.1	8.0	8.1	7.6	7.9	7.8	7.8	-1.2	8.2	8.0	8.0	8.1	7.9	8.2	8.0	8.0	-1.0	GTP-binding protein
VFA0512	3.4	3.0	3.1	3.2	3.0	2.9	3.2	3.0	-1.1	3.2	3.0	2.9	3.0	2.8	2.8	3.0	2.9	-1.1	hypothetical protein
VFA0513	2.8	2.4	2.2	2.5	2.7	2.6	2.7	2.7	1.1	2.7	2.7	2.2	2.5	2.2	2.5	2.2	2.3	-1.1	DNA integration/recombination/inversion protein
VFA0514	2.8	1.8	1.7	2.1	1.7	1.6	1.7	1.7	-1.4	2.2	1.9	1.8	2.0	1.6	1.7	1.6	1.6	-1.3	hypothetical protein
VFA0515	3.8	3.2	3.2	3.4	3.2	3.4	3.4	3.3	-1.0	3.2	3.2	3.2	3.2	3.4	3.0	3.3	3.2	1.0	transposase
VFA0516	4.8	4.3	4.2	4.4	4.2	3.8	4.4	4.1	-1.2	4.5	4.4	4.2	4.4	3.9	3.8	3.8	3.8	-1.5	hypothetical protein
VFA0517	1.7	1.8	1.8	1.8	2.0	1.8	1.9	1.9	1.1	1.8	1.8	1.9	1.8	1.7	2.1	1.9	1.9	1.0	hypothetical protein
VFA0518	1.7	1.7	1.6	1.6	1.8	1.6	1.7	1.7	1.0	1.7	1.7	1.7	1.7	1.4	1.5	1.6	1.5	-1.1	hypothetical protein
VFA0519	3.2	3.1	3.3	3.2	3.3	3.4	3.2	3.3	1.1	3.2	3.3	3.5	3.3	3.4	3.4	3.5	3.5	1.1	hypothetical protein
VFA0520	4.0	3.5	3.2	3.6	3.5	3.2	3.6	3.4	-1.1	3.8	3.0	3.3	3.4	3.4	3.3	3.0	3.2	-1.1	hypothetical protein
VFA0521	3.1	2.9	2.7	2.9	3.2	3.0	2.9	3.0	1.1	2.8	2.9	2.7	2.8	3.1	3.1	3.0	3.0	1.2	hypothetical protein
VFA0522	3.3	3.2	3.2	3.2	3.6	3.2	3.1	3.3	1.0	3.3	3.1	3.2	3.2	3.1	3.3	3.8	3.4	1.1	DNA repair protein RadC
VFA0523	4.4	4.5	4.2	4.4	4.6	4.5	4.4	4.5	1.1	4.4	4.4	4.4	4.4	4.6	4.8	4.4	4.6	1.2	DNA-binding protein
VFA0524	3.5	3.4	3.5	3.5	3.7	3.6	3.5	3.6	1.1	3.6	3.5	3.4	3.5	3.3	3.4	3.5	3.4	-1.1	ribonuclease H
VFA0528to05	2.4	2.5	2.0	2.3	2.4	2.1	3.0	2.5	1.1	2.2	2.4	2.2	2.3	2.0	2.2	1.9	2.0	-1.2	methyl-accepting chemotaxis protein
VFA0531	6.1	6.3	6.4	6.5	6.6	6.3	6.4	6.5	-1.0	6.8	6.5	6.4	6.5	6.2	6.2	6.2	6.1	-1.3	uridine phosphorylase
VFA0532	6.3	6.5	5.8	6.2	6.0	6.1	6.0	6.0	-1.1	6.3	6.5	6.4	6.4	5.7	6.4	6.0	6.0	-1.3	hypothetical protein
VFA0533	6.3	6.1	6.0	6.1	5.7	6.1	6.0	5.9	-1.1	6.2	6.2	6.3	6.2	6.0	6.1	5.9	6.0	-1.2	hypothetical protein
VFA0534	6.6	5.8	5.3	5.9	5.5	5.5	6.0	5.7	-1.2	6.2	5.8	5.8	5.9	5.5	5.8	5.7	5.7	-1.2	hypothetical protein
VFA0535	7.9	7.7	7.7	7.8	7.3	7.5	7.7	7.5	-1.2	7.8	7.5	7.6	7.7	7.6	7.6	7.7	7.7	1.0	type I restriction-modification system methylation subunit
VFA0536	7.6	7.4	7.4	7.5	6.5	7.3	7.2	7.4	-1.4	7.4	7.3	7.2	7.4	7.4	7.3	7.0	7.4	-1.2	hypothetical protein
VFA0537	8.0	7.9	7.7	7.9	7.0	7.7	7.5	7.4	-1.4	7.8	7.7	7.8	7.8	7.6	7.5	7.6	7.6	-1.2	type I restriction-modification system methylation subunit
VFA0538	7.7	7.1	7.3	7.4	6.5	6.9	7.4	6.9	-1.4	7.4	6.9	7.2	7.2	6.9	6.3	6.9	6.7	-1.4	type I restriction-modification system methylation subunit
VFA0539	7.6	7.4	7.4	7.5	6.9	7.1	7.5	7.2	-1.2	7.4	7.1	7.3	7.3	7.0	7.2	7.2	7.2	-1.1	type I restriction-modification system restriction subunit
VFA0540	6.9	6.7	6.7	6.8	6.4	6.5	6.9	6.6	-1.1	6.7	6.6	6.7	6.6	6.5	6.3	6.6	6.5	-1.1	hypothetical protein
VFA0541	7.3	7.5	7.2	7.3	7.4	7.4	7.6	7.4	-1.1	7.3	7.0	7.4	7.4	7.6	7.4	7.5	7.5	-1.1	DNA integration/recombination/inversion protein
VFA0549	4.0	3.8	3.6	3.8	3.5	3.5	4.5	3.8	1.0	4.0	4.2	4.3	4.2	3.8	3.7	3.1	3.5	-1.5	hypothetical protein
VFA0550	4.7	4.8	4.5	4.7	4.2	4.4	5.2	4.6	-1.0	4.7	5.0	5.2	4.9	5.4	5.0	3.6	4.7	-1.2	hypothetical cytosolic protein
VFA0551	4.6	4.1	3.5	4.1	3.4	3.4	3.5	3.4	-1.6	4.0	4.0	3.6	3.9	3.3	4.0	3.1	3.5	-1.3	hypothetical protein
VFA0552	6.2	5.6	5.4	5.7	5.6	5.6	6.1	5.8	-1.1	5.9	5.4	5.5	5.6	5.5	5.8	5.4	5.6	-1.0	hypothetical cytosolic protein
VFA0553	8.7	8.8	8.8	8.8	8.5	8.9	8.8	8.7	-1.0	8.6	8.6	8.6	8.6	8.9	8.9	9.1	8.9	-1.3	ATP-dependent RNA helicase
VFA0554	7.6	7.0	5.8	6.8	6.7	6.3	6.9	6.6	-1.1	7.6	6.8	5.8	6.7	5.5	6.2	5.7	5.8	-1.9	hypothetical cytosolic protein
VFA0556	8.1	7.8	7.7	7.9	7.4	7.4	7.8	7.5	-1.1	7.9	7.8	7.8	7.8	7.8	7.9	7.9	7.8	-1.0	hypothetical protein
VFA0557	8.3	8.3	8.3	8.3	8.5	8.6	8.6	8.5	-1.2	8.1	8.3	8.3	8.3	8.5	8.4	8.4	8.4	-1.1	oligopeptide-binding protein OppA
VFA0558	8.2	8.1	7.7	8.0	7.6	7.9	7.9	7.8	-1.2	8.1	7.9	8.0	8.0	7.9	7.9	7.9	7.9	-1.1	coproporphyrinogen III oxidase
VFA0559	6.8	6.3	6.2	6.4	5.9	6.2	6.4	6.3	-1.4	6.4	6.2	6.2	6.2	6.4	5.8	6.0	6.8	-1.0	hypothetical protein
VFA0560	8.0	8.1	7.9	8.0	7.8	7.8	8.0	7.9	-1.1	7.9	7.9	7.9	7.9	7.9	7.6	7.8	7.8	-1.1	sensory transduction protein kinase
VFA0561	8.8	8.6	8.6	8.7	8.4	8.5	8.8	8.6	-1.1	8.7	8.6	8.6	8.6	8.6	8.2	8.6	8.5	-1.1	transcriptional regulator
VFA0562	8.5	8.7	8.4	8.6	7.9	8.4	8.1	8.1	-1.3	8.4	8.5	8.6	8.5	8.3	8.2	8.4	8.3	-1.2	hypothetical protein
VFA0563	6.7	7.0	6.3	6.6	6.5	6.6	6.3	6.5	-1.1	6.5	6.9	6.8	6.7	6.5	6.7	7.0	6.7	-1.0	hypothetical protein
VFA0564	5.1	5.7	5.8	5.9	5.7	5.7	5.6	5.6	-1.0	5.6	5.6	5.6	5.6	5.6	5.6	5.2	5.7	-1.7	TetP protein
VFA0565	8.4	8.0	7.9	8.1	8.1	7.7	8.2	8.0	-1.1	8.4	8.0	8.1	8.1	8.1	8.0	8.2	8.1	-1.0	molybdenum cofactor biosynthesis protein
VFA0566	3.0	2.8	2.1	2.6	2.5	2.5	2.8	2.6	-1.0	2.9	2.5	2.6	2.7	2.4	2.5	2.3	2.4	-1.0	hypothetical protein
VFA0567	6.6	6.5	6.1	6.4	5.7	5.6	6.3	5.9	-1.3	6.4	6.6	6.3	6.4	6.3	6.9	6.4	6.5	1.1	sensory box/GGDEF family protein
VFA0569	9.8	9.7	9.5	9.7	9.2	9.4	9.4	9.3	-1.4	9.8	9.5	9.5	9.6	9.2	9.4	9.2	9.3	-1.2	hypothetical protein
VFA0571	5.6	5.4	5.0	5.4	5.6	5.7	6.0	5.8	-1.3	5.6	5.6	5.1	5.4	5.5	6.2	6.1	5.9	-1.4	DNA integration/recombination/inversion protein
VFA0573	7.3	7.5	6.6	7.2	7.5	7.2	7.4	7.4	1.1	7.5	7.7	7.3	7.5	7.4	8.1	7.4	7.6	1.1	hypothetical protein
VFA0573to05	4.0	3.6	3.4	3.7	3.8	3.7	4.0	3.8	1.1	3.7	3.9	3.6	3.7	3.6	4.1	3.6	3.8	1.0	hypothetical protein
VFA0573to05	3.1	3.4	3.1	3.2	3.4	3.5	3.3	3.4	1.2	3.3	3.7	3.3	3.4	3.6	3.4	3.2	3.4	-1.0	hypothetical protein
VFA0574.5	3.2	3.2	2.8	3.1	3.4	3.1	3.0	3.2	1.1	3.1	3.3	3.0	3.1	3.0	3.0	2.8	3.0	-1.1	hypothetical protein
VFA0575to05	3.6	3.3	2.8	3.2	3.4	3.1	3.9	3.4	1.2	3.3	3.4	2.9	3.2	2.9	3.0	2.7	2.9	-1.3	hypothetical protein
VFA0575to05	1.7	1.7	1.6	1.7	1.7	1.7	1.9	1.8	1.1	1.6	1.7	1.4	1.6	1.6	1.7	1.5	1.6	1.0	hypothetical protein
VFA0577	3.1	2.6	2.4	2.7	2.7	2.7	3.4	2.9	1.1	2.3	2.7	2.3	2.5	2.4	2.1	2.2	2.2	-1.2	enterotoxin
VFA0578	3.0	2.9	3.0	2.9	3.3	3.0	3.0	3.1	1.1	2.9	3.0	3.1	3.0	3.1	3.2	3.2	3.3	1.2	OrfU
VFA0579	4.0	4.1	3.4	3.8	3.7	4.0	4.1	3.9	1.1	4.0	3.9	3.8	3.9	3.4	3.8	3.8	3.7	-1.2	hypothetical protein
VFA0580	3.9	3.4	3.0	3.4	3.0	2.9	3.8	3.2	-1.0	3.4	3.4	3.0	3.2	2.7	2.9	2.5	2.7	-1.5	hypothetical protein
VFA0581	3.7	3.5	3.1	3.4	3.3	3.3	3.5	3.4	-1.0	3.6	3.5	3.4	3.5	3.3	3.3	3.3	3.3	-1.2	RstA
VFA0582to05	6.4	6.4	6.1	6.3	6.0	6.0	7.0	6.3	-1.0	6.6	6.9	6.5	6.7	6.5	6.7	5.5	6.2	-1.3	cryptic phage CTXphi transcriptional repressor rstR
VFA0582to05	3.6	3.4	2.7	3.2	3.4	3.1	3.4	3.3	-1.1	3.3	3.1	3.2	3.2	3.4	3.3	3.0	3.2	1.0	cryptic phage CTXphi transcriptional repressor rstR
VFA0583	7.3	6.8	7.1	7.1	7.1	6.4	7.3	6.9	-1.1	7.3	6.8	7.0	7.0	6.9	6.4	6.9	6.7	-1.2	hypothetical protein
VFA0584	5.8	5.8	5.4	5.7	5.2	5.4	5.5	5.4	-1.1	5.6	5.5	5.6	5.6	5.6	5.0	5.2	5.4	-1.2	hypothetical protein
VFA0585	10.4	9.8	10.1	10.1	10.2	10.2	10.5	10.3	1.1	10.4	9.6	9.9	10.0	10.1					

VFA0617	7.6	7.3	7.4	7.4	7.0	7.2	7.1	7.1	-1.2	7.3	7.1	7.4	7.3	7.4	7.2	7.5	7.4	1.1	hypothetical protein	
VFA0621	7.1	6.5	6.4	6.6	6.1	6.0	6.6	6.2	-1.4	6.8	6.6	6.4	6.6	6.1	6.3	6.2	6.3	6.2	-1.3	hypothetical protein
VFA0622	6.4	6.1	5.6	6.0	5.1	5.4	5.8	5.4	-1.5	6.2	6.1	6.1	6.1	5.6	5.6	5.5	5.6	5.6	-1.5	hypothetical protein
VFA0623to06:	5.7	5.3	4.9	5.3	4.5	4.4	5.3	4.7	-1.5	5.6	5.5	5.5	5.5	6.1	6.4	5.9	6.1	6.1	1.5	hypothetical protein
VFA0624	7.8	7.7	7.8	7.7	7.7	7.4	7.9	7.7	-1.2	7.6	7.8	7.7	7.7	7.4	7.3	7.5	7.4	7.3	-1.3	hypothetical protein
VFA0625	8.3	8.5	8.5	8.4	8.6	8.4	9.0	8.7	-1.0	8.2	8.7	8.4	8.4	8.2	8.1	8.1	8.2	8.1	-1.2	hypothetical protein
VFA0626	8.1	8.3	8.3	8.2	7.9	8.0	8.2	8.1	-1.1	7.9	8.5	8.2	8.2	8.1	8.1	8.0	8.2	8.1	-1.1	hypothetical protein
VFA0627	7.0	7.0	7.0	7.0	6.6	6.9	6.8	6.8	-1.2	6.8	7.3	7.0	7.0	6.8	7.0	7.0	6.9	6.9	-1.1	hypothetical protein
VFA0628	7.0	7.0	6.5	6.8	6.7	7.0	7.0	6.9	-1.0	6.8	7.0	6.8	6.8	6.7	6.8	6.7	6.7	6.7	-1.1	3-methyl-2-oxobutanoate hydroxymethyltransferase
VFA0629	7.2	7.1	6.9	7.1	6.3	6.6	7.2	6.7	-1.3	7.0	7.5	7.0	7.2	6.7	7.1	6.7	6.8	6.8	-1.2	hypothetical protein
VFA0629to06:	5.9	5.6	5.2	5.5	5.0	5.4	5.5	5.3	-1.2	5.8	5.6	5.3	5.6	5.3	5.4	5.1	5.3	5.3	-1.3	hypothetical protein
VFA0629to06:	5.8	5.1	4.7	5.2	4.7	4.6	5.0	4.8	-1.3	5.4	5.4	4.9	5.2	4.7	4.8	4.5	4.7	4.5	-1.5	hypothetical protein
VFA0629to06:	3.0	3.0	2.4	2.8	2.8	3.0	2.9	2.9	1.1	2.8	3.2	2.5	2.8	2.9	3.4	2.7	3.0	3.0	1.1	hypothetical protein
VFA0629to06:	3.0	3.2	2.7	3.0	3.0	3.2	3.3	3.2	1.1	2.8	3.4	2.7	3.0	2.8	3.2	2.9	3.0	3.0	1.0	hypothetical protein
VFA0630	7.2	7.3	7.2	7.2	6.8	7.0	7.2	7.0	-1.2	7.0	7.5	7.3	7.2	7.2	7.0	7.1	7.1	7.1	-1.1	hypothetical protein
VFA0631	7.6	7.7	7.7	7.6	7.2	7.7	7.6	7.5	-1.2	7.3	7.9	7.7	7.6	7.6	7.4	7.7	7.6	7.6	-1.0	hypothetical protein
VFA0632	8.3	8.4	8.4	8.4	7.9	8.3	8.3	8.2	-1.1	8.1	8.6	8.4	8.4	8.2	8.4	8.4	8.3	8.3	-1.0	hypothetical protein
VFA0633	5.2	4.9	4.8	4.9	4.2	4.3	5.0	4.5	-1.4	4.8	5.0	4.5	4.7	4.4	4.4	4.0	4.3	4.3	-1.4	hypothetical protein
VFA0634	5.5	5.5	5.1	5.4	5.2	5.2	5.3	5.2	-1.4	5.2	5.2	4.8	5.1	5.0	5.2	4.8	5.0	5.0	-1.4	hypothetical protein
VFA0635	7.5	7.4	7.3	7.4	7.4	7.7	7.7	7.6	-1.2	7.4	7.5	7.2	7.4	7.7	7.6	7.6	7.7	7.7	1.2	hypothetical protein
VFA0636	8.1	8.0	7.8	8.0	8.3	8.4	8.5	8.4	1.3	8.0	8.1	7.8	8.0	8.4	8.2	8.4	8.4	8.4	1.3	hypothetical protein
VFA0636to06:	3.8	3.4	3.4	3.6	3.6	3.5	3.6	3.6	-1.0	3.7	3.6	3.4	3.6	3.6	3.1	3.4	3.4	3.4	-1.2	hypothetical protein
VFA0636to06:	4.6	4.6	3.9	4.4	5.0	4.4	5.3	4.9	1.4	4.4	5.0	4.4	4.6	4.2	4.5	4.1	4.3	4.3	-1.3	hypothetical protein
VFA0638	5.7	5.3	5.1	5.4	4.5	4.7	5.1	4.8	-1.5	5.4	5.1	4.8	5.1	4.4	4.7	4.9	4.7	4.7	-1.4	hypothetical protein
VFA0639	6.9	6.8	6.8	6.8	6.1	6.5	6.7	6.4	-1.3	6.7	6.8	6.7	6.7	6.5	6.6	6.8	6.6	6.6	-1.0	hypothetical protein
VFA0640	6.7	6.6	6.5	6.6	5.8	6.3	6.4	6.1	-1.4	6.5	6.5	6.4	6.5	6.6	6.4	6.6	6.5	6.5	1.0	lactoylglutathione lyase
VFA0641	6.3	6.3	6.2	6.2	5.7	6.3	6.3	6.2	-1.3	6.3	6.3	6.2	6.1	6.0	6.3	5.9	6.1	6.1	-1.1	hypothetical protein
VFA0642	6.9	6.8	6.2	6.6	6.7	6.6	7.2	6.8	1.1	6.8	7.2	6.8	7.0	6.4	6.8	6.2	6.5	6.5	-1.4	hypothetical protein
VFA0643	5.0	4.3	4.5	4.6	4.2	3.7	4.7	4.2	-1.3	4.3	4.3	4.4	4.3	3.9	3.7	3.9	3.8	3.8	-1.4	phosphotransferase family protein
VFA0643to06:	4.3	3.7	3.1	3.7	3.9	3.5	4.0	3.8	1.1	4.1	4.1	3.3	3.8	3.4	3.4	3.2	3.3	3.3	-1.4	phosphotransferase family protein
VFA0643to06:	3.6	3.3	2.9	3.3	4.0	3.5	4.5	4.0	1.7	3.1	3.6	3.2	3.3	2.9	3.4	3.0	3.1	3.1	-1.2	phosphotransferase family protein
VFA0644	6.3	6.0	2.7	3.2	3.0	2.7	3.2	3.2	1.2	3.8	3.5	3.2	3.2	3.8	3.5	2.9	2.9	2.9	-1.2	hypothetical protein
VFA0646	6.6	6.1	6.1	6.3	6.3	5.8	6.7	6.3	-1.0	6.2	6.5	6.1	6.3	5.6	5.8	5.9	5.8	5.8	-1.4	hypothetical protein
VFA0647	6.2	6.1	5.8	6.0	5.6	5.9	5.9	5.8	-1.2	6.1	6.2	5.9	6.1	5.6	6.1	5.5	5.7	5.7	-1.2	hypothetical protein
VFA0648	6.6	6.4	6.3	6.5	5.9	6.6	6.6	6.4	-1.1	6.1	6.5	6.2	6.3	6.2	6.3	6.5	6.4	6.4	1.0	hypothetical protein
VFA0649	7.2	6.6	6.9	6.9	6.7	6.6	6.9	6.8	-1.1	6.9	6.7	6.6	6.7	6.0	6.0	6.9	6.9	6.9	-1.1	hypothetical protein
VFA0650	6.7	6.3	6.2	6.4	6.1	6.2	6.4	6.2	-1.1	6.4	6.2	5.7	6.1	6.1	6.6	6.3	6.3	6.3	-1.1	hypothetical protein
VFA0650to06:	4.6	4.5	4.2	4.4	4.1	4.4	4.6	4.4	-1.1	4.2	4.6	4.3	4.4	4.2	4.4	4.1	4.2	4.2	-1.1	hypothetical protein
VFA0650to06:	4.2	3.7	3.6	3.9	3.5	3.8	4.1	3.8	-1.0	4.0	4.0	3.5	3.8	3.6	3.9	3.5	3.7	3.7	-1.1	hypothetical protein
VFA0651	10.2	10.4	10.2	10.3	10.1	10.3	10.2	10.2	-1.0	10.1	10.3	10.3	10.2	10.5	10.6	10.6	10.5	10.5	1.3	hypothetical protein
VFA0652	8.6	9.0	8.8	8.8	8.4	8.9	8.5	8.6	-1.1	8.4	8.9	8.8	8.7	8.9	8.8	8.9	8.9	8.9	-1.1	hypothetical protein
VFA0653	6.5	6.5	6.1	6.4	6.1	6.4	6.5	6.4	-1.0	6.4	6.9	6.1	6.4	6.2	6.5	6.4	6.4	6.4	-1.1	lysine acetyltransferase
VFA0654	7.0	6.9	6.8	6.9	6.6	6.9	7.1	6.9	-1.0	6.8	7.1	6.7	6.9	6.8	6.8	6.9	6.8	6.8	-1.0	hypothetical protein
VFA0655	8.1	8.3	8.4	8.2	7.8	8.2	8.0	8.0	-1.2	8.0	8.5	8.3	8.3	8.3	8.1	8.2	8.2	8.2	-1.1	hypothetical protein
VFA0655to06:	5.6	5.5	5.1	5.4	4.8	5.5	5.4	5.2	-1.1	5.4	5.7	5.1	5.4	5.0	5.2	4.8	5.0	5.0	-1.3	hypothetical protein
VFA0655to06:	2.3	2.3	2.1	2.2	2.2	2.2	2.4	2.3	1.0	2.1	2.5	2.3	2.3	2.2	2.2	2.2	2.2	2.2	-1.1	hypothetical protein
VFA0656	7.6	7.2	7.2	7.4	7.0	7.3	7.4	7.2	-1.1	7.4	7.3	7.2	7.3	7.5	7.5	7.6	7.6	7.6	-1.1	hypothetical protein
VFA0657	2.4	2.2	1.9	2.1	1.9	2.1	1.9	2.0	-1.1	2.2	2.2	1.7	2.0	1.8	2.2	1.9	2.0	2.0	-1.0	hypothetical protein
VFA0657_x	2.3	2.0	1.9	2.1	1.9	1.9	2.0	2.0	-1.1	1.9	2.0	2.0	2.0	1.8	1.9	1.8	1.9	1.9	-1.1	hypothetical protein
VFA0658	7.0	6.6	6.5	6.7	6.6	6.8	6.8	6.7	1.0	6.9	6.8	6.5	6.7	6.6	6.8	6.5	6.6	6.6	-1.1	hypothetical protein
VFA0658to06:	3.8	3.2	3.1	3.4	3.3	3.3	3.6	3.4	1.0	3.9	3.6	3.4	3.6	3.2	3.3	3.3	3.3	3.3	-1.3	hypothetical protein
VFA0658to06:	6.3	6.0	2.4	2.9	6.3	6.0	6.4	6.3	-1.1	6.2	6.3	6.2	6.2	6.3	6.6	6.2	6.3	6.2	-1.3	hypothetical protein
VFA0659	2.2	2.4	2.1	2.2	2.0	2.2	2.0	2.0	-1.1	2.2	2.5	2.0	2.2	2.1	2.3	1.9	2.1	2.1	-1.1	hypothetical protein
VFA0660	6.6	6.1	5.8	6.2	6.0	5.9	6.6	6.2	1.0	6.5	6.4	5.8	6.2	5.6	5.7	5.4	5.6	5.6	-1.6	prolyl endopeptidase
VFA0661	8.0	7.5	7.3	7.6	7.2	7.2	7.7	7.4	-1.2	7.7	7.4	7.5	7.6	7.6	7.1	7.4	7.4	7.4	-1.1	hypothetical protein
VFA0662	6.9	6.0	5.9	6.3	5.9	5.8	6.3	6.0	-1.2	6.6	6.0	6.2	6.3	6.7	5.5	5.6	5.6	5.6	-1.5	acetyltransferase
VFA0664	6.4	5.9	5.2	5.8	6.1	5.6	6.1	5.8	-1.0	6.1	5.6	5.6	5.8	5.4	5.4	5.5	5.4	5.4	-1.3	hypothetical protein
VFA0665	8.1	7.9	7.8	7.9	7.4	7.7	7.9	7.7	-1.2	7.9	7.7	7.7	7.8	7.7	7.8	7.9	7.8	7.8	1.0	hypothetical cytosolic protein
VFA0666	7.7	7.5	7.5	7.5	7.1	7.3	7.5	7.3	-1.2	7.5	7.3	7.4	7.4	7.1	7.3	7.4	7.3	7.3	-1.1	ComA operon protein 2
VFA0667	6.5	6.3	6.1	6.3	6.2	6.2	6.3	6.2	-1.1	6.4	6.3	6.3	6.4	6.2	6.5	6.3	6.3	6.3	-1.0	hypothetical protein
VFA0668	6.2	6.0	5.0	5.7	5.5	5.3	5.4	5.4	-1.3	6.2	5.8	5.6	5.9	5.5	5.9	5.5	5.6	5.6	-1.2	hypothetical protein
VFA0668to06:	4.6	4.0	3.7	4.1	3.6	3.4	3.9	3.6	-1.4	4.4	3.6	3.7	3.9	4.1	4.1	3.7	4.0	4.0	1.0	hypothetical protein
VFA0668to06:	3.6	3.7	2.6	3.3	3.4	3.2	3.7	3.4	-1.1	3.4	3.8	3.3	3.5	3.2	3.7	3.5	3.5	3.5	-1.0	hypothetical protein
VFA0670	8.8	8.5	8.5	8.6	8.2	8.3	8.2	8.2	-1.3	8.5	8.6	8.4	8.5	8.4	8.5	8.6	8.5	8.5	1.0	hypothetical protein
VFA0674to06:	2.7	2.5	2.5	2.6	2.5	2.3	2.4	2.4	-1.1	2.6	2.5	2.4	2.5	2.6	2.6	2.7	2.7	2.7	1.1	hypothetical protein
VFA0675	4.9	4.3	4.0	4.4	3.9	4.1	4.9	4.3	-1.1	4.2	4.2	3.7	4.0	3.8	4.2	4.1	4.0	4.0	-1.0	hypothetical protein
VFA0676	7.9	7.7	7.4	7.7	7.6	7.5	8.0	7.7	-1.0	7.8	7.8	7.6	7.7	7.4	7.8	7.6	7.6	7.6	-1.1	hypothetical protein
VFA0678	7.6	7.3	7.2	7.4	7.2	7.5	7.6	7.4	-1.0	7.5	7.3	7.4	7.4	7.4	7.3	7.2	7.3	7.3	-1.1	MoxR protein
VFA0679	6.7	6.2	5.8	6.2	5.9	6.0	6.2	6.0	-1.2	6.3	5.7	6.0	6.0	5.5	5.3	5.4	5.4	5.4	-1.1	hypothetical cytosolic protein
VFA0680	5.4	4.1	3.5	4.3	3.3	3.8	4.1	3.7	-1.5	4.9										



VFA0719	7.1	7.2	7.0	7.1	7.0	6.8	7.1	7.0	-1.1	6.9	7.0	7.0	7.0	6.9	7.0	7.0	7.0	1.0	hypothetical protein
VFA0720	5.2	4.6	4.4	4.3	4.6	4.4	4.7	4.7	-1.2	4.9	4.4	4.8	4.2	4.8	4.5	4.5	4.5	-1.2	hypothetical protein
VFA0721	5.6	4.8	4.5	5.0	4.9	4.3	5.6	4.9	-1.0	5.4	4.7	4.8	5.0	4.0	4.2	4.5	4.2	-1.7	hypothetical protein
VFA0723	2.0	2.0	1.9	2.0	2.0	1.9	2.0	2.0	-1.1	1.9	1.9	1.8	1.9	1.9	2.0	1.8	1.9	1.0	hypothetical protein
VFA0724	5.9	5.3	5.3	5.5	5.5	5.6	5.9	5.7	1.1	5.5	5.6	5.5	5.5	5.8	5.3	5.6	5.6	1.0	transcriptional regulators, LysR family
VFA0725	3.8	3.9	3.4	3.7	3.7	4.0	4.3	4.0	1.3	3.5	3.7	3.4	3.5	3.8	3.9	3.2	3.6	1.1	chologlycine hydrolase family
VFA0725b	9.1	8.1	8.9	9.0	8.7	8.7	8.9	8.6	-1.2	8.9	8.7	9.1	9.0	8.7	9.0	9.2	9.1	1.1	acyltransferase
VFA0729	7.0	6.4	6.7	6.7	6.2	6.3	6.6	6.4	-1.3	6.9	6.2	6.6	6.6	6.9	6.4	6.8	6.7	1.1	transporter, MFS superfamily
VFA0730	4.8	4.3	3.8	4.3	4.1	3.8	4.1	4.0	-1.0	4.5	3.9	4.0	4.1	3.9	4.0	3.9	3.9	1.1	transcriptional regulators, LysR family
VFA0731	4.6	4.6	4.4	4.5	4.2	4.5	4.3	4.3	-1.2	4.6	4.4	4.4	4.5	4.4	4.7	4.5	4.6	1.1	glucan 1,6-alpha-glucosidase
VFA0732	7.3	7.3	7.2	7.3	6.9	7.4	7.1	7.1	-1.1	7.0	7.3	7.3	7.2	7.2	7.0	7.2	7.1	-1.1	transcriptional regulator
VFA0733	7.3	7.3	7.2	7.3	6.9	7.4	7.1	7.1	-1.1	7.0	7.2	7.1	7.1	7.0	6.9	7.1	7.0	-1.1	two component sensor histidine kinase
VFA0734	6.0	6.1	6.1	6.1	5.8	6.1	6.0	6.0	-1.1	5.6	6.2	6.0	6.0	6.0	5.6	5.9	5.8	-1.1	hypothetical protein
VFA0735	5.1	4.8	4.6	4.8	4.5	4.9	5.1	4.9	-1.0	4.9	4.7	4.9	4.8	5.0	4.9	4.5	4.8	-1.1	hypothetical protein
VFA0736	4.4	4.4	4.6	4.5	4.3	4.7	4.7	4.5	1.0	4.2	4.7	4.4	4.4	4.5	4.7	4.5	4.5	-1.1	ABC transporter permease protein
VFA0737	4.3	4.4	4.4	4.3	4.3	4.3	4.6	4.4	1.1	4.1	4.3	4.1	4.2	4.6	4.3	4.2	4.3	-1.1	ABC transporter ATP-binding protein
VFA0738	3.6	3.7	3.6	3.6	3.6	3.9	3.9	3.6	1.1	3.9	3.7	3.7	3.8	3.6	4.0	4.1	3.9	1.1	hypothetical protein
VFA0739	7.8	7.6	7.3	7.6	7.1	7.4	7.4	7.3	-1.2	7.8	7.5	7.4	7.6	7.2	7.5	7.4	7.4	-1.2	acetyltransferase
VFA0740	4.4	4.1	3.5	4.0	3.7	3.7	3.7	3.7	-1.2	4.3	3.8	3.3	3.8	3.5	3.7	3.2	3.5	-1.2	zinc finger protein
VFA0741	6.8	6.4	6.2	6.5	5.9	6.3	6.4	6.2	-1.2	6.7	6.1	6.3	6.4	6.1	6.3	6.3	6.2	-1.1	hypothetical protein
VFA0742	4.0	3.5	3.6	3.7	3.7	3.5	3.8	3.7	-1.0	3.6	4.1	3.5	3.7	3.6	3.4	3.8	3.6	-1.1	hypothetical protein
VFA0743	4.1	3.8	3.8	3.9	3.8	3.7	4.0	3.9	-1.0	4.0	3.7	3.8	3.8	3.9	3.8	3.7	3.8	-1.0	hypothetical protein
VFA0744	5.8	5.4	4.9	5.3	5.3	5.2	5.5	5.3	-1.0	5.5	5.2	4.9	5.2	5.3	5.4	5.0	5.2	1.0	transcriptional regulators, LysR family
VFA0748	8.6	8.8	8.9	8.7	8.3	8.6	8.3	8.4	-1.3	8.6	8.5	8.7	8.6	8.5	8.6	8.8	8.7	1.1	adenosylmethionine-8-amino-7-oxononanoate transaminase
VFA0749	8.6	8.2	7.8	8.2	8.9	8.2	8.9	8.7	1.4	8.5	8.4	7.9	8.3	7.9	7.9	8.0	8.0	-1.2	hypothetical protein
VFA0750	7.8	7.6	7.5	7.6	7.6	7.9	7.9	7.8	1.1	7.6	7.4	7.5	7.5	7.9	7.7	7.9	7.8	1.3	ribosomal-protein-S5-alanine acetyltransferase
VFA0751	10.3	7.3	7.2	8.1	8.1	8.5	8.1	8.2	-1.2	8.2	8.1	8.0	8.0	8.4	8.1	8.4	8.3	1.3	transcriptional regulatory protein TyrR
VFA0754	6.7	6.6	6.1	6.5	6.3	6.4	6.2	6.3	-1.1	6.4	6.5	6.3	6.4	6.7	6.9	6.8	6.8	1.3	peptide methionine sulfoxide reductase
VFA0755	4.5	4.2	3.3	4.0	4.0	3.8	4.5	4.1	-1.0	4.0	3.7	3.6	3.8	3.2	3.6	3.2	3.3	-1.4	hypothetical protein
VFA0771	6.7	6.4	6.2	6.4	6.0	6.5	6.5	6.4	-1.0	6.5	6.1	6.3	6.3	6.3	6.4	6.4	6.4	1.1	transcriptional regulators, LysR family
VFA0772	6.0	5.6	5.5	5.7	4.8	5.2	5.4	5.1	-1.5	5.7	5.4	5.5	5.5	6.2	6.2	4.9	5.1	-1.3	homogentisate export protein
VFA0773	2.9	2.9	2.7	2.9	10.5	9.4	10.4	10.1	1.4	9.9	9.4	9.3	9.7	8.9	9.4	8.8	9.0	-1.0	hypothetical protein
VFA0774	8.5	8.6	8.5	8.5	8.1	8.6	8.6	8.4	-1.1	8.4	8.4	8.5	8.4	8.7	8.6	8.8	8.7	-1.2	hypothetical protein
VFA0776	7.3	7.4	7.4	7.4	6.5	7.1	7.0	6.8	-1.4	7.2	7.4	7.5	7.4	7.1	7.2	7.1	7.1	-1.2	TonB protein
VFA0785	6.6	6.2	6.4	6.4	6.7	6.3	7.0	6.7	1.2	6.2	6.6	6.2	6.3	6.3	6.3	6.3	6.3	-1.0	transcriptional regulator, AraC family
VFA0786	3.9	3.7	3.5	3.7	3.9	3.7	3.9	3.8	1.1	4.0	3.9	3.8	3.9	3.4	4.1	3.7	3.7	-1.1	PTS system, glucose-specific II BC component
VFA0788	5.3	4.6	3.8	4.5	4.6	3.6	5.6	4.5	-1.0	5.0	4.9	4.2	4.7	5.6	4.6	4.6	4.6	-1.1	hypothetical protein
VFA0789	4.8	4.3	3.9	4.3	4.1	3.7	4.4	4.1	-1.2	4.4	4.4	4.2	4.3	3.7	3.9	3.6	3.8	-1.5	lactoylglutathione lyase
VFA0791	5.7	4.9	4.1	4.9	4.9	4.3	5.3	4.8	-1.1	5.1	4.6	4.3	4.7	3.9	4.4	3.8	4.0	-1.0	transcriptional regulators, LysR family
VFA0792	5.4	5.1	5.1	5.2	4.9	4.9	5.0	5.0	-1.2	5.2	4.9	5.0	5.0	4.9	4.7	5.0	4.9	-1.1	proline iminopeptidase
VFA0793	6.1	5.7	5.5	5.8	5.8	5.7	5.9	5.8	-1.0	5.6	5.6	5.4	5.6	5.9	5.9	5.8	5.9	1.3	transcriptional regulators, LysR family
VFA0794	5.3	4.7	4.6	4.9	4.3	4.2	4.9	4.5	-1.3	5.1	4.4	4.3	4.6	4.1	4.0	4.2	4.1	-1.4	acetate:propionate kinase
VFA0795	3.9	3.4	3.2	3.5	3.2	3.0	2.9	3.0	-1.4	3.5	3.0	3.0	3.1	2.8	3.1	2.4	2.7	-1.3	two component response regulator
VFA0796	5.8	5.3	5.2	5.4	5.4	5.2	5.7	5.4	-1.0	5.4	5.2	5.3	5.3	5.7	5.0	5.0	4.9	-1.3	sensor protein
VFA0797	7.2	5.8	5.9	6.3	5.2	5.1	5.5	5.3	-2.5	7.0	5.4	5.7	6.0	5.3	5.1	5.1	5.2	-1.8	transporter
VFA0798	7.3	5.6	5.2	6.0	4.6	4.6	5.0	4.7	-2.1	7.1	5.0	5.4	5.8	4.7	4.3	4.5	4.5	-2.4	maltose transport system permease protein MalF
VFA0800	8.0	6.3	6.6	6.9	7.0	6.8	7.1	7.0	-1.0	7.9	5.9	6.3	6.7	5.8	5.2	5.8	5.6	-2.1	maltose/maltodextrin transport ATP-binding protein MalK
VFA0802	7.1	7.2	7.1	7.1	7.1	7.2	7.3	7.2	1.0	6.9	7.1	7.0	7.0	6.9	7.0	6.8	6.9	-1.0	chemotaxis protein CheV
VFA0803	9.9	9.7	10.0	9.8	9.3	9.7	9.4	9.4	-1.3	9.8	9.4	9.7	9.6	9.8	9.3	9.8	9.6	1.0	serine/threonine sodium symporter
VFA0808	8.8	7.2	7.2	7.7	6.8	6.6	6.8	6.7	-2.0	8.6	6.8	7.2	7.5	6.6	6.5	6.8	6.6	-1.8	glycogen branching enzyme
VFA0809	9.6	7.4	7.4	8.1	7.6	7.3	7.6	7.5	-1.5	9.5	6.8	7.2	7.8	6.1	6.1	6.1	6.1	-3.3	4-alpha-glucanotransferase
VFA0810	5.3	4.7	4.6	4.9	4.3	4.2	4.9	4.5	-1.3	5.0	4.9	4.2	4.7	5.6	4.9	4.4	4.4	-4.0	glycogen phosphorylase
VFA0813	6.6	6.0	6.2	6.2	5.9	5.8	6.1	5.9	-1.2	6.4	6.0	6.1	6.2	6.0	5.7	5.7	5.8	-1.0	formate transporter
VFA0814	7.7	7.9	7.6	7.7	8.0	8.1	8.3	8.1	-1.3	7.5	8.2	7.6	7.8	8.1	8.6	8.3	8.3	-1.5	hypothetical protein
VFA0815	7.0	6.6	6.5	6.7	6.4	6.5	7.0	6.6	-1.4	6.8	6.7	6.4	6.6	6.5	6.8	6.6	6.7	1.0	DNA-3-methyladenine glycosylase
VFA0816	5.6	5.4	4.7	5.2	4.6	4.6	4.9	4.7	-1.1	5.2	5.1	4.8	5.0	4.5	5.2	4.9	4.9	-1.1	hypothetical protein
VFA0817	5.8	5.4	5.1	5.4	4.4	4.9	5.1	4.8	-1.5	5.4	5.3	5.1	5.3	4.9	4.9	4.8	4.9	-1.3	SCO2 protein precursor
VFA0819	6.1	5.2	4.9	5.4	4.8	4.7	5.5	5.0	-1.3	5.9	5.0	4.8	5.2	4.9	5.2	5.3	5.1	-1.1	transporter, drug/metabolite exporter family
VFA0821	5.8	5.3	5.3	5.4	5.2	5.1	5.6	5.3	-1.0	5.6	5.4	5.3	5.4	5.2	5.3	5.2	5.2	-1.1	glutathione S-transferase
VFA0823	6.3	5.7	5.4	5.8	4.7	4.8	5.6	5.0	-1.7	6.2	5.6	5.5	5.8	5.7	5.8	5.7	5.7	-1.1	vanilic acid utilization protein VluB
VFA0825	5.1	3.8	3.6	4.2	3.1	3.2	3.0	3.1	-2.1	4.8	3.7	3.5	4.0	3.6	3.5	3.7	3.6	-1.3	ferric anguibactin transport system permease protein FatC
VFA0827to08:	2.9	2.9	2.7	2.9	2.3	2.4	2.7	2.5	-1.3	2.6	3.0	2.5	2.7	2.3	2.3	2.4	2.4	-1.3	Ferric anguibactin-binding protein
VFA0828	8.9	8.8	8.4	8.7	8.7	8.7	8.9	8.8	-1.0	8.9	9.0	8.4	8.8	8.6	9.0	8.9	8.9	1.1	glutaredoxin 2
VFA0829	7.4	7.1	7.1	7.2	7.0	7.1	7.4	7.2	-1.1	7.1	6.7	6.8	6.9	6.9	6.8	6.9	6.8	-1.0	sodium/proline symporter
VFA0833	7.6	7.6	7.6	7.6	7.5	7.8	7.8	7.7	1.0	7.5	7.7	7.6	7.6	7.6	7.5	7.5	7.6	1.0	transcriptional regulator, AraC family
VFA0834	6.6	6.7	6.4	6.5	6.0	7.5	6.4	6.6	1.0	6.7	5.9	6.4	6.3	6.4	5.9	6.5	6.3	-1.1	NivV precursor
VFA0835	6.2	5.6	5.5	5.8	6.5	6.8	6.7	6.7	-1.4	5.7	5.1	5.3	5.4	5.6	5.2	5.5	5.4	1.0	YobM family integral membrane protein
VFA0836	8.1	8.1	8.0	8.1	7.5	8.1	7.7	7.8	-1.2	7.9	7.9	7.9	7.9	8.0	8.0	8.0	8.0	1.1	Tas protein
VFA0837	6.6	6.8	6.6	6.7	6.0	6.7	6.3	6.3	-1.3	6.5	6.9	6.7	6.7	6.8	7.0	6.8	6.8	1.1	putative ATPase involved in pili biogenesis
VFA0838	6.1	5.7	5.1	5.6	5.1	5.2	5.7	5.4	-1.2	6.1	5.3	5.4	5.6	5.2	5.4	5.4	5.3	-1.2	hypothetical protein
VFA0844	4.5	4.1	4.1	4.2	4.1	4.0	4.4	4.2	-1.1	4.1	4.3	3.8	4.1	3.9	4.4	4.3	4.2	1.1	outer membrane protein P1 precursor
VFA0845	6.5	6.7	6.6	6.6	6.5	6.8	6.7	6.7	-1.0	6.6	6.9	6.7	6.7	6.9	7.0	6.9	6.9	-1.3	hypothetical protein
VFA0846	6.7	6.3	6.1	6.3	6.1	6.2													

VFA0886	3.1	2.7	2.4	2.7	2.6	2.5	2.9	2.7	-1.0	2.9	2.7	2.7	2.8	2.7	2.3	2.4	2.5	-1.2	zinc metalloprotease
VFA0887	4.9	4.4	3.9	4.4	4.1	4.1	4.6	4.3	-1.1	4.3	4.3	4.2	4.3	3.7	3.5	4.0	3.7	-1.5	hypothetical protein
VFA0888	5.1	4.4	3.8	4.4	4.0	4.6	4.8	4.5	-1.0	5.0	4.6	4.0	4.5	4.2	4.6	4.0	4.3	-1.2	hypothetical protein
VFA0889	7.5	7.6	7.2	7.4	6.6	7.3	7.3	7.1	-1.3	7.4	7.5	7.5	7.5	7.4	7.4	7.4	7.4	-1.1	TagD-like protein/thioperoxidase
VFA0890	7.3	7.4	6.8	7.2	6.6	7.0	6.9	6.8	-1.2	7.2	7.5	7.1	7.2	6.9	7.1	6.9	6.9	-1.2	thioredoxin peroxidase
VFA0891to08	3.7	3.0	3.0	3.2	3.4	3.1	3.6	3.4	-1.1	3.8	3.7	2.8	3.4	2.9	3.3	2.6	2.9	-1.4	methyl-accepting chemotaxis protein
VFA0891to08	2.3	1.9	1.8	2.0	2.1	2.2	2.3	2.2	-1.1	2.2	2.4	2.2	2.2	2.1	2.0	1.9	2.0	-1.2	methyl-accepting chemotaxis protein
VFA0892	6.1	5.6	5.3	5.7	5.8	5.3	6.1	5.7	-1.1	6.3	5.8	5.2	5.8	5.3	5.5	5.1	5.3	-1.4	hypothetical protein
VFA0893	6.5	6.3	6.0	6.2	6.1	6.1	6.3	6.2	-1.0	6.3	6.2	6.1	6.2	6.4	6.4	6.2	6.3	-1.1	transcriptional regulator, AraC family
VFA0896	4.8	4.4	4.2	4.5	3.8	4.2	4.1	4.0	-1.4	4.2	4.5	4.5	4.4	3.9	4.1	4.0	4.0	-1.3	multidrug resistance protein A
VFA0897	7.1	7.4	7.3	7.3	7.0	7.2	7.2	7.1	-1.1	7.1	7.5	7.4	7.3	7.2	7.1	7.2	7.2	-1.1	transcriptional regulators, LysR family
VFA0898	4.2	3.9	3.8	4.0	4.2	3.9	3.9	4.0	-1.0	3.9	4.0	3.9	4.0	4.0	3.6	3.6	3.7	-1.2	hypothetical protein
VFA0900	3.3	3.6	3.2	3.4	3.6	3.4	3.4	3.5	-1.1	3.5	3.4	3.3	3.4	3.2	3.2	3.6	3.3	-1.0	arylsulfatase regulator (Fe-S oxidoreductase)
VFA0901	3.4	2.9	3.0	3.1	3.1	3.0	3.0	3.0	-1.0	3.2	3.0	2.8	3.0	2.6	2.9	2.7	2.7	-1.2	MoxR protein
VFA0902	2.5	2.2	1.9	2.2	2.6	2.0	2.6	2.4	-1.2	2.3	2.3	2.2	2.3	2.1	2.1	2.0	2.1	-1.2	hypothetical protein
VFA0903	2.4	2.3	2.3	2.3	2.1	2.2	2.3	2.2	-1.1	2.3	2.3	2.0	2.2	2.4	2.5	2.2	2.3	-1.1	hypothetical protein
VFA0903to09	3.3	3.3	3.1	3.2	3.0	3.2	3.1	3.1	-1.1	3.3	3.3	2.8	3.1	2.7	3.1	2.6	2.8	-1.3	hypothetical protein
VFA0903to09	4.4	4.4	4.1	4.3	4.5	4.5	4.8	4.6	-1.2	4.2	4.8	4.4	4.5	4.0	4.7	4.3	4.3	-1.1	hypothetical protein
VFA0904	3.9	3.8	3.5	3.7	3.8	3.9	3.9	3.8	-1.1	3.5	3.9	3.5	3.6	3.9	3.8	3.5	3.7	-1.1	hypothetical protein
VFA0905	2.6	2.1	1.9	2.2	2.2	2.1	2.4	2.3	-1.0	2.5	2.2	2.3	2.3	2.2	2.3	2.0	2.2	-1.1	hypothetical protein
VFA0906	3.7	3.2	3.1	3.4	2.6	2.9	3.5	3.0	-1.2	3.2	3.3	3.0	3.2	2.7	3.1	2.9	2.9	-1.2	acriflavine resistance periplasmic protein
VFA0907	4.7	4.3	3.9	4.3	3.9	4.2	4.5	4.2	-1.1	4.3	4.5	4.1	4.3	4.1	3.9	3.6	3.9	-1.4	acriflavine resistance plasma membrane protein
VFA0909	6.5	5.7	5.2	5.8	5.1	5.1	5.8	5.3	-1.4	6.3	5.3	5.3	5.6	4.9	5.2	4.9	5.0	-1.5	hypothetical protein
VFA0910	4.1	3.0	2.6	3.2	2.8	2.8	3.4	3.0	-1.2	3.5	3.3	2.8	3.2	2.6	2.8	2.9	2.8	-1.2	hypothetical protein
VFA0911	4.9	4.4	3.7	4.3	4.0	3.9	4.6	4.1	-1.2	4.7	4.3	3.9	4.3	3.5	4.1	3.5	3.7	-1.5	transcriptional regulators, LysR family
VFA0912	6.4	5.6	5.2	5.7	5.2	5.2	5.9	5.5	-1.2	6.0	4.8	5.3	5.4	5.1	5.0	5.0	5.0	-1.3	ABC transporter ATP-binding protein
VFA0913	6.7	5.7	5.3	6.0	6.1	5.6	6.3	5.9	-1.1	6.4	5.6	5.3	6.8	6.5	5.1	5.2	5.3	-1.2	hypothetical protein
VFA0914	5.6	5.2	5.3	5.4	4.9	5.5	5.5	5.3	-1.0	5.4	5.2	5.2	5.3	5.4	5.1	5.4	5.3	-1.0	hypothetical protein
VFA0915	6.6	6.3	6.1	6.3	6.5	6.7	6.9	6.7	-1.3	6.4	6.5	6.0	6.3	6.1	6.7	6.3	6.4	-1.1	probable maltose O-acetyltransferase
VFA0916	5.5	5.2	5.3	5.3	5.2	4.7	5.1	5.0	-1.2	5.5	5.2	5.2	5.3	5.1	5.0	5.1	5.1	-1.2	Na(+)-driven multidrug efflux pump
VFA0917	7.4	7.2	6.8	7.1	7.3	6.9	7.7	7.3	-1.1	7.3	7.3	6.8	7.2	6.9	7.3	7.2	7.2	-1.0	deoxycydidylate deaminase
VFA0923	6.7	6.9	6.7	7.0	6.7	6.8	7.0	6.5	-1.7	7.3	6.8	6.8	6.8	6.5	6.3	6.5	6.4	-1.3	6-oxo-acyl-CoA reductase
VFA0924	7.1	6.0	5.8	6.3	5.3	4.8	5.9	5.4	-1.9	6.9	5.7	5.9	6.2	5.8	5.4	6.0	5.8	-1.3	LuxI, autoinducer synthesis associated
VFA0926	6.8	6.7	6.6	6.7	6.2	6.5	6.6	6.4	-1.2	6.8	6.7	6.6	6.7	6.6	6.7	6.7	6.7	-1.0	hypothetical membrane associated protein
VFA0927	6.3	6.3	6.1	6.2	6.0	6.0	6.4	6.2	-1.0	6.0	6.6	6.2	6.3	6.7	6.5	6.5	6.6	-1.2	hypothetical protein
VFA0928	3.3	3.2	2.9	3.2	3.4	3.2	3.6	3.4	-1.2	3.3	3.2	3.2	3.2	3.3	3.2	2.9	3.1	-1.1	hypothetical protein
VFA0929	4.2	3.9	3.6	3.9	3.7	3.5	4.3	3.7	-1.1	4.1	3.9	3.4	3.8	3.7	3.3	3.7	3.7	-1.2	hypothetical protein
VFA0930	4.9	4.7	4.7	4.8	4.9	4.8	4.9	4.8	-1.0	4.7	4.7	4.9	4.8	4.6	4.2	4.6	4.5	-1.2	carboxypeptidase G2 precursor
VFA0933	6.2	5.5	5.5	5.7	6.0	5.2	6.5	5.9	-1.1	5.8	5.4	5.3	5.5	5.0	4.5	4.9	4.8	-1.7	hypothetical protein
VFA0934	6.9	6.5	6.2	6.6	6.0	6.1	6.5	6.2	-1.3	6.8	6.2	6.3	6.4	6.1	6.3	6.1	6.2	-1.2	hypothetical protein
VFA0935	6.9	6.4	6.0	6.4	6.3	6.0	6.7	6.3	-1.1	6.8	6.4	6.2	6.4	6.0	5.9	5.9	5.9	-1.4	transcriptional regulators, LysR family
VFA0936	7.6	7.4	7.2	7.4	7.2	7.2	7.5	7.3	-1.1	7.4	7.2	7.3	7.4	7.1	7.0	7.0	7.0	-1.0	lipase/acylhydrolase family protein
VFA0937	7.2	6.8	6.9	7.0	6.8	6.8	7.2	6.9	-1.0	7.0	6.9	6.7	6.9	6.8	6.7	6.9	6.8	-1.1	phosphoglycolate phosphatase
VFA0938	6.8	6.6	6.7	6.7	6.2	6.4	6.7	6.4	-1.2	6.6	6.6	6.5	6.6	6.3	6.1	6.6	6.3	-1.2	threonine efflux protein
VFA0940	8.1	8.2	8.3	8.2	7.8	7.7	8.0	7.9	-1.3	7.9	8.4	8.2	8.2	7.8	8.1	7.8	7.9	-1.2	PTS system, fructose-specific IIBC component
VFA0943	5.1	4.3	4.2	4.5	4.5	4.4	4.9	4.6	-1.0	4.9	4.6	4.3	4.6	4.5	4.2	4.2	4.3	-1.2	catabolite repressor-activator
VFA0944	1.7	1.7	1.6	1.7	1.7	1.5	1.6	1.7	-1.0	1.6	1.7	1.6	1.7	1.6	1.6	1.5	1.6	-1.5	hypothetical protein
VFA0945	5.6	5.7	5.1	5.5	5.4	5.5	5.5	5.5	-1.0	5.3	5.6	5.6	5.5	4.8	5.1	5.1	5.0	-1.4	hypothetical protein
VFA0946	3.8	3.6	3.0	3.5	3.3	3.4	3.9	3.6	-1.1	3.7	3.8	3.5	3.7	2.9	3.1	3.2	3.1	-1.2	hypothetical protein
VFA0947_x	2.2	2.2	2.2	2.2	2.2	2.3	2.3	2.3	-1.1	2.2	2.3	2.2	2.2	2.2	2.3	2.2	2.2	-1.0	hypothetical protein
VFA0948	5.1	4.9	4.2	4.8	4.5	4.7	5.0	4.7	-1.0	4.6	5.1	4.5	4.7	4.2	4.2	3.9	4.1	-1.5	hypothetical protein
VFA0949	5.7	5.2	5.1	5.3	5.3	5.8	5.3	5.4	-1.1	5.5	5.5	5.1	5.3	5.4	4.7	4.5	4.5	-1.2	hypothetical protein
VFA0950	6.0	5.9	5.4	5.8	5.7	5.8	6.2	5.9	-1.1	5.9	6.1	5.7	5.9	5.5	5.7	5.6	5.6	-1.2	hypothetical protein
VFA0951	4.8	4.1	3.6	4.2	3.9	4.1	4.5	4.2	-1.0	4.4	4.0	3.6	4.0	4.1	4.2	4.0	4.1	-1.1	hypothetical protein
VFA0952	4.2	3.7	3.6	3.8	3.3	3.5	3.8	3.5	-1.2	3.6	3.9	3.2	3.6	3.0	3.2	3.3	3.3	-1.2	hypothetical protein
VFA0953	3.9	3.1	3.4	3.5	3.1	3.4	3.6	3.4	-1.1	3.4	3.7	3.4	3.5	3.0	3.6	3.0	3.1	-1.3	VgrG protein
VFA0954	5.0	4.6	4.0	4.5	4.5	4.4	4.7	4.5	-1.0	4.7	4.7	4.3	4.6	4.2	4.7	4.2	4.3	-1.2	hemolysin co-regulated protein
VFA0955	7.0	6.9	6.7	6.9	6.4	6.6	6.6	6.6	-1.2	6.6	6.9	6.8	6.8	7.0	7.0	6.9	7.0	-1.2	hypothetical protein
VFA0956	7.8	7.5	7.3	7.5	7.1	7.2	7.3	7.2	-1.3	7.7	7.3	7.4	7.5	7.2	7.4	7.3	7.3	-1.2	hydrolase (HAD superfamily)
VFA0957	5.3	4.9	5.1	5.1	4.9	4.7	4.9	4.9	-1.2	5.1	5.0	4.6	4.9	4.5	4.5	4.5	4.5	-1.3	transporter, MFS superfamily
VFA0960	6.4	6.2	6.2	6.3	5.7	5.7	5.8	5.7	-1.4	6.3	5.9	6.2	6.1	5.7	5.2	5.9	5.6	-1.4	maltose/maltodextrin-binding protein
VFA0961	3.7	3.9	3.4	3.7	3.7	3.4	3.6	3.6	-1.0	3.6	3.5	3.3	3.4	3.0	3.8	3.6	3.2	-1.1	hypothetical protein
VFA0962	3.5	3.3	3.0	3.3	3.2	3.1	3.5	3.3	-1.0	3.3	3.3	3.3	3.3	3.2	3.0	3.1	3.1	-1.2	pyruvate formate-lyase activating enzyme
VFA0963	7.3	7.2	7.0	7.2	7.1	7.0	7.5	7.2	-1.0	7.2	7.3	7.1	7.2	7.0	6.9	7.1	7.0	-1.2	transcriptional regulators, LysR family
VFA0964	4.6	3.7	3.3	3.9	3.6	3.4	3.8	3.6	-1.2	4.3	3.5	3.4	3.7	3.2	3.3	3.4	3.3	-1.3	integral membrane protein
VFA0965	7.0	6.6	6.2	6.6	6.1	6.5	6.5	6.4	-1.2	6.7	6.6	6.4	6.5	6.0	6.2	5.9	6.0	-1.4	NADPH-dependent FMN reductase
VFA0966	6.8	6.6	6.4	6.6	7.9	6.8	8.1	7.6	-1.0	6.8	7.1	6.4	6.7	6.1	6.4	5.7	6.1	-1.6	L-serine dehydratase
VFA0967	4.7	4.7	4.6	4.7	4.8	4.4	5.0	4.7	-1.0	4.5	4.8	4.6	4.6	4.2	4.3	4.2	4.2	-1.3	nucleoside permease NupC
VFA0969	4.5	4.2	4.2	4.3	4.1	3.9	4.0	4.0	-1.2	4.3	4.3	4.3	4.3	3.9	3.7	4.0	3.9	-1.3	guanine deaminase
VFA0970	5.9	5.4	5.1	5.5	4.6	5.0	5.1	4.9	-1.4	5.5	5.1	5.2	5.2	5.0	5.1	5.3	5.1	-1.1	hypothetical protein
VFA0971	5.7	4.9	5.0	5.2	4.3	4.8	5.1	4.7	-1.4	5.3	4.8	4.7	4.9	4.2	4.6	4.4	4.4	-1.4	vitamin B12 transport ATP-binding protein BtuD
VFA0972	6.1	5.7	5.7	5.9	5.4	5.6	5.6	5.5	-1.3	6.0	5.6	5.7	5.7	5.7	5.3	5.6	5.5	-1.2	ABC transporter, FeoCD family
VFA0973	6.6	6.4	6.3	6.4	6.0	6.3	6.4	6.2											

VFA1010to10	3.2	2.8	2.3	2.7	2.5	2.4	2.7	2.5	-1.2	2.9	2.7	2.2	2.6	2.0	2.2	2.1	2.1	-1.4	beta-hexosaminidase
VFA1011	3.2	2.7	2.2	2.7	2.4	2.1	3.1	2.5	-1.1	3.0	2.7	2.6	2.8	2.3	2.3	2.1	2.2	-1.4	hypothetical protein
VFA1013	6.6	6.3	5.2	6.0	7.0	6.0	7.4	6.8	1.7	6.3	6.4	5.7	6.1	5.3	5.9	5.3	5.5	-1.6	hypothetical protein
VFA1018	6.5	6.5	6.3	6.4	6.5	6.7	7.0	6.7	1.2	6.7	6.9	6.8	6.8	6.8	6.9	6.5	6.7	-1.0	hypothetical protein
VFA1019	6.2	6.3	6.2	6.2	5.9	6.5	6.9	6.4	1.1	6.2	6.5	6.6	6.4	6.1	6.2	5.9	6.2	-1.2	hypothetical cytosolic protein
VFA1020	5.1	5.4	4.8	5.1	4.4	4.7	6.5	5.2	1.0	5.3	5.8	5.7	5.6	6.1	6.1	3.4	5.2	-1.4	possible anti-sigma factor antagonist
VFA1021	5.2	5.6	5.2	5.3	4.6	4.9	5.9	5.2	-1.1	5.3	5.7	5.6	5.5	6.2	5.8	5.8	5.6	1.0	OmpA family protein
VFA1022	5.2	5.2	5.0	5.1	4.5	4.9	5.6	5.0	-1.1	4.9	5.5	5.4	5.3	5.5	5.3	4.4	5.1	-1.1	transporter
VFA1023	5.6	5.3	5.0	5.3	4.7	4.9	5.9	5.2	-1.1	5.4	5.4	5.3	5.4	5.4	5.3	4.1	4.9	-1.3	hypothetical protein
VFA1024	5.9	5.7	5.3	5.6	5.6	5.3	6.0	5.6	1.0	5.8	6.0	5.9	5.9	5.6	5.8	5.1	5.5	-1.3	transcriptional regulator
VFA1025	7.6	7.8	7.3	7.6	7.9	8.0	8.3	8.1	1.4	7.5	8.1	7.7	7.8	7.7	8.3	7.7	7.9	1.1	transcriptional regulator
VFA1026	9.5	9.8	9.4	9.5	10.3	9.7	10.3	10.1	1.5	9.3	10.0	9.6	9.7	9.3	9.7	9.1	9.4	-1.2	transcriptional regulator, LuxO family
VFA1027	7.5	7.5	7.3	7.4	8.1	7.3	8.2	7.9	1.4	7.3	7.6	7.3	7.4	7.0	7.2	6.7	7.0	-1.3	glycosyltransferase
VFA1028	3.8	3.6	3.6	3.7	3.4	3.1	4.9	3.8	1.1	3.7	3.8	4.1	3.9	4.6	4.3	3.2	4.0	-1.1	glycosyltransferase
VFA1029	3.2	3.4	3.1	3.2	2.6	3.0	4.4	3.3	1.1	3.3	3.5	3.9	3.5	4.6	3.7	2.5	3.6	1.0	putative glycosyltransferase
VFA1030	4.0	3.8	3.5	3.8	3.2	3.4	4.5	3.7	-1.0	3.9	4.2	3.8	4.0	4.3	4.1	3.4	4.0	-1.0	oligosaccharide translocase
VFA1036	4.8	4.3	4.4	4.5	4.0	4.0	5.5	4.5	1.0	4.6	5.3	5.0	5.0	5.3	4.9	3.4	4.5	-1.4	glycosyltransferase
VFA1032	4.0	3.8	3.8	3.8	3.2	3.2	4.6	3.7	-1.1	3.8	3.8	4.3	4.0	4.4	4.1	2.9	3.8	-1.1	probable maltose O-acetyltransferase
VFA1033	4.3	4.2	3.8	4.1	3.5	3.7	4.9	4.0	-1.0	3.9	4.1	4.6	4.2	4.5	4.1	3.4	4.0	-1.1	glycosyltransferase
VFA1034	3.8	3.6	3.6	3.7	3.4	3.6	4.4	3.8	1.1	3.7	3.6	3.8	3.7	3.7	3.8	2.8	3.4	-1.2	chain length regulator (capsular polysaccharide biosynthesis)
VFA1035	4.7	4.6	4.3	4.5	3.7	4.0	5.6	4.4	-1.0	4.6	5.1	5.1	4.9	5.0	5.3	3.5	4.6	-1.2	glycosyltransferase
VFA1037	5.5	5.4	5.2	5.4	5.1	4.9	5.9	5.3	-1.0	5.3	5.6	5.4	5.4	5.5	5.5	5.0	5.3	-1.1	bacterial sugar transferase
VFA1040	5.8	5.2	4.9	5.3	4.9	4.9	5.0	4.9	-1.3	5.5	5.0	4.9	5.2	4.7	4.9	4.8	4.8	-1.3	glutaredoxin
VFA1041	7.1	6.5	6.2	6.6	6.3	6.6	7.0	6.6	1.0	7.0	6.4	6.4	6.6	6.6	6.4	6.2	6.4	-1.1	protein YgiW precursor
VFA1042	7.0	6.6	6.4	6.7	6.6	7.3	7.2	7.0	1.3	6.6	6.3	6.3	6.4	6.1	6.2	6.2	6.2	-1.1	ABC transporter component, lysophospholipase L1 transport
VFA1043	6.0	6.7	6.7	6.7	6.0	6.7	7.0	6.2	-1.2	6.0	6.7	6.7	6.7	6.8	6.5	6.5	6.8	-1.2	637 Cok thioesterase I
VFA1045	6.3	5.4	4.5	5.4	4.8	4.4	5.3	4.8	-1.5	6.0	5.2	4.7	5.3	4.5	4.9	4.5	4.6	-1.6	hypothetical protein
VFA1046	8.1	7.5	7.4	7.7	7.2	7.3	7.4	7.3	-1.4	7.9	7.3	7.4	7.6	7.2	7.4	7.5	7.4	-1.1	transcriptional regulator, LysR family
VFA1047	7.7	7.4	7.3	7.5	7.5	7.3	7.7	7.5	1.0	7.6	7.3	7.3	7.4	7.2	7.2	7.5	7.3	-1.1	Mg2+ transporter MgtE
VFA1048	5.5	4.7	4.6	4.9	4.9	4.8	5.4	5.0	1.1	5.2	5.1	4.7	5.0	4.8	4.8	4.9	4.8	-1.1	transcriptional regulators, LysR family
VFA1049	5.6	5.3	5.3	5.8	3.7	3.6	3.8	3.0	-1.0	4.0	3.6	3.8	3.9	3.9	3.5	3.6	3.6	-1.1	33AD1 oxidase family
VFA1050	5.1	4.9	4.6	4.9	5.0	4.4	5.5	4.9	-1.0	4.5	5.0	4.4	4.6	4.5	4.8	4.2	4.5	-1.1	glycine betaine-binding protein
VFA1052	6.0	5.8	5.8	5.9	6.0	5.6	6.0	5.9	-1.0	5.8	6.0	5.8	5.8	5.6	5.6	5.5	5.6	-1.2	sulfate transporter
VFA1053	8.0	8.3	8.0	8.1	8.0	8.2	8.3	8.1	1.0	7.9	8.8	8.2	8.3	8.0	8.5	8.0	8.2	-1.1	transcriptional regulator, MerR family
VFA1054	7.3	7.1	6.7	7.0	7.5	7.1	7.8	7.5	1.4	7.3	7.3	6.8	7.1	6.6	7.0	6.8	6.8	-1.2	acetyltransferase
VFA1055	5.4	4.7	4.9	5.0	4.6	4.4	4.5	4.1	-1.2	4.9	4.9	4.8	4.9	4.4	4.3	4.4	4.4	-1.4	transporter, drug/metabolite exporter family
VFA1056	5.7	5.1	4.5	5.1	4.7	5.0	5.1	4.9	-1.1	5.6	5.0	5.0	5.2	5.0	5.2	5.0	5.1	-1.1	hypothetical protein
VFA1057	5.7	5.7	5.5	5.7	5.3	5.6	5.6	5.5	-1.1	5.6	5.7	5.7	5.7	5.5	5.5	5.2	5.4	-1.2	predicted phosphatase
VFA1058	6.2	4.0	3.5	4.5	3.2	2.6	4.0	3.3	-2.4	6.0	3.5	3.5	4.3	2.6	2.9	2.7	2.7	-3.0	hypothetical protein
VFA1059	5.2	5.0	4.4	4.9	4.9	4.5	5.2	4.8	-1.0	5.0	4.9	4.5	4.8	4.5	4.4	4.2	4.4	-1.3	hypothetical protein
VFA1060	5.1	4.5	4.2	4.6	4.0	4.0	4.4	4.1	-1.4	4.9	4.6	4.4	4.6	4.4	4.6	4.0	4.4	-1.0	hypothetical protein
VFA1061	5.5	5.0	4.8	5.1	4.8	5.1	5.4	5.1	-1.0	5.2	4.7	4.5	4.8	4.9	4.6	4.8	4.8	-1.0	transcriptional regulators, LysR family
VFA1062	8.3	8.0	8.3	8.2	8.0	8.4	8.2	8.2	1.0	8.3	8.0	8.0	8.1	8.4	8.1	8.5	8.3	1.2	transporter, NRAMP family
VFA1063	6.7	6.4	5.7	6.3	5.6	5.8	6.0	5.8	-1.2	6.6	6.2	5.8	6.2	5.5	6.1	5.7	5.8	-1.4	transcriptional regulator, MarR family
VFA1064	5.5	5.2	5.0	5.3	4.7	5.0	5.3	5.0	-1.2	5.3	5.4	5.1	5.3	5.4	5.2	5.1	5.2	-1.1	transporter
VFA1065	5.4	5.8	5.8	6.0	5.8	5.3	5.9	5.5	-1.3	6.2	5.7	5.6	5.8	5.5	5.2	5.4	5.3	-1.4	hypothetical protein
VFA1067	4.0	3.2	3.1	3.4	3.4	3.5	4.2	3.7	-1.2	3.5	3.2	3.3	3.3	3.3	2.8	2.6	2.9	-1.3	hypothetical protein
VFA1068	6.4	6.0	5.9	6.1	5.6	5.5	6.1	5.7	-1.3	6.2	6.1	5.9	6.1	5.4	5.8	5.6	5.6	-1.4	peptidase E
VFA1070	5.7	4.8	4.1	4.9	3.6	3.9	3.8	3.8	-2.1	5.1	3.9	4.3	4.4	3.8	2.9	3.5	3.4	-2.1	hypothetical protein
VFA1071	5.5	4.9	4.3	4.9	3.8	4.4	4.3	4.2	-1.6	5.0	4.4	4.4	4.6	4.1	3.5	4.3	4.0	-1.6	methyI-accepting chemotaxis protein
VFA1075	5.5	2.9	2.9	3.1	2.9	3.0	4.4	3.1	-1.1	3.2	3.0	3.0	3.2	3.2	2.8	2.8	2.9	-1.3	possible heptosyltransferase
VFA1076	2.0	1.6	1.5	1.7	1.6	1.6	1.7	1.6	-1.1	2.1	1.6	1.9	1.9	1.9	1.5	1.6	1.7	-1.2	possible diguanylate phosphodiesterase
VFA1076to10	2.1	1.9	1.6	1.8	1.6	1.7	1.8	1.7	-1.1	1.8	1.8	1.6	1.7	1.7	1.8	1.6	1.7	-1.0	possible diguanylate phosphodiesterase
VFA1076to10	2.7	2.6	2.1	2.5	2.6	2.4	2.8	2.6	-1.1	2.7	2.6	2.2	2.5	2.2	2.7	2.3	2.4	-1.1	possible diguanylate phosphodiesterase
VFA1078	6.3	5.9	5.7	6.0	5.6	5.8	6.3	5.9	-1.1	6.1	5.9	5.5	5.9	5.4	5.6	5.4	5.5	-1.3	acetyltransferase/hydrolyase family protein
VFA1082	6.2	6.5	6.3	6.0	4.7	5.8	5.7	5.4	-1.0	6.1	6.2	6.0	6.1	6.2	5.7	5.9	5.9	-1.1	transcriptional regulator, AraC family
VFA1082to10	1.8	1.8	1.6	1.8	1.7	1.8	1.8	1.8	-1.0	2.0	1.9	1.7	1.9	1.9	1.7	1.8	1.8	-1.1	transcriptional regulator, AraC family
VFA1082to10	4.3	4.0	3.5	3.9	3.5	3.5	3.7	3.5	-1.3	4.0	3.7	3.7	3.8	3.6	3.7	3.6	3.6	-1.1	transcriptional regulator, AraC family
VFA1083	1.4	1.5	1.4	1.5	1.5	1.6	1.5	1.5	1.0	1.5	1.5	1.4	1.5	1.3	1.7	1.4	1.5	-1.0	hypothetical protein
VFA1085	4.8	4.5	3.8	4.4	4.4	4.3	4.4	4.3	-1.0	4.6	4.7	4.4	4.6	4.1	4.4	4.0	4.2	-1.3	hypothetical protein
VFA1086	5.9	5.5	5.0	5.5	5.3	5.5	5.6	5.5	-1.0	5.6	5.2	4.9	5.2	5.0	5.4	5.2	5.2	-1.0	transcriptional regulators, LysR family
VFA1087	4.0	4.0	3.9	4.0	4.1	4.2	3.9	4.1	1.1	3.8	4.2	4.0	4.0	3.8	4.1	4.1	4.0	1.0	ABC transporter substrate-binding protein
VFA1088	3.1	3.0	2.8	3.0	3.0	3.0	3.0	3.0	1.0	2.8	3.0	2.8	2.9	2.9	2.9	2.6	2.8	-1.0	hypothetical protein
VFA1089	2.7	2.7	2.1	2.5	2.6	2.5	2.6	2.6	1.0	2.6	2.5	2.4	2.5	2.4	2.4	2.3	2.4	-1.1	ABC transporter permease protein
VFA1090	2.3	2.0	1.8	2.1	1.9	2.0	2.2	2.0	-1.0	2.2	2.0	1.9	2.0	2.0	1.8	1.9	1.9	-1.1	ABC transporter permease protein
VFA1091	5.5	5.4	5.0	5.3	5.7	5.1	5.9	5.6	1.2	5.2	5.6	5.1	5.3	5.0	5.4	5.1	5.2	-1.1	iron(III)-transport ATP-binding protein StuC
VFA1092	5.9	6.0	5.5	5.8	5.9	5.3	6.3	5.8	1.0	5.7	6.2	5.5	5.8	5.3	5.4	5.1	5.3	-1.5	hypothetical protein
VFA1093	4.5	3.8	3.5	4.0	3.8	3.6	3.9	3.8	-1.2	4.0	3.6	3.7	3.8	3.4	3.3	3.0	3.2	-1.0	hypothetical protein
VFA1094	5.9	5.3	5.2	5.5	4.3	4.8	4.6	4.6	-1.9	5.9	4.4	4.7	5.0	4.1	4.2	3.9	4.1	-1.9	cold shock protein
VFA1096	5.1	4.6	4.7	4.8	4.0	4.0	4.7	4.2	-1.5	4.9	4.3	4.5	4.6	3.9	3.9	4.1	4.0	-1.5	hypothetical protein
VFA1097	3.8	3.8	3.5	3.7	3.3	3.4	3.7	3.5	-1.2	3.9	3.6	3.3	3.6	3.0	3.1	3.2	3.1	-1.4	hypothetical protein
VFA1100	4.5	3.8	4.0	4.1	4.4	4.2	4.2	4.3	1.1	4.7	4.3	4.2	4.4	4.1	4.0	3.9	4.0	-1.3	outer membrane protein
VFA1101	1.6	1.6	1.5	1.6	1.7	1.6	1.5	1.6	1.1	1.									

VFA1128to111	4.2	3.4	3.5	3.7	3.6	3.4	3.6	3.5	-1.1	3.8	3.6	3.4	3.6	3.4	3.5	3.4	3.5	-1.1	hypothetical protein
VFA1128to112	2.2	1.9	2.2	2.0	1.9	2.0	2.0	2.0	-1.2	2.0	2.0	2.0	2.1	2.0	1.7	1.9	2.0	-1.2	hypothetical protein
VFA1129-1	4.0	3.8	3.6	3.8	3.6	3.4	4.0	3.6	-1.1	3.9	3.7	3.6	3.7	3.2	3.2	3.3	3.2	-1.4	hypothetical protein
VFA1129-2	6.7	6.6	6.5	6.6	6.3	6.3	6.6	6.4	-1.1	6.5	6.7	6.4	6.5	6.2	6.2	6.3	6.3	-1.2	hypothetical protein
VFA1130	2.7	2.6	2.7	2.7	2.7	2.8	2.7	2.7	-1.0	2.8	2.5	2.5	2.6	2.4	2.7	2.5	2.5	-1.0	hypothetical protein
VFA1131	2.1	1.8	1.8	1.9	1.9	1.8	1.9	1.8	-1.1	2.3	1.8	1.7	1.9	1.8	2.1	1.8	1.7	-1.0	hypothetical protein
VFA1132	5.3	5.2	4.9	5.1	5.1	4.5	5.3	5.0	-1.1	5.0	4.9	5.0	5.0	4.8	4.7	4.5	4.7	-1.2	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VFA1133	7.2	7.7	7.1	7.3	7.2	6.8	7.3	7.1	-1.2	7.2	7.3	7.4	7.3	7.0	6.8	6.9	6.9	-1.3	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VFA1134	7.0	7.2	6.7	6.9	6.7	6.3	7.1	6.7	-1.2	6.8	6.9	7.0	6.9	6.5	6.2	6.5	6.4	-1.4	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VFA1135	6.6	6.9	6.4	6.7	6.4	5.8	6.7	6.3	-1.3	6.5	6.7	6.9	6.7	6.2	5.9	6.3	6.1	-1.5	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VFA1135_x	6.8	7.0	6.6	6.8	6.1	5.8	6.8	6.2	-1.5	6.5	6.8	6.8	6.7	6.3	6.0	6.1	6.1	-1.5	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VFA1137	3.6	3.3	2.9	3.3	3.3	3.1	3.5	3.3	-1.0	3.6	3.2	3.1	3.3	2.7	3.3	2.9	3.0	-1.3	anaerobic glycerol-3-phosphate dehydrogenase subunit C
VFA1138	1.9	1.8	1.7	1.8	1.8	1.7	1.8	1.8	-1.0	1.6	1.7	1.7	1.7	1.8	1.7	1.6	1.7	-1.0	structural protein P5
VFA1139	2.0	2.0	1.8	1.9	2.1	1.9	2.0	2.0	-1.0	2.0	1.9	2.0	2.0	2.1	2.0	1.9	2.0	-1.0	hypothetical protein
VFA1140	3.3	2.8	2.1	2.7	2.4	2.6	2.8	2.6	-1.1	3.0	2.4	2.5	2.6	2.4	2.5	2.2	2.4	-1.2	hypothetical protein
VFA1141	2.3	2.1	1.9	2.1	2.2	2.1	2.2	2.2	-1.1	2.3	2.0	1.9	2.1	1.8	2.0	2.0	1.9	-1.1	hypothetical protein
VFA1142	5.6	4.8	4.7	5.0	4.6	4.7	5.2	4.8	-1.1	4.9	4.5	4.8	4.8	4.2	4.4	4.4	4.3	-1.3	transcriptional regulators, LysR family
VFA1143	3.3	2.9	2.5	2.9	2.6	2.6	2.8	2.7	-1.2	3.2	3.0	2.9	3.1	2.7	2.7	2.9	2.7	-1.2	hypothetical membrane spanning protein
VFA1145	7.3	7.1	6.9	7.1	6.7	7.0	7.0	6.9	-1.2	7.2	7.2	7.1	7.1	7.0	7.2	7.2	7.1	-1.0	hypothetical protein
VFA1146	4.8	4.1	3.7	4.2	4.1	3.6	3.7	3.5	-1.6	4.3	4.1	4.0	4.2	3.6	3.6	3.4	3.5	-1.5	carbamate kinase
VFA1147	6.4	5.9	5.9	6.1	6.1	5.6	6.2	5.9	-1.1	6.2	5.8	5.9	6.0	5.9	5.6	5.5	5.7	-1.2	hydrolase (HAD superfamily)
VFA1148	7.4	7.3	7.1	7.3	7.3	7.1	7.6	7.3	-1.0	7.3	7.2	7.2	7.2	7.1	7.1	7.2	7.1	-1.1	transcriptional regulators, LysR family
VFA1149	4.9	4.6	4.4	4.6	4.3	4.1	4.8	4.4	-1.2	4.6	4.4	4.4	4.5	4.1	4.4	4.3	4.2	-1.2	acriflavin resistance plasma membrane protein
VFA1150	4.0	3.6	3.0	3.5	3.2	3.3	3.6	3.4	-1.1	3.5	3.4	3.2	3.4	3.7	3.7	3.4	3.6	-1.1	acriflavin resistance periplasmic protein
VFA1151	3.9	3.6	3.5	3.7	3.6	3.4	3.8	3.6	-1.1	3.5	3.8	3.7	3.7	3.9	4.2	3.9	4.0	-1.2	hypothetical protein
VFA1152	4.1	3.9	3.7	3.9	3.9	4.1	4.4	4.1	-1.2	4.0	4.0	3.8	3.9	3.5	4.1	4.0	3.9	-1.0	acriflavin resistance periplasmic protein
VFA1153	5.9	5.4	5.4	5.6	5.2	5.4	5.4	5.4	-1.2	5.9	5.1	5.5	5.5	5.6	5.7	5.6	5.6	-1.1	methyltransferase
VFA1154	7.6	7.4	7.2	7.4	7.3	7.2	7.7	7.4	-1.0	7.6	7.5	7.1	7.4	7.3	7.7	7.4	7.5	-1.1	hypothetical protein
VFA1155	7.0	6.4	6.2	6.5	6.1	6.1	6.4	6.2	-1.3	6.9	6.2	6.6	6.5	6.3	6.2	6.5	6.3	-1.1	hypothetical protein
VFA1156	7.1	6.6	6.6	6.7	6.3	6.4	6.6	6.4	-1.2	7.0	6.4	6.7	6.7	6.6	6.2	6.7	6.5	-1.1	ATP-dependent DNA helicase RecQ
VFA1157	6.7	6.2	6.1	6.3	5.6	6.1	6.3	6.0	-1.2	6.3	5.9	5.9	6.0	6.2	6.1	6.1	6.1	-1.1	ATP-dependent DNA helicase RecQ
VFA1160	6.5	5.9	5.9	6.1	6.0	5.7	6.3	6.0	-1.1	6.4	5.7	5.9	6.0	5.9	5.7	5.8	5.8	-1.1	transcriptional regulator
VFA1161	8.7	8.7	8.6	8.6	8.3	8.4	8.4	8.4	-1.2	8.6	8.5	8.6	8.6	8.3	8.5	8.5	8.5	-1.1	pyridoxamine 5'-phosphate oxidase
VFA1162-1	9.6	9.7	9.7	9.7	9.7	9.7	9.7	9.7	-1.0	9.6	9.8	9.7	9.7	9.8	9.7	9.7	9.7	-1.0	iron-regulated protein FrpC
VFA1162to116	5.8	5.3	4.7	5.3	5.1	5.0	5.7	5.3	-1.0	5.2	5.3	5.0	5.2	5.2	5.2	4.9	5.1	-1.1	iron-regulated protein FrpC
VFA1162to111	4.1	4.0	3.7	3.9	4.1	4.1	4.2	4.1	-1.2	4.0	4.3	3.9	4.1	4.0	4.0	3.9	4.0	-1.1	iron-regulated protein FrpC
VFA1163	10.7	10.7	10.5	10.8	10.9	10.9	11.1	10.9	-1.2	10.7	10.8	10.6	10.7	10.9	11.2	11.0	11.0	-1.2	type I secretion outer membrane protein
VFA1164	9.3	9.1	8.7	9.0	9.4	9.4	9.7	9.5	-1.4	9.2	9.3	8.9	9.1	9.1	9.6	9.2	9.3	-1.1	outer membrane porin F
VFA1165	8.0	7.6	7.6	7.7	7.4	7.6	7.8	7.6	-1.1	7.7	7.6	7.4	7.6	7.2	7.1	7.2	7.2	-1.1	type I protein secretion ATP-binding protein
VFA1166	8.3	8.0	8.0	8.1	7.9	8.1	8.3	8.1	-1.0	8.0	7.9	7.8	7.9	7.5	7.8	7.8	7.7	-1.2	diguanylate cyclase/phosphodiesterase domain 1 (GGDEF)
VFA1167	8.0	7.9	7.7	7.9	7.9	7.9	8.1	8.0	-1.1	7.7	7.8	7.6	7.7	7.6	7.9	7.9	7.8	-1.1	hypothetical protein
VFA1168	7.6	7.4	7.2	7.4	7.6	7.4	7.9	7.7	-1.2	7.3	7.5	7.2	7.3	7.2	7.5	7.4	7.4	-1.0	type I secretion adaptor protein (Hyd family)
VFA1169	6.5	5.9	6.2	6.2	5.6	5.8	5.9	5.8	-1.3	6.1	5.5	5.7	5.8	5.5	5.2	5.6	5.4	-1.3	transcriptional activator CtrR
VFA1170	7.0	7.0	6.6	6.8	6.2	6.5	6.5	6.4	-1.3	6.8	6.7	6.6	6.7	6.5	6.7	6.8	6.7	-1.0	hypothetical protein
VFA1171	8.0	7.6	7.7	7.8	7.6	8.1	8.8	8.2	-1.0	8.6	9.0	8.7	8.7	9.2	9.2	8.1	8.8	-1.1	DNA-binding protein ParB
VFA1172	7.8	7.4	7.6	7.6	7.4	7.9	8.7	8.0	-1.3	8.4	8.8	8.6	8.6	8.6	9.0	8.0	8.7	-1.1	plasmid partition protein A
VFA1172to001	4.1	3.5	3.1	3.6	3.3	3.5	3.7	3.5	-1.1	3.6	3.6	3.4	3.5	3.2	3.4	2.7	3.1	-1.3	plasmid partition protein A
VFA1172to001	3.2	3.0	2.6	2.9	2.6	2.7	3.6	3.0	-1.0	2.6	3.2	2.8	2.9	2.7	2.4	2.3	2.5	-1.3	plasmid partition protein A
VFB02	5.7	5.6	5.1	5.5	5.6	5.4	5.8	5.6	-1.1	5.3	5.5	5.3	5.4	5.2	5.5	5.0	5.2	-1.1	DNA primase TracC
VFB02to03	5.6	5.4	5.6	5.5	5.7	5.9	5.8	5.8	-1.2	5.3	5.4	5.3	5.4	5.6	5.3	5.6	5.5	-1.1	DNA primase TracC
VFB02to03CC	3.8	3.6	3.1	3.5	3.2	3.5	3.3	3.3	-1.1	3.7	3.9	3.5	3.7	3.2	3.7	3.6	3.5	-1.2	DNA primase TracC
VFB03	9.0	9.1	9.2	9.1	9.4	9.7	9.5	9.6	-1.4	8.9	9.3	9.0	9.1	9.5	9.2	9.5	9.4	-1.2	hypothetical protein
VFB08	3.7	3.5	3.0	3.4	3.3	2.9	3.3	3.2	-1.2	3.3	3.0	3.3	3.2	3.0	3.1	2.9	3.0	-1.2	hypothetical protein
VFB08to09	6.8	7.0	7.3	7.0	7.0	7.0	6.9	7.0	-1.0	6.9	7.0	7.4	7.1	7.7	7.0	7.4	7.3	-1.2	hypothetical protein
VFB08to09CC	9.6	9.9	10.2	9.9	10.3	10.0	10.0	10.1	-1.1	9.8	10.1	10.3	10.1	10.5	9.9	10.3	10.2	-1.1	hypothetical protein
VFB09	7.0	6.9	6.7	6.9	7.1	7.1	7.5	7.2	-1.3	6.8	7.1	6.7	6.9	7.1	7.4	6.9	7.1	-1.2	hypothetical protein
VFB10	7.5	7.4	7.2	7.4	7.4	7.3	7.8	7.5	-1.1	7.4	7.5	7.2	7.3	7.5	7.4	7.5	7.5	-1.1	hypothetical protein
VFB11	5.7	5.3	5.4	5.5	5.6	5.3	6.0	5.6	-1.1	5.3	5.5	5.1	5.3	5.3	5.0	5.1	5.2	-1.1	hypothetical protein
VFB15	6.6	6.7	6.6	6.7	6.2	6.5	6.4	6.4	-1.2	6.5	6.5	6.7	6.6	6.6	6.5	6.9	6.7	-1.1	resolvasase/recombinase
VFB16	7.9	8.2	7.7	7.9	8.2	8.2	8.2	8.2	-1.2	7.9	8.5	7.8	8.1	8.0	8.7	8.3	8.3	-1.2	hypothetical protein
VFB16to17	3.1	2.9	2.9	2.9	2.5	2.8	3.0	2.8	-1.1	2.8	3.2	2.8	2.9	2.7	2.8	2.6	2.7	-1.2	hypothetical protein
VFB16to17CC	4.0	4.0	3.7	3.9	4.1	3.8	4.3	4.1	-1.2	4.0	4.1	3.7	3.9	3.4	3.5	3.5	3.5	-1.4	hypothetical protein
VFB17	7.4	7.2	7.2	7.2	7.3	6.9	7.3	7.2	-1.3	7.2	7.4	7.1	7.2	7.2	7.6	7.5	7.4	-1.1	hypothetical protein
VFB18	8.6	8.4	8.3	8.4	8.8	8.6	9.0	8.8	-1.1	8.5	8.3	8.3	8.4	8.3	8.2	8.4	8.3	-1.1	DNA-binding protein RDGA
VFB20	6.3	6.5	6.1	6.3	6.2	6.6	6.4	6.4	-1.1	5.9	6.9	6.1	6.3	5.8	6.9	6.2	6.3	-1.0	hypothetical protein
VFB21	6.2	7.0	6.6	6.6	6.4	7.0	6.4	6.6	-1.0	5.9	7.5	6.5	6.6	6.1	7.3	6.8	6.7	-1.1	hypothetical protein
VFB22	7.9	8.9	8.8	8.5	8.1	8.9	8.3	8.4	-1.1	7.6	9.1	8.4	8.4	8.3	8.9	8.6	8.6	-1.2	hypothetical protein
VFB23	7.2	8.0	7.9	7.7	7.0	7.9	7.5	7.5	-1.2	6.8	8.0	7.4	7.4	7.0	7.9	7.6	7.5	-1.0	hypothetical protein
VFB24	7.0	7.6	7.7	7.4	6.5	7.4	7.0	7.0	-1.4	6.4	7.5	7.0	7.0	6.6	7.2	7.2	7.0	-1.1	hypothetical protein
VFB25	6.9	7.4	7.5	7.3	6.3	7.2	6.7	6.7	-1.4	6.4	7.3	6.9	6.9	6.6	7.0	7.1	6.9	-1.0	hypothetical protein
VFB26	7.2	7.9	7.9	7.7	6.9	7.7	7.1	7.2	-1.4	7.0	7.8	7.6	7.4	7.1	7.6	7.5	7.4	-1.0	hypothetical protein
VFB27	6.7	7.5	7.6	7.3	6.3	7.4	6.7	6.8	-1.4	6.6	7.5	7.0	7.0	6.7	7.3	7.0	7.0	-1.0	hypothetical protein
VFB28	7.3	8.1	8.1	7.8															

**Table S3.** Genes whose repression requires the presence of both H-NOX<sub>vf</sub> and NO

<b>VF locus*</b>	<b>Fold change<sup>†</sup></b> <b>(wild-type+NO/ wild-type)</b>	<b>Fold change<sup>†</sup></b> <b>(hnoX+NO/ hnoX)</b>	<b>Annotation<sup>†</sup></b>
VF_0006	0.2	1.4	Cystine transport system, ATP-binding protein, YecC
VF_0007	0.2	1.6	Cystine transport system, permease protein, YecS
VF_0616	0.6	1.3	Fe-S cluster-synthesis regulatory protein, IscR
VF_0637	0.3	1.2	Inositol-5-monophosphate dehydrogenase, GuaB
VF_0808	0.2	0.8	Fused <i>N</i> -acetyl glucosamine-specific PTS enzyme: IIC and IIB components, NagE
<b>VF_0927</b>	<b>0.4</b>	<b>0.9</b>	<b>Hypothetical protein</b>
<b>VF_1227</b>	<b>0.7</b>	<b>1.2</b>	<b>Heme-degrading protein, HuvX</b>
<b>VF_1234</b>	<b>0.3</b>	<b>1.3</b>	<b>Hemin receptor, HutA</b>
VF_1512	0.6	1.2	Thiopurine S-methyltransferase, Tpm
VF_2440	0.6	1.1	DNA-damage-inducible SOS response protein, DinF
<b>VFA_0157</b>	<b>0.4</b>	<b>1.0</b>	<b>Putative permease</b>
<b>VFA_0191</b>	<b>0.3</b>	<b>1.0</b>	<b>Ferrichrome receptor precursor, FhuE</b>
VFA_0192	0.3	0.9	Hypothetical protein
<b>VFA_0193</b>	<b>0.4</b>	<b>0.9</b>	<b>ToIQ protein</b>
VFA_0199	0.3	0.8	Chitooligosaccharide transport system, ATP-binding protein, OppD
<b>VFA_0333</b>	<b>0.2</b>	<b>0.7</b>	<b>Protease II, PtrB</b>
VFA_0702	0.5	1.1	Glycine cleavage system protein H, GcvH
<b>VFA_0784</b>	<b>0.5</b>	<b>1.1</b>	<b>Ferrichrome outer-membrane transporter, FhuA</b>
<b>VFA_0827</b>	<b>0.4</b>	<b>1.0</b>	<b>Ferric anguibactin-binding protein, VctP</b>

VFA\_0848            0.5            1.1            **Hypothetical protein**

---

\* From [www.ncbi.nlm.nih.gov/blast](http://www.ncbi.nlm.nih.gov/blast); entries in bold font contain a conserved palindromic motif in their promoter region that resembles the consensus binding site of Fur (Fig. S4).

† Average fold-change calculated from assays of three independent RNA samples. The RNA was isolated from cultures of wild-type or *hnoX*-insertion mutant cells that had been either left untreated or exposed to 80  $\mu$ M DEA-NONOate for 30 min. The 20 ORFs listed include all of those that were differentially regulated in wild type, but not in the *hnoX* mutant, after exposure to NO, as revealed by a differential-contrast analysis using a false discovery rate of 0.05 (Supplemental Materials and Methods).

## Supporting Figure Legends

**Fig. S1.** Venn diagram representing the proportion of genes differentially expressed between the different experimental treatments (estimated false-discovery rate  $\leq 0.05$ ). The upper left circle (WT vs. WT+NO) represents the genes (697 total) differentially expressed when the wild-type *V. fischeri* ES114 gene expression levels were compared between the control treatment and the NO treatment. The upper right circle (*hnoX* vs. *hnoX*+NO) represents the genes differentially expressed when the gene expression levels of the *hnoX* insertion mutant were compared between the control treatment and the NO treatment (1,037 genes total). The bottom circle (Difference) represents the genes (123 total) whose expression levels were affected by the NO treatment, in either the wild-type or the mutant strains, but in a different way in each strain (in magnitude or in direction). The expression levels of another 2,697 genes were not affected by the NO treatment compared to the control treatment in either strain. The intersections between the three sets of genes can be divided into four classes. The first class contains the 359 genes whose expression levels were affected by the NO treatment in the same direction in both the wild-type and the mutant strains. Therefore, we do not expect the regulation of these genes to be affected by the activity of H-NOX. The second class contains 36 genes whose expression levels were affected by the NO treatment in both wild-type and mutant strains, but in different direction. The third class contains 47 genes whose expression levels were affected by the NO treatment only in the *hnoX* mutant strain. These latter two classes represent genes whose change of expression level is likely to be the result of indirect effects due to a failure of the *hnoX* mutant strain to respond appropriately to the NO treatment. The fourth class contains 40 genes whose expression levels were affected by the NO treatment only in the wild-type strain. These are the genes that are likely to be more directly affected by the activity of H-NOX. Each class may contain additional members whose responses did not meet the required statistical cut-offs.

**Fig. S2.** Viability of *V. fischeri* wild type and the  $\Delta hnoX$  mutant after challenge with NO. One half of an MS medium culture of each strain was treated with the NO generator DEA-NONOate to a final concentration of either 40  $\mu$ M (anaerobically) or 500  $\mu$ M (aerobically). After one hour, the viability (as determined by CFUs) of the challenged wild type (closed bars) and the  $\Delta hnoX$  mutant (open bars) was calculated relative to that of the untreated control cultures. Error bars indicate the SEM of viability from triplicate cultures in one experiment. Similar experiments were performed three times, and a representative result is shown.

**Fig. S3.** Sequence logo of the predicted Fur-binding site in *V. fischeri* ES114. The logo was derived from the alignment of the promoter sequences of the co-expressed loci from Fig. 2. The logo picture was created using WebLogo (<http://weblogo.berkeley.edu/>) (16).

**Fig. S4.** The *hnoX* mutant had the same low growth rate as wild type in a low-iron medium lacking hemin. The wild type (circles) and  $\Delta hnoX$  mutant (squares) were grown in MS medium containing 10 mM *N*-acetyl glucosamine and 10  $\mu$ M EDDHA. At the arrow, half of the cultures (open symbols) were exposed to 80  $\mu$ M NO generator. The two strains had essentially the same growth rates as each other, both in the presence and absence of NO.

**Fig. S5.** The  $\Delta hnoX$  mutant produces a similar level of luminescence per cell as wild type when grown in culture. Cultures of wild type (open circles) and  $\Delta hnoX$  (closed circles) were grown in MS medium containing 10 mM *N*-acetyl glucosamine. Peak luminescence was reached at an OD of approximately 0.4 in both cultures.



**Fig. S6.** Carriage of the plasmid encoding a wild-type copy of *hnoX* (pComhnoX) had no differential effect on the growth rates of either the wild-type or  $\Delta hnoX$  strains. Cultures were grown in MS medium containing 10 mM *N*-acetyl glucosamine, 50  $\mu$ M EDDHA and 10  $\mu$ M hemin. Blue diamonds: wild type + vector (pVSV105); pink squares: wild type + pComhnoX; yellow triangles:  $\Delta hnoX$  + vector (pVSV105); blue crosses:  $\Delta hnoX$  + pComhnoX

**Fig. S7.** Addition of either hemin or a NOS inhibitor to the surrounding seawater did not compromise the squid's capacity to support normal levels *V. fischeri* growth in the light organ. The number of *V. fischeri* cells was determined at 24 h post-inoculation in light organs of animals when they were exposed to 0.2  $\mu$ M hemin (panel A, open bar) or 100  $\mu$ M SMTC (panel B, open bar)

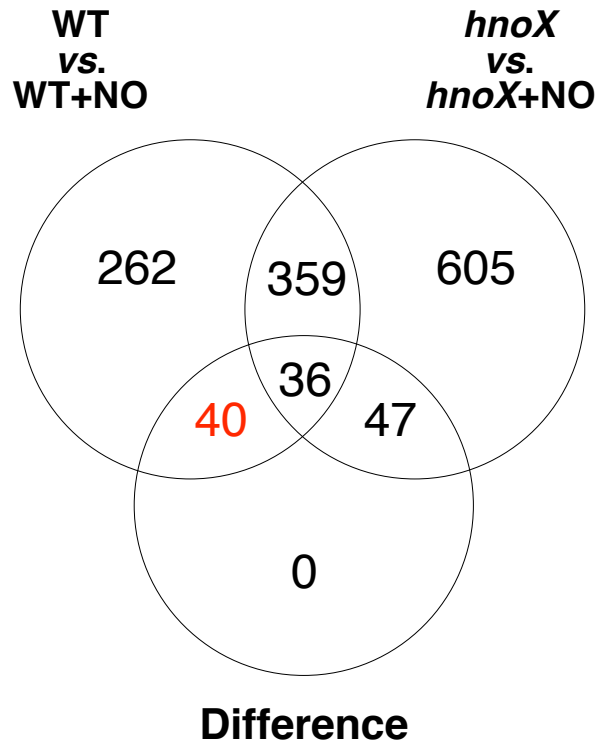
**Fig. S8.** Heat map summarizing the expression profile of all *V. fischeri* genes that were differentially expressed in wild type upon NO exposure, but unchanged in the *hnoX* insertion mutant. The analysis used a four-way contrast analysis with a false-discovery rate cut-off of 0.05 (15). Genes, or intergenic region (\*), are identified by their locus tags (rows), and experimental treatment triplicates are grouped in vertical columns (WT = wild-type cells; *hnoX* = insertion-mutant cells; NO = nitric-oxide treatment). The expression-level values were normalized to their z-scores for each row (red = low expression level, white = high expression level).

## Supporting References

1. Boon, EM, Huang, SH, & Marletta, MA (2005) A molecular basis for NO selectivity in soluble guanylate cyclase. *Nat Chem Biol* 1:53-59.
2. Karow, DS, Pan, D, Tran, R, Pellicena, P, Presley, A, Mathies, RA, & Marletta, MA (2004) Spectroscopic characterization of the soluble guanylate cyclase-like heme domains from *Vibrio cholerae* and *Thermoanaerobacter tengcongensis*. *Biochemistry* 43:10203-10211.
3. Boon, EM, Davis, JH, Tran, R, Karow, DS, Huang, SH, Pan, D, Miazgowicz, MM, Mathies, RA, & Marletta, MA (2006) Nitric oxide binding to prokaryotic homologs of the soluble guanylate cyclase beta1 H-NOX domain. *The Journal of biological chemistry* 281:21892-21902.
4. Winger, JA, Derbyshire, ER, & Marletta, MA (2007) Dissociation of nitric oxide from soluble guanylate cyclase and heme-nitric oxide/oxygen binding domain constructs. *The Journal of biological chemistry* 282:897-907.
5. Miller, JH (1992) A short course in bacterial genetics. *Cold Spring Harbor Laboratory Press, Cold Spring Harbor, N. Y.*
6. Bose, JL, Kim, U, Bartkowski, W, Gunsalus, RP, Overley, AM, Lyell, NL, Visick, KL, & Stabb, EV (2007) Bioluminescence in *Vibrio fischeri* is controlled by the redox-responsive regulator ArcA. *Mol Microbiol* 65:538 - 553.
7. Bailey, TL & Elkan, C (1994) in *Proceedings of the Second International Conference on Intelligent Systems for Molecular Biology*, eds. Altman, R., Brutlag, D., Karp, P., Lathrop, R., & Searls, D. (The AAI Press, Menlo Park), pp. 28-36.
8. Bailey, TL & Gribskov, M (1998) Combining evidence using p-values: application to sequence homology searches. *Bioinformatics* 14:48-54.
9. McCann, J, Stabb, EV, Millikan, DS, & Ruby, EG (2003) Population Dynamics of *Vibrio fischeri* during Infection of *Euprymna scolopes*. *Appl. Environ. Microbiol.* 69:5928-5934.

10. Dunn, AK & Stabb, EV (2008) Genetic Analysis of Trimethylamine N-Oxide Reductases in the Light Organ Symbiont *Vibrio fischeri* ES114. *J. Bacteriol.* 190:5814-5823.
11. Newman, MC & Unger, MA (2003) in *Fundamentals of Ecotoxicology*, eds. Newman, M. C. & Unger, M. A. (CRC Press, Boca Raton), pp. 174-178.
12. Dunn, AK, Martin, MO, & Stabb, EV (2005) Characterization of pES213, a small mobilizable plasmid from *Vibrio fischeri*. *Plasmid* 54:114-134.
13. Boettcher, KJ & Ruby, EG (1990) Depressed light emission by symbiotic *Vibrio fischeri* of the sepiolid squid *Euprymna scolopes*. *J. Bacteriol.* 172:3701-3706.
14. Dunn, AK, Millikan, DS, Adin, DM, Bose, JL, & Stabb, EV (2006) New rfp- and pES213-Derived Tools for Analyzing Symbiotic *Vibrio fischeri* Reveal Patterns of Infection and lux Expression In Situ. *Appl. Environ. Microbiol.* 72:802-810.
15. Smyth, GK (2004) in *Statistical Applications in Genetics and Molecular Biology* (Berkeley Electronic Press, Berkeley).
16. Crooks, GE, Hon, G, Chandonia, JM, & Brenner, SE (2004) WebLogo: a sequence logo generator. *Genome Res* 14:1188-1190.

Fig. S1



-2697 other genes unaffected

Fig. S2

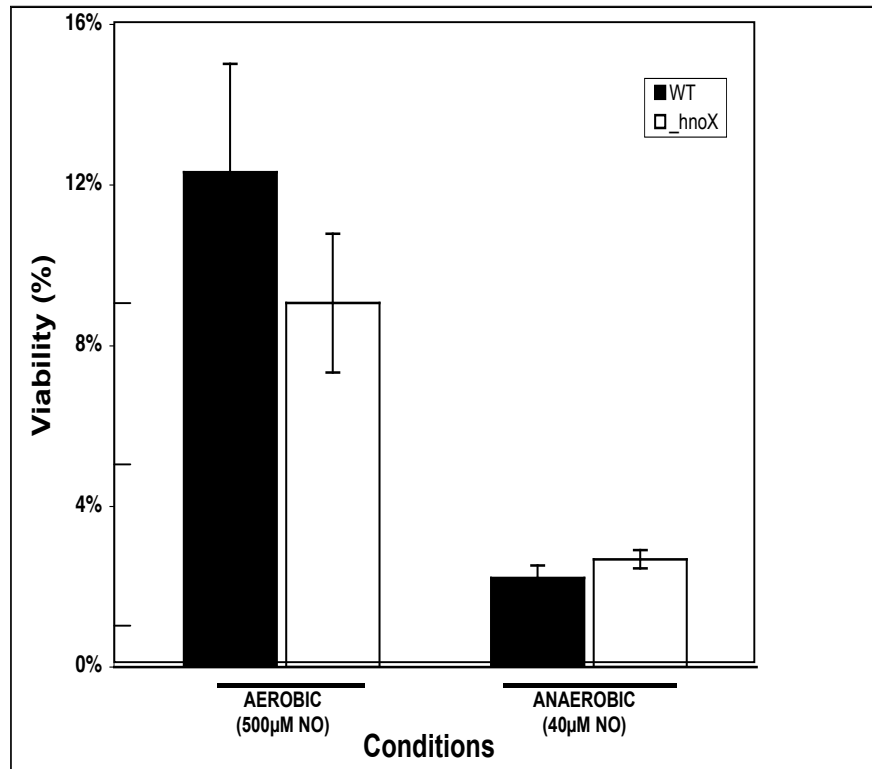


Fig. S3

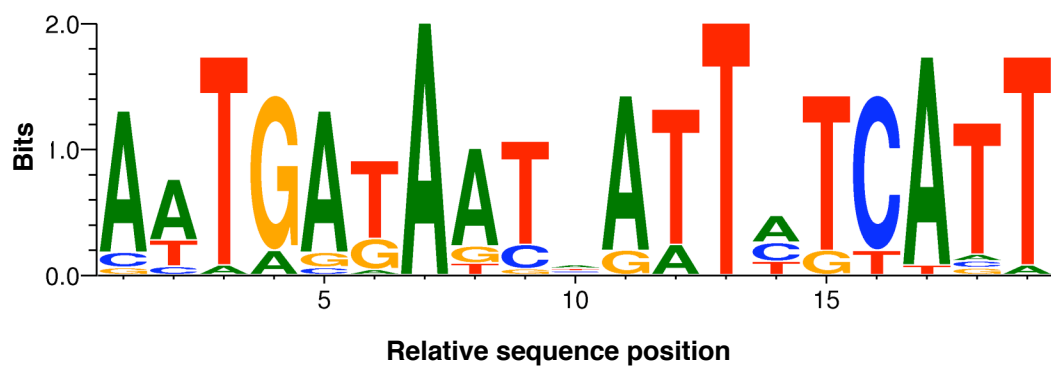


Fig. S4

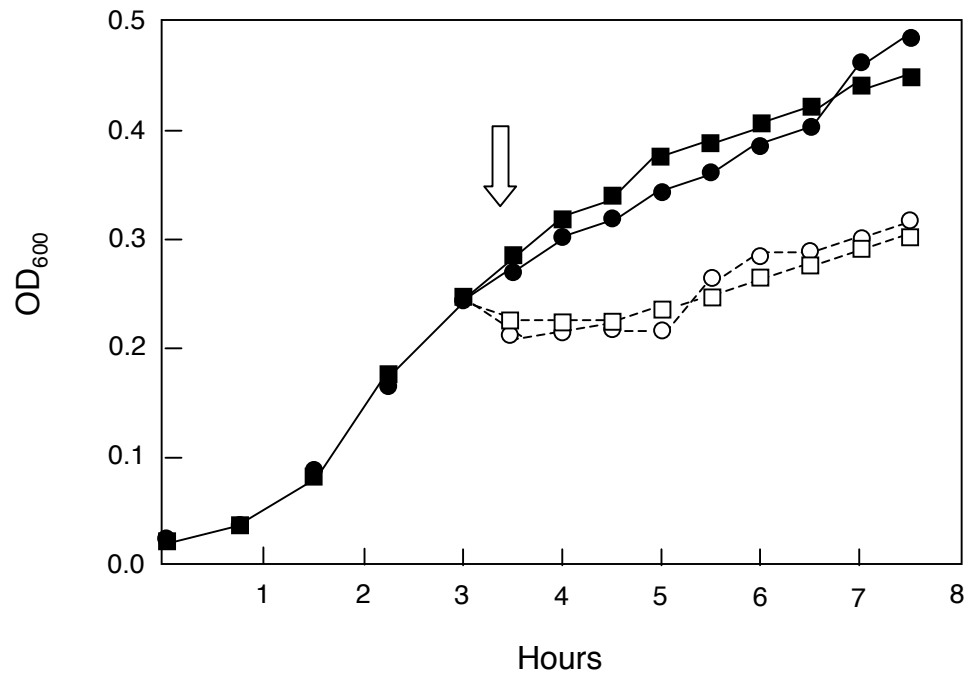


Fig. S5

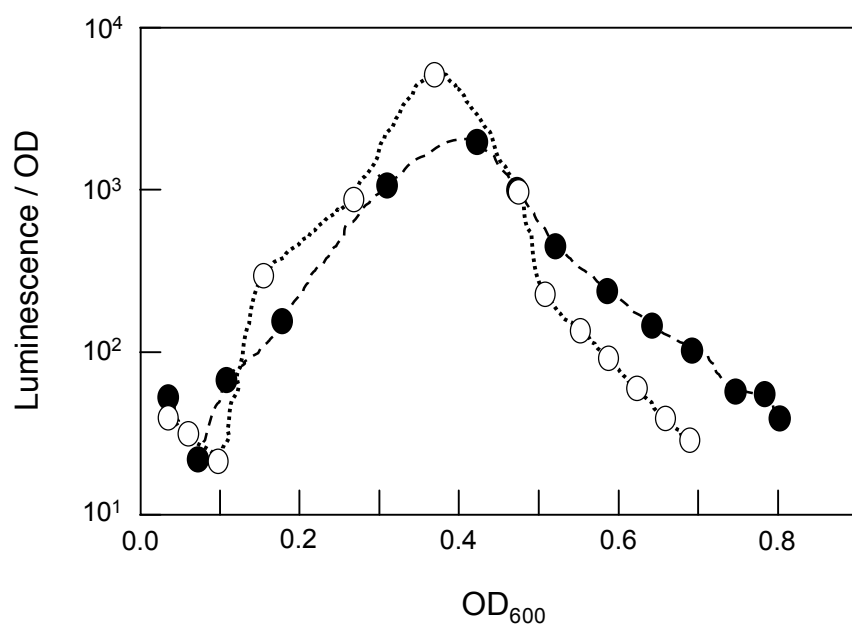




Fig. S6

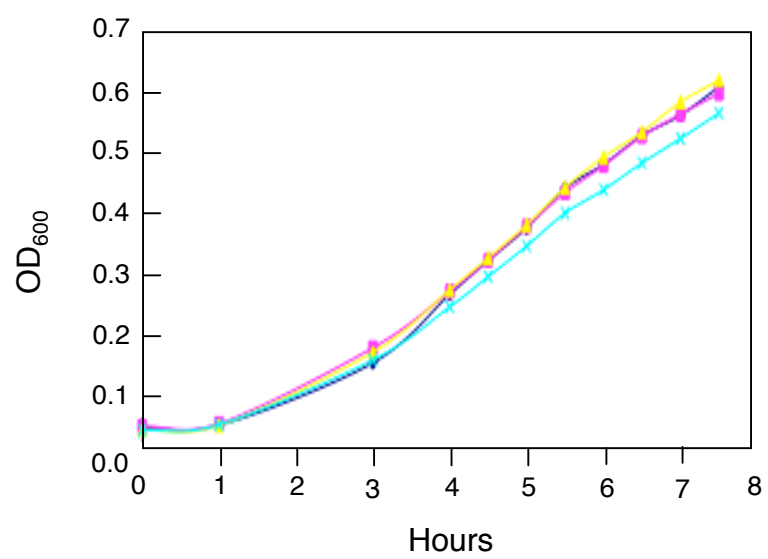


Fig. S7

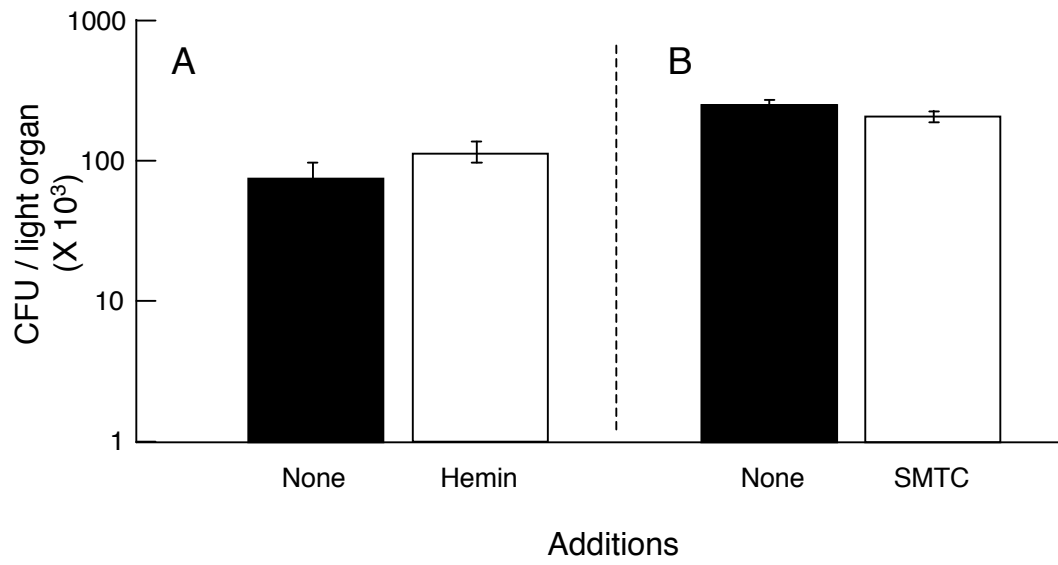


Fig. S8

