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Degradation of pyridine by a novel bacterial strain, *Sphingobacterium multivorum* JPB23, isolated from coal-coking wastewater

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ABSTRACT

A bacterial strain, JPB23, that uses pyridine as sole carbon, nitrogen, and energy source was isolated from the wastewater of a coal-coking plant. Using morphological observation, assessment of its physiological characteristics, and a 16S rRNA sequence analysis, we identified the strain as *Sphingobacterium multivorum*. The bacterium degraded 3,000 mg/L pyridine completely within 10 d. The optimum degradation conditions were pH 5.0 or 9.0 and a temperature range of 30°C–37°C. Glucose (500 mg/L) stimulated the growth of strain JPB23 and increased the removal of pyridine; in contrast, 1,000 mg/L glucose delayed the degradation of pyridine. A comparative transcriptome analysis was performed to clarify the molecular mechanisms of pyridine degradation by *S. multivorum* JPB23. Candidate genes encoding succinate-semialdehyde dehydrogenase, amidase, ammonia monooxygenase, nitrate reductase, nitrite reductase, nitric oxide reductase, and nitrous-oxide reductase are considered to participate in the pyridine degradation pathway. Our results lay the foundation for determining the molecular mechanisms of the pyridine degradation pathways in bacteria.

Keywords: Pyridine; Biodegradation; *Sphingobacterium multivorum* JPB23; Coal-coking wastewater; Transcriptome analysis; Nitrogen transformation

1. Introduction

Pyridine is an industrial solvent and a raw material for herbicide synthesis and is widely used in the chemical, pharmaceutical, and oil industries [1]. Large quantities of pyridine are frequently detected in the wastewater from coking plants, pharmaceutical factories, and other industries [2]. Pyridine is a hazardous substance and one of the most important pollutants in China [3]. With its toxicity and nauseous odor, the discharge of pyridine-containing waste damages human health and the environment [4]. Therefore, the pyridine produced by industrial activities should be eliminated before it enters the environment.

Many treatment technologies have been developed to remove pyridine from contaminated environments, including adsorption methods [3,5], sorption on zeolites [6], and biodegradation [1,7]. Of these, biodegradation is a low-cost and highly efficient method of pyridine removal [8]. Previous investigations have mainly focused on the isolation of pyridine-degrading microorganisms, and the effects of pH, temperature, and the addition of carbon source on these strains [9–12]. Since the 1910s, several microorganisms capable of degrading pyridine and its derivatives have been

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isolated and investigated, including *Micrococcus luteus* [13], *Nocardioides* sp. [14], *Pseudomonas* sp. [15], *Gordonia terrea* [16], *Paracoccus* sp. [10,17], *Shinella zoogloeoides* [18], *Arthrobacter* sp. [19], *Achromobacter* sp. [11], *Shewanella algae* [20], and *Rhizobium* sp. [12]. Recently, bioaugmentation strategies have been developed to enhance the biodegradation of pyridine, such as activated sludge systems [21–23], an electricity-assisted anaerobic system [24], aerobic granulation [25], and a dynamic membrane bioreactor [26].

Two main pyridine degradation pathways have been identified in bacteria. In both pathways, the initial reduction of pyridine produces 1,4-dihydropyridine. In pathway 1, the N–C_2 ring of 1,4-dihydropyridine undergoes hydrolytic cleavage and subsequent deamination to glutaric dialdehyde, followed by sequential oxidation to glutarate semialdehyde, glutarate, and glutaryl-coenzyme A [7,27]. In pathway 2, hydrolysis or a dioxygenase attacks the C_2–C_3 double bond, forming N-formylaminovinylacetaldehyde, which is immediately oxidized to the corresponding semialdehyde. The hydrolysis of the C_6–N bond then liberates formamide and succinate semialdehyde. Formamide is hydrolyzed to form formate and NH_3, and succinate semialdehyde is oxidized to succinate [7,9]. In the metabolic pathway of pyridine in *Nocardia* KM-2, the initial degradation reaction involves the hydroxylation of the ring and the formation of 3-hydroxypyridine. Subsequently, the degradation pathways is identical to pathway 2 [8]. Wang et al. [28] detected a distinct pyridine biodegradation mechanism in *Paracoccus* sp. NJUST30, in which pyridine degradation begins with the hydroxylation of the pyridine ring to form 2,3-dihydro-pyridine-2,3-diol or 2,3-dihydro-pyridine-2,4-diol, followed by the cleavage of the pyridine ring, generating 2,4-dihydroxy-2H-pyridine-3-one, 2-carbonyl-succinic acid, 1,2-dihydro-pyridine-2-ol, piperidin-2-ol, and 4-formylamino-butyric acid as the main intermediates [28]. Several enzymes involved in the pyridine degradation pathways have been identified by measuring their enzymatic activities [7,9,13,27]. However, the corresponding genes have seldom been reported.

In this study, a novel pyridine-degrading strain, *Sphingobacterium multivorum* JPB23, was isolated from coke plant wastewater. Strain JPB23 is, to the best of our knowledge, the first documented pyridine-degrading *S. multivorum* isolate. We investigated the pyridine degradation characteristics and growth behavior of this isolate. We also used an RNA sequencing analysis to obtain a global view of the transcriptional regulation of *S. multivorum* JPB23 in response to pyridine exposure. Candidate genes that potentially participate in the pyridine degradation pathway were identified. Our results provide a valuable genetic resource to explore the molecular mechanisms of the pyridine degradation pathway by *S. multivorum* JPB23.

2. Materials and methods

2.1. Media

Pure cultures were enriched and maintained in Luria–Bertani medium (10.0 g/L tryptone, 5.0 g/L yeast extract, and 5.0 g/L NaCl). Mineral salt medium (MSM; 1.5 g/L Na_2HPO_4, 1.5 g/L KH_2PO_4, 0.2 g/L $MgSO_4·7H_2O$, 0.01 g/L $CaCl_2·2H_2O$, and 1 mL of trace elements solution; pH 7.0) was used for bacterial isolation and the biodegradation experiments. The trace element solution contained 1.69 g/L $MnSO_4·H_2O$, 0.38 g/L $CuSO_4·5H_2O$, 1.15 g/L $ZnSO_4·7H_2O$, 0.024 g/L $Na_2MoO_4·2H_2O$, 1.16g/L H_3BO_3, 2.78 g/L $FeSO_4·7H_2O$, and 0.24 g/L $CoCl_2·6H_2O$. The pyridine solutions were filter-sterilized and added to MSM as the carbon and nitrogen source for bacterial growth.

2.2. Isolation of pyridine-degrading bacteria

Samples of coal-coking wastewater were collected from Shanxi Nanyao Group Changjinyuan Coking Co. Ltd (Changzhi, Shanxi Province, China). Liquid MSM (50 mL) supplemented with 500 mg/L pyridine was inoculated with the samples (0.5 mL), which were incubated on a rotary shaker (180 rpm, 30°C) to enrich the pyridine-degrading bacteria. After incubation for 10 d, serial dilutions (10^{-1}–10^{-7}) of the enrichment cultures were spread onto MSM plates supplemented with 1,000 mg/L pyridine. The pyridine-degrading bacterial colonies were screened and purified three times with the streak plate method.

2.3. Identification of the isolate

The morphological, physiological, and biochemical features of the isolate were characterized. The cell morphology was examined with a scanning electron microscope (TM3000, Hitachi). The cells were Gram-stained with the Gram-staining procedure described by Solano et al. [29]. Nine phenotypic traits, including carbohydrate fermentation and extracellular enzymes, were tested with standard protocols [30]. The utilization of 71 carbon sources and the tolerance of 18 chemicals were determined with the Biolog Gen III MicroPlate, according to the manufacturer's instructions. Bacterial chromosomal DNA was isolated with a QIAamp DNA Mini Kit (Qiagen, Germany). The 16S rRNA gene was amplified with the primers 27F (5′-GAGTTTGATCCTGGCTCAG-3′) and 1492R (5′-AGAAAGGAGGTGATCCAGCC-3′). PCR was performed under the following conditions: initial denaturation at 95°C for 5 min; 30 cycles of 94°C for 30 s, 55°C for 30 s, and 72°C for 1 min 30 s; and a final extension step at 72°C for 10 min. The product was ligated into the pMD18-T vector (TaKaRa, Japan) and sequenced. The sequencing result was submitted to GenBank for BLAST analysis. The nucleotide sequence of the 16S rRNA of *S. multivorum* JPB23 was registered in GenBank under accession number KX658650.

The 16S rRNA sequence was compared with those of the type strains in the EzTaxon-e server [31]. Species with the top 40 highest similarity scores to strain JPB23 were used for multilocus sequence analysis. A phylogenetic analysis was performed with the software package MEGA version 6.0 [32] after a multiple-sequence alignment of the data via CLUSTALW [33]. Phylogenetic trees were constructed with the neighbor-joining (NJ) algorithm [34].

2.4. Pyridine degradation experiments

A single colony was grown to the logarithmic growth phase in LB medium containing 500 mg/L pyridine on a rotary shaker (30°C, 180 rpm). The cells were harvested by centrifugation at 5,000 × g for 5 min. The pellet was washed three times with MSM and resuspended in MSM to an optical density of 1.5 at a wavelength of 600 nm (OD_{600}) using a TU-1901 spectrophotometer (Persee Analytics, Inc., China). This cell culture was added to 50 mL of fresh MSM (2%, v/v) containing 500–3,000 mg/L pyridine. The effects of pH (6, 7, 8, 9, or 10), temperature (25°C, 30°C, or 37°C), and added carbon (0, 500, or 1,000 mg/L glucose) on pyridine degradation and cell growth in MSM containing 1,000 mg/L pyridine were investigated. The incubation temperature was 30°C unless otherwise specified. Each parameter was tested in three parallel Erlenmeyer flasks to ensure the accuracy of the analysis. Subsamples were collected at regular intervals to measure the biomass and pyridine concentration.

2.5. Biomass and pyridine determination

The cell density and pyridine concentration were monitored spectrophotometrically by measuring the absorbance at wavelengths of 600 and 256 nm, respectively, with a TU-1901 spectrophotometer (Persee) [9]. To measure the pyridine concentration, samples of the suspension culture were centrifuged at 5,000 × g for 10 min. The concentration of free pyridine in the supernatant was determined with spectrophotometry. The percentage of pyridine removed was calculated as the amount of pyridine removed divided by the initial amount of pyridine present.

2.6. RNA-seq analysis

The inoculating cell suspension (1 mL; described in "Pyridine degradation experiments") was added to 50 mL of MSM supplemented with 1,000 mg/L pyridine (Pyr), and incubated at 30°C with shaking at 180 rpm for 72 h. In the control experiment, 1 mL of inoculating cell suspension was added to 50 mL of MSM supplemented with 1,000 mg/L glucose and 2 g/L $(NH_4)_2SO_4$ as the carbon source and nitrogen source, respectively (CT). Total RNA was extracted from 5 mL samples with the RNeasy Mini Kit (Qiagen) and the rRNA was removed with the Ribo-Zero Magnetic Kit (Epicentre). The RNA sequence reads were obtained with the Illumina HiSeq™ 4000 (Hangzhou Woosen Biotechnology Co., Ltd, China). The reads were filtered by removing any reads containing adapters or more than 10% unknown nucleotides and low-quality reads containing more than 50% low-quality bases (Q-value ≤ 10). The transcriptome was assembled de novo with the short-reads assembly program Trinity [35]. The gene expression levels were calculated as reads per kilobase of gene per million reads [36]. Genes were considered significantly differentially expressed if the q-value (false discovery rate) was <0.05 and the $\log_2$ fold change in gene expression in the Pyr vs. the CT condition was <−1 (downregulated) or >1 (upregulated).

3. Results

3.1. Isolation and identification of pyridine-degrading strains

We isolated 12 indigenous bacterial strains from the coal-coking wastewater that were able to grow on pyridine as the sole carbon and nitrogen source. The percentage of pyridine removal was determined by their incubation in MSM containing 1,000 mg/L pyridine for 5 d (30°C, 180 rpm). Eleven of the 12 strains degraded 34.4%–57.6% of the pyridine at an initial concentration of 1,000 mg/L. Strain JPB23 removed 99.5% of the pyridine from medium containing 1,000 mg/L pyridine, which was the highest pyridine biodegradation capacity. Therefore, strain JPB23 was studied further.

As shown in Fig. 1, strain JPB23 is a Gram-negative rod-shaped bacterium, 1.1–1.9 μm in length and 0.5 μm in width. The 1490-nt 16S rRNA sequence of strain JPB23 was used as the query to search the type strain 16S rRNA sequence database using the EzTaxon-e server. Nine type strains of *Sphingobacterium* species shared >97% similarity with strain JPB23. The 16S rRNA sequence of *S. multivorum* IAM14316^T shared the highest similarity (99.86%) with that of strain JPB23. We constructed and analyzed phylogenetic trees based on the 16S rRNA sequences. Strain JPB23 formed a robust clade with *S. multivorum* IAM14316^T on the NJ tree (Fig. 2). The results revealed that strain JPB23 is a member of the genus *Sphingobacterium* in the family Sphingobacteriaceae. The biochemical characteristics of strain JPB23 are listed in Table S1. The utilization of carbon sources and tolerance of various chemicals were determined with the Biolog Gen III MicroPlate and compared with standard databases in the Biolog system. The physiological characteristics of strain JPB23 were nearly identical to those of *S. multivorum*, except in its utilization of N-acetyl-d-galactosamine and gelatin, and its tolerance of troleandomycin. Based on these analyses, we conclude that strain JPB23 is *S. multivorum*. JPB23 is the first-documented *Sphingobacterium* isolate capable of degrading pyridine.

3.2. Effect of initial pyridine concentration on pyridine degradation and cell growth

To evaluate the pyridine-degradation capacity of strain JPB23, it was added to MSM containing 500, 1,000, 1,500, 2,500,

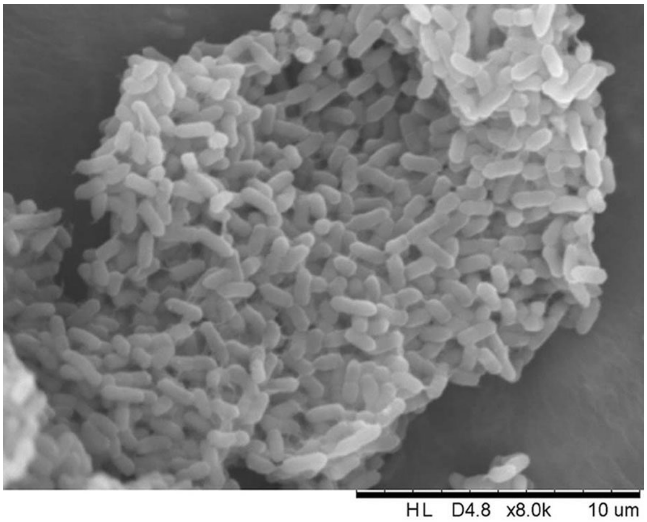


Fig. 1. Scanning electron micrograph of *Sphingobacterium multivorum* JPB23 cells

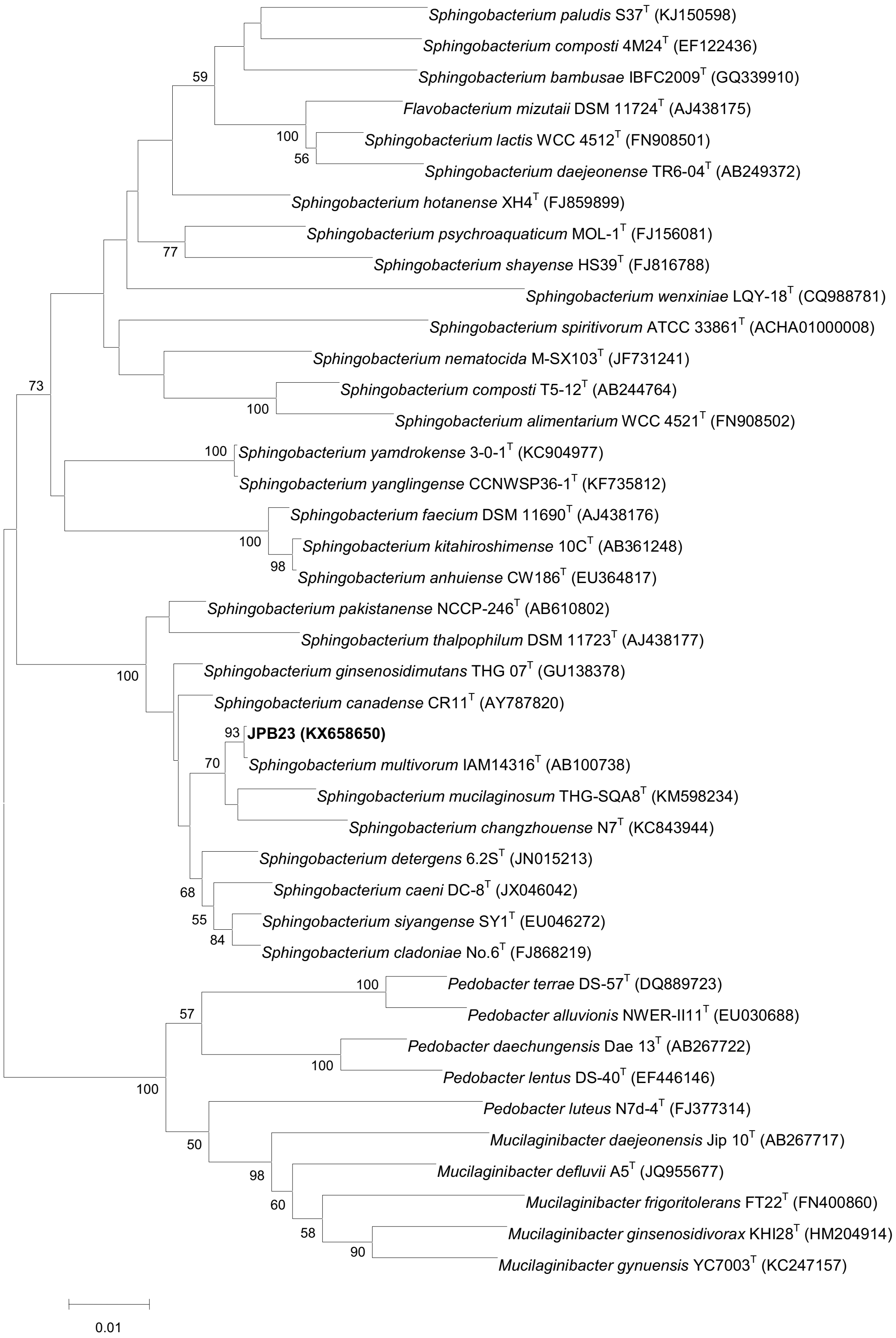


Fig. 2. Neighbour-joining phylogenetic tree based on 16S rRNA gene sequences of strain JPB23 and related taxa. Bootstrap values (1,000 replications) are shown as percentages at each node only if they are 50% or greater. Bar, 0.01 substitutions per nucleotide position.

and 3,000 mg/L pyridine and incubated aerobically at 30°C on a shaker at 180 rpm. As shown in Fig. 3, JPB23 degraded pyridine at a relatively constant rate. At initial pyridine concentrations of 500, 1,000, 1,500, 2,500, and 3,000 mg/L, complete degradation was achieved within 4, 5, 6, 9, and 10 d, respectively, with average degradation rates of 125, 200, 250, 277, and 300 mg/L/d, respectively (Fig. 3a). The degradation rate was higher in medium with a high initial pyridine concentration, indicating that strain JPB23 has a considerable pyridine-degradation capacity. Correspondingly, the biomass increased with the degradation of pyridine. As the initial pyridine concentration increased, the maximum biomass increased markly. The OD$_{600}$ values of the cultures of strain JPB23 peaked at 0.427 ± 0.019, 0.543 ± 0.027, 0.718 ± 0.028, 0.834 ± 0.040, and 1.089 ± 0.040, respectively (Fig. 3b). At low initial pyridine concentrations (500, 1,000, and 1,500 mg/L), the OD$_{600}$ values of the cultures continued to increase, and cell growth was in the log phase. At high initial pyridine concentrations of 2,500 and 3,000 mg/L, the growth of JPB23 plateaued on days 8 and 9, respectively. As the initial pyridine concentration increased, the duration of the log phase and the maximum OD$_{600}$ value of the culture increased. When growth plateaued, the pyridine concentration in the medium had dropped to the minimum value, and the percentage of pyridine removal was 99%. Therefore, cell biomass and pyridine degradation were correlated. Therefore, strain JPB23 effectively utilizes pyridine as sole carbon, nitrogen, and energy source, and transforms it into biomass.

The pyridine-degradation capacity and rate of strain JPB23 are higher than those of other pyridine-degrading strains (*Pseudomonas* sp. P12 [15], *Shewanella putrefaciens*, *Bacillus sphaericus* [37], *Streptomyces* sp. HJ02 [9], and *Rhizobium* sp. NJUST18 [12]). Therefore, it has potential utility in the treatment of pyridine-containing wastewater.

3.3. Effect of initial pH on pyridine degradation and cell growth

Pyridine degradation was significantly affected by pH. The degradation of 1,000 mg/L pyridine by strain JPB23 at various initial pH values is shown in Fig. 4a. JPB23 degraded pyridine over a wide range of pH values (pH 5.0–9.0). The optimal pH values for pyridine degradation were 5.0 and 9.0, at which pyridine was degraded completely within 3 d. At initial pH values of 6.0 and 8.0, complete pyridine degradation was achieved within 4 d, and the degradation rate at pH 8.0 was higher than that at pH 6.0. At an initial pH value of 7.0, pyridine was completely degraded within 5 d. The highest pyridine degradation rate was at pHs 5.0 and 9.0, followed by pHs 8.0, 6.0, and 7.0. Therefore, weakly acidic or weakly alkaline conditions enhance the degradation of pyridine by strain JPB23. At an initial pH of 10.0, pyridine degradation was slow, and a prolonged lag phase was observed. On day 5, only 49.83% of the pyridine had been removed, consistent with the studies of Mathur et al. [37] and Shen et al. [12].

To further investigate the effect of pH on pyridine degradation, we also measured the OD$_{600}$ of JPB23 cultures at various pH values. As shown in Fig. 4b, the growth trend of strain JPB23 differed according to the initial pH. The growth rates at different initial pH values (pH 5.0–9.0) did not differ significantly before day 2. At initial pH values of 5.0, 8.0, and 9.0, the OD$_{600}$ values of the cultures increased rapidly after day 2 and peaked on day 3. The transition from exponential to stationary phase occurred on day 3, after which OD$_{600}$ decreased slightly. At initial pH values of 6.0 and 7.0, the growth rates were lower than those at initial pH values of 5.0, 8.0, and 9.0. At an initial pH of 6.0, the OD$_{600}$ values of the cultures peaked at 4–5 d. Pyridine was degraded completely at the times of the peak OD$_{600}$ values. Strain JPB23 showed the highest growth rate at pH 9.0, followed by pHs 5.0, 8.0, 6.0, and 7.0 (Fig. 4b), and this pattern is similar to that of the pyridine-degradation rate (Fig. 4a). Therefore, pyridine degradation correlated positively with cell growth.

3.4. Effect of temperature on pyridine degradation and cell growth

Fig. 5 shows the effects of temperature on pyridine degradation and cell growth at an initial pH of 7.0. Strain JPB23 grew in MSM at 25°C–37°C. At 30 or 37°C, pyridine was removed completely within 5 or 4 d, respectively (Fig. 5a). The pyridine-degradation rate was higher at 30°C than at

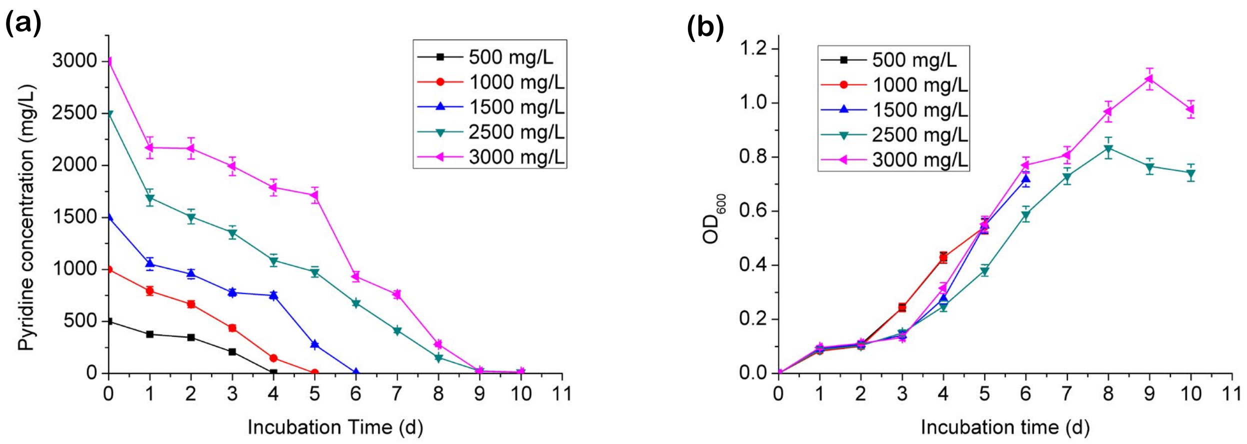


Fig. 3. Effect of initial pyridine concentration on pyridine degradation (a) and cell growth (b).

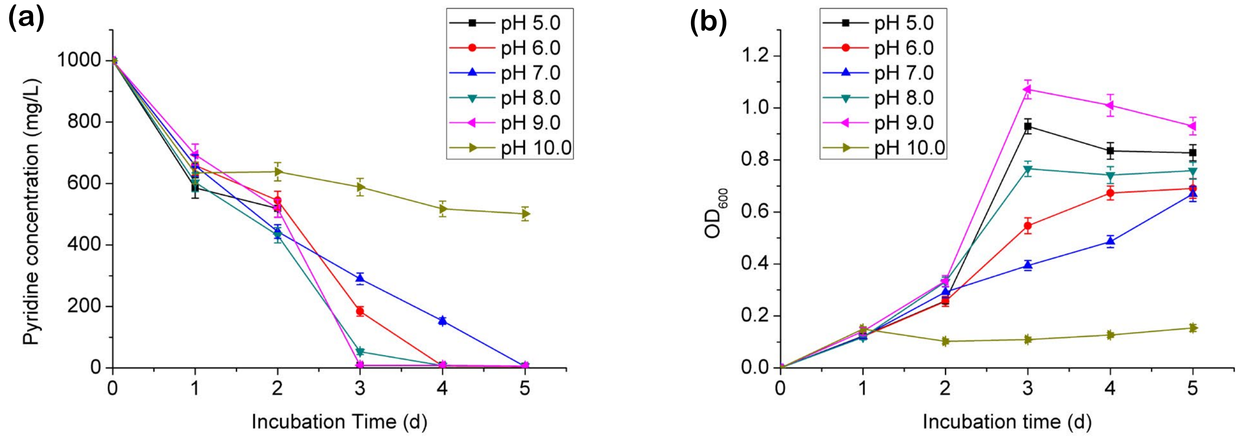


Fig. 4. Effect of initial pH value on pyridine degradation (a) and cell growth (b).

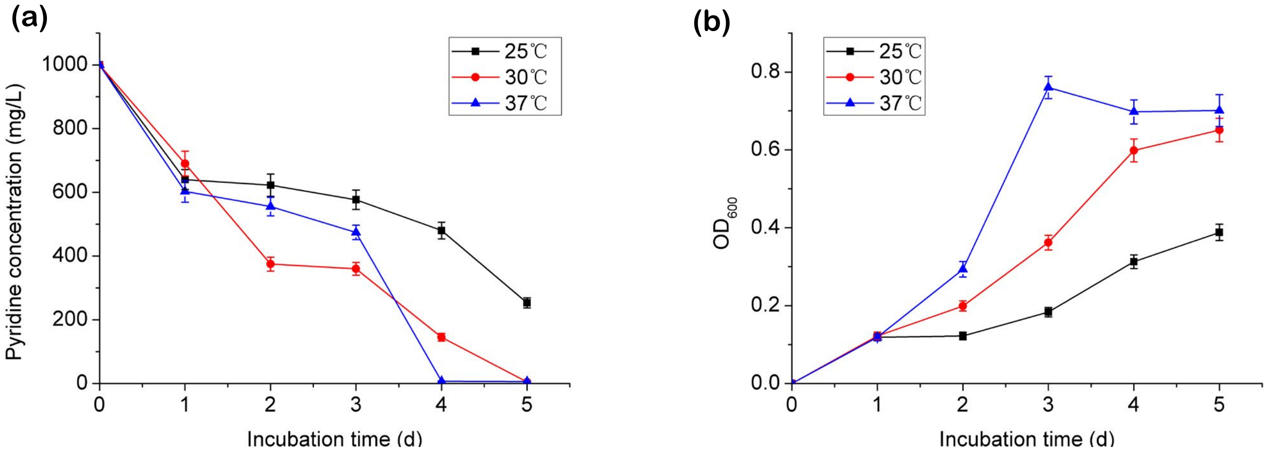


Fig. 5. Effect of temperature on pyridine degradation (a) and cell growth (b).

37°C during the first 3 d. Thereafter, the pyridine-degradation rate was significantly lower at 30°C than at 37°C. At 25°C, pyridine degradation was slow, and 253.17 mg/L pyridine remained in the medium after 5 d. As shown in Fig. 5b, the growth rate was higher at 37°C than at 30°C in the logarithmic growth phase, but the OD_{600} value at 30°C (0.651) was similar to that at 37°C (0.701) after 5 d. Growth at 25°C was slow, and after 5 d, the OD_{600} value (0.388) was half that at 37°C. Therefore, temperatures of 30°C and 37°C are suitable for pyridine degradation and cell growth.

3.5. Effect of additional carbon on pyridine degradation and cell growth

Fig. 6 shows the effects of the addition of glucose on pyridine degradation and cell growth. Cultures with 0 and 500 mg/L additional glucose degraded 1,000 mg/L pyridine within 5 and 4 d, respectively (Fig. 6a). In cultures with 1,000 mg/L additional glucose, 75.18% of the pyridine was degraded within 5 d. Pyridine degradation was enhanced by the addition of 500 mg/L glucose, but inhibited by 1,000 mg/L glucose. This is consistent with the study by Shen et al. [12]. As indicated in Fig. 6b, glucose enhanced the growth of strain JPB23 in a concentration-dependent manner, suggesting that the addition of glucose increased the accumulation of biomass. Therefore, *S. multivorum* JPB23 preferentially utilized glucose added as a supplementary carbon source. The addition of a low concentration of glucose enhanced the accumulation of biomass and therefore also pyridine degradation. With the addition of a high concentration of glucose, strain JPB23 preferentially utilized glucose for biomass growth, and then used pyridine when the glucose was exhausted, resulting in a delay in pyridine degradation.

3.6. Transcriptomic analysis of pyridine-induced genes

To better understand the pyridine-biodegradation mechanism of strain JPB23, transcriptomic analysis was used to identify genes that were differentially expressed between cultures with and without added pyridine. High-throughput RNA sequencing was performed with the Illumina HiSeq™ 4000 System. The transcriptome was assembled de novo with

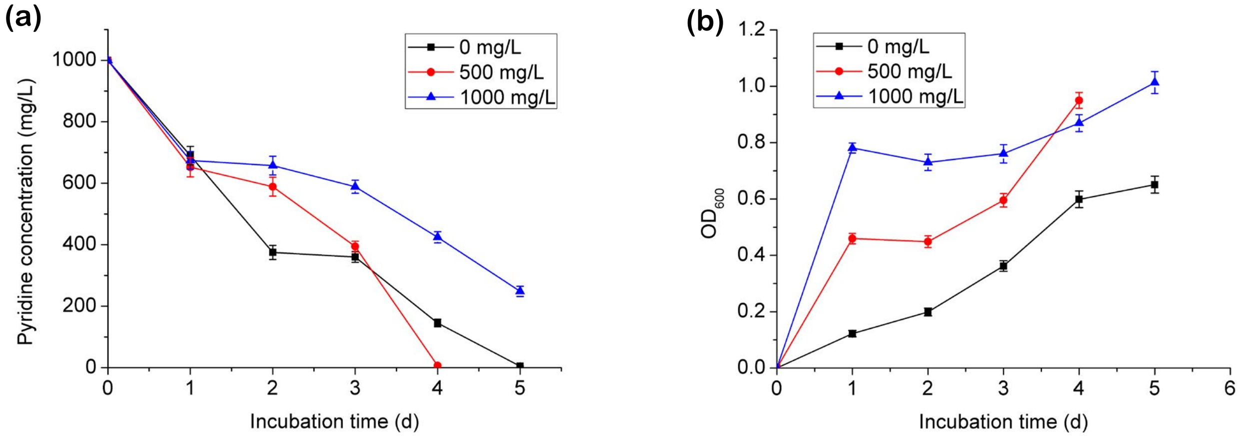


Fig. 6. Effect of glucose addition on pyridine degradation (a) and cell growth (b).

the short-reads assembly program Trinity, which is suitable for the assembly of transcriptome from RNA-seq data without a reference genome [35]. A total of more than 1.9 × 10^7 unique reads were obtained, and >97% of all the reads mapped to reference genes. From a total of 4,561 genes, 2,578 genes (56.6%) showed differential expression patterns; 2,157 genes (47.4%) were significantly upregulated by pyridine (Table S2), 222 of which were >10-fold unregulated ($\log_2$FC > 3.32); and 421 genes (9.2%) were downregulated by the addition of pyridine (Fig. 7).

Fourteen candidate genes involved in the pyridine-degradation pathway were identified based on the differentially expressed gene analysis and the existing literature (Fig. 8), including: (1) three genes (Unigene0000474, Unigene0000475, and Unigene0004334) encoding succinate-semialdehyde dehydrogenase, which catalyzes the dehydrogenation of succinate semialdehyde; (2) one gene (Unigene0002756) encoding an amidase family protein, which potentially participates in the aminohydrolysis of formamide; (3) one gene (Unigene0002919) encoding ammonia monooxygenase, which is involved in ammonia oxidation; (4) one gene (Unigene0002044) encoding nitrate reductase, which reduces nitrate into nitrite; (5) two genes (Unigene0002529 and Unigene0002655) encoding nitrite reductase, which catalyzes the reduction of nitrite; (6) three genes encoding accessory proteins for nitric oxide reductase (Unigene0000426 and Unigene0003038) and nitric oxide reductase (Unigene 0000428), which participate in the reduction of nitric oxide, generating nitrous oxide; and (7) three genes encoding nitrous oxide reductase (Unigene0001287) and regulatory proteins for nitrous oxide reductase (Unigene0003294 and Unigene0003295), which are involved in the reduction of nitrous oxide to dinitrogen.

4. Discussion

The isolation of pyridine degraders is important for the biotreatment of pyridine. To date, several bacteria have been showed to be capable of pyridine biodegradation. However, the biodegradation of pyridine by *Sphingobacterium* has not been reported until now. The genus *Sphingobacterium* was proposed by Yabuuchi et al. [38] to include Gram-negative rods.

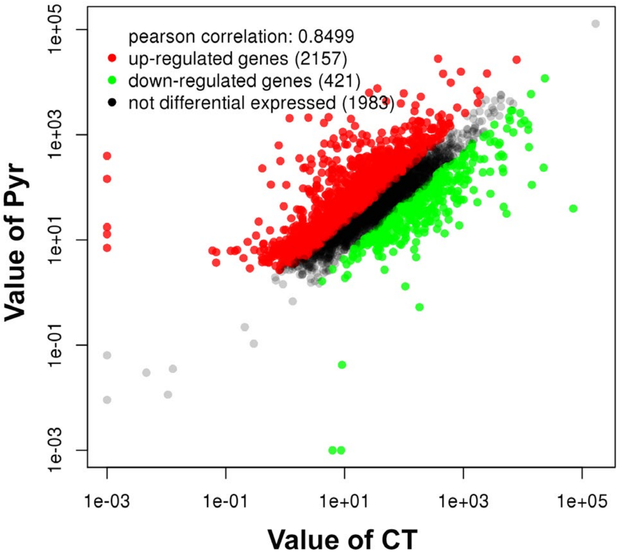
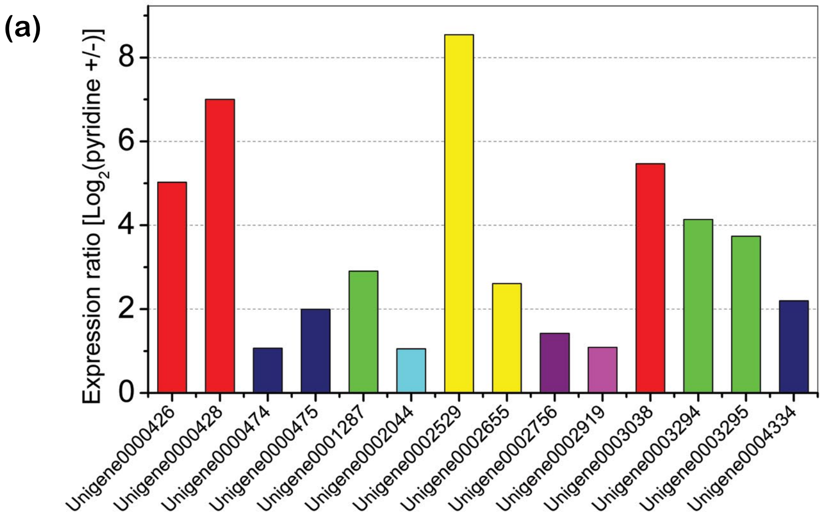


Fig. 7. Scatter plot of DEGs between the control (CT) and pyridine-addition (Pyr) libraries. Red spots represent the upregulated DEGs, green spots indicate the downregulated DEGs, and black spots represent the genes without significant differential expression.

Previous studies have shown that these bacteria are capable of degrading a number of insecticides [39–42] and organic pollutants [43,44]. In this study, we report the biodegradation of pyridine by a member of the genus *Sphingobacterium*.

The pyridine-degradation capacity of microorganisms is affected by various factors, including pH and temperature. Our results show that *S. multivorum* JPB23 degrades pyridine at pH 5.0–9.0, and that weakly acidic or weakly alkaline conditions enhance its cell growth and pyridine degradation (Fig. 4). In contrast, pyridine degradation by *Rhizobium* sp. NJUST18 [12], *S. putrefaciens*, and *B. sphaericus* [37] peaks at an initial pH of 7.0, and alkaline conditions (pH 7.0–9.0) are suitable for pyridine degradation by *Achromobacter* sp. DN-06 [11] (optimum, pH 8.0). Pyridine degradation was slow at initial pH values <6.0. Pyridine-degrading strains



(b)

GeneID	log$_2$(Pyridine +/-)	Description
Unigene0000426	5.03	accessory protein for nitric oxide reductase, *norD*
Unigene0000428	7.00	cytochrome b-containing subunit I of nitric oxide reductase, *norB*
Unigene0000474	1.07	succinate-semialdehyde dehydrogenase (NADP($^+$))
Unigene0000475	2.00	succinate-semialdehyde dehydrogenase (NADP($^+$))
Unigene0001287	2.91	nitrous-oxide reductase, *nosZ*
Unigene0002044	1.05	nitrate reductase catalytic subunit
Unigene0002529	8.55	nitrite reductase, copper-containing
Unigene0002655	2.61	nitrite reductase, copper-containing
Unigene0002756	1.42	amidase family protein
Unigene0002919	1.09	ammonia monooxygenase
Unigene0003038	5.47	accessory protein for nitric oxide reductase, *NorE*
Unigene0003294	4.14	4Fe-4S binding protein, regulatory protein for nitrous oxide reductase, *nosR*
Unigene0003295	3.74	4Fe-4S binding protein, regulatory protein for nitrous oxide reductase, *nosR*
Unigene0004334	2.20	succinate-semialdehyde dehydrogenase (NADP($^+$))

Fig. 8. Expression ratio (a) and description (b) of candidate genes involved in pyridine degradation.

have various optimal pH values. Li et al. [9] investigated the effect of temperature on pyridine degradation by *Streptomyces* sp. HJ02. The optimal temperature was 30°C and the pyridine-degradation rate was significantly higher at 30°C than at 37°C [9]. The optimum temperature for pyridine degradation by *S. multivorum* JPB23 is 30–37°C. The results of this study show that pyridine degradation by this strain correlates positively with cell growth. *S. multivorum* JPB23 displayed a significant pyridine-degradation ability only when the OD_{600} value exceeded 0.6. Therefore, we added glucose to the medium to promote cell growth. The addition of glucose enhanced the accumulation of biomass (Fig. 6), but the addition of >1,000 mg/L glucose delayed the degradation of pyridine. In contrast, the addition of 500 mg/L glucose promoted both cell growth and pyridine degradation. Li et al. also reported that the addition of sucrose inhibited pyridine degradation by *Streptomyces* sp. HJ02 [9]. Therefore, both the concentration and type of carbon sources affect pyridine degradation. Investigating the effects of various factors on pyridine degradation should facilitate the use of *S. multivorum* JPB23 to remove pyridine from industrial wastewater.

Based on our transcriptomic analysis, genes encoding succinate-semialdehyde dehydrogenase were upregulated in response to pyridine (Fig. 8). We infer that the pyridine-degradation pathway of *S. multivorum* JPB23 is identical to one of the metabolic pathways proposed by Watson and Cain [7], in which succinate semialdehyde is one of the main intermediates. The proposed pyridine-degradation pathway of *S. multivorum* JPB23 is described in Fig. 9. The pyridine ring is cleaved between C_2 and C_3, and the C_6–N bond is hydrolyzed to liberate succinate semialdehyde and formamide. Succinate semialdehyde is further oxidized to succinate by succinate-semialdehyde dehydrogenase. Succinate may then enter the tricarboxylic acid cycle for energy production. Formamide is attacked by amidase to produce formate and NH_3. NH_3 is transformed to NH_2OH by ammonia monooxygenase, and then to NO_3^- by an unidentified enzyme. NO_3^- is transformed to NO_2^- and then to NO by nitrate reductase and nitrite reductase, respectively. NO is converted to N_2O by nitric oxide reductase and finally to N_2 by nitrous oxide reductase. Ten genes involved in nitrogenous transformation showed higher expression ratios, especially Unigene0000426 and Unigene0000428, which had gene expression ratios of

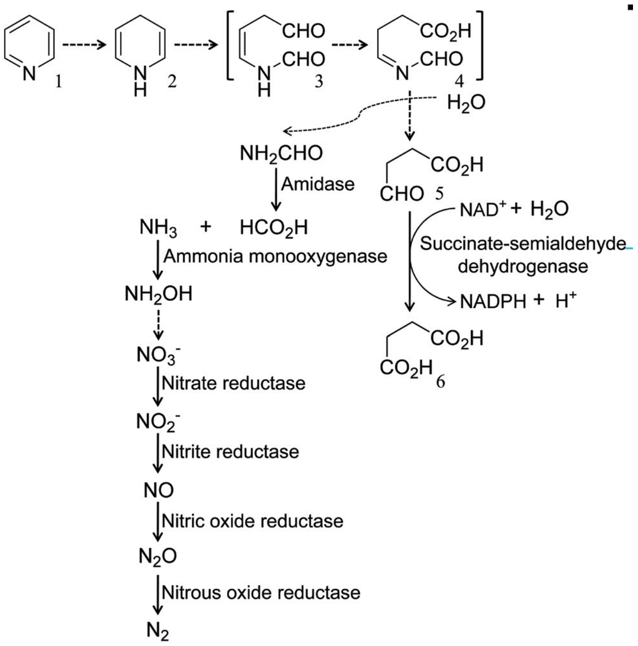


Fig. 9. Proposed pathway for the degradation of pyridine by JPB23 stain. The dashes arrows represent the speculated information. 1, pyridine; 2, 1,4-dihydropyridine; 3, N-formylaminovimylacetaldehyde; 4, N-formylaminovimylacetic acid; 5, succinic semialdehyde; 6, succinic acid.

>13 (Fig. 8). Therefore, strain JPB23 is highly likely to be a denitrifying bacterium.

Pyridine-degradation pathways have been investigated in *Nocardia* Z1, *Bacillus* 4 [7], *Nocardia* KM-2 [8], *Streptomyces* sp. HJ02 [9], and *Paracoccus* sp. NJUST30 [28]. However, nitrogen transformation initiated from pyridine has only been reported in *Paracoccus* sp. BW001 [17] and *S. zoogloeoides* BC026 [18]. Our RNA-seq analysis indicated that the mechanism of pyridine degradation in *S. multivorum* JPB23 is similar to the pathway used by *Bacillus* 4 [7] and *Streptomyces* sp. HJ02 [9], with succinate semialdehyde, formamide, and formic acid as the main intermediates. However, nitrogen transformation was not described in *Bacillus* 4 or *Streptomyces* sp. HJ02. Based on the present study, we propose a nitrogen transformation pathway initiated from pyridine in *S. multivorum* JPB23 that is identical to that of *Paracoccus* sp. BW001 [17] and *S. zoogloeoides* BC026 [18]. Further, investigations are required to clarify the molecular mechanism underlying the formation of succinate semialdehyde in *S. multivorum* JPB23.

5. Conclusion

Strain JPB23, which is capable of degrading pyridine, was isolated from the wastewater of a coal-coking plant. According to a 16S rRNA sequence analysis, the strain was identified as *Sphingobacterium* sp. Strain JPB23 degraded 3,000 mg/L pyridine completely within 10 d, and pyridine degradation correlated positively with cell growth. The effects of pH, temperature, and glucose addition on pyridine degradation by strain JPB23 were investigated. The optimum degradation conditions were pH 5.0 or 9.0 and a temperature of 30–37°C. The addition of 500 mg/L glucose promoted both cell growth and pyridine degradation; in contrast, the addition of >1,000 mg/L glucose delayed the degradation of pyridine. An RNA-seq analysis suggested that candidate genes involved in succinate-semialdehyde dehydrogenation, formamide aminohydrolysis, ammonia oxidation, and nitrogen transformation participate in the pyridine-degradation pathway. The pyridine degradation pathway was proposed. The metabolism of pyridine was ripped between C_2 and C_3, and pyridine was hydrolyzed to succinate semialdehyde and formamide. Formamide was attacked by amidase to produce formate and NH_3, and NH_3 was ultimately transformed into N_2.

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Supplementary information

Table S1
Characteristics of strain JPB23

Characteristics	Result*	Characteristics	Result	Characteristics	Result
Gram's dye	+	L-Fucose	w	Citric acid	−
Methyl red	−	L-Rhamnose	w	α-Keto-glutaric acid	−
V-P	+	Inosine	−	D-malic acid	−
Indole	−	D-Sorbitol	−	L-Malic acid	−
Malonate	+	D-Mannitol	−	Bromo-Succinic acid	−
KOH	−	D-Arabitol	−	Tween 40	−
Starch hydrolysis	−	myo-Inositol	−	γ-Amino-butryric acid	−
Lecithinase	−	Glycerol	w	α-HydroxyButyric acid	−
Catalase	−	D-Glucose-6- Phosphate	−	β-Hydroxy-D, L-Butyric acid	−
Oxidase	−	D-Fructose-6-Phosphate	w	α-Keto-Butyric acid	−
Utilization of carbon sources (BIOLOG Gen III)		D-Aspartic acid	−	Acetoacetic acid	w
Dextrin	+	D-Serine	−	Propionic acid	−
D-Maltose	+	Gelatin	+	Acetic acid	w
D-Trehalose	+	Glycyl-L-Proline	w	Formic acid	−
D-Cellobiose	+	L-Alanine	−	Growth at (BIOLOG Gen III)	
Gentiobiose	+	L-Arginine	−	1% NaCl	+
Sucrose	+	L-Aspartic acid	−	4% NaCl	−
D-Turanose	+	L-Glutamic acid	−	1% Sodium lactate	+
Stachyose	−	L-Histidine	−	Troleandomycin	+
D-Raffinose	+	L-Pyroglutamic acid	−	Rifamycin SV	+
α-D-Lactose	+	L-Serine	−	Minocycline	−
D-Melibiose	w	Pectin	+	Lincomycin	−
β-Methyl-D-Glucoside	+	D-Galacturonic acid	+	Guanidine hydrochloride	−
D-Salicin	+	L-Galactonic acid Lactone	−	Niaproof 4	−
N-Acetyl-D-Glucosamine	+	D-Gluconic acid	−	Vancomycin	w
N-Acetyl-β-D-Mannosamine	−	D-Glucuronic acid	w	Tetrazolium violet	+
N-Acetyl-D-Galactosamine	+	Glucuronamide	w	Tetrazolium blue	+
N-Acetyl Neuraminic acid	w	Mucic acid	−	Nalidixic acid	−
α-D-Glucose	+	Quinic acid	−	Lithium chloride	−
D-Mannose	+	D-Saccharic acid	−	Otassium tellurite	−
D-Fructose	+	p-Hydroxy-phenylacetic acid	−	Aztreonam	+
D-Galactose	+	Methyl pyruvate	−	Sodium butyrate	w
3-Methyl Glucose	−	D-Lactic acid Methyl Ester	−	Sodium bromate	−
D-Fucose	−	L-Lactic acid	−		

*+, Positive; −, negative; w, weakly positive.

Table S2
Genes upregulated by pyridine

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0000003	2.026478751	Conserved hypothetical protein
Unigene0000004	4.347062534	Hypothetical protein
Unigene0000008	1.031113409	Major facilitator superfamily protein
Unigene0000009	2.022203379	Methylase
Unigene0000011	3.551964774	ABC transporter
Unigene0000012	1.443149656	Transposase
Unigene0000016	2.574739554	Hypothetical protein
Unigene0000017	8.647629696	Senescence-associated protein, partial
Unigene0000018	2.489922533	Hypothetical protein
Unigene0000019	1.828056793	Hypothetical protein
Unigene0000021	3.035787849	Globin-coupled sensor protein
Unigene0000022	6.214479587	Porin
Unigene0000024	1.735611925	Concanavalin A-like lectin/glucanases superfamily protein
Unigene0000026	3.071741497	Uncharacterized protein
Unigene0000030	1.1484153	Uncharacterized membrane protein
Unigene0000031	2.167873394	LysR family transcriptional regulator
Unigene0000035	2.168401044	Ankyrin
Unigene0000036	1.444522657	(S)-ureidoglycine aminohydrolase
Unigene0000037	1.162004801	MFS transporter
Unigene0000038	2.644417411	Malonyl-CoA synthase
Unigene0000040	1.204245472	D-alanyl-D-alanine carboxypeptidase
Unigene0000042	1.255825008	Diguanylate phosphodiesterase
Unigene0000043	1.076609868	Spermidine/putrescine ABC transporter substrate-binding protein
Unigene0000044	1.475265219	GGDEF-domain containing protein
Unigene0000050	1.627179863	Autoinducer 2 aldolase
Unigene0000051	1.928830255	Short-chain dehydrogenase
Unigene0000052	2.117806902	Autoinducer 2 aldolase
Unigene0000053	7.735781529	Iron ABC transporter permease
Unigene0000054	5.471661278	Bacterial extracellular solute-binding family protein
Unigene0000055	5.934495181	Inositol monophosphatase
Unigene0000059	3.424661864	Pyruvate dehydrogenase complex E1 component subunit beta
Unigene0000060	1.760577761	Dihydrolipoamide dehydrogenase
Unigene0000061	3.06768043	Pyruvate dehydrogenase complex dihydrolipoamide acetyltransferase
Unigene0000063	1.094783388	ATP-dependent acyl-CoA ligase
Unigene0000065	1.202889119	Acetoacetate decarboxylase
Unigene0000067	7.013288121	N-carbamoylputrescine amidase
Unigene0000069	1.609051222	Agmatine deiminase
Unigene0000070	1.191332752	Acetyl-/propionyl-CoA carboxylase alpha chain
Unigene0000076	1.428318307	ABC transporter permease
Unigene0000079	2.723955646	Glycine betaine/L-proline-binding protein
Unigene0000080	1.971113113	ABC transporter permease
Unigene0000083	1.527227554	Replication initiation protein
Unigene0000086	1.04900036	LuxR family transcriptional regulator
Unigene0000091	2.647613759	Inositol monophosphatase
Unigene0000093	1.336379385	Hypothetical protein
Unigene0000096	1.542829241	Spermidine/putrescine ABC transporter permease
Unigene0000097	2.136118583	ABC transporter ATP-binding protein
Unigene0000099	1.407810087	Type VI secretion protein
Unigene0000100	2.185571383	DNA methylase N-4/N-6 domain protein
Unigene0000101	1.878083862	GGDEF domain-containing protein

Unigene0000102	2.921523394	Lytic transglycosylase
Unigene0000107	2.430306086	Transcriptional regulator LsrR
Unigene0000108	1.929394088	Autoinducer 2 kinase LsrK
Unigene0000109	1.521241892	EamA family transporter
Unigene0000111	1.7626564	Elongation factor G
Unigene0000112	2.430124182	Translation elongation factor Tu
Unigene0000114	1.383630381	Conjugal transfer protein TrbF
Unigene0000115	1.525573991	Conjugal transfer protein TrbG
Unigene0000118	2.528476934	Long-chain fatty acid--coa ligase
Unigene0000119	2.208583124	Long-chain-fatty-acid--coa ligase
Unigene0000120	1.634658391	D-amino acid aminotransferase
Unigene0000122	1.442576476	D-aminopeptidase
Unigene0000124	1.100007333	Plasmid maintenance system antidote protein
Unigene0000125	1.893022022	Uncharacterized protein
Unigene0000127	1.337320458	Hypothetical protein
Unigene0000129	2.403135489	Methylmalonyl-CoA carboxyltransferase
Unigene0000130	1.78566246	Methylmalonyl-CoA carboxyltransferase
Unigene0000132	2.084897194	Hypothetical protein
Unigene0000133	3.036214784	Hypothetical protein
Unigene0000134	1.601791637	Hypothetical protein
Unigene0000135	2.283621627	Transcriptional regulator, MarR family
Unigene0000136	2.190681358	HTH-type transcriptional repressor CytR
Unigene0000137	2.303587092	Transporter
Unigene0000138	1.547450361	Flavin-nucleotide-binding protein
Unigene0000139	2.48767305	ROK family transcriptional regulator
Unigene0000140	1.434840233	Transcriptional regulator
Unigene0000141	2.029830856	ABC transporter ATP-binding protein
Unigene0000151	1.39737284	DEAD/DEAH box helicase
Unigene0000153	1.263327199	Hypothetical protein
Unigene0000154	3.068134813	Hypothetical protein
Unigene0000156	1.338252465	Anion permease
Unigene0000157	1.929078552	Alanine racemase
Unigene0000158	1.534986445	Polar amino acid ABC transporter, inner membrane subunit
Unigene0000159	1.023215991	lysE type translocator family protein
Unigene0000161	2.076135763	Methylase/helicase
Unigene0000162	3.339680255	16S RNA G1207 methylase RsmC
Unigene0000163	1.276901489	Methylase, partial
Unigene0000164	2.976361778	Methylase
Unigene0000165	1.935953082	Sugar ABC transporter substrate-binding protein
Unigene0000166	1.392334883	Sugar ABC transporter ATP-binding protein
Unigene0000167	1.080187878	Aspartate aminotransferase family protein
Unigene0000171	1.244329665	Possible C4-dicarboxylate-binding periplasmic protein
Unigene0000172	1.953740416	TRAP-type C4-dicarboxylate transport system, large permease component
Unigene0000173	1.519304153	TRAP-type C4-dicarboxylate transport system, large permease component
Unigene0000174	2.473252113	Phosphohydrolase
Unigene0000175	2.031779986	Membrane Protein
Unigene0000176	1.658306031	2-methylthioadenine synthetase
Unigene0000177	1.668635186	2-methylthioadenine synthetase
Unigene0000178	1.293500236	Thiamin biosynthesis protein
Unigene0000182	1.642359295	Sodium-independent anion transporter
Unigene0000183	2.360695622	Phosphoadenosine phosphosulfate reductase
Unigene0000185	4.582896602	L,D-transpeptidase
Unigene0000186	1.167231502	Penicillin-binding protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0000188	2.070603446	Acetyl-CoA hydrolase
Unigene0000189	2.139550636	3-oxoadipate CoA-transferase
Unigene0000190	1.760746617	3-oxoadipate CoA-transferase
Unigene0000191	1.010383783	RNA polymerase subunit sigma-70
Unigene0000193	1.24845792	2-(S)-hydroxypropyl-CoM dehydrogenase XecE
Unigene0000194	2.235329908	ABC transporter permease
Unigene0000195	1.736191894	Aspartate aminotransferase family protein
Unigene0000196	1.878915245	Aldehyde dehydrogenase family protein
Unigene0000197	2.080063236	Aldehyde dehydrogenase family protein
Unigene0000198	2.095475182	NitT/TauT family transport system permease protein
Unigene0000201	1.031136695	DNA-binding transcriptional regulator, LysR family
Unigene0000202	4.573479173	Peptidase S41
Unigene0000203	4.996501854	Rrf2 family transcriptional regulator
Unigene0000205	1.929214397	Peptide ABC transporter substrate-binding protein
Unigene0000208	3.217079935	3-oxoacyl-(acyl-carrier-protein) reductase protein
Unigene0000209	3.009833295	GntR family transcriptional regulator
Unigene0000210	1.456421941	RNA polymerase sigma-54 factor
Unigene0000213	1.140916147	Error-prone DNA polymerase
Unigene0000214	3.146486275	Ceramide glucosyltransferase
Unigene0000215	2.056375691	Serine/threonine protein kinase
Unigene0000216	1.406087221	Glycosyl transferase 21 family protein
Unigene0000218	1.792811693	Conjugal transfer coupling protein TraG
Unigene0000220	1.349633537	Conjugal transfer protein TraC
Unigene0000221	2.11133267	Conjugal transfer protein TraG
Unigene0000223	1.429625089	Relaxase
Unigene0000224	1.749641152	Dtr system oriT relaxase
Unigene0000226	1.74389903	Ketol-acid reductoisomerase
Unigene0000228	1.098519009	Hypothetical protein
Unigene0000233	1.672566834	Peptide ABC transporter substrate-binding protein
Unigene0000234	2.023541745	Amino acid ABC transporter
Unigene0000235	2.175387996	2-aminohexano-6-lactam racemase
Unigene0000236	2.12810622	MurR/RpiR family transcriptional regulator
Unigene0000237	2.608328054	Glutamine synthetase
Unigene0000238	2.794805698	TraM recognition site of TraD and TraG, partial
Unigene0000239	1.260040057	Conjugative coupling factor TraD, PFGI-1 class
Unigene0000243	2.050249179	Enoyl-CoA hydratase/carnithine racemase
Unigene0000245	1.985349004	Acyl-CoA dehydrogenase
Unigene0000246	1.745677182	MFS transporter
Unigene0000251	1.8253037	NHL repeat family protein
Unigene0000252	1.94648445	L-arabinose transporter ATP-binding protein
Unigene0000253	3.635200484	Sugar ABC transporter substrate-binding protein
Unigene0000254	2.811623817	Replication initiation protein RepC
Unigene0000255	4.191854699	Short-chain dehydrogenase
Unigene0000256	6.737179409	Membrane protein
Unigene0000260	1.671032043	Porin
Unigene0000261	2.054757849	LysR family transcriptional regulator
Unigene0000269	2.450977654	Transporter, partial
Unigene0000270	2.557109073	DNA uptake protein
Unigene0000271	1.639154969	Guanine deaminase
Unigene0000272	3.031313359	Cysteine desulfurase
Unigene0000273	1.674436757	Conjugal transfer protein TrbL

Unigene0000274	1.959424436	P-type conjugative transfer protein TrbG
Unigene0000275	1.978285438	Membrane protein
Unigene0000276	1.89329415	Oligosaccharyl transferase-like protein
Unigene0000277	1.878029884	Oligosaccharyl transferase-like protein
Unigene0000279	3.345777249	ABC-type uncharacterized transport system permease component
Unigene0000280	1.889335461	Acriflavin resistance protein
Unigene0000281	1.400796293	Iron ABC transporter substrate-binding protein
Unigene0000284	1.046768393	Signal recognition particle-docking protein FtsY
Unigene0000286	2.671230851	Transketolase
Unigene0000287	2.489208019	Transketolase
Unigene0000288	2.307585994	Transketolase
Unigene0000291	1.318150488	Peptidyl-prolyl cis-trans isomerase
Unigene0000292	3.067783103	Sarcosine dehydrogenase
Unigene0000293	1.8940065	Sarcosine dehydrogenase
Unigene0000294	2.345995377	Sarcosine dehydrogenase
Unigene0000296	1.328583535	Ring hydroxylating alpha subunit family protein
Unigene0000305	2.071490012	ABC transporter
Unigene0000306	1.158633601	Tryptophan synthase subunit alpha
Unigene0000313	1.109227324	Integrating conjugative element protein
Unigene0000314	1.551109697	Cytochrome c oxidase, cbb3-type subunit I
Unigene0000315	3.298788027	Cytochrome-c oxidase, cbb3-type subunit I
Unigene0000316	3.910812999	Chemotaxis protein
Unigene0000318	3.85077447	Chemotaxis protein
Unigene0000321	1.289423982	Ectoine/hydroxyectoine ABC transporter permease subunit EhuD
Unigene0000328	1.412507082	Membrane protein involved in the export of O-antigen and teichoic acid
Unigene0000329	1.537538699	lipopolysaccharide biosynthesis protein
Unigene0000332	1.874823424	Glycosyl transferase family 1
Unigene0000334	2.713331645	Glycosyl transferase family 1
Unigene0000335	1.259569975	DNA (cytosine-5-)-methyltransferase
Unigene0000337	1.610105533	DNA helicase
Unigene0000339	1.542920178	Alanine-phosphoribitol ligase
Unigene0000340	3.079346504	GMC family oxidoreductase
Unigene0000341	1.407455722	3-ketoacyl-ACP reductase
Unigene0000344	1.15854359	Methyl-accepting chemotaxis protein
Unigene0000345	1.911411732	Winged helix-turn-helix domain-containing protein
Unigene0000348	3.315562622	Lactate dehydrogenase
Unigene0000350	2.202315721	Lactate dehydrogenase
Unigene0000351	3.073447077	Lactate dehydrogenase
Unigene0000362	1.513359676	MFS transporter
Unigene0000363	2.793180236	Hydrophobe/amphiphile efflux-1 family RND transporter
Unigene0000364	1.313305972	Malto-oligosyltrehalose trehalohydrolase
Unigene0000368	1.470072705	Alpha/beta-hydrolase family protein
Unigene0000369	1.384634744	Alpha/beta-hydrolase family protein
Unigene0000370	1.283775416	Aldehyde dehydrogenase
Unigene0000373	1.207305948	Peptidase S15, partial
Unigene0000374	4.477901434	Chemotaxis protein CheA
Unigene0000375	5.011797556	Methyl-accepting chemotaxis protein
Unigene0000376	5.381404824	Hypothetical protein
Unigene0000377	1.04573337	WYL domain-containing protein
Unigene0000379	1.836489715	Brex phage defense system ATPase BrxC
Unigene0000381	2.783801919	AMP-dependent synthetase
Unigene0000382	2.517806159	Asparagine synthetase B
Unigene0000385	1.268373459	Hypothetical protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0000386	2.113356031	Histidine kinase
Unigene0000388	1.52420024	Pyridoxamine 5′-phosphate oxidase-related, FMN-binding protein
Unigene0000391	1.038819892	DNA topoisomerase IV subunit B
Unigene0000392	1.160700569	DNA topoisomerase IV subunit B
Unigene0000393	1.699107927	Iron ABC transporter permease
Unigene0000394	1.361490792	Iron ABC transporter permease
Unigene0000398	2.627250067	Integrase
Unigene0000399	1.811767618	Integrase
Unigene0000402	3.571958131	Pilus assembly protein
Unigene0000403	3.692107992	Pilus assembly protein CpaC
Unigene0000404	3.485430917	Protein kinase
Unigene0000405	2.98878942	Pilus assembly protein
Unigene0000406	4.120525905	CtpF protein
Unigene0000411	1.201162959	Phage tail tape-measure protein
Unigene0000414	1.057783587	Sugar ABC transporter permease
Unigene0000415	2.810643131	ABC transporter ATP-binding protein
Unigene0000416	1.690143178	ABC transporter ATP-binding protein
Unigene0000424	2.492824276	Methyl-accepting chemotaxis (MCP) signaling domain protein
Unigene0000425	3.62633663	Chemotaxis protein
Unigene0000426	5.026947871	Accessory protein for nitric oxide reductase, norD
Unigene0000427	6.325257387	Oxygen-independent coproporphyrinogen III oxidase
Unigene0000428	7.000318755	Cytochrome b-containing subunit I of nitric oxide reductase, norB
Unigene0000430	2.206963664	Hypothetical protein
Unigene0000433	1.173316678	DNA repair protein RadC
Unigene0000438	1.72443432	Thiamine diphosphokinase
Unigene0000444	2.372095357	Amino acid ABC transporter permease
Unigene0000445	1.185928639	Chloride channel protein
Unigene0000446	1.176047718	Sodium-independent anion transporter
Unigene0000447	2.061348844	ABC transporter permease
Unigene0000448	2.474271243	Ferric iron ABC transporter permease
Unigene0000449	6.923889571	MFS transporter
Unigene0000450	2.33850206	Iron ABC transporter substrate-binding protein
Unigene0000451	1.249594149	DNA replication protein
Unigene0000454	1.652355604	Uncharacterized protein
Unigene0000456	1.339147536	Conjugal transfer protein TrbF
Unigene0000458	2.451120989	Entry-exclusion protein
Unigene0000459	1.420852355	Conjugal transfer protein TrbL
Unigene0000460	1.066075608	Precorrin-3B C(17)-methyltransferase
Unigene0000461	1.531657663	Precorrin-6A synthase (deacetylating)
Unigene0000462	2.636230194	Methionine synthase
Unigene0000465	2.65782535	Head morphogenesis protein
Unigene0000466	1.972325937	Head morphogenesis protein SPP1
Unigene0000467	1.009605582	Two-component sensor histidine kinase
Unigene0000468	2.803557473	PAS domain-containing sensor histidine kinase
Unigene0000469	1.310960581	Sensor histidine kinase
Unigene0000470	1.489214918	His Kinase A domain protein
Unigene0000471	3.556685752	Uncharacterized protein
Unigene0000473	2.024718423	Histidinol phosphate phosphatase
Unigene0000474	1.069292711	Succinate-semialdehyde dehydrogenase (NADP(+))
Unigene0000475	1.995146114	Succinate-semialdehyde dehydrogenase (NADP(+))
Unigene0000476	3.344099752	2-deoxyribose-5-phosphate aldolase

Unigene0000477	1.991138797	4-aminobutyrate transaminase
Unigene0000478	1.875805296	Uncharacterized protein
Unigene0000479	1.340411751	Exodeoxyribonuclease V subunit beta
Unigene0000482	1.520748418	Gluconolactonase
Unigene0000483	2.188856963	Dehydrogenase
Unigene0000485	2.810205295	Flotillin family protein
Unigene0000486	1.778121348	ABC transporter ATP-binding protein
Unigene0000487	3.559105673	ABC transporter substrate-binding protein
Unigene0000489	1.232191814	Chorismate synthase
Unigene0000490	1.710037632	Riboflavin biosynthesis protein RibBA
Unigene0000492	1.741529608	PadR family transcriptional regulator, partial
Unigene0000493	1.193389214	Homoprotocatechuate degradative operon repressor
Unigene0000503	1.125813236	DNA-binding transcriptional regulator, XRE-family HTH domain
Unigene0000504	2.301287149	FAD-dependent oxidoreductase
Unigene0000505	2.467971052	FAD-dependent oxidoreductase
Unigene0000506	2.45314815	Iron siderophore receptor protein
Unigene0000509	9.656095324	Hypothetical protein
Unigene0000510	1.83588413	Hypothetical protein
Unigene0000511	2.657618969	Membrane protein
Unigene0000512	1.876618971	Hypothetical protein
Unigene0000514	1.867552215	Methylase
Unigene0000516	1.75908544	Methylase
Unigene0000519	1.298163829	Hypothetical protein
Unigene0000520	1.019953762	Methylase
Unigene0000523	3.243053341	RRNA intron-encoded homing endonuclease
Unigene0000524	2.686757946	Methenyltetrahydrofolate cyclohydrolase
Unigene0000525	2.274790785	Formyltetrahydrofolate deformylase
Unigene0000526	1.12150668	Formyltetrahydrofolate deformylase
Unigene0000527	2.0384987	Serine hydroxymethyltransferase
Unigene0000528	1.865280826	Dihydroorotase
Unigene0000529	2.526844134	ABC transporter permease
Unigene0000530	1.68637614	Nucleoside/nucleotide kinase family protein
Unigene0000531	2.318863905	Sugar ABC transporter ATP-binding protein
Unigene0000533	1.875317409	6-phospho-3-hexuloisomerase
Unigene0000534	1.440456868	Glucosamine--fructose-6-phosphate aminotransferase
Unigene0000540	1.217618419	Nopaline ABC transporter nucleotide-binding protein/ATPase
Unigene0000541	1.267478534	Amino acid ABC transporter substrate-binding protein
Unigene0000542	1.773662756	(2Fe-2S)-binding protein
Unigene0000543	1.415000655	Branched-chain amino acid ABC transporter permease
Unigene0000544	1.822081499	Branched-chain amino acid ABC transporter permease
Unigene0000551	1.468183225	Hypothetical protein
Unigene0000553	1.404341464	Cellulose synthase
Unigene0000555	2.041033908	Serine/threonine dehydratase
Unigene0000556	3.00702879	Sugar ABC transporter ATP-binding protein
Unigene0000557	2.862912211	Sugar ABC transporter ATP-binding protein
Unigene0000558	1.510367452	ArsR family transcriptional regulator
Unigene0000559	1.852470875	Hypothetical protein
Unigene0000560	1.165555652	Sorbosone dehydrogenase
Unigene0000563	2.111142286	Aldehyde dehydrogenase
Unigene0000566	1.853079749	Branched-chain amino acid ABC transporter
Unigene0000567	1.986104185	Conjugal transfer protein TrbE
Unigene0000568	1.469180267	Conjugal transfer protein TrbE
Unigene0000569	4.983083145	Flagellin

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0000570	5.945113083	Flagellin
Unigene0000571	4.11940353	Flagellin C
Unigene0000572	2.513487764	Replication protein A
Unigene0000573	1.212415336	sprT domain-containing protein
Unigene0000574	1.150724196	Replication protein A
Unigene0000575	2.841915967	ABC transporter permease
Unigene0000576	3.268016159	Amino acid ABC transporter
Unigene0000577	2.40371112	Octopine transport system permease protein occM
Unigene0000578	1.860316854	Amino acid ABC transporter
Unigene0000583	1.919968963	D-xylose ABC transporter ATP-binding protein
Unigene0000585	1.300629701	Sugar ABC transporter ATPase
Unigene0000586	1.777653818	Glycerol-3-phosphate dehydrogenase
Unigene0000587	1.518019018	von Willebrand factor type A domain protein
Unigene0000591	1.126529378	6-phosphogluconate dehydrogenase
Unigene0000592	1.534235154	Glycerol dehydrogenase
Unigene0000594	1.443462294	IdnD L-idonate 5-dehydrogenase
Unigene0000600	1.617162318	Transposase
Unigene0000602	8.574310591	Hypothetical protein
Unigene0000603	2.895241043	Hypothetical protein
Unigene0000605	1.493576581	ABC transporter permease, partial
Unigene0000606	2.289068567	Spermidine/putrescine ABC transporter ATP-binding protein
Unigene0000609	2.642442099	Spermidine/putrescine ABC transporter substrate-binding protein
Unigene0000617	1.515583085	DUF2312 domain-containing protein
Unigene0000618	1.828142353	Hypothetical protein
Unigene0000619	1.197542005	Uncharacterized conserved protein, UPF0335 family
Unigene0000621	4.549512616	Spermidine/putrescine ABC transporter substrate-binding protein
Unigene0000622	4.11425002	Gamma-aminobutyraldehyde dehydrogenase
Unigene0000623	2.483025917	ABC transporter substrate-binding protein
Unigene0000625	3.268776451	ABC transporter permease
Unigene0000626	4.215111671	Sugar ABC transporter substrate-binding protein
Unigene0000627	1.714180419	Histidinol dehydrogenase
Unigene0000628	3.402116043	Hydrolase
Unigene0000629	1.074777983	Hydrolase
Unigene0000630	1.642837647	ABC transporter substrate-binding protein
Unigene0000631	2.749313946	Fe^{3+}/spermidine/putrescine ABC transporter ATP-binding protein
Unigene0000632	1.368522494	Glutathione-dependent disulfide-bond oxidoreductase
Unigene0000633	2.368861432	Spermidine/putrescine ABC transporter ATP-binding protein
Unigene0000634	1.224620912	Spermidine/putrescine ABC transporter permease
Unigene0000635	1.769129698	Histidinol phosphate phosphatase
Unigene0000636	2.414138513	Polyamine ABC transporter ATP-binding protein
Unigene0000637	1.210575983	Aldehyde dehydrogenase family protein
Unigene0000638	2.054579051	Nicotinate phosphoribosyltransferase
Unigene0000640	1.790664164	Iron ABC transporter permease
Unigene0000641	1.743570352	Hemophore HasA outer membrane receptor HasR
Unigene0000644	2.544084601	Transposase
Unigene0000645	2.698310906	Transposase
Unigene0000647	1.775742833	Iron(III) transport system ATP-binding protein
Unigene0000648	1.924274157	Iron ABC transporter permease
Unigene0000649	1.816699455	Phosphonoacetaldehyde hydrolase
Unigene0000650	1.268812706	Iron ABC transporter permease
Unigene0000651	1.150619507	Hypothetical protein

Unigene0000653	1.748782501	Chitinase
Unigene0000656	1.104990543	Hypothetical protein
Unigene0000664	1.780561237	Arsenical resistance protein ArsH
Unigene0000667	1.375454119	Arsenical resistance protein ArsH
Unigene0000668	10.7640994	Hypothetical protein
Unigene0000669	1.689460842	D-ribose transporter ATP-binding protein
Unigene0000670	1.111781578	D-ribose transporter ATP-binding protein
Unigene0000671	1.735417225	Pentose kinase
Unigene0000674	1.545295384	Sugar ABC transporter ATP-binding protein
Unigene0000675	1.393347853	Sugar ABC transporter permease
Unigene0000676	1.23520522	Ribose import ATP-binding protein RbsA
Unigene0000677	2.519101937	Lantibiotic ABC transporter permease
Unigene0000678	1.667842968	Monosaccharide-transporting ATPase
Unigene0000679	2.843191393	Oxidoreductase
Unigene0000680	1.888178863	Probable sugar ABC transporter, permease protein
Unigene0000681	1.273899259	Sugar ABC transporter permease
Unigene0000682	1.609475993	Deacylase
Unigene0000683	1.271318374	ABC transporter ATP-binding protein
Unigene0000686	1.04510045	Formate dehydrogenase
Unigene0000687	2.222627899	Hydrolase
Unigene0000688	2.608769232	Hydrolase
Unigene0000690	2.283322175	Chemotaxis protein
Unigene0000691	1.905743029	Methyl-accepting chemotaxis protein
Unigene0000692	3.37924026	Methyl-accepting chemotaxis sensory transducer with Cache sensor
Unigene0000694	1.35895676	Chemotaxis protein
Unigene0000695	3.63970327	Chemotaxis protein
Unigene0000696	3.061958747	Methyl-accepting chemotaxis protein (MCP) signalling domain-containing protein, partial
Unigene0000698	3.328660796	Chemotaxis protein
Unigene0000699	3.86195474	Chemotaxis protein
Unigene0000700	3.626178662	Chemotaxis protein
Unigene0000701	2.164106932	Chemotaxis protein
Unigene0000703	1.500146387	Chemotaxis protein
Unigene0000704	1.365325614	Chemotaxis protein CheW
Unigene0000705	2.209802335	Chemoreceptor McpA
Unigene0000706	7.609060514	Hypothetical protein
Unigene0000711	2.10987446	Hypothetical protein
Unigene0000712	2.018095754	Phage protein
Unigene0000717	3.687687332	Electron transfer flavoprotein subunit alpha
Unigene0000718	2.596017689	Integrase
Unigene0000719	1.273690928	5-oxoprolinase
Unigene0000720	5.257144431	Protein dehydratase
Unigene0000721	4.589245266	Aldolase
Unigene0000722	1.712304662	Electron transfer flavoprotein alpha subunit
Unigene0000724	1.363673219	Deoxyribodipyrimidine photolyase
Unigene0000727	1.482584295	D-serine ammonia-lyase
Unigene0000731	1.415005618	Pseudouridine synthase
Unigene0000732	1.469324392	Type I pantothenate kinase
Unigene0000736	1.976237961	Integrase
Unigene0000737	2.307076708	PF03235 family protein
Unigene0000738	1.005877767	Heme ABC exporter, ATP-binding protein CcmA
Unigene0000739	2.077475058	Acyl CoA:acetate/3-ketoacid CoA transferase
Unigene0000742	2.762458008	L-aspartate oxidase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0000743	1.101656849	Oxidoreductase
Unigene0000747	1.833453875	Hypothetical protein
Unigene0000748	2.138983014	Hypothetical protein
Unigene0000750	1.608407639	Thioredoxin family protein
Unigene0000752	1.416364283	virB8 family protein
Unigene0000754	1.317176066	SH3 domain-containing protein
Unigene0000760	3.012319801	LysR family transcriptional regulator
Unigene0000762	1.820168937	HlyD family type I secretion periplasmic adaptor subunit
Unigene0000763	1.19169953	Conjugal transfer protein TraG
Unigene0000772	1.578758837	Cobalamin synthesis G family protein
Unigene0000773	1.559504629	Cobaltochelatase subunit CobN
Unigene0000774	2.443322662	Nucleoside triphosphate pyrophosphohydrolase
Unigene0000776	1.158582347	N-acetyltransferase
Unigene0000779	1.62709124	Phenylalanine--tRNA ligase subunit alpha
Unigene0000780	1.776081181	6-aminohexanoate hydrolase
Unigene0000782	1.237938474	Acetolactate synthase isozyme 2 large subunit
Unigene0000786	2.42762252	Septum site-determining protein MinD
Unigene0000787	3.134927259	ABC transporter substrate-binding protein
Unigene0000788	1.5814349	Amidohydrolase 3
Unigene0000795	1.391230362	Molybdenum ABC transporter ATP-binding protein
Unigene0000796	2.12205638	ABC transporter ATP-binding protein
Unigene0000799	3.43824918	Dipeptide transport ATP-binding protein DppD
Unigene0000800	1.695586216	Peptide ABC transporter permease
Unigene0000801	1.538301396	Peptide ABC transporter permease
Unigene0000802	2.104723651	D-ala-D-ala transporter subunit
Unigene0000803	3.042176844	ABC transporter substrate-binding protein
Unigene0000804	1.404560051	Peptide ABC transporter ATP-binding protein
Unigene0000805	2.61767884	ABC transporter
Unigene0000807	1.924719831	ABC transporter ATP-binding protein
Unigene0000808	1.961596233	ABC transporter
Unigene0000809	1.926115821	Peptide ABC transporter substrate-binding protein
Unigene0000811	1.876795286	Molybdate ABC transporter permease
Unigene0000813	1.749021128	Isoleucine--tRNA ligase
Unigene0000814	2.009655509	ABC transporter ATP-binding protein
Unigene0000817	1.754776359	Isoleucine--tRNA ligase
Unigene0000818	1.113814227	GTPase HflX
Unigene0000820	2.126752302	IclR family transcriptional regulator
Unigene0000821	2.417719167	ABC transporter substrate-binding protein
Unigene0000824	1.035580758	TIGR01244 family protein
Unigene0000825	2.444485169	Oxidoreductase
Unigene0000826	3.070522704	Uracil-DNA glycosylase
Unigene0000828	1.075749378	Guanine deaminase
Unigene0000829	2.00831726	ABC transporter ATP-binding protein
Unigene0000832	1.401111076	Chromosome segregation protein SMC
Unigene0000833	5.09320789	Mannitol 2-dehydrogenase MtlK
Unigene0000834	1.348623467	Pyridoxamine 5′-phosphate oxidase
Unigene0000838	1.077319625	Microcin ABC transporter ATP-binding protein
Unigene0000840	2.323508079	Gluconokinase
Unigene0000842	1.412913061	Transposase
Unigene0000843	1.332680441	Branched-chain amino acid ABC transporter permease
Unigene0000844	2.272004048	Transposase

Unigene0000845	1.286235522	Molybdenum cofactor synthesis domain-containing protein
Unigene0000846	1.202183506	NAD(P)-dependent dehydrogenase, short-chain alcohol dehydrogenase family
Unigene0000851	1.237357714	Hypothetical protein
Unigene0000860	1.338620123	Transcriptional regulator
Unigene0000861	2.298346218	IS6 family transposase
Unigene0000862	2.0651138	Menaquinone biosynthesis methyltransferase
Unigene0000868	1.676375651	Glycine--tRNA ligase subunit alpha
Unigene0000873	4.040233274	Glycosyl transferase
Unigene0000875	1.965768385	Hypothetical conserved protein
Unigene0000876	2.001255248	Anion permease
Unigene0000878	1.172688555	GntR family transcriptional regulator
Unigene0000884	1.381756847	Xylose isomerase
Unigene0000886	1.680013727	Glycerate kinase
Unigene0000887	1.168442627	Uncharacterized protein
Unigene0000888	1.551126842	Fumarate hydratase, class II
Unigene0000891	1.306184707	Heme ABC transporter ATP-binding protein
Unigene0000893	1.297233365	5'-nucleotidase /3'-nucleotidase /exopolyphosphatase
Unigene0000894	3.075551436	Methyl-accepting chemotaxis sensory transducer
Unigene0000895	2.944537926	Chemotaxis protein
Unigene0000896	1.038975378	Cation transporter
Unigene0000897	1.061679561	Ring-hydroxylating oxygenase subunit alpha
Unigene0000898	2.386678979	ABC transporter permease
Unigene0000901	1.072411719	Hypothetical protein
Unigene0000902	2.377171134	Mll0865 protein
Unigene0000904	1.340422664	Hypothetical protein
Unigene0000905	2.074912043	Terminase
Unigene0000906	1.077889019	Acetate kinase
Unigene0000907	1.363253545	Energy-dependent translational throttle protein EttA
Unigene0000908	1.749873809	Membrane protein
Unigene0000910	4.334582925	Hypothetical protein
Unigene0000911	1.261585578	Hypothetical protein
Unigene0000912	1.025104306	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase
Unigene0000913	1.954541152	Methylmalonyl-CoA mutase
Unigene0000916	7.921010465	MFS transporter, partial
Unigene0000917	1.937274684	Nitrile hydratase
Unigene0000918	1.831949468	Lysine transporter LysE
Unigene0000921	2.004758963	tRNA (N6-threonylcarbamoyladenosine(37)-N6)-methyltransferase TrmO
Unigene0000922	2.261071663	Phytanoyl-CoA dioxygenase
Unigene0000923	1.275202403	Transglutaminase-like cysteine peptidase, BTLCP
Unigene0000924	3.306715404	Serine chemoreceptor protein
Unigene0000925	1.108014374	Double-strand break repair helicase AddA
Unigene0000926	2.842494485	Urea carboxylase-associated protein 1
Unigene0000927	1.450273233	Amidohydrolase
Unigene0000930	2.664550417	BMP family ABC transporter substrate-binding protein
Unigene0000931	1.996311282	Conjugal transfer protein TraG
Unigene0000932	1.742913963	Transcriptional regulator
Unigene0000933	1.025407068	Luciferase family oxidoreductase
Unigene0000934	1.148225339	Membrane protein
Unigene0000938	2.946315464	Carbohydrate ABC transporter substrate-binding protein, CUT1 family
Unigene0000940	3.120569238	L-2-hydroxyglutarate oxidase LhgO
Unigene0000941	3.985454689	Hydroxyglutarate oxidase
Unigene0000943	1.822489005	Uncharacterized protein
Unigene0000944	1.207874956	MFS transporter

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0000945	1.397737422	Phosphoribosylamine--glycine ligase
Unigene0000946	1.675704262	N-methylproline demethylase
Unigene0000953	5.174360301	Tripartite tricarboxylate transporter TctA
Unigene0000954	1.575892799	Tad-like Flp pilus-assembly family protein
Unigene0000956	1.309543274	Chromosome segregation protein SMC
Unigene0000958	1.95625612	Uncharacterized conserved protein YcbK, DUF882 family
Unigene0000959	1.196708278	Hypothetical protein
Unigene0000963	1.289263882	ABC transporter substrate-binding protein
Unigene0000964	1.803673442	ABC transporter substrate-binding protein
Unigene0000965	2.43082396	Phosphoribosylformylglycinamidine cyclo-ligase
Unigene0000966	1.381849474	Phosphoribosylglycinamide formyltransferase
Unigene0000967	1.400813697	2-methylcitrate dehydratase
Unigene0000969	2.160717626	Heavy metal-binding protein
Unigene0000971	2.0834856	Phosphohistidine phosphatase
Unigene0000972	1.385043604	DNA-packaging protein
Unigene0000973	1.151381824	AsnC family transcriptional regulator
Unigene0000974	1.025178141	2-polyprenylphenol 6-hydroxylase
Unigene0000975	1.165046217	Alcohol dehydrogenase
Unigene0000977	2.652412079	Methyl-accepting chemotaxis protein
Unigene0000978	1.82010829	Hypothetical protein
Unigene0000979	1.019426962	DNA-binding transcriptional regulator
Unigene0000981	1.905520685	Aminoglycoside phosphotransferase
Unigene0000987	1.275841772	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex ATPase subunit type 1 TsaE
Unigene0000989	2.033060982	Binding-protein-dependent transport systems inner membrane component
Unigene0000990	2.089343121	Oxidoreductase
Unigene0000996	1.898884941	Membrane protein
Unigene0000997	1.932176267	Xylulokinase
Unigene0000998	1.118077381	Fis family transcriptional regulator
Unigene0001000	1.423977032	Nucleoside-diphosphate sugar epimerase
Unigene0001001	1.335851361	Glucose-1-phosphate cytidylyltransferase
Unigene0001005	1.956458169	Relaxase
Unigene0001006	1.037470597	tRNA dihydrouridine synthase DusB
Unigene0001013	1.120450652	3-deoxy-manno-octulosonate cytidylyltransferase
Unigene0001015	1.281926791	Cold-shock protein
Unigene0001017	1.240217665	Tetratricopeptide TPR_2 repeat protein
Unigene0001019	2.206088664	methylmalonyl-CoA mutase family protein
Unigene0001020	1.844619564	ArsR family transcriptional regulator
Unigene0001021	4.416733702	Uncharacterized protein
Unigene0001022	2.047050445	Glutathione S-transferase
Unigene0001023	1.731923567	Succinyl-diaminopimelate desuccinylase
Unigene0001025	2.296702598	Ribose transport system ATP-binding protein
Unigene0001026	1.10136074	Tryptophan synthase subunit beta
Unigene0001028	2.023226991	Hypothetical protein
Unigene0001032	2.985830469	C4-dicarboxylate ABC transporter substrate-binding protein
Unigene0001034	1.945756986	Bacterial regulatory s, gntR family protein
Unigene0001036	3.598370844	CagE TrbE VirB component of type IV transporter system
Unigene0001037	3.722820601	Copper-translocating P-type ATPase
Unigene0001038	3.569520938	Copper chaperone
Unigene0001042	1.613509548	TRAP transporter solute receptor, TAXI family protein
Unigene0001043	2.512915915	MAPEG family protein

Unigene0001045	2.034089723	Hypothetical protein
Unigene0001049	3.569683213	Two-component sensor histidine kinase
Unigene0001050	2.805318694	Two-component sensor histidine kinase
Unigene0001051	1.713802471	Cysteine desulfurase-like protein
Unigene0001052	1.575882424	Integrase
Unigene0001054	1.663640893	tRNA (guanosine(37)-N1)-methyltransferase TrmD
Unigene0001057	1.061957195	Alanine--tRNA ligase
Unigene0001058	1.372380553	Elongation factor 4
Unigene0001060	2.135958769	Three-Cys-motif partner protein
Unigene0001063	1.12405081	Pirin domain-containing protein
Unigene0001065	1.426245128	Enoyl-CoA hydratase
Unigene0001067	1.784074361	Phosphoglycerate kinase
Unigene0001068	1.144625283	Penicillin-binding protein 1C
Unigene0001069	2.513095217	ABC transporter substrate-binding protein
Unigene0001070	1.729104862	MFS transporter
Unigene0001071	1.428536607	LuxR family transcriptional regulator
Unigene0001073	1.19139272	Plasmid partitioning protein RepA
Unigene0001074	1.126430096	Aldehyde oxidase
Unigene0001075	2.167384221	Replication initiation protein
Unigene0001077	1.875371764	NAD(P)-dependent oxidoreductase
Unigene0001083	1.363921156	Lysine--tRNA ligase
Unigene0001084	1.254238126	Glutamate--tRNA ligase GltX
Unigene0001085	1.005951062	NADH dehydrogenase
Unigene0001089	1.150119907	Band 7 protein
Unigene0001094	3.291009049	Phage prohead protease, HK97 family/phage major capsid protein, HK97 family
Unigene0001096	1.115189071	GAF domain-containing protein
Unigene0001097	1.97006545	Phosphodiesterase
Unigene0001099	1.632427895	Alpha/beta hydrolase
Unigene0001102	2.496311248	BMP family ABC transporter substrate-binding protein
Unigene0001106	2.42119459	Polysaccharide inhibition protein
Unigene0001107	1.095109244	Lactoylglutathione lyase
Unigene0001109	2.313656818	Hypothetical protein
Unigene0001110	1.047764863	Membrane protease subunit
Unigene0001111	1.563484471	Hydrolase
Unigene0001112	1.613159799	Lactate dehydrogenase
Unigene0001115	3.379666119	Branched-chain amino acid ABC transporter permease
Unigene0001117	1.258070527	L-fuconate dehydratase
Unigene0001119	1.126384069	PTS fructose transporter subunit IIA
Unigene0001124	3.77994866	2-isopropylmalate synthase
Unigene0001125	1.486560982	CoA-transferase
Unigene0001127	1.268751953	LysR family transcriptional regulator
Unigene0001132	1.342357145	MFS transporter
Unigene0001134	2.060145932	GMC family oxidoreductase
Unigene0001135	2.303244785	DeoR family transcriptional regulator
Unigene0001138	1.85050874	Cobalamin biosynthesis protein CobW
Unigene0001139	1.036118815	Nitroreductase
Unigene0001140	1.100332182	Mob protein
Unigene0001145	3.460590442	Flagellar motor switch protein
Unigene0001149	5.958746668	Hypothetical protein
Unigene0001152	1.602930475	Protein SlyX
Unigene0001153	1.345984123	50S ribosomal protein L20
Unigene0001155	6.440864757	Hemin ABC transporter substrate-binding protein
Unigene0001156	2.112988843	Site-specific recombinase XerD

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0001158	1.919959185	N-formylglutamate amidohydrolase
Unigene0001159	4.337534095	Two-component system, OmpR family, phosphate regulon response regulator OmpR
Unigene0001160	2.555220645	3-oxoacyl-ACP reductase
Unigene0001171	1.085075321	Membrane protein
Unigene0001174	1.08492947	Transposase IS116/IS110/IS902 family protein
Unigene0001176	1.755700188	Signal peptide protein
Unigene0001178	5.126081826	Rod-binding protein
Unigene0001179	1.02665196	Cytidine deaminase
Unigene0001183	3.764591254	DNA-binding protein
Unigene0001187	2.888417276	Hypothetical protein
Unigene0001188	1.406175791	Arabinose ABC transporter permease
Unigene0001189	2.923607301	LacI family transcriptional regulator
Unigene0001190	2.408297	LacI family transcriptional regulator
Unigene0001191	1.816375328	ATP-binding protein
Unigene0001195	1.456897896	ABC transporter permease
Unigene0001196	2.921637181	Hypothetical protein
Unigene0001199	1.511477764	Tn3 family transposase
Unigene0001201	2.340883456	Diguanylate cyclase domain protein
Unigene0001202	1.804966078	Diguanylate cyclase domain protein
Unigene0001211	1.182104278	Cell envelope biogenesis protein OmpA
Unigene0001212	1.986117048	Uncharacterized conserved protein, DUF2147 family
Unigene0001214	4.296474021	Uncharacterized protein
Unigene0001215	3.028860346	Transposase
Unigene0001222	7.212223229	Hemin-degrading HemS.ChuX domain protein
Unigene0001224	2.697835605	N-acetyltransferase
Unigene0001226	3.193967094	2-nitropropane dioxygenase
Unigene0001227	2.712583704	Diguanylate cyclase
Unigene0001229	1.439320533	Transglycosylase domain protein
Unigene0001230	1.016103821	Taurine ABC transporter substrate-binding protein
Unigene0001231	1.649888455	Dimethylamine/trimethylamine dehydrogenase
Unigene0001232	1.043043025	Polar amino acid ABC transporter, inner membrane subunit
Unigene0001235	1.540276166	Sulfate ABC transporter permease subunit CysW
Unigene0001236	1.310745901	CDP-diacylglycerol--serine O-phosphatidyltransferase
Unigene0001239	1.420862381	Gamma-glutamyltransferase
Unigene0001242	1.251811475	Beta-Ala-His dipeptidase
Unigene0001243	1.127480285	Oxidoreductase
Unigene0001248	1.428511642	DUF2312 domain-containing protein
Unigene0001249	1.707672531	FAD-binding oxidoreductase
Unigene0001250	3.660324375	Hypothetical protein
Unigene0001251	2.671033361	Peptide ABC transporter substrate-binding protein
Unigene0001252	4.587721441	Pilus assembly protein TadD
Unigene0001254	3.069655086	Chromosome partitioning protein ParA
Unigene0001256	2.979077358	Succinoglycan biosynthesis transporter ExoP
Unigene0001258	2.022852649	DNA helicase
Unigene0001260	1.046413055	Triose-phosphate isomerase
Unigene0001261	2.612107692	NAD-glutamate dehydrogenase
Unigene0001262	1.445285673	Acetolactate synthase
Unigene0001264	1.040589183	Septum formation inhibitor MinC
Unigene0001265	2.439032486	Hypothetical protein
Unigene0001267	14.09816371	Hypothetical protein

Unigene0001268	1.493635093	X-Pro dipeptidase
Unigene0001269	2.289411482	FAD-dependent oxidoreductase
Unigene0001270	1.288077733	Hypothetical protein
Unigene0001271	1.388358469	Alkaline phosphatase
Unigene0001272	1.86801982	3-isopropylmalate dehydrogenase
Unigene0001273	2.430349466	F0F1 ATP synthase subunit A
Unigene0001276	1.326028191	Glutamate synthase
Unigene0001283	1.750843203	Glutamine synthetase
Unigene0001286	2.023367689	asp/Glu/Hydantoin racemase family protein
Unigene0001287	2.907125103	Nitrous-oxide reductase, nosZ
Unigene0001289	1.451632903	Aspartate-semialdehyde dehydrogenase
Unigene0001292	1.928155089	Acetylpolyamine aminohydrolase
Unigene0001295	1.692662315	P-type conjugative transfer protein VirB9
Unigene0001297	1.452663817	Agmatinase
Unigene0001298	1.668907305	Hypothetical protein
Unigene0001299	1.497491211	LysR family transcriptional regulator
Unigene0001302	3.568997974	Hemolysin-type calcium-binding repeat-containing protein
Unigene0001304	1.172948721	Nicotinamide N-methyase
Unigene0001317	1.63964186	2-oxoglutarate dehydrogenase E1 component
Unigene0001318	1.106901378	Oxidoreductase
Unigene0001320	1.328699714	2-aminoethylphosphonate--pyruvate transaminase PhnW
Unigene0001322	2.169169802	Glycerol-3-phosphate dehydrogenase
Unigene0001326	1.935219372	Homogentisate 1,2-dioxygenase
Unigene0001327	2.198797254	Dihydroorotate dehydrogenase
Unigene0001335	3.306627655	Sodium-translocating pyrophosphatase
Unigene0001341	1.751191268	Nucleoside hydrolase
Unigene0001343	1.230924223	Aldehyde dehydrogenase
Unigene0001347	2.367203007	ABC transporter substrate-binding protein
Unigene0001348	1.567623993	Membrane protein
Unigene0001354	1.971730785	ATP-binding protein
Unigene0001356	1.019803666	2-deoxy-D-gluconate 3-dehydrogenase
Unigene0001360	1.294529383	Enolase
Unigene0001361	2.311695025	Beta-carotene 15,15′-monooxygenase
Unigene0001362	1.451025646	SfnB family sulfur acquisition oxidoreductase
Unigene0001363	1.336644389	5′-methylthioadenosine/S-adenosylhomocysteine nucleosidase, partial
Unigene0001365	1.513559929	Hypothetical protein
Unigene0001366	1.732383849	GCN5-like N-acetyltransferase
Unigene0001367	1.940024857	Site-specific DNA recombinase
Unigene0001369	1.15858667	raqprd family integrative conjugative element protein
Unigene0001370	1.532386261	Dienelactone hydrolase
Unigene0001372	2.025908354	Plasmid partitioning protein RepA
Unigene0001373	2.481503478	Spermidine/putrescine ABC transporter substrate-binding protein
Unigene0001379	2.192481478	Quinone oxidoreductase, type IV
Unigene0001380	1.085302952	Replicase family domain-containing protein
Unigene0001381	1.290299992	FCD domain-containing protein
Unigene0001382	2.730840536	GntR family transcriptional regulator
Unigene0001383	2.453573298	Transcriptional regulator
Unigene0001384	1.686707735	Tryptophan--tRNA ligase
Unigene0001386	1.345297274	Transcriptional regulator
Unigene0001388	2.503516358	Hypothetical protein
Unigene0001389	1.276909807	Oligoendopeptidase F
Unigene0001392	2.349931945	AraC-type DNA-binding protein
Unigene0001393	3.857716525	Hypothetical protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0001394	2.023027877	Hypothetical protein
Unigene0001395	1.304669861	IMP dehydrogenase
Unigene0001396	1.189153796	MFS transporter
Unigene0001403	1.779373012	PcfJ-like protein
Unigene0001404	1.995307069	Aminotransferase
Unigene0001405	1.75897915	Flagellar biosynthesis protein FlhB
Unigene0001406	2.486154722	YicC family protein
Unigene0001407	2.827905737	Enoyl-CoA hydratase
Unigene0001408	1.123924435	Diaminopimelate decarboxylase
Unigene0001413	1.54152806	Protease inhibitor Inh
Unigene0001416	1.121122913	Mannose-1-phosphate guanyltransferase
Unigene0001419	3.432335989	Transposase
Unigene0001420	2.084206527	Molecular chaperone DnaJ
Unigene0001421	1.730275377	GntR family transcriptional regulator
Unigene0001425	2.194552537	LysR family transcriptional regulator
Unigene0001431	1.565982151	Branched chain amino acid aminotransferase
Unigene0001433	1.758561408	Relaxase
Unigene0001434	2.233453488	Hypothetical protein
Unigene0001436	3.036876132	Signal transduction histidine kinase
Unigene0001439	2.324179382	Deoxycytidylate deaminase
Unigene0001440	3.419241898	Hypothetical protein
Unigene0001444	1.362407632	Transcriptional regulator, MerR family
Unigene0001446	2.262667029	Methylase
Unigene0001447	2.496101021	GntR family transcriptional regulator, partial
Unigene0001448	1.814950095	FMNH2-dependent monooxygenase
Unigene0001453	2.750805505	ABC transporter permease
Unigene0001454	3.065636775	MFS transporter
Unigene0001457	1.125409056	Glutathione S-transferase
Unigene0001460	1.102074925	Proline racemase
Unigene0001462	1.749113753	AAA domain-containing protein
Unigene0001466	1.362487016	WGR domain-containing protein
Unigene0001468	1.253429402	Cobalt ABC transporter ATP-binding protein
Unigene0001471	2.56645599	1-aminocyclopropane-1-carboxylate deaminase
Unigene0001472	1.168146099	Methionyl-tRNA formyltransferase
Unigene0001473	1.680598819	Phosphoesterase
Unigene0001474	2.832544936	Replication initiation protein RepC
Unigene0001476	1.11151576	Hydrolase
Unigene0001477	1.240229976	Bacterial regulatory s, luxR family protein
Unigene0001478	3.097546926	Acetyltransferase
Unigene0001482	2.239289096	Thioesterase
Unigene0001483	1.098086319	Purine ribonucleoside efflux pump NepI
Unigene0001485	1.494178847	SAM-dependent methyltransferase
Unigene0001489	1.135641186	N-methylproline demethylase
Unigene0001490	3.339942686	Transposase
Unigene0001491	4.11949817	Membrane protein
Unigene0001493	1.289163206	Lytic transglycosylase catalytic
Unigene0001494	1.365240917	Membrane protein
Unigene0001496	1.285613765	Hypothetical protein
Unigene0001499	1.839935697	GntR family transcriptional regulator
Unigene0001504	1.042365324	Bacterial regulatory s, gntR family protein
Unigene0001505	1.268250472	DNA cytosine methyltransferase

Unigene0001507	3.661658303	Cell wall-associated hydrolase
Unigene0001511	1.619355391	Agmatinase
Unigene0001512	2.923109677	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase
Unigene0001518	1.182551158	Relaxase
Unigene0001520	3.102052541	Bifunctional diguanylate cyclase/phosphodiesterase
Unigene0001521	1.141663948	Glutathione synthase
Unigene0001523	1.548340153	GntR family transcriptional regulator
Unigene0001533	1.4953135	Hypothetical protein
Unigene0001539	2.767105898	Hypothetical protein
Unigene0001540	2.521598079	Polysaccharide inhibition protein
Unigene0001543	1.153555061	Transcriptional regulator BetI
Unigene0001544	2.013492767	2′-deoxycytidine 5′-triphosphate deaminase
Unigene0001545	3.284518257	AMP-dependent synthetase
Unigene0001546	1.756590654	Pilus assembly protein
Unigene0001551	2.512053015	Transposase
Unigene0001553	13.64746967	Hypothetical protein
Unigene0001554	2.576829037	Amino acid ABC transporter substrate-binding protein
Unigene0001557	1.618963038	Acyltransferase
Unigene0001560	1.595911657	cys-tRNA(pro)/cys-tRNA(cys) deacylase
Unigene0001561	2.439480226	Nodulation protein NodT
Unigene0001562	2.240368813	Nodulation protein NodT
Unigene0001563	2.308153521	OsmC/Ohr family protein
Unigene0001564	1.17246521	AsnC family transcriptional regulator
Unigene0001565	1.903560763	Conjugal transfer protein TraG
Unigene0001568	2.541171135	Hypothetical protein
Unigene0001573	1.399261133	ABC transporter family protein
Unigene0001574	1.323968701	Short-chain dehydrogenase
Unigene0001575	1.700561988	Two-component system response regulator
Unigene0001579	1.625011133	RutC family protein
Unigene0001586	1.878241322	Response regulator
Unigene0001587	1.971830088	Hypothetical protein
Unigene0001598	2.125974886	ABC transporter ATP-binding protein
Unigene0001599	1.544834721	Aminotransferase DegT
Unigene0001600	1.803081874	Hybrid sensor histidine kinase/response regulator
Unigene0001603	1.113480853	Site-specific DNA-methyltransferase
Unigene0001604	3.200754876	Cyanate transporter
Unigene0001606	5.007057892	Transcriptional regulator TonB family
Unigene0001608	2.185637172	Carbohydrate-binding protein
Unigene0001609	1.423652421	Permease
Unigene0001613	2.341685702	Copper-translocating P-type ATPase
Unigene0001614	1.282133743	AAA-like domain protein
Unigene0001617	1.157338087	Glyoxalase
Unigene0001618	2.00835539	Two-component sensor histidine kinase
Unigene0001619	2.287065442	Two-component sensor histidine kinase
Unigene0001620	4.600334728	Flagellar motor switch protein FliM
Unigene0001621	1.406773158	Terminase
Unigene0001622	2.394298248	Aspartate aminotransferase
Unigene0001623	1.392924822	Pseudouridylate synthase
Unigene0001624	2.620867757	ABC transporter permease
Unigene0001625	2.616240003	ABC transporter permease
Unigene0001626	1.423216355	Cellulose biosynthesis protein BcsN
Unigene0001628	1.314698241	Aconitate hydratase 1
Unigene0001629	2.678880992	Glutamine synthetase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0001630	1.679370267	4-hydroxy-2-oxo-heptane-1,7-dioate aldolase HpcH
Unigene0001631	1.375355192	Gamma-aminobutyraldehyde dehydrogenase
Unigene0001634	1.434718377	Hypothetical protein
Unigene0001635	1.053094448	Lytic transglycosylase
Unigene0001636	1.530948068	GGDEF-domain containing protein
Unigene0001644	2.904596306	Diguanylate cyclase
Unigene0001645	1.790643865	Flavin reductase
Unigene0001647	1.766555418	Sugar ABC transporter substrate-binding protein
Unigene0001650	3.321290147	Thiolase
Unigene0001656	2.394244317	Competence protein ComM
Unigene0001657	1.67634013	Desaturase
Unigene0001659	1.801686001	Uracil phosphoribosyltransferase
Unigene0001661	1.353038592	Membrane-bound lysozyme-inhibitor of c-type lysozyme family protein
Unigene0001662	1.558783863	Cold shock protein
Unigene0001668	1.39005013	Methyltransferase-like protein KIAA1627
Unigene0001669	1.42087115	Monovalent cation/H^+ antiporter subunit A
Unigene0001672	6.191220103	Adenosylmethionine--8-amino-7-oxononanoate transaminase
Unigene0001675	4.031008978	Conserved protein
Unigene0001676	3.611158992	Uncharacterized protein
Unigene0001679	1.69534261	DUF1173 domain-containing protein
Unigene0001687	1.566306679	LysR family transcriptional regulator
Unigene0001688	4.429072812	ABC transporter substrate-binding protein
Unigene0001691	7.681924484	Oxygen-independent coproporphyrinogen III oxidase
Unigene0001693	1.193058125	LysR family transcriptional regulator
Unigene0001694	1.876595136	Branched-chain amino acid ABC transporter permease
Unigene0001697	1.245075307	TRANSPOSASE
Unigene0001698	3.09099269	Alanine dehydrogenase
Unigene0001699	2.311631498	Alanine dehydrogenase
Unigene0001701	4.360841665	Branched chain amino acid ABC transporter substrate-binding protein
Unigene0001702	1.691697477	Cytochrome C peroxidase
Unigene0001703	1.468435902	Thioredoxin reductase TrxB
Unigene0001704	2.963096538	Ferrochelatase
Unigene0001706	4.314821462	Amino acid ABC transporter substrate-binding protein
Unigene0001707	1.197486942	MFS transporter
Unigene0001708	2.445110797	Cytosine deaminase
Unigene0001711	1.13839042	Antitoxin of toxin-antitoxin stability system
Unigene0001713	1.020208258	DUF3011 domain-containing protein
Unigene0001722	1.186948814	Anion permease
Unigene0001725	1.156914174	eamA-like transporter family protein
Unigene0001727	1.630884913	30S ribosomal protein S4
Unigene0001730	2.263081178	Transcriptional regulator
Unigene0001733	2.056974823	FAD-dependent oxidoreductase
Unigene0001739	1.38606685	GntR family transcriptional regulator
Unigene0001740	3.942775893	ABC transporter substrate-binding protein
Unigene0001744	1.306833612	Spermidine synthase
Unigene0001746	2.48085748	MarC family transcriptional regulator
Unigene0001748	1.036101777	Glutathione-dependent formaldehyde-activating GFA
Unigene0001753	1.541685227	Heme biosynthesis protein HemY
Unigene0001754	3.150584278	Chromosome partitioning protein
Unigene0001757	2.036232442	Membrane protein
Unigene0001759	1.098600959	Endonuclease, Uma2 family (restriction endonuclease fold)

Unigene0001764	2.6195107	ABC transporter substrate-binding protein
Unigene0001768	1.230166424	Ornithine carbamoyltransferase
Unigene0001769	1.31287195	Acetylornithine transaminase
Unigene0001770	1.633180357	Diguanylate cyclase domain protein
Unigene0001782	1.662631324	Hypothetical protein
Unigene0001783	4.775542377	Hypothetical protein
Unigene0001787	1.328618218	Benzoate transporter family protein
Unigene0001790	1.794923777	L-dehydroascorbate transporter large permease subunit
Unigene0001794	1.28873391	ABC transporter permease
Unigene0001797	2.039465143	Branched chain amino acid ABC transporter substrate-binding protein
Unigene0001798	1.049814316	Ornithine cyclodeaminase/mu-crystallin
Unigene0001800	3.930114442	Chemotaxis protein
Unigene0001802	3.691840775	EAL domain-containing protein
Unigene0001804	1.407917506	Peptide ABC transporter
Unigene0001805	1.742354301	Peptidase M48 family protein
Unigene0001807	1.486615544	LysR family transcriptional regulator
Unigene0001810	4.784366801	Flagellar motor protein MotB
Unigene0001811	1.251250476	Type IV secretion system protein VirB10
Unigene0001812	1.43987951	Adenosylcobinamide-GDP ribazoletransferase
Unigene0001813	2.000897245	Methyltransferase
Unigene0001815	1.299146575	Acetylornithine deacetylase
Unigene0001817	2.810372789	Glyoxalase
Unigene0001822	4.125614453	Xanthine uracil permease
Unigene0001824	1.657405517	Phosphoglycerate dehydrogenase
Unigene0001827	2.178114703	Transcriptional regulator, LysR family
Unigene0001828	1.022883383	Hypothetical conserved protein
Unigene0001829	2.161753758	Amino acid ABC transporter substrate-binding protein
Unigene0001832	2.108031145	Amino acid ABC transporter substrate-binding protein
Unigene0001833	1.756679708	Long-chain fatty acid transporter
Unigene0001837	1.7997197	Hypothetical protein
Unigene0001841	1.945623416	Phosphonate ABC transporter substrate-binding protein
Unigene0001844	1.065877056	Methyltransferase
Unigene0001846	1.85228507	Uncharacterized protein
Unigene0001847	1.34662138	GLE1 domain-containing protein
Unigene0001850	1.467724775	MFS sugar transporter
Unigene0001851	1.278428799	Diacylglycerol kinase
Unigene0001852	1.060142729	Transcriptional regulator, MerR family
Unigene0001856	1.045994543	Anti-sigma factor
Unigene0001857	3.091137233	GcrA cell cycle regulator
Unigene0001861	5.748007077	Type VI secretion protein
Unigene0001864	1.705214598	Choline-sulfatase
Unigene0001869	1.652464122	PAS domain-containing sensor histidine kinase
Unigene0001871	2.11027551	MFS transporter
Unigene0001872	1.958588908	AfpU protein
Unigene0001874	1.951398099	PilZ domain-containing protein
Unigene0001876	3.776563668	Plasmid partitioning protein RepA
Unigene0001877	2.477571631	Hypothetical protein
Unigene0001879	1.461132481	Glutamine amidotransferase
Unigene0001880	4.005208391	Hypothetical protein
Unigene0001881	2.044571492	Binding-protein-dependent transport system inner membrane component
Unigene0001882	1.390972061	Hypothetical protein
Unigene0001884	5.029093898	Chromosome partitioning protein ParA
Unigene0001885	1.567213769	GGDEF-domain containing protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0001887	1.521745723	Mercuric reductase
Unigene0001888	1.428274568	Heme exporter protein B
Unigene0001889	1.469840106	Potassium transporter
Unigene0001892	1.414983826	Hypothetical protein
Unigene0001896	1.631613287	TetR family transcriptional regulator
Unigene0001899	1.337175192	ATP-binding protein
Unigene0001905	2.187636433	Lysine transporter LysE
Unigene0001906	5.874666531	Glycosyltransferase
Unigene0001913	1.822012042	GntR family transcriptional regulator
Unigene0001915	2.613266658	LuxR family transcriptional regulator
Unigene0001916	1.35222044	Histidine utilization repressor
Unigene0001917	1.241311182	Hypothetical protein
Unigene0001918	6.717090768	PG1 protein, homology to Homo sapiens
Unigene0001920	2.605623338	SNF2-related protein
Unigene0001921	2.861819387	Conjugal transfer protein TraG
Unigene0001922	1.492929621	Peptidase S41
Unigene0001924	1.175900236	Acyl-CoA dehydrogenase
Unigene0001925	3.522788808	Sugar ABC transporter substrate-binding protein
Unigene0001930	1.181093908	Glycine/betaine ABC transporter permease
Unigene0001933	1.486892103	Membrane protein
Unigene0001942	2.183561663	Tiorf63 protein
Unigene0001948	2.061601992	YecA family protein
Unigene0001949	3.48462581	DEAD/DEAH box helicase
Unigene0001951	1.845420752	TetR family transcriptional regulator, partial
Unigene0001952	1.166444289	Cytochrome-c oxidase, cbb3-type subunit I
Unigene0001954	2.194785746	Twitching motility protein PilT
Unigene0001955	2.49609912	Prevent-host-death protein
Unigene0001966	2.202186167	DDE transposase
Unigene0001968	3.582837303	Hypothetical protein
Unigene0001972	1.571545584	Polyribonucleotide nucleotidyltransferase
Unigene0001973	1.611428731	IS110 family transposase
Unigene0001976	1.36538721	DNA topoisomerase 4 subunit A
Unigene0001977	1.687629969	Lactate dehydrogenase
Unigene0001982	4.545476848	Flagellar M-ring protein FliF
Unigene0001988	1.816173674	Methylmalonate-semialdehyde dehydrogenase
Unigene0001989	2.212534419	Transcriptional regulator
Unigene0001990	1.701370822	Hypothetical protein
Unigene0001994	2.662034259	Cytosine/purines uracil thiamine allantoin permease
Unigene0001995	4.196007187	Aldehyde dehydrogenase
Unigene0001997	2.892635332	Oxidoreductase
Unigene0001998	3.05454757	AraC family transcriptional regulator
Unigene0001999	1.288536921	Xaa-Pro aminopeptidase
Unigene0002005	1.908487048	TetR family transcriptional regulator
Unigene0002006	1.246017499	AAA family ATPase
Unigene0002008	2.063112759	mu-like prophage FluMu gp41 family protein
Unigene0002009	3.377376469	Dihydroxyacetone kinase, L subunit
Unigene0002010	1.371341568	2-polyprenyl-6-methoxyphenol hydroxylase
Unigene0002011	2.208324029	Hypothetical protein
Unigene0002012	1.257724986	Aldehyde oxidase
Unigene0002014	1.849915933	Hypothetical protein
Unigene0002015	1.468798189	Hypothetical protein

Unigene0002017	1.580552734	2-hydroxymuconic semialdehyde hydrolase
Unigene0002019	1.360966992	MFS transporter
Unigene0002021	1.697555651	Aminotransferase
Unigene0002022	1.206275049	MFS transporter
Unigene0002025	1.631712361	Metallophosphatase
Unigene0002026	2.323058076	ABC transporter ATP-binding protein
Unigene0002027	1.105021213	2-deoxy-D-gluconate 3-dehydrogenase
Unigene0002029	2.128934232	MBL fold metallo-hydrolase
Unigene0002030	1.937867741	Triose-phosphate isomerase
Unigene0002032	1.479114066	EamA family transporter
Unigene0002033	1.184637945	D-amino-acid oxidase
Unigene0002040	1.579390376	Iron(III) transport system substrate-binding protein
Unigene0002043	2.544338999	ATPase
Unigene0002044	1.05351792	Nitrate reductase catalytic subunit
Unigene0002045	1.095047689	Transcriptional regulator
Unigene0002046	1.663973722	Agmatinase
Unigene0002050	1.523837883	X-Pro aminopeptidase
Unigene0002053	1.493078497	Nicotinate phosphoribosyltransferase
Unigene0002056	1.275092993	Polysaccharide biosynthesis protein GumN
Unigene0002057	3.149163386	Quinate dehydrogenase
Unigene0002059	1.877743897	Antirestriction protein ArdC
Unigene0002060	1.534582909	Heparinase
Unigene0002061	1.015910531	Peptidase M14
Unigene0002063	1.197746694	Trifunctional transcriptional regulator/proline dehydrogenase/L-glutamate gamma-semialdehyde dehydrogenase
Unigene0002065	2.642834552	Trehalose/maltose-binding protein MalE
Unigene0002068	1.886078589	Acetylornithine transaminase
Unigene0002070	2.772972376	Glutamine synthetase
Unigene0002071	2.109964241	ABC transporter
Unigene0002073	1.14633484	Aldehyde dehydrogenase
Unigene0002076	1.493791738	Sugar ABC transporter ATP-binding protein
Unigene0002077	1.162275562	Galactonate dehydratase
Unigene0002081	2.56976248	Hypothetical protein
Unigene0002082	2.471748739	GGDEF domain-containing protein
Unigene0002085	5.898595007	Hemoglobin/transferrin/lactoferrin receptor protein
Unigene0002086	1.475473275	Fe^{3+}/spermidine/putrescine ABC transporter ATP-binding protein
Unigene0002090	4.503184569	Hypothetical protein
Unigene0002092	1.536357636	Cysteine desulfurase
Unigene0002093	1.96338692	Hypothetical protein
Unigene0002097	2.731941485	DNA-binding protein
Unigene0002099	1.380887492	Hypothetical protein
Unigene0002100	1.428801997	Glutamine synthetase 1
Unigene0002101	1.561620904	Aldo/keto reductase
Unigene0002102	1.641063572	Phosphate ABC transporter ATP-binding protein
Unigene0002103	2.58972028	Aspartate aminotransferase family protein
Unigene0002105	1.286899409	MOSC domain-containing protein
Unigene0002108	1.443240279	GntR family transcriptional regulator
Unigene0002111	1.628395676	Cell division protein ZapA
Unigene0002114	1.134375299	Endonuclease III
Unigene0002115	2.772828942	Hypothetical protein
Unigene0002116	1.963003945	Phosphoserine phosphatase SerB
Unigene0002122	1.084211414	Coproporphyrinogen III oxidase
Unigene0002123	1.417083118	ABC transporter ATP-binding protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0002125	2.497638484	PAS domain-containing sensor histidine kinase
Unigene0002128	1.023855731	FAD-dependent oxidoreductase
Unigene0002132	1.130961331	Cytochrome
Unigene0002133	3.064435029	Sugar ABC transporter
Unigene0002135	1.505660202	2-ketoarginine decarboxylase
Unigene0002137	2.331571249	Peptidase M17
Unigene0002139	4.807990085	Hypothetical protein
Unigene0002140	1.02711282	LysR family transcriptional regulator
Unigene0002145	1.366025671	glucan 1,4-alpha-glucosidase
Unigene0002148	2.177739187	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
Unigene0002149	2.260427342	Transcriptional regulator
Unigene0002150	2.674122977	ABC transporter substrate-binding protein
Unigene0002152	1.363770345	Beta-aryl ether-cleaving protein
Unigene0002154	1.480265167	Segregation and condensation protein B
Unigene0002155	1.424287803	HTH domain protein
Unigene0002156	1.705074965	Aminotransferase
Unigene0002157	1.931177965	Hypothetical protein
Unigene0002160	3.192459118	ABC-type sugar transport system periplasmic component
Unigene0002161	2.498060713	Cro/Cl family transcriptional regulator
Unigene0002162	3.358659955	Transposase IS3/IS911 family protein
Unigene0002167	1.614084365	Aspartyl/glutamyl-tRNA amidotransferase subunit A
Unigene0002168	1.052328828	Aspartyl/glutamyl-tRNA amidotransferase subunit A
Unigene0002169	1.275589239	Protein of uncharacterized function
Unigene0002171	2.978809356	Exported protein
Unigene0002173	1.921835916	Cation transporter
Unigene0002176	2.267362391	Thiol oxidoreductase
Unigene0002177	1.347957612	Glutamine synthetase
Unigene0002184	3.202332691	Aspartate aminotransferase family protein
Unigene0002186	2.607975999	Ribose ABC transporter substrate-binding protein
Unigene0002188	2.191893055	MltA-interacting MipA family protein
Unigene0002189	1.159592664	INTEGRATING CONJUGATIVE ELEMENT PARB
Unigene0002194	2.551457523	TRANSPOSASE
Unigene0002195	1.031371288	Septum formation protein Maf
Unigene0002198	1.807984751	S-adenosylmethionine uptake transporter
Unigene0002200	2.879758146	Glycoside hydrolase family 5
Unigene0002201	1.523281272	DUF1127 domain-containing protein
Unigene0002204	1.127052091	Cytosine/adenosine deaminase
Unigene0002205	2.601706977	Transposase
Unigene0002206	1.220050434	3-phosphoshikimate 1-carboxyvinyltransferase AroA
Unigene0002208	1.144341853	GTP pyrophosphokinase
Unigene0002210	4.277418652	Xylose isomerase
Unigene0002213	2.358717586	Aldehyde dehydrogenase PuuC
Unigene0002216	1.075526961	GGDEF domain-containing protein
Unigene0002218	1.493146863	Adenine phosphoribosyltransferase
Unigene0002221	1.337493916	CTP synthase
Unigene0002222	1.71011958	Bacteriocin-protection, YdeI/OmpD-Associated family protein
Unigene0002223	2.213187177	Aminoacyl-tRNA hydrolase
Unigene0002225	1.022730728	Sugar ABC transporter substrate-binding protein
Unigene0002227	1.293908168	LacI family transcriptional regulator
Unigene0002229	3.271072242	ATP F0F1 synthase subunit alpha
Unigene0002233	1.11072029	DNA mismatch repair protein MutS

Unigene0002234	6.767650848	Acyl-CoA dehydrogenase
Unigene0002237	2.093121613	Acetyl-CoA hydrolase
Unigene0002240	1.033934102	Transposase
Unigene0002243	3.425968967	Flagellar biosynthetic protein FliP
Unigene0002244	2.475525285	NAD(+) synthase
Unigene0002247	1.351253252	MFS transporter
Unigene0002248	1.743896362	DDE transposase
Unigene0002254	1.61302138	Methyltransferase
Unigene0002256	2.387335553	LuxR family transcriptional regulator
Unigene0002257	1.264518826	YggS family pyridoxal phosphate enzyme
Unigene0002259	3.3582117	UDP-galactopyranose mutase
Unigene0002260	1.350143714	Argininosuccinate lyase
Unigene0002265	2.530663823	HxlR family transcriptional regulator
Unigene0002269	2.190569228	LacI family transcriptional regulator
Unigene0002270	1.172584942	Alkaline phosphatase
Unigene0002282	1.753303181	Transposase, Mutator family
Unigene0002285	2.290707247	[acyl-carrier-protein] S-malonyltransferase
Unigene0002290	2.133392777	GguC protein
Unigene0002292	2.267580363	IgA FC receptor
Unigene0002294	4.027586591	Putrescine/spermidine ABC transporter substrate-binding protein
Unigene0002295	2.429121605	GGDEF domain-containing protein
Unigene0002300	2.142033597	Transporter
Unigene0002302	1.462513335	Cupin
Unigene0002306	1.658529127	Antirepressor
Unigene0002308	2.079098489	Membrane protein
Unigene0002309	1.859642094	Arabinose transporter
Unigene0002311	1.385504289	Hypothetical protein
Unigene0002315	2.162642321	Holliday junction resolvase RuvX
Unigene0002322	1.044140038	Membrane protein
Unigene0002330	1.603004472	Glycerol-3-phosphate acyltransferase
Unigene0002334	2.328736856	Oxidoreductase
Unigene0002335	2.310312775	ABC transporter permease
Unigene0002337	1.265707752	ArsR family transcriptional regulator
Unigene0002338	2.074898763	Transcriptional regulator
Unigene0002339	1.700240634	Hypothetical protein
Unigene0002341	1.251236778	Lysophospholipase
Unigene0002342	1.258422714	LysR family transcriptional regulator
Unigene0002343	1.403846278	DUF2793 domain-containing protein
Unigene0002345	2.481381925	Hypothetical protein
Unigene0002348	1.787726748	Sugar ABC transporter ATP-binding protein
Unigene0002351	3.842474027	Lipoprotein
Unigene0002352	1.753448436	4-hydroxybenzoate polyprenyltransferase
Unigene0002353	5.289171586	Hypothetical protein
Unigene0002354	3.099149659	Hypothetical protein
Unigene0002356	2.835356208	Transposase
Unigene0002357	2.028214228	Conjugal transfer protein TraA
Unigene0002360	6.436936633	Hypothetical protein
Unigene0002363	2.089276582	VirB4 family type IV secretion/conjugal transfer ATPase
Unigene0002365	1.717540273	Hypothetical protein
Unigene0002366	1.766614313	Mannose-6-phosphate isomerase
Unigene0002367	2.512335468	AMP-dependent synthetase
Unigene0002369	3.933157424	TRAP dicarboxylate transporter-DctP subunit
Unigene0002370	1.32973771	Choline dehydrogenase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0002371	1.354238185	DNA invertase
Unigene0002373	2.11686544	Cell wall-associated hydrolase
Unigene0002374	7.28162594	Transposase
Unigene0002378	2.586287121	Spermidine/putrescine-binding periplasmic protein PotD
Unigene0002381	1.804619632	Plasmid partitioning protein
Unigene0002383	1.508931163	Hypothetical protein
Unigene0002387	5.223931557	Lytic transglycosylase catalytic
Unigene0002388	1.096017422	Oxidoreductase
Unigene0002389	1.07791422	Arginase
Unigene0002390	1.531179763	Hypothetical protein
Unigene0002391	2.769131629	MFS transporter
Unigene0002392	1.318282127	Glycine dehydrogenase (aminomethyl-transferring)
Unigene0002393	1.714237224	Crp/Fnr family transcriptional regulator
Unigene0002394	1.154000842	NADH-ubiquinone oxidoreductase
Unigene0002396	1.150332405	L,D-transpeptidase
Unigene0002397	1.012876824	Dihydroxy-acid dehydratase
Unigene0002398	6.614817385	Peptidase
Unigene0002400	2.199647877	Membrane protein
Unigene0002401	2.110179277	DUF1625 domain-containing protein
Unigene0002403	1.73908316	Transposase
Unigene0002405	1.44916704	Glutamate synthase subunit alpha
Unigene0002409	2.458299685	Diguanylate cyclase domain protein
Unigene0002412	1.588761774	tRNA-binding protein
Unigene0002413	1.590725537	Pyrroline-5-carboxylate reductase
Unigene0002419	3.556393095	Chemotaxis protein
Unigene0002422	1.098351351	Peptidase
Unigene0002423	1.878765787	Phosphonate ABC transporter periplasmic phosphonate binding protein
Unigene0002424	1.846942996	Homocysteine methyltransferase
Unigene0002425	1.401009754	Amidohydrolase family protein
Unigene0002428	2.699163323	Branched-chain amino acid ABC transporter substrate-binding protein
Unigene0002433	1.484780232	Multifunctional 2',3′-cyclic-nucleotide 2′-phosphodiesterase/5′-nucleotidase/3′-nucleotidase
Unigene0002436	4.785583499	flagellar protein
Unigene0002437	2.822272681	CoA-binding protein
Unigene0002438	1.877876226	Thymidylate synthase
Unigene0002442	1.701902289	Cysteine synthase
Unigene0002443	1.182294498	MFS transporter
Unigene0002445	2.708700898	Dihydrodipicolinate synthase family protein
Unigene0002446	2.218032545	Capsid protein
Unigene0002450	1.138596378	Histidine utilization repressor
Unigene0002451	1.156745193	TetR family transcriptional regulator
Unigene0002454	1.899469252	Helix-turn-helix transcriptional regulator
Unigene0002455	1.202494732	Dihydroorotase
Unigene0002456	2.523389191	Replication initiation protein RepC
Unigene0002457	2.443374012	Ribonucleotide-diphosphate reductase subunit alpha
Unigene0002458	2.080935523	Ribonucleotide-diphosphate reductase subunit alpha
Unigene0002471	1.750296874	Sugar ABC transporter, permease protein
Unigene0002472	1.150406891	Membrane protein
Unigene0002473	1.307779224	Amino acid ABC transporter ATPase
Unigene0002474	1.068260917	Exodeoxyribonuclease III
Unigene0002475	2.393643264	Phage portal protein

Unigene0002478	1.875883712	Integrase family protein
Unigene0002479	1.476438685	Transcriptional regulator
Unigene0002481	1.06925288	Hypothetical protein
Unigene0002483	1.792092837	Copper-translocating P-type ATPase
Unigene0002486	1.420923282	Pyridoxine 5′-phosphate synthase PdxJ
Unigene0002493	1.53348784	Helicase subunit of the DNA excision repair complex
Unigene0002494	1.067331242	MFS transporter
Unigene0002495	1.670699707	D-ribose transporter ATP-binding protein
Unigene0002496	2.463956257	Formimidoylglutamate deiminase
Unigene0002497	1.165966154	Bcr/CflA family drug resistance efflux transporter
Unigene0002498	2.47836369	Hypothetical protein
Unigene0002500	1.068483502	Aspartate aminotransferase family protein
Unigene0002501	1.270906775	deoxyguanosinetriphosphate triphosphohydrolase
Unigene0002503	1.457139007	Phosphomannomutase
Unigene0002504	1.215235013	Hypothetical protein
Unigene0002505	1.588482973	Uncharacterized membrane protein HdeD, DUF308 family
Unigene0002506	3.436399179	Plasmid partitioning protein
Unigene0002508	1.334388497	GTP-binding protein TypA/BipA
Unigene0002514	1.646472774	Sugar phosphate isomerase
Unigene0002515	1.724241337	Membrane protein
Unigene0002519	1.422029959	ATP-binding protein
Unigene0002520	1.772931296	MFS transporter
Unigene0002524	1.053146931	lipo-like protein
Unigene0002529	8.546199162	Nitrite reductase, copper-containing
Unigene0002530	1.300607277	Aspartate aminotransferase AspC
Unigene0002531	1.610318391	Carbonate dehydratase
Unigene0002536	2.008351173	Threonine dehydrogenase
Unigene0002538	1.459190478	Sarcosine oxidase subunit alpha family protein
Unigene0002539	2.177684839	Rhamnose ABC transporter substrate-binding protein
Unigene0002543	1.166785793	MFS transporter
Unigene0002547	3.189152674	Plasmid partitioning protein
Unigene0002548	3.318585111	Histidinol-phosphate aminotransferase 1
Unigene0002549	3.378337086	OHCU decarboxylase
Unigene0002550	3.997070921	OHCU decarboxylase
Unigene0002553	1.103588993	MurR/RpiR family transcriptional regulator
Unigene0002556	1.484328312	Myo-inositol 2-dehydrogenase
Unigene0002557	2.592889196	Conjugal transfer protein TraA
Unigene0002558	1.033374564	Sugar kinase ribokinase family
Unigene0002561	2.739048909	Hypothetical protein
Unigene0002562	1.565440902	Uncharacterized protein
Unigene0002567	1.593459282	AAA family ATPase
Unigene0002568	1.215201419	Hypothetical protein
Unigene0002569	1.361523146	Ornithine cyclodeaminase
Unigene0002570	1.08607424	DUF159 family protein
Unigene0002571	2.391631773	Bifunctional hydroxymethylpyrimidine kinase/phosphomethylpyrimidine kinase
Unigene0002572	2.428004632	Hypothetical protein
Unigene0002573	1.880525541	ABC transporter permease
Unigene0002579	2.959373492	Spermidine/putrescine ABC transporter
Unigene0002581	3.346240878	Sugar ABC transporter substrate-binding protein
Unigene0002583	1.221064103	Site-specific recombinase XerD
Unigene0002589	4.777770516	Cell wall-associated hydrolase
Unigene0002590	1.848990574	SAM-dependent methyltransferase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0002593	1.525916803	Hybrid sensor histidine kinase/response regulator
Unigene0002595	2.783681461	Diguanylate cyclase
Unigene0002596	2.804691117	LacI family transcriptional regulator
Unigene0002599	2.218503523	Phosphoglycolate phosphatase
Unigene0002600	1.681286157	DNA protecting protein DprA
Unigene0002601	1.814696034	Amino acid ABC transporter substrate-binding protein
Unigene0002602	2.919812807	Cytosine-specific methyltransferase
Unigene0002608	1.791671845	Integrating conjugative element protein
Unigene0002610	2.377454578	ABC transporter permease
Unigene0002611	1.070273625	Aspartate dehydrogenase
Unigene0002613	1.55259672	Beta-ketoacyl-[acyl-carrier-protein] synthase II
Unigene0002614	1.015190908	Chromosomal replication initiator protein DnaA
Unigene0002615	2.242256846	Carbamoyl phosphate synthase small subunit
Unigene0002617	2.010440143	Ti-type conjugative transfer system protein TraG
Unigene0002618	1.022717737	Mobilization protein
Unigene0002621	1.620818269	MFS transporter
Unigene0002622	1.191065455	Lactoylglutathione lyase
Unigene0002624	1.035590523	DNA-directed RNA polymerase sigma-70 factor
Unigene0002625	1.147490637	ADP-ribose pyrophosphatase
Unigene0002626	1.492372813	MurR/RpiR family transcriptional regulator
Unigene0002627	1.192419685	LysR family transcriptional regulator
Unigene0002629	1.062767435	MBL fold metallo-hydrolase
Unigene0002632	3.747597502	4-hydroxyphenylacetate 3-hydroxylase
Unigene0002636	1.611798452	Membrane protein
Unigene0002640	1.425753021	ArdC gene in pSa-like protein
Unigene0002641	1.966166157	Xylulokinase
Unigene0002644	1.312346494	GntR family transcriptional regulator
Unigene0002647	9.74918789	Hypothetical protein
Unigene0002648	2.042289693	SNF2-related protein
Unigene0002649	2.769054083	Helix-turn-helix transcriptional regulator
Unigene0002651	2.961336476	Transcriptional regulator
Unigene0002652	2.728433011	Transcriptional regulator
Unigene0002654	2.781918349	Cytoplasmic protein
Unigene0002655	2.611134668	Nitrite reductase, copper-containing
Unigene0002656	1.414136606	Alpha/beta hydrolase
Unigene0002661	1.793347371	Pyrimidine-specific ribonucleoside hydrolase RihA
Unigene0002662	2.616600634	50S ribosomal protein L25/general stress protein Ctc
Unigene0002663	1.526841822	Chemotaxis protein
Unigene0002667	1.931165494	Sugar ABC transporter substrate-binding protein
Unigene0002669	1.493235754	ABC transporter permease
Unigene0002670	3.004677746	MarR family transcriptional regulator
Unigene0002674	4.291798841	Chemotaxis response regulator protein-glutamate methylesterase 2
Unigene0002675	1.498872573	Acyl carrier protein
Unigene0002680	1.337546022	Fumarylacetoacetate hydrolase
Unigene0002681	1.295485607	Peptide ABC transporter ATP-binding protein
Unigene0002682	1.142215878	Sulfate transporter subunit
Unigene0002685	6.522019644	Transglutaminase
Unigene0002686	1.933112185	Amidohydrolase
Unigene0002687	1.127624247	Hypothetical protein
Unigene0002691	2.103532952	Carbohydrate kinase
Unigene0002692	1.693265242	Phasin

Unigene0002695	2.131162269	Single-stranded DNA-binding protein
Unigene0002698	2.24435623	Peptidoglycan transglycosylase
Unigene0002704	1.010361333	Hypothetical protein
Unigene0002706	1.428445407	Conjugal transfer protein
Unigene0002707	3.384436628	ABC transporter permease
Unigene0002708	1.470190432	Ribulokinase
Unigene0002709	1.542874702	ErfK/YbiS/YcfS/YnhG
Unigene0002720	3.289693215	DNA-binding protein HRm
Unigene0002730	1.344376346	Caspase domain protein
Unigene0002734	1.239548367	Opacity porin family protein
Unigene0002735	1.601275563	Primase 2
Unigene0002740	2.017269348	Plasmid partitioning protein
Unigene0002742	2.795498596	DUF1419 domain-containing protein
Unigene0002743	1.467508302	Toprim-like protein
Unigene0002745	1.271039904	Glycerophosphodiester phosphodiesterase
Unigene0002748	1.222576138	LysR family transcriptional regulator
Unigene0002750	2.10914314	Iron import ATP-binding/permease protein IrtB
Unigene0002751	1.226373264	FMN-dependent NADH-azoreductase AzoR
Unigene0002753	2.563744938	ABC transporter
Unigene0002756	1.42305491	Amidase family protein
Unigene0002757	1.488887856	Cystathionine beta-lyase
Unigene0002760	1.531908507	Short-chain dehydrogenase/reductase
Unigene0002761	1.516358598	Bacterial regulatory s, lacI family protein
Unigene0002762	1.763806408	ATP-dependent helicase
Unigene0002763	1.110492536	NAD-dependent malic enzyme
Unigene0002764	1.492582595	Surface antigen variable number repeat-containing protein
Unigene0002765	3.198452396	Glycosyl transferase
Unigene0002769	2.280068185	Bifunctional phosphoribosylaminoimidazolecarboxamide formyltransferase/ IMP cyclohydrolase
Unigene0002773	1.536445113	50S ribosomal protein L21
Unigene0002774	1.272213585	Alcohol dehydrogenase
Unigene0002775	5.34087362	PilZ domain-containing protein
Unigene0002778	1.543236961	Glutamine ABC transporter ATP-binding protein
Unigene0002781	6.834399054	Binding-protein-dependent transport systems inner membrane component
Unigene0002787	1.652434877	Hypothetical protein
Unigene0002789	1.326436028	Outer membrane protein assembly factor BamA
Unigene0002791	2.412385085	Ribose transport system permease protein
Unigene0002794	3.035034927	Hypothetical protein
Unigene0002796	3.369076919	Flagellar biosynthesis protein FlhA
Unigene0002797	1.050929968	Glucose-6-phosphate dehydrogenase
Unigene0002798	1.350861524	ABC transporter ATP-binding protein
Unigene0002799	1.760553351	Alanine-phosphoribitol ligase
Unigene0002800	2.046302846	Alanine-phosphoribitol ligase
Unigene0002801	5.6770766	Hypothetical protein
Unigene0002802	4.996861231	Chemotaxis protein
Unigene0002803	2.065554504	23S rRNA [adenine(2030)-N(6)]-methyltransferase RlmJ
Unigene0002806	1.524182651	50S ribosomal protein L1
Unigene0002807	4.685693649	Fis family transcriptional regulator
Unigene0002811	1.105119359	Inositol monophosphatase
Unigene0002812	1.619708088	Glutaminase
Unigene0002813	1.136946334	DDE transposase
Unigene0002814	2.282156471	Flavo, family protein
Unigene0002819	2.828775583	Integrase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0002821	1.537404076	DNA-methyltransferase
Unigene0002822	1.051947411	Acyl-CoA thioester hydrolase
Unigene0002826	1.862506843	Fructose-1,6-bisphosphate aldolase
Unigene0002828	1.876536466	HAD hydrolase, IA, variant 1 family protein
Unigene0002829	1.577376271	tRNA (adenosine(37)-N6)-threonylcarbamoyltransferase complex transferase subunit TsaD
Unigene0002830	1.388713418	CopG family transcriptional regulator
Unigene0002832	2.159133214	Nuclease
Unigene0002834	1.416550438	Transcriptional regulator, GntR family
Unigene0002835	6.245666481	Transcriptional regulator, AraC family
Unigene0002836	2.258261409	Hypothetical protein
Unigene0002839	1.79964711	3-oxoacyl-ACP reductase
Unigene0002840	1.641705953	3-oxoacyl-[acyl-carrier-protein] reductase
Unigene0002845	4.318568481	Biotin biosynthesis protein BioC
Unigene0002847	1.448955341	Glycosyltransferase
Unigene0002848	3.029949849	GDP-mannose 4,6-dehydratase
Unigene0002849	3.707031456	Sel1 repeat family protein
Unigene0002850	1.41063617	30S ribosomal protein S1
Unigene0002851	1.274516848	LysR family transcriptional regulator
Unigene0002854	1.717258724	Acrylyl-CoA reductase AcuI
Unigene0002855	2.967623244	Acetolactate synthase 3 large subunit
Unigene0002858	3.047676553	Alkaline phosphatase
Unigene0002863	2.368834433	Sugar ABC transporter ATP-binding protein
Unigene0002864	2.093584712	Glycerol kinase
Unigene0002866	1.415739519	MerR family transcriptional regulator
Unigene0002868	1.80574926	LacI family transcriptional regulator
Unigene0002869	2.895262455	Transcriptional regulator
Unigene0002870	1.653358542	Amidohydrolase
Unigene0002874	3.421856918	C4-dicarboxylate transporter DctA
Unigene0002875	1.067512552	Potassium transporter Kup
Unigene0002876	1.48224024	Transcription termination factor Rho
Unigene0002886	2.287905544	1-aminocyclopropane-1-carboxylate deaminase
Unigene0002889	1.137357672	CoA-binding protein
Unigene0002891	1.9623408	Regulator of CtrA degradation
Unigene0002892	2.04530563	ABC-type amino acid transport periplasmic component
Unigene0002894	1.340761639	Cytochrome oxidase
Unigene0002899	2.361023564	Pyridoxal kinase
Unigene0002901	1.108157957	Cysteine desulfurase
Unigene0002902	1.510845074	Peptide chain release factor 3
Unigene0002908	1.856583854	Urease accessory protein
Unigene0002910	6.839193407	TonB-dependent heme/hemoglobin receptor family protein
Unigene0002911	1.34366545	Histidine--tRNA ligase
Unigene0002915	3.040087659	Hypothetical protein
Unigene0002917	2.867991042	Dihydrodipicolinate synthase family protein
Unigene0002919	1.089429517	Ammonia monooxygenase
Unigene0002920	1.179963668	Aldo/keto reductase
Unigene0002921	1.956158114	Phosphoenolpyruvate carboxykinase (ATP)
Unigene0002922	1.833286272	Acetyl-CoA acetyltransferase
Unigene0002927	1.988453201	Phage regulatory protein, rha family
Unigene0002929	1.790508867	N-methylproline demethylase
Unigene0002932	1.876144595	Replication initiation protein RepC

Unigene0002933	1.060808521	DNA primase
Unigene0002937	2.478184122	Sensory box protein
Unigene0002943	1.344358937	Cation: proton antiporter
Unigene0002944	1.620613266	Acetylornithine deacetylase
Unigene0002946	2.177962398	ATPase AAA
Unigene0002949	1.110536101	Modification methylase
Unigene0002952	2.36708635	Leucyl aminopeptidase
Unigene0002957	2.945299704	Acetate--CoA ligase
Unigene0002958	2.532799924	Hypothetical protein
Unigene0002959	2.455073337	ABC transporter substrate-binding protein
Unigene0002960	1.451027113	Antirestriction protein ArdC
Unigene0002964	1.575815196	Methyltransferase
Unigene0002966	3.698382124	Peptide ABC transporter substrate-binding protein
Unigene0002968	1.872416763	Phage tail tape measure protein
Unigene0002969	1.475307121	Hypothetical protein
Unigene0002974	2.264511666	Hypothetical protein
Unigene0002976	1.11228755	PEP-utilizing protein mobile subunit
Unigene0002978	1.341092057	Chaperonin GroL
Unigene0002980	2.711320192	TetR family transcriptional regulator
Unigene0002986	1.787993914	4-hydroxybutyrate dehydrogenase
Unigene0002988	1.320545384	Carboxylesterase
Unigene0002989	1.377138948	PAAR motif family protein
Unigene0002991	2.223497269	dTDP-glucose 4,6-dehydratase AcbB
Unigene0002996	1.578163805	Acyl-CoA dehydrogenase, partial
Unigene0002999	1.2017231	Hypothetical protein
Unigene0003003	3.203688247	Hypothetical protein
Unigene0003004	1.161815796	ErfK/YbiS/YcfS/YnhG family protein
Unigene0003005	1.70409978	Glutamine-hydrolyzing GMP synthase
Unigene0003007	1.070632213	Phosphate regulon sensor kinase PhoR
Unigene0003008	1.383424343	Oxidoreductase
Unigene0003009	1.089949857	Cobyrinic acid a,c-diamide synthase
Unigene0003011	2.165453614	MFS transporter
Unigene0003013	1.052680652	Conjugal transfer protein
Unigene0003014	3.323613195	BMP family ABC transporter substrate-binding protein
Unigene0003017	3.911670222	Site-specific recombinase XerD
Unigene0003021	2.325283506	Permeases of the major facilitator superfamily
Unigene0003022	1.381056609	2,3-bisphosphoglycerate-dependent phosphoglycerate mutase
Unigene0003024	2.426050786	Transposase
Unigene0003030	1.355152742	Membrane protein
Unigene0003031	1.060880866	Molybdenum cofactor guanylyltransferase
Unigene0003035	1.066547157	Colicin V production protein
Unigene0003037	1.742009179	Response regulator
Unigene0003038	5.467426811	Accessory protein for nitric oxide reductase, NorE
Unigene0003039	1.611624974	Chromosome partitioning protein ParA
Unigene0003040	3.353514527	Opacity-associated protein
Unigene0003041	2.226969	ABC transporter permease
Unigene0003048	2.189981747	Conjugal transfer protein TrbB
Unigene0003049	2.044378251	Beta-lactamase
Unigene0003050	1.495436264	P-type conjugative transfer ATPase TrbB
Unigene0003051	1.580550934	Site-specific DNA-methyltransferase
Unigene0003052	3.935220168	Hypothetical protein
Unigene0003054	2.071771361	Sugar kinase
Unigene0003056	1.085277786	Peptide ABC transporter substrate-binding protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0003061	2.739884738	Acetyltransferase domain protein
Unigene0003063	3.390355376	Adenosylhomocysteinase
Unigene0003064	1.502648296	50S ribosomal protein L13
Unigene0003068	2.135738497	Hypothetical protein
Unigene0003072	2.997445554	F0F1 ATP synthase assembly protein
Unigene0003073	1.357524787	Phosphoribosylamine--glycine ligase
Unigene0003074	1.505874575	DNA-binding protein
Unigene0003076	1.444656577	ABC transporter permease
Unigene0003081	2.113109441	Virulence factor
Unigene0003083	1.071316353	Conjugative transfer ATPase, PFL_4706 family
Unigene0003084	2.05992078	Hypothetical protein
Unigene0003085	2.315648619	Chemotaxis protein CheW
Unigene0003086	2.965825943	RNA polymerase subunit sigma-70
Unigene0003087	1.69928403	Swarming motility protein YneE
Unigene0003088	2.134413437	ABC transporter permease
Unigene0003090	18.59328838	Hypothetical protein
Unigene0003094	2.47427169	Antirepressor
Unigene0003095	1.534672743	CTP synthase, partial
Unigene0003097	1.499838581	Amino acid ABC transporter
Unigene0003099	4.110695497	Uncharacterized protein
Unigene0003105	12.78214506	Hypothetical protein
Unigene0003109	2.725035796	Methylase
Unigene0003110	2.926990432	Methylase
Unigene0003111	1.262095686	Uncharacterized conserved protein
Unigene0003113	2.25797033	Iron import ATP-binding/permease protein IrtA
Unigene0003114	2.270088381	Pesticin receptor precursor
Unigene0003115	1.715960496	Bifunctional diguanylate cyclase/phosphodiesterase
Unigene0003116	1.490376807	Bifunctional diguanylate cyclase/phosphodiesterase
Unigene0003117	1.515670276	Magnesium-translocating P-type ATPase
Unigene0003118	1.291039066	IS21 family transposase
Unigene0003119	1.30911992	IS3 family transposase ISRtr2
Unigene0003120	2.654098501	VWA domain-containing protein
Unigene0003122	2.555151102	Hypothetical protein
Unigene0003125	2.047720319	Conjugal transfer protein TraG
Unigene0003126	1.748567546	Replication protein
Unigene0003127	2.474822559	Phage tail fiber protein
Unigene0003128	2.652550188	DUF2163 domain-containing protein
Unigene0003129	1.503629695	Leucine--tRNA ligase
Unigene0003132	1.940906275	Peptide ABC transporter permease
Unigene0003133	1.345974963	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione acylhydrolase
Unigene0003134	1.81748194	Transposase
Unigene0003135	3.216611064	LacI family transcriptional regulator
Unigene0003137	1.107515665	Gluconolaconase
Unigene0003141	1.333684854	Esterase/lipase
Unigene0003142	1.2915839	Alkaline phosphatase
Unigene0003143	1.158077679	Phosphonate C-P lyase system protein PhnK
Unigene0003144	1.497706537	Carbon-phosphorus lyase complex subunit PhnI
Unigene0003145	1.298666338	Copper-translocating P-type ATPase
Unigene0003150	1.119476929	Amino acid ABC transporter
Unigene0003155	1.08114618	NAD(P)H dehydrogenase
Unigene0003159	6.406867843	Hypothetical protein

Unigene0003160	3.048058816	Hypothetical protein
Unigene0003164	1.716027383	Hypothetical protein
Unigene0003167	2.581861054	Hypothetical protein
Unigene0003168	2.010348427	Uncharacterized protein
Unigene0003169	1.510454886	Porin
Unigene0003170	1.684005109	NADP-specific glutamate dehydrogenase Gdh
Unigene0003171	2.861625783	Glycosyl transferase family 1
Unigene0003174	1.058571663	Xanthine permease XanP
Unigene0003175	1.628773372	TonB-dependent siderophore receptor
Unigene0003179	1.347647241	Hypothetical protein
Unigene0003181	1.435183642	Urease subunit alpha
Unigene0003182	1.010100419	Urease accessory protein UreF
Unigene0003183	3.964902669	Propionyl-CoA synthetase, partial
Unigene0003184	2.683095804	Propionyl-CoA synthetase
Unigene0003185	2.506988254	Chemoreceptor McpA
Unigene0003186	2.002736145	Peptidase
Unigene0003187	1.440423235	Phosphoenolpyruvate--protein phosphotransferase
Unigene0003194	1.283006447	Monovalent cation/H^+ antiporter subunit A
Unigene0003195	1.662331526	ATP-binding protein
Unigene0003196	1.752298272	LuxR family transcriptional regulator
Unigene0003199	3.008066258	50S ribosomal protein L9
Unigene0003200	1.375609405	Acyl-CoA dehydrogenase
Unigene0003201	1.466444075	Membrane transport family protein
Unigene0003209	1.191710829	Sodium-independent anion transporter
Unigene0003212	1.967258751	Hypothetical protein
Unigene0003213	2.719752839	Thiamine/thiamine pyrophosphate ABC transporter, permease protein
Unigene0003214	2.459038978	Thiamine transport system permease protein ThiP
Unigene0003216	3.286271333	Serine acetyltransferase
Unigene0003217	2.02499156	Alpha-2-macroglobulin family protein
Unigene0003218	1.677062982	Alpha-2-macroglobulin family protein
Unigene0003219	2.003849677	GTA TIM-barrel-like domain protein
Unigene0003220	1.95884518	Phage tail protein
Unigene0003221	1.275080026	DDE transposase
Unigene0003222	1.231986944	Uncharacterized protein
Unigene0003225	1.64069184	ACP phosphodiesterase
Unigene0003226	2.14751431	VirB4 family type IV secretion/conjugal transfer ATPase
Unigene0003227	2.848121928	VirB4 family type IV secretion/conjugal transfer ATPase
Unigene0003228	1.767394306	2,3-dihydroxy-2,3-dihydro-p-cumate dehydrogenase CmtB
Unigene0003229	1.297702527	Thymidine kinase Tdk
Unigene0003234	1.401925615	DNA polymerase III subunit epsilon
Unigene0003237	1.196653939	Dihydrolipoyl dehydrogenase
Unigene0003238	1.58067877	Branched-chain alpha-keto acid dehydrogenase subunit E2
Unigene0003241	2.024111714	Oxygen-independent coproporphyrinogen III oxidase
Unigene0003243	1.289173248	Cobaltochelatase subunit CobN
Unigene0003245	1.888648407	Asp/Glu/hydantoin racemase
Unigene0003246	1.620586818	ABC transporter ATP-binding protein
Unigene0003248	1.800694201	Sugar kinase
Unigene0003250	5.137142986	Flagellar basal-body rod protein FlgG
Unigene0003251	5.335323709	Flagellar basal body L-ring protein
Unigene0003252	1.93641947	Adenine deaminase
Unigene0003253	1.341474227	aldose epimerase
Unigene0003258	2.266906336	MexE family multidrug efflux RND transporter periplasmic adaptor subunit
Unigene0003259	1.104664022	Esterase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0003260	1.369314048	Bacterial low temperature requirement A family protein
Unigene0003261	1.17350303	Bacterial low temperature requirement A family protein
Unigene0003262	1.622262086	Serine/threonine-protein kinase HipA
Unigene0003264	1.1686665	Type IV secretory pathway, VirD2 components
Unigene0003267	1.053311608	Tol biopolymer transport system, periplasmic component-related protein
Unigene0003269	1.6254553	Uncharacterized protein
Unigene0003270	4.781668475	ABC-type branched-chain amino acid transport system periplasmic component
Unigene0003271	1.412596674	MltA-interacting MipA family protein
Unigene0003272	1.338654908	Scaffolding protein
Unigene0003274	2.24891957	Integrating conjugative element protein PilL, PFGI-1 class
Unigene0003277	2.252835335	CHAD domain-containing protein
Unigene0003278	1.745817634	GntR family transcriptional regulator
Unigene0003279	2.116842772	Hybrid sensor histidine kinase/response regulator
Unigene0003280	1.938881112	Hybrid sensor histidine kinase/response regulator
Unigene0003281	1.476494873	Isocitrate dehydrogenase
Unigene0003282	1.10026013	eamA-like transporter family protein
Unigene0003285	1.419171908	Uncharacterized protein
Unigene0003286	1.84121266	Putative membrane protein
Unigene0003287	1.665112143	ABC transporter substrate-binding protein
Unigene0003290	5.672693448	Iron ABC transporter substrate-binding protein
Unigene0003291	6.001305104	Iron ABC transporter substrate-binding protein
Unigene0003294	4.140492917	4Fe-4S binding protein, regulatory protein for nitrous oxide reductase, nosR
Unigene0003295	3.738446167	4Fe-4S binding protein, regulatory protein for nitrous oxide reductase, nosR
Unigene0003296	1.226161348	Hypothetical protein
Unigene0003297	1.036450829	Hypothetical protein
Unigene0003300	1.558552028	Hydroxymethylbilane synthase
Unigene0003303	2.681296609	Diguanylate cyclase
Unigene0003304	1.278408161	Diguanylate cyclase domain protein
Unigene0003312	2.19538727	Amino acid transporter
Unigene0003315	2.591780006	Amino acid transporter
Unigene0003316	2.837959348	Monosaccharide ABC transporter substrate-binding protein, CUT2 family
Unigene0003319	1.185282936	Serine--tRNA ligase
Unigene0003325	1.517520799	ABC transporter permease
Unigene0003328	1.271868118	Aminoacyl-tRNA deacylase
Unigene0003329	2.032207676	Transketolase CbbT
Unigene0003330	2.381070809	Type I glyceraldehyde-3-phosphate dehydrogenase
Unigene0003331	1.3850021	Serine/threonine phosphatase
Unigene0003335	1.416126609	Na^+/H^+ antiporter subunit D, partial
Unigene0003340	1.097521533	Hypothetical protein
Unigene0003342	1.836729251	Cytochrome c oxidase subunit I
Unigene0003344	1.659033491	Type II restriction endonuclease
Unigene0003346	1.102920973	Acetyl/propionyl-CoA carboxylase subunit alpha
Unigene0003347	2.2300475	Acetyl/propionyl-CoA carboxylase subuit alpha
Unigene0003348	1.93644235	Histidine kinase
Unigene0003349	2.004293047	Histidine kinase
Unigene0003350	3.040763542	Mn^{2+} and Fe^{2+} transporter of the NRAMP family
Unigene0003355	1.745429305	Aspartate aminotransferase
Unigene0003356	1.309617436	Aspartate aminotransferase
Unigene0003360	1.180415907	Ammonia channel protein
Unigene0003361	1.887373751	Ammonia channel
Unigene0003367	1.512049144	Lysophospholipase

Unigene0003368	4.626815243	Cupin
Unigene0003375	1.055646989	ribonuclease D
Unigene0003376	3.113419422	Membrane protein
Unigene0003377	1.70310886	DNA-binding protein
Unigene0003379	1.846724169	5-carboxymethyl-2-hydroxymuconate isomerase
Unigene0003381	1.358268551	Branched-chain amino acid ABC transporter permease, partial
Unigene0003383	2.138417128	ATPase
Unigene0003393	2.00125457	Dihydrolipoyl dehydrogenase
Unigene0003394	1.877235701	Dihydrolipoyl dehydrogenase
Unigene0003395	1.332776201	tRNA pseudouridine(55) synthase TruB
Unigene0003396	1.101007839	Ribosome-binding factor A
Unigene0003397	3.019221338	L,D-transpeptidase
Unigene0003398	3.031739041	L,D-transpeptidase
Unigene0003403	1.320082558	Lipoprotein
Unigene0003408	1.50193262	Argininosuccinate lyase
Unigene0003409	1.779448131	Sigma-54-dependent Fis family transcriptional regulator
Unigene0003410	1.40723469	Sigma-54-dependent Fis family transcriptional regulator
Unigene0003415	1.81367403	Amino acid/amide ABC transporter ATP-binding protein 2, HAAT family
Unigene0003416	1.534500835	ABC transporter ATP-binding protein
Unigene0003417	2.274817684	Monosaccharide ABC transporter ATP-binding protein, CUT2 family
Unigene0003418	2.112834954	ABC transporter permease
Unigene0003419	1.122971704	DNA translocase FtsK
Unigene0003422	1.618377579	Integrating conjugative element protein
Unigene0003426	1.253352307	Magnesium transporter
Unigene0003427	1.349930649	Peptide deformylase
Unigene0003428	1.658086725	Mu-like prophage FluMu gp41 family protein
Unigene0003429	1.339033691	Mu-like prophage FluMu gp41 family protein
Unigene0003431	1.723626316	Glutamine synthetase
Unigene0003432	1.524471149	3-oxoacyl-[acyl-carrier-protein] synthase 2
Unigene0003433	2.116990918	NADPH: quinone oxidoreductase
Unigene0003434	1.051010103	Mannose-1-phosphate guanylyltransferase, partial
Unigene0003436	1.169003939	Glutamate-5-semialdehyde dehydrogenase
Unigene0003438	1.34289125	Organic solvent ABC transporter substrate-binding protein
Unigene0003439	3.303608181	Uncharacterized protein
Unigene0003440	1.824733448	Conjugative coupling factor TraD, PFGI-1 class
Unigene0003443	1.377559172	ATP phosphoribosyltransferase regulatory subunit
Unigene0003444	1.417534034	Sarcosine oxidase subunit alpha
Unigene0003445	1.245625304	Sarcosine oxidase subunit beta
Unigene0003446	3.416876804	NAD synthetase
Unigene0003447	2.943241621	NAD(P) transhydrogenase subunit alpha
Unigene0003448	1.087621979	Transcription accessory protein
Unigene0003450	1.209376362	His Kinase A domain protein
Unigene0003454	2.125589131	Acyl-CoA dehydrogenase
Unigene0003455	2.176510092	3-hydroxyacyl-CoA dehydrogenase
Unigene0003458	2.074942818	Hypothetical protein
Unigene0003459	2.760817785	Hypothetical protein
Unigene0003461	1.356810256	Soluble lytic murein transglycosylase
Unigene0003462	1.231497271	Lysine transporter LysE
Unigene0003467	1.375608326	Aminotransferase
Unigene0003469	1.088502023	LuxR family transcriptional regulator
Unigene0003470	1.138693014	MarR family transcriptional regulator
Unigene0003474	3.67087345	Kazal-type serine protease inhibitor domain protein
Unigene0003475	4.141193996	Acetaldehyde dehydrogenase 2

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0003476	3.297444335	Iron ABC transporter substrate-binding protein
Unigene0003477	1.339043041	Malic enzyme
Unigene0003480	1.37465618	Transposon Tn3 transposase
Unigene0003483	3.323489191	ATP synthase F0 subunit B
Unigene0003484	3.259699948	F0F1 ATP synthase subunit B′
Unigene0003485	2.253625567	FAD-dependent oxidoreductase
Unigene0003488	2.212751797	Shikimate dehydrogenase
Unigene0003497	1.681821063	Conjugal transfer protein TraG
Unigene0003498	1.908949728	Methylmalonyl-CoA epimerase
Unigene0003499	3.404548034	Thiamine ABC transporter substrate binding subunit
Unigene0003502	1.30783867	Glycine/betaine ABC transporter substrate-binding protein
Unigene0003509	1.529989298	Guanylate kinase
Unigene0003510	1.034658502	Diguanylate cyclase
Unigene0003514	2.068058839	Thiamine ABC transporter, ATP-binding protein
Unigene0003515	1.517353007	Transcriptional regulator
Unigene0003516	1.510432356	Glycosyl transferase
Unigene0003519	2.652468134	Hypothetical protein
Unigene0003520	1.392587404	Acyl-CoA synthetase (AMP-forming)/AMP-acid ligase II
Unigene0003521	1.428858033	Transcriptional regulator, PaaX family
Unigene0003522	1.138669854	ABC-type branched-chain amino acid transport system periplasmic component
Unigene0003523	2.645073607	RNA-binding region RNP-1
Unigene0003524	1.119497174	RNA-binding region RNP-1
Unigene0003525	1.449884779	ABC transporter ATP-binding protein
Unigene0003528	3.012292435	Transposase
Unigene0003531	2.399386572	AraC family transcriptional regulator
Unigene0003535	1.593602057	Integrase
Unigene0003539	2.136229032	Protein LemA
Unigene0003540	1.172298622	Membrane protein
Unigene0003541	2.265011763	Short chain dehydrogenase
Unigene0003542	5.528453973	U32 family peptidase
Unigene0003543	6.734653725	Protease
Unigene0003545	1.7533137	Exopolysaccharide production repressor family protein
Unigene0003546	1.01462486	Hypothetical protein
Unigene0003547	2.024916244	Hypothetical protein
Unigene0003548	1.375003711	Amino acid ABC transporter substrate-binding protein
Unigene0003549	1.728305511	Amino acid ABC transporter permease
Unigene0003552	1.626948415	Sugar kinase
Unigene0003553	2.534590334	Transcriptional regulator
Unigene0003554	1.010885495	Pyruvate dehydrogenase complex repressor
Unigene0003557	1.63391428	Sugar ABC transporter substrate-binding protein
Unigene0003558	1.146574561	Riboflavin biosynthesis protein RibD
Unigene0003559	1.751181847	Serine hydroxymethyltransferase
Unigene0003561	1.121035139	Recombinase XerC
Unigene0003564	2.010015882	Iron ABC transporter permease
Unigene0003565	3.491337499	Hemoglobin/transferrin/lactoferrin receptor protein
Unigene0003569	2.07588286	Flagellar biosynthetic protein FliR
Unigene0003576	1.684445274	Metallophosphoesterase
Unigene0003577	1.360778406	DNA-directed RNA polymerase subunit beta
Unigene0003580	1.78589219	Replication initiation protein RepC
Unigene0003585	4.611531492	tonB-system energizer ExbB
Unigene0003586	4.33184741	tonB-system energizer ExbB

Unigene0003591	1.412122159	Glyoxalase
Unigene0003592	1.851398549	Cysteine synthase
Unigene0003596	1.646996215	Two-component sensor histidine kinase
Unigene0003598	2.139968635	Phosphoserine aminotransferase
Unigene0003599	1.330036925	Phosphoserine aminotransferase
Unigene0003609	2.101534835	Amino acid transporter
Unigene0003613	5.054812574	Flagellar transcriptional regulator FtcR
Unigene0003614	4.347779262	Flagellar hook-associated protein FlgK
Unigene0003618	1.329192246	Heme biosynthesis protein HemY
Unigene0003620	1.717902712	Glycerol-3-phosphate dehydrogenase
Unigene0003621	1.286452372	Plasmid partitioning protein RepA
Unigene0003623	1.179637866	Beta-glucosidase
Unigene0003625	1.47874725	S-(hydroxymethyl)glutathione dehydrogenase
Unigene0003629	1.577937184	Dihydropyrimidinase
Unigene0003630	1.447176645	Zn-dependent hydrolase
Unigene0003631	1.981389122	Hydrolase
Unigene0003632	1.777502625	Cytosine deaminase
Unigene0003639	1.20763943	Nitrogen fixation protein FixG
Unigene0003641	1.324693245	Cupin
Unigene0003644	1.485770526	Lactate dehydrogenase
Unigene0003645	1.671689305	Lactate dehydrogenase
Unigene0003649	2.985222953	Membrane protein
Unigene0003658	2.591558977	Cobalamin biosynthesis protein CobW
Unigene0003659	2.868407978	Hypothetical protein
Unigene0003661	1.055461614	Farnesyl-diphosphate synthase
Unigene0003665	1.992184877	Membrane protein
Unigene0003666	1.005641666	Type I secretion system permease/ATPase
Unigene0003667	1.146476366	Type I secretion protein
Unigene0003670	1.463829419	Cytochrome bd ubiquinol oxidase subunit I
Unigene0003672	1.566449513	Methyl-accepting chemotaxis protein
Unigene0003674	1.833359663	DNA-directed RNA polymerase subunit alpha
Unigene0003677	1.714867801	Molybdopterin oxidoreductase
Unigene0003678	1.468651522	GNAT family N-acetyltransferase
Unigene0003681	1.779779294	Phosphopentomutase
Unigene0003682	1.131827926	Phosphopentomutase
Unigene0003683	2.714884112	Virulence factor SrfB-like protein
Unigene0003684	2.947535369	Virulence protein SrfB
Unigene0003685	2.854931534	Acyl-CoA reductase
Unigene0003686	1.780152211	Type 12 methyltransferase
Unigene0003689	1.330929375	AraC family transcriptional regulator
Unigene0003691	1.124526938	Membrane protein
Unigene0003694	2.646545643	VIRULENCE factor SrfB-like protein
Unigene0003695	2.403709999	Virulence factor SrfC-like protein
Unigene0003696	2.825148239	Branched chain amino acid ABC transporter substrate-binding protein
Unigene0003698	4.091191418	Acyl-CoA dehydrogenase
Unigene0003699	2.863816172	Beta-mannosidase
Unigene0003706	1.286241153	Helicase
Unigene0003708	2.073262165	Collagen-like protein
Unigene0003709	1.79936956	Hypothetical protein
Unigene0003712	1.217966973	RpiR family transcriptional regulator
Unigene0003714	1.151154023	Diguanylate cyclase (GGDEF) domain-containing protein
Unigene0003716	1.32682619	Histidine kinase
Unigene0003719	1.904041574	5,10-methylene tetrahydromethanopterin reductase

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0003722	1.410363966	Gamma-glutamylputrescine oxidoreductase PuuB
Unigene0003723	2.240717867	Gluconate 5-dehydrogenase Gno
Unigene0003726	1.064784792	Hypothetical protein
Unigene0003727	3.497717111	Inverse autotransporter beta-barrel domain-containing protein
Unigene0003728	1.733551582	EamA family transporter
Unigene0003729	1.630968701	Hydroxypyruvate isomerase
Unigene0003732	2.443489787	Histidine kinase
Unigene0003734	1.011054356	Anthranilate synthase component I
Unigene0003735	1.387920259	ExsB family transcriptional regulator
Unigene0003744	1.225239659	MFS permease
Unigene0003745	2.38202864	L-arabinose 1-dehydrogenase
Unigene0003747	2.297979896	Hypothetical protein
Unigene0003748	1.360451113	Glycine cleavage system transcriptional activator
Unigene0003749	1.347711505	3-deoxy-8-phosphooctulonate synthase
Unigene0003750	1.791800731	3-deoxy-8-phosphooctulonate synthase
Unigene0003754	2.9124946	Acetohydroxy acid isomeroreductase, catalytic domain protein
Unigene0003755	3.891352351	Acetohydroxy acid isomeroreductase, catalytic domain protein
Unigene0003756	2.376089573	Replication protein C
Unigene0003757	2.356091186	Hypothetical protein
Unigene0003759	1.288914724	RNA pseudouridine synthase
Unigene0003763	1.03895819	GGDEF domain-containing protein
Unigene0003765	1.86399495	Poly(3-hydroxyalkanoate) synthetase
Unigene0003766	1.588388738	Poly-beta-hydroxybutyrate polymerase PhbC
Unigene0003767	1.945455187	Rhizopine-binding protein
Unigene0003771	1.493673411	Tetraacyldisaccharide 4′-kinase, partial
Unigene0003772	1.521428795	Tetraacyldisaccharide 4′-kinase
Unigene0003774	3.211831092	Glutaryl-CoA dehydrogenase
Unigene0003775	1.843889555	D-amino acid dehydrogenase small subunit
Unigene0003778	1.771274791	Phosphodiesterase
Unigene0003782	1.124356092	SLC13 family permease
Unigene0003783	1.184477083	SLC13 family permease
Unigene0003786	1.411818453	Amidophosphoribosyltransferase
Unigene0003787	2.928780061	Methylase
Unigene0003790	2.835685036	dTDP-glucose 4,6-dehydratase
Unigene0003791	1.766318163	dTDP-4-dehydrorhamnose 3,5-epimerase
Unigene0003792	3.11144665	Oxidoreductase
Unigene0003793	1.941911333	Sensor histidine kinase
Unigene0003794	1.711817779	DNA-binding response regulator
Unigene0003796	1.807927582	Gluconate 5-dehydrogenase
Unigene0003797	1.523502989	Carbohydrate kinase
Unigene0003799	2.376289825	Crp/Fnr family transcriptional regulator
Unigene0003800	3.945171641	Transglutaminase
Unigene0003801	3.584027259	Transglutaminase
Unigene0003802	3.747546714	Hybrid sensor histidine kinase/response regulator
Unigene0003803	4.542763774	Hybrid sensor histidine kinase/response regulator
Unigene0003804	1.435934202	3-isopropylmalate dehydratase large subunit
Unigene0003805	1.202092311	3-isopropylmalate dehydratase large subunit
Unigene0003808	1.060322241	Glycosyl transferase family 1
Unigene0003809	1.912036935	Hypothetical protein
Unigene0003810	1.390085934	Metallophosphoesterase domain-containing protein
Unigene0003813	1.081809814	Sensor histidine kinase

Unigene0003814	1.475258345	Cytochrome o ubiquinol oxidase subunit I
Unigene0003815	2.195366267	Oxidoreductase
Unigene0003816	2.686289786	Hypothetical protein
Unigene0003817	1.60972909	TIGR00701 family protein
Unigene0003818	1.1638452	Uroporphyrinogen decarboxylase
Unigene0003823	4.661674519	C4-dicarboxylate ABC transporter
Unigene0003824	4.118401988	TRAP-type mannitol/chloroaromatic compound transport system large permease component
Unigene0003827	1.880344154	Transcriptional regulator, RpiR family
Unigene0003828	1.883144263	Argininosuccinate synthase
Unigene0003829	1.891139162	MarR family transcriptional regulator
Unigene0003833	2.950430675	Transketolase
Unigene0003835	1.094321121	Pyrroline-5-carboxylate reductase
Unigene0003838	1.532090307	Hypothetical protein
Unigene0003840	9.123154899	Hypothetical protein
Unigene0003841	17.14253323	Hypothetical protein
Unigene0003842	3.305074694	GDP-fucose synthetase
Unigene0003843	2.160477495	Glycosyl transferase, group 1
Unigene0003844	1.879976728	Aspartate--tRNA ligase
Unigene0003848	2.077287189	Alkaline phosphatase
Unigene0003853	2.008855832	Carboxynorspermidine decarboxylase
Unigene0003854	1.037649899	Glutamate--cysteine ligase
Unigene0003857	2.895392588	Glutathione S-transferase
Unigene0003858	1.812234465	Acyl-CoA dehydrogenase
Unigene0003862	3.625320834	ATP synthase subunit beta
Unigene0003863	2.133925011	Glycine cleavage system protein T
Unigene0003864	2.102498422	Glycine cleavage system protein T
Unigene0003868	1.472628554	Multidrug ABC transporter ATP-binding protein
Unigene0003869	1.499288775	Glycine cleavage system protein T
Unigene0003871	1.738850417	Diguanylate cyclase domain protein
Unigene0003872	1.849678093	Bifunctional diguanylate cyclase/phosphodiesterase
Unigene0003875	2.091875751	Methylase/helicase
Unigene0003876	1.626825613	Methylase
Unigene0003877	1.003133741	Ribosomal protein L3 N(5)-glutamine methyltransferase
Unigene0003884	1.627752343	ABC transporter substrate-binding protein
Unigene0003885	1.077865266	Glutamine ABC transporter ATP-binding protein
Unigene0003887	1.175912816	Hypothetical protein
Unigene0003888	3.231201113	UDP-galactopyranose mutase
Unigene0003889	3.283190716	Glycosyl transferase
Unigene0003892	1.949860584	Type IV secretory pathway, VirD2 components (relaxase)
Unigene0003893	1.117241531	Aspartate kinase
Unigene0003894	1.524281332	Phosphoenolpyruvate--protein phosphotransferase
Unigene0003895	1.171808953	ACR family transporter
Unigene0003897	2.980305003	Iron ABC transporter
Unigene0003900	1.610531234	Glucose-1-phosphate adenylyltransferase
Unigene0003901	1.701410089	Amino acid ABC transporter permease
Unigene0003902	1.346802472	ABC transporter family protein
Unigene0003906	1.714056331	VirB4 family type IV secretion/conjugal transfer ATPase
Unigene0003908	2.833067707	Hypothetical protein
Unigene0003910	2.907949379	Conjugal transfer protein TrbL
Unigene0003921	1.700195852	50S ribosomal protein L2
Unigene0003922	1.900313575	30S ribosomal protein S5
Unigene0003924	1.970363969	Spermidine/putrescine ABC transporter ATP-binding protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0003925	2.788030416	Iron ABC transporter substrate-binding protein
Unigene0003929	1.169317389	Oxidoreductase
Unigene0003931	1.287009075	Peptidoglycan-binding protein LysM
Unigene0003932	1.590563122	Alkylated DNA repair dioxygenase
Unigene0003934	1.197746743	Uncharacterized protein
Unigene0003935	1.683598396	Hydrophobe/amphiphile efflux-1 family RND transporter
Unigene0003936	1.360939944	Hydrophobe/amphiphile efflux-1 family RND transporter
Unigene0003937	2.608796488	Cytochrome c oxidase subunit I
Unigene0003938	1.310460695	Multidrug efflux RND transporter permease subunit
Unigene0003940	2.300690277	LysR family transcriptional regulator
Unigene0003941	3.064573392	Egg lysin
Unigene0003942	2.825621973	Acid phosphatase/phosphotransferase
Unigene0003951	1.373063678	Beta-galactosidase
Unigene0003952	1.971665489	Glycosyl transferase
Unigene0003953	1.390333442	Amino acid ABC transporter permease
Unigene0003963	2.569876084	Hypothetical protein
Unigene0003964	1.623688078	Dehydrogenase
Unigene0003966	1.03424983	Chromate transporter
Unigene0003967	1.617734166	Sarcosine dehydrogenase
Unigene0003969	2.921550023	Dehydration responsive domain protein, partial
Unigene0003970	1.722815675	Uncharacterized protein
Unigene0003976	1.236557362	Deacetyase
Unigene0003977	1.944575434	Oxidoreductase
Unigene0003979	1.55187329	Adenine deaminase
Unigene0003980	1.974662636	Adenine deaminase
Unigene0003981	1.30328316	glycyl-tRNA synthetase subunit beta
Unigene0003982	3.770536992	Conserved hypothetical exported protein
Unigene0003983	1.302709737	glycyl-tRNA synthetase subunit beta
Unigene0003984	1.701868574	ATP-dependent peptidase M41 family protein
Unigene0003988	1.786706729	4-hydroxy-tetrahydrodipicolinate reductase
Unigene0003989	1.510609676	ABC transporter ATP-binding protein
Unigene0003993	1.641098372	S-adenosylmethionine--diacylglycerol 3-amino-3-carboxypropyl transferase
Unigene0004002	3.997005198	Pseudoazurin
Unigene0004005	1.414978544	Hypothetical protein
Unigene0004006	1.659021575	Phage integrase protein
Unigene0004008	1.594142274	Cytosine deaminase
Unigene0004009	1.467197881	Amino acid ABC transporter permease
Unigene0004010	1.043846923	Disulfide bond formation protein DsbA
Unigene0004014	1.230758365	Chromosome partitioning protein ParA
Unigene0004016	1.024982586	Cobyrinic acid a,c-diamide synthase
Unigene0004019	1.590334587	Lactate dehydrogenase
Unigene0004020	2.364367659	Lactate dehydrogenase
Unigene0004025	2.444496743	DUF1073 domain-containing protein
Unigene0004026	1.77141374	Terminase
Unigene0004038	1.794134497	lysM domain protein
Unigene0004039	1.47217609	LysM protein LysM
Unigene0004040	1.277235512	Conserved hypothetical exported protein
Unigene0004042	1.068520962	DNA cytosine methyltransferase
Unigene0004044	1.03418263	LacI family transcriptional regulator
Unigene0004048	1.159287817	Allophanate hydrolase
Unigene0004049	1.438268047	Acetyl-/propionyl-CoA carboxylase alpha chain

Unigene0004050	1.584936146	Allophanate hydrolase
Unigene0004051	2.683525432	Acetyl-CoA acetyltransferase
Unigene0004052	3.503378748	Acetyl-CoA acetyltransferase
Unigene0004053	3.198049308	Acetyl-CoA acetyltransferase
Unigene0004054	1.149534712	DMT(drug/metabolite transporter) superfamily permease
Unigene0004055	1.718164888	ABC transporter permease
Unigene0004057	2.311463751	Glycosyl transferase
Unigene0004059	1.239863322	Branched-chain amino acid ABC transporter permease, partial
Unigene0004061	1.333971799	AAA domain protein
Unigene0004064	2.080273308	MarR family transcriptional regulator
Unigene0004065	2.863385437	Coproporphyrinogen III oxidase
Unigene0004070	1.883383081	O-acetylhomoserine aminocarboxypropyltransferase
Unigene0004071	2.1144811	ABC transporter permease
Unigene0004072	1.676433158	DNA-binding protein
Unigene0004073	1.079372604	Chloramphenicol phosphotransferase
Unigene0004074	1.163580869	Hypothetical protein
Unigene0004082	3.788505673	Chemotaxis protein CheA
Unigene0004083	2.591429458	Chemotaxis protein
Unigene0004084	3.256255531	Chemotaxis response regulator protein-glutamate methylesterase
Unigene0004085	1.150937163	FUSC family protein
Unigene0004088	1.03295738	UDP-glucose--undecaprenyl-phosphate glucose-1-phosphate transferase GumD
Unigene0004091	1.122574273	LuxR family transcriptional regulator
Unigene0004093	1.323005032	Hypothetical protein
Unigene0004094	1.21303599	Transcriptional regulator
Unigene0004095	1.853255651	Conjugal transfer protein TrbJ
Unigene0004096	1.157213245	P-type conjugative transfer protein TrbL
Unigene0004098	1.284470173	NAD$^+$ synthase
Unigene0004099	1.30661213	Plasmid partitioning protein RepB
Unigene0004101	1.72512306	Pyridoxal 4-dehydrogenase
Unigene0004102	1.002956525	NAD(P)-dependent oxidoreductase
Unigene0004103	3.1106417	ABC transporter substrate-binding protein
Unigene0004104	1.668612148	ABC transporter ATP-binding protein
Unigene0004105	1.831681777	AAA domain-containing protein
Unigene0004107	1.559899888	Sulfate ABC transporter ATP-binding protein
Unigene0004108	3.198724366	Spermidine/putrescine ABC transporter ATP-binding protein
Unigene0004109	2.844338237	ABC transporter permease
Unigene0004110	5.51850982	Thiazole synthase ThiG
Unigene0004111	4.845363123	Thiamine-phosphate diphosphorylase
Unigene0004112	6.008714248	Thiazole synthase
Unigene0004113	6.629659935	Thiamine biosynthesis protein ThiS
Unigene0004114	5.487541061	Phosphomethylpyrimidine synthase ThiC
Unigene0004115	1.910269321	Hybrid sensor histidine kinase/response regulator
Unigene0004116	1.998923556	Hybrid sensor histidine kinase/response regulator
Unigene0004117	1.053258547	GntR family transcriptional regulator
Unigene0004118	1.142659054	Sigma-54-dependent Fis family transcriptional regulator
Unigene0004119	2.198735193	Hypothetical protein
Unigene0004120	1.825779498	ABC transporter substrate-binding protein
Unigene0004129	6.402806482	DUF2325 domain-containing protein
Unigene0004130	2.21060782	DUF423 domain-containing protein
Unigene0004134	1.132285476	Aldehyde dehydrogenase
Unigene0004138	2.591856198	PG1 protein, homology to Homo sapiens
Unigene0004139	1.978469876	NADP-dependent malic enzyme
Unigene0004141	1.328181793	Miniconductance mechanosensitive channel

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0004142	1.609940933	TRAP dicarboxylate transporter, DctM subunit
Unigene0004143	3.66025393	Methyl-accepting chemotaxis protein
Unigene0004144	4.034730057	Methyl-accepting chemotaxis protein
Unigene0004150	1.467618057	Xanthine dehydrogenase small subunit
Unigene0004152	1.972413529	Amino acid ABC transporter permease
Unigene0004153	1.560525286	Sugar isomerase
Unigene0004154	2.031340099	NnrU family protein
Unigene0004157	2.502574357	Lactate dehydrogenase
Unigene0004158	2.374504472	DNA topoisomerase III, partial
Unigene0004159	2.531830263	DNA topoisomerase III
Unigene0004160	1.470084005	Short-chain dehydrogenase
Unigene0004161	1.945443836	Glycerol-3-phosphate dehydrogenase
Unigene0004162	1.5599533	Methylhydantoinase
Unigene0004167	3.099297535	Sulfite reductase subunit beta
Unigene0004168	2.896904153	Sulfite reductase [NADPH] flavoprotein, alpha-component
Unigene0004173	3.207394526	DDE transposase
Unigene0004174	1.27989178	Hypothetical protein
Unigene0004177	3.745560381	Flagellar protein
Unigene0004178	5.580841352	Flagellum-specific ATP synthase FliI
Unigene0004179	4.033675693	Flagellum-specific ATP synthase FliI
Unigene0004181	1.058852471	Glycogen branching protein
Unigene0004183	1.502698007	16S rRNA (cytidine(1402)-2’-O)-methyltransferase
Unigene0004186	1.468771285	Glycine/betaine ABC transporter permease
Unigene0004193	1.786088632	Redox-regulated ATPase YchF
Unigene0004194	1.271588284	GTP-binding protein
Unigene0004202	1.835583555	DUF4400 domain-containing protein
Unigene0004203	1.438511867	Recombinase zinc beta ribbon domain-containing protein
Unigene0004204	2.047182789	ABC transporter permease
Unigene0004205	1.817755213	Choline dehydrogenase
Unigene0004207	1.033934336	UDP-glucose 6-dehydrogenase
Unigene0004209	2.455280164	Replication initiation protein
Unigene0004210	1.399912592	Hypothetical protein
Unigene0004211	1.122283146	Cell division protein
Unigene0004217	1.299788606	3-oxoacyl-[acyl-carrier-protein] synthase III
Unigene0004218	1.138306472	Spermidine/putrescine ABC transporter ATP-binding protein
Unigene0004219	1.597129937	Spermidine/putrescine ABC transporter substrate-binding protein
Unigene0004220	1.686897683	Trimethylamine dehydrogenase Tmd
Unigene0004233	1.533619168	Metal-binding protein
Unigene0004236	5.301242786	Hypothetical protein
Unigene0004237	2.836274998	Iron ABC transporter permease
Unigene0004238	2.143589539	Iron ABC transporter permease
Unigene0004239	3.716355052	Binding--dependent transport system inner membrane component family protein
Unigene0004248	1.78427797	2-isopropylmalate synthase
Unigene0004250	1.866756279	AAA domain-containing protein
Unigene0004252	1.130723606	Branched-chain amino acid ABC transporter permease
Unigene0004254	1.804748352	MFS transporter
Unigene0004255	1.8619248	Oxidoreductase
Unigene0004257	1.459476802	GCN5 family acetyltransferase
Unigene0004258	2.915221924	Beta tubulin, autoregulation binding site
Unigene0004259	1.3887464	GTA TIM-barrel-like domain protein
Unigene0004260	3.034639296	GTA TIM-barrel-like domain protein

Unigene0004261	2.054512353	Acetyl-CoA acetyltransferase
Unigene0004262	2.425961307	3-hydroxyacyl-CoA dehydrogenase
Unigene0004263	1.987449689	3-methyl-2-oxobutanoate dehydrogenase (2-methylpropanoyl-transferring) subunit alpha
Unigene0004264	1.01162258	Leucyl aminopeptidase
Unigene0004265	1.047190229	DNA polymerase III subunit chi
Unigene0004266	1.278896985	ATP-binding protein
Unigene0004271	1.718523982	Galactonate dehydratase
Unigene0004279	1.247913468	Ribonuclease J
Unigene0004280	1.417001794	MBL fold metallo-hydrolase
Unigene0004281	1.214034254	Biotin biosynthesis protein
Unigene0004283	1.089053685	NADH dehydrogenase subunit D
Unigene0004291	1.777774689	Hypothetical protein
Unigene0004295	2.100525213	Predicted arabinose efflux permease, MFS family
Unigene0004297	1.629765715	Rossman fold protein, TIGR00730 family
Unigene0004304	2.008867861	Ribose ABC transporter permease
Unigene0004305	1.537028827	D-ribose transporter ATP-binding protein
Unigene0004306	1.525539727	ABC transporter
Unigene0004307	2.353381132	Sugar ABC transporter permease
Unigene0004315	1.13808537	Spermidine/putrescine ABC transporter substrate-binding protein
Unigene0004318	1.269939042	VirB4 family type IV secretion/conjugal transfer ATPase
Unigene0004319	2.966353095	Conjugal transfer protein TrbC
Unigene0004320	2.467963542	P-type conjugative transfer ATPase TrbB
Unigene0004321	1.797516711	Conjugative transfer protein TrbE
Unigene0004329	3.263685683	GNAT family N-acetyltransferase
Unigene0004331	1.528051876	Ribose ABC transporter permease
Unigene0004332	1.151005987	Type I methionyl aminopeptidase
Unigene0004334	2.196495009	Succinate-semialdehyde dehydrogenase (NADP(+))
Unigene0004336	1.527415996	Conjugal transfer protein TraG
Unigene0004337	2.182444804	Conjugal transfer protein TraG
Unigene0004338	4.031169536	Sel1 repeat family protein
Unigene0004339	3.673938438	Sel1 repeat family protein
Unigene0004341	1.590739745	Outer membrane autotransporter barrel domain-containing protein
Unigene0004342	1.269922478	Outer membrane autotransporter barrel domain-containing protein
Unigene0004345	1.539650138	ROK family transcriptional regulator
Unigene0004346	1.1673033	Amidase
Unigene0004347	1.591567269	Oxidoreductase
Unigene0004348	2.098771552	Predicted dehydrogenase
Unigene0004349	2.530192922	Predicted dehydrogenase
Unigene0004360	3.678464661	Glyoxylate carboligase
Unigene0004361	3.150916627	2-hydroxy-3-oxopropionate reductase
Unigene0004367	1.220209562	AAA domain-containing protein
Unigene0004368	1.496091578	Chromosome partition protein smc
Unigene0004375	1.657574409	3-oxoacyl-ACP reductase
Unigene0004385	2.461650264	Alpha-glucosidase
Unigene0004386	2.24311802	Alpha-glucoside ABC transporter substrate-binding protein, partial
Unigene0004390	1.246868856	Phosphatidate cytidylyltransferase
Unigene0004394	1.675751477	Amino acid ABC transporter substrate-binding protein
Unigene0004395	1.367811344	Aminotransferase class-III family protein
Unigene0004399	5.433324504	Uncharacterized PROTEIN
Unigene0004400	3.745532717	Uncharacterized PROTEIN
Unigene0004404	1.258248805	GTPase
Unigene0004407	2.528557207	Flagellar protein

(continued)

Table S2 *Continued*

GeneID	$\log_2$ Ratiov(Pyridine ±)	Description
Unigene0004408	1.241953199	Glycerol-3-phosphate dehydrogenase
Unigene0004410	2.995348178	D-ribose ABC transporter substrate-binding protein
Unigene0004411	1.472181856	Carbohydrate kinase
Unigene0004412	2.187907574	Bifunctional imidazolonepropionase/histidine ammonia-lyase
Unigene0004413	2.268529331	Urocanate hydratase
Unigene0004418	2.890886978	ABC transporter permease
Unigene0004420	1.942216783	ABC transporter family protein
Unigene0004421	3.023156191	Phage tail protein
Unigene0004424	1.167340101	FAD-binding oxidoreductase
Unigene0004425	1.366438906	Molecular chaperone Hsp70
Unigene0004433	1.437783695	Choline ABC transporter ATP-binding protein
Unigene0004434	1.810631426	Glycine betaine transport system permease protein OpuAB
Unigene0004435	2.147770979	Glycine betaine ABC transporter substrate-binding protein
Unigene0004436	1.189201683	MFS transporter
Unigene0004439	1.315160893	Nitrate/sulfonate/bicarbonate ABC transporter periplasmic protein-like protein
Unigene0004440	1.533122653	ABC transporter-like protein
Unigene0004441	1.619027951	ABC transporter permease
Unigene0004442	1.323578908	Acetyltransferase (GNAT) domain-containing protein
Unigene0004443	1.163322313	Membrane protein involved in the export of O-antigen and teichoic acid
Unigene0004444	1.615127099	Membrane protein involved in the export of O-antigen and teichoic acid
Unigene0004445	1.330970893	Membrane protein involved in the export of O-antigen and teichoic acid
Unigene0004446	1.255363536	Glycerol-3-phosphate transporter ATP-binding subunit
Unigene0004447	1.35341019	ABC transporter ATP-binding protein
Unigene0004449	2.009986167	Hypothetical protein
Unigene0004450	1.073270315	Hypothetical protein
Unigene0004451	3.511891092	Lactate dehydrogenase, partial
Unigene0004452	1.777512994	Lactate dehydrogenase
Unigene0004453	2.133029106	Maebl
Unigene0004455	1.18580235	Dihydrodipicolinate synthase family protein
Unigene0004456	2.760845693	Copper oxidase
Unigene0004457	4.744717352	Copper oxidase
Unigene0004458	1.133911855	Transcriptional regulator protein
Unigene0004459	1.10456099	HTH DNA binding domain-containing protein
Unigene0004460	1.347135613	3-ketoacyl-ACP reductase
Unigene0004468	1.146654145	Glutamate synthase
Unigene0004469	1.723817775	Glutamate synthase conserved region-containing protein, partial
Unigene0004470	1.632616586	Glutamate synthase subunit alpha
Unigene0004474	3.07561617	Conjugal transfer protein TrbE
Unigene0004475	2.294151656	Conjugal transfer protein TrbC
Unigene0004476	3.139939304	Conjugal transfer protein TrbB
Unigene0004477	2.101607272	AAA ATPase
Unigene0004478	1.050548454	Dipeptide epimerase
Unigene0004479	1.937891671	3-phenylpropionic acid transporter
Unigene0004480	2.045337075	3-phenylpropionic acid transporter
Unigene0004481	1.504476754	Hypothetical protein
Unigene0004483	2.448804212	Conjugal transfer protein TraG
Unigene0004484	3.093452781	Nuclease
Unigene0004492	2.524019799	Electron transfer flavoprotein-ubiquinone oxidoreductase, partial
Unigene0004493	1.17763593	Electron transfer flavoprotein-ubiquinone oxidoreductase
Unigene0004494	1.326484228	1-carboxy-3-chloro-3,4-dihydroxycyclo hexa-1,5-diene dehydrogenase
Unigene0004495	1.678693512	Inositol 2-dehydrogenase 1

Unigene0004496	1.269609165	1-carboxy-3-chloro-3,4-dihydroxycyclo hexa-1,5-diene dehydrogenase
Unigene0004497	2.034979177	Histidine kinase
Unigene0004498	2.857616833	PAS domain-containing sensor histidine kinase
Unigene0004503	1.606451572	ABC transporter ATP-binding protein
Unigene0004509	1.209427684	TrbL/VirB6 plasmid conjugal transfer protein
Unigene0004510	1.946750015	Chromosome partitioning protein ParB
Unigene0004512	1.129574961	Alpha-D-glucose phosphate-specific phosphoglucomutase
Unigene0004516	1.051152989	Glycogen debranching enzyme GlgX, partial
Unigene0004518	1.454242334	Glycine C-acetyltransferase
Unigene0004520	1.305222171	Glycine C-acetyltransferase
Unigene0004522	1.119286462	Aldehyde-activating protein
Unigene0004523	1.827511601	DUF1049 domain-containing protein
Unigene0004524	1.524593608	Carbon monoxide dehydrogenase
Unigene0004527	2.069604694	ABC transporter ATP-binding protein
Unigene0004530	1.251833303	ABC transporter ATP-binding protein
Unigene0004531	1.920409316	Hydantoinase subunit beta
Unigene0004535	1.933538602	Transcriptional regulator
Unigene0004536	1.419697951	Transcriptional regulator
Unigene0004537	2.115493014	EamA family transporter
Unigene0004538	1.019726299	Proline iminopeptidase
Unigene0004540	1.595186611	MerR family transcriptional regulator
Unigene0004542	1.345629124	Monosaccharide ABC transporter substrate-binding protein, CUT2 family
Unigene0004545	1.796104009	2,5-dihydroxypyridine 5,6-dioxygenase
Unigene0004547	1.467446231	ABC transporter, membrane spanning protein PstA
Unigene0004548	1.20395828	Phosphate ABC transporter ATP-binding protein
Unigene0004551	1.508266444	Aspartate ammonia-lyase
Unigene0004552	1.377842463	Aspartate ammonia-lyase
Unigene0004553	2.520857385	ABC transporter permease
Unigene0004554	3.303795071	BMP family ABC transporter substrate-binding protein
Unigene0004555	2.943639581	ABC transporter permease
Unigene0004556	2.561257977	Sugar ABC transporter ATP-binding protein
Unigene0004557	2.098136765	Autoinducer 2 import ATP-binding protein LsrA
Unigene0004558	2.292876768	Antibiotic resistance protein
Unigene0004560	1.516950339	ycaO-type kinase domain protein
Unigene0004561	1.570417701	heme ABC transporter ATP-binding protein
Unigene0004566	1.431598395	Regulator
Unigene0004567	1.450782944	MBL fold metallo-hydrolase