Supplemental Methods:

Sample Collection

Duplicate surface samples were collected from the Amazon River plume aboard the R/V Knorr in June 2010 (4 52.71'N, 51 21.59'W) during a period of high river discharge. The collection site (Station 10, 4° 52.71'N, 51° 21.59'W; S = 21.0; T = 29.6°C), located ~ 500 Km to the north of the Amazon River mouth, was characterized by the presence of coastal diatoms in the top 8 m of the water column. Sampling was conducted between 0700 and 0900 local time by gently impeller pumping (modified Rule 1800 submersible sump pump) surface water through 10 m of tygon tubing (3 cm) to the ship's deck where it then flowed through a 156 μm mesh into 20 L carboys. In the lab, cells were partitioned into two size fractions by sequential filtration (using a Masterflex peristaltic pump) of the pre-filtered seawater through a 2.0 μm pore-size, 142 mm diameter polycarbonate (PCTE) membrane filter (Sterlitech Corporation, Kent, CWA) and a 0.22 μm pore-size, 142 mm diameter Supor membrane filter (Pall, Port Washington, NY). Metagenomic and non-selective metatranscriptomic analyses were conducted on both pore-size filters; poly(A)-selected (eukaryote-dominated) metatranscriptomic analyses were conducted only on the larger pore-size filter (2.0 μm pore-size). All filters were immediately submerged in RNAlater (Applied Biosystems, Austin, TX) in sterile 50 mL conical tubes, incubated at room temperature overnight and then stored at -80^{o}C until extraction. Filtration and stabilization of each sample was completed within 30 min of water collection. Additionally, samples were collected and preserved for flow cytometry. After staining with 1X SYBR Green II and incubating in the dark for at least 10 minutes, samples were analyzed using a Beckman Coulter Cyan flow cytometer with an excitation wavelength of 488nm and emission detection filter of 530nm. Bacterial cells were quantified using a combination of light scatter and fluorescence detection with a bead standard of known concentration used to calculate the volume counted by the machine.

Total Community RNA Processing for Metatranscriptomes

Prior to RNA extraction, the filters were thawed, removed from the preservative solution, placed in Whirl-Pak® bags (Nasco, Fort Artkinson, WI), and flash-frozen in liquid nitrogen. RNA extraction and DNA removal were carried out as previously described (1-3). In brief, a lysis tube was prepared for each sample consisting of a sterile 50 mL conical tube containing 8 mL of RLT Lysis Solution (Qiagen, Valencia, CA), 3 grams of RNA PowerSoil beads (Mo-Bio, Carlsbad, CA), and internal standards (described below). Filters inside the bags were broken into small pieces using a rubber mallet and transferred to the lysis tubes. Tubes were vortexed for 10 min to lyse cells, and RNA was purified from cell lysate using an RNeasy Kit (Qiagen, Valencia, CA) followed by two successive treatments with the Turbo DNA-free kit (Invitrogen, Carlsbad, CA) to completely remove residual DNA. Ribosomal RNA (rRNA) was selectively removed using community-specific biotinylated-rRNA probes prepared with DNA from a sample collected simultaneously (4). To maximize the removal of rRNA, probes were created for Bacterial and Archaeal 16S and 23S rRNA and Eukaryotic 18S and 28S rRNA. Probe-bound rRNA was removed via hybridization to streptavidin-coated magnetic beads (New England Biolabs, Ipswich, MA), and successful removal of rRNA from the samples was confirmed using either an Experion automated electrophoresis system (Bio-Rad Laboratories, Hercules, CA) or a Bioanalyzer (Agilent Technologies, Santa Clara, CA). rRNA-depleted samples were linearly amplified using the MessageAmp II-Bacteria Kit (Applied Biosystems, Austin, TX), and amplified mRNA was converted into cDNA using the Superscript III First Strand synthesis system (Invitrogen, Carlsbad, CA) with random primers, followed by the NEBnext mRNA second strand synthesis module (New England Biolabs, Ipswich, MA), both according to manufacturer protocols. Synthesized cDNA was purified using the QIAquick PCR purification kit (Qiagen, Valencia, CA) followed by EtOH precipitation, resuspended in 100 μL of TE buffer and stored at -80^{o} C until library preparation for sequencing.

Poly(A)-tail Selected RNA Processing for Metatranscriptomes

To ensure sufficient coverage of eukaryotic transcriptomes, a second metatranscriptome protocol was used that selectively sequenced messages with poly(A) tails; this was carried out for the >2.0 μm pore-size filter only. Samples were prepared as described above with the following exceptions. Each lysis tube was prepared with 9 mL of RLT Lysis Solution, 250 μL of zirconium beads (OPS Diagnostics, Lebanon, NJ, USA), and an internal poly(A)-tailed mRNA standard (see below). Following lysis, poly(A)-tailed mRNA was isolated from total RNA using an Oligotex mRNA kit (Qiagen, Valencia, CA), and mRNA was linearly amplified with a MessageAmp II-aRNA Amplification Kit (Applied Biosystems, Austin, TX). Double stranded cDNA was prepared as described above except without ethanol precipitation.

DNA Processing for Metagenomes

DNA was extracted and purified as previously described (5-7) with some modification. Briefly, each filter was thawed, removed from the preservative solution, and rinsed three times in autoclaved, filter-sterilized, 0.1% phosphate-buffered saline (PBS) to remove any residual RNAlater. Each filter was shattered as described above and placed in a tube containing DNA extraction buffer [DEB: 0.1 M Tris-HCl (pH 8), 0.1 M Na-EDTA (pH 8), 0.1 M $Na_2H_2PO_4$ (pH 8), 1.5 M NaCl, 5% CTAB]. All liquid from the rinses as well as the original RNAlater was pushed through a 0.2μm Sterivex-GP filter capsule (EMD Millipore, Billerica, MA), which was subsequently rinsed 3 times to salvage any lost cells. The capsule was opened and the filter sliced into pieces and added to the tube with the original membrane filter and an internal genomic DNA standard (described below). Following treatments with proteinase-K, lysozyme, and sodium dodecyl sulfate, DNA was purified via phenol:chloroform extraction and isopropanol precipitation.

Sequencing

cDNA and DNA was sheared ultrasonically to ~200-250 base pair fragments and TruSeq libraries (Illumina Inc., San Diego, CA) were constructed for paired-end (2 x 150) sequencing using the Illumina Genome Analyzer IIx sequencing platform (Illumina Inc., San Diego, CA).

Internal Standards

Omics processing included the addition of internal standards (8) to allow for calculation of volume-based absolute copy numbers for each gene or transcript type, rather than just relative quantification (i.e., counts L^{-1} rather than percent of sequence library). Two mRNA standards without poly(A) tails (to mimic prokaryotic and organelle mRNAs) were synthesized by *in vitro* transcription using a method modified from (1). The standards were constructed by linearizing a pTXB1 vector (New England Biolabs, Ipswich, MA) with *Nco*I restriction enzyme (New England Biolabs, Ipswich, MA) or pFN18A Halotag T7 Flexi Vector (Promega, Madison, WI) with *Bam*HI restriction enzyme (New England Biolabs, Ipswich, MA). Each was purified by phenol:chloroform:isoamyl alcohol extraction and ethanol precipitation. The 5' nucleotide overhangs were removed using Mung Bean Nuclease (New England Biolabs, Ipswich, MA), followed by purification via phenol:chloroform:isoamyl alcohol extraction and ethanol precipitation. Complete digestion of the vector was confirmed on a 1% agarose gel. The DNA fragment was then transcribed *in vitro* using the Riboprobe *in vitro* Transcription System (Promega, Madison, WI) according to the manufacturer's protocol using a T7 RNA polymerase to create 916 nt (pTXB1 standard) or 970 nt (pFN18A) artificial transcripts. Residual DNA was removed using RQ1 RNase-Free DNase and the RNA was purified by phenol:chloroform:isoamyl alcohol extraction and ethanol precipitation. The RNA standards were quantified using the Quant-iT Ribogreen RNA Reagent and Kit (Invitrogen, Carlsbad, CA), and RNA nucleotide length was confirmed with an Experion automated electrophoresis system (Bio-Rad Laboratories, Hercules, CA). A known number of each standard (pTXB1 = 2.104×10^{10} copies; pFN18A = 1.172×10^{10} copies) was added independently to each lysis tube immediately prior to the addition of the sample filter.

An mRNA standard with a poly(A) tail (to mimic eukaryotic nuclear mRNA) was created from an HAP-1 Protelomerase viral gene. To create the standard, a 544 bp amplicon containing a poly(A) tail and a T7 promoter was produced from the template DNA through PCR. The PCR amplicons were then used as the template DNA for an *in vitro* transcription reaction to produce the resulting 499 nucleotide poly(A)-tailed mRNA. The addition of 2.0×10^9 copies of the standard occurred immediately prior to cell lysis.

The genomic internal standard for metagenomic samples consisted of *Thermus thermophilus* DSM7039 [HB8] genomic DNA (American Type Culture Collection, Manassas, VA) added immediately prior to cell lysis. The amount of DNA standard added was estimated to be ~ 1% (8.4 ng per liter filtered) of sample DNA based on yields of DNA from a typical filter (Table S1).

16S and 18S rRNA tag sequencing

DNA was PCR-amplified in four replicate 20 µl reactions using bacterial 16S ribosomal RNA gene primers. The bacteria-specific forward primer began at 27F in the V2 region and included a 454B FLX linker (GCCTTGCCAGCCCGCTCAG *TC* AGRGTTTGATYMTGGCTCAG). The reverse primer began at 338R and included a 454A linker and a unique 8 base pair barcode (denoted by N in primer sequence; GCCTCCCTCGCGCCATCAG NNNNNNNN *CA* TGCWGCCWCCCGTAGGWGT) (Modified from (9)). Products from replicate amplifications were combined and purified with the S.N.A.P. UV-Free Gel Purification Kit (Invitrogen, Carlsbad, CA) by gel isolation from a 0.8% agarose gel. Purified samples were sent for pyrosequencing on a Roche-454 FLX Pyrosequencer at Engencore at the University of South Carolina using titanium chemistry (http://engencore.sc.edu/).

Bioinformatics

Following sequencing, paired-end Illumina reads were joined using the She-ra program (10) with the default parameters and a quality metric score of 0.5. Paired reads were trimmed using Seqtrim (11) with default settings. To remove rRNA, tRNA, and internal standard sequences from the metatranscriptome reads, a Blastn search was performed against a database containing representative ribosomal RNA and tRNA sequences along with the internal standard sequences. All reads with a bit score greater ≥ 50 to one of the sequences in the database were removed (1). To remove internal standard sequences from the metagenome reads, a Blastn search against the *T. thermophilus* HB8 genome was carried out, and any hits from the metagenome sequences with a bit score ≥ 50 were queried against the RefSeq protein database using a Blastx search; hits matching *Thermus thermophilus* proteins with a bit score ≥ 40 were designated as internal standard.

Reads representing genes or transcripts of 74 selected biogeochemically-relevant genes were identified using a Blastx search against a custom database consisting of multiple reference sequences from diverse taxa for each gene, along with paralogs having sequences most similar to the gene of interest. This gene-specific reference database was tested on a subset of Amazon reads using a bit score ≥ 40, and re-analysis of the positive reads against the RefSeq protein database was used to adjust the composition of the database. To obtain an estimate of error that was propagated through the calculations, a Poisson distribution was generated for each gene using the rpois function in R with the lamba parameter equal to the count of reads and 10,000 randomly sampled values returned. The Poisson distributions were converted to normalized count distributions (copies L^{-1}) and then averaged together for replicate samples. The resulting distributions were used to calculate expression ratios for each gene by dividing the transcripts L^{-1} distribution by the genes L^{-1} distribution. Expression ratios between size fractions were considered significantly different when separated by 2 standard deviations. For comparison, a one-tailed statistical comparison was also performed using Welch's T-test, an adaptation of the standard T-test for two samples with unequal variances. Of the 55 genes identified to have significantly different ratios based on 2 standard deviations of the Poisson distribution, 50 of these (91%) had p-values of 0.1 or less with the Welsh's T-test, while the remaining 5 had p-values of <0.14.

Cell numbers of the transcriptionally dominant prokaryotic organisms (those contributing the most transcripts to samples from this station) were estimated based on the metagenomic coverage of each reference genome. The number of protein encoding reads identified in the metagenomes (ACM3 and ACM4) for each taxon (found with a Blastx analysis of the metagenomic reads against the Refseq protein database) was divided by the number of protein encoding genes present in the reference genome for corresponding taxon. This average fold-coverage of the genes was used as an index of genome copy number, and we assumed one genome copy per cell.

Three of the most dominant prokaryotic organisms were used for a genome-wide comparative expression analysis between the two size fractions. Protein encoding reads binning to each of the three taxonomic bins were identified using Blastx against the Refseq protein database. KEGG GENE assignments for reads binning to CB0205, HTCC7211, and HTCC2080 were obtained by annotating the reference proteins against KEGG GENES using the KEGG Automatic Annotation Server (KAAS) (12) and KEGG pathway reconstruction was performed using MinPath (13). For each individual gene or pathway in a taxonomic bin, Poisson distributions were randomly generated using the rpois function in R with the lambda parameter equal to the count of reads, with 10,000 randomly sampled values returned. The resulting distributions were then averaged between replicate samples, and the mean and standard deviation from the resulting distributions were determined. These calculations were performed on each of the two size fractions, and each gene within a taxonomic bin was compared between the fractions. Genes or pathways were designated as differentially expressed when at least 2 standard deviations existed between the average values for each size fraction.

Ribosomal RNA gene sequences in the metagenomes were identified by mapping paired reads to 16S and 18S rRNA sequence databases with Bowtie2 (2.0.0-beta5) using local alignment mode with default options. Hits were classified with the classify.seqs program in mothur (1.24.0) (14) using a minimum bootstrap cutoff of 80%. Each end of the paired-end reads was also mapped individually to 16S and 18S rRNA sequence databases using the Bowtie2 end-to-end alignment mode with default options. Both members of the paired-end reads were classified with RTAX (v0.983) (15) in forward and reverse directions, and the read with the higher RTAX value of the pair was retained. The Greengenes 16S rRNA 99% OTUs (v.12.10) database (16) was used for classification of paired reads using mothur, the Greengenes 16S rRNA 97% OTUs (v.12.10) was used for unpaired reads using RTAX (due to limitations of the program), and a custom database of 18S rRNA genes modified from the Silva-euks (v.108) database (17) after removal of sequences with more than 5 ambiguous bases (1953 seqs), homopolymers greater than 10 bp (527 seqs), and long polymers of 6bp repeats (7 seqs). Eukaryotic taxonomy strings in this database were manually reduced to Kingdom, Phylum, Class, Order, Family, Genus, and Species.

Ribosomal RNA gene sequences from the tag sequencing were processed on the Data Intensive Academic Grid (DIAG) shared computational cloud at the University of Maryland School of Medicine Institute for Genome Sciences (IGS) with the AmpliconNoise pipeline (18), using recommended procedures for quality control (CleanMinMax.pl, PyroNoiseT, SeqDistT, SeqNoiseT). Maximum sequence length was set to 250 base pairs (Parse.pl), and chimeras were identified and removed (PerseusD). Sequences were clustered into operational taxonomic units (OTUs) using Qiime, and sequences from each sample were unweighted (unweight_fasta.py), concatenated, and subjected to primers removal. OTUs were identified using uclust (pick_otus.py), and representative sequences were selected (pick_rep_set.py). The taxonomy of OTUs was determined in MacQiime (assign_taxonomy.py), retraining the RDP Classifier to use the October 2012 Greengenes taxonomic database (16).

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Supplemental Figure Legends:

Figure S1. Taxonomic composition of the prokaryotic community in the Amazon River plume in June 2010 (Station 10).

Figure S2. Comparative taxonomic composition of free-living (FL) and particle-associated (PA) prokaryotic communities at six stations along the Amazon River plume in June 2010 as identified from taxonomic assignments of protein-encoding metagenomic reads.

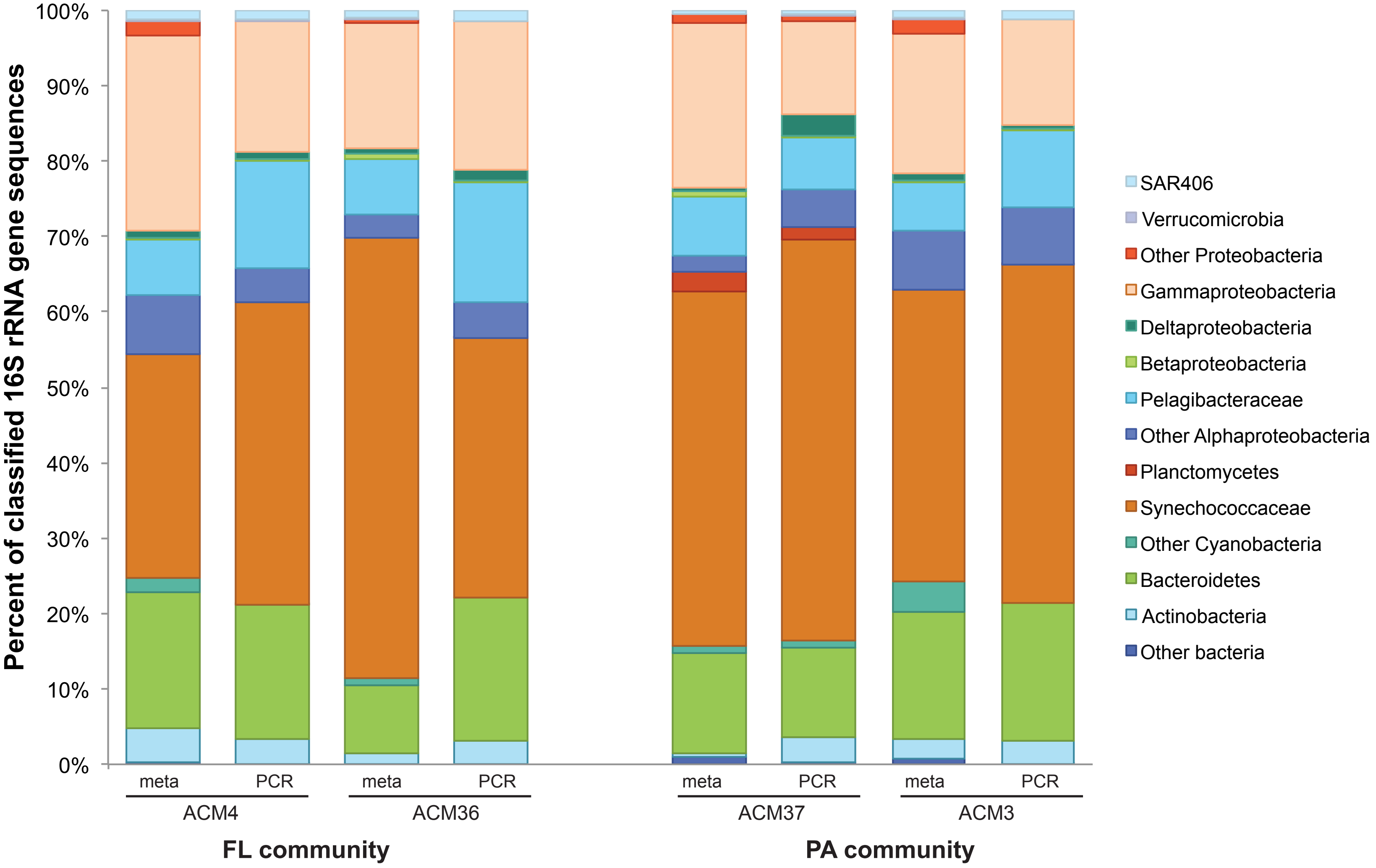
Figure S3. Relative contribution of the top 24 prokaryotic taxa to the genes and transcripts in the particle-associated community of the Amazon River plume.

Figure S4. Percent identity of metagenomic reads to the reference genome for universal single-copy genes *rpoB* (red), *gyrB* (green), and *recA* (blue) for the three most abundant taxa in the FL (dashed line) and PA (solid line) communities.

Figure S5. The importance of cell abundance versus gene regulation to the differential contribution of PA cells to the Amazon Plume metatranscriptome for three major bacterial taxa. For each taxon, the direction and magnitude of the difference in PA cells compared to FL cells that is attributed to each factor is shown for the 25 genes with the most positive and most negative differences, and KEGG pathway assignments are indicated by color-coded circles.

Figure S6. Photosynthesis-related genes in the *Synechococcus* sp. CB0205 bin exhibiting significantly different regulation between microenvironments. Gene functional annotations are based on KEGG pathways ko00195, ko00196, ko00710. Maroon = upregulated in free-living cells. No photosynthesis genes were upregulated in particle-associated cells

Fig. S1



Percent of classified 16S rRNA gene sequences
100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
meta
PCR
meta
PCR
meta
PCR
meta
PCR
ACM4
ACM36
ACM37
ACM3
FL community
PA community
SAR406
Verrucomicrobia
Other Proteobacteria
Gammaproteobacteria
Deltaproteobacteria
Betaproteobacteria
Pelagibacteraceae
Other Alphaproteobacteria
Planctomycetes
Synechococcaceae
Other Cyanobacteria
Bacteroidetes
Actinobacteria
Other bacteria

Fig. S2

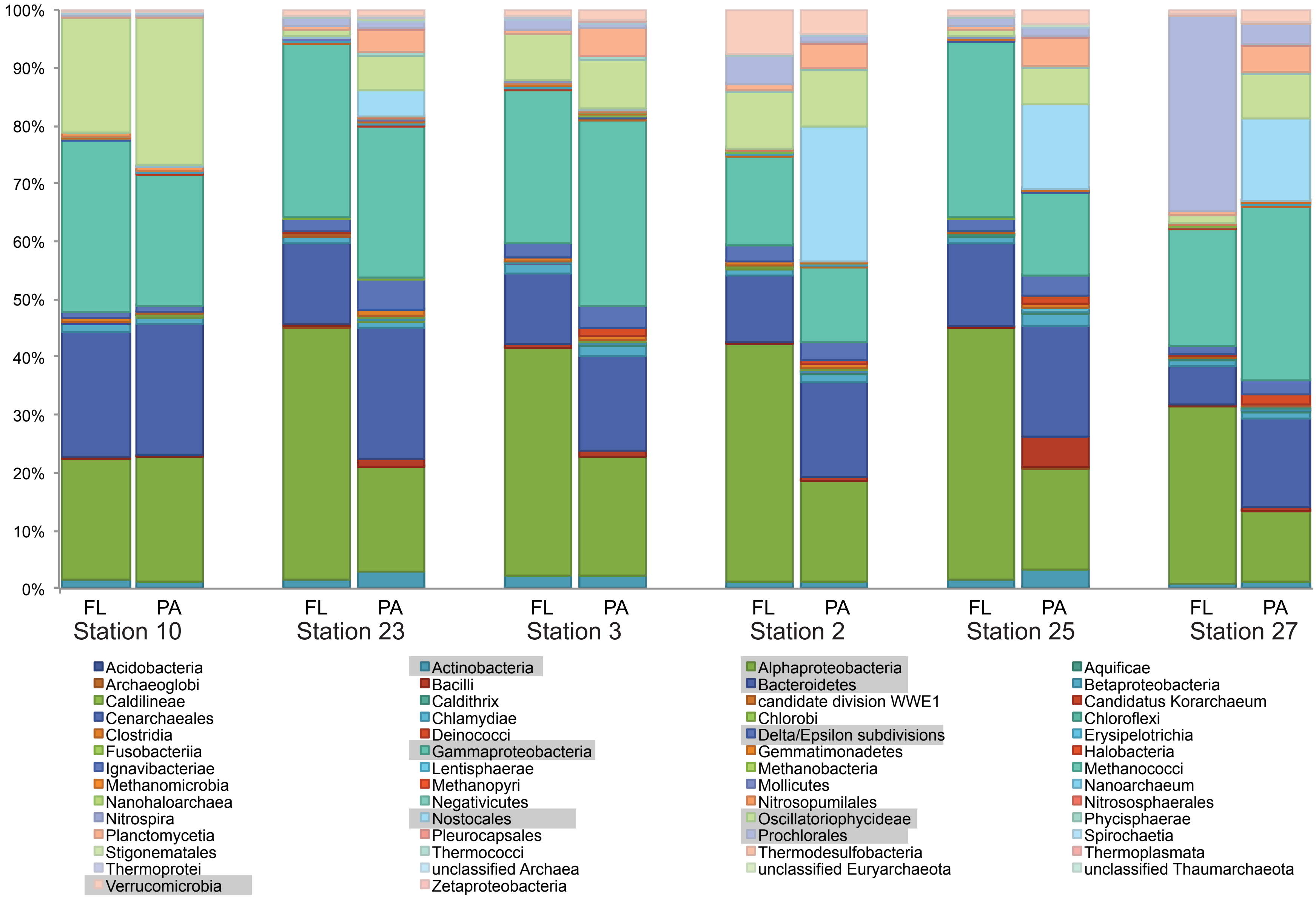

100%
90%
80%
70%
60%
50%
40%
30%
20%
10%
0%
FL
PA
Station 10
FL
PA
Station 23
FL
PA
Station 3
FL
PA
Station 2
FL
PA
Station 25
FL
PA
Station 27
Acidobacteria
Archaeoglobi
Caldilineae
Cenarchaeales
Clostridia
Fusobacteriia
Ignavibacteriae
Methanomicrobia
Nanohaloarchaea
Nitrospira
Planctomycetia
Stigonematales
Thermoprotei
Verrucomicrobia
Actinobacteria
Bacilli
Caldithrix
Chlamydiae
Deinococci
Gammaproteobacteria
Lentisphaerae
Methanopyri
Negativicutes
Nostocales
Pleurocapsales
Thermococci
unclassified Archaea
Zetaproteobacteria
Alphaproteobacteria
Bacteroidetes
candidate division WWE1
Chlorobi
Delta/Epsilon subdivisions
Gemmatimonadetes
Methanobacteria
Mollicutes
Nitrosopumilales
Oscillatoriophycideae
Prochlorales
Thermodesulfobacteria
unclassified Euryarchaeota
Aquificae
Betaproteobacteria
Candidatus Korarchaeum
Chloroflexi
Erysipelotrichia
Halobacteria
Methanococci
Nanoarchaeum
Nitrososphaerales
Phycisphaerae
Spirochaetia
Thermoplasmata
unclassified Thaumarchaeota

Fig. S3

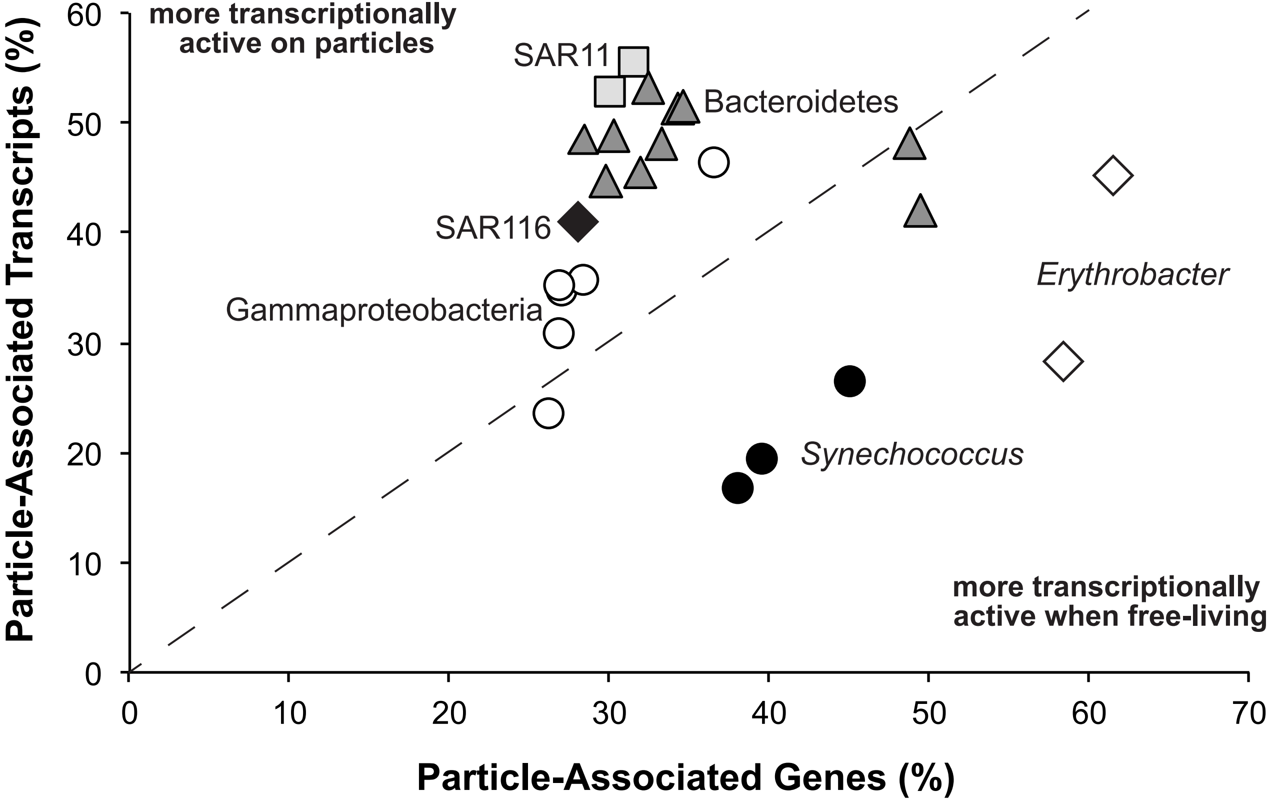

more transcriptionally active on particles
SAR11
Bacteroidetes
SAR116
Gammaproteobacteria
Erythrobacter
Synechococcus
more transcriptionally active when free-living
Particle-Associated Transcripts (%)
Particle-Associated Genes (%)
0
10
20
30
40
50
60
70

Fig. S4

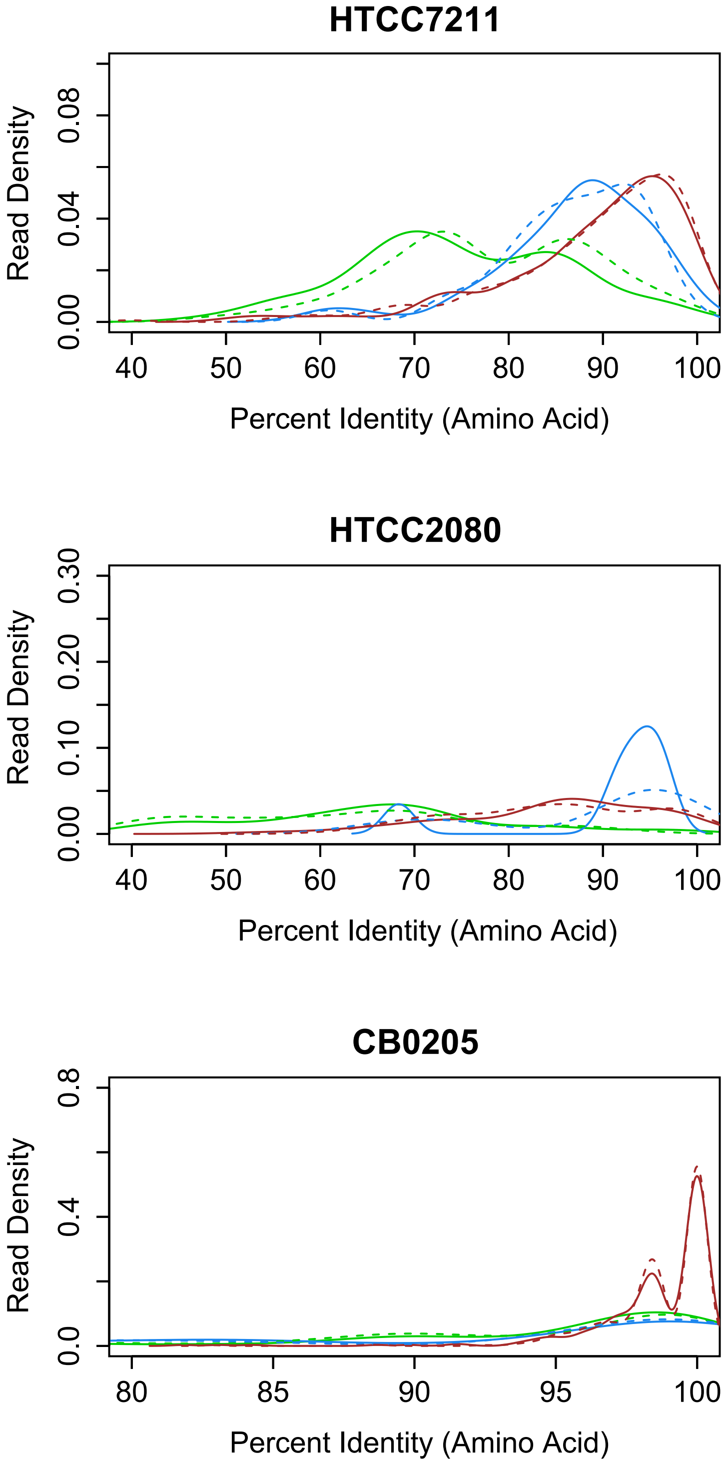
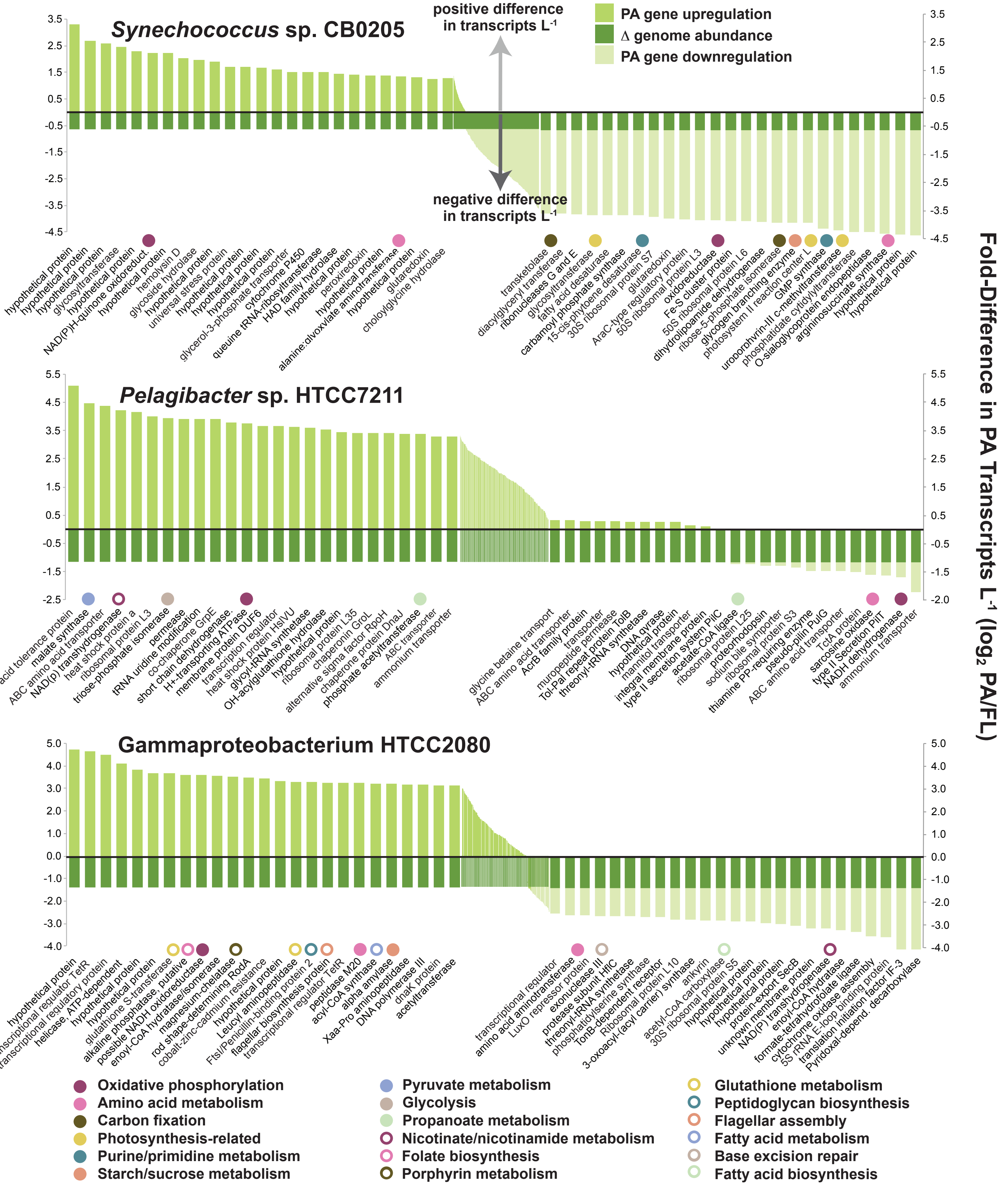

HTCC7211
Read Density
0.00
0.04
0.08
40
50
60
70
80
90
100
Percent Identity (Amino Acid)
HTCC2080
Read Density
0.00
0.10
0.20
0.30
40
50
60
70
80
90
100
Percent Identity (Amino Acid)
CB0205
Read Density
0.0
0.4
0.8
80
85
90
95
100
Percent Identity (Amino Acid)

Figure S5



Synechococcus sp. CB0205
positive difference in transcripts L-1
negative difference in transcripts L-1
PA gene upregulation
Δ genome abundance
PA gene downregulation
3.5
2.5
1.5
0.5
-0.5
-1.5
-2.5
-3.5
-4.5
hypothetical protein
hypothetical protein
hypothetical protein
glycosyltransferase
hypothetical protein
NAD(P)H-quinone oxidoreduct.
hypothetical protein
hemolysin D
glycoside hydrolase
hypothetical protein
universal stress protein
hypothetical protein
hypothetical protein
hypothetical protein
glycerol-3-phosphate transporter
cytochrome P450
queuine tRNA-ribosyltransferase
HAD family hydrolase
hypothetical protein
peroxiredoxin
hypothetical protein
alanine:glyoxylate aminotransferase
hypothetical protein
glutaredoxin
choloylglycine hydrolase
transketolase
diacylglyceryl transferase
ribonucleases G and E
glycosyltransferase
fatty acid desaturase
carbamoyl phosphate synthase
15-cis-phytoene desaturase
30S ribosomal protein S7
glutaredoxin
AraC-type regulatory protein
50S ribosomal protein L3
oxidoreductase
Fe-S cluster protein
50S ribosomal protein L6
dihydrolipoamide dehydrogenase
ribose-5-phosphate isomerase
glycogen branching enzyme
photosystem II reaction center L
GMP synthase
uroporphyrin-III c-methyltransferase
phosphatidate cytidylyltransferase
O-sialoglycoprotein endopeptidase
argininosuccinate synthase
hypothetical protein
hypothetical protein
Pelagibacter sp. HTCC7211
5.5
4.5
3.5
2.5
1.5
0.5
-0.5
-1.5
-2.5
-2.0
acid tolerance protein
malate synthase
ABC amino acid transporter
NAD(p) transhydrogenase
heat shock protein a
ribosomal protein L3
triose-phosphate isomerase
permease
tRNA uridine modification
co-chaperone GrpE
short chain dehydrogenase.
H+-transporting ATPase
membrane protein DUF6
transcription regulator
heat shock protein HslVU
glycyl-tRNA synthetase
OH-acylglutathione hydrolase
hypothetical protein
ribosomal protein L35
chaperonin GroL
alternative sigma factor RpoH
chaperone protein DnaJ
phosphate acetyltransferase
ABC transporter
ammonium transporter
glycine betaine transport
ABC amino acid transporter
AcrB family protein
transporter
muropeptide permease
Tol-Pal repeat protein TolB
threonyl-tRNA synthetase
DNA gyrase
hypothetical protein
mannitol transporter
integral membrane protein
type II secretion system PilC
acetate-CoA ligase
ribosomal protein L25
proteorhodopsin
sodium bile symporter
ribosomal protein S3
thiamine PP-requiring enzyme
pseudo-pilin PulG
ABC amino acid transporter
TctA protein
sarcosine oxidase
type II Secretion PilT
NADH dehydrogenase
ammonium transporter
Gammaproteobacterium HTCC2080
5.0
4.0
3.0
2.0
1.0
0.0
-1.0
-2.0
-3.0
-4.0
hypothetical protein
transcriptional regulator TetR
transcriptional regulatory protein
helicase, ATP-dependent
hypothetical protein
hypothetical protein
glutathione S-transferase
alkaline phosphatase, putative
possible NADH oxidoreductase
enoyl-CoA hydratase/isomerase
magnesium-chelatase
rod shape-determining RodA
cobalt-zinc-cadmium resistance
hypothetical protein
Leucyl aminopeptidase
FtsI/Penicillin-binding protein 2
flagellar biosynthesis protein
transcriptional regulator TetR
peptidase M20
acyl-CoA synthase
alpha amylase
Xaa-Pro aminopeptidase
DNA polymerase III
dnaK protein
acetyltransferase
transcriptional regulator
amino acid aminotransferase
LuxO repressor protein
exonuclease III
protease subunit HflC
threonyl-tRNA synthetase
phosphatidylserine synthase
TonB-dependent receptor
Ribosomal protein L10
3-oxoacyl-(acyl carrier) synthase
ankyrin
acetyl-CoA carboxylase
30S ribosomal protein S5
hypothetical protein
hypothetical protein
protein-export SecB
unknown membrane protein
NAD(P) transhydrogenase
enoyl-CoA hydratase
formate-tetrahydrofolate ligase
cytochrome oxidase assembly
5S rRNA E-loop binding protein
translation initiation factor IF-3
Pyridoxal-depend. decarboxylase
Fold-Difference in PA Transcripts L-1 (log2 PA/FL)
● Oxidative phosphorylation
● Amino acid metabolism
● Carbon fixation
● Photosynthesis-related
● Purine/primidine metabolism
● Starch/sucrose metabolism
● Pyruvate metabolism
● Glycolysis
● Propanoate metabolism
○ Nicotinate/nicotinamide metabolism
○ Folate biosynthesis
○ Porphyrin metabolism
○ Glutathione metabolism
○ Peptidoglycan biosynthesis
○ Flagellar assembly
○ Fatty acid metabolism
○ Base excision repair
○ Fatty acid biosynthesis

Figure S6

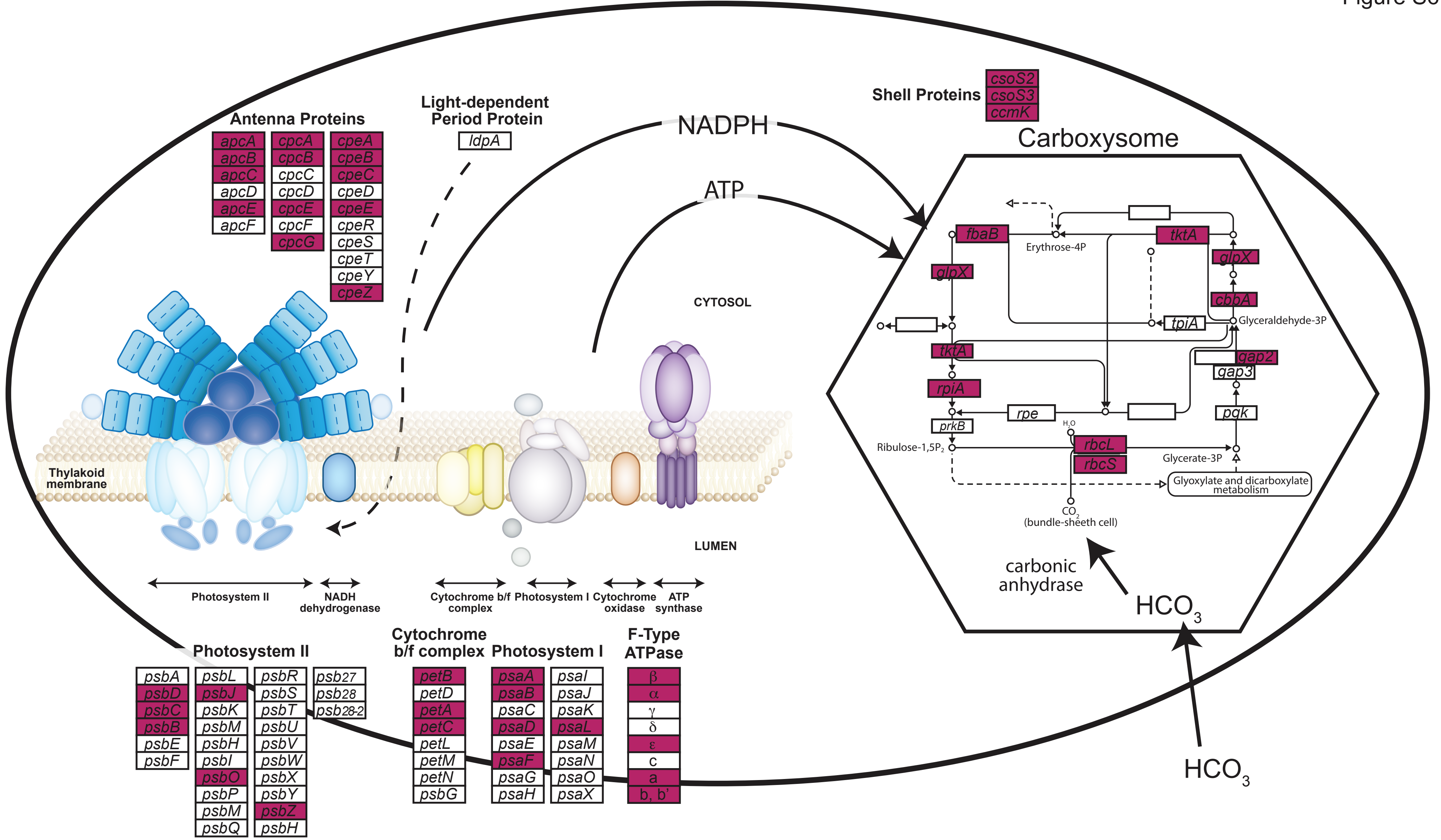

Antenna Proteins
apcA
apcB
apcC
apcD
apcE
apcF
cpcA
cpcB
cpcC
cpcD
cpcE
cpcF
cpcG
cpeA
cpeB
cpeC
cpeD
cpeE
cpeR
cpeS
cpeT
cpeY
cpeZ
Light-dependent Period Protein
ldpA
NADPH
ATP
Shell Proteins
csoS2
csoS3
ccmK
Carboxysome
CYTOSOL
LUMEN
Thylakoid membrane
fbaB
Erythrose-4P
tktA
glpX
glpX
cbbA
tpiA
Glyceraldehyde-3P
tktA
rpiA
gap2
gap3
rpe
pgk
prkB
H2O
Ribulose-1,5P2
rbcL
rbcS
Glycerate-3P
Glyoxylate and dicarboxylate metabolism
CO2 (bundle-sheeth cell)
carbonic anhydrase
HCO3
HCO3
Photosystem II
NADH dehydrogenase
Cytochrome b/f complex
Photosystem I
Cytochrome oxidase
ATP synthase
Photosystem II
psbA
psbD
psbC
psbB
psbE
psbF
psbL
psbJ
psbK
psbM
psbH
psbI
psbO
psbP
psbM
psbQ
psbR
psbS
psbT
psbU
psbV
psbW
psbX
psbY
psbZ
psbH
psb27
psb28
psb28-2
Cytochrome b/f complex
petB
petD
petA
petC
petL
petM
petN
petG
Photosystem I
psaA
psaB
psaC
psaD
psaE
psaF
psaG
psaH
psaI
psaJ
psaK
psaL
psaM
psaN
psaO
psaX
F-Type ATPase
β
α
γ
δ
ε
c
a
b, b'

Table S1. Internal standard addition and recoveries.

	Sample	Standard Copies Added	Standard Copies Recovered	Sequencing Depth (%)	Volume Filtered (L)	Normalization Factor
	Metatranscriptomes					
Standard 1 (pTXB1, 916 nt)	ACM11	2.10×10^{10}	19,640	9.25×10^{-5}	5.9	1.81×10^{5}
	ACM29	2.10×10^{10}	13,769	6.54×10^{-5}	4.8	3.18×10^{5}
	ACM12	2.10×10^{10}	22,233	10.57×10^{-5}	5.9	1.60×10^{5}
	ACM30	2.10×10^{10}	7,793	3.70×10^{-5}	3.3	8.18×10^{5}
Standard 2 (pFN18A, 970 nt)	ACM11	1.17×10^{10}	11,350	9.68×10^{-5}	5.9	1.75×10^{5}
	ACM29	1.17×10^{10}	6,313	5.39×10^{-5}	4.8	3.87×10^{5}
	ACM12	1.17×10^{10}	8,404	7.17×10^{-5}	5.9	2.36×10^{5}
	ACM30	1.17×10^{10}	3,139	2.68×10^{-5}	3.3	1.13×10^{6}
	Metagenomes					
Thermus thermophilus HB8 (Genomic DNA)	ACM4	1.86×10^{7}	1.428	7.66×10^{-6}	4.8	2.72×10^{6}
	ACM36[†]	-	-	-	5.2	-
	ACM3	2.02×10^{7}	1.654	8.19×10^{-6}	5.2	2.35×10^{6}
	ACM37	1.86×10^{7}	0.287	1.54×10^{-6}	4.8	1.35×10^{7}
	Poly(A) Metatranscriptomes					
Standard 3 (HAP-1, 499 nt)	ACM8	2.00×10^{9}	17,455	8.73×10^{-4}	5.5	2.08×10^{4}
	ACM27	2.00×10^{9}	11,362	5.68×10^{-4}	7.4	1.54×10^{3}

[†] Standards were added incorrectly to sample ACM36; gene normalization was estimated based on replicate sample ACM4.

Table S2. IDs and descriptions of 74 biogeochemically relevant genes.

ID	Gene/Protein	Description
pepA	Glutamyl aminopeptidase	Calcium-stimulated exopeptidase that selectively hydrolyze acidic amino acid residues with a preference for certain Glutamine
pepL	Leucyl aminopeptidase	Hydrolytic exopeptidase with a preference for certain Leucine and hydrophobic amino acid substrates
pepM	Methionyl aminopeptidase	Ubiquitous, essential exopeptidase that cleaves N-terminal Methionine residues from cellular proteins
pepN	Alanyl aminopeptidase	Broad specificity exopeptidase that cleaves amino acid residues from the N-terminus of peptides and protein substrates with a preference for certain Alanine
pepP/pepX	Prolyl aminopeptidase (PAP) or Xaa-Pro aminopeptidase (XAP)	PAPs preferentially cleave N-terminal proline residues from cellular proteins; XAPs are prolidases that catalyze the cleavage of Xaa-Pro dipeptides or act on aminoacyl-hydroxyproline analogs but does not act on Pro-Pro bonds
GAPDH	Glyceraldehyde-3-phosphate dehydrogenase	Catalyzes the reversible interconversion of glyceraldehyde-3-phosphate and 1,3-diphosphoglycerate
pgi	Glucose-6-phosphate isomerase	Catalyzes the reversible isomerization of glucose-6-phosphate and fructose-6-phosphate
metF	Methylenetetrahydrofolate reductase	Catalyzes the reduction of 5,10-methylenetetrahydrofolate to 5-methyltetrahydrofolate, which is then further used in the final step of methionine biosynthesis
bglA	Beta-glucosidase	Catalyzes the hydrolysis of terminal non-reducing residues in beta-glucosides with release of glucose
pcaH	Protocatechuate 3,4-dioxygenase (3,4-PCD)	Part of the β-ketoadipate pathway that catalyzes the conversion of protocatechuate to citric acid cycle intermediates
vanA	Vanillate demethylase	Involved in vanillate (a lignin-derived monoaryl) degradation by vanillate-utilizing aerobic bacteria
phaC	Polyhydroxyalkanoate synthase	Catalyzes the polymerization of (R)-3-hydroxybutyryl-CoA to form the polyhydroxyalkanoate polymer, the last step in polyhydroxyalkanoate biosynthesis
phaP	Phasin	Coats the surface of the polyhydroxyalkanoate granules, preventing them from coalescing, in turn stabilizing the granules
phaR	Polyhydroxyalkanoate regulator	Transcriptional regulator of polyhydroxyalkanoate biosynthesis
phaZ	Polyhydroxyalkanoate depolymerase	Responsible for intracellular degradation of polyhydroxyalkanoate
amoA	Ammonia monooxygenase subunit A	Catalyzes oxidation of ammonia to hydroxylamine, the first step in the oxidation of ammonia to nitrite.
amtB	Ammonium transporter B	Membrane-bound ammonium/methylammonium transport B protein thought to be required during low [NH(x)]
cphA	Cyanophycin synthetase	Catalyzes the synthesis of cyanophycin granule polypeptide (CGP), which is used as a temporary nitrogen reserve.
cphB	Cyanophycinase	Hydrolyzes cyanophicin to the dipeptide β-Asp-Arg, the first step in making stored amino acids available to the cell
glnA	Glutamine synthetase	Catalyzes the ATP-dependent cycle whereby ammonia is incorporated into glutamate to form glutamine, the first step for ammonia assimilation into organic nitrogen
napA	Nitrate reductase subunit A	Large subunit of the Nap periplasmic nitrate reductase that catalyzes the first step of the denitrification process by conversion of nitrate to nitrite
nirK	Nitrite reductase	Key enzyme in the dissimilatory denitrification process that catalyzes the reduction of nitrite to NO
phnD	Phosphonate ABC transporter, periplasmic binding protein	Periplasmic binding protein of an ABC-type transporter system required for utilization of phosphonates and organophosphorus compounds
phnE	Phosphonate ABC transporter, integral membrane protein	Integral membrane protein of an ABC-type transporter system required for utilization of phosphonates and organophosphorus compounds
phnG	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the corresponding hydrocarbons.
phnH	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the corresponding hydrocarbons
phnM	C-P lyase	Part of a membrane associated C-P lyase complex required for hydrolysis of C-P bonds to yield inorganic phosphate and the

		corresponding hydrocarbons
phoA	Alkaline phosphatase	Dephosphorylates organic phosphates and is induced under phosphate starvation as a means to generate free phosphate groups for uptake and use
phoD	Alkaline phosphatase	Belongs to the Pho regulon and codes for codes for alkaline phosphatase D (APaseD), which is a secreted phosphodiesterase
phoU	Alkaline phosphatase	Serves as a signal transduction mediator, being involved in free inorganic P transport and acting as a regulator of the phosphate-specific transport system
phoX	Alkaline phosphatase	Encodes an alkaline phosphatase that uses Ca^{2+} as a cofactor and can be responsible for extracellular phosphatase activity under phosphorus limitation
pitA	Low affinity PO_4 transporter	Low-affinity inorganic phosphate transporter and when inorganic phosphate is abundant, pitA is its major uptake system
ppk1	Polyphosphate kinase	Reversibly synthesizes inorganic polyphosphate, a storage polymer made up of tens to hundreds of phosphate residues linked together by high-energy bonds
ppk2	Polyphosphate kinase	Can polymerize into an actin-like filament concurrent with its reversible synthesis of inorganic polyphosphate
pstA	Phosphate ABC transporter, permease	Membrane permease in the high-affinity phosphate-specific transport (Pst) system that facilitates the transport of phosphate across the membrane
pstC	Phosphate ABC transporter, permease	Membrane permease in the high-affinity phosphate-specific transport (Pst) system that facilitates the transport of phosphate across the membrane
pstS	Phosphate ABC transporter, periplasmic binding protein	Phosphate-binding lipoprotein found within the periplasm of the cell, it is part of the high-affinity phosphate-specific transport (Pst) system
aprA	Adenosine-5'-phosphosulfate reductase (Apr), alpha subunit	Subunit A of dissimilatory adenosine-5'-phosphosulfate (APS) reductase aprAB gene complex that catalyzes the reduction of APS to AMP and sulfite during sulfur reduction
aprB	Adenosine-5'-phosphosulfate reductase (Apr), beta subunit	Subunit B of dissimilatory adenosine-5'-phosphosulfate (APS) reductase aprAB gene complex that catalyzes the reduction of APS to AMP and sulfite during sulfur reduction
cysI	Sulfite reductase	Assimilatory sulfite reduction enzyme that catalyzes the reaction of sulfite to sulfide
cysK	Cysteine synthase	Involved in sulfur metabolism and synthesizes cysteine, the predominant mechanism by which inorganic sulfur is reduced and incorporated into organic compounds
dddD	Type III acyl coenzyme A transferase	Mediates the cleavage of DMSP forming DMS and a 3-carbon compound
dddQ	DMSP lyase	Mediates the cleavage of DMSP forming DMS and a 3-carbon compound
dmdA	DMSP demethylase	Catalyzes the first step in the DMSP demethylation pathway - cleavage of a methyl group from DMSP, eventually resulting in methionine formation and C oxidation
soxA	Cytochrome *c* (diheme)	One of the seven structural proteins involved in sulfur oxidation it combines with the SoxX protein form a cytochrome c complex that is located in the periplasm of the cell and is involved in electron transport
soxB	Sulfate thiohydrolase	One of the seven structural proteins involved in sulfur oxidation it is a type of cytochrome c protein that is located in the periplasm and is involved in the electron transport chain
fliC	Filament protein; flagellin	Structural filament protein, synthesized in the cytosol, composed of monomeric subunits that are polymerized into the long helical filament of the bacterial flagellum
fliF	MS-ring protein	Transmembrane flagellar MS-ring protein, part of the flagellar basal body, that anchors the flagellum to the cytoplasmic membrane
fliG	Flagellar motor switch protein	Essential for assembly, rotation and clockwise/counter-clockwise switching of the bacterial flagellum
motA	Flagellar motor protein	Along with MotB couples flagellar rotation to proton/sodium motive force across the membrane and forms the stator elements of the rotary flagellar machine, required for flagellar rotation
motB	Flagellar motor protein	Along with MotA couples flagellar rotation to proton/sodium motive force across the membrane and forms the stator elements of the rotary flagellar machine, required for flagellar rotation
cheA	Histidine kinase	A cytoplasmic histidine kinase that donates phosphate groups to

		CheY and CheB, which control flagellar responses and sensory adaptation, respectively
cheB	Methylesterase	A phosphorylation-activated response regulator involved in reversible modification of bacterial chemotaxis receptors. It is required for tumbling movement and regulates tumbling frequency based on perceived tumble-modulating signals (i.e. nutrient concentration) formed by the chemoreceptors
cheR	Methyltransferase	Involved in reversible modification of bacterial chemotaxis receptors, it plays a role in the chemosensory response and adaptation of the cell to chemical stimuli
cheW	Signaling protein	Plays a role in coupling methyl-accepting chemotaxis proteins, it regulates motility behavior by two distinct signals, one that stimulates and one that inhibits the intracellular phosphorylation cascade by its effect on the histidine kinase CheA
thiC	Phosphomethylpyrimidine synthase	Catalyzes the pyrimidine branch of the Thiamin biosynthesis pathway, converting 5-aminoimidazole ribonucleotide to hydroxymethylpyrimidine phosphate
thiL	Thiamin-monophosphate kinase	Catalyzes the final step of the thiamin pyrophosphate biosynthesis pathway
pdxH	Pyridoxine 5'-phosphate oxidase	Catalyzes the oxidation of pyridoxine 5'-phosphate to pyridoxal 5'-phosphate in the final step of vitamin B6 biosynthesis
pdxJ	Pyridoxine 5'-phosphate synthase	Catalyzes the condensation of 1-deoxy-d-xylulose-5-phosphate and 1-amino-3-oxo-4-(phosphohydroxy)propan-2-one to pyridoxine 5'-phosphate, a reaction involved in de novo biosynthesis of pyridoxine (vitamin B6) and pyridoxal phosphate
fecA	Ferric dicitrate transporter	TonB-ExbB-dependent ferric-siderophore specific outer membrane receptor protein. When intracellular iron is low, exogenous ferric citrate binds to the FecA receptor, which signals for and aids in translocation of ferric citrate into the cell
feoB	Fe(II) G protein-like transporter	Membrane-bound G protein-like transporter, essential for Fe(II) uptake in bacteria during conditions of low oxygen
Ftr1	High affinity Fe(II) permease	Permease component of a high-affinity Fe(II) uptake system. Expression may be increased during Fe limitation
afuA/futA/hitA/idiA	Periplasmic Fe(III) ABC transporter	Iron-deficiency-induced, periplasmic iron-binding protein component of a ferric iron ABC-transporter system
afuB/futB	Fe(III) ABC transporter permease	Hydrophobic ferric iron ABC transporter permease protein
PR	Proteorhodopsin	Mediates light-driven proton pumps for harvesting and conversion of light into energy
bchX	Chlorophyll iron protein	Part of a photosynthetic gene cluster involved in redox reactions of the bacteriochlorophyll biosynthesis pathway
pufL	Photosynthetic reaction center subunit L	The light subunit of the photosynthetic reaction center, it helps provide the scaffolding for the chromophore in the reaction center
pufM	Photosynthetic reaction center subunit M	The medium subunit of the photosynthetic reaction center, it helps provide the scaffolding for the chromophore in the reaction center
psbB	Photosystem II CP47 chlorophyll apoprotein	Photosystem II protein that binds to chlorophyll and is found in plants, algae, and cyanobacteria
cpcD	Phycocyanin-assoc. linker polypeptide	Structural component of the phycobilisome
α-*ca*	α carbonic anhydrase	Zinc metalloenzyme found in bacteria, archaea, and eukaryota that participates in CO_2 diffusion, interconversion of CO_2 and HCO_3 during photosynthesis, pH homeostasis, and ion transport
ε-*ca*	ε carbonic anhydrase	Zinc metalloenzyme found in cyanobacteria carboxysomes and chemolithoautotrophs that participates in CO_2 diffusion, interconversion of CO_2 and HCO_3 during photosynthesis, pH homeostasis, and ion transport
rbcL (IA)	Ribulose 1,5-bisphosphate carboxylase/oxygenase form IA (RuBisCO IA)	Catalyzes the first, rate-limiting step of the Calvin cycle, the primary pathway for photosynthetic carbon reduction in the oceans; rbcL IA has been found in α, β, and γ-proteobacteria, cyanobacteria and prochlorales
rbcL (II)	Ribulose 1,5-bisphosphate carboxylase/oxygenase form II (RuBisCO II)	Catalyzes the first, rate-limiting step of the Calvin cycle, the primary pathway for photosynthetic carbon reduction in the oceans; rbcL II has been found in α, β, and γ-proteobacteria, and eukaryotes

Table S3. Gene expression ratios in the *Synechococcus* sp. CB0205 bin.

NCBI GI	Protein Description	Mean Expression Ratio (FL)	Mean Expression Ratio (PA)	PA Regulation
497998808	hypothetical protein SCB02_00319	0.0159	0.0511	Up
497998935	hypothetical protein SCB02_00599	0.0039	0.016	Up
497999395	hypothetical protein SCB02_01633	0.0223	0.1099	Up
497999396	hypothetical protein SCB02_01638	0.0421	0.1981	Up
498000149	tRNA nucleotidyltransferase/poly(A) polymerase	0.014	0.0326	Up
498000159	glycosyltransferase	0.002	0.011	Up
498000180	hypothetical protein SCB02_03348	0.0304	0.1832	Up
498000306	queuine tRNA-ribosyltransferase	0.0105	0.0296	Up
498000620	hypothetical protein SCB02_04388	0.0309	0.051	Up
498000622	dihydrobiliverdin:ferredoxin oxidoreductase	0.0305	0.072	Up
498000774	NAD(P)H-quinone oxidoreductase subunit N	0.0103	0.0485	Up
498000927	putative enolase-phosphatase E-1	0.0086	0.0233	Up
498001071	hypothetical protein SCB02_05303	0.3047	0.7016	Up
498001275	outer envelope membrane protein	0.0193	0.0296	Up
498001991	hypothetical protein SCB02_07563	0.0106	0.0325	Up
498002581	sugar kinase	0.0242	0.0526	Up
498002588	hypothetical protein SCB02_09140	0.0031	0.0116	Up
498002720	serine:pyruvate/alanine:glyoxylate aminotransferase	0.1162	0.2943	Up
498002799	thioredoxin peroxidase	0.0792	0.2075	Up
498003008	hypothetical protein SCB02_10519	0.0041	0.0404	Up
498003662	alpha-glucosidase	0.01	0.0388	Up
498003678	superfamily II DNA/RNA helicase	0.0876	0.1566	Up
498003936	putative L-cysteine/cystine lyase	0.023	0.0477	Up
497992572	hypothetical protein SCB02_00062	0.0039	0.0015	Down
497998706	protein phosphatase 2C	0.0088	0.003	Down
497998744	30S ribosomal protein S14	0.0903	0.0132	Down
497998754	polynucleotide phosphorylase/polyadenylase	0.017	0.0051	Down
497998755	hypothetical protein SCB02_00354	0.0159	0.0056	Down
497998831	hypothetical protein SCB02_00369	0.01	0.0031	Down
497998836	methionine sulfoxide reductase B	0.0263	0.0072	Down
497998838	putative lipidA disaccharide synthetase	0.0134	0.0035	Down
497998840	acetyl-CoA carboxylase biotin carboxylase subunit	0.0127	0.0033	Down
497998842	hypothetical protein SCB02_00389	0.0148	0.004	Down
497998855	ATPase	0.0201	0.0099	Down
497998861	FeS assembly ATPase SufC	0.0196	0.0059	Down
497998888	ferredoxin-thioredoxin reductase catalytic chain	0.0203	0.0088	Down
497998890	transcriptional regulator	0.0176	0.0046	Down
497998893	phycobilisome rod-core linker polypeptide cpcG	0.0612	0.0169	Down
497998906	Rho termination factor domain-containing protein	0.0246	0.0088	Down
497998908	hypothetical protein SCB02_00569	0.0138	0.0034	Down
497998918	peroxiredoxin	0.0076	0.0024	Down
497998942	peroxiredoxin	0.0386	0.0167	Down
497998956	periplasmic trypsin-like serine protease	0.0301	0.0048	Down
497998977	RND family outer membrane efflux protein	0.0109	0.0049	Down
497999018	photosystem II complex extrinsic protein precursor U	0.0269	0.0168	Down
497999025	hypothetical protein SCB02_00786	0.0503	0.0175	Down
497999029	2-methylthioadenine synthetase	0.0049	0.0022	Down
497999031	major facilitator superfamily permease	0.0084	0.002	Down
497999034	Fe-S oxidoreductase	0.0108	0.0068	Down
497999038	6-pyruvoyl tetrahydropterin synthase	0.0231	0.0053	Down
497999047	zeta-carotene desaturase	0.0166	0.0058	Down
497999080	porin	0.0277	0.0136	Down
497999098	porin	0.0505	0.0211	Down
497999102	glycosyl transferase family protein	0.0045	0.0015	Down
497999105	glycosyltransferase	0.0069	0.0034	Down
497999112	hypothetical protein SCB02_00966	0.0083	0.0024	Down
497999113	photosystem II D2 protein (photosystem q(a) protein)	0.043	0.0195	Down
497999117	copper-transporting ATPase	0.006	0.0015	Down
497999144	RNA-binding protein	0.0412	0.0168	Down
497999166	phytoene synthase	0.0186	0.0041	Down
497999169	phytoene dehydrogenase	0.0156	0.0019	Down
497999172	NAD(P)H-quinone oxidoreductase subunit F	0.0383	0.0084	Down
497999182	NAD(P)H-quinone oxidoreductase subunit 4	0.0112	0.004	Down
497999184	nucleoside-diphosphate-sugar transferase	0.0206	0.0069	Down
497999190	methylenetetrahydrofolate reductase	0.0107	0.0023	Down
497999193	NADH:ubiquinone oxidoreductase subunit J	0.0489	0.0082	Down
497999206	NADH:ubiquinone oxidoreductase subunit H	0.0332	0.0109	Down
497999210	citrate synthase	0.0112	0.0031	Down
497999212	NAD(P)H-quinone oxidoreductase subunit H	0.0214	0.0076	Down
497999253	TM2 domain-containing protein	0.0062	0.0027	Down
497999262	glutathione synthetase	0.0128	0.0022	Down
497999283	arginyl-tRNA synthetase	0.0114	0.0016	Down
497999304	guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	0.0126	0.0047	Down
497999312	two-component response regulator	0.0068	0.002	Down
497999338	50S ribosomal protein L10	0.0666	0.0183	Down
497999369	50S ribosomal protein L1	0.0394	0.0072	Down
497999371	50S ribosomal protein L11	0.1236	0.0245	Down
497999373	transcription antitermination protein NusG	0.0385	0.0065	Down
497999374	putative kinase	0.0075	0.0034	Down
497999379	aspartyl/glutamyl-tRNA amidotransferase subunit B	0.0091	0.002	Down
497999386	arginine decarboxylase	0.0041	0.0022	Down
497999391	putative flavoprotein	0.01	0.0023	Down
497999419	hypothetical protein SCB02_01718	0.2035	0.0677	Down
497999425	glycine dehydrogenase	0.0111	0.0018	Down
497999427	glycine cleavage system protein H	0.0104	0.0037	Down
497999429	50S ribosomal protein L9	0.0245	0.0053	Down
497999439	DnaB replicative helicase	0.0076	0.003	Down
497999442	putative membrane protein of ABC transport system	0.012	0.0023	Down

497999576	putative urea ABC transporter, substrate binding protein	0.0335	0.0057	Down
497999578	hypothetical protein SCB02_02052	0.0503	0.0038	Down
497999603	uroporphyrin-III c-methyltransferase	0.0259	0.0022	Down
497999605	ferredoxin-nitrite reductase	0.025	0.0084	Down
497999612	formate and nitrite transporters	0.0995	0.0158	Down
497999614	hypothetical protein SCB02_02092	0.0153	0.0051	Down
497999620	assimilatory nitrate reductase (ferredoxin) precursor	0.0065	0.0017	Down
497999627	nitrate permease NapA	0.0123	0.0016	Down
497999629	major facilitator superfamily permease	0.0041	0.0013	Down
497999648	polyphosphate kinase	0.0025	0.0008	Down
497999650	formyltetrahydrofolate deformylase	0.0104	0.0027	Down
497999669	molecular chaperone DnaK	0.0127	0.0024	Down
497999678	argininosuccinate synthase	0.0205	0.0016	Down
497999690	excinuclease ABC subunit B	0.0057	0.0009	Down
497999730	trigger factor	0.0084	0.0028	Down
497999746	ATP-dependent Clp protease proteolytic subunit ClpP	0.0117	0.003	Down
497999748	glycosyl transferase, group 2 family protein	0.0246	0.0057	Down
497999757	sulfolipid biosynthesis protein (UDP-sulfoquinovose synthase)	0.0458	0.0071	Down
497999772	putative penicillin-binding protein	0.0038	0.001	Down
497999776	GMP synthase	0.0286	0.0025	Down
497999781	elongation factor P	0.0301	0.0065	Down
497999813	putative cyclophilin-type peptidyl-prolyl cis-trans isomerase	0.0071	0.0033	Down
497999815	glyceraldehyde 3-phosphate dehydrogenase	0.0422	0.0112	Down
497999820	UDP-N-acetylmuramate--L-alanine ligase	0.0072	0.0013	Down
497999822	chaperone protein DnaJ	0.0079	0.002	Down
497999832	Na+/H+ antiporter	0.0418	0.0114	Down
497999848	phosphorylase	0.008	0.0041	Down
497999852	acyl carrier protein	0.0217	0.0066	Down
497999932	3-oxoacyl-acyl-carrier-protein] synthase II	0.0706	0.01	Down
497999934	transketolase	0.0321	0.0041	Down
497999936	thiamine biosynthesis protein ThiC	0.0232	0.014	Down
497999938	hypothetical protein SCB02_02826	0.0233	0.0053	Down
497999940	cysteine synthase A	0.0081	0.0018	Down
497999957	lysyl-tRNA synthetase	0.0068	0.0011	Down
497999971	signal recognition particle-docking protein FtsY	0.0118	0.0031	Down
497999977	hypothetical protein SCB02_02916	0.0352	0.0082	Down
497999980	hypothetical protein SCB02_02921	0.0167	0.0031	Down
497999982	DNA gyrase/topoisomerase IV, subunit A	0.0065	0.0024	Down
497999988	excinuclease ABC subunit A	0.0066	0.0022	Down
497999990	DNA repair ATPase RecN	0.0043	0.0013	Down
497999992	DNA polymerase III subunit beta	0.0067	0.004	Down
498000001	phosphoribosylformylglycinamidine synthase II	0.0169	0.0051	Down
498000004	amidophosphoribosyltransferase	0.0207	0.0061	Down
498000007	photosystem II reaction center protein Z	0.0449	0.0142	Down
498000019	preprotein translocase subunit SecA	0.011	0.0038	Down
498000035	Mg2+ transporter	0.0113	0.0058	Down
498000058	S-adenosyl-L-homocysteine hydrolase	0.0151	0.0022	Down
498000087	rod shape-determining protein MreB	0.0051	0.0018	Down
498000093	argininosuccinate lyase	0.0092	0.0023	Down
498000103	hypothetical protein SCB02_03193	0.013	0.0023	Down
498000109	glycosyl transferase family protein	0.0089	0.0031	Down
498000114	amino acid permease-associated region	0.0086	0.002	Down
498000123	carbamoyltransferase	0.0127	0.0045	Down
498000128	hypothetical protein SCB02_03238	0.021	0.0032	Down
498000131	isocitrate dehydrogenase	0.0175	0.0049	Down
498000135	Heme oxygenase (decyclizing)	0.0505	0.0226	Down
498000140	glycosyl transferase family protein	0.0181	0.0081	Down
498000142	ABC-type multidrug transport system, ATPase and permease components	0.0154	0.0067	Down
498000145	glycosyltransferase	0.0087	0.0039	Down
498000172	hypothetical protein SCB02_03393	0.008	0.0033	Down
498000199	hypothetical protein SCB02_03418	0.013	0.0035	Down
498000210	GDP-mannose 4,6-dehydratase	0.0129	0.0051	Down
498000212	dTDP-glucose 4-6-dehydratase-like protein	0.0233	0.006	Down
498000216	UDP-glucose 6-dehydrogenase	0.0087	0.0021	Down
498000219	photosystem II reaction center protein J	0.0666	0.0133	Down
498000221	photosystem II reaction center L	0.0997	0.0101	Down
498000224	cytochrome b559 subunit beta	0.0402	0.0162	Down
498000226	Ycf48-like protein	0.0214	0.0113	Down
498000229	rubredoxin	0.0167	0.0039	Down
498000231	NADH:ubiquinone oxidoreductase subunit A	0.0319	0.0051	Down
498000233	NADH dehydrogenase subunit B	0.052	0.007	Down
498000235	magnesium chelatase, ATPase subunit D	0.0063	0.0024	Down
498000249	DegT/DnrJ/EryC1/StrS aminotransferase family protein	0.0085	0.0025	Down
498000257	imidazoleglycerol-phosphate dehydratase	0.014	0.0044	Down
498000269	lignostilbene-alpha,beta-dioxygenase and related enzyme	0.004	0.0016	Down
498000271	hypothetical protein SCB02_03573	0.0178	0.0048	Down
498000276	phosphoglucomutase/phosphomannomutase family protein	0.0079	0.0025	Down
498000281	hypothetical protein SCB02_03653	0.174	0.0597	Down
498000312	hypothetical protein SCB02_03668	0.0267	0.0095	Down
498000316	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	0.01	0.0017	Down
498000318	serine hydroxymethyltransferase	0.0134	0.0032	Down
498000325	glycosyltransferase	0.0099	0.004	Down
498000326	isopropylmalate isomerase large subunit	0.0177	0.0038	Down
498000328	alpha mannosidase	0.0053	0.0028	Down
498000331	Sec-independent protein translocase protein TatA	0.0601	0.0215	Down
498000334	hypothetical protein SCB02_03788	0.0051	0.0021	Down
498000338	CRP family global nitrogen regulatory protein	0.0131	0.0032	Down
498000341	putative inorganic carbon transporter/0-antigen polymerase (ICT/OAP) family protein	0.0051	0.0018	Down
498000366	hypothetical protein SCB02_03863	0.019	0.0099	Down
498000372	beta carotene hydroxylase	0.0176	0.0037	Down
498000381	coenzyme A biosynthesis bifunctional protein CoaBC (DNA/pantothenate metabolism flavoprotein)	0.0101	0.0026	Down
498000401	photosystem II manganese-stabilizing protein	0.034	0.0091	Down
498000406	Sulfate adenylyltransferase	0.031	0.0083	Down

498000408	cell division protein FtsH	0.033	0.0085	Down
498000410	chorismate synthase	0.0192	0.0038	Down
498000415	Fe-S oxidoreductase	0.0115	0.0049	Down
498000432	ATP-dependent Clp protease adaptor protein ClpS	0.0168	0.0034	Down
498000435	L,L-diaminopimelate aminotransferase	0.0065	0.0014	Down
498000437	ribonucleases G and E	0.0254	0.0032	Down
498000443	cyclopropane-fatty-acyl-phospholipid synthase family protein	0.013	0.0023	Down
498000460	Lon protease domain-containing protein	0.0238	0.0049	Down
498000463	elongation factor Tu	0.1445	0.0376	Down
498000466	elongation factor G	0.1601	0.0211	Down
498000468	30S ribosomal protein S7	0.0486	0.0057	Down
498000472	hypothetical protein SCB02_04086	0.004	0.002	Down
498000478	ferredoxin-dependent glutamate synthase	0.0243	0.0041	Down
498000481	lipoyl synthase	0.0097	0.0048	Down
498000485	photosystem I P700 chlorophyll a apoprotein A1	0.0941	0.0518	Down
498000493	photosystem I P700 chlorophyll a apoprotein A1	0.1211	0.0508	Down
498000503	photosystem I P700 chlorophyll a apoprotein A2	0.0839	0.0468	Down
498000505	universal stress protein	0.0212	0.0116	Down
498000517	photosystem II PsbB protein	0.1362	0.0488	Down
498000524	30S ribosomal protein S1	0.0674	0.0091	Down
498000533	S-adenosylmethionine synthetase	0.0191	0.0053	Down
498000537	phycobilisome rod-core linker polypeptide (L-RC 28.5)	0.0741	0.0141	Down
498000559	hypothetical protein SCB02_04258	0.062	0.0092	Down
498000561	phycobilisome linker polypeptide, C-phycoerythrin class I-associated protein	0.0557	0.0101	Down
498000563	phycobilisome linker polypeptide, C-phycoerythrin-associated protein	0.0309	0.0048	Down
498000565	phycobilisome linker polypeptide, C-phycoerythrin class I-associated protein	0.044	0.0072	Down
498000567	phycoerythrin linker gene region	0.0043	0.0016	Down
498000574	hypothetical protein SCB02_04318	0.0059	0.0014	Down
498000587	bilin biosynthesis protein CpeZ	0.013	0.0016	Down
498000609	C-phycoerythrin class I alpha chain	0.31	0.1243	Down
498000613	C-phycoerythrin class I beta chain	0.3171	0.0625	Down
498000615	phycoerythrobilin:ferredoxin oxidoreductase	0.0109	0.0016	Down
498000624	R-phycocyanin II beta chain	0.0537	0.0154	Down
498000633	phycocyanin, alpha subunit	0.1074	0.0657	Down
498000635	HEAT repeat-containing PBS lyase	0.0096	0.0028	Down
498000638	phosphoribosylaminoimidazole synthetase	0.0229	0.003	Down
498000647	hypothetical protein SCB02_04445	0.0253	0.0095	Down
498000650	hypothetical protein SCB02_04525	0.0182	0.0074	Down
498000693	cell division protein	0.0119	0.0067	Down
498000702	photosystem I protein PsaD	0.0802	0.0258	Down
498000704	anthranilate synthase component I	0.0099	0.0018	Down
498000705	phosphoenolpyruvate carboxylase	0.0129	0.0017	Down
498000707	hypothetical protein SCB02_04605	0.0124	0.0053	Down
498000716	hypothetical protein SCB02_04620	0.0277	0.0083	Down
498000722	hypothetical protein SCB02_04659	0.0374	0.0149	Down
498000753	recombinase A	0.0077	0.003	Down
498000756	50S ribosomal protein L3	0.1743	0.0191	Down
498000776	30S ribosomal protein S3	0.0864	0.012	Down
498000787	50S ribosomal protein L29	0.0987	0.0277	Down
498000790	50S ribosomal protein L5	0.0403	0.0066	Down
498000796	30S ribosomal protein S8	0.0558	0.0161	Down
498000798	50S ribosomal protein L6	0.1213	0.0128	Down
498000800	50S ribosomal protein L15	0.0536	0.0228	Down
498000808	preprotein translocase subunit SecY	0.0331	0.0075	Down
498000812	adenylate kinase	0.0279	0.004	Down
498000814	30S ribosomal protein S13	0.1065	0.0301	Down
498000833	DNA-directed RNA polymerase subunit alpha	0.0368	0.0069	Down
498000837	50S ribosomal protein L13	0.0908	0.0204	Down
498000842	30S ribosomal protein S9	0.0752	0.0099	Down
498000843	alanine racemase	0.0069	0.0028	Down
498000854	photosystem I reaction centre subunit XI	0.0653	0.0091	Down
498000870	carboxyl-terminal protease	0.0043	0.0012	Down
498000907	cytochrome b6	0.0625	0.0259	Down
498000909	cytochrome b6-f complex subunit IV	0.0792	0.0509	Down
498000911	Calcium/calmodulin dependent protein kinase II association-domain protein	0.0041	0.0016	Down
498000925	photosystem I reaction center subunit IV	0.0448	0.0171	Down
498000931	cell division protein sepF	0.0347	0.0116	Down
498000980	putative transporter, membrane component	0.0065	0.002	Down
498000989	GPH family sugar transporter	0.0095	0.0021	Down
498000991	DNA-binding protein HU	0.042	0.0161	Down
498001008	iron ABC transporter ATP-binding protein	0.0044	0.0019	Down
498001020	GTPase CgtA	0.0075	0.0035	Down
498001022	translation initiation factor IF-2	0.0226	0.0066	Down
498001058	trypsin-like serine protease	0.0207	0.0082	Down
498001079	ribose-5-phosphate isomerase A	0.0363	0.0037	Down
498001081	DNA-directed RNA polymerase subunit beta	0.0417	0.0059	Down
498001088	DNA-directed RNA polymerase subunit gamma	0.0263	0.0051	Down
498001089	DNA-directed RNA polymerase subunit beta'	0.0316	0.0074	Down
498001091	ribosomal RNA large subunit methyltransferase N	0.0199	0.0038	Down
498001095	hypothetical protein SCB02_05393	0.0472	0.0186	Down
498001101	hypothetical protein SCB02_05398	0.06	0.0101	Down
498001103	DEAD/DEAH box helicase-like protein	0.0067	0.0029	Down
498001126	adenylosuccinate lyase	0.0107	0.004	Down
498001131	nitrogen regulatory protein P-II	0.0297	0.0108	Down
498001137	phycobilisome linker polypeptide, allophycocyanin-associated, core (LC 7.7)	0.0536	0.0136	Down
498001147	allophycocyanin subunit beta	0.0653	0.025	Down
498001150	allophycocyanin alpha chain	0.2001	0.0351	Down
498001152	anchor polypeptide LCM	0.0408	0.0083	Down
498001154	H+-transporting ATP synthase	0.3173	0.0461	Down
498001158	F0F1 ATP synthase subunit A	0.1588	0.0272	Down
498001160	F0F1 ATP synthase subunit B'	0.0835	0.0131	Down
498001164	F0F1 ATP synthase subunit B	0.0473	0.0085	Down
498001165	F0F1 ATP synthase subunit alpha	0.0547	0.0162	Down
498001167	F0F1 ATP synthase subunit epsilon	0.0341	0.0088	Down

498001203	F0F1 ATP synthase subunit beta	0.0551	0.0099	Down
498001204	chaperonin GroEL	0.0131	0.003	Down
498001206	phosphoglyceromutase	0.0152	0.0054	Down
498001212	hypothetical protein SCB02_05778	0.0089	0.004	Down
498001232	hypothetical protein SCB02_05853	0.0071	0.0032	Down
498001258	50S ribosomal protein L21	0.0617	0.0124	Down
498001260	phosphoribosylamine--glycine ligase	0.0066	0.0033	Down
498001271	UDP-3-O-3-hydroxymyristoyl] N-acetylglucosamine deacetylase	0.0117	0.0018	Down
498001277	(3R)-hydroxymyristoyl-ACP dehydratase	0.0336	0.0086	Down
498001279	peptide methionine sulfoxide reductase MsrA	0.0083	0.0017	Down
498001285	hypothetical protein SCB02_05933	0.0151	0.0052	Down
498001287	multifunctional aminopeptidase A	0.0077	0.0027	Down
498001291	tyrosyl-tRNA synthetase	0.0127	0.0037	Down
498001301	long-chain acyl-CoA synthetase	0.017	0.0025	Down
498001319	branched-chain alpha-keto acid dehydrogenase subunit E2	0.0212	0.0097	Down
498001323	branched-chain alpha-keto acid dehydrogenase subunit E2	0.0225	0.0038	Down
498001335	apolipoprotein N-acyltransferase	0.0092	0.0036	Down
498001350	hypothetical protein SCB02_06085	0.0079	0.0021	Down
498001353	hypothetical protein SCB02_06100	0.0046	0.0022	Down
498001358	cell division protein FtsH3	0.0106	0.004	Down
498001362	putative riboflavin kinase/FAD synthase	0.0231	0.0117	Down
498001409	thiamine-phosphate pyrophosphorylase	0.0078	0.002	Down
498001412	hypothetical protein SCB02_06212	0.0282	0.0146	Down
498001417	30S ribosomal protein S16	0.153	0.0205	Down
498001452	pyruvate dehydrogenase E1 alpha subunit	0.0247	0.0068	Down
498001458	tRNA-specific 2-thiouridylase MnmA	0.0103	0.003	Down
498001477	photosystem II CP43 protein	0.0652	0.0254	Down
498001497	peptidyl-prolyl cis-trans isomerase	0.0261	0.0076	Down
498001511	3-beta hydroxysteroid dehydrogenase/isomerase family protein	0.0481	0.0143	Down
498001523	hypothetical protein SCB02_06467	0.017	0.0043	Down
498001539	thioredoxin reductase	0.0095	0.0046	Down
498001561	hypothetical protein SCB02_06507	0.0368	0.0177	Down
498001563	hypothetical protein SCB02_06522	0.0162	0.0037	Down
498001570	putative nicotinamide nucleotide transhydrogenase, subunit alpha 2	0.0141	0.003	Down
498001573	putative nicotinamide nucleotide transhydrogenase, subunit beta	0.0403	0.012	Down
498001575	hypothetical protein SCB02_06557	0.022	0.0044	Down
498001582	glutamyl-tRNA synthetase	0.0062	0.0032	Down
498001607	50S ribosomal protein L19	0.182	0.0241	Down
498001609	methionine aminopeptidase	0.0167	0.0061	Down
498001614	hypothetical protein SCB02_06642	0.0224	0.0046	Down
498001618	TRAP-T family tripartite transporter	0.0127	0.0021	Down
498001630	glutamate-1-semialdehyde aminotransferase	0.0365	0.0092	Down
498001636	putative glycolate oxidase subunit GlcD	0.0084	0.0022	Down
498001638	hypothetical protein SCB02_06712	0.0145	0.0035	Down
498001645	permease	0.0069	0.0015	Down
498001686	hypothetical protein SCB02_06806	0.0127	0.0043	Down
498001688	bifunctional phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase protein	0.024	0.0118	Down
498001696	RND family multidrug efflux protein	0.0026	0.0007	Down
498001701	putative membrane protein	0.0099	0.0051	Down
498001706	hypothetical protein SCB02_06886	0.0364	0.0062	Down
498001723	AraC-type regulatory protein, putative	0.0081	0.0009	Down
498001768	Methyltransferase type 11	0.0119	0.0031	Down
498001854	hypothetical protein SCB02_07278	0.0033	0.0014	Down
498001878	Rho termination factor domain-containing protein	0.0454	0.0189	Down
498001886	hypothetical protein SCB02_07333	0.0696	0.0052	Down
498001900	hypothetical protein SCB02_07428	0.0132	0.0051	Down
498001937	hypothetical protein SCB02_07468	0.0537	0.0127	Down
498001954	hypothetical protein SCB02_07518	0.0098	0.0023	Down
498001974	hypothetical protein SCB02_07583	0.0109	0.0044	Down
498002000	ABC-type multidrug transport system, ATPase and permease components	0.0195	0.0113	Down
498002084	ATP phosphoribosyltransferase catalytic subunit	0.0163	0.0081	Down
498002335	CO2 hydration protein ChpX	0.0101	0.0044	Down
498002355	NAD(P)H-quinone oxidoreductase chain 4	0.0366	0.0079	Down
498002357	NAD(P)H-quinone oxidoreductase subunit F	0.03	0.006	Down
498002359	putative carboxysome shell polypeptide CsoS3	0.0098	0.003	Down
498002378	carboxysome shell polypeptide, CsoS2	0.0262	0.0044	Down
498002379	ribulose bisphosphate carboxylase, small chain	0.2919	0.0674	Down
498002381	ribulose bisophosphate carboxylase	0.1115	0.0202	Down
498002383	carboxysome shell peptide	0.1185	0.0157	Down
498002398	MFS superfamily sulfate permease	0.0256	0.0065	Down
498002401	Ca2+/Na+ antiporter	0.0223	0.0039	Down
498002407	ammonium transporter	0.1559	0.0512	Down
498002412	di/tricarboxylate transporter	0.0167	0.0046	Down
498002414	hypothetical protein SCB02_08605	0.0086	0.0032	Down
498002415	Trk family sodium transporter	0.0136	0.0032	Down
498002418	light-independent protochlorophyllide reductase subunit B	0.0194	0.0077	Down
498002419	protochlorophyllide reductase iron-sulfur ATP-binding protein	0.1673	0.069	Down
498002438	Zn-dependent membrane associated protease	0.0337	0.0056	Down
498002443	GTP cyclohydrolase I	0.0369	0.0134	Down
498002445	short chain dehydrogenase	0.0089	0.0028	Down
498002449	acyl-ACP reductase	0.0131	0.0054	Down
498002451	aldehyde decarbonylase	0.027	0.0071	Down
498002456	small subunit ribosomal protein S1	0.0305	0.005	Down
498002457	hypothetical protein SCB02_08730	0.0145	0.0033	Down
498002459	hypothetical protein SCB02_08735	0.0081	0.0026	Down
498002464	hypothetical protein SCB02_08760	0.0261	0.009	Down
498002469	acetolactate synthase 3 catalytic subunit	0.028	0.0051	Down
498002486	cob(I)alamin adenosyltransferase	0.0117	0.006	Down
498002496	hypothetical protein SCB02_08820	0.0062	0.0025	Down
498002510	ferredoxin	0.0465	0.0097	Down
498002522	carbohydrate kinase	0.007	0.0037	Down
498002540	glycosyl transferase family 39	0.0122	0.0075	Down
498002568	cytochrome C6	0.0215	0.0061	Down

498002569	nucleoside-diphosphate-sugar epimerase	0.0262	0.0044	Down
498002571	glycogen branching enzyme	0.0177	0.0018	Down
498002573	acyl esterase	0.0041	0.0016	Down
498002577	hypothetical protein SCB02_09100	0.0181	0.0067	Down
498002579	hypothetical protein SCB02_09105	0.0046	0.0009	Down
498002590	phosphofructokinase	0.0057	0.0026	Down
498002594	homoserine kinase	0.0135	0.0019	Down
498002598	threonyl-tRNA synthetase	0.0098	0.002	Down
498002605	cation efflux system protein	0.0096	0.0031	Down
498002606	membrane associated GTPase	0.0108	0.0018	Down
498002614	hypothetical protein SCB02_09240	0.018	0.0084	Down
498002616	menaquinone biosynthesis protein MenD (2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate	0.0056	0.0014	Down
498002623	glycogen synthase	0.0136	0.0041	Down
498002627	3-phosphoshikimate 1-carboxyvinyltransferase	0.0124	0.0026	Down
498002631	3-octaprenyl-4-hydroxybenzoate decarboxylase	0.0064	0.0015	Down
498002633	nitrilase	0.0117	0.0032	Down
498002636	solanesyl diphosphate synthase	0.023	0.0047	Down
498002638	acetyl-coenzyme A synthetase	0.0078	0.0032	Down
498002649	heavy metal ABC transporter (HMT) family permease/ATP-binding protein	0.0128	0.0033	Down
498002654	carbamoyl phosphate synthase small subunit	0.018	0.0022	Down
498002658	tRNA/rRNA methyltransferase (SpoU):RNA methyltransferase TrmH	0.0202	0.0034	Down
498002660	aspartyl/glutamyl-tRNA amidotransferase subunit A	0.0234	0.0037	Down
498002661	DNA polymerase III subunit alpha	0.006	0.0024	Down
498002662	hypothetical protein SCB02_09450	0.0415	0.0139	Down
498002663	30S ribosomal protein S15	0.084	0.0155	Down
498002689	hypothetical protein SCB02_09535	0.0101	0.004	Down
498002697	preprotein translocase subunit SecD	0.0152	0.0034	Down
498002705	permease	0.0108	0.0014	Down
498002716	methyltransferase, UbiE/COQ5 family protein	0.0054	0.0009	Down
498002718	glutamine synthetase, glutamate--ammonia ligase	0.0136	0.0048	Down
498002723	pyridoxal-dependent decarboxylase family protein	0.0051	0.0015	Down
498002730	insulinase family protein	0.0044	0.0017	Down
498002736	ABC transporter	0.013	0.0034	Down
498002737	ABC-transporter, membrane spanning component	0.0066	0.0011	Down
498002753	glycosyltransferase	0.0164	0.004	Down
498002754	30S ribosomal protein S2	0.0897	0.0177	Down
498002755	translation elongation factor Ts	0.0223	0.0059	Down
498002759	sulfite reductase subunit beta	0.0141	0.0045	Down
498002760	glycyl-tRNA synthetase beta subunit	0.0162	0.0039	Down
498002761	fatty acid desaturase	0.0236	0.0029	Down
498002763	geranylgeranyl hydrogenase	0.0243	0.0063	Down
498002766	GTP-binding protein TypA	0.0226	0.0086	Down
498002770	permease	0.0135	0.002	Down
498002772	cytochrome c assembly protein	0.0237	0.0053	Down
498002775	fructose 1,6-bisphosphatase II	0.022	0.0082	Down
498002777	glutamyl-tRNA reductase	0.0121	0.0023	Down
498002779	glucose-1-phosphate adenylyltransferase	0.0192	0.0068	Down
498002789	Uracil phosphoribosyltransferase	0.0135	0.0022	Down
498002792	pentapeptide repeat-containing protein	0.0094	0.0028	Down
498002793	hydrogenase accessory membrane protein	0.0515	0.0101	Down
498002797	phosphoribosylformylglycinamidine synthase I	0.0388	0.0056	Down
498002803	two component transcriptional regulator, winged helix family protein	0.0505	0.0114	Down
498002806	hypothetical protein SCB02_09907	0.0284	0.0099	Down
498002812	zinc metallopeptidase	0.0135	0.0043	Down
498002815	proton extrusion protein PcxA	0.0095	0.0033	Down
498002821	methionyl-tRNA synthetase	0.0062	0.0014	Down
498002827	30S ribosomal protein S18	0.2506	0.0542	Down
498002829	50S ribosomal protein L33	0.077	0.0307	Down
498002831	phenylalanyl-tRNA synthetase subunit beta	0.0085	0.0017	Down
498002835	allophycocyanin alpha, B subunit	0.0323	0.0185	Down
498002836	DnaJ domain-containing protein	0.0053	0.0011	Down
498002848	hypothetical protein SCB02_10052	0.0139	0.005	Down
498002852	methionine synthase (5-methyltetrahydrofolate--homocysteine methyltransferase)	0.0061	0.0008	Down
498002858	hypothetical protein SCB02_10077	0.0542	0.0252	Down
498002879	excinuclease ABC subunit C	0.0081	0.0034	Down
498002881	flavin reductase-like domain-containing protein	0.0527	0.021	Down
498002885	hypothetical protein SCB02_10124	0.0079	0.0015	Down
498002887	D-alanyl-D-alanine carboxypeptidase	0.0067	0.0021	Down
498002888	hypothetical protein SCB02_10134	0.0286	0.0065	Down
498002894	diaminopimelate epimerase	0.0179	0.0054	Down
498002896	leucyl-tRNA synthetase	0.0053	0.0018	Down
498002897	glucose-6-phosphate isomerase	0.0086	0.0024	Down
498002900	protease	0.005	0.0027	Down
498002905	N-acetyl-gamma-glutamyl-phosphate reductase	0.0142	0.0027	Down
498002914	molecular chaperone DnaK	0.0063	0.0022	Down
498002915	putative phosphate ABC transporter	0.0393	0.0067	Down
498002916	putative phosphate ABC transporter	0.0211	0.0055	Down
498002918	phosphate ABC transporter ATP-binding protein	0.0141	0.0023	Down
498002922	inositol-1(or 4)-monophosphatase	0.0077	0.0024	Down
498002924	ATP phosphoribosyltransferase regulatory subunit	0.0069	0.0027	Down
498002928	hypothetical protein SCB02_10269	0.0324	0.0159	Down
498002937	glucosylglycerol-phosphate synthase	0.005	0.0017	Down
498002953	50S ribosomal protein L28	0.0407	0.0086	Down
498003040	glutaredoxin	0.0133	0.0015	Down
498003042	rhomboid family protein	0.0148	0.0052	Down
498003079	1-deoxy-D-xylulose-5-phosphate synthase	0.0271	0.0047	Down
498003083	hypothetical protein SCB02_10731	0.0191	0.0049	Down
498003085	pyruvate kinase	0.0181	0.0035	Down
498003086	peptide ABC transporter permease	0.0085	0.0017	Down
498003090	ATP-dependent Clp protease proteolytic subunit	0.0201	0.0069	Down
498003092	Thf1-like protein	0.0239	0.0061	Down
498003100	cytochrome b6-f complex subunit PetN	0.0663	0.0189	Down
498003175	endolysin	0.0146	0.0044	Down

498003271	hypothetical protein SCB02_11216	0.0097	0.0038	Down
498003304	fructose-1,6-bisphosphate aldolase	0.0286	0.0057	Down
498003306	hypothetical protein SCB02_11286	0.0029	0.0009	Down
498003314	cell division protein FtsH4	0.0102	0.0043	Down
498003317	hypothetical protein SCB02_11321	0.0115	0.0036	Down
498003320	Fe-S cluster protein	0.0207	0.0022	Down
498003331	hypothetical protein SCB02_11371	0.0079	0.0027	Down
498003332	magnesium-protoporphyrin IX monomethyl ester cyclase	0.0197	0.0042	Down
498003333	putative modulator of DNA gyrase; TldD	0.0087	0.0018	Down
498003345	transcription-repair coupling factor	0.0033	0.0006	Down
498003348	carboxyl-terminal processing protease	0.0083	0.002	Down
498003350	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	0.0144	0.0034	Down
498003375	Hsp33-like chaperonin	0.0069	0.0022	Down
498003378	hypothetical protein SCB02_11536	0.0255	0.0072	Down
498003380	peptide chain release factor 3	0.0092	0.0016	Down
498003415	hypothetical protein SCB02_11631	0.0095	0.0024	Down
498003563	sirohydrochlorin cobaltochelatase	0.0037	0.0012	Down
498003568	hypothetical protein SCB02_12028	0.0114	0.0019	Down
498003573	carbamoyl phosphate synthase large subunit	0.0101	0.0022	Down
498003577	Sodium:alanine symporter family protein	0.0118	0.0039	Down
498003597	hypothetical protein SCB02_12153	0.019	0.0102	Down
498003607	hypothetical protein SCB02_12205	0.0406	0.0129	Down
498003614	ABC-type phosphate transport system, substrate binding protein	0.0377	0.006	Down
498003615	putative phosphate ABC transporter	0.0128	0.0017	Down
498003616	putative phosphate ABC transporter	0.0064	0.0024	Down
498003619	chromate transporter	0.004	0.0014	Down
498003623	transcriptional regulator	0.0514	0.0081	Down
498003625	two component transcriptional regulator	0.0089	0.004	Down
498003628	hypothetical protein SCB02_12310	0.033	0.007	Down
498003633	oxidoreductase, FAD-dependent	0.0048	0.001	Down
498003637	glutamine synthetase catalytic region	0.0113	0.0042	Down
498003642	ANL40	0.0311	0.0067	Down
498003653	fatty acid desaturase, type 2	0.015	0.0058	Down
498003659	tRNA (uracil-5-)-methyltransferase Gid	0.0122	0.002	Down
498003665	two-component response regulator	0.021	0.0085	Down
498003680	RNA-binding protein RbpD	0.0488	0.0101	Down
498003683	membrane bound transcriptional regulator-like protein	0.0299	0.0052	Down
498003700	biotin synthase	0.0158	0.0022	Down
498003702	hypothetical protein SCB02_12692	0.0215	0.003	Down
498003703	diaminopimelate decarboxylase	0.0188	0.0026	Down
498003705	ATPase	0.0291	0.0086	Down
498003709	glyceraldehyde-3-phosphate dehydrogenase	0.0099	0.0024	Down
498003715	phosphatidate cytidylyltransferase	0.0136	0.0011	Down
498003726	aminopeptidase N	0.0086	0.0016	Down
498003731	ferredoxin-NADP oxidoreductase	0.0197	0.0027	Down
498003756	2-isopropylmalate synthase	0.014	0.005	Down
498003758	hypothetical protein SCB02_12972	0.0061	0.0023	Down
498003764	inosine 5-monophosphate dehydrogenase	0.042	0.0128	Down
498003780	putative beta-lactamase	0.0042	0.0014	Down
498003786	hypothetical protein SCB02_13074	0.0122	0.0043	Down
498003790	homoserine dehydrogenase	0.0113	0.0043	Down
498003797	fused dienelactone hydrolase/uncharacterized domain	0.0052	0.0026	Down
498003812	GTP-binding protein YchF	0.0109	0.0049	Down
498003815	membrane fusion protein	0.0104	0.0046	Down
498003818	UGMP family protein	0.0532	0.0043	Down
498003819	photosystem I reaction center subunit III	0.056	0.0188	Down
498003823	Sec-independent protein secretion pathway component TatC	0.0109	0.0032	Down
498003825	cytochrome b6-f complex iron-sulfur subunit	0.0506	0.008	Down
498003828	apocytochrome f	0.0322	0.0096	Down
498003830	prolipoprotein diacylglyceryl transferase	0.0149	0.0019	Down
498003841	putative exopolyphosphatase	0.0059	0.0016	Down
498003858	chaperonin GroEL	0.008	0.0023	Down
498003859	hypothetical protein SCB02_13301	0.0273	0.0084	Down
498003899	hypothetical protein SCB02_13396	0.0184	0.0046	Down
498003905	NAD(P)H-quinone oxidoreductase subunit 2	0.0851	0.0092	Down
498003913	glycosyltransferase of family UDP-glucose:tetrahydrobiopterin glucosyltransferase	0.0153	0.0034	Down
498003915	DMT family permease	0.027	0.0084	Down
498003919	hypothetical protein SCB02_13476	0.0216	0.0089	Down
498003926	AAA family ATPase	0.0049	0.0019	Down
498003943	indole-3-glycerol-phosphate synthase	0.0183	0.0037	Down
498003945	dihydrolipoamide dehydrogenase	0.0181	0.0019	Down
498003950	UDP-N-acetylglucosamine 1-carboxyvinyltransferase	0.0101	0.0027	Down
498003965	D-alanine--D-alanine ligase	0.0083	0.0029	Down
498003973	cell division protein FtsZ	0.0469	0.0125	Down
498003977	integral membrane protein	0.0118	0.0032	Down
498003978	ATP-dependent Clp protease-like protein	0.0108	0.0019	Down
498003979	ATP-dependent Clp protease proteolytic subunit	0.0171	0.0055	Down
498004011	kinase	0.0184	0.0066	Down
497998709	menaquinone biosynthesis methyltransferase	0.0036	0.0025	-
497998725	glycosyltransferase	0.0038	0.0028	-
497998745	GTP-binding protein LepA	0.0142	0.0142	-
497998833	hypothetical protein SCB02_00359	0.0101	0.0043	-
497998862	HIT (histidine triad) family protein	0.0332	0.0306	-
497998910	membrane protein-related protein	0.0168	0.0078	-
497998912	phosphatidylcholine-hydrolyzing phospholipase D family protein	0.0038	0.0067	-
497998917	hypothetical protein SCB02_00564	0.0062	0.0116	-
497998933	RND family multidrug efflux transporter	0.0007	0.0006	-
497998951	HAD superfamily hydrolase	0.0028	0.0028	-
497998975	hypothetical protein SCB02_00676	0.0302	0.0237	-
497999016	inositol monophosphate family protein	0.0109	0.0073	-
497999045	pyrimidine reductase, riboflavin biosynthesis	0.0111	0.0084	-
497999053	hypothetical protein SCB02_00846	0.0032	0.0046	-
497999069	ribosome-binding factor A	0.0051	0.0047	-
497999096	porin	0.0089	0.0056	-

497999136	two-component system response regulator	0.0066	0.0042	-
497999164	tRNA nucleotidyltransferase/poly(A) polymerase	0.0056	0.0026	-
497999186	hypothetical protein SCB02_01121	0.0164	0.0106	-
497999222	ABC-type multidrug transport system, ATPase and permease components	0.0024	0.0011	-
497999229	adenylylsulfate kinase	0.0049	0.0027	-
497999241	two component LuxR family transcriptional regulator	0.008	0.0043	-
497999243	hypothetical protein SCB02_01256	0.0079	0.0044	-
497999256	hypothetical protein SCB02_01286	0.0065	0.0062	-
497999259	thioesterase	0.0041	0.0016	-
497999281	Ion transport protein	0.0041	0.004	-
497999285	glutaredoxin	0.0055	0.013	-
497999314	ABC transporter ATP-binding protein	0.0032	0.0024	-
497999336	two-component sensor histidine kinase	0.0024	0.0018	-
497999352	general (type II) secretion pathway protein D precursor	0.0029	0.0041	-
497999399	GntR family regulatory protein	0.0034	0.0053	-
497999423	hypothetical protein SCB02_01713	0.0101	0.0084	-
497999434	Delta-9 acyl-phospholipid desaturase	0.0267	0.0169	-
497999459	hypothetical protein SCB02_01798	0.0096	0.0075	-
497999482	hypothetical protein SCB02_01828	0.0046	0.0055	-
497999484	hypothetical protein SCB02_01833	0.009	0.0056	-
497999487	hypothetical protein SCB02_01843	0.008	0.004	-
497999561	CTP synthetase	0.011	0.0115	-
497999582	urease accessory protein UreG	0.0078	0.0042	-
497999607	hypothetical protein SCB02_02062	0.008	0.0059	-
497999610	hypothetical protein SCB02_02067	0.0041	0.0083	-
497999632	molybdenum cofactor biosynthesis protein A	0.0034	0.002	-
497999665	Fe-S oxidoreductas	0.0055	0.003	-
497999676	ABC transporter, substrate binding protein, phosphate	0.0031	0.0012	-
497999694	hypothetical protein SCB02_02267	0.0107	0.0062	-
497999698	hypothetical protein SCB02_02277	0.0127	0.0085	-
497999704	phage integrase family protein	0.0036	0.0082	-
497999726	putative cell envelope-related function transcriptional attenuator	0.0024	0.0022	-
497999750	ATP-dependent protease ATP-binding subunit ClpX	0.0046	0.0032	-
497999767	hypothetical protein SCB02_02417	0.0092	0.0046	-
497999789	hypothetical protein SCB02_02477	0.0147	0.0175	-
497999836	general secretion pathway protein E	0.01	0.0077	-
497999838	twitching motility protein	0.0026	0.0013	-
497999859	putative ribonuclease III	0.0071	0.0031	-
497999946	peptidase, M20D family protein	0.0052	0.0025	-
497999954	serine/threonine protein kinase	0.0022	0.0019	-
497999965	hypothetical protein SCB02_02881	0.0101	0.004	-
497999998	threonine synthase	0.0715	0.0685	-
498000002	hypothetical protein SCB02_02971	0.0057	0.0082	-
498000017	DNA mismatch repair protein MutS	0.0022	0.0013	-
498000044	translation initiation factor IF-3	0.017	0.0136	-
498000046	tRNA delta(2)-isopentenylpyrophosphate transferase	0.0101	0.0109	-
498000048	DNA gyrase subunit B	0.027	0.0298	-
498000052	hypothetical protein SCB02_03086	0.0143	0.0462	-
498000055	crcB protein	0.0202	0.0404	-
498000057	glutathione peroxidase	0.023	0.0113	-
498000080	A/G-specific adenine glycosylase	0.0067	0.0076	-
498000147	UvrD/REP helicase	0.0125	0.0154	-
498000158	glycosly transferase	0.0044	0.0097	-
498000161	lipopolysaccharide synthesis sugar transferase	0.0076	0.0035	-
498000163	sugar transferase	0.0211	0.0145	-
498000166	lipolytic protein G-D-S-L family	0.0045	0.0019	-
498000169	glycosyltransferase	0.0098	0.0073	-
498000174	glycosyltransferase	0.0052	0.0051	-
498000184	hypothetical protein SCB02_03358	0.0195	0.0411	-
498000189	glycosyltransferase	0.008	0.0115	-
498000195	glycosyl transferase family 2	0.0119	0.0082	-
498000197	hypothetical protein SCB02_03388	0.01	0.0103	-
498000202	methyltransferase FkbM	0.0082	0.0094	-
498000206	hypothetical protein SCB02_03408	0.0031	0.0038	-
498000208	hypothetical protein SCB02_03413	0.0023	0.0038	-
498000214	putative GDP-L-fucose synthetase	0.0132	0.0143	-
498000251	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	0.004	0.0033	-
498000254	deoxyribodipyrimidine photolyase	0.0064	0.0037	-
498000262	hypothetical protein SCB02_03543	0.0016	0.004	-
498000296	oxidoreductase	0.0105	0.0159	-
498000330	pentapeptide repeat-containing protein	0.0156	0.0248	-
498000333	photosystem II reaction center protein H	0.1507	0.0682	-
498000345	cob(I)alamin adenosyltransferase	0.0055	0.004	-
498000347	deoxycytidine triphosphate deaminase	0.0061	0.0027	-
498000355	ferredoxin	0.0024	0.003	-
498000360	soluble lytic transglycosylase	0.0034	0.0038	-
498000362	phosphoglucosamine mutase	0.0063	0.0059	-
498000476	hypothetical protein SCB02_04081	0.0278	0.0173	-
498000491	hypothetical protein SCB02_04116	0.0018	0.0047	-
498000530	transcriptional regulator NrdR	0.0156	0.0093	-
498000552	hypothetical protein SCB02_04238	0.0075	0.0076	-
498000582	hypothetical protein SCB02_04308	0.0077	0.0124	-
498000589	hypothetical protein SCB02_04323	0.0019	0.0017	-
498000598	hypothetical protein SCB02_04343	0.0027	0.0017	-
498000617	hypothetical protein SCB02_04383	0.0115	0.0064	-
498000645	rare lipoprotein A	0.0082	0.011	-
498000701	ATPase	0.0083	0.0043	-
498000748	hypothetical protein SCB02_04654	0.0168	0.0098	-
498000772	putative ldpA protein	0.0148	0.0192	-
498000930	formamidopyrimidine-DNA glycosylase	0.0034	0.0022	-
498000937	peptidoglycan-binding LysM	0.0042	0.003	-
498000939	putative aldehyde dehydrogenase	0.0037	0.002	-
498001033	putative glutathione S-transferase	0.0019	0.0025	-
498001034	aspartoacylase	0.003	0.0042	-

498001097	hypothetical protein SCB02_05383	0.0105	0.0065	-
498001145	cell division protein FtsW	0.0051	0.0034	-
498001169	hypothetical protein SCB02_05573	0.0048	0.0048	-
498001172	hypothetical protein SCB02_05588	0.0014	0.0025	-
498001196	forkhead-associated protein	0.0255	0.0458	-
498001200	FHA modulated glycosyl transferase/transpeptidase	0.006	0.0069	-
498001218	DnaK family protein	0.0124	0.0188	-
498001227	3-hydroxyisobutyrate dehydrogenase related protein	0.0021	0.002	-
498001241	ribosomal protein L11 methyltransferase	0.0085	0.005	-
498001245	cytochrome c-550	0.0299	0.018	-
498001247	ribonuclease Z	0.0072	0.008	-
498001306	transporter, major facilitator family protein	0.0072	0.0049	-
498001339	superoxide dismutase	0.0091	0.0051	-
498001371	hypothetical protein SCB02_06140	0.0142	0.0189	-
498001372	hypothetical protein SCB02_06145	0.0109	0.0188	-
498001380	two-component sytem response regulator	0.0103	0.0117	-
498001439	prohibitin family protein	0.0046	0.0019	-
498001448	hypothetical protein SCB02_06272	0.0157	0.0201	-
498001464	Type II alternative RNA polymerase sigma factor, sigma-70 family protein	0.0012	0.0013	-
498001537	hypothetical protein SCB02_06462	0.0042	0.0045	-
498001605	CPA1 family Na+/H+ antiporter	0.0063	0.0066	-
498001632	TRAP-T family tripartite transporter	0.0075	0.0037	-
498001658	hypothetical protein SCB02_06747	0.0063	0.0096	-
498001671	ABC transporter	0.006	0.0036	-
498001673	hypothetical protein SCB02_06782	0.0028	0.0035	-
498001708	RNA polymerase sigma factor, sigma-70 family protein	0.0017	0.001	-
498001710	hypothetical protein SCB02_06856	0.0115	0.0073	-
498001725	putative DNA repair ATPase	0.0016	0.001	-
498001726	DNA repair exonuclease	0.0036	0.0017	-
498001746	cytochrome c oxidase subunit I	0.0012	0.0016	-
498001750	flavoprotein related to choline dehydrogenase	0.0029	0.0025	-
498001783	hypothetical protein SCB02_07041	0.002	0.0029	-
498001786	hypothetical protein SCB02_07046	0.001	0.0014	-
498001790	neuromedin U	0.0029	0.0012	-
498001797	regulatory proteins, Crp family protein	0.0235	0.037	-
498001801	ferritin	0.0068	0.0058	-
498001806	Beta-lactamase-like protein	0.0032	0.0014	-
498001808	SAM-dependent methyltransferase	0.0039	0.0082	-
498001810	transcriptional regulator	0.0054	0.0081	-
498001812	hypothetical protein SCB02_07126	0.0336	0.0221	-
498001814	hypothetical protein SCB02_07131	0.004	0.0039	-
498001857	metallo-beta-lactamase superfamily hydrolase	0.0061	0.0045	-
498001867	asparagine synthase	0.0027	0.0016	-
498001923	hypothetical protein SCB02_07393	0.0033	0.0045	-
498001960	dienelactone hydrolase	0.0049	0.0037	-
498002007	putative cytochrome P450	0.0068	0.0192	-
498002045	porin-like protein	0.0757	0.1048	-
498002386	hypothetical protein SCB02_08510	0.008	0.0082	-
498002405	hypothetical protein SCB02_08575	0.0442	0.0452	-
498002416	VIC family potassium channel protein	0.0119	0.0081	-
498002417	light-independent protochlorophyllide reductase subunit N	0.0175	0.0128	-
498002428	hypothetical protein SCB02_08655	0.0049	0.0033	-
498002454	creatininase	0.0033	0.004	-
498002463	hypothetical protein SCB02_08755	0.0183	0.0134	-
498002493	ribosome recycling factor	0.036	0.0202	-
498002506	hypothetical protein SCB02_08860	0.0025	0.0013	-
498002512	hypothetical protein SCB02_08875	0.0081	0.0072	-
498002520	putative photosystem II reaction center Psb27 protein	0.0264	0.0193	-
498002525	single-stranded DNA-binding protein	0.0109	0.0105	-
498002542	hypothetical protein SCB02_08965	0.0103	0.0071	-
498002543	hypothetical protein SCB02_08970	0.0092	0.008	-
498002558	hypothetical protein SCB02_09025	0.0083	0.014	-
498002559	putative pterin-4-alpha-carbinolamine dehydratase	0.0094	0.0095	-
498002560	asparagine synthase (glutamine-hydrolyzing)	0.0121	0.0158	-
498002561	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB	0.004	0.0052	-
498002574	hypothetical protein SCB02_09090	0.0071	0.0029	-
498002607	photosystem II protein D1	0.0746	0.0655	-
498002612	zinc transporter ZupT	0.0085	0.0047	-
498002613	hypothetical protein SCB02_09235	0.0056	0.0032	-
498002647	methionine-S-sulfoxide reductase	0.0084	0.0075	-
498002650	hypothetical protein SCB02_09400	0.0036	0.0069	-
498002652	anthranilate phosphoribosyltransferase	0.0101	0.0058	-
498002656	hypothetical protein SCB02_09420	0.0067	0.0081	-
498002679	hypothetical protein SCB02_09505	0.0035	0.0027	-
498002694	pyruvate dehydrogenase E1 beta subunit	0.0199	0.0147	-
498002717	hypothetical protein SCB02_09622	0.0096	0.0063	-
498002719	allophycocyanin subunit beta	0.0252	0.0133	-
498002739	DevA-like ABC transporter ATPase component	0.0058	0.0049	-
498002756	hypothetical protein SCB02_09727	0.0068	0.0074	-
498002764	putative carboxypeptidase	0.0035	0.0021	-
498002767	hypothetical protein SCB02_09777	0.0077	0.004	-
498002780	6-phosphogluconate dehydrogenase	0.0026	0.0027	-
498002782	putative 6-phosphogluconolactonase (DevB, Pgl)	0.0038	0.0027	-
498002783	hypothetical protein SCB02_09832	0.0655	0.1034	-
498002801	hypothetical protein SCB02_09897	0.0316	0.0355	-
498002809	uridine kinase	0.0024	0.0029	-
498002814	bifunctional adenosylcobalamin biosynthesis protein (adenosylcobinamide kinase /	0.0084	0.0102	-
498002816	hypothetical protein SCB02_09947	0.0168	0.0141	-
498002819	hypothetical protein SCB02_09962	0.0121	0.0126	-
498002842	epimerase, PhzC/PhzF-like protein	0.0029	0.0015	-
498002844	NAD(P)H-dependent glycerol-3-phosphate dehydrogenase	0.0063	0.0078	-
498002846	hypothetical protein SCB02_10047	0.0179	0.0392	-
498002898	DnaB-like helicase	0.0066	0.0038	-
498002909	peptidylprolyl isomerase	0.0089	0.0038	-

498002910	5'-methylthioadenosine phosphorylase	0.0052	0.0033	-
498002912	hypothetical protein SCB02_10219	0.0041	0.0047	-
498002931	hypothetical protein SCB02_10274	0.0212	0.0152	-
498002935	hypothetical protein SCB02_10284	0.0035	0.0087	-
498002936	heat shock protein 90	0.0063	0.0068	-
498002946	hypothetical protein SCB02_10319	0.0035	0.0021	-
498002951	glycerol kinase	0.0031	0.0017	-
498002952	small mechanosensitive ion channel	0.0053	0.0046	-
498002963	glycosyl transferase, group 2 family protein	0.0036	0.0022	-
498002966	hypothetical protein SCB02_10389	0.0037	0.0042	-
498002988	hypothetical protein SCB02_10459	0.0033	0.0024	-
498002991	hypothetical protein SCB02_10474	0.0028	0.0028	-
498003031	hypothetical protein SCB02_10556	0.0016	0.0016	-
498003033	hypothetical protein SCB02_10561	0.0038	0.0044	-
498003043	putative Zn peptidase	0.0048	0.0025	-
498003050	ATPase	0.0032	0.0032	-
498003059	hypothetical protein SCB02_10651	0.008	0.0042	-
498003061	SAM-dependent methyltransferase	0.0016	0.0012	-
498003064	hypothetical protein SCB02_10671	0.0103	0.0059	-
498003084	hypothetical protein SCB02_10736	0.0126	0.0207	-
498003088	FtsH ATP-dependent protease-like protein	0.0095	0.0059	-
498003098	hypothetical protein SCB02_10781	0.1285	0.0826	-
498003102	ATP-dependent Clp protease adaptor	0.011	0.013	-
498003156	hypothetical protein SCB02_10906	0.0034	0.0066	-
498003157	hypothetical protein SCB02_10911	0.0032	0.0028	-
498003159	hypothetical protein SCB02_10921	0.005	0.0024	-
498003163	phosphoribosylaminoimidazole carboxylase ATPase subunit	0.0033	0.0015	-
498003168	hypothetical protein SCB02_10951	0.0233	0.0259	-
498003169	hypothetical protein SCB02_10956	0.0174	0.0134	-
498003229	CBS	0.0125	0.0063	-
498003234	nucleotide sugar epimerase	0.0067	0.0035	-
498003243	hypothetical protein SCB02_11111	0.0042	0.0032	-
498003245	fumarate hydratase	0.0048	0.006	-
498003278	3-isopropylmalate dehydrogenase	0.0108	0.0101	-
498003324	hypothetical protein SCB02_11346	0.0147	0.006	-
498003334	putative modulator of DNA gyrase	0.004	0.0025	-
498003373	hypothetical protein SCB02_11511	0.0047	0.0043	-
498003374	ABC-type cobalt transport system, ATPase component	0.0036	0.0029	-
498003377	hypothetical protein SCB02_11531	0.0181	0.0074	-
498003384	small-conductance mechanosensitive channel	0.0024	0.0018	-
498003387	ribonucleotide reductase	0.0035	0.0033	-
498003397	hypothetical protein SCB02_11581	0.0043	0.0093	-
498003399	choloylglycine hydrolase	0.0025	0.0061	-
498003530	hypothetical protein SCB02_11898	0.0032	0.0072	-
498003532	hypothetical protein SCB02_11903	0.0027	0.0043	-
498003543	ATLS1-like light-inducible protein	0.0088	0.0048	-
498003576	hypothetical protein SCB02_12058	0.008	0.0107	-
498003579	glutathione reductase (NADPH)	0.0061	0.0048	-
498003582	glutathione S-transferase	0.0033	0.0035	-
498003591	putative universal stress protein f	0.0016	0.0052	-
498003592	hypothetical protein SCB02_12128	0.0034	0.0036	-
498003593	hypothetical protein SCB02_12133	0.004	0.0073	-
498003603	selenophosphate synthase/FAD/NAD(P)-binding domain-containing protein	0.002	0.0017	-
498003609	hypothetical protein SCB02_12215	0.0039	0.0075	-
498003611	major facilitator superfamily permease / multidrug efflux transporter	0.0041	0.0056	-
498003622	CHAD domain containing protein	0.0051	0.0044	-
498003627	porin	0.0476	0.0613	-
498003632	rubredoxin	0.0123	0.0205	-
498003634	reductase	0.0386	0.0479	-
498003635	hypothetical protein SCB02_12345	0.0221	0.0388	-
498003638	cation transport ATPase	0.0022	0.0019	-
498003661	carotenoid isomerase	0.0068	0.0046	-
498003663	hypothetical protein SCB02_12487	0.0213	0.0178	-
498003664	hypothetical protein SCB02_12492	0.0084	0.0066	-
498003666	hypothetical protein SCB02_12502	0.0267	0.0228	-
498003692	PsbP	0.0169	0.0086	-
498003707	hypothetical protein SCB02_12717	0.0033	0.0087	-
498003755	putative sn-glycerol-3-phosphate ABC transporter, permease protein	0.0037	0.0106	-
498003757	hypothetical protein SCB02_12967	0.0094	0.0081	-
498003759	Fe-S oxidoreductase	0.0018	0.0014	-
498003760	lycopene cyclase (CrtL-type)	0.0033	0.0036	-
498003765	thioredoxin	0.018	0.0084	-
498003777	cytochrome cM	0.0116	0.0101	-
498003787	SufE protein	0.0045	0.0027	-
498003799	hypothetical protein SCB02_13119	0.0102	0.0175	-
498003817	hypothetical protein SCB02_13194	0.0262	0.014	-
498003864	putative multidrug efflux ABC transporter	0.0216	0.027	-
498003866	protoheme IX farnesyltransferase	0.0179	0.0234	-
498003870	putative cytochrome c oxidase, subunit 2	0.0215	0.0178	-
498003872	cytochrome c oxidase, subunit I	0.0181	0.0136	-
498003906	ABC transporter ATP-binding protein	0.0065	0.0048	-
498003923	putative inner membrane protein translocase component YidC	0.0122	0.0104	-
498003928	spectrin repeat-containing protein	0.0153	0.0105	-
498003929	hypothetical protein SCB02_13521	0.0084	0.0027	-
498003937	UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	0.0043	0.0019	-
498003953	pentapeptide repeat-containing protein	0.0045	0.0038	-
498003963	(dimethylallyl)adenosine tRNA methylthiotransferase	0.0052	0.0039	-
498003987	hypothetical protein SCB02_13711	0.0013	0.0084	-
498003992	glycyl-tRNA synthetase subunit alpha	0.0166	0.0118	-
498004010	hypothetical protein SCB02_13759	0.0118	0.0068	-

Table S4. Gene expression ratios in the *Pelagibacter* sp. HTCC7211 bin.

NCBI GI	Protein Description	Mean Expression Ratio (FL)	Mean Expression Ratio (PA)	PA Regulation
495819520	DNA-directed RNA polymerase, beta' subunit	0.0114	0.0456	Up
495819535	cytochrome c oxidase, subunit II	0.0183	0.0947	Up
495819590	tRNA uridine 5-carboxymethylaminomethyl modification enzyme GidA	0.0537	0.8066	Up
495819592	glycine betaine transport ATP-binding protein opuAA	0.0026	0.0196	Up
495819601	general amino acid ABC transporter, ATP-binding protein	0.0037	0.0778	Up
495819605	ATP-dependent Zn protease	0.0142	0.0398	Up
495819621	Receptor family ligand binding domain protein	0.058	0.1563	Up
495819635	2-isopropylmalate synthase	0.3554	3.2775	Up
495819639	chaperone protein DnaK	0.0231	0.1487	Up
495819692	3-hydroxyacyl-CoA dehydrogenase	0.0058	0.0458	Up
495819722	integral membrane protein	0.0692	0.5633	Up
495819728	serine hydroxymethyltransferase	0.0075	0.0468	Up
495819738	HflK protein	0.0227	0.1614	Up
495819741	acyl carrier protein	0.0928	0.293	Up
495819758	translation elongation factor G	0.0175	0.0527	Up
495819798	cytochrome-c oxidase	0.0817	0.5174	Up
495819802	alanyl-tRNA synthetase	0.0013	0.0063	Up
495819841	glutamine synthetase, catalytic domain, putative	0.035	0.0827	Up
495819850	trap dicarboxylate transporter - dctp subunit	0.0678	0.4403	Up
495819874	citrate (si)-synthase	0.0067	0.0329	Up
495819902	ribosomal protein L2	0.0121	0.0645	Up
495819920	pirin	0.0094	0.0766	Up
495819927	DNA-directed RNA polymerase, alpha subunit	0.0201	0.068	Up
495819970	glutamate synthase large subunit	0.0154	0.0478	Up
495819989	acid tolerance regulatory protein actr	0.0111	0.3769	Up
495820016	cell division protein FtsZ	0.0097	0.0334	Up
495820052	heat shock protein HslVU, ATPase subunit HslU	0.003	0.0376	Up
495820074	Bacterial extracellular solute-binding protein, family 7	0.0507	0.1481	Up
495820146	GTP cyclohydrolase I	0.0104	0.0589	Up
495820147	NAD(p) transhydrogenase subunit beta	0.1718	3.2063	Up
495820166	alanine dehydrogenase	0.0091	0.0805	Up
495820193	translation elongation factor Tu	0.1686	0.331	Up
495820205	H+-transporting two-sector ATPase (subunit b)	0.0041	0.0556	Up
495820243	import inner membrane translocase, subunit Tim44	0.0049	0.0455	Up
495820250	taurine transport system periplasmic protein	0.0515	0.221	Up
495820272	OmpA family protein	0.055	0.4371	Up
495820285	malate synthase	0.0009	0.02	Up
495820304	ABC proline/glycine betaine transporter, periplasmic substrate-binding protein	0.0179	0.075	Up
495820329	heAt shock protein a	0.0752	1.3574	Up
495820360	substrate-binding region of ABC-type glycine betaine transport system	0.0625	0.2092	Up
495820365	ABC transporter	0.0526	0.1471	Up
495820376	spermidine/putrescine-binding periplasmic protein	0.1081	0.3382	Up
495820390	translation initiation factor IF-2	0.0029	0.021	Up
495820391	ATP-dependent protease La	0.0047	0.032	Up
495820433	DNA-directed RNA polymerase, beta subunit	0.0113	0.0274	Up
495820456	ABC transporter, QAT family, substrate-binding protein, putative	0.0124	0.0423	Up
495820460	carbamoyl-phosphate synthase, large subunit	0.0031	0.0115	Up
495820606	glutamine synthetase, type III	0.0034	0.0172	Up
495820631	leucyl aminopeptidase	0.0042	0.0186	Up
495820666	NADH dehydrogenase (quinone), D subunit	0.0104	0.063	Up
495820681	ribosomal protein S11	0.0211	0.0957	Up
495820706	betaine-aldehyde dehydrogenase	0.0014	0.0083	Up
495820716	co-chaperone GrpE	0.0052	0.0779	Up
495820729	Integral membrane protein DUF6	0.0685	0.8739	Up
495820782	non-specific DNA-binding protein HBsu	0.1866	0.611	Up
495820856	thioredoxin-disulfide reductase	0.0107	0.0638	Up
495820892	permease	0.0024	0.0362	Up
495820976	triose-phosphate isomerase	0.02	0.3099	Up
495821028	extracellular solute-binding protein, family 5	0.0159	0.0739	Up
495821044	putative permease, major facilitator superfamily	0.004	0.0156	Up
495821048	protease DO	0.0105	0.0469	Up
495821054	30S ribosomal protein S1	0.015	0.0487	Up
495821062	protein RecA	0.0188	0.1162	Up
495821077	ATP synthase F1, alpha subunit	0.0188	0.0984	Up
495821094	H+-transporting two-sector ATPase (subunit b)	0.0388	0.1869	Up
495821103	xanthine/uracil/vitamin C permease family protein	0.109	0.2955	Up
495821111	smc protein	0.0021	0.0128	Up
495821156	ATP-binding component of ABC transporter	0.0058	0.0572	Up
495821159	chaperonin GroL	0.0431	0.4632	Up
495821160	ribosomal protein S4	0.0072	0.032	Up
495821187	ABC transporter	0.1852	0.7251	Up
495821262	oxidoreductase, aldo/keto reductase family	0.0021	0.0171	Up
495821376	tartrate dehydrogenase	0.0033	0.0278	Up
495821387	catalase/peroxidase HPI	0.0202	0.1227	Up
495821393	formate dehydrogenase, alpha subunit	0.0064	0.019	Up
495821415	polyribonucleotide nucleotidyltransferase	0.0119	0.0488	Up
495821419	conserved hypothetical protein	0.0111	0.0651	Up
495821420	alternative sigma factor RpoH	0.0044	0.0465	Up
495821440	cytochrome B/c1	0.0109	0.0422	Up
495821487	transcription termination factor Rho	0.0067	0.026	Up
495821508	aminomethyltransferase, glycin cleavage system T protein	0.0462	0.1439	Up
495821524	V-type H(+)-translocating pyrophosphatase	0.0698	0.132	Up
495821537	chaperone protein DnaJ	0.0048	0.0505	Up
495821544	ammonium transporter family protein	0.0633	0.6174	Up
495819481	ATP synthase F0, A subunit	0.0139	0.0366	-
495819485	gxgxg motif-containing protein	0.0109	0.0219	-
495819490	FolC bifunctional protein	0.011	0.0576	-
495819493	Na+/H+ antiporter NhaA	0.007	0.0119	-

495819498	glutamyl-tRNA(Gln) amidotransferase subunit A	0.0043	0.014	-
495819500	ribosomal protein L14	0.0123	0.0383	-
495819503	acetyl-CoA carboxylase, biotin carboxylase	0.0073	0.0103	-
495819511	spermidine/putrescine transport system permease protein potb	0.0043	0.0215	-
495819525	phosphoribosylformylglycinamidine synthase II	0.0026	0.0051	-
495819529	histidyl-tRNA synthetase	0.0038	0.0094	-
495819532	ABC-type branched-chain amino acid transport system, permease protein I	0.006	0.0367	-
495819536	phenylalanyl-tRNA synthetase, beta subunit	0.0008	0.0061	-
495819537	nucleotidyltransferase/DNA polymerase involved in DNA repair/SOS mutagenesis and repair	0.0012	0.0028	-
495819541	NAD+ synthetase	0.0043	0.0214	-
495819551	ribosomal protein L20	0.0075	0.0174	-
495819557	NADH dehydrogenase i chain a	0.0168	0.1133	-
495819573	ABC transporter, membrane spanning protein (glycine betaine)	0.0055	0.0182	-
495819597	putative coenzyme F420-reducing hydrogenase, beta subunit family protein	0.0019	0.0025	-
495819598	prolyl-tRNA synthetase	0.003	0.0054	-
495819617	conserved hypothetical protein TIGR00701	0.0011	0.0073	-
495819640	acetyl-CoA carboxylase, carboxyl transferase, alpha subunit	0.0029	0.0054	-
495819641	pyruvate, phosphate dikinase	0.0022	0.0075	-
495819643	glycine betaine/L-proline transport system permease	0.0043	0.0054	-
495819675	putative 3-hydroxyisobutyrate dehydrogenase	0.0014	0.0073	-
495819684	tryptophanyl-tRNA synthetase	0.0039	0.0128	-
495819686	glutamate synthase, large subunit	0.0014	0.0032	-
495819688	glutamine synthetase, type I	0.0134	0.0327	-
495819691	type II Secretion PilQ	0.0259	0.0853	-
495819702	signal recognition particle protein	0.0035	0.0085	-
495819705	methylenetetrahydrofolate reductase	0.0235	0.037	-
495819720	ATP synthase F1, gamma subunit	0.004	0.007	-
495819724	ammonium transporter family protein	0.026	0.0124	-
495819727	branched-chain amino acid transport system/permease component	0.0046	0.0087	-
495819731	preprotein translocase SecG subunit	0.0197	0.0251	-
495819753	5-methylcytosine-specific restriction enzyme A	0.0038	0.0196	-
495819755	pyruvate dehydrogenase (acetyl-transferring), homodimeric type	0.0033	0.0058	-
495819765	trigger factor	0.0022	0.0069	-
495819766	DNA primase	0.0016	0.0044	-
495819768	flavin-containing monooxygenase FMO	0.0048	0.0169	-
495819780	2-isopropylmalate synthase/homocitrate synthase family protein	0.0014	0.0081	-
495819788	type 4 fimbrial biogenesis protein PilP	0.0775	0.1379	-
495819799	succinate dehydrogenase, flavoprotein subunit	0.0039	0.0096	-
495819822	ribosomal protein S21	0.0149	0.0428	-
495819823	amidophosphoribosyltransferase	0.0029	0.0057	-
495819826	choline dehydrogenase	0.0016	0.0077	-
495819827	electron transfer flavoprotein-ubiquinone oxidoreductase	0.0034	0.0043	-
495819854	formate--tetrahydrofolate ligase	0.0043	0.018	-
495819856	ribonucleoside-diphosphate reductase, beta subunit	0.0148	0.0242	-
495819857	glutamyl-tRNA synthetase	0.0019	0.0042	-
495819876	galactarate dehydratase, putative	0.03	0.0465	-
495819901	30S ribosomal protein S16	0.0187	0.0279	-
495819904	tRNA (guanine-N1)-methyltransferase	0.0092	0.0364	-
495819931	RNA polymerase sigma factor	0.0058	0.0091	-
495819935	glycine amidinotransferase	0.0018	0.0097	-
495819939	segregation and condensation protein B	0.0025	0.0209	-
495819948	nitrogen-fixing NifU domain protein	0.0032	0.0229	-
495819949	acetate--CoA ligase	0.0049	0.0047	-
495819951	dna-directed rna polymerase omega subunit	0.0114	0.036	-
495819966	hydroxyacylglutathione hydrolase	0.0028	0.0326	-
495819968	mannitol transporter	0.0182	0.0202	-
495819974	conserved hypothetical protein	0.0065	0.0447	-
495819983	ribosomal protein S3	0.0085	0.0074	-
495819987	3-demethylubiquinone-9 3-O-methyltransferase	0.0017	0.0109	-
495819988	probable NADH-ubiquinone oxireductase	0.0012	0.0047	-
495820000	ribonuclease E/G	0.0012	0.0079	-
495820003	ribosomal protein S2	0.0092	0.0359	-
495820035	histidine triad protein	0.0014	0.0088	-
495820048	gamma-butyrobetaine,2-oxoglutarate dioxygenase, putative	0.001	0.0058	-
495820064	transporter	0.0405	0.0496	-
495820075	nucleoside diphosphate kinase	0.0025	0.0101	-
495820076	ribonucleoside-diphosphate reductase, alpha subunit	0.0186	0.0324	-
495820077	thiamine pyrophosphate-requiring enzyme	0.0187	0.0152	-
495820079	anthranilate phosphoribosyltransferase	0.0019	0.0096	-
495820099	argininosuccinate synthase	0.0012	0.0059	-
495820101	ribosomal protein S13p/S18e	0.0412	0.2372	-
495820103	CarD-like transcriptional regulator family protein	0.0063	0.0236	-
495820105	D-galactarate dehydratase/Altronate	0.0151	0.0331	-
495820109	methylenetetrahydrofolate dehydrogenase	0.006	0.0152	-
495820111	malate dehydrogenase, NAD-dependent	0.005	0.0324	-
495820118	transporter, major facilitator family	0.0009	0.0055	-
495820126	adenylylsulfate kinase	0.0269	0.0361	-
495820129	phosphoribosylformylglycinamidine synthase I	0.0046	0.0087	-
495820131	conserved hypothetical protein	0.0035	0.008	-
495820133	protein TolQ	0.0158	0.034	-
495820134	phosphate acetyltransferase	0.0017	0.0176	-
495820137	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase	0.0058	0.0152	-
495820138	exodeoxyribonuclease I	0.0023	0.0108	-
495820140	sodium Bile symporter family protein	0.0089	0.0081	-
495820141	glycine betaine/L-proline transport system permease protein	0.0055	0.0073	-
495820148	type II Secretion PilT	0.0327	0.0237	-
495820162	chromosome partitioning protein	0.0041	0.0231	-
495820168	preprotein translocase, SecY subunit	0.0087	0.0142	-
495820175	ATP-dependent Clp protease, ATP-binding subunit ClpX	0.0085	0.0177	-
495820177	UDP-3-O-(3-hydroxymyristoyl) N-acetylglucosamine deacetylase	0.0038	0.0118	-
495820199	adenylylsulfate reductase, alpha subunit	0.0227	0.0398	-
495820201	selenocysteine lyase chain A	0.0028	0.0079	-
495820212	Tol-Pal system beta propeller repeat protein TolB	0.0152	0.0185	-

495820215	isoleucyl-tRNA synthetase	0.0024	0.009	-
495820216	Na+/solute symporter, Ssf family	0.3479	0.5602	-
495820229	conserved hypothetical protein	0.0172	0.065	-
495820232	ATP synthase F1, beta subunit	0.0327	0.0893	-
495820235	acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	0.002	0.0086	-
495820242	ribosomal protein L1	0.0043	0.0247	-
495820249	LexA repressor	0.0099	0.021	-
495820278	ribosomal protein S6	0.0051	0.0166	-
495820288	ribosomal protein L16	0.0157	0.084	-
495820297	DNA uptake lipoprotein	0.0007	0.0059	-
495820299	phosphoribosylaminoimidazole-succinocarboxamide synthase	0.0023	0.0137	-
495820303	conserved hypothetical integral membrane protein	0.0051	0.0256	-
495820307	3-oxoacyl-(acyl-carrier-protein) synthase	0.0045	0.025	-
495820310	protein-export membrane protein SecD	0.0021	0.0137	-
495820312	creatinase	0.0011	0.0043	-
495820326	glycyl-tRNA synthetase, beta subunit	0.0015	0.0183	-
495820335	bacteriorhodopsin	0.8933	0.8271	-
495820356	putative monomeric sarcosine oxidase	0.0168	0.028	-
495820369	dihydroxy-acid dehydratase	0.0087	0.0168	-
495820374	6-O-methylguanine DNA methyltransferase	0.0046	0.0225	-
495820377	spermine/spermidine synthase	0.0052	0.0128	-
495820400	lipoprotein	0.0318	0.085	-
495820415	integral membrane protein MviN	0.0016	0.0108	-
495820435	50S ribosomal protein L5	0.0083	0.066	-
495820449	DNA topoisomerase I	0.0018	0.0048	-
495820452	ribosomal protein L7/L12	0.0424	0.1562	-
495820455	homoserine O-acetyltransferase	0.0025	0.0077	-
495820467	potassium uptake protein	0.0042	0.0136	-
495820469	UDP-N-acetylmuramoylalanyl-D-glutamate	0.0015	0.0057	-
495820550	dimethylglycine dehydrogenase	0.0083	0.0174	-
495820564	ketol-acid reductoisomerase	0.0048	0.0184	-
495820567	short chain dehydrogenase	0.0017	0.0235	-
495820577	mannitol transporter	0.0033	0.0042	-
495820587	threonyl-tRNA synthetase	0.0048	0.0058	-
495820588	methionine adenosyltransferase	0.0033	0.0108	-
495820593	ureidoglycolate dehydrogenase	0.0035	0.0105	-
495820599	D-amino-acid dehydrogenase small chain	0.003	0.0049	-
495820605	DNA gyrase, B subunit	0.0035	0.0117	-
495820615	3-isopropylmalate dehydratase, large subunit	0.0023	0.0087	-
495820620	ribosomal protein L11	0.0137	0.0728	-
495820637	50S ribosomal protein L19	0.0115	0.0654	-
495820640	lysine/ornithine decarboxylase	0.002	0.0158	-
495820642	LSU ribosomal protein L10P	0.0182	0.0518	-
495820662	mechanosensitive ion channel	0.0033	0.007	-
495820672	replicative DNA helicase	0.0031	0.0091	-
495820702	ribosomal protein S12	0.0209	0.0843	-
495820704	rod shape-determining protein MreB	0.0109	0.0289	-
495820731	argininosuccinate lyase	0.002	0.0067	-
495820732	methylmalonate-semialdehyde dehydrogenase	0.0044	0.0197	-
495820740	conserved hypothetical protein	0.0013	0.0127	-
495820747	type II Secretion PilY1	0.0087	0.0144	-
495820749	ABC transporter, permease protein	0.0027	0.0059	-
495820752	acetolactate synthase, large subunit, biosynthetic type	0.0013	0.0058	-
495820765	excinuclease ABC, B subunit	0.0016	0.0059	-
495820766	DNA gyrase, A subunit	0.0048	0.0058	-
495820774	extracellular solute-binding protein, family 1	0.0813	0.3771	-
495820778	HesB/YadR/YfhF	0.0031	0.0136	-
495820791	sarcosine dehydrogenase	0.0007	0.0027	-
495820800	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	0.0028	0.0122	-
495820807	phenylalanyl-tRNA synthetase, alpha subunit	0.0018	0.0107	-
495820814	glycine dehydrogenase	0.0039	0.0096	-
495820816	L-lactate dehydrogenase	0.0016	0.0074	-
495820822	ribosomal protein L3	0.0026	0.0415	-
495820835	excinuclease ABC, A subunit	0.0021	0.0109	-
495820838	putative tricarboxylic transport TctC	0.0482	0.1568	-
495820842	glycine betaine transporter, ATP-binding protein	0.0032	0.0075	-
495820843	TctA protein	0.0128	0.0101	-
495820847	ammonium transporter	0.0537	0.193	-
495820849	cytochrome c oxidase, subunit I	0.0425	0.0635	-
495820869	Integral membrane protein DUF6	0.0012	0.0045	-
495820881	putative pseudo-pilin PulG	0.0914	0.0737	-
495820884	DNA-directed DNA polymerase gamma/tau subunit	0.0028	0.0102	-
495820895	flavin Mononucleotide Binding Protein	0.0021	0.005	-
495820896	glutamyl-tRNA(gln) amidotransferase chain B	0.0023	0.0111	-
495820902	amino acid ABC transporter	0.0133	0.0107	-
495820907	histone deacetylase family protein	0.0017	0.008	-
495820912	quinolinate synthetase complex, A subunit	0.0043	0.0149	-
495820918	ribosomal protein L6	0.0054	0.0178	-
495820919	tail-specific proteinase	0.0019	0.0084	-
495820932	hypothetical protein PB7211_1033	0.0038	0.0068	-
495820939	chromosomal replication initiator protein DnaA	0.002	0.0096	-
495820965	adenosylhomocysteinase	0.0075	0.0473	-
495820978	CTP synthase	0.0036	0.007	-
495820980	ribosomal protein L25, Ctc-form	0.0236	0.0226	-
495820991	glycerol kinase	0.0016	0.0035	-
495820993	putative hemimethylated DNA binding domain protein	0.0096	0.0337	-
495821000	NADH dehydrogenase i chain b	0.0334	0.023	-
495821002	NADH dehydrogenase (quinone), G subunit	0.0036	0.0135	-
495821021	proline dipeptidase	0.0015	0.008	-
495821027	transcription termination factor	0.0074	0.0118	-
495821030	penicillin-binding protein 1A	0.0046	0.0076	-
495821035	adenosylmethionine-8-amino-7-oxononanoate aminotransferase	0.0058	0.0306	-
495821051	conserved hypothetical protein	0.0042	0.0458	-
495821059	adenylylsulfate reductase membrane anchor	0.0423	0.0785	-

495821061	GTP-binding protein LepA	0.0016	0.0049	-
495821075	adenylosuccinate lyase	0.0037	0.0192	-
495821081	ATP-dependent protease	0.0083	0.031	-
495821095	single-strand binding protein family protein	0.0119	0.0347	-
495821097	sarcosine oxidase alpha subunit	0.0044	0.0102	-
495821104	amino acid ABC transporter, permease protein	0.013	0.0163	-
495821116	acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	0.0058	0.0164	-
495821128	aconitate hydratase 1	0.0024	0.0069	-
495821130	glycine cleavage system H protein	0.0093	0.0199	-
495821131	ubiquinol-cytochrome c reductase, iron-sulfur subunit	0.0055	0.038	-
495821132	delta-aminolevulinic acid dehydratase	0.0037	0.0085	-
495821133	conserved hypothetical protein	0.0073	0.0308	-
495821134	transcription regulator	0.0039	0.0493	-
495821137	ribosomal protein S20	0.0068	0.0417	-
495821157	NADP-dependent malic enzyme	0.0042	0.0128	-
495821189	imidazoleglycerol-phosphate dehydratase	0.0072	0.0231	-
495821197	30S ribosomal protein S14	0.0146	0.0611	-
495821209	O-acetylhomoserine (thiol)-lyase	0.0096	0.02	-
495821230	ribosomal protein L13	0.0078	0.0514	-
495821233	conserved hypothetical protein	0.0618	0.0818	-
495821248	ribosomal protein L35	0.0048	0.0517	-
495821253	translation elongation factor Ts	0.0043	0.0251	-
495821273	preprotein translocase, SecA subunit	0.0018	0.0103	-
495821291	DNA polymerase III, alpha subunit	0.0014	0.0065	-
495821294	2-polyprenylphenol 6-hydroxylase	0.0008	0.0068	-
495821302	acetolactate synthase, small subunit	0.0036	0.0086	-
495821309	isocitrate lyase	0.0023	0.0192	-
495821311	outer membrane protein TolC	0.0014	0.0095	-
495821319	conserved hypothetical protein	0.0054	0.0366	-
495821325	muropeptide permease	0.0073	0.0089	-
495821331	morn repeat protein	0.0018	0.0158	-
495821333	homocysteine S-methyltransferase	0.002	0.0029	-
495821335	octaprenyl-diphosphate synthase	0.0034	0.0154	-
495821355	glutamate synthase subunit 1	0.0132	0.0608	-
495821364	tol-pal system protein YbgF, putative	0.0089	0.0349	-
495821391	acetyl-CoA carboxylase, biotin carboxyl carrier protein	0.0138	0.0485	-
495821403	dihydrodipicolinate synthase	0.0033	0.0145	-
495821406	cysteinyl-tRNA synthetase	0.0015	0.0112	-
495821409	cytochrome c oxidase assembly protein CtaG	0.0051	0.023	-
495821412	sarcosine oxidase	0.0061	0.0176	-
495821433	3-deoxy-7-phosphoheptulonate synthase	0.011	0.0477	-
495821442	NADH oxidoreductase (quinone), F subunit	0.0021	0.0059	-
495821454	AcrB/AcrD/AcrF family protein	0.0047	0.0058	-
495821481	chaperonin GroS	0.0543	0.2835	-
495821507	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase	0.002	0.0035	-
495821518	membrane protein	0.0238	0.0371	-
495821519	RIP metalloprotease RseP	0.006	0.0103	-
495821522	hypothetical protein PB7211_1417	0.017	0.0204	-
495821531	probable integral membrane protein	0.0043	0.0047	-
495821538	conserved hypothetical protein	0.0084	0.0138	-
495821542	sarcosine oxidase beta subunit	0.0072	0.0053	-
495821548	NADH dehydrogenase i chain l	0.0043	0.0064	-
495821550	glycine betaine transporter, ATP-binding protein	0.0042	0.009	-
495821560	type II Secretion System PilC	0.018	0.0184	-
495821568	metallo-beta-lactamase family protein	0.002	0.0091	-

Table S5. Gene expression ratios in the gammaproteobacterium HTCC2080 bin.

NCBI GI	Protein Description	Mean Expression Ratio (FL)	Mean Expression Ratio (PA)	PA Regulation
494440354	hypothetical protein	0.0154	0.0868	Up
494440403	dnaK protein	0.0403	0.3517	Up
494440409	bifunctional isocitrate dehydrogenase kinase/phosphatase protein	0.0375	0.3177	Up
494440423	Secreted Zn-dependent peptidase, insulinase family protein	0.0529	0.2275	Up
494440451	probable acid-CoA ligase	0.0478	0.3195	Up
494440531	Alpha amylase, catalytic subdomain	0.1094	1.0107	Up
494440576	C-terminal processing peptidase	0.0221	0.1555	Up
494440618	Leucyl aminopeptidase	0.0399	0.3909	Up
494440739	isoquinoline 1-oxidoreductase, beta subunit	0.4149	2.4925	Up
494440758	enoyl-CoA hydratase/isomerase family protein	0.061	0.7257	Up
494441092	signal peptide peptidase SppA, 67K type	0.023	0.0509	Up
494441139	acyl-CoA synthase	0.025	0.1787	Up
494441143	acyl-CoA synthase	0.1803	1.6682	Up
494441150	transcriptional regulator, TetR family protein	0.156	1.4948	Up
494441152	putative lipoprotein	0.1305	0.3226	Up
494441170	putative TonB-dependent receptor	0.0562	0.1313	Up
494441263	invasion protein IbeA	0.0198	0.121	Up
494441273	peptidase M20	0.006	0.0568	Up
494441340	putative acyl coenzyme A dehydrogenase (HcaD-like) protein	0.0524	0.2198	Up
494441342	hypothetical protein	0.0209	0.2073	Up
494441355	aminotransferase, class III	0.0608	0.1833	Up
494441435	Magnesium-chelatase, subunit H	0.0199	0.2316	Up
494441467	cobalt-zinc-cadmium resistance protein (CzcA)-like	0.0113	0.1214	Up
494441545	cobalt-zinc-cadmium resistance protein (CzcA)-like	0.0775	0.3368	Up
494441547	phosphoenolpyruvate carboxykinase (ATP)	0.1487	0.9292	Up
494441555	ribonucleotide-diphosphate reductase alpha subunit	0.0284	0.0945	Up
494441566	Cell division protein FtsI/penicillin-binding protein 2	1.188	11.6239	Up
494441632	oxidoreductase, short chain dehydrogenase/reductase family protein	0.105	0.6064	Up
494441786	acyl-CoA dehydrogenase-like protein	0.028	0.0857	Up
494441804	putative indolepyruvate ferredoxin oxidoreductase alpha subunit	0.0154	0.079	Up
494441857	TonB-dependent receptor	0.0247	0.1271	Up
494442038	2,4-dienoyl-CoA reductase FadH1	0.2144	1.5905	Up
494442120	glutathione S-transferase	0.0032	0.0405	Up
494442294	putative transcriptional regulator, Fis family protein	0.0489	0.1822	Up
494442514	Acetyltransferase	0.0083	0.0724	Up
494442681	helicase, ATP-dependent	0.0068	0.1158	Up
494442774	hypothetical protein	0.0252	0.0736	Up
494442862	Glutamate synthase domain 2	0.048	0.1487	Up
494442911	putative type 4 fimbrial biogenesis pily1-related protein signal peptide	0.0367	0.1738	Up
494443014	L-carnitine dehydratase/bile acid-inducible protein F	0.0301	0.1995	Up
494443015	5-oxoprolinase (ATP-hydrolyzing)	0.0525	0.4344	Up
494443109	TPR domain protein	0.012	0.0414	Up
494443148	acyl-CoA dehydrogenase-like protein	0.0061	0.0316	Up
494443189	acriflavin resistance protein	0.0089	0.0685	Up
494440127	protease subunit HflC	0.0559	0.0238	Down
494440167	Beta-glucosidase	0.1017	0.0507	Down
494440245	Ribosomal protein L10	1.4544	0.5637	Down
494440247	DNA-directed RNA polymerase subunit beta	0.2435	0.1589	Down
494440267	50S ribosomal protein L5	0.4236	0.1986	Down
494440272	30S ribosomal protein S5	0.8106	0.2938	Down
494440275	protein translocase subunit SecY	0.5032	0.2822	Down
494440652	Ankyrin	0.2788	0.1054	Down
494440764	aminotransferase, class III	0.152	0.0712	Down
494440790	putative unknown membrane associated protein	0.0873	0.0257	Down
494440793	Branched-chain amino acid aminotransferase I	0.2981	0.1329	Down
494441146	Outer membrane protein	0.0547	0.031	Down
494441371	Pyridoxal-dependent decarboxylase	0.2288	0.0358	Down
494441741	Cytochrome oxidase assembly protein	0.067	0.0155	Down
494442055	formate--tetrahydrofolate ligase	0.0599	0.016	Down
494442274	putative TonB-dependent outer membrane receptor	0.6055	0.2498	Down
494442351	enoyl-CoA hydratase/isomerase family protein	0.0753	0.0212	Down
494442352	acetyl-CoA carboxylase carboxyltransferase	0.0674	0.0251	Down
494442353	hypothetical protein	0.07	0.024	Down
494442365	Flagellar biosynthesis protein FliR	0.2362	0.1502	Down
494442593	translation initiation factor IF-3	0.6376	0.0998	Down
494442597	threonyl-tRNA synthetase	0.0645	0.0274	Down
494442812	protein-export protein SecB	0.1159	0.0375	Down
494442833	NAD(P) transhydrogenase subunit alpha	0.1068	0.0314	Down
494442915	Inorganic diphosphatase	0.1243	0.0813	Down
494443095	Na(+)-translocating NADH-quinone reductase subunit F	0.1295	0.0695	Down
494443140	ribosomal 5S rRNA E-loop binding protein Ctc/L25/TL5	0.2073	0.0469	Down
494440042	ribulose-phosphate 3-epimerase	0.035	0.0274	-
494440089	metallo-beta-lactamase family protein	0.0231	0.0242	-
494440093	hypothetical protein	0.0134	0.0438	-
494440094	hypothetical protein	0.0087	0.0127	-
494440108	Gamma-glutamyltransferase	0.0119	0.0677	-
494440168	putative sodium/hexose cotransport protein	0.0521	0.0306	-
494440170	Glycine hydroxymethyltransferase	0.0923	0.0965	-
494440248	DNA-directed RNA polymerase subunit beta'	0.3469	0.4348	-
494440251	translation elongation factor G	0.1887	0.3033	-
494440252	conserved repeat domain protein	0.0099	0.0119	-
494440261	30S ribosomal protein S3	0.8761	0.789	-
494440262	50S ribosomal protein L16	0.119	0.2637	-
494440279	DNA-directed RNA polymerase subunit alpha	0.2874	0.2363	-
494440293	UDP-glucose pyrophosphorylase	0.0441	0.0378	-
494440303	acyl-CoA dehydrogenase-like protein	0.014	0.0245	-
494440310	Oar-like outer membrane protein protein, OmpA family	0.1152	0.1737	-
494440380	hypothetical protein	0.0192	0.0263	-

494440393	hypothetical protein	0.0438	0.0315	-
494440413	transcriptional regulator, TetR family protein	0.0024	0.0602	-
494440424	pyruvate dehydrogenase subunit E1	0.0704	0.0576	-
494440428	acyl-CoA synthase	0.0223	0.0122	-
494440448	TonB-dependent receptor	0.0157	0.0285	-
494440463	putative esterase	0.0186	0.0196	-
494440471	hypothetical protein	0.018	0.0638	-
494440472	putative ferredoxin	0.0188	0.0437	-
494440474	Transcriptional regulator	0.01	0.0349	-
494440489	Cytochrome c-type biogenesis protein CcmF	0.0328	0.0639	-
494440493	chromosome segregation protein	0.0265	0.0298	-
494440496	transcriptional regulatory protein	0.0052	0.1165	-
494440501	citrate synthase	0.0363	0.1259	-
494440504	succinate dehydrogenase flavoprotein subunit	0.0666	0.0642	-
494440507	dihydrolipoamide acetyltransferase	0.1104	0.0719	-
494440511	Succinyl-CoA synthetase, alpha subunit	0.2277	0.4655	-
494440530	Multi-sensor Hybrid Histidine Kinase	0.015	0.078	-
494440535	major facilitator family transporter	0.0056	0.0393	-
494440566	hypothetical protein	0.0734	0.0535	-
494440570	thioredoxin reductase 1	0.0424	0.0755	-
494440586	hypothetical protein	0.0009	0.0114	-
494440593	acyl-CoA synthase	0.005	0.0122	-
494440606	sodium/proton antiporter	0.0392	0.0437	-
494440623	hypothetical protein	0.0515	0.0712	-
494440631	long-chain-fatty-acid--CoA ligase	0.0233	0.0405	-
494440650	ATP-dependent protease ATP-binding subunit	0.0694	0.1366	-
494440658	3-oxoacyl-(acyl carrier protein) synthase	0.2047	0.0787	-
494440666	DNA polymerase III delta prime subunit	0.1052	0.0713	-
494440687	sensor histidine kinase	0.0385	0.0522	-
494440715	hypothetical protein	0.0057	0.0113	-
494440752	probable choline transporter	0.0171	0.0163	-
494440761	hypothetical protein	0.0208	0.0159	-
494440791	periplasmic protein TonB	0.1021	0.1436	-
494440794	Lipid A export ATP-binding/permease protein MsbA	0.0925	0.1682	-
494440795	TonB system biopolymer transport component	0.2686	0.1925	-
494440796	TonB system biopolymer transport component	0.1305	0.104	-
494440804	Ubiquinone biosynthesis hydroxylase, UbiH/UbiF/VisC/COQ6	0.0433	0.2344	-
494440806	aminopeptidase P II	0.0154	0.034	-
494440814	D-erythrose-4-phosphate dehydrogenase	0.0336	0.1945	-
494440818	TonB-dependent receptor	0.3984	0.2619	-
494440824	S-adenosyl-L-homocysteine hydrolase	0.0568	0.0634	-
494440844	RNA polymerase sigma factor	0.2212	0.1325	-
494440852	50S ribosomal subunit protein L28	0.1896	0.1055	-
494440860	Exonuclease III	0.0567	0.0245	-
494440886	Sodium-transporting two-sector ATPase	0.2831	0.2967	-
494440889	F-type H+-transporting ATPase c chain	0.7616	0.473	-
494440890	F0F1 ATP synthase subunit A	0.532	0.282	-
494440893	Putative ParA family protein	0.0523	0.0365	-
494440897	putative inner membrane protein translocase component YidC	0.0155	0.0318	-
494440905	DNA gyrase subunit B	0.0228	0.0485	-
494440908	glycyl-tRNA synthetase subunit alpha	0.0268	0.0819	-
494440911	potassium uptake protein TrkH	0.013	0.0388	-
494440912	potassium transporter peripheral membrane component	0.0147	0.0161	-
494440923	cytochrome c oxidase, subunit II	0.3062	0.5784	-
494440924	Cytochrome-c oxidase	0.2258	0.3464	-
494440926	cytochrome c oxidase, subunit III	0.1771	0.1709	-
494440936	hypothetical protein	0.0655	0.1077	-
494440942	N-acetylglutamate synthase	0.0159	0.0309	-
494440961	TPR domain protein	0.003	0.0082	-
494441008	flagellar biosynthesis protein	0.0519	0.4975	-
494441030	transcription termination factor Rho	0.065	0.135	-
494441060	deoxyribodipyrimidine photolyase, putative	0.0061	0.0078	-
494441063	dihydroorotate dehydrogenase/oxidoreductase, FAD-binding protein	0.0359	0.0457	-
494441066	hypothetical protein	0.0395	0.1249	-
494441070	hypothetical protein	0.0279	0.1783	-
494441078	hypothetical protein	0.0308	0.0315	-
494441085	hypothetical protein	0.0048	0.0105	-
494441138	Amidohydrolase family protein	0.0118	0.024	-
494441144	hypothetical protein	0.0238	0.029	-
494441145	hypothetical protein	0.0718	0.0737	-
494441153	TonB-dependent receptor	0.0857	0.0749	-
494441188	hypothetical protein	0.0087	0.0084	-
494441189	methionine synthase I	0.0068	0.0271	-
494441191	methionine synthase I	0.0362	0.033	-
494441216	hypothetical protein	0.0056	0.0074	-
494441219	alcohol dehydrogenase, zinc-containing	0.0086	0.0352	-
494441226	Alcohol dehydrogenase, class IV	0.0146	0.0246	-
494441251	Alcohol dehydrogenase large subunit	0.0217	0.0307	-
494441260	hypothetical protein	0.0078	0.0042	-
494441261	TPR domain protein	0.0092	0.027	-
494441262	TonB-dependent receptor	0.0848	0.1119	-
494441265	hypothetical protein	0.0075	0.0146	-
494441274	MFS permease	0.0568	0.0609	-
494441287	UvrD/REP helicase	0.0023	0.0154	-
494441290	rarD protein	0.0376	0.0725	-
494441312	GTP-binding protein LepA	0.1105	0.0709	-
494441339	hypothetical protein	0.0087	0.0076	-
494441389	aminomethyl transferase family protein	0.0067	0.009	-
494441408	phosphoenolpyruvate carboxylase	0.032	0.0151	-
494441412	glucose-6-phosphate 1-dehydrogenase	0.0846	0.1687	-
494441414	glucokinase	0.1339	0.099	-
494441439	Photosynthetic reaction center H-chain	0.0038	0.0152	-
494441544	Secretion protein HlyD	0.1055	0.1084	-
494441560	Bacterioferritin	0.0098	0.0364	-

494441567	putative rod shape-determining protein RodA	1.782	19.8767	-
494441570	D-alanyl-D-alanine carboxypeptidase	0.0139	0.0172	-
494441573	peptide chain release factor RF-3	0.0454	0.1303	-
494441576	glutamine synthetase, putative	0.0791	0.1553	-
494441607	Kynureninase	0.0098	0.0272	-
494441621	Cysteine synthase	0.0435	0.0438	-
494441638	Acyl-CoA hydrolase-like protein	0.0412	0.0734	-
494441639	short chain dehydrogenase	0.0617	0.0457	-
494441640	acetyl-coenzyme A synthetase	0.0202	0.0294	-
494441641	Putative cyclase	0.0108	0.0321	-
494441642	taurine dioxygenase	0.0231	0.0597	-
494441643	sodium/alanine symporter	0.0176	0.037	-
494441646	Catalase	0.1254	1.049	-
494441659	alcohol dehydrogenase, iron-containing	0.0574	0.15	-
494441669	ATP-dependent metalloprotease FtsH	0.093	0.1107	-
494441685	SmpB protein	0.1181	0.1418	-
494441688	30S ribosomal protein S15	0.5528	0.3424	-
494441696	DNA polymerase III, epsilon subunit	0.0101	0.0903	-
494441708	putative integral membrane protein	0.0196	0.0594	-
494441716	monooxygenase, flavin-binding family protein	0.0261	0.026	-
494441730	leucyl-tRNA synthetase	0.0112	0.0958	-
494441756	LuxO repressor protein	0.0318	0.0139	-
494441824	amidophosphoribosyltransferase	0.0578	0.0436	-
494441830	tryptophan synthase subunit beta	0.0541	0.0673	-
494441856	acetoin dehydrogenase complex, E1 component, alpha subunit	0.0137	0.0467	-
494441870	cytochrome P450	0.0119	0.021	-
494441872	glutathione-dependent formaldehyde-activating, GFA	0.0103	0.0211	-
494441898	putative PQQ-dependent polyvinyl alcohol dehydrogenase precursor	0.0096	0.0228	-
494441911	putative TonB-dependent receptor	0.0347	0.039	-
494441918	cyclohexanone monooxygenase	0.0098	0.0144	-
494441942	hypothetical protein	0.0146	0.1202	-
494441945	putative integral membrane transport protein	0.006	0.018	-
494441946	cytochrome P450 family protein	0.0134	0.0541	-
494441963	Phosphoesterase, PA-phosphatase related protein	0.036	0.0475	-
494441970	probable oxidoreductase	0.015	0.0179	-
494441971	hypothetical protein	1.1194	5.6645	-
494441999	arylsulfatase B precursor	0.0065	0.0041	-
494442009	hypothetical protein	0.0257	0.0325	-
494442010	hypothetical protein	0.0212	0.0482	-
494442013	putative beta-ketoacyl synthase	0.0488	0.1003	-
494442054	N-acyl-D-glutamate amidohydrolase	0.0175	0.0232	-
494442059	formate dehydrogenase alpha subunit	0.034	0.0245	-
494442061	sarcosine dehydrogenase	0.0372	0.0307	-
494442071	hypothetical protein	0.0658	0.0237	-
494442074	hypothetical protein	0.0331	0.0825	-
494442088	putative saccharopine dehydrogenase	0.02	0.0175	-
494442089	4-aminobutyrate aminotransferase	0.0074	0.0163	-
494442093	YfmJ	0.0127	0.0845	-
494442097	hypothetical protein	0.0159	0.037	-
494442101	sarcosine oxidase, alpha subunit family protein	0.0064	0.0166	-
494442106	hypothetical protein	0.014	0.0373	-
494442110	TonB-dependent receptor	0.0685	0.041	-
494442112	TonB-dependent receptor	0.0139	0.0334	-
494442122	Acyl-CoA synthetases (AMP-forming)/AMP-acid ligases II	0.0046	0.0223	-
494442149	RND family efflux transporter	0.0759	0.0433	-
494442150	proton/peptide symporter family protein	0.0076	0.0192	-
494442171	hypothetical protein	0.0122	0.0222	-
494442186	ammonium transporter	0.0878	0.1078	-
494442198	sulfatase family protein	0.0231	0.0744	-
494442226	Xaa-Pro aminopeptidase family enzyme	0.0296	0.2694	-
494442232	probable long chain fatty acid CoA ligase	0.0211	0.0389	-
494442260	hypothetical protein	0.0416	0.0326	-
494442261	hypothetical protein	0.0134	0.0231	-
494442286	Spermidine/putrescine ABC transporter ATP-binding subunit	0.0482	0.0883	-
494442290	hypothetical protein	0.0093	0.0391	-
494442300	tRNA nucleotidyltransferase, putative	0.0158	0.1236	-
494442308	Parvulin-like peptidyl-prolyl isomerase	0.048	0.035	-
494442354	transcriptional regulator	0.0277	0.0128	-
494442371	DNA gyrase subunit A	0.0584	0.1392	-
494442407	Helix-turn-helix, AraC type	0.025	0.0473	-
494442433	translocase	0.0181	0.0315	-
494442444	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	0.0428	0.1319	-
494442459	ubiquinol--cytochrome c reductase, cytochrome b	0.1952	0.1547	-
494442464	hypothetical protein	0.1431	0.0486	-
494442489	Twin-arginine translocation protein TatB	0.0376	0.0476	-
494442491	Glutamyl-tRNA(Gln) amidotransferase A subunit	0.0157	0.0823	-
494442502	hypothetical protein	0.0068	0.0106	-
494442516	possible NADH oxidoreductase	0.0169	0.2043	-
494442528	cAMP-binding protein - catabolite gene activator and regulatory subunit of cAMP-dependent protein kinase	0.0646	0.0358	-
494442529	adenylate cyclase PLUS two component hybrid sensor and regulator	0.0237	0.0927	-
494442590	phenylalanyl-tRNA synthetase alpha subunit	0.1198	0.1435	-
494442595	hypothetical protein	0.0101	0.0196	-
494442636	hypothetical protein	0.0035	0.0204	-
494442668	oligopeptide ABC transporter periplasmic oligopeptide-binding protein	0.0068	0.0067	-
494442669	Phosphoglycerate mutase 1	0.0216	0.069	-
494442674	alkaline phosphatase, putative	0.0047	0.0571	-
494442704	isocitrate lyase	0.2878	0.2803	-
494442711	hypothetical protein	0.0803	0.057	-
494442714	chaperone protein HscA	0.0814	0.0533	-
494442718	cysteine desulfurase	0.1292	0.1793	-
494442724	phosphoribosylformylglycinamidine synthase	0.0272	0.0534	-
494442728	Alpha-methylacyl-CoA racemase	0.0051	0.0132	-
494442740	protein kinase C inhibitor	0.0299	0.0429	-

494442749	probable phosphate transporter	0.0895	0.1058	-
494442750	hypothetical protein	0.0537	0.0954	-
494442752	Phosphate-selective porin O and P	0.0214	0.0179	-
494442788	hypothetical protein	0.1741	0.1196	-
494442799	efflux transporter, RND family, MFP subunit	0.0287	0.0367	-
494442816	Glutamate--ammonia ligase	0.0225	0.0373	-
494442821	DNA topoisomerase IV subunit A	0.0177	0.0497	-
494442824	translation elongation factor P	0.0446	0.0304	-
494442832	anti-sigm factor, ChrR	0.1323	0.1085	-
494442836	ABC transporter, ATP-binding/permease protein	0.0141	0.0565	-
494442883	L-threonine 3-dehydrogenase	0.035	0.0499	-
494442897	NAD synthase	0.024	0.0391	-
494442898	competence protein ComL	0.0226	0.0328	-
494442913	diguanylate cyclase/phosphodiesterase (GGDEF & EAL domains)	0.0769	0.0773	-
494442917	phosphatidylserine synthase	0.0519	0.0218	-
494442952	Bacterioferritin	0.0563	0.0845	-
494442984	uridylate kinase	0.0854	0.0876	-
494442985	ribosome recycling factor	0.1446	0.0755	-
494442990	probable outer membrane protein	0.065	0.0418	-
494442991	hypothetical protein	0.1416	0.4198	-
494443006	putative citrate lyase beta subunit	0.0161	0.0259	-
494443007	MmgE/PrpD	0.0079	0.0149	-
494443008	4-hydroxyphenylacetate 3-hydroxylase family protein	0.0067	0.0075	-
494443013	3-oxoadipate enol-lactone hydrolase	0.0136	0.0239	-
494443016	5-oxoprolinase (ATP-hydrolyzing)	0.0121	0.0242	-
494443026	Methenyltetrahydrofolate cyclohydrolase	0.0204	0.0501	-
494443027	major facilitator superfamily MFS_1	0.0117	0.089	-
494443062	hypothetical protein	0.0146	0.0464	-
494443085	lipid A export ATP-binding/permease protein MsbA	0.0257	0.027	-
494443087	MotA/TolQ/ExbB proton channel	0.0238	0.0747	-
494443098	hypothetical protein	0.0576	0.0315	-
494443100	Bacterial ring hydroxylating dioxygenase, alpha subunit:Immunoglobulin/major histocompatibility	0.0092	0.0267	-
494443101	aminomethyltransferase	0.0242	0.0353	-
494443103	phytoene dehydrogenase	0.0114	0.0117	-
494443108	hypothetical protein	0.0018	0.0256	-
494443110	hypothetical protein	0.0134	0.058	-
494443111	TonB-dependent receptor	0.0535	0.0596	-
494443119	hypothetical protein	0.0084	0.0233	-
494443150	hypothetical protein	0.0103	0.0105	-
494443158	sulfatase family protein	0.0275	0.106	-
494443166	Na(+)-translocating NADH-quinone reductase subunit B	0.1354	0.1162	-
494443168	glyceraldehyde-3-phosphate dehydrogenase	0.0498	0.0284	-
494443175	DNA topoisomerase I	0.0153	0.0309	-
494443180	hypothetical protein	0.0355	0.2272	-
494443181	hypothetical protein	0.0316	0.227	-
494443188	hypothetical protein	0.0192	0.5064	-
494443204	hypothetical protein	0.0397	0.0468	-
494443205	Isoleucyl-tRNA synthetase, class Ia	0.034	0.037	-