

Supporting information:

The induction of two biosynthetic enzymes helps *Escherichia coli* sustain heme synthesis and activate catalase during hydrogen peroxide stress.

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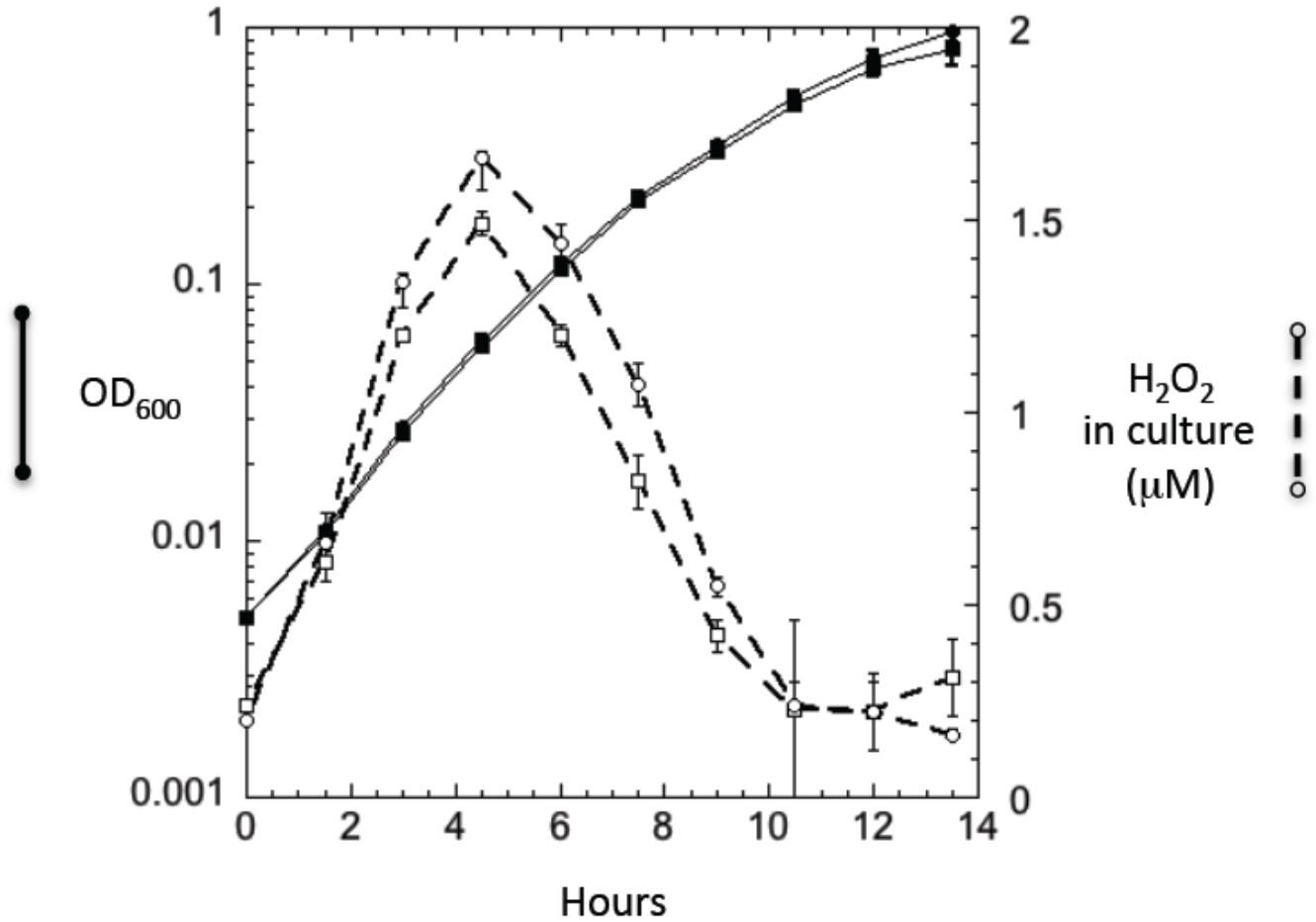


Figure S1. Growth and H₂O₂ accumulation in oxic cultures of Hpx⁻ and Hpx2⁻ cells. Anoxic exponential cultures were diluted into oxic glucose medium at time zero. Closed symbols represent biomass (OD₆₀₀), and open symbols represent H₂O₂ levels in the medium. The H₂O₂ rapidly equilibrates across membranes, so these values should also represent intracellular concentrations (Seaver & Imlay, 2001b). Virtually no H₂O₂ accumulates in sterile medium (not shown). In this study the biochemical measurements reported in other figures were performed after 2-3 hours of aeration, corresponding to H₂O₂ levels of ~ 1 μM.

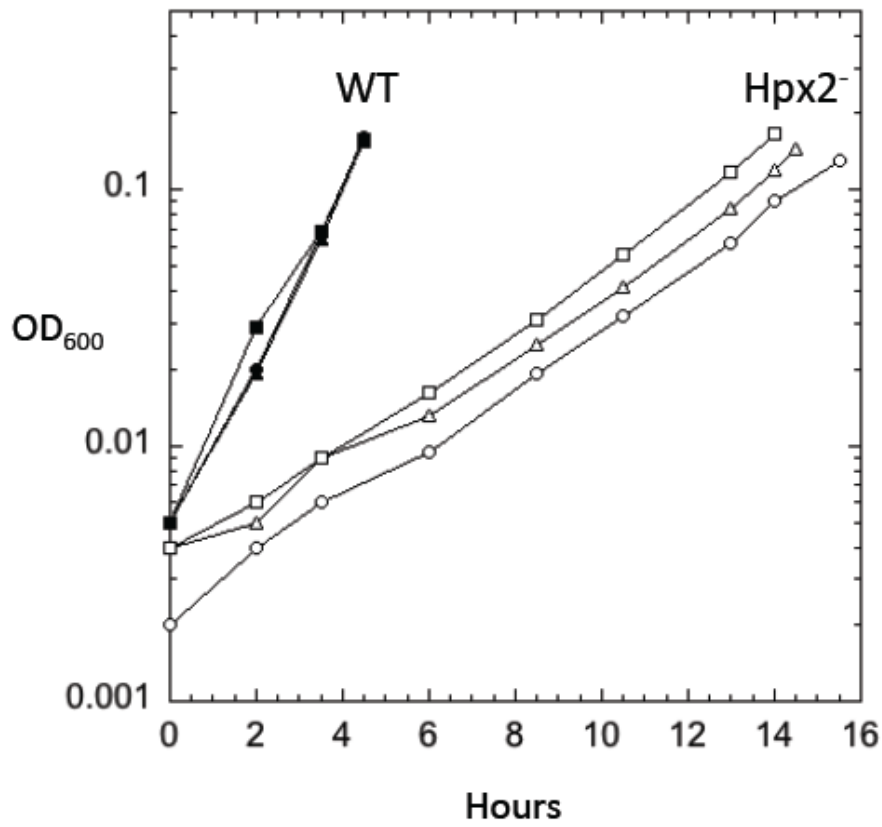


Figure S2. Growth of the triplicate wild-type (solid symbols, MG1655) and Hpx2⁻ (open symbols, SMA1385) cultures that were used for RNA sequencing analysis. Samples were collected near 0.150 OD₆₀₀.

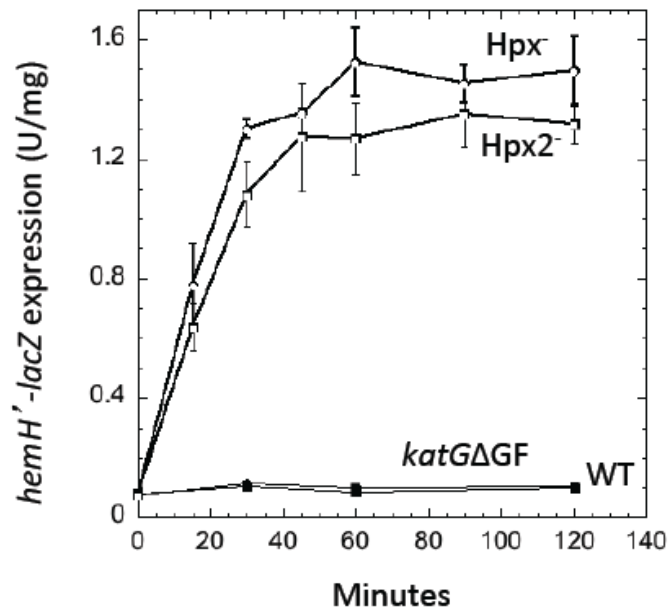


Figure S3. Time course of induction of the *hemH'*-*lacZ* transcriptional fusion. Exponentially growing cells in anoxic LB medium were diluted at time zero into oxic medium, and β -galactosidase activity was monitored. Data represent the mean of three independent experiments. Strains used were SMA1023 (WT), SMA1119 (Hpx⁻), SMA1391 (*katG*ΔGF) and SMA1397 (Hpx2⁻). No difference in induction was observed in Hpx⁻ and Hpx2⁻ strains, indicating that the increased heme demand of the latter strain had no effect upon *hemH* transcription.

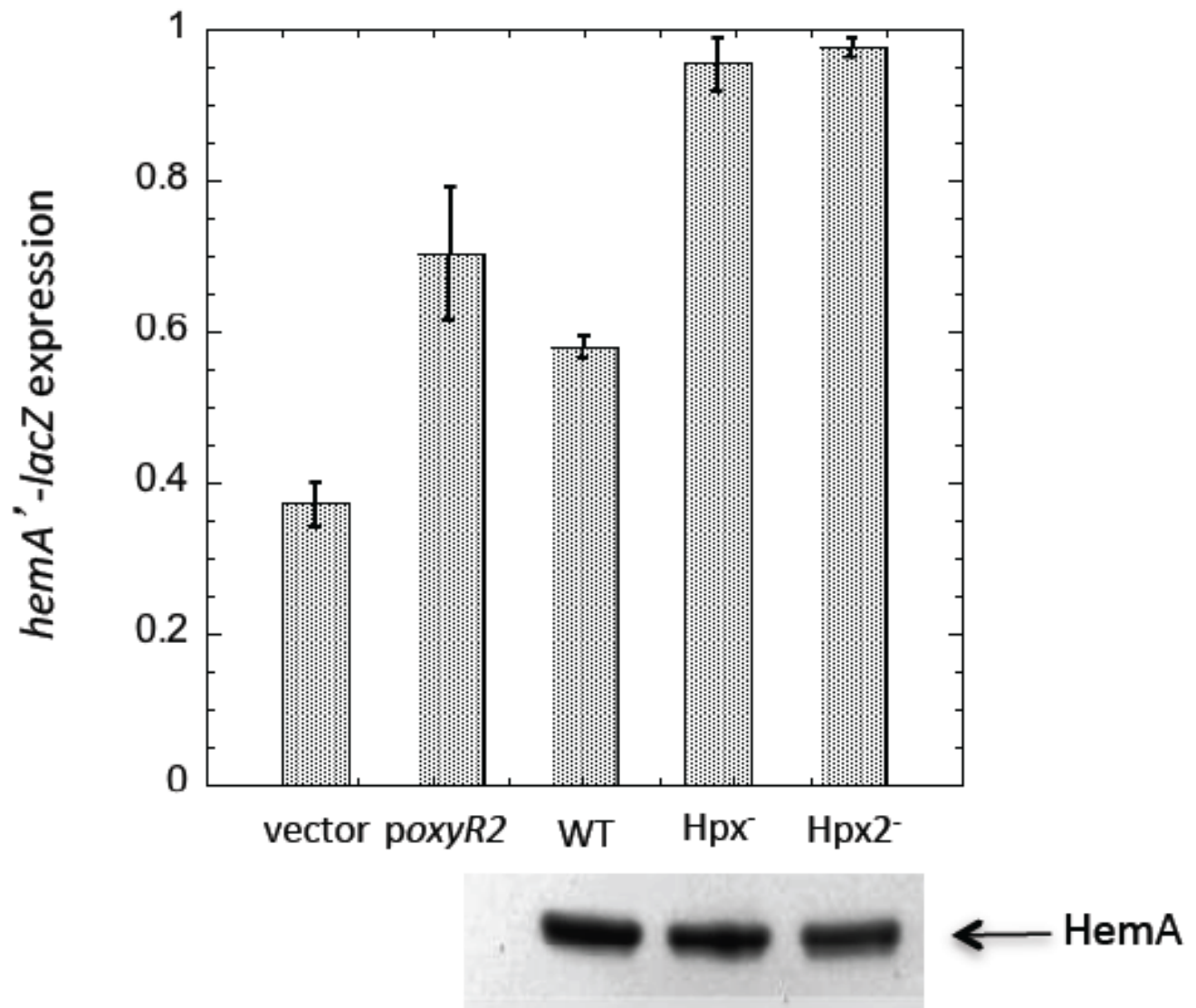


Figure S4. HemA levels do not substantially change during H₂O₂ stress. Cells were diluted into oxic glucose medium at time zero. (A) β -galactosidase activity from a *hemA'*-*lacZ* fusion was monitored. (B) Protein levels were assessed in the same strains by western blot after three hours of aeration. Data are representative of three independent experiments. The *hemA*::*lacZ* strains were SMA1067 (WT with vector), SMA1059 (WT *poxyR2* plasmid), SMA1053 (WT), SMA1121 (*Hpx*⁻), SMA1559 (*Hpx2*⁻).

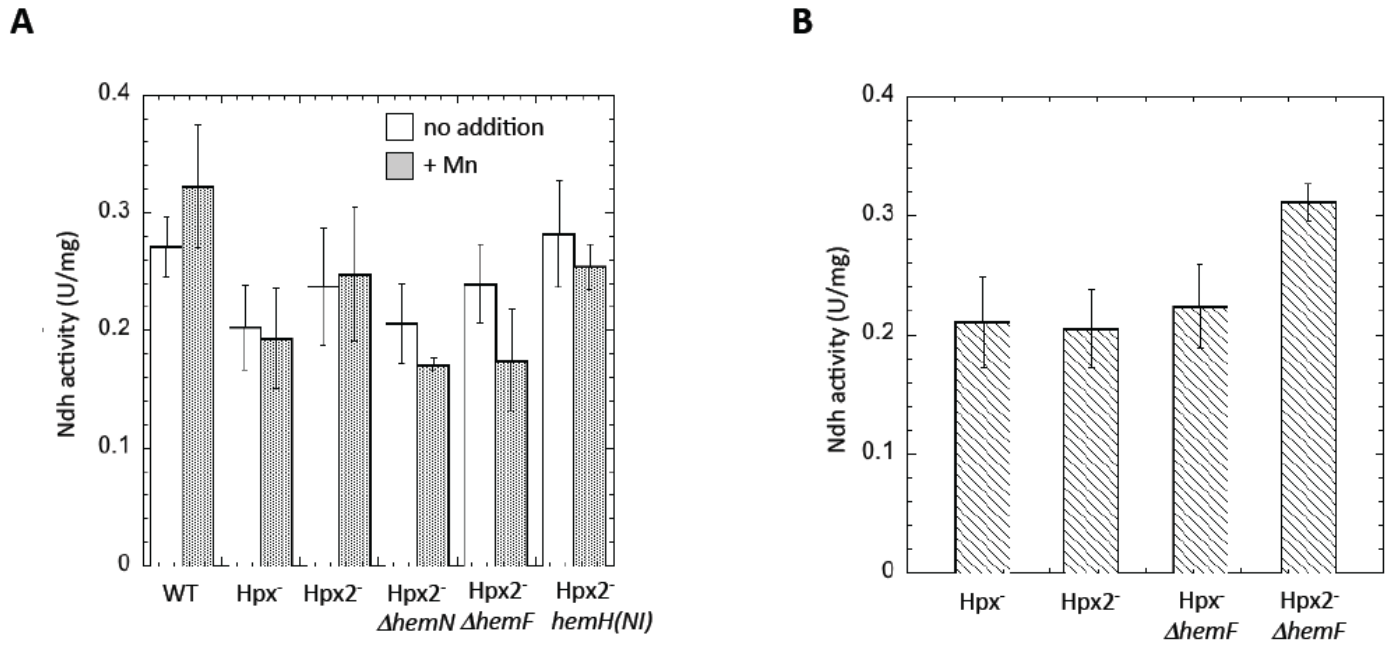


Figure S5. NADH dehydrogenase activities are unaffected by *hemH*, *hemN*, and *hemF* mutations during H₂O₂ stress. Activities were measured using the NADH:ferricyanide oxidoreductase assay.

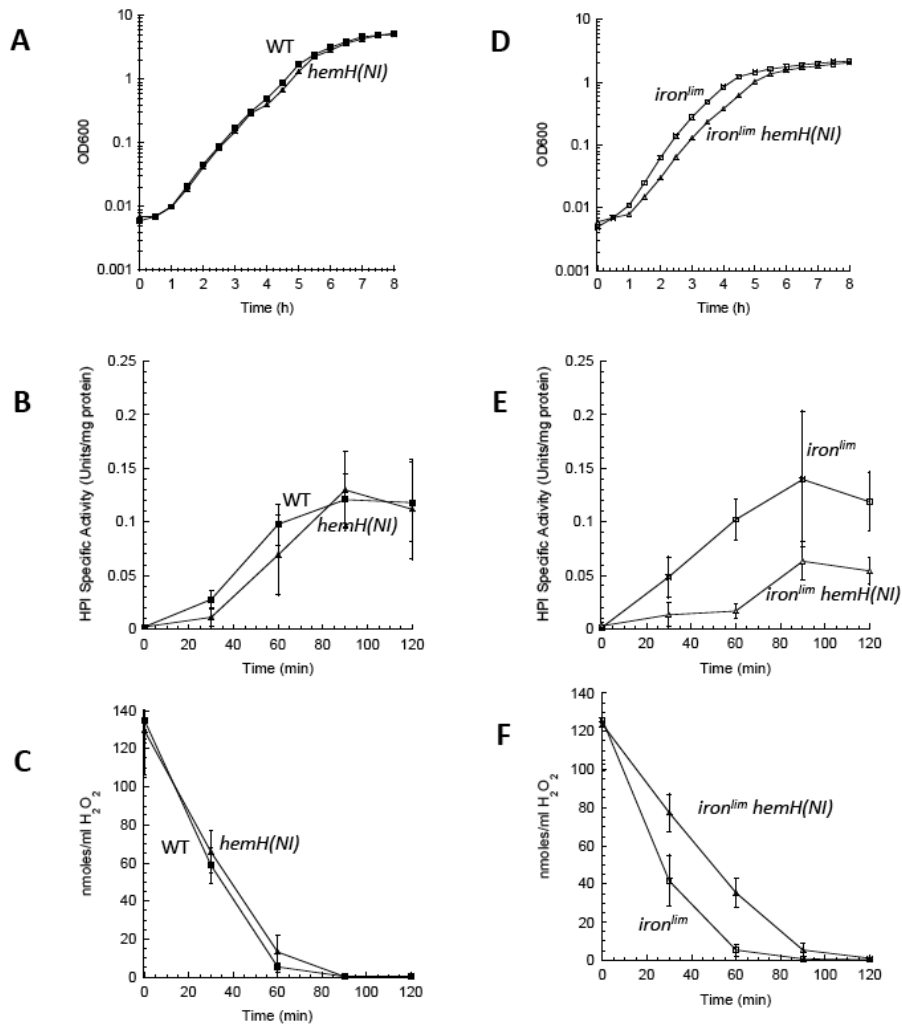


Figure S6. During H_2O_2 stress, iron-deficient cells exhibit a greater need for *hemH* induction. Cells with wild-type iron-import genes (panels A-C) were compared to iron-limited mutants (D-F) that lacked both Feo, the ferrous importer, and TonB, which powers the siderophore and ferric-citrate iron import systems (denoted *iron^{lim}*). At time zero, exponentially growing cells were diluted into fresh LB medium containing 0.3 mM H_2O_2 . This dose was chosen because it imposes little growth lag upon iron-replete *hemH(NI)* strains. Biomass (OD₆₀₀) (panels A, D), KatG peroxidase activities (B, E), and residual H_2O_2 (C, F) were monitored. Data represent the mean of three independent experiments. The strains were JI370 ($\Delta ahpF$), SMA1129 [$\Delta ahpF$ *hemH(NI)*], JEM557 ($\Delta ahpF$ $\Delta tonB$ $\Delta feoABC$), and SMA1169 [$\Delta ahpF$ $\Delta tonB$ $\Delta feoABC$ *hemH(NI)*].

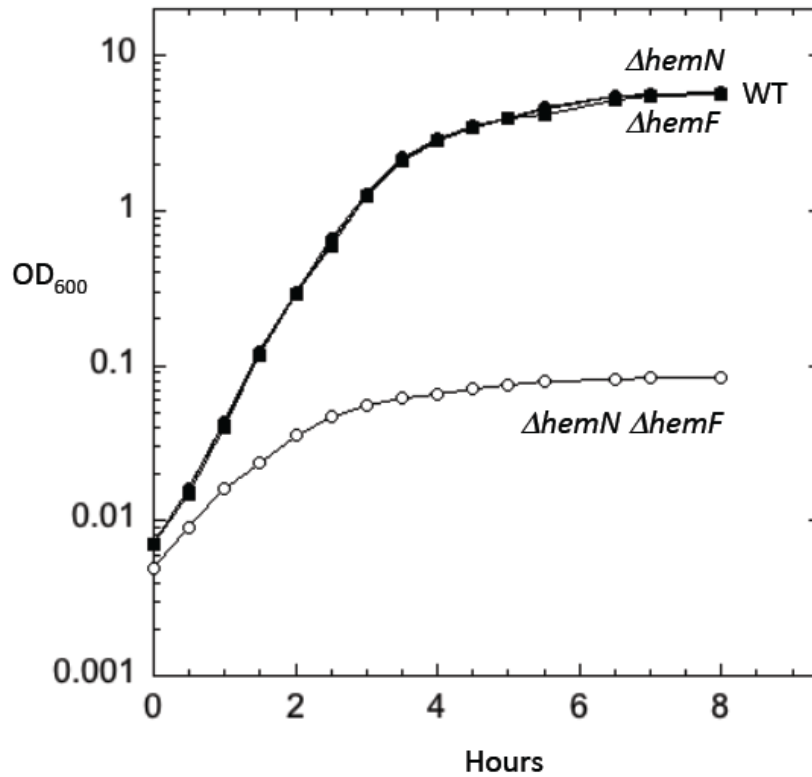


Figure S7. Either HemF or HemN is sufficient to support wild-type growth in unstressed cells.

Anoxic cultures in LB medium were diluted into oxic medium at time zero. Data are representative of three independent experiments. Strains used were MG1655 (WT), SMA1497 ($\Delta hemF$), SMA1499 ($\Delta hemN$), and SMA1557 ($\Delta hemF \Delta hemN$). Heme synthesis is essential in this medium only under oxic conditions.

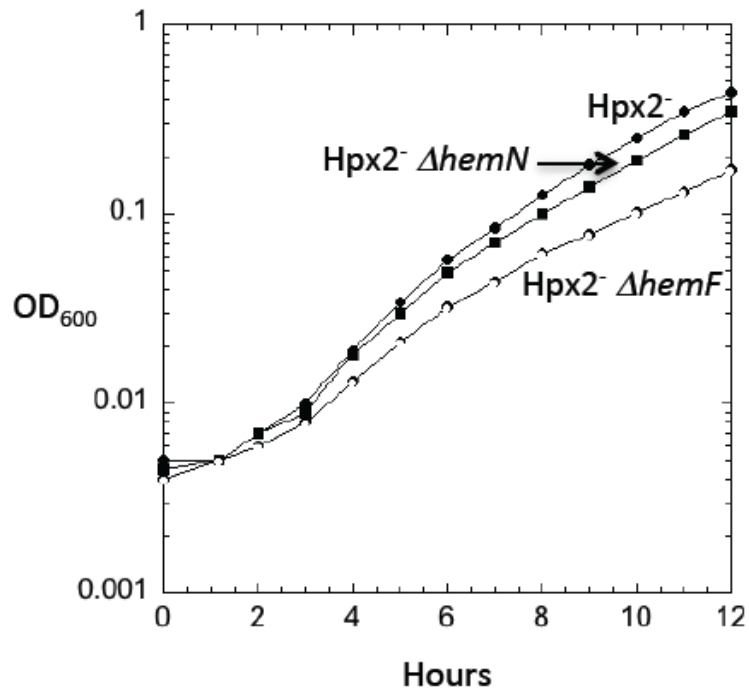


Figure S8. HemF induction helps cells cope with low-grade H₂O₂ stress in glucose medium. *Hpx2⁻* strains were diluted at time zero into oxic glucose medium. Data are representative of three independent experiments. Strains used were SMA1383 (*Hpx2⁻*) SMA1503 (*Hpx2⁻ΔhemF*), and SMA1505 (*Hpx2⁻ΔhemN*).

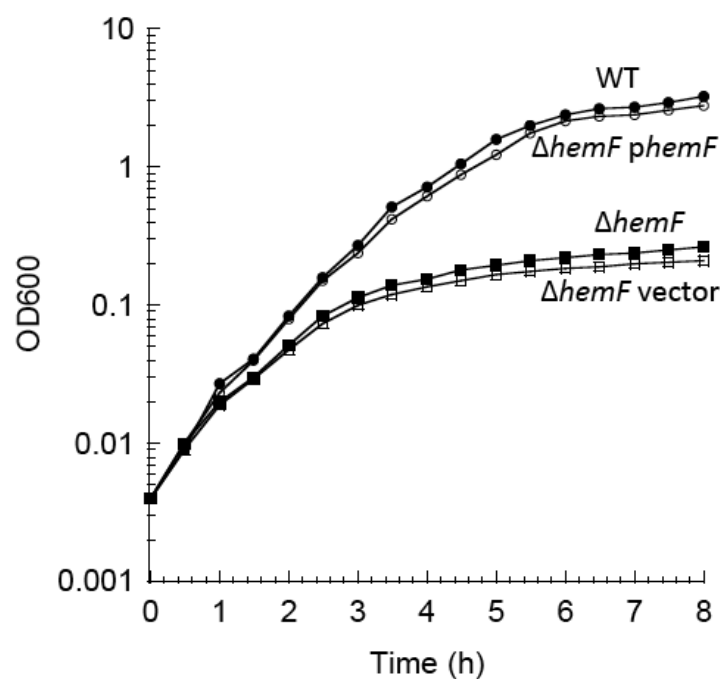


Figure S9. Complementation of the H₂O₂-sensitivity phenotype of *hemF* mutants. Anoxic cultures in LB medium were diluted into oxic medium at time zero. Data are representative of three independent experiments. Strains used were SMA1383 (Hpx2⁻) SMA1503 (Hpx2⁻ $\Delta hemF$), SMA1553 (Hpx2⁻ $\Delta hemF$ with vector), SMA1555 (Hpx2⁻ $\Delta hemF$ with *phemF*).

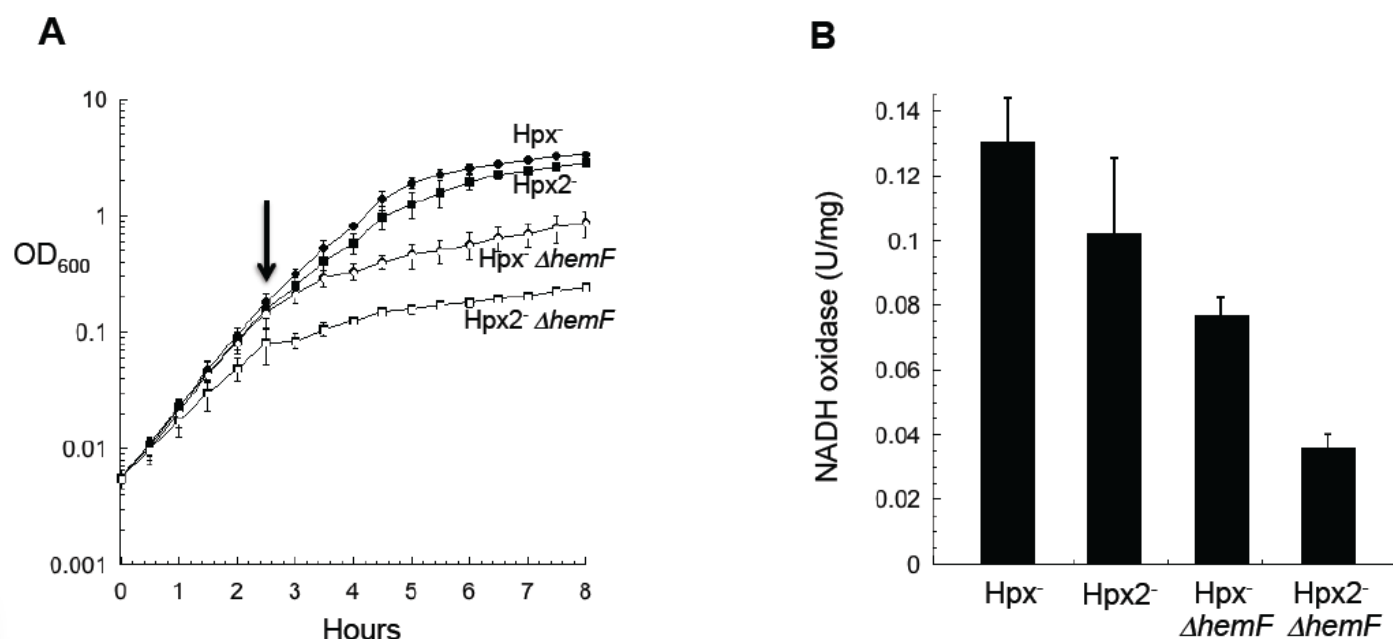


Figure S10. The synthesis of KatG exacerbates the inadequacy of HemN at activating cytochrome oxidase. Anoxic cultures in LB were diluted into oxic medium at time zero. (A) Cell growth. (B) At the time point indicated by the arrow in panel A, membrane vesicles were prepared and NADH oxidase activity was assayed. Hpx2⁻ strains synthesize (inactive) heme-containing KatG, whereas Hpx⁻ strains do not. Data indicate the mean of three independent experiments. The strains were LC106 (Hpx⁻), SMA1383 (Hpx2⁻), SMA1539 (Hpx⁻ Δ hemF) and SMA1503 (Hpx2⁻ Δ hemF).

Supplementary tables.

Table S1. The genes most strongly induced in Hpx2⁻ strains.

Name	Regulator ^a	Fold induction ^b	FDR ^c	Function
<i>oxyS</i>	OxyR	261.01	2.36E-211	NcRNA
<i>katG</i>	OxyR	57.37	0.00E+00	Catalase-peroxidase HPI, heme b-containing
<i>flu</i>	OxyR	52.77	3.25E-206	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter
<i>ymfM</i>	YmfT (SOS)	43.43	7.82E-94	E14 prophage; putative protein
<i>ymfN</i>	YmfT (SOS)	40.90	2.61E-198	E14 prophage; predicted DNA-binding transcriptional regulator
<i>ymfT</i>	YmfT (SOS)	36.71	2.85E-131	E14 prophage; predicted DNA-binding transcriptional regulator
<i>ymfO</i>	YmfT (SOS)	34.09	1.86E-51	E14 prophage; conserved protein
<i>ymfL</i>	YmfT (SOS)	33.48	6.18E-168	E14 prophage; predicted DNA-binding transcriptional regulator
<i>grxA</i>	OxyR	29.65	9.80E-220	Glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)
<i>pspA</i>	PspF	25.55	0.00E+00	Regulatory protein for phage-shock-protein operon
<i>cirA</i>	Fur	20.74	1.81E-226	Catecholate siderophore receptor CirA
<i>pspG</i>	PspF	20.42	4.12E-156	Phage shock protein G
<i>trxC</i>	OxyR	19.72	0.00E+00	Thioredoxin 2
<i>sufD</i>	OxyR, Fur	19.55	0.00E+00	Component of SufBCD Fe-S cluster assembly scaffold
<i>norW</i>	NorR	18.89	4.55E-160	NADH:flavorubredoxin oxidoreductase
<i>fhuE</i>	Fur	18.83	0.00E+00	Ferric-rhodotorulic acid outer membrane transporter
<i>sufC</i>	OxyR, Fur	17.74	0.00E+00	SufBCD Fe-S cluster assembly scaffold protein, ATP-binding protein
<i>tisB</i>	LexA (SOS)	17.44	1.33E-270	Toxic membrane persister formation peptide, LexA-regulated
<i>isrC</i>	OxyR	17.20	9.32E-52	NcRNA
<i>pspC</i>	PspF	16.43	0.00E+00	DNA-binding transcriptional activator
<i>sufS</i>	OxyR, Fur	15.90	0.00E+00	Cysteine desulfurase, stimulated by SufE; selenocysteine lyase, PLP-dependent
<i>pspB</i>	PspF	15.70	1.00E-255	DNA-binding transcriptional regulator of psp operon
<i>yaaA</i>	OxyR	15.34	0.00E+00	Peroxide resistance protein, lowers intracellular iron
<i>ymfJ</i>	(SOS)	15.26	2.86E-212	E14 prophage; putative protein

<i>sufB</i>	OxyR, Fur	15.01	1.45E-295	Component of SufBCD Fe-S cluster assembly scaffold
<i>yjjZ</i>	Fur	14.53	7.17E-91	Hypothetical protein
<i>pspD</i>	PspF	13.80	1.32E-195	Peripheral inner membrane phage-shock protein
<i>hemH</i>	OxyR	13.69	0.00E+00	Ferrochelatase
<i>entE</i>	Fur	13.65	1.04E-236	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase multienzyme complex
<i>ymfP</i>	YmFT (SOS)	13.08	9.02E-47	E14 prophage; conserved protein
<i>sufA</i>	OxyR, Fur	11.13	5.33E-320	Fe-S cluster assembly protein
<i>fecA</i>	Fur	11.06	3.92E-141	KpLE2 phage-like element; ferric citrate outer membrane transporter
<i>entB</i>	Fur	10.98	9.42E-210	Isochorismatase
<i>sufE</i>	OxyR, Fur	10.81	1.33E-208	Sulfur acceptor protein
<i>entC</i>	Fur	10.74	9.88E-272	Isochorismate synthase 1
<i>nrdE</i>	Fur	10.70	1.37E-286	Ribonucleoside-diphosphate reductase 2, alpha subunit
<i>recN</i>	LexA (SOS)	10.34	3.70E-212	Recombination and repair protein
<i>norV</i>	NorR	9.97	1.82E-173	Anaerobic nitric oxide reductase flavorubredoxin
<i>entA</i>	Fur	9.79	6.72E-170	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
<i>xisE</i>	(SOS)	9.61	3.48E-114	E14 prophage; predicted excisionase
<i>nrdI</i>	Fur	9.09	6.33E-133	Flavodoxin required for NrdEF cluster assembly
<i>dps</i>	OxyR	8.99	4.81E-246	Fe-binding and storage protein; stress-inducible DNA-binding protetin
<i>nrdF</i>	Fur	8.93	9.91E-106	Ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like protein
<i>entH</i>	Fur	8.84	1.20E-85	Thioesterase required for efficient enterobactin production
<i>entF</i>	Fur	8.74	1.45E-189	Enterobactin synthase multienzyme complex component, ATP-dependent
<i>sulA</i>	LexA (SOS)	8.70	4.13E-240	SOS cell division inhibitor
<i>mntH</i>	OxyR, Fur	8.55	2.26E-139	Manganese/divalent cation transporter
<i>ymfQ</i>	ymFT (SOS)	8.41	2.58E-13	Prohage e14 tail protein homolog
<i>fepA</i>	Fur	8.09	2.45E-106	Iron-enterobactin outer membrane transporter
<i>nrdH</i>	Fur	7.80	2.04E-150	Hydrogen donor for NrdEF electron transport system; glutaredoxin-like protein
<i>yfiP</i>		7.64	9.75E-131	Conserved protein, DTW domain

<i>fes</i>	Fur	7.61	2.86E-156	Enterobactin/ferric enterobactin esterase
<i>ybiX</i>	Fur?	7.51	3.20E-135	Conserved protein, Fe(II)-dependent oxygenase superfamily
<i>ybdZ</i>	Fur	7.49	1.46E-52	Stimulator of EntF adenylation activity, MbtH-like
<i>ymfR</i>	YmfT (SOS)	6.79	3.14E-09	E14 prophage; putative protein
<i>entD</i>	Fur	6.75	4.24E-62	Phosphopantetheinyltransferase component of enterobactin synthase multienzyme complex
<i>glnK</i>	Fur?	6.56	1.73E-16	Nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB
<i>gor</i>	OxyR	6.43	4.15E-297	Glutathione oxidoreductase
<i>fruB</i>		6.22	3.35E-39	Fused fructose-specific PTS enzymes: IIA component/HPr component
<i>fecR</i>	Fur	6.00	1.32E-188	KpLE2 phage-like element; transmembrane signal transducer for ferric citrate transport
<i>fecB</i>	Fur	5.84	7.56E-101	KpLE2 phage-like element; iron-dictrate transporter subunit
<i>hemF</i>	OxyR	5.68	8.01E-296	Coproporphyrinogen III oxidase
<i>nanA</i>		5.66	1.54E-102	N-acetylneuraminate lyase
<i>intE</i>	(SOS)	5.48	1.99E-132	E14 prophage; predicted integrase
<i>mltF</i>		5.32	4.93E-225	Membrane-bound lytic transglycosylase F, murein hydrolase
<i>yeiB</i>		5.30	3.59E-202	Putative inner membrane protein
<i>ssuE</i>		5.22	7.41E-16	NAD(P)H-dependent FMN reductase
<i>yebG</i>	LexA (SOS)	5.20	7.90E-115	Conserved protein regulated by LexA
<i>xthA</i>		5.16	8.35E-249	Exonuclease III
<i>glpE</i>		4.95	2.26E-191	Thiosulfate:cyanide sulfurtransferase (rhodanese)
<i>yddB</i>		4.93	6.39E-140	Putative porin protein
<i>ssuA</i>		4.83	1.81E-21	Aliphatic sulfonate binding protein, SsuABC ABC transporter
<i>folE</i>		4.54	2.78E-129	GTP cyclohydrolase I
<i>fecI</i>	Fur	4.46	1.33E-129	KpLE2 phage-like element; RNA polymerase, sigma 19 factor
<i>pspE</i>	PspF	4.45	1.16E-154	Thiosulfate:cyanide sulfurtransferase (rhodanese)
<i>yijE</i>		4.27	8.10E-39	Inner membrane protein, predicted permease
<i>uxuA</i>	OxyR	4.27	8.16E-64	Mannonate hydrolase
<i>yncE</i>	Fur	4.22	2.09E-110	ATP-binding protein, periplasmic, function unknown

<i>adhE</i>		4.14	2.47E-94	Fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
<i>clpS</i>	OxyR?	4.09	1.44E-120	Regulatory protein for ClpA substrate specificity
<i>clpA</i>	OxyR?	4.06	4.16E-131	ATPase and specificity subunit of ClpA-ClpP ATP-dependent serine protease, chaperone activity
<i>ryhB</i>	Fur	3.92	2.70E-27	NcRNA
<i>uxuB</i>	OxyR	3.87	3.84E-39	D-mannonate oxidoreductase, NAD-dependent
<i>tauB</i>		3.73	2.02E-10	Taurine transporter subunit
<i>ssuD</i>		3.70	5.38E-19	Alkanesulfonate monooxygenase, FMNH(2)-dependent
<i>dppA</i>		3.69	3.34E-100	Dipeptide transporter
<i>uof</i>	OxyR	3.65	1.61E-140	<i>RyhB</i> -regulated fur leader peptide
<i>fepB</i>	Fur	3.64	5.81E-70	Iron-enterobactin transporter subunit
<i>dinB</i>	LexA (SOS)	3.63	1.42E-58	DNA polymerase IV

^aTranscriptional regulator that controls expression of the gene. Known members of the OxyR, Fur, or SOS regulons are indicated. ^bFold induction represents the ratio of gene expression in Hpx2⁻ cells relative to expression in wild-type cells. ^cFDR: false discovery rate adjusted p-values.

Table S2. Gene-expression ratios for known members of the OxyR regulon.

Gene	Ordered Locus Name	Fold Induction	FDR	Function	Role
<i>oxyS</i>	b4458	261.01	2.36E-211	Small regulatory RNA	
<i>dps</i>	b0812	8.99	4.81E-246	Fe-binding and storage protein	Iron scavenging
<i>katG</i>	b3942	57.37	0	Catalase	H ₂ O ₂ scavenging
<i>grxA</i>	b0849	29.65	9.80E-220	Glutaredoxin A	Disulfide reduction
<i>trxC</i>	b2582	19.72	0	Thioredoxin C	
<i>dsbG*</i>	b0604	0.36	6.41E-42	Periplasmic disulfide bond chaperone-isomerase	
<i>gor</i>	b3500	6.43	4.15E-297	Glutathione oxidoreductase	
<i>mntH</i>	b2392	8.55	2.26E-139	Manganese transporter	Manganese import
<i>uof</i>	b4637	3.65	1.61E-140	Posttranscriptional regulation of <i>fur</i> levels	Iron import control
<i>fur</i>	b0683	3.09	1.12E-127	Ferric uptake regulator	
<i>fhuF*</i>	b4367	0.40	2.48E-79	Ferric iron reductase	
<i>sufA</i>	b1684	11.13	5.33E-320	Fe-S cluster assembly and repair system	Fe-S cluster assembly and repair
<i>sufB</i>	b1683	15.01	1.45E-295		
<i>sufC</i>	b1682	17.74	0		
<i>sufD</i>	b1681	19.55	0		
<i>sufS</i>	b1680	15.90	0		
<i>sufE</i>	b1679	10.81	1.33E-208		
<i>hemF</i>	b2436	5.68	8.01E-296	Coproporphyrinogen III oxidase	Heme biosynthesis
<i>hemH</i>	b0475	13.69	0	Ferrochelataase	
<i>yaaA</i>	b0006	15.34	0	Unknown function	Control of iron levels
<i>uxuA</i>	b4322	4.27	8.16E-64	D-mannoate dehydratase/oxidoreductase	D-glucuronate degradation pathway
<i>uxuB</i>	b4323	3.87	3.84E-39		
<i>yhjA</i>	b3518	1.89	3.33E-13	Predicted cytochrome <i>c</i> peroxidase	
<i>ybjC*</i>	b0850	0.44	2.43E-18	Inner membrane protein; unknown function	
<i>nfsA*</i>	b0851	0.45	1.25E-52	NADPH nitroreductase	
<i>isrC</i>	b4435	17.20	9.32E-52	Small regulatory RNA	
<i>flu</i>	b2000	52.77	3.25E-206	Antigen 43	Cell adhesion

¹Sources: Zheng et al., 2001; Kehres et al., 2000. *Genes negatively regulated by OxyR.

Table S3. The heme proteins of *Escherichia coli*. Their relative rates of synthesis under growth conditions similar to those of this study have been reported by Li *et al.* (Li *et al.*, 2014).

Gene	Protein	Biological process	Prostetic group	Induction
<i>katG</i>	Catalase G	H ₂ O ₂ scavenging	Protoheme IX, heme B	Aerobiosis
<i>katE</i>	Catalase E		Protoheme IX, heme D	
<i>cyoABCD</i>	Cytochrome <i>bo</i> oxidase	Electron transfer	Protoheme IX, heme B	
<i>cydAB</i>	Cytochrome <i>bd</i> oxidase-I		Protoheme IX, heme D	
<i>appCB</i>	Cytochrome <i>bd</i> oxidase-II		Protoheme IX, (heme D?)	
<i>fdo</i>	Formate dehydrogenase-O		Protoheme IX, heme B/D	
<i>cybC</i>	Soluble cytochrome b562 (cryptic)		Protoheme IX, heme B	
<i>sdhCDAB</i>	Succinate dehydrogenase	Electron transfer, TCA cycle	Protoheme IX, heme B	
<i>bfr</i>	Bacterioferritin	Iron storage	Protoheme IX, heme B	
<i>dosCP</i>	C-di-GMP cyclase(<i>C</i>)/phosphodiesterase (<i>D</i>)	Regulation of [c-di-GMP], biofilm formation	Protoheme IX, heme B	
<i>yhjA</i>	Cytochrome C peroxidase	Unknown	Protoheme IX, heme B	Anaerobiosis
<i>nrfA</i>	Nitrite reductase	Anaerobic respiration	*Siroheme	
<i>nirB</i>				
<i>napABCGH</i>	Periplasmic nitrate reductase	Anaerobic respiration	Protoheme IX, heme B (covalently bound)	
<i>hmp</i>	Flavohemoglobin	Nitric oxide dioxygenase, ferrisiderophore/ferric citrate reductase	Protoheme IX, heme B	Ana/aerobiosis
<i>efeUOB</i>	Ferrous iron transporter (cryptic)	Uptake of ferrous iron under conditions of iron limitation and low pH	Protoheme IX, heme B	
<i>cysIJ</i>	Sulfite reductase	Sulfate assimilation	*Siroheme	

*Siroheme synthesis departs from the pathway of heme synthesis after the HemD step and does not involve coproporphyrinogen III oxidase (HemN/HemF) or ferrochelatase (HemH).

Table S4. Strains and plasmids used in this study.

Strain	Relevant features	Reference
MG1655	F ⁻ wild type	<i>E.coli</i> genetic stock center
BW25113	<i>lacI rrnB ΔlacZ hsdK ΔaraBAD ΔrhaBAD</i>	(Datsenko and Wanner, 2000)
DH5α pir ⁺	<i>supE44 ΔlacU169 (φ80lacZΔM15) hsdR17 recA1 endA1 girA96 thi-1 relA1 pir⁺</i>	J.M. Slauch
JI361	MG1655 Δ <i>katG</i> 17::Tn10	(Seaver and Imlay, 2001b)
JI370	MG1655 Δ <i>ahpF</i> ::kan	(Seaver and Imlay, 2001b)
JI372	MG1655 Δ <i>ahpF</i> ::kan Δ(<i>katE</i> 12::Tn10)1	(Seaver and Imlay, 2001b)
JEM218	MG1655 Δ(<i>ahpCF</i> 1::cat)1 Δ(<i>katE</i> 12::Tn10)1	Lab stock
LC106	MG1655 Δ <i>ahpF</i> ::kan Δ(<i>katE</i> 12::Tn10)1 Δ(<i>katG</i> ::Tn10)1	(Seaver and Imlay, 2004)
SMA1427	MG1655 Δ(<i>mntH</i> 2::cat)	This work
SP61	MG1655 Δ <i>dps</i> ::cat	Lab stock
SMA1161	MG1655 Δ <i>hemH</i> 1::cat	This work
SMA1459	BW25113 Δ <i>hemF</i> 1::cat	This work
SMA1497	MG1655 Δ(<i>hemF</i> 1::cat)	P1 (SMA1459) x MG1655
SMA1475	BW25113 Δ <i>hemN</i> 1::cat	This work
SMA1499	MG1655 Δ(<i>hemN</i> 1::cat)	P1 (SMA1475) x MG1655
SMA1557	SMA1497 Δ <i>hemN</i> ::cat1	P1 (SMA1475) x SMA1497
SMA1367	BW25113 <i>katG</i> Δ <i>FG</i> ~ <i>zij</i> -8::cat	This work
SMA1379	MG1655 <i>katG</i> Δ <i>FG</i> ~ <i>zij</i> -8	P1 (SMA1367) MG1655
SMA1383	JI372 <i>katG</i> Δ <i>FG</i> ~ <i>zij</i> -8	P1 (SMA1367) x JI372
SMA1385	JEM218 <i>katG</i> Δ <i>FG</i> ~ <i>zij</i> -8	P1 (SMA1367) x JEM218
SMA1027	BW25113 <i>hemH</i> (<i>NI</i>)1::cat	This work
SMA1035	MG1655 <i>hemH</i> ((<i>NI</i>)1::cat)	P1 (SMA1027) x MG1655
SMA1129	JI370 <i>hemH</i> ((<i>NI</i>)1::cat)	P1(SMA1027) x JI370
SMA1399	SMA1383 <i>hemH</i> ((<i>NI</i>)1::cat)	P1 (SMA1027) x SMA1383
SMA1539	LC106 Δ <i>hemF</i> 1::cat	P1 (SMA1459) x LC106
SMA1503	SMA1383 Δ(<i>hemF</i> 1::cat)	P1 (SMA1459) x SMA1383
SMA1553	SMA1503 with pBR322	This work
SMA1555	SMA1533 with pSM16	This work
SMA1505	SMA1383 Δ(<i>hemN</i> 1::cat)	P1 (SMA1475) x SMA1383
SMA1306	JI370 Δ <i>katG</i> 17::Tn10	P1 (JI361) x JI370
SMA1308	SMA1129 Δ <i>katG</i> 17::Tn10	P1 (JI361) x JI370
SMA1247	JI370 Δ <i>dps</i> ::cat	P1 (SP61) x JI370
SMA1249	SMA1129 Δ <i>dps</i> ::cat	P1 (SP61) x SMA1129
SMA1274	SMA1247 with pCKR101	This work
SMA1275	SMA1247 with pDps	This work
SMA1276	SMA1247 with pDpr	This work
SMA1277	SMA1249 with pCKR101	This work
SMA1278	SMA1249 with pDps	This work
SMA1279	SMA1249 with pDpr	This work
JEM557	Δ(<i>feoABC</i> 1::cat) Δ(<i>tonB</i> 1::cat)	Lab stock
SMA1169	JEM557 <i>hemH</i> ((<i>NI</i>)1::cat)	P1 (SMA1027) x JEM557
SMA1519	JI370 Δ <i>hemF</i> 1::cat	P1 (SMA1459) x JI370
SMA1521	JI370 Δ <i>hemN</i> 1::cat	P1 (SMA1475) x JI370

SJ98	MG1655 $\Delta lacZ::cat$	(Jang and Imlay, 2010)
SJ130	MG1655 $\Delta(lacZ::cat)$	(Jang and Imlay, 2010)
SJ108	LC106 $\Delta(lacZ::cat)$	(Jang and Imlay, 2010)
SMA1381	SJ130 <i>katG</i> Δ FG~ <i>zij-8</i>	P1 (SMA1367) x SJ130
SMA1363	Jl372 $\Delta(lacZ::cat)$	P1 (SJ98) x Jl372
SMA1387	SMA1363 <i>katG</i> Δ FG~ <i>zij-8</i>	P1 (SMA1367) x SMA1363
SMA1021	SJ130 att λ ::[SJ501:: <i>hemH'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1023	SJ130 att λ ::[SJ501:: <i>hemH'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1119	SJ108 att λ ::[SJ501:: <i>hemH'</i> - <i>lacZ</i> +] <i>cat</i> ^R	P1 (SMA1021) x SJ108
SMA1391	SMA1381 att λ ::[SJ501:: <i>hemH'</i> - <i>lacZ</i> +] <i>cat</i> ^R	P1 (SMA1021) x SMA1381
SMA1397	SMA1387 att λ ::[SJ501:: <i>hemH'</i> - <i>lacZ</i> +] <i>cat</i> ^R	P1 (SMA1021) x SMA1387
SMA1061	SMA1023 with pACYC184	This work
SMA1025	SMA1023 with pGS058	This work
SMA1043	SJ130 att λ ::[SJ501:: <i>hemH(NI)1'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1049	SJ130 att λ ::[SJ501:: <i>hemH(NI)1'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1079	SJ108 att λ ::[SJ501:: <i>hemH(NI)1'</i> - <i>lacZ</i> +] <i>cat</i> ^R	P1 (SMA1043) x SJ108
SMA1063	SMA1049 with pACYC184	This work
SMA1055	SMA1049 with pGS058	This work
SMA1047	SJ130 att λ ::[SJ501:: <i>hemA'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1053	SJ130 att λ ::[SJ501:: <i>hemA'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1121	SJ108 att λ ::[SJ501:: <i>hemA'</i> - <i>lacZ</i> +] <i>cat</i> ^R	P1 (SMA1047) x SJ108
SMA1389	SMA1381 <i>katG</i> Δ FG~ <i>zij-8</i> att λ ::[SJ501:: <i>hemA'</i> - <i>lacZ</i> +] <i>cat</i> ^R	P1 (SMA1047) x SMA1381
SMA1559	SMA1387 <i>katG</i> Δ FG~ <i>zij-8</i> att λ ::[SJ501:: <i>hemA'</i> - <i>lacZ</i> +] <i>cat</i> ^R	This work
SMA1067	SMA1053 with pACYC184	This work
SMA1059	SMA1053 with pGS058	This work
SMA1151	MG1655 with pACYC184	This work
SMA1149	MG1655 with pGS058	This work
SMA1153	SMA1035 with pACYC184	This work
SMA1039	SMA1035 with pGS058	This work
SMA1507	SMA1497 with pACYC184	This work
SMA1509	SMA1497 with pGS058	This work
SMA1511	SMA1499 with pACYC184	This work
SMA1513	SMA1499 with pGS058	This work
SMA1431	SMA1427 with pGS058	This work

Plasmid	Relevant features	Reference
pSJ501	pAH125 derivative with <i>cat</i> flanked by flp sites	(Jang and Imlay, 2010)
pINT-ts	CRIM helper plasmid containing <i>int</i> _{λ} Amp ^r	(Haldimann and Wanner, 2001)
pSM11	pSJ501:: <i>hemH'</i> - <i>lacZ</i> ⁺	This work
pSM12	pSJ501:: <i>hemH(NI)1'</i> - <i>lacZ</i> ⁺	This work
pSM14	pSJ501:: <i>hemA'</i> - <i>lacZ</i> ⁺	This work
pKD3	<i>bla</i> FRT <i>cat</i> FRT PS1 PS2 oriR6K	(Datsenko and Wanner, 2000)
pKD46	<i>bla</i> P _{bad} <i>gam</i> <i>bet</i> <i>exo</i> pSC101 oriTS	(Datsenko and Wanner, 2000)

pCP20	<i>bla cat cl857</i> λ P _R <i>flp</i> pSC101 oriTS	(Cherepanov and Wachernagel, 1995)
pACYC184	Tet ^r Cm ^r p15A ori	(Kullik et al.,1995)
pGS058	pACYC184 containing <i>oxyR2</i> [A233V]	(Kullik et al.,1995)
pCKR101	P _{lac} -lacI ^q P _{tac} polylinker Amp ^r (20-50 copies per cell)	Jeff Gardner
<i>pdpS</i>	pCKR101 <i>dps</i> ⁺ insert	(Park et al. 2005)
<i>pdpR</i>	pCKR101 <i>dpr</i> ⁺ insert	(Park et al. 2005)
<i>pkatGΔFG</i>	pET20b(+) containing <i>katGΔFG</i>	(Li and Goodwin, 2004)
pBR322	Tet ^r Cm ^r pMB1 ori (10-100 copies per cell)	Bob Gennis
pSM16	pBR322 containing <i>hemF</i>	This work

Table S5. Primers used for the qRT-PCR.

Primer	Sequence	Amplicon size (bp)
<i>hemF_fw</i>	5'-TGCTCAACCTTCAGGATACG-3'	119
<i>hemF_rv</i>	5'-ATTACGCAACACCCGACTAC-3'	
<i>hemH_fw</i>	5'-CGAAGCTGTATGCCTCTGTC-3'	121
<i>hemH_rv</i>	5'-TAGCTCATTCCCAGCGCTAC-3'	
<i>rrsG_fw</i>	5'-CCTCCCGAAGGTTAAGCTAC-3'	125
<i>rrsG_rv</i>	5'-GTCGGAATCGCTAGTAATCG-3'	

Table S6. Full list of gene-expression ratios for Hpx2⁻ cells relative to wild-type cells. FDR: false discovery rate adjusted p-values.

Name	Fold induction	FDR	
<i>oxyS</i>	261.01	2.36E-211	ncRNA
<i>oweE</i>	61.53	1.18E-53	pseudo
<i>katG</i>	57.37	0.00E+00	catalase-peroxidase HPI, heme b-containing
<i>flu</i>	52.77	3.25E-206	CP4-44 prophage; antigen 43 (Ag43) phase-variable biofilm formation autotransporter
<i>ymfM</i>	43.43	7.82E-94	e14 prophage; putative protein
<i>ymfN</i>	40.90	2.61E-198	e14 prophage; predicted DNA-binding transcriptional regulator
<i>ymfT</i>	36.71	2.85E-131	e14 prophage; predicted DNA-binding transcriptional regulator
<i>ymfO</i>	34.09	1.86E-51	e14 prophage; conserved protein
<i>ymfL</i>	33.48	6.18E-168	e14 prophage; predicted DNA-binding transcriptional regulator
<i>grxA</i>	29.65	9.80E-220	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (RNR1a)
<i>pspA</i>	25.55	0.00E+00	regulatory protein for phage-shock-protein operon
<i>cirA</i>	20.74	1.81E-226	catecholate siderophore receptor CirA
<i>pspG</i>	20.42	4.12E-156	phage shock protein G
<i>trxC</i>	19.72	0.00E+00	thioredoxin 2
<i>sufD</i>	19.55	0.00E+00	component of SufBCD Fe-S cluster assembly scaffold
<i>norW</i>	18.89	4.55E-160	NADH:flavorubredoxin oxidoreductase
<i>fhuE</i>	18.83	0.00E+00	ferric-rhodotorulic acid outer membrane transporter
<i>sufC</i>	17.74	0.00E+00	SufBCD Fe-S cluster assembly scaffold protein, ATP-binding protein
<i>tisB</i>	17.44	1.33E-270	toxic membrane persister formation peptide, LexA-regulated
<i>isrC</i>	17.20	9.32E-52	ncRNA
<i>pspC</i>	16.43	0.00E+00	DNA-binding transcriptional activator
<i>sufS</i>	15.90	0.00E+00	cysteine desulfurase, stimulated by SufE; selenocysteine lyase
<i>pspB</i>	15.70	1.00E-255	DNA-binding transcriptional regulator of psp operon
<i>yaaA</i>	15.34	0.00E+00	peroxide resistance protein, lowers intracellular iron
<i>ymfJ</i>	15.26	2.86E-212	e14 prophage; putative protein
<i>sufB</i>	15.01	1.45E-295	component of SufBCD Fe-S cluster assembly scaffold
<i>yjjZ</i>	14.53	7.17E-91	hypothetical protein
<i>pspD</i>	13.80	1.32E-195	peripheral inner membrane phage-shock protein
<i>hemH</i>	13.69	0.00E+00	ferrochelataase
<i>entE</i>	13.65	1.04E-236	2,3-dihydroxybenzoate-AMP ligase component of enterobactin synthase
<i>ymfP</i>	13.08	9.02E-47	e14 prophage; conserved protein
<i>sufA</i>	11.13	5.33E-320	Fe-S cluster assembly protein
<i>fecA</i>	11.06	3.92E-141	KpLE2 phage-like element; ferric citrate outer membrane transporter
<i>entB</i>	10.98	9.42E-210	isochorismatase
<i>sufE</i>	10.81	1.33E-208	sulfur acceptor protein
<i>entC</i>	10.74	9.88E-272	isochorismate synthase 1
<i>nrdE</i>	10.70	1.37E-286	ribonucleoside-diphosphate reductase 2, alpha subunit

<i>recN</i>	10.34	3.70E-212	recombination and repair protein
<i>norV</i>	9.97	1.82E-173	anaerobic nitric oxide reductase flavorubredoxin
<i>entA</i>	9.79	6.72E-170	2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase
<i>xisE</i>	9.61	3.48E-114	e14 prophage; predicted excisionase
<i>yhiD</i>	-9.29	5.99E-65	putative Mg(2+) transport ATPase, inner membrane protein
<i>hdeB</i>	-9.20	2.07E-163	acid-resistance protein
<i>nrdI</i>	9.09	6.33E-133	flavodoxin required for NrdEF cluster assembly
<i>dps</i>	8.99	4.81E-246	Fe-binding and storage protein; stress-inducible DNA-binding protein
<i>nrdF</i>	8.93	9.91E-106	ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like protein
<i>entH</i>	8.84	1.20E-85	thioesterase required for efficient enterobactin production
<i>entF</i>	8.74	1.45E-189	enterobactin synthase multienzyme complex component, ATP-dependent
<i>sulA</i>	8.70	4.13E-240	SOS cell division inhibitor
<i>mntH</i>	8.55	2.26E-139	manganese/divalent cation transporter
<i>ymfQ</i>	8.41	2.58E-13	prohage e14 tail protein homolog
<i>fepA</i>	8.09	2.45E-106	iron-enterobactin outer membrane transporter
<i>nrdH</i>	7.80	2.04E-150	hydrogen donor for NrdEF electron transport system
<i>hdeD</i>	-7.70	7.76E-103	acid-resistance membrane protein
<i>hdeA</i>	-7.69	8.00E-98	stress response protein acid-resistance protein
<i>yfiP</i>	7.64	9.75E-131	conserved protein, DTW domain
<i>fes</i>	7.61	2.86E-156	enterobactin/ferric enterobactin esterase
<i>ybiX</i>	7.51	3.20E-135	conserved protein, Fe(II)-dependent oxygenase superfamily
<i>ybdZ</i>	7.49	1.46E-52	stimulator of EntF adenylation activity, MbtH-like
<i>gadE</i>	-7.31	1.01E-94	DNA-binding transcriptional activator
<i>sodB</i>	-7.24	6.32E-271	superoxide dismutase, Fe
<i>uraA</i>	-7.17	4.79E-48	uracil permease
<i>ymfR</i>	6.79	3.14E-09	e14 prophage; putative protein
<i>entD</i>	6.75	4.24E-62	phosphopantetheinyltransferase component of enterobactin synthase
<i>arrS</i>	-6.60	2.57E-05	ncRNA
<i>glnK</i>	6.56	1.73E-16	nitrogen assimilation regulatory protein for GlnL, GlnE, and AmtB
<i>yoeH</i>	-6.49	2.53E-74	pseudo
<i>gor</i>	6.43	4.15E-297	glutathione oxidoreductase
<i>yoeG</i>	-6.32	1.15E-100	pseudo
<i>yobF</i>	-6.24	3.72E-185	hypothetical protein
<i>fruB</i>	6.22	3.35E-39	fused fructose-specific PTS enzymes: IIA component/HPr component
<i>lysP</i>	-6.21	3.56E-199	lysine transporter
<i>fecR</i>	6.00	1.32E-188	transmembrane signal transducer for ferric citrate transport
<i>yahA</i>	-5.90	1.10E-190	c-di-GMP-specific phosphodiesterase
<i>cspC</i>	-5.85	9.57E-195	stress protein, member of the CspA-family
<i>fecB</i>	5.84	7.56E-101	KpLE2 phage-like element; iron-dicitrate transporter subunit

<i>malE</i>	-5.73	3.42E-134	maltose transporter subunit
<i>hemF</i>	5.68	8.01E-296	coproporphyrinogen III oxidase
<i>nanA</i>	5.66	1.54E-102	N-acetylneuraminate lyase
<i>csrC</i>	5.65	4.05E-131	ncRNA
<i>malK</i>	-5.64	2.82E-56	fused maltose transport subunit, ATP-binding component
<i>intE</i>	5.48	1.99E-132	e14 prophage; predicted integrase
<i>mltF</i>	5.32	4.93E-225	membrane-bound lytic transglycosylase F, murein hydrolase
<i>yeiB</i>	5.30	3.59E-202	putative inner membrane protein
<i>gcvH</i>	-5.29	3.60E-117	glycine cleavage complex lipoylprotein
<i>ssuE</i>	5.22	7.41E-16	NAD(P)H-dependent FMN reductase
<i>yebG</i>	5.20	7.90E-115	conserved protein regulated by LexA
<i>xthA</i>	5.16	8.35E-249	exonuclease III
<i>gadC</i>	-5.10	1.00E-89	glutamate:gamma-aminobutyric acid antiporter
<i>gadB</i>	-5.00	1.08E-64	glutamate decarboxylase B, PLP-dependent
<i>glpE</i>	4.95	2.26E-191	thiosulfate:cyanide sulfurtransferase (rhodanese)
<i>yddB</i>	4.93	6.39E-140	putative porin protein
<i>ssuA</i>	4.83	1.81E-21	aliphatic sulfonate binding protein, SsuABC ABC transporter
<i>folE</i>	4.54	2.78E-129	GTP cyclohydrolase I
<i>fecI</i>	4.46	1.33E-129	KpLE2 phage-like element; RNA polymerase, sigma 19 factor
<i>pspE</i>	4.45	1.16E-154	thiosulfate:cyanide sulfurtransferase (rhodanese)
<i>mepS</i>	-4.41	1.44E-152	mutational suppressor of prc thermosensitivity, outer membrane lipoprotein
<i>lysC</i>	-4.36	3.84E-200	aspartokinase III
<i>codB</i>	-4.30	2.72E-23	cytosine transporter
<i>yijE</i>	4.27	8.10E-39	inner membrane protein, predicted permease
<i>uxuA</i>	4.27	8.16E-64	mannonate hydrolase
<i>yncE</i>	4.22	2.09E-110	ATP-binding protein, periplasmic, function unknown
<i>gadW</i>	-4.22	2.41E-72	transcriptional activator of <i>gadA</i> and <i>gadBC</i> ; repressor of <i>gadX</i>
<i>caiF</i>	-4.15	1.19E-80	DNA-binding transcriptional activator
<i>adhE</i>	4.14	2.47E-94	fused acetaldehyde-CoA dehydrogenase/ alcohol dehydrogenase
<i>clpS</i>	4.09	1.44E-120	regulatory protein for ClpA substrate specificity
<i>clpA</i>	4.06	4.16E-131	ATPase and specificity subunit of ClpA-ClpP ATP-dependent protease
<i>proX</i>	-4.02	1.09E-91	glycine betaine transporter subunit
<i>malM</i>	-3.98	2.35E-83	maltose regulon periplasmic protein
<i>ryhB</i>	3.92	2.70E-27	ncRNA
<i>arcZ</i>	-3.91	2.86E-12	ncRNA
<i>ansP</i>	-3.90	1.96E-69	L-asparagine transporter
<i>uxuB</i>	3.87	3.84E-39	D-mannonate oxidoreductase, NAD-dependent
<i>glsA</i>	-3.86	6.99E-37	glutaminase 1
<i>hdhA</i>	-3.78	4.18E-104	7-alpha-hydroxysteroid dehydrogenase, NAD-dependent
<i>bfr</i>	-3.75	9.11E-138	bacterioferritin, iron storage and detoxification protein

<i>tauB</i>	3.73	2.02E-10	taurine transporter subunit
<i>malG</i>	-3.70	7.96E-52	maltose transporter subunit
<i>ssuD</i>	3.70	5.38E-19	alkanesulfonate monooxygenase, FMNH(2)-dependent
<i>dppA</i>	3.69	3.34E-100	dipeptide transporter
<i>uof</i>	3.65	1.61E-140	ryhB-regulated fur leader peptide
<i>fepB</i>	3.64	5.81E-70	iron-enterobactin transporter subunit
<i>dinB</i>	3.63	1.42E-58	DNA polymerase IV
<i>mdtK</i>	-3.63	1.45E-56	multidrug efflux system transporter
<i>slp</i>	-3.61	1.46E-54	outer membrane lipoprotein
<i>tsx</i>	-3.60	1.09E-88	nucleoside channel, receptor of phage T6 and colicin K
<i>recX</i>	3.58	2.13E-27	regulatory protein for RecA
<i>ythA</i>	3.56	8.71E-08	hypothetical protein
<i>pqqL</i>	3.55	6.49E-95	putative peptidase
<i>trpL</i>	-3.51	7.34E-13	trp operon leader peptide
<i>lamB</i>	-3.50	9.73E-62	maltose outer membrane porin (maltoporin)
<i>dapB</i>	-3.49	1.03E-82	dihydrodipicolinate reductase
<i>rsmB</i>	3.47	4.58E-199	16S rRNA m(5)C967 methyltransferase, SAM-dependent
<i>icdC</i>	3.45	2.29E-13	pseudo
<i>dinI</i>	3.43	2.28E-76	DNA damage-inducible protein I
<i>umuD</i>	3.41	1.43E-18	DNA polymerase V, subunit D
<i>argI</i>	-3.40	7.62E-14	ornithine carbamoyltransferase 1
<i>cspI</i>	3.36	1.17E-11	Qin prophage; cold shock protein
<i>yeeR</i>	3.35	5.62E-27	CP4-44 prophage; predicted membrane protein
<i>upp</i>	-3.33	3.93E-46	uracil phosphoribosyltransferase
<i>fmt</i>	3.33	8.66E-150	10-formyltetrahydrofolate:L-methionyl-tRNA(fMet) N-formyltransferase
<i>dinD</i>	3.32	1.60E-46	DNA-damage-inducible protein
<i>ypdK</i>	-3.32	1.07E-42	expressed protein, membrane-associated
<i>cho</i>	3.30	2.76E-84	endonuclease of nucleotide excision repair
<i>plaP</i>	-3.26	7.30E-130	putrescine importer, low affinity
<i>micA</i>	3.25	2.08E-03	ncRNA
<i>uxaC</i>	3.24	9.71E-49	uronate isomerase
<i>yihT</i>	3.23	7.49E-05	putative aldolase
<i>dadX</i>	3.21	1.24E-63	alanine racemase 2, PLP-binding
<i>ybbW</i>	3.21	6.79E-04	putative allantoin transporter
<i>yddA</i>	3.19	5.15E-63	fused predicted multidrug transporter subunits of ABC superfamily
<i>recA</i>	3.18	6.34E-148	DNA strand exchange and recombination protein
<i>rhaA</i>	3.17	1.97E-04	L-rhamnose isomerase
<i>gntT</i>	3.16	1.32E-56	gluconate transporter, high-affinity GNT I system
<i>ytfK</i>	-3.16	3.66E-57	conserved protein, DUF1107 family
<i>ydiE</i>	3.15	7.71E-45	hemin uptake protein HemP homolog
<i>galS</i>	3.14	5.65E-36	DNA-binding transcriptional repressor
<i>def</i>	3.14	4.60E-143	peptide deformylase
<i>dadA</i>	3.10	6.57E-58	D-amino acid dehydrogenase

<i>mdtJ</i>	-3.10	4.09E-20	multidrug efflux system transporter
<i>fur</i>	3.09	1.12E-127	transcriptional dual regulator of siderophore biosynthesis and transport
<i>ydjM</i>	3.08	4.74E-17	inner membrane protein regulated by LexA
<i>insH1</i>	3.07	1.03E-05	IS5 transposase and trans-activator
<i>gadA</i>	-3.06	7.26E-17	glutamate decarboxylase A, PLP-dependent
<i>ssuC</i>	3.05	3.75E-04	putative alkanesulfonate transporter subunit
<i>narU</i>	-3.05	8.00E-24	nitrate/nitrite transporter
<i>fruK</i>	3.02	1.77E-22	fructose-1-phosphate kinase
<i>rutA</i>	3.02	4.34E-05	pyrimidine oxygenase, FMN-dependent
<i>rbsD</i>	-3.01	1.21E-22	putative cytoplasmic sugar-binding protein
<i>uxaA</i>	3.00	8.84E-48	altronate hydrolase
<i>trxB</i>	2.99	2.94E-109	thioredoxin reductase, FAD/NAD(P)-binding
<i>istR</i>	2.98	1.67E-04	ncRNA
<i>ygaM</i>	-2.97	5.03E-58	ribosome-binding protein, probably membrane-anchored, function unknown
<i>gcvT</i>	-2.97	3.30E-56	aminomethyltransferase, subunit (T protein) of glycine cleavage complex
<i>fiu</i>	2.95	1.84E-47	catecholate siderophore receptor Fiu
<i>mdtE</i>	-2.93	1.01E-24	anaerobic multidrug efflux transporter, ArcA-regulated
<i>fecE</i>	2.93	4.70E-99	KpLE2 phage-like element; iron-dicitrate transporter subunit
<i>fecC</i>	2.92	1.59E-48	KpLE2 phage-like element; iron-dicitrate transporter subunit
<i>pta</i>	2.90	4.31E-84	phosphate acetyltransferase
<i>codA</i>	-2.90	5.33E-68	cytosine/isoguanine deaminase
<i>leuC</i>	2.90	3.67E-72	3-isopropylmalate dehydratase large subunit
<i>abgA</i>	2.86	6.99E-10	p-aminobenzoyl-glutamate hydrolase, A subunit
<i>ynaE</i>	2.85	5.05E-05	cold shock protein, function unknown, Rac prophage
<i>leuB</i>	2.84	1.03E-75	3-isopropylmalate dehydrogenase, NAD(+)-dependent
<i>ndk</i>	-2.84	3.87E-97	nucleoside diphosphate kinase/AP endonuclease/3'-phosphodiesterase
<i>asnW</i>	-2.84	1.10E-17	tRNA
<i>tauA</i>	2.82	4.58E-07	taurine transporter subunit
<i>ybiI</i>	2.82	3.92E-42	DksA-type zinc finger protein
<i>ompC</i>	-2.81	5.04E-66	outer membrane porin protein C
<i>ybaT</i>	-2.80	3.75E-40	putative amino acid transporter
<i>argG</i>	-2.80	1.03E-44	argininosuccinate synthetase
<i>aceF</i>	2.80	6.81E-35	pyruvate dehydrogenase, dihydrolipoyltransacetylase component E2
<i>ilvX</i>	-2.80	7.65E-26	hypothetical protein
<i>glpD</i>	2.79	4.56E-64	sn-glycerol-3-phosphate dehydrogenase, aerobic, FAD/NAD(P)-binding
<i>yhiM</i>	-2.77	7.86E-10	acid resistance protein, inner membrane
<i>ariR</i>	-2.77	2.86E-16	RcsB connector protein for regulation of biofilm and acid-resistance
<i>glpR</i>	2.77	7.49E-90	DNA-binding transcriptional repressor
<i>glnL</i>	2.76	5.65E-36	sensory histidine kinase in two-component regulatory system with GlnG
<i>leuA</i>	2.76	3.15E-46	2-isopropylmalate synthase
<i>dsbG</i>	-2.76	6.41E-42	thiol:disulfide interchange protein, periplasmic
<i>rpoB</i>	2.75	1.14E-35	RNA polymerase, beta subunit
<i>yncJ</i>	2.75	9.05E-18	hypothetical protein

<i>malF</i>	-2.74	3.30E-41	maltose transporter subunit
<i>yahM</i>	-2.73	4.77E-18	hypothetical protein
<i>insH1</i>	2.73	1.13E-02	IS5 transposase and trans-activator
<i>yahI</i>	2.72	9.66E-04	carbamate kinase-like protein
<i>yjdJ</i>	-2.71	1.07E-39	putative acyltransferase with acyl-CoA N-acyltransferase domain
<i>nanT</i>	2.71	7.00E-16	sialic acid transporter
<i>ybhI</i>	2.70	1.05E-04	putative transporter
<i>mipA</i>	-2.70	8.31E-78	scaffolding protein for murein synthesizing machinery
<i>argA</i>	-2.68	2.66E-48	fused acetylglutamate kinase (inactive)/amino acid N-acetyltransferase
<i>yhaH</i>	-2.68	3.26E-33	inner membrane protein, DUF805 family
<i>tnaA</i>	-2.67	9.61E-29	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
<i>yoaC</i>	-2.67	6.37E-54	conserved protein, DUF1889 family
<i>mdtI</i>	-2.67	4.68E-06	multidrug efflux system transporter
<i>csgD</i>	2.66	3.56E-48	DNA-binding transcriptional activator for csgBA
<i>csgE</i>	2.64	1.09E-18	curlin secretion specificity factor
<i>cpxP</i>	2.64	1.36E-51	inhibitor of the cpx response; periplasmic adaptor protein
<i>dctR</i>	-2.63	6.07E-22	putative DNA-binding transcriptional regulator
<i>modA</i>	-2.63	1.42E-46	molybdate transporter subunit
<i>glpG</i>	2.62	1.93E-91	rhomboid intramembrane serine protease
<i>metV</i>	-2.61	2.04E-30	tRNA
<i>ypfM</i>	2.61	8.03E-52	hypothetical protein
<i>argD</i>	-2.60	2.38E-35	acetylornithine aminotransferase/succinyldiaminopimelate aminotransferase
<i>epd</i>	2.60	6.26E-86	D-erythrose 4-phosphate dehydrogenase
<i>agaS</i>	-2.60	1.62E-02	tagatose-6-phosphate ketose/aldose isomerase
<i>astA</i>	2.60	1.39E-12	arginine succinyltransferase
<i>polB</i>	2.60	1.05E-35	DNA polymerase II
<i>uspG</i>	-2.59	1.14E-63	universal stress protein UP12
<i>metW</i>	-2.58	1.92E-25	tRNA
<i>paaC</i>	2.57	1.97E-02	ring 1,2-phenylacetyl-CoA epoxidase subunit
<i>nadB</i>	-2.55	2.18E-67	quinolinate synthase, L-aspartate oxidase (B protein) subunit
<i>hyfH</i>	2.55	1.44E-03	hydrogenase 4, Fe-S subunit
<i>ygiL</i>	-2.54	1.23E-06	putative fimbrial-like adhesin protein
<i>nanE</i>	2.54	1.33E-17	putative N-acetylmannosamine-6-P epimerase
<i>mdtF</i>	-2.54	3.34E-21	anaerobic multidrug efflux transporter, ArcA-regulated
<i>glf</i>	-2.53	9.59E-23	UDP-galactopyranose mutase, FAD/NAD(P)-binding
<i>fhuF</i>	-2.52	2.48E-79	ferric iron reductase involved in ferric hydroxamate transport
<i>argF</i>	-2.50	1.21E-47	ornithine carbamoyltransferase 2, chain F; CP4-6 prophage
<i>putA</i>	2.47	4.23E-58	transcriptional regulator/proline dehydrogenase/P5C dehydrogenase
<i>proV</i>	-2.47	1.81E-33	glycine betaine transporter subunit
<i>aspU</i>	-2.47	2.67E-05	tRNA
<i>ybiU</i>	-2.46	3.66E-59	hypothetical protein
<i>gatC</i>	-2.46	2.48E-13	galactitol-specific enzyme IIC component of PTS
<i>yodC</i>	-2.46	1.58E-08	hypothetical protein

<i>fecD</i>	2.45	2.52E-35	KpLE2 phage-like element; iron-dicitrate transporter subunit
<i>ybaY</i>	-2.45	3.19E-43	outer membrane lipoprotein
<i>gltF</i>	-2.45	4.15E-41	periplasmic protein
<i>katE</i>	-2.44	8.66E-30	catalase HP11, heme d-containing
<i>tauC</i>	2.43	2.19E-05	taurine transporter subunit
<i>astD</i>	2.43	5.21E-17	succinylglutamic semialdehyde dehydrogenase
<i>puuA</i>	-2.42	1.71E-24	gamma-Glu-putrescine synthase
<i>yedN</i>	2.41	4.22E-04	pseudo
<i>yceB</i>	-2.40	6.43E-61	lipoprotein, DUF1439 family
<i>proW</i>	-2.40	5.56E-20	glycine betaine transporter subunit
<i>dctA</i>	-2.40	6.42E-27	C4-dicarboxylic acid, orotate and citrate transporter
<i>yjdI</i>	-2.40	5.30E-10	hypothetical protein
<i>umuC</i>	2.39	8.41E-18	DNA polymerase V, subunit C
<i>yfiB</i>	-2.38	2.91E-22	putative positive effector of YfiN activity, OM lipoprotein
<i>uvrA</i>	2.37	3.71E-47	damage recognition protein of nucleotide excision repair excinuclease
<i>msyB</i>	-2.37	3.56E-15	multicopy suppressor of secY and secA
<i>nudI</i>	-2.36	2.22E-17	nucleoside triphosphatase
<i>yeeS</i>	2.36	5.01E-04	CP4-44 prophage; predicted DNA repair protein
<i>nrdD</i>	2.36	7.96E-52	anaerobic ribonucleoside-triphosphate reductase
<i>leuT</i>	-2.36	1.53E-29	tRNA
<i>yebE</i>	2.34	1.79E-28	inner membrane protein, DUF533 family
<i>gabD</i>	2.34	3.38E-31	succinate-semialdehyde dehydrogenase I, NADP-dependent
<i>ycjM</i>	2.34	7.35E-05	putative glucosyltransferase
<i>trpT</i>	-2.33	8.79E-10	tRNA
<i>cadB</i>	2.33	8.36E-04	putative lysine/cadaverine transporter
<i>pnuC</i>	-2.33	4.58E-56	nicotinamide riboside transporter
<i>metN</i>	2.33	9.21E-67	DL-methionine transporter subunit
<i>yoel</i>	-2.32	2.82E-16	hypothetical protein
<i>dinQ</i>	2.31	3.70E-37	damage inducible protein
<i>glmZ</i>	-2.30	5.51E-23	ncRNA
<i>ydjI</i>	2.30	5.28E-09	putative aldolase
<i>ydiF</i>	2.29	1.22E-05	fused predicted acetyl-CoA:acetoacetyl-CoA transferase
<i>waaH</i>	2.29	1.78E-06	putative glycosyl transferase
<i>ydhY</i>	2.29	3.23E-02	putative 4Fe-4S ferridoxin-type protein
<i>acnA</i>	2.28	8.66E-30	aconitate hydratase 1
<i>borD</i>	-2.28	2.53E-37	DLP12 prophage; predicted lipoprotein
<i>ybjC</i>	-2.27	2.43E-18	conserved protein, DUF1418 family
<i>fimB</i>	-2.27	2.94E-50	tyrosine recombinase/inversion of on/off regulator of fimA
<i>yfiF</i>	2.27	1.95E-67	putative methyltransferase
<i>osmE</i>	-2.26	4.77E-41	DNA-binding transcriptional activator
<i>uvrD</i>	2.26	8.58E-61	DNA-dependent ATPase I and helicase II
<i>abgB</i>	2.26	1.36E-07	p-aminobenzoyl-glutamate hydrolase, B subunit
<i>ygaY</i>	-2.25	1.14E-13	pseudo

<i>dinG</i>	2.25	1.41E-43	ATP-dependent DNA helicase
<i>argH</i>	-2.25	4.87E-42	argininosuccinate lyase
<i>uidA</i>	2.25	1.58E-06	beta-D-glucuronidase
<i>dppB</i>	2.25	3.50E-16	dipeptide/heme transporter
<i>nfsA</i>	-2.24	1.25E-52	nitroreductase A, NADPH-dependent, FMN-dependent
<i>evgA</i>	-2.24	1.39E-25	response regulator in two-component regulatory system with EvgS
<i>yqaE</i>	-2.24	3.42E-35	cyaR sRNA-regulated protein
<i>uspF</i>	-2.24	5.15E-36	stress-induced protein, ATP-binding protein
<i>yeaC</i>	-2.24	5.63E-27	hypothetical protein
<i>hisC</i>	2.24	3.91E-14	histidinol-phosphate aminotransferase
<i>gtrB</i>	-2.22	2.49E-24	CPS-53 (KpLE1) prophage; bactoprenol glucosyl transferase
<i>ybiV</i>	-2.22	2.44E-42	sugar phosphatase; preference for fructose-1-P, ribose-5-P and glucose-6-P
<i>mscS</i>	-2.22	4.87E-56	mechanosensitive channel protein, small conductance
<i>fliK</i>	2.22	2.83E-03	flagellar hook-length control protein
<i>iscR</i>	2.22	4.23E-33	DNA-binding transcriptional repressor
<i>serW</i>	-2.22	4.59E-08	tRNA
<i>ilvB</i>	2.22	8.63E-05	acetolactate synthase I, large subunit
<i>ydfK</i>	2.22	9.85E-03	cold shock protein, function unknown, Qin prophage
<i>dtgD</i>	-2.20	1.95E-24	dipeptide and tripeptide permease D
<i>yihQ</i>	2.20	6.81E-06	alpha-glucosidase
<i>argC</i>	-2.20	1.19E-49	N-acetyl-gamma-glutamylphosphate reductase, NAD(P)-binding
<i>yjbD</i>	-2.19	1.77E-28	hypothetical protein
<i>arcA</i>	-2.19	1.91E-68	DNA-binding response regulator in two-component regulatory system
<i>fepC</i>	2.19	1.23E-28	iron-enterobactin transporter subunit
<i>yggL</i>	-2.19	2.62E-30	conserved protein, DUF469 family
<i>gatB</i>	-2.19	5.97E-14	galactitol-specific enzyme IIB component of PTS
<i>yjhE</i>	2.19	7.61E-04	pseudo
<i>nadA</i>	-2.18	4.62E-38	quinolinate synthase, subunit A
<i>uxuR</i>	2.18	5.66E-54	DNA-binding transcriptional repressor
<i>scpB</i>	2.18	1.23E-05	methylmalonyl-CoA decarboxylase, biotin-independent
<i>ycfJ</i>	2.17	1.11E-14	hypothetical protein
<i>yiaR</i>	2.16	4.52E-03	putative L-xylulose 5-phosphate 3-epimerase
<i>glgS</i>	-2.16	1.40E-37	putative glycogen synthesis protein
<i>pyrI</i>	-2.16	1.20E-08	aspartate carbamoyltransferase, regulatory subunit
<i>ibsD</i>	2.16	3.85E-02	toxic membrane protein
<i>yjfM</i>	-2.16	3.53E-03	CP4-57 prophage; putative protein
<i>paal</i>	2.15	1.09E-02	thioesterase, with ring-hydroxylated phenylacetyl-coenzyme A thioesters
<i>lhgO</i>	2.15	2.55E-17	L-2-hydroxyglutarate oxidase
<i>leuD</i>	2.15	2.82E-29	3-isopropylmalate dehydratase small subunit
<i>ffs</i>	2.15	4.12E-03	ncRNA
<i>tauD</i>	2.15	2.05E-09	taurine dioxygenase, 2-oxoglutarate-dependent
<i>aceE</i>	2.14	2.77E-37	pyruvate dehydrogenase, decarboxylase component E1, thiamin-binding
<i>yneM</i>	2.14	1.18E-18	expressed protein, membrane-associated

<i>yagU</i>	-2.14	4.49E-38	inner membrane protein, DUF1440 family
<i>yiaB</i>	-2.14	7.51E-03	inner membrane protein, YiaAB family
<i>yciT</i>	2.14	1.37E-55	global regulator of transcription; DeoR family
<i>sdhD</i>	-2.13	1.01E-29	succinate dehydrogenase, membrane subunit, binds cytochrome b556
<i>grxD</i>	-2.13	2.60E-32	glutaredoxin-4
<i>pyrE</i>	-2.13	1.45E-09	orotate phosphoribosyltransferase
<i>artJ</i>	-2.12	4.59E-27	arginine binding protein, periplasmic
<i>yeaQ</i>	-2.12	4.13E-28	conserved protein, UPF0410 family
<i>abgR</i>	2.11	3.89E-17	putative DNA-binding transcriptional regulator of abgABT operon
<i>yqhD</i>	2.10	1.85E-41	aldehyde reductase, NADPH-dependent
<i>fumA</i>	-2.10	3.97E-38	fumarate hydratase (fumarase A), aerobic Class I
<i>rpsI</i>	-2.10	6.37E-35	30S ribosomal subunit protein S9
<i>ilvC</i>	-2.09	1.69E-17	ketol-acid reductoisomerase, NAD(P)-binding
<i>ilvN</i>	2.09	1.91E-04	acetolactate synthase I, small subunit
<i>deoA</i>	2.09	2.09E-23	thymidine phosphorylase
<i>metU</i>	-2.09	2.29E-19	tRNA
<i>ygeN</i>	2.08	3.26E-03	pseudo
<i>rpmE</i>	-2.08	2.87E-41	50S ribosomal subunit protein L31
<i>ygiM</i>	2.08	1.84E-32	SH3 domain protein
<i>rutF</i>	2.08	5.59E-03	flavin:NADH reductase
<i>norR</i>	2.08	9.04E-23	anaerobic nitric oxide reductase DNA-binding transcriptional activator
<i>ybjM</i>	-2.08	6.25E-14	inner membrane protein
<i>ybiC</i>	-2.07	1.26E-50	putative dehydrogenase
<i>rpoC</i>	2.07	5.36E-22	RNA polymerase, beta prime subunit
<i>ydiO</i>	2.06	2.37E-05	putative acyl-CoA dehydrogenase
<i>ycgX</i>	2.06	3.74E-06	hypothetical protein
<i>dinF</i>	2.06	4.84E-17	oxidative stress resistance protein; predicted MATE family efflux pump
<i>ygiW</i>	-2.06	1.19E-50	hypothetical protein
<i>rplM</i>	-2.06	1.48E-31	50S ribosomal subunit protein L13
<i>flhC</i>	-2.05	1.01E-17	DNA-binding transcriptional dual regulator with FlhD
<i>ymdF</i>	-2.05	1.57E-13	hypothetical protein
<i>glyS</i>	2.05	7.37E-21	glycine tRNA synthetase, beta subunit
<i>mglC</i>	-2.04	1.32E-11	methyl-galactoside transporter subunit
<i>lexA</i>	2.04	4.84E-46	DNA-binding transcriptional repressor of SOS regulon
<i>zraP</i>	2.04	9.83E-04	Zn-dependent periplasmic chaperone
<i>yaiY</i>	2.03	6.45E-07	inner membrane protein, DUF2755 family
<i>ybgD</i>	-2.03	9.40E-03	putative fimbrial-like adhesin protein
<i>sibC</i>	2.03	1.75E-06	ncRNA
<i>ymgA</i>	-2.02	5.41E-09	RcsB connector protein for regulation of biofilm
<i>ypjF</i>	-2.02	2.32E-04	CP4-57 prophage; toxin of the YpjF-YfjZ toxin-antitoxin system
<i>cspA</i>	2.02	3.26E-16	RNA chaperone and anti-terminator, cold-inducible
<i>glyQ</i>	2.02	7.88E-10	glycine tRNA synthetase, alpha subunit
<i>puuD</i>	-2.02	1.82E-22	gamma-Glu-GABA hydrolase

<i>yphA</i>	-2.02	2.32E-28	putative inner membrane protein
<i>folP</i>	2.01	8.88E-36	7,8-dihydropteroate synthase
<i>astC</i>	2.01	5.19E-14	succinylornithine transaminase, PLP-dependent
<i>rzpR</i>	2.01	1.23E-02	pseudo
<i>kup</i>	-2.01	9.31E-20	potassium transporter
<i>entS</i>	2.01	2.93E-40	enterobactin exporter, iron-regulated
<i>xisD</i>	2.01	2.40E-03	pseudo
<i>yhcO</i>	-2.01	2.00E-19	putative barnase inhibitor
<i>paaE</i>	2.01	1.45E-03	ring 1,2-phenylacetyl-CoA epoxidase, NAD(P)H oxidoreductase component
<i>rlmE</i>	2.00	1.52E-44	23S rRNA U2552 2'-O-ribose methyltransferase, SAM-dependent
<i>hscB</i>	2.00	3.33E-37	DnaJ-like molecular chaperone specific for IscU
<i>yfhH</i>	-2.00	2.86E-19	putative DNA-binding transcriptional regulator
<i>ybaN</i>	2.00	2.89E-28	inner membrane protein, DUF454 family
<i>yecF</i>	-1.99	3.77E-20	conserved protein, DUF2594 family
<i>sra</i>	-1.99	7.04E-24	stationary-phase-induced ribosome-associated protein
<i>yohP</i>	-1.99	5.96E-11	hypothetical protein
<i>dmlA</i>	1.99	1.91E-16	D-malate oxidase, NAD-dependent; probable tartrate dehydrogenase
<i>ackA</i>	1.99	2.54E-53	acetate kinase A and propionate kinase 2
<i>ileS</i>	1.98	1.12E-22	isoleucyl-tRNA synthetase
<i>emrB</i>	-1.98	1.78E-16	multidrug efflux system protein
<i>wrbA</i>	-1.98	6.28E-33	NAD(P)H:quinone oxidoreductase
<i>ftsH</i>	1.98	4.04E-52	protease, ATP-dependent zinc-metallo
<i>fepE</i>	1.98	3.01E-04	regulator of length of O-antigen component of lipopolysaccharide chains
<i>ddpX</i>	1.98	4.31E-04	D-ala-D-ala dipeptidase, Zn-dependent
<i>rpsO</i>	-1.98	8.74E-41	30S ribosomal subunit protein S15
<i>yjcD</i>	-1.97	3.47E-25	putative permease
<i>ydfE</i>	1.97	7.12E-03	pseudo
<i>ykgC</i>	-1.97	5.82E-09	putative pyridine nucleotide-disulfide oxidoreductase
<i>kbaZ</i>	-1.97	8.82E-03	tagatose 6-phosphate aldolase 1, kbaZ subunit
<i>mhpD</i>	1.97	1.12E-02	2-keto-4-pentenoate hydratase
<i>yicL</i>	-1.97	1.05E-35	putative inner membrane protein
<i>shiA</i>	1.97	3.69E-30	shikimate transporter
<i>ymgC</i>	-1.96	7.53E-05	hypothetical protein
<i>proM</i>	-1.96	7.45E-13	tRNA
<i>mutS</i>	1.96	2.08E-33	methyl-directed mismatch repair protein
<i>ycgZ</i>	-1.96	2.65E-07	RcsB connector protein for regulation of biofilm and acid-resistance
<i>argV</i>	-1.96	5.62E-17	tRNA
<i>ibpB</i>	1.95	3.64E-09	heat shock chaperone
<i>cnu</i>	-1.95	4.58E-15	oriC-binding complex H-NS/Cnu
<i>can</i>	-1.95	9.66E-42	carbonic anhydrase
<i>nuoN</i>	-1.95	7.23E-32	NADH:ubiquinone oxidoreductase, membrane subunit N
<i>valZ</i>	-1.95	2.56E-23	tRNA
<i>lysY</i>	-1.94	7.57E-33	tRNA

<i>pgk</i>	1.94	2.50E-15	phosphoglycerate kinase
<i>pflA</i>	-1.94	5.65E-16	pyruvate formate lyase activating enzyme 1
<i>glpA</i>	1.94	8.57E-03	sn-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit
<i>fbp</i>	-1.93	6.13E-35	fructose-1,6-bisphosphatase I
<i>tonB</i>	1.93	3.77E-31	membrane spanning protein in TonB-ExbB-ExbD transport complex
<i>bdm</i>	-1.93	1.39E-12	biofilm-dependent modulation protein
<i>ubiH</i>	1.93	4.34E-25	2-octaprenyl-6-methoxyphenol hydroxylase, FAD/NAD(P)-binding
<i>ydjJ</i>	1.93	2.27E-03	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>cyaY</i>	-1.93	1.91E-16	frataxin; iron-binding and oxidizing protein
<i>tpx</i>	1.93	5.03E-49	lipid hydroperoxide peroxidase
<i>sibE</i>	1.92	5.65E-10	ncRNA
<i>uvrB</i>	1.92	5.87E-39	excinuclease of nucleotide excision repair
<i>valT</i>	-1.92	8.46E-19	tRNA
<i>mprA</i>	-1.92	2.24E-26	transcriptional repressor of microcin B17 synthesis and multidrug efflux
<i>insQ</i>	1.92	4.07E-33	IS609 transposase B
<i>pyrB</i>	-1.92	5.73E-06	aspartate carbamoyltransferase, catalytic subunit
<i>yehR</i>	-1.91	1.56E-03	lipoprotein, DUF1307 family
<i>bioA</i>	1.91	9.79E-43	7,8-diaminopelargonic acid synthase, PLP-dependent
<i>hybF</i>	1.91	2.49E-04	protein involved with the maturation of hydrogenases 1 and 2
<i>metI</i>	1.91	4.13E-33	DL-methionine transporter subunit
<i>yedE</i>	-1.91	3.35E-35	putative inner membrane protein
<i>insZ</i>	1.91	7.57E-05	pseudo
<i>hisD</i>	1.90	4.73E-19	bifunctional histidinal dehydrogenase/ histidinol dehydrogenase
<i>agaV</i>	-1.90	3.75E-03	N-acetylgalactosamine-specific enzyme IIB component of PTS
<i>argW</i>	-1.90	7.50E-03	tRNA
<i>galP</i>	-1.90	7.76E-36	D-galactose transporter
<i>yraQ</i>	-1.90	7.57E-17	putative permease
<i>csgF</i>	1.90	4.08E-09	outer membrane protein required for curli nucleation by CsgB
<i>phoE</i>	-1.90	2.26E-06	outer membrane phosphoporin protein E
<i>yqgE</i>	1.90	1.37E-29	hypothetical protein
<i>yqgF</i>	1.90	2.15E-30	putative Holliday junction resolvase
<i>fabB</i>	1.89	5.72E-10	3-oxoacyl-[acyl-carrier-protein] synthase I
<i>shoB</i>	-1.89	1.67E-15	toxic membrane protein
<i>ldrD</i>	1.89	2.09E-12	toxic polypeptide, small
<i>ygiV</i>	-1.89	1.23E-21	transcriptional repressor for mcbR biofilm gene
<i>ytjA</i>	-1.89	2.24E-34	hypothetical protein
<i>arsR</i>	-1.89	1.02E-04	DNA-binding transcriptional repressor
<i>yhjA</i>	1.89	3.33E-13	putative cytochrome C peroxidase
<i>infA</i>	-1.89	1.44E-21	translation initiation factor IF-1
<i>yhjR</i>	-1.89	1.60E-32	hypothetical protein
<i>gpmM</i>	1.89	3.30E-40	phosphoglycero mutase III, cofactor-independent
<i>yecJ</i>	-1.89	1.43E-15	hypothetical protein
<i>eutL</i>	1.89	3.96E-09	putative carboxysome structural protein; role in ethanolamine utilization?

<i>ddpF</i>	1.89	3.52E-04	D,D-dipeptide permease system, ATP-binding component
<i>purA</i>	1.88	5.73E-27	adenylosuccinate synthetase
<i>gntP</i>	1.88	2.79E-07	fructuronate transporter
<i>putP</i>	-1.88	4.53E-15	proline:sodium symporter
<i>yzgL</i>	-1.88	4.06E-05	pseudo
<i>ybeT</i>	1.88	1.55E-02	conserved protein, Sell family
<i>fruA</i>	1.88	2.95E-16	fused fructose-specific PTS enzymes: IIBcomponent/IIC components
<i>kdsB</i>	-1.88	4.18E-28	3-deoxy-manno-octulosonate cytidyltransferase
<i>yhbV</i>	1.88	4.19E-04	putative protease
<i>cynX</i>	1.88	1.55E-05	putative cyanate transporter
<i>hycG</i>	1.87	6.16E-04	hydrogenase 3 and formate hydrogenase complex, HycG subunit
<i>fixC</i>	1.87	2.46E-02	putative oxidoreductase with FAD/NAD(P)-binding domain
<i>ycaR</i>	-1.87	2.93E-10	peroxide and acid resistance protein, UPF0434 family
<i>kefC</i>	-1.87	1.78E-14	potassium:proton antiporter
<i>pntB</i>	-1.87	5.98E-23	pyridine nucleotide transhydrogenase, beta subunit
<i>astB</i>	1.87	1.37E-08	succinylarginine dihydrolase
<i>hisL</i>	1.87	5.75E-21	his operon leader peptide
<i>mscL</i>	-1.87	2.56E-28	mechanosensitive channel protein, high conductance
<i>prfA</i>	1.87	9.02E-38	peptide chain release factor RF-1
<i>ybhF</i>	1.87	5.37E-19	fused predicted transporter subunits of ABC superfamily
<i>gatD</i>	-1.87	1.02E-07	galactitol-1-phosphate dehydrogenase, Zn-dependent and NAD(P)-binding
<i>sdhC</i>	-1.86	1.41E-28	succinate dehydrogenase, membrane subunit, binds cytochrome b556
<i>yhiI</i>	-1.86	7.24E-17	putative membrane fusion protein (MFP) of efflux pump
<i>flkB</i>	-1.86	2.18E-35	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
<i>mgtA</i>	-1.86	4.99E-24	magnesium transporter
<i>ptsI</i>	1.86	1.66E-30	PEP-protein phosphotransferase of PTS system (enzyme I)
<i>leuV</i>	-1.86	1.61E-21	tRNA
<i>fis</i>	-1.86	3.07E-20	global DNA-binding transcriptional dual regulator
<i>gpt</i>	-1.86	6.87E-22	guanine-hypoxanthine phosphoribosyltransferase
<i>fusA</i>	1.85	1.45E-19	protein chain elongation factor EF-G, GTP-binding
<i>yihR</i>	1.85	4.16E-02	putative aldose-1-epimerase
<i>ydjN</i>	-1.85	1.14E-45	putative transporter
<i>zinT</i>	-1.85	1.01E-08	zinc and cadmium binding protein, periplasmic
<i>nuoA</i>	-1.85	2.82E-36	NADH:ubiquinone oxidoreductase, membrane subunit A
<i>fucU</i>	-1.85	1.24E-18	L-fucose mutarotase
<i>rpmA</i>	-1.85	1.51E-21	50S ribosomal subunit protein L27
<i>dkgA</i>	-1.85	9.29E-20	2,5-diketo-D-gluconate reductase A
<i>yaaI</i>	-1.85	4.36E-02	conserved protein, UPF0412 family
<i>hemA</i>	1.85	3.53E-41	glutamyl tRNA reductase
<i>yccX</i>	-1.85	1.08E-16	weak acylphosphatase
<i>rcnR</i>	-1.84	1.24E-08	DNA-binding transcriptional repressor of rcnA
<i>mcbR</i>	-1.84	1.06E-20	colanic acid and biofilm gene transcriptional regulator, MqsR-controlled
<i>glyA</i>	1.84	2.46E-28	serine hydroxymethyltransferase

<i>insF1</i>	-1.84	9.87E-06	IS3 transposase B
<i>gspF</i>	-1.84	3.06E-02	general secretory pathway component, cryptic
<i>lysW</i>	-1.84	1.12E-21	tRNA
<i>rmuC</i>	1.84	1.88E-22	putative recombination limiting protein
<i>bssS</i>	-1.84	2.08E-22	biofilm regulator
<i>yagH</i>	1.84	1.54E-05	CP4-6 prophage; predicted xylosidase/arabinosidase
<i>argB</i>	-1.84	1.39E-14	acetylglutamate kinase
<i>yfiM</i>	-1.84	2.68E-06	required for high salt suppression of motility; probable lipoprotein
<i>lpxT</i>	-1.83	2.00E-17	lipid A 1-diphosphate synthase
<i>cynT</i>	1.83	9.71E-03	carbonic anhydrase
<i>alsB</i>	-1.83	6.43E-08	D-allose transporter subunit
<i>tyrP</i>	-1.83	2.68E-14	tyrosine transporter
<i>yfiN</i>	-1.83	1.17E-13	putative membrane-anchored diguanylate cyclase
<i>ppa</i>	-1.83	7.88E-43	inorganic pyrophosphatase
<i>ssrS</i>	1.83	8.92E-06	ncRNA
<i>yhaI</i>	-1.83	1.02E-03	inner membrane protein, DUF805 family
<i>fepG</i>	1.83	1.88E-11	iron-enterobactin transporter subunit
<i>yoaA</i>	1.83	8.45E-28	conserved protein with nucleoside triphosphate hydrolase domain
<i>iraP</i>	-1.83	8.42E-28	anti-RssB factor, RpoS stabilizer during Pi starvation; anti-adaptor protein
<i>yahN</i>	-1.83	1.35E-03	amino acid exporter for proline, lysine, glutamate, homoserine
<i>ybgK</i>	1.83	6.54E-19	putative allophanate hydrolase, subunit 2
<i>torA</i>	1.83	1.42E-05	trimethylamine N-oxide (TMAO) reductase I, catalytic subunit
<i>ydhX</i>	1.83	7.31E-03	putative 4Fe-4S ferridoxin-type protein
<i>slyX</i>	-1.83	5.88E-18	protein required for phi X174 lysis
<i>hisR</i>	-1.83	8.73E-15	tRNA
<i>kefF</i>	-1.82	3.33E-13	potassium-efflux system ancillary protein for KefC
<i>rluB</i>	-1.82	1.02E-18	23S rRNA pseudouridine(2605) synthase
<i>rhmD</i>	1.82	3.60E-02	L-rhamnonate dehydratase
<i>rpmG</i>	-1.82	8.37E-33	50S ribosomal subunit protein L33
<i>insH1</i>	1.82	2.17E-06	pseudo
<i>ycgJ</i>	-1.82	4.30E-17	hypothetical protein
<i>ribB</i>	-1.82	7.83E-35	3,4-dihydroxy-2-butanone-4-phosphate synthase
<i>efp</i>	-1.81	1.71E-44	polyproline-specific translation elongation factor EF-P
<i>glnA</i>	1.81	3.45E-14	glutamine synthetase
<i>yjjI</i>	-1.80	2.23E-04	hypothetical protein
<i>rpsS</i>	1.80	1.10E-08	30S ribosomal subunit protein S19
<i>ydiH</i>	1.80	1.07E-10	hypothetical protein
<i>cstA</i>	1.80	1.86E-20	carbon starvation protein
<i>glnG</i>	1.80	5.56E-18	response regulator in two-component regulatory system with GlnL
<i>wcaF</i>	-1.80	2.95E-02	putative acyl transferase
<i>prlC</i>	1.80	1.57E-30	oligopeptidase A
<i>ilvL</i>	1.80	6.37E-09	ilvG operon leader peptide
<i>yqjG</i>	-1.80	4.51E-22	putative S-transferase

<i>glnB</i>	-1.80	4.51E-22	regulatory protein P-II for glutamine synthetase
<i>yciW</i>	1.80	4.16E-31	putative oxidoreductase
<i>yciH</i>	-1.80	2.57E-07	initiation factor function partial mimic, SUI1 family
<i>osmY</i>	-1.79	3.63E-28	periplasmic protein
<i>ysaB</i>	-1.79	1.43E-08	hypothetical protein
<i>dgoA</i>	1.79	2.19E-02	2-oxo-3-deoxygalactonate 6-phosphate aldolase
<i>insII</i>	1.79	1.18E-02	pseudo
<i>ldrC</i>	1.79	9.47E-03	toxic polypeptide, small
<i>yneG</i>	1.79	6.38E-04	hypothetical protein
<i>nagC</i>	1.79	3.38E-33	transcriptional dual regulator, repressor of N-acetylglucosamine
<i>fdnG</i>	1.79	6.84E-06	formate dehydrogenase-N, alpha subunit, nitrate-inducible
<i>maa</i>	-1.78	3.69E-30	maltose O-acetyltransferase
<i>yihL</i>	-1.78	1.87E-05	putative DNA-binding transcriptional regulator
<i>dgoK</i>	1.78	1.21E-07	2-oxo-3-deoxygalactonate kinase
<i>rplF</i>	1.78	1.79E-11	50S ribosomal subunit protein L6
<i>yhcA</i>	-1.78	3.42E-04	putative periplasmic chaperone protein
<i>cmtB</i>	-1.78	4.42E-02	putative mannitol-specific enzyme IIA component of PTS
<i>ddpB</i>	1.78	7.89E-03	D-ala-D-ala transporter subunit
<i>torD</i>	1.78	2.40E-03	TorA-maturation chaperone
<i>trkA</i>	1.78	6.19E-26	NAD-binding component of TrK potassium transporter
<i>iscS</i>	1.78	2.45E-23	cysteine desulfurase (tRNA sulfurtransferase), PLP-dependent
<i>rplU</i>	-1.77	1.50E-29	50S ribosomal subunit protein L21
<i>fepD</i>	1.77	5.07E-21	iron-enterobactin transporter subunit
<i>evgS</i>	-1.77	4.46E-08	histidine kinase in two-component regulatory system with EvgA
<i>ugpB</i>	-1.77	2.04E-30	glycerol-3-phosphate transporter subunit
<i>yqiA</i>	1.77	1.48E-17	acyl CoA esterase
<i>ygaU</i>	-1.77	2.94E-19	hypothetical protein
<i>rdlD</i>	-1.77	3.87E-02	ncRNA
<i>serU</i>	1.77	4.23E-04	tRNA
<i>rimK</i>	-1.77	1.43E-14	ribosomal protein S6 modification protein
<i>nagA</i>	1.77	6.69E-28	N-acetylglucosamine-6-phosphate deacetylase
<i>yghA</i>	-1.76	2.30E-18	putative oxidoreductase
<i>tdk</i>	-1.76	8.70E-26	thymidine kinase/deoxyuridine kinase
<i>glnU</i>	-1.76	1.47E-14	tRNA
<i>ybhQ</i>	-1.76	1.51E-14	inner membrane protein
<i>elaA</i>	-1.76	6.03E-10	putative acyltransferase with acyl-CoA N-acyltransferase domain
<i>yqfA</i>	1.76	1.67E-21	inner membrane protein, hemolysin III family HyllIII
<i>yciF</i>	-1.76	3.62E-12	putative rubrerythrin/ferritin-like metal-binding protein
<i>dld</i>	1.76	1.73E-31	D-lactate dehydrogenase, FAD-binding, NADH independent
<i>yfaY</i>	1.76	2.69E-24	hypothetical protein
<i>ydaU</i>	1.76	1.60E-03	Rac prophage; conserved protein
<i>ridA</i>	-1.76	8.31E-24	conserved protein, UPF0131 family
<i>hycC</i>	1.75	4.87E-02	hydrogenase 3, membrane subunit

<i>emrA</i>	-1.75	6.29E-21	multidrug efflux system
<i>yjhZ</i>	-1.75	1.86E-02	pseudo
<i>argQ</i>	-1.75	3.30E-22	tRNA
<i>pheP</i>	-1.75	2.98E-19	phenylalanine transporter
<i>tyrA</i>	-1.75	4.69E-11	fused chorismate mutase T/prephenate dehydrogenase
<i>ydhR</i>	1.75	1.49E-24	putative monooxygenase
<i>spy</i>	1.75	4.74E-17	periplasmic ATP-independent protein refolding chaperone, stress-induced
<i>fliG</i>	1.75	1.75E-02	flagellar motor switching and energizing component
<i>yciA</i>	-1.75	4.85E-24	acyl-CoA esterase
<i>ygeO</i>	1.75	4.38E-03	pseudo
<i>yiaT</i>	-1.75	1.44E-02	putative outer membrane protein
<i>yecA</i>	-1.75	1.59E-16	conserved protein, UPF0149 family
<i>aceA</i>	1.74	2.56E-12	isocitrate lyase
<i>yccJ</i>	-1.74	2.95E-23	hypothetical protein
<i>nuoB</i>	-1.74	1.01E-31	NADH:ubiquinone oxidoreductase, chain B
<i>eda</i>	-1.74	3.67E-23	2-keto-3-deoxygluconate 6-phosphate aldolase/oxaloacetate decarboxylase
<i>fhuB</i>	-1.74	6.15E-16	fused iron-hydroxamate transporter subunits
<i>lsrG</i>	1.74	1.20E-04	autoinducer-2 (AI-2) degrading protein LsrG
<i>yaeH</i>	-1.74	1.64E-30	conserved protein, UPF0325 family
<i>yffQ</i>	-1.74	7.27E-03	CPZ-55 prophage; putative protein
<i>yeeJ</i>	1.74	3.65E-07	putative adhesin
<i>aidB</i>	-1.74	9.09E-09	DNA alkylation damage repair protein
<i>valW</i>	-1.74	1.26E-08	tRNA
<i>ldrA</i>	1.74	3.29E-02	toxic polypeptide, small
<i>metE</i>	1.74	2.69E-14	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase
<i>amtB</i>	1.74	4.47E-09	ammonium transporter
<i>nlpA</i>	-1.74	3.61E-36	cytoplasmic membrane lipoprotein-28
<i>dksA</i>	-1.73	1.09E-27	DNA-binding transcriptional regulator of rRNA transcription
<i>ecpA</i>	-1.73	6.10E-15	cryptic Mat fimbriin gene
<i>nac</i>	1.73	3.14E-07	DNA-binding transcriptional dual regulator of nitrogen assimilation
<i>gadX</i>	-1.73	5.05E-19	DNA-binding transcriptional dual regulator
<i>ygiS</i>	-1.73	1.58E-14	periplasmic-binding component of ABC superfamily
<i>yjbM</i>	-1.73	4.08E-02	hypothetical protein
<i>elaB</i>	-1.73	7.82E-19	ribosome-binding protein, probably membrane-anchored, function unknown
<i>sfsB</i>	-1.73	3.36E-05	DNA-binding transcriptional activator of maltose metabolism
<i>hisB</i>	1.73	6.57E-15	fused histidinol-phosphatase/imidazoleglycerol-phosphate dehydratase
<i>pyrD</i>	-1.72	3.42E-29	dihydro-orotate oxidase, FMN-linked
<i>yceM</i>	1.72	5.32E-14	putative oxidoreductase with NAD(P)-binding Rossmann-fold domain
<i>rplV</i>	1.72	1.52E-07	50S ribosomal subunit protein L22
<i>narJ</i>	1.72	1.06E-03	molybdenum-cofactor-assembly chaperone subunit of nitrate reductase 1
<i>yghW</i>	-1.72	4.19E-03	hypothetical protein
<i>pheM</i>	1.72	1.59E-07	phenylalanyl-tRNA synthetase operon leader peptide
<i>ybbM</i>	-1.72	9.43E-11	inner membrane protein, UPF0014 family

<i>ybiJ</i>	1.72	3.47E-15	hypothetical protein
<i>yhfZ</i>	-1.72	1.50E-06	hypothetical protein
<i>atpG</i>	1.71	9.98E-13	F1 sector of membrane-bound ATP synthase, gamma subunit
<i>dsrB</i>	-1.71	1.73E-09	hypothetical protein
<i>yfdY</i>	-1.71	2.46E-07	putative inner membrane protein
<i>yfaZ</i>	-1.71	2.28E-08	outer membrane protein, possible porin
<i>raiA</i>	1.71	1.09E-18	cold shock protein associated with 30S ribosomal subunit
<i>metZ</i>	-1.71	5.00E-09	tRNA
<i>yihV</i>	1.71	9.80E-04	putative sugar kinase
<i>yjfP</i>	-1.71	1.54E-09	acyl CoA esterase
<i>nupG</i>	-1.71	2.05E-18	nucleoside transporter
<i>msrB</i>	-1.71	2.36E-25	methionine sulfoxide reductase B
<i>clpB</i>	1.71	1.86E-14	protein disaggregation chaperone
<i>hcaF</i>	1.71	1.26E-03	3-phenylpropionate dioxygenase, small (beta) subunit
<i>lysQ</i>	-1.71	1.15E-13	tRNA
<i>glyT</i>	-1.71	4.69E-18	tRNA
<i>phoA</i>	-1.71	1.27E-21	bacterial alkaline phosphatase
<i>metB</i>	1.71	1.40E-24	cystathionine gamma-synthase, PLP-dependent
<i>ygiK</i>	1.71	6.17E-04	alpha-glucosidase
<i>bioF</i>	1.70	3.55E-28	8-amino-7-oxononanoate synthase
<i>yaaH</i>	-1.70	6.53E-11	inner membrane protein, Grp1_Fun34_YaaH family
<i>yrdA</i>	-1.70	1.26E-28	hypothetical protein
<i>mliC</i>	1.70	1.54E-11	inhibitor of c-type lysozyme, membrane-bound; predicted lipoprotein
<i>sgrS</i>	1.70	1.12E-13	ncRNA
<i>ruvA</i>	1.70	2.23E-19	component of RuvABC resolvase, regulatory subunit
<i>pepP</i>	1.70	1.44E-15	proline aminopeptidase P II
<i>argZ</i>	-1.70	1.12E-21	tRNA
<i>tsr</i>	1.70	4.55E-07	methyl-accepting chemotaxis protein I, serine sensor receptor
<i>ycfZ</i>	-1.70	3.16E-02	inner membrane protein
<i>lysZ</i>	-1.70	3.52E-22	tRNA
<i>yeeZ</i>	1.70	4.26E-27	putative epimerase, with NAD(P)-binding Rossmann-fold domain
<i>ykgM</i>	-1.70	9.96E-04	50S ribosomal protein L31 type B
<i>yjdO</i>	-1.70	6.39E-03	hypothetical protein
<i>rplY</i>	-1.70	5.62E-17	50S ribosomal subunit protein L25
<i>rplB</i>	1.70	4.89E-08	50S ribosomal subunit protein L2
<i>ppsA</i>	-1.70	4.36E-19	phosphoenolpyruvate synthase
<i>hlyE</i>	1.70	1.00E-05	hemolysin E
<i>dppD</i>	1.70	1.09E-14	dipeptide/heme transporter
<i>ppdC</i>	1.70	9.89E-03	hypothetical protein
<i>ddpD</i>	1.70	1.18E-03	D,D-dipeptide permease system, ATP-binding component
<i>dppC</i>	1.70	2.89E-08	dipeptide/heme transporter
<i>araB</i>	1.70	4.35E-03	L-ribulokinase
<i>argE</i>	-1.69	3.54E-26	acetylornithine deacetylase

<i>pstS</i>	-1.69	1.12E-13	periplasmic phosphate binding protein, high-affinity
<i>nrdG</i>	1.69	3.37E-05	anaerobic ribonucleotide reductase activating protein
<i>yhhJ</i>	-1.69	7.93E-13	putative permease subunit, ABC transporter superfamily
<i>lhr</i>	1.69	4.37E-19	putative ATP-dependent helicase
<i>yneO</i>	1.69	4.04E-07	pseudo
<i>chiP</i>	1.69	1.37E-03	chitoporin, uptake of chitosugars
<i>opgC</i>	-1.69	3.25E-14	protein for succinylation of osmoregulated periplasmic glucans (OPGs)
<i>galT</i>	1.69	1.74E-12	galactose-1-phosphate uridylyltransferase
<i>yniD</i>	1.69	3.80E-03	hypothetical protein
<i>holC</i>	1.69	1.44E-12	DNA polymerase III, chi subunit
<i>ycaC</i>	-1.69	2.70E-29	putative hydrolase, isochorismatase family
<i>paoC</i>	1.69	1.85E-04	PaoABC aldehyde oxidoreductase, Moco-containing subunit
<i>yjdM</i>	-1.69	9.03E-14	hypothetical protein
<i>yegU</i>	1.69	1.01E-05	putative hydrolase
<i>yqhA</i>	-1.69	5.92E-30	putative inner membrane protein, UPF0114 family
<i>csgB</i>	1.69	2.36E-02	curlin nucleator protein, minor subunit in curli complex
<i>ynfL</i>	1.68	7.13E-07	putative DNA-binding transcriptional regulator
<i>nepI</i>	-1.68	4.77E-08	putative transporter
<i>yqiD</i>	-1.68	3.34E-22	membrane-anchored ribosome-binding protein
<i>atpI</i>	-1.68	4.80E-20	ATP synthase, membrane-bound accessory factor
<i>ddpC</i>	1.68	1.54E-03	D-ala-D-ala transporter subunit
<i>ybgL</i>	1.68	2.53E-13	conserved protein, UPF0271 family
<i>yceH</i>	1.68	1.60E-23	conserved protein, UPF0502 family
<i>ptsG</i>	-1.68	1.25E-20	fused glucose-specific PTS enzymes: IIB component/IIC component
<i>glnX</i>	-1.68	6.44E-11	tRNA
<i>yehE</i>	-1.68	1.98E-12	hypothetical protein
<i>puuP</i>	-1.68	7.81E-06	putrescine importer
<i>yjbI</i>	1.68	1.17E-02	pseudo
<i>speE</i>	-1.68	7.03E-16	spermidine synthase (putrescine aminopropyltransferase)
<i>rplW</i>	1.68	5.40E-10	50S ribosomal subunit protein L23
<i>yjhB</i>	1.68	3.06E-09	putative transporter
<i>yfdX</i>	-1.67	5.66E-04	hypothetical protein
<i>ycaP</i>	-1.67	2.18E-10	putative inner membrane protein, UPF0702 family
<i>pgaC</i>	-1.67	3.85E-03	biofilm PGA synthase PgaCD, catalytic subunit
<i>cbrA</i>	1.67	7.87E-03	colicin M resistance protein; predicted oxidoreductase
<i>yfiR</i>	-1.67	4.37E-14	putative periplasmic inhibitor of YfiN activity
<i>betA</i>	1.67	1.06E-12	choline dehydrogenase, a flavoprotein
<i>hchA</i>	-1.67	2.07E-11	glyoxalase III and Hsp31 molecular chaperone
<i>rpsH</i>	1.67	1.17E-10	30S ribosomal subunit protein S8
<i>yebZ</i>	-1.67	1.13E-16	inner membrane protein
<i>hcaB</i>	1.67	7.98E-04	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase
<i>rplS</i>	-1.67	5.69E-23	50S ribosomal subunit protein L19
<i>yeaH</i>	1.67	1.92E-10	UPF0229 family protein

<i>yahG</i>	1.67	2.16E-02	hypothetical protein
<i>aqpZ</i>	-1.67	2.34E-07	aquaporin Z
<i>yeiP</i>	-1.66	3.46E-26	elongation factor P-like protein
<i>mrp</i>	-1.66	3.79E-15	antiporter inner membrane protein
<i>rcaA</i>	-1.66	1.65E-10	DNA-binding transcriptional activator, co-regulator with RcsB
<i>fliM</i>	1.66	2.99E-02	flagellar motor switching and energizing component
<i>fadE</i>	-1.66	2.60E-13	acyl coenzyme A dehydrogenase
<i>xdhB</i>	1.66	5.71E-03	xanthine dehydrogenase, FAD-binding subunit
<i>srIE</i>	1.66	3.23E-02	glucitol/sorbitol-specific enzyme IIB component of PTS
<i>pntA</i>	-1.66	4.19E-24	pyridine nucleotide transhydrogenase, alpha subunit
<i>rpsC</i>	1.66	7.52E-07	30S ribosomal subunit protein S3
<i>cspB</i>	1.66	4.45E-07	Qin prophage; cold shock protein
<i>pflB</i>	1.66	7.05E-25	pyruvate formate lyase I
<i>nfsB</i>	-1.66	9.10E-25	dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive
<i>trpB</i>	1.66	4.29E-16	tryptophan synthase, beta subunit
<i>sdaA</i>	1.65	1.05E-20	L-serine deaminase I
<i>prmC</i>	1.65	4.71E-09	N5-glutamine methyltransferase, modifies release factors RF-1 and RF-2
<i>ymgG</i>	-1.65	8.01E-08	conserved protein, UPF0757 family
<i>hupA</i>	-1.65	2.68E-19	HU, DNA-binding transcriptional regulator, alpha subunit
<i>rpsG</i>	1.65	3.87E-18	30S ribosomal subunit protein S7
<i>hyfB</i>	1.65	5.93E-03	hydrogenase 4, membrane subunit
<i>galK</i>	1.65	2.75E-18	galactokinase
<i>guaC</i>	-1.65	6.35E-26	GMP reductase
<i>tktA</i>	1.65	5.95E-08	transketolase 1, thiamin-binding
<i>tdcE</i>	1.65	2.05E-05	pyruvate formate-lyase 4/2-ketobutyrate formate-lyase
<i>fhlA</i>	-1.65	5.56E-12	DNA-binding transcriptional activator
<i>mak</i>	-1.65	1.43E-09	manno(fructo)kinase
<i>exbD</i>	1.65	1.87E-22	membrane spanning protein in TonB-ExbB-ExbD complex
<i>acnB</i>	1.65	1.33E-09	bifunctional aconitate hydratase 2/2-methylisocitrate dehydratase
<i>ompW</i>	-1.65	2.52E-04	outer membrane protein W
<i>ybeZ</i>	1.65	1.48E-25	putative protein with nucleoside triphosphate hydrolase domain
<i>dosP</i>	1.65	1.77E-04	oxygen sensor, c-di-GMP phosphodiesterase, heme-regulated
<i>yfhL</i>	-1.65	3.08E-06	putative 4Fe-4S cluster-containing protein
<i>hrpA</i>	1.65	3.37E-22	putative ATP-dependent helicase
<i>topB</i>	1.65	1.99E-20	DNA topoisomerase III
<i>ddpA</i>	1.65	8.95E-07	D-ala-D-a la transporter subunit
<i>glnE</i>	1.64	4.66E-15	fused deadenylyltransferase/adenylyltransferase for glutamine synthetase
<i>nei</i>	1.64	1.35E-10	endonuclease VIII/ 5-formyluracil/5-hydroxymethyluracil DNA glycosylase
<i>gcvP</i>	-1.64	5.38E-13	glycine decarboxylase, subunit (protein P) of glycine cleavage complex
<i>glnW</i>	-1.64	1.05E-12	tRNA
<i>araA</i>	1.64	1.13E-03	L-arabinose isomerase
<i>tyrU</i>	-1.64	6.33E-18	tRNA
<i>nrdA</i>	1.64	3.41E-23	ribonucleoside-diphosphate reductase 1, alpha subunit

<i>emrY</i>	-1.64	4.16E-03	putative multidrug efflux system
<i>argY</i>	-1.64	1.11E-19	tRNA
<i>yciZ</i>	1.64	1.01E-09	hypothetical protein
<i>ogt</i>	1.64	1.88E-09	O-6-alkylguanine-DNA:cysteine-protein methyltransferase
<i>recB</i>	1.64	1.25E-25	exonuclease V (RecBCD complex), beta subunit
<i>gltT</i>	-1.64	1.41E-12	tRNA
<i>lacY</i>	-1.64	1.20E-02	lactose permease
<i>yebY</i>	-1.64	6.72E-18	hypothetical protein
<i>yfiL</i>	-1.64	8.97E-08	lipoprotein
<i>adk</i>	-1.63	1.66E-20	adenylate kinase
<i>frdC</i>	-1.63	1.74E-08	fumarate reductase (anaerobic), membrane anchor subunit
<i>nhaA</i>	-1.63	4.38E-20	sodium-proton antiporter
<i>pflD</i>	1.63	3.96E-05	putative formate acetyltransferase 2 (pyruvate formate lyase II)
<i>gntK</i>	-1.63	1.95E-04	gluconate kinase 2
<i>leuW</i>	-1.63	8.13E-13	tRNA
<i>btuR</i>	1.63	1.88E-14	cob(I)alamin adenosyltransferase/cobinamide adenosyltransferase
<i>rpsN</i>	1.63	5.62E-12	30S ribosomal subunit protein S14
<i>prfB</i>	1.63	9.47E-28	peptide chain release factor RF-2
<i>ybeY</i>	1.63	2.10E-20	metal-binding heat shock protein required for rRNA maturation
<i>ftnA</i>	-1.63	4.66E-12	ferritin iron storage protein (cytoplasmic)
<i>ypfG</i>	1.63	3.08E-09	hypothetical protein
<i>eutC</i>	1.63	2.78E-06	ethanolamine ammonia-lyase, small subunit (light chain)
<i>surE</i>	1.63	3.24E-21	broad specificity 5'(3')-nucleotidase and polyphosphatase
<i>valS</i>	1.62	1.21E-23	valyl-tRNA synthetase
<i>yqiK</i>	-1.62	9.66E-17	hypothetical protein
<i>deoB</i>	1.62	1.13E-13	phosphopentomutase
<i>psaA</i>	-1.62	4.99E-04	miscRNA
<i>ptsH</i>	1.62	2.05E-25	phosphohistidinoprotein-hexose phosphotransferase of PTS system (Hpr)
<i>tnaB</i>	-1.62	1.40E-02	tryptophan transporter of low affinity
<i>yjiX</i>	1.62	5.25E-03	hypothetical protein
<i>yliF</i>	-1.62	4.92E-10	putative membrane-anchored diguanylate cyclase
<i>rplR</i>	1.62	3.30E-08	50S ribosomal subunit protein L18
<i>yoaE</i>	1.62	2.85E-22	fused predicted membrane protein/conserved protein
<i>panB</i>	1.62	9.19E-19	3-methyl-2-oxobutanoate hydroxymethyltransferase
<i>yncL</i>	-1.62	8.01E-06	hypothetical protein
<i>argX</i>	-1.62	4.04E-12	tRNA
<i>rnhB</i>	1.62	1.74E-11	ribonuclease HII, degrades RNA of DNA-RNA hybrids
<i>wcaD</i>	-1.62	2.07E-02	putative colanic acid polymerase
<i>leuP</i>	-1.62	5.95E-08	tRNA
<i>nagB</i>	1.62	5.65E-26	glucosamine-6-phosphate deaminase
<i>dnaK</i>	1.61	1.31E-14	chaperone Hsp70, co-chaperone with DnaJ
<i>ytfH</i>	-1.61	3.91E-03	putative transcriptional regulator, HxlR-type, DUF24 family
<i>yiiS</i>	-1.61	1.43E-16	conserved protein, UPF0381 family

<i>rph</i>	-1.61	1.00E-13	defective ribonuclease PH
<i>sbp</i>	-1.61	1.65E-19	sulfate transporter subunit
<i>yihG</i>	-1.61	5.12E-08	inner membrane protein, Predicted acyltransferase
<i>ftsK</i>	1.61	2.26E-21	DNA translocase at septal ring sorting daughter chromosomes
<i>flgE</i>	1.61	1.17E-02	flagellar hook protein
<i>yjH</i>	-1.61	4.49E-09	CP4-57 prophage; putative protein
<i>paaK</i>	1.61	9.34E-09	phenylacetyl-CoA ligase
<i>metL</i>	1.61	6.34E-18	fused aspartokinase II/homoserine dehydrogenase II
<i>amiA</i>	1.61	1.09E-24	N-acetylmuramoyl-L-alanine amidase I
<i>glnV</i>	-1.61	1.74E-08	tRNA
<i>nudB</i>	1.61	8.77E-17	dihydroneopterin triphosphate pyrophosphatase
<i>dtpB</i>	-1.60	6.82E-14	dipeptide and tripeptide permease B
<i>tgt</i>	-1.60	1.76E-16	tRNA-guanine transglycosylase
<i>yibB</i>	-1.60	1.80E-04	conserved protein, pfam09612 family
<i>yodB</i>	-1.60	1.09E-04	cytochrome b561 homolog
<i>ushA</i>	-1.60	1.99E-22	bifunctional UDP-sugar hydrolase/5'-nucleotidase
<i>fucI</i>	1.60	8.04E-04	L-fucose isomerase
<i>minE</i>	-1.60	1.82E-20	cell division topological specificity factor
<i>glnH</i>	-1.60	7.04E-24	glutamine transporter subunit
<i>lysA</i>	-1.60	2.32E-12	diaminopimelate decarboxylase, PLP-binding
<i>rplT</i>	-1.60	1.53E-22	50S ribosomal subunit protein L20
<i>yqjE</i>	-1.60	5.05E-19	inner membrane protein, DUF1469 family
<i>speD</i>	-1.60	4.35E-09	S-adenosylmethionine decarboxylase
<i>yeeE</i>	-1.60	2.73E-10	inner membrane protein, UPF0394 family
<i>ppiC</i>	-1.60	3.33E-12	peptidyl-prolyl cis-trans isomerase C (rotamase C)
<i>ymgE</i>	-1.59	2.61E-04	putative inner membrane protein
<i>yehM</i>	1.59	2.09E-02	hypothetical protein
<i>flhA</i>	1.59	1.51E-04	putative flagellar export pore protein
<i>eutK</i>	1.59	8.30E-04	putative carboxysome structural protein; role in ethanolamine utilization?
<i>yifE</i>	-1.59	4.23E-19	conserved protein, UPF0438 family
<i>uspD</i>	-1.59	1.94E-18	stress-induced protein
<i>nuoM</i>	-1.59	5.32E-08	NADH:ubiquinone oxidoreductase, membrane subunit M
<i>ydH</i>	-1.59	1.33E-09	hypothetical protein
<i>hpt</i>	-1.59	2.66E-20	hypoxanthine phosphoribosyltransferase
<i>rhlB</i>	1.59	1.21E-18	ATP-dependent RNA helicase
<i>yedF</i>	-1.59	2.46E-11	conserved protein, UPF0033 family
<i>yehI</i>	1.59	4.36E-06	hypothetical protein
<i>yfaL</i>	1.59	4.03E-10	adhesin
<i>recC</i>	1.59	1.73E-21	exonuclease V (RecBCD complex), gamma chain
<i>trmD</i>	-1.59	1.43E-16	tRNA m(1)G37 methyltransferase, SAM-dependent
<i>hokD</i>	1.59	8.29E-10	Qin prophage; small toxic polypeptide
<i>slyA</i>	-1.59	2.51E-18	DNA-binding transcriptional activator
<i>yidC</i>	-1.59	3.34E-22	membrane protein insertase

<i>suhB</i>	-1.58	4.23E-19	inositol monophosphatase
<i>ecnA</i>	-1.58	5.05E-08	entericidin A membrane lipoprotein, antidote entericidin B
<i>yjgH</i>	-1.58	4.88E-07	conserved protein, UPF0131 family
<i>gpp</i>	1.58	2.90E-21	guanosine pentaphosphatase/exopolyphosphatase
<i>sugE</i>	-1.58	3.28E-17	multidrug efflux system protein
<i>yjhR</i>	-1.58	7.02E-04	pseudo
<i>lpxB</i>	1.58	1.81E-21	tetraacyldisaccharide-1-P synthase
<i>flhD</i>	-1.58	2.64E-06	DNA-binding transcriptional dual regulator with FlhC
<i>gudX</i>	1.58	1.67E-02	glucarate dehydratase-related protein, substrate unknown
<i>ycaD</i>	-1.58	9.81E-13	putative MFS-type transporter
<i>yghO</i>	1.58	2.52E-02	pseudo
<i>rpmB</i>	-1.58	5.80E-26	50S ribosomal subunit protein L28
<i>csiD</i>	1.58	1.78E-11	carbon starvation protein
<i>symE</i>	1.58	1.87E-03	toxic peptide regulated by antisense sRNA symR
<i>ugpA</i>	-1.58	2.35E-04	glycerol-3-phosphate transporter subunit
<i>ugd</i>	-1.58	1.86E-13	UDP-glucose 6-dehydrogenase
<i>bacA</i>	-1.57	4.02E-09	undecaprenyl pyrophosphate phosphatase
<i>yiiR</i>	-1.57	5.86E-07	putative inner membrane protein, DUF805 family
<i>ruvB</i>	1.57	2.75E-22	ATP-dependent DNA helicase, component of RuvABC resolvosome
<i>dgoD</i>	1.57	5.13E-05	galactonate dehydratase
<i>trpE</i>	-1.57	4.51E-04	component I of anthranilate synthase
<i>carA</i>	-1.57	3.44E-16	carbamoyl phosphate synthetase small subunit, glutamine amidotransferase
<i>metK</i>	1.57	5.57E-22	S-adenosylmethionine synthetase
<i>rpsA</i>	-1.57	9.96E-17	30S ribosomal subunit protein S1
<i>queC</i>	-1.57	5.35E-10	7-cyano-7-deazaguanine (preQ0) synthase; queuosine biosynthesis
<i>bioC</i>	1.57	6.65E-13	malonyl-CoA methyltransferase, SAM-dependent
<i>exuR</i>	1.57	4.35E-20	DNA-binding transcriptional repressor
<i>insL1</i>	1.57	1.19E-03	IS186 transposase
<i>pitA</i>	-1.57	5.48E-15	phosphate transporter, low-affinity; tellurite importer
<i>yffS</i>	-1.57	1.83E-03	CPZ-55 prophage; putative protein
<i>fadM</i>	-1.57	2.06E-06	long-chain acyl-CoA thioesterase III
<i>uspA</i>	-1.57	2.99E-17	universal stress global response regulator
<i>mdfA</i>	-1.57	6.92E-12	multidrug efflux system protein
<i>narH</i>	1.57	3.22E-04	nitrate reductase 1, beta (Fe-S) subunit
<i>alaA</i>	-1.57	5.57E-22	valine-pyruvate aminotransferase 2
<i>ppc</i>	1.57	2.22E-16	phosphoenolpyruvate carboxylase
<i>eutR</i>	1.56	1.45E-05	eut operon transcriptional activator, AraC family
<i>melB</i>	-1.56	8.29E-06	melibiose:sodium symporter
<i>bcsQ</i>	-1.56	4.61E-05	pseudo
<i>fliD</i>	1.56	1.49E-02	flagellar filament capping protein
<i>rpsT</i>	-1.56	1.53E-18	30S ribosomal subunit protein S20
<i>rpsU</i>	-1.56	2.69E-14	30S ribosomal subunit protein S21
<i>sibA</i>	1.56	1.67E-05	ncRNA

<i>ydbD</i>	1.56	3.39E-06	putative PF10971 family periplasmic methylglyoxal resistance protein
<i>rsmJ</i>	1.56	6.49E-11	16S rRNA m(2)G1516 methyltransferase, SAM-dependent
<i>ivbL</i>	1.56	8.02E-06	ilvB operon leader peptide
<i>alaV</i>	-1.56	7.13E-18	tRNA
<i>malS</i>	-1.56	6.27E-06	alpha-amylase
<i>mhpF</i>	1.55	2.79E-02	acetaldehyde-CoA dehydrogenase II, NAD-binding
<i>ssrA</i>	1.55	2.62E-13	miscRNA
<i>leuU</i>	-1.55	1.42E-05	tRNA
<i>rimO</i>	-1.55	1.16E-15	ribosomal protein S12 methylthiotransferase; radical SAM superfamily
<i>hypB</i>	1.55	3.28E-03	GTP hydrolase involved in nickel liganding into hydrogenases
<i>nanM</i>	-1.55	3.00E-11	N-acetylneuraminic acid mutarotase
<i>qorA</i>	-1.55	1.66E-15	quinone oxidoreductase, NADPH-dependent
<i>yjiK</i>	-1.55	1.35E-04	hypothetical protein
<i>exbB</i>	1.55	1.85E-20	membrane spanning protein in TonB-ExbB-ExbD complex
<i>yeeP</i>	1.55	7.04E-05	pseudo
<i>kdpE</i>	1.55	2.53E-05	response regulator in two-component regulatory system with KdpD
<i>crl</i>	-1.55	1.86E-14	sigma factor-binding protein, RNA polymerase holoenzyme formation
<i>wbbH</i>	-1.55	1.88E-12	O-antigen polymerase
<i>dsbB</i>	-1.55	5.06E-12	oxidoreductase for reoxidation of DsbA protein disulfide isomerase I
<i>ydhV</i>	1.55	3.11E-02	putative oxidoreductase
<i>rpsL</i>	1.55	2.01E-17	30S ribosomal subunit protein S12
<i>kdpB</i>	1.55	2.96E-03	potassium translocating ATPase, subunit B
<i>aceK</i>	1.55	2.53E-06	isocitrate dehydrogenase kinase/phosphatase
<i>ybhL</i>	-1.55	1.13E-17	inner membrane protein, UPF0005 family
<i>ilvG</i>	-1.55	4.37E-09	pseudo
<i>ykfC</i>	1.55	1.09E-08	pseudo
<i>frmB</i>	-1.55	3.31E-07	S-formylglutathione hydrolase
<i>rimM</i>	-1.55	1.88E-14	16S rRNA processing protein
<i>ygfF</i>	-1.55	6.62E-03	putative NAD(P)-binding oxidoreductase
<i>aroE</i>	-1.54	2.01E-10	dehydroshikimate reductase, NAD(P)-binding
<i>ygaV</i>	1.54	8.23E-03	tributyltin-inducible repressor of ygaVP
<i>tap</i>	1.54	2.28E-02	methyl-accepting protein IV
<i>csgG</i>	1.54	5.72E-09	curli production assembly/transport outer membrane lipoprotein
<i>treF</i>	1.54	1.06E-10	cytoplasmic trehalase
<i>asnC</i>	-1.54	1.17E-05	DNA-binding transcriptional dual regulator
<i>ycgR</i>	1.54	4.20E-02	flagellar velocity braking protein, c-di-GMP-regulated
<i>lrp</i>	-1.54	1.95E-14	DNA-binding transcriptional dual regulator, leucine-binding
<i>hisH</i>	1.54	7.66E-08	imidazole glycerol phosphate synthase, glutamine amidotransferase subunit
<i>solA</i>	-1.54	3.08E-20	N-methyltryptophan oxidase, FAD-binding
<i>waaL</i>	-1.54	1.35E-02	O-antigen ligase
<i>rarA</i>	1.54	4.27E-18	DNA-dependent ATPase, processing recombination intermediates at replication forks
<i>tfaE</i>	1.54	2.17E-02	e14 prophage; predicted tail fiber assembly protein
<i>trpC</i>	1.54	3.63E-11	fused indole-3-glycerolphosphate synthetase/N-(5-phosphoribosyl)anthranilate isomerase

<i>glmM</i>	1.54	3.05E-15	phosphoglucosamine mutase
<i>argR</i>	-1.54	1.34E-15	DNA-binding transcriptional dual regulator, L-arginine-binding
<i>rplP</i>	1.54	4.52E-06	50S ribosomal subunit protein L16
<i>metF</i>	1.54	2.69E-13	5,10-methylenetetrahydrofolate reductase
<i>yfeN</i>	-1.54	1.24E-04	putative outer membrane protein
<i>rpsE</i>	1.54	2.17E-06	30S ribosomal subunit protein S5
<i>yihN</i>	-1.53	1.78E-03	inner membrane protein, predicted transporter
<i>cynS</i>	1.53	4.92E-03	cyanate aminohydrolase
<i>yiaS</i>	1.53	2.47E-03	L-ribulose-5-phosphate 4-epimerase
<i>pbpG</i>	1.53	1.64E-17	D-alanyl-D-alanine endopeptidase
<i>yegQ</i>	1.53	3.18E-18	putative peptidase
<i>wcaL</i>	1.53	1.45E-03	putative glycosyl transferase
<i>galU</i>	-1.53	9.52E-16	glucose-1-phosphate uridylyltransferase
<i>erpA</i>	-1.53	8.87E-14	iron-sulfur cluster insertion protein
<i>slmA</i>	-1.53	1.48E-13	DNA-binding anti-FtsZ division inhibitor
<i>slt</i>	1.53	3.34E-23	lytic murein transglycosylase, soluble
<i>yliI</i>	1.53	1.72E-10	soluble aldose sugar dehydrogenase
<i>yhfL</i>	-1.53	1.23E-02	small lipoprotein
<i>xerD</i>	1.53	9.23E-13	site-specific tyrosine recombinase
<i>cueO</i>	-1.53	2.77E-08	multicopper oxidase (laccase)
<i>cadC</i>	-1.53	1.35E-05	DNA-binding transcriptional activator
<i>crcB</i>	-1.53	4.56E-08	putative fluoride exporter; associated with chromosome condensation
<i>gabT</i>	1.53	3.36E-10	4-aminobutyrate aminotransferase, PLP-dependent
<i>yieP</i>	-1.53	3.99E-19	putative transcriptional regulator
<i>ynbC</i>	1.53	5.19E-04	putative hydrolase
<i>scpC</i>	1.53	1.82E-02	propionyl-CoA:succinate CoA transferase
<i>ydiU</i>	1.53	1.06E-17	conserved protein, UPF0061 family
<i>atpB</i>	-1.53	5.58E-15	F0 sector of membrane-bound ATP synthase, subunit a
<i>yjeJ</i>	-1.53	7.57E-05	hypothetical protein
<i>deoC</i>	1.53	7.13E-07	2-deoxyribose-5-phosphate aldolase, NAD(P)-linked
<i>yhhQ</i>	-1.52	3.83E-07	inner membrane protein, DUF165 family
<i>pepN</i>	1.52	7.07E-10	aminopeptidase N
<i>ybcW</i>	-1.52	8.78E-03	DLP12 prophage; putative protein
<i>ispU</i>	-1.52	1.06E-15	undecaprenyl pyrophosphate synthase
<i>ymiA</i>	1.52	3.31E-03	hypothetical protein
<i>yicS</i>	-1.52	1.93E-07	putative periplasmic protein
<i>arsB</i>	-1.52	7.97E-04	arsenite/antimonite transporter
<i>betB</i>	1.52	2.09E-10	betaine aldehyde dehydrogenase, NAD-dependent
<i>tfaX</i>	1.52	4.10E-02	pseudo
<i>alaS</i>	1.52	4.44E-17	alanyl-tRNA synthetase
<i>lspA</i>	1.52	4.48E-11	prolipoprotein signal peptidase (signal peptidase II)
<i>yfbP</i>	-1.52	3.53E-05	TPR-like repeats-containing protein
<i>yaaW</i>	-1.52	8.35E-03	conserved protein, UPF0174 family

<i>rpmI</i>	-1.52	5.57E-15	50S ribosomal subunit protein L35
<i>rpmF</i>	-1.52	7.09E-14	50S ribosomal subunit protein L32
<i>yoaB</i>	-1.52	1.45E-15	putative reactive intermediate deaminase
<i>dmsB</i>	-1.52	2.58E-02	dimethyl sulfoxide reductase, anaerobic, subunit B
<i>ribD</i>	1.52	1.65E-11	diaminohydroxyphosphoribosylaminopyrimidine deaminase
<i>yjgN</i>	-1.52	1.46E-02	inner membrane protein, DUF898 family
<i>yfcD</i>	-1.52	2.27E-19	putative NUDIX hydrolase
<i>chbC</i>	-1.52	2.33E-03	N,N'-diacetylchitobiose-specific enzyme IIC component of PTS
<i>trpA</i>	1.52	1.16E-11	tryptophan synthase, alpha subunit
<i>ymbA</i>	-1.52	8.87E-08	hypothetical protein
<i>yicC</i>	-1.52	5.68E-21	conserved protein, UPF0701 family
<i>tyrV</i>	-1.52	1.01E-07	tRNA
<i>asd</i>	-1.52	7.01E-16	aspartate-semialdehyde dehydrogenase, NAD(P)-binding
<i>yciK</i>	1.52	9.09E-10	putative oxoacyl-(acyl carrier protein) reductase, EmrKY-TolC system
<i>rplD</i>	1.51	8.79E-08	50S ribosomal subunit protein L4
<i>ycjG</i>	1.51	6.80E-11	L-Ala-D/L-Glu epimerase
<i>yhbX</i>	-1.51	2.03E-04	putative hydrolase, inner membrane
<i>folB</i>	-1.51	7.92E-05	bifunctional dihydroneopterin aldolase/dihydroneopterin triphosphate 2'-epimerase
<i>sfmA</i>	-1.51	3.43E-02	putative fimbrial-like adhesin protein
<i>aceB</i>	1.51	4.32E-12	malate synthase A
<i>yffJ</i>	-1.51	9.66E-03	CP4-57 prophage; putative protein
<i>iscU</i>	1.51	2.25E-13	iron-sulfur cluster assembly scaffold protein
<i>ygiN</i>	-1.51	6.03E-17	quinol monooxygenase
<i>rhyb</i>	-1.51	2.81E-20	5-aminolevulinate dehydratase (porphobilinogen synthase)
<i>hcaC</i>	-1.51	2.67E-15	CDP-diglyceride synthase
<i>yhjD</i>	-1.51	2.81E-08	putative alternate lipid exporter, suppressor of msbA and KDO essentiality
<i>mgo</i>	1.51	1.28E-05	malate dehydrogenase, FAD/NAD(P)-binding domain
<i>rseB</i>	1.51	2.37E-17	anti-sigma E factor, binds RseA
<i>fdhE</i>	1.51	1.30E-15	formate dehydrogenase formation protein
<i>yfbO</i>	-1.51	6.84E-03	hypothetical protein
<i>fbaA</i>	1.51	5.87E-16	fructose-bisphosphate aldolase, class II
<i>iraD</i>	-1.50	8.19E-05	RpoS stabilizer after DNA damage, anti-RssB factor
<i>yeeW</i>	-1.50	2.05E-02	pseudo
<i>frsA</i>	1.50	9.41E-11	fermentation-respiration switch protein; PTS Enzyme IIA(Glc)-binding protein
<i>glyY</i>	-1.50	2.06E-07	tRNA
<i>eno</i>	1.50	8.88E-16	enolase
<i>degQ</i>	-1.50	6.22E-14	serine endoprotease, periplasmic
<i>lsrF</i>	1.50	8.53E-04	putative autoinducer-2 (AI-2) aldolase
<i>ydhQ</i>	-1.50	5.38E-07	hypothetical protein
<i>yhaV</i>	-1.50	1.91E-15	toxin of the SohB(PrIF)-YhaV toxin-antitoxin system
<i>fdoH</i>	1.50	2.41E-06	formate dehydrogenase-O, Fe-S subunit
<i>yffT</i>	1.50	3.33E-02	CP4-57 prophage; putative protein
<i>yfcV</i>	2.88	1.40E-01	putative fimbrial-like adhesin protein

<i>yobI</i>	-1.96	1.40E-01	hypothetical protein
<i>ppdA</i>	1.93	5.94E-02	hypothetical protein
<i>paaF</i>	1.93	6.28E-02	2,3-dehydroadipyl-CoA hydratase
<i>psuK</i>	-1.91	8.97E-02	pseudouridine kinase
<i>rcbA</i>	1.89	6.84E-02	double-strand break reduction protein, Rac prophage
<i>hyfD</i>	1.88	7.75E-02	hydrogenase 4, membrane subunit
<i>stfP</i>	1.83	5.74E-02	e14 prophage; putative protein
<i>fliI</i>	1.80	9.37E-02	flagellum-specific ATP synthase
<i>ydfD</i>	-1.80	2.33E-01	Qin prophage; putative protein
<i>elfD</i>	1.77	7.68E-02	putative periplasmic pilin chaperone
<i>exoD</i>	1.77	6.63E-02	pseudo
<i>ebgC</i>	1.77	1.16E-01	cryptic beta-D-galactosidase, beta subunit
<i>insHI</i>	-1.74	1.07E-01	IS5 transposase and trans-activator
<i>yffM</i>	-1.74	7.77E-02	CPZ-55 prophage; putative protein
<i>yojO</i>	-1.73	3.30E-01	hypothetical protein
<i>sgcB</i>	1.72	8.25E-02	putative enzyme IIB component of PTS
<i>yncH</i>	1.72	8.70E-02	hypothetical protein
<i>asnV</i>	-1.71	1.34E-01	tRNA
<i>yghT</i>	-1.71	7.23E-02	putative ATP-binding protein
<i>yjiL</i>	1.71	5.82E-02	putative ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase
<i>thiQ</i>	-1.70	5.11E-02	thiamin transporter subunit
<i>araD</i>	1.69	5.23E-02	L-ribulose-5-phosphate 4-epimerase
<i>thiF</i>	1.68	6.94E-02	adenylyltransferase, modifies ThiS C-terminus
<i>ssnA</i>	1.67	1.78E-01	putative chlorohydrolase/aminohydrolase
<i>nrfD</i>	-1.67	1.20E-01	formate-dependent nitrite reductase, membrane subunit
<i>gspG</i>	-1.66	1.78E-01	pseudopilin, cryptic, general secretion pathway
<i>yhaB</i>	-1.65	2.50E-01	hypothetical protein
<i>yahF</i>	1.65	6.65E-02	putative acyl-CoA synthetase and succinyl-CoA synthetase domain
<i>dsrA</i>	-1.65	3.16E-01	ncRNA
<i>mhpB</i>	1.64	1.78E-01	2,3-dihydroxyphenylpropionate 1,2-dioxygenase
<i>yfaH</i>	-1.63	1.06E-01	pseudo
<i>stfQ</i>	1.63	9.73E-02	Qin prophage; predicted side tail fiber assembly protein
<i>fliN</i>	1.62	3.34E-01	flagellar motor switching and energizing component
<i>aaeX</i>	-1.62	1.88E-01	membrane protein of efflux system
<i>yfcP</i>	1.62	5.92E-02	putative fimbrial-like adhesin protein
<i>ygbL</i>	1.61	5.48E-02	putative class II aldolase
<i>ygiZ</i>	1.60	3.78E-01	inner membrane protein
<i>hcaC</i>	1.60	8.48E-02	3-phenylpropionate dioxygenase, predicted ferredoxin subunit
<i>paaG</i>	1.59	2.09E-01	1,2-epoxyphenylacetyl-CoA isomerase, oxepin-CoA-forming
<i>ykfM</i>	1.59	7.53E-02	hypothetical protein
<i>yceO</i>	1.59	1.92E-01	hypothetical protein
<i>stfE</i>	1.59	1.90E-01	pseudo
<i>yhfX</i>	1.59	9.96E-02	putative amino acid racemase

<i>phnN</i>	1.58	1.14E-01	ribose 1,5-bisphosphokinase
<i>pinQ</i>	1.58	1.77E-01	Qin prophage; predicted site-specific recombinase
<i>yhjH</i>	1.57	2.09E-01	cyclic-di-GMP phosphodiesterase, FlhDC-regulated
<i>tfaR</i>	1.57	2.95E-01	Rac prophage; predicted tail fiber assembly protein
<i>ygiJ</i>	1.57	3.94E-01	hypothetical protein
<i>yiaQ</i>	1.57	2.47E-01	3-keto-L-gulonate 6-phosphate decarboxylase
<i>motB</i>	1.56	1.78E-01	protein that enables flagellar motor rotation
<i>hyaB</i>	1.55	1.77E-01	hydrogenase 1, large subunit
<i>ybeU</i>	1.55	1.36E-01	conserved protein, DUF1266 family
<i>yccM</i>	-1.55	5.92E-02	putative 4Fe-4S membrane protein
<i>yhiS</i>	1.55	6.57E-02	pseudo
<i>ygaQ</i>	1.54	1.07E-01	pseudo
<i>yegK</i>	1.54	2.24E-01	hypothetical protein
<i>agaB</i>	1.53	1.86E-01	N-acetylgalactosamine-specific enzyme IIB component of PTS
<i>ykgO</i>	-1.53	9.94E-02	RpmJ-like protein
<i>rhaB</i>	1.52	2.62E-01	rhamnulokinase
<i>afuC</i>	1.52	6.16E-02	CP4-6 prophage; predicted ferric transporter subunit
<i>ygfK</i>	1.52	7.82E-02	putative oxidoreductase, Fe-S subunit
<i>fliH</i>	1.52	1.95E-01	negative regulator of Flil ATPase activity
<i>ppdB</i>	1.52	8.97E-02	hypothetical protein
<i>ycjN</i>	1.51	2.24E-01	putative sugar transporter subunit: periplasmic-binding component of ABC superfamily
<i>yrhA</i>	1.51	2.38E-01	pseudo
<i>glcE</i>	1.50	5.11E-02	glycolate oxidase FAD binding subunit
<i>ydaY</i>	1.50	8.82E-02	pseudo
<i>pykF</i>	1.50	1.87E-14	pyruvate kinase I
<i>sdiA</i>	1.50	6.25E-10	quorum-sensing transcriptional activator
<i>yigF</i>	-1.50	8.81E-04	putative inner membrane protein
<i>glyU</i>	1.50	3.20E-03	tRNA
<i>ygdD</i>	-1.50	7.80E-04	inner membrane protein, UPF0382 family
<i>yeaG</i>	1.50	9.67E-11	protein kinase, function unknown; autokinase
<i>yegP</i>	-1.50	3.28E-13	conserved protein, UPF0339 family
<i>lyxK</i>	1.50	7.25E-02	L-xylulose kinase
<i>gluS</i>	-1.50	2.15E-13	glutamate transporter
<i>yadS</i>	-1.50	1.87E-06	inner membrane protein, UPF0126 family
<i>ilvD</i>	1.50	2.61E-06	dihydroxyacid dehydratase
<i>ldrB</i>	1.50	7.18E-03	toxic polypeptide, small
<i>relB</i>	1.50	1.31E-11	Qin prophage; bifunctional antitoxin of the RelE-RelB toxin-antitoxin system
<i>glcA</i>	-1.50	3.01E-09	glycolate transporter
<i>yibT</i>	-1.49	5.73E-13	hypothetical protein
<i>fadI</i>	-1.49	2.67E-05	beta-ketoacyl-CoA thiolase, anaerobic, subunit
<i>ycjX</i>	1.49	1.33E-09	conserved protein with nucleoside triphosphate hydrolase domain
<i>yjhX</i>	-1.49	1.38E-02	hypothetical protein
<i>thrB</i>	1.49	1.70E-11	homoserine kinase

<i>asr</i>	1.49	6.16E-04	acid shock-inducible periplasmic protein
<i>ypdC</i>	1.49	9.12E-06	putative DNA-binding protein
<i>yegJ</i>	-1.49	1.33E-02	hypothetical protein
<i>mdtO</i>	1.49	1.23E-01	membrane translocase (MDR) of MdtNOP efflux pump, PET family
<i>oppD</i>	1.49	3.66E-04	oligopeptide transporter subunit
<i>lrhA</i>	1.49	3.86E-15	DNA-binding transcriptional repressor of flagellar, motility and chemotaxis genes
<i>folX</i>	-1.49	9.16E-16	D-erythro-7,8-dihydroneopterin triphosphate 2'-epimerase and dihydroneopterin aldolase
<i>yohF</i>	-1.49	1.21E-04	putative oxidoreductase with NAD(P)-binding Rossmann-fold domain
<i>ydfZ</i>	-1.49	4.65E-04	selenoprotein, function unknown
<i>leuL</i>	1.49	2.12E-05	leu operon leader peptide
<i>ylbE</i>	1.49	8.01E-02	pseudo
<i>ptsP</i>	1.49	2.75E-11	PEP-protein phosphotransferase (enzyme I)/GAF domain containing protein
<i>mutT</i>	-1.49	3.22E-04	nucleoside triphosphate pyrophosphohydrolase, marked preference for dGTP
<i>loiP</i>	-1.49	2.57E-14	Phe-Phe periplasmic metalloprotease, OM lipoprotein; heat shock protein that binds Era
<i>cca</i>	1.49	2.63E-17	tRNA nucleotidyl transferase/2'3'-cyclic phosphodiesterase/2'nucleotidase and phosphatase
<i>eptB</i>	1.49	5.69E-10	KDO phosphoethanolamine transferase, Ca(2+)-inducible
<i>hokE</i>	1.49	2.29E-01	toxic polypeptide, small
<i>ggt</i>	-1.49	1.27E-10	gamma-glutamyltranspeptidase
<i>bfd</i>	1.49	7.53E-11	bacterioferritin-associated ferredoxin
<i>pepD</i>	1.49	9.62E-19	aminoacyl-histidine dipeptidase (peptidase D)
<i>glpX</i>	-1.49	8.85E-11	fructose 1,6-bisphosphatase II
<i>alaC</i>	1.48	5.61E-08	valine-pyruvate aminotransferase 3
<i>rplL</i>	-1.48	2.08E-18	50S ribosomal subunit protein L7/L12
<i>dnaJ</i>	1.48	2.26E-11	chaperone Hsp40, co-chaperone with DnaK
<i>dut</i>	-1.48	6.53E-17	deoxyuridinetriphosphatase
<i>yhjV</i>	-1.48	2.20E-07	putative transporter
<i>yeaD</i>	1.48	5.63E-08	hypothetical protein
<i>ydeO</i>	-1.48	9.50E-03	UV-inducible global regulator, EvgA-, GadE-dependent
<i>rpmD</i>	1.48	2.80E-07	50S ribosomal subunit protein L30
<i>ydiS</i>	1.48	6.49E-02	putative oxidoreductase with FAD/NAD(P)-binding domain
<i>acrZ</i>	-1.48	1.02E-08	AcrAB-TolC efflux pump accessory protein, membrane-associated
<i>yejH</i>	1.48	8.27E-08	putative ATP-dependent DNA or RNA helicase
<i>ydaW</i>	1.48	1.51E-02	pseudo
<i>hha</i>	-1.48	5.10E-16	modulator of gene expression, with H-NS
<i>nmpC</i>	-1.48	2.49E-13	pseudo
<i>ycjS</i>	1.48	7.17E-02	putative oxidoreductase, NADH-binding
<i>yqiC</i>	-1.48	3.40E-15	hypothetical protein
<i>degS</i>	-1.48	5.38E-13	serine endoprotease, periplasmic
<i>yciG</i>	-1.48	8.36E-10	hypothetical protein
<i>nuoC</i>	-1.48	2.90E-14	NADH:ubiquinone oxidoreductase, fused CD subunit
<i>ycaM</i>	-1.48	7.42E-03	putative transporter
<i>yqgB</i>	-1.48	8.09E-07	hypothetical protein
<i>ysgA</i>	-1.47	9.94E-14	putative hydrolase

<i>yphE</i>	1.47	8.39E-02	fused predicted sugar transporter subunits of ABC superfamily: ATP-binding components
<i>crp</i>	-1.47	3.96E-09	DNA-binding transcriptional dual regulator
<i>wzzB</i>	-1.47	2.57E-17	regulator of length of O-antigen component of lipopolysaccharide chains
<i>gntU</i>	-1.47	4.78E-03	gluconate transporter, low affinity GNT 1 system
<i>tynA</i>	1.47	2.82E-05	tyramine oxidase, copper-requiring
<i>rplE</i>	1.47	2.02E-08	50S ribosomal subunit protein L5
<i>yafT</i>	-1.47	1.19E-02	lipoprotein
<i>yhjJ</i>	1.47	1.36E-15	putative zinc-dependent peptidase
<i>rpmC</i>	1.47	2.27E-05	50S ribosomal subunit protein L29
<i>lpd</i>	1.47	3.81E-08	lipoamide dehydrogenase, E3 component is part of three enzyme complexes
<i>rpoA</i>	1.47	2.34E-08	RNA polymerase, alpha subunit
<i>yihS</i>	1.47	6.02E-02	aldose-ketose isomerase; D-mannose isomerase
<i>abgT</i>	1.47	8.34E-03	p-aminobenzoyl-glutamate transporter; membrane protein
<i>pphB</i>	1.47	1.24E-02	serine/threonine-specific protein phosphatase 2
<i>ygfZ</i>	1.47	5.13E-15	iron-sulfur cluster repair protein, plumbagin resistance
<i>ydiQ</i>	1.47	1.88E-01	putative electron transfer flavoprotein subunit
<i>yahO</i>	-1.47	1.50E-10	periplasmic protein, function unknown, YhcN family
<i>dnaC</i>	1.47	1.59E-08	DNA biosynthesis protein
<i>fldB</i>	-1.47	4.40E-15	flavodoxin 2
<i>oppC</i>	1.47	1.26E-02	oligopeptide transporter subunit
<i>yceI</i>	-1.47	1.88E-10	secreted protein
<i>ydfG</i>	-1.47	2.69E-14	malonic semialdehyde reductase; L-allo-threonine dehydrogenase
<i>hisP</i>	-1.47	4.58E-09	histidine/lysine/arginine/ornithine transporter subunit
<i>sapC</i>	-1.47	2.40E-05	antimicrobial peptide transport ABC transporter permease
<i>sucB</i>	1.47	5.68E-06	dihydrolipoyltranssuccinase
<i>atoC</i>	1.47	7.72E-05	fused response regulator of ato operon, sigma54 interaction protein
<i>gtrS</i>	-1.47	3.29E-07	serotype-specific glucosyl transferase, CPS-53 (KpLE1) prophage
<i>aroK</i>	-1.47	9.26E-15	shikimate kinase I
<i>hda</i>	-1.47	2.50E-14	ATPase regulatory factor involved in DnaA inactivation
<i>rdgC</i>	-1.46	3.07E-13	nucleoid-associated ssDNA and dsDNA binding protein
<i>yqcC</i>	1.46	1.51E-03	hypothetical protein
<i>cpdA</i>	1.46	2.99E-16	3',5' cAMP phosphodiesterase
<i>frwB</i>	1.46	3.56E-01	putative enzyme IIB component of PTS
<i>rzpD</i>	1.46	2.03E-01	DLP12 prophage; predicted murein endopeptidase
<i>tufA</i>	1.46	4.60E-11	protein chain elongation factor EF-Tu (duplicate of tufB)
<i>yhhN</i>	-1.46	1.36E-13	putative inner membrane protein, TMEM86 family
<i>paaY</i>	-1.46	6.28E-10	putative hexapeptide repeat acetyltransferase
<i>ydeE</i>	1.46	9.59E-05	putative transporter
<i>treB</i>	-1.46	1.14E-11	fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component
<i>lysS</i>	1.46	1.92E-10	lysine tRNA synthetase, constitutive
<i>pliG</i>	-1.46	4.80E-12	hypothetical protein
<i>ibsC</i>	1.46	1.17E-01	toxic membrane protein
<i>uspB</i>	-1.46	4.04E-11	universal stress (ethanol tolerance) protein B

<i>yjiH</i>	1.46	3.39E-01	putative inner membrane protein
<i>ygcR</i>	1.46	3.22E-01	putative flavoprotein
<i>dcyD</i>	1.46	1.30E-09	D-cysteine desulfhydrase, PLP-dependent
<i>nanK</i>	1.46	5.14E-06	N-acetylmannosamine kinase
<i>gltW</i>	-1.46	1.95E-07	tRNA
<i>ybaZ</i>	1.46	1.14E-04	excision repair protein, alkyltransferase-like protein ATL
<i>ybdR</i>	1.46	9.38E-07	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>rfbA</i>	-1.46	4.44E-07	glucose-1-phosphate thymidyltransferase
<i>holA</i>	1.46	1.08E-12	DNA polymerase III, delta subunit
<i>stpA</i>	-1.46	7.82E-14	DNA binding protein, nucleoid-associated
<i>flgC</i>	-1.46	8.52E-01	flagellar component of cell-proximal portion of basal-body rod
<i>thiG</i>	1.46	1.13E-01	thiamin biosynthesis ThiGH complex subunit
<i>azoR</i>	1.46	2.49E-10	NADH-azoreductase, FMN-dependent
<i>nuoI</i>	-1.46	9.91E-09	NADH:ubiquinone oxidoreductase, chain I
<i>thiP</i>	-1.46	1.37E-01	fused thiamin transporter subunits of ABC superfamily: membrane components
<i>yphB</i>	1.46	1.85E-03	hypothetical protein
<i>yfcR</i>	1.46	2.05E-01	putative fimbrial-like adhesin protein
<i>priA</i>	1.46	1.11E-09	Primosome factor n' (replication factor Y)
<i>rpsP</i>	-1.46	5.20E-14	30S ribosomal subunit protein S16
<i>gnsB</i>	1.46	3.18E-05	Qin prophage; multicopy suppressor of secG(Cs) and fabA6(Ts)
<i>pheL</i>	1.46	1.57E-07	pheA gene leader peptide
<i>ftsP</i>	1.45	2.23E-13	septal ring component that protects the divisome from stress; multicopy suppressor of ftsI(T)
<i>fabI</i>	-1.45	1.65E-15	enoyl-[acyl-carrier-protein] reductase, NADH-dependent
<i>yhaL</i>	-1.45	7.78E-06	hypothetical protein
<i>ycdT</i>	-1.45	2.18E-06	diguanylate cyclase, membrane-anchored
<i>bsmA</i>	-1.45	2.82E-05	biofilm peroxide resistance protein
<i>pflC</i>	1.45	9.84E-02	pyruvate formate lyase II activase
<i>fic</i>	-1.45	3.08E-07	stationary-phase adenosine monophosphate-protein transferase domain protein
<i>rbbA</i>	-1.45	2.38E-09	fused ribosome-associated ATPase: ATP-binding protein/predicted membrane protein
<i>purP</i>	-1.45	3.39E-12	adenine permease, high affinity; adenine:H ⁺ symporter
<i>wcaJ</i>	-1.45	7.24E-02	colanic biosynthesis UDP-glucose lipid carrier transferase
<i>yiaF</i>	-1.45	7.44E-15	hypothetical protein
<i>frdB</i>	-1.45	2.98E-06	fumarate reductase (anaerobic), Fe-S subunit
<i>yhbY</i>	-1.45	6.48E-14	RNA binding protein associated with pre-50S ribosomal subunits
<i>yifK</i>	-1.45	1.92E-15	putative transporter
<i>blc</i>	-1.45	7.30E-10	outer membrane lipoprotein (lipocalin), cell division and growth function
<i>lpxK</i>	-1.45	4.92E-10	lipid A 4'kinase
<i>ygfT</i>	1.45	1.83E-02	fused predicted oxidoreductase: Fe-S subunit/nucleotide-binding subunit
<i>patA</i>	1.45	4.72E-09	putrescine:2-oxoglutaric acid aminotransferase, PLP-dependent
<i>aldA</i>	-1.45	1.04E-06	aldehyde dehydrogenase A, NAD-linked
<i>yaaJ</i>	-1.45	6.37E-05	putative transporter
<i>atpE</i>	-1.45	5.37E-07	F0 sector of membrane-bound ATP synthase, subunit c
<i>feoC</i>	-1.45	3.18E-06	putative DNA-binding transcriptional regulator

<i>emrE</i>	-1.45	1.19E-05	DLP12 prophage; multidrug resistance protein
<i>yhjB</i>	-1.45	9.74E-05	putative response regulator, LuxR-like HTH domain, function unknown
<i>ygcN</i>	-1.45	1.03E-03	putative oxidoreductase with FAD/NAD(P)-binding domain
<i>waaA</i>	-1.45	3.28E-13	3-deoxy-D-manno-octulosonic-acid transferase (KDO transferase)
<i>chpS</i>	-1.45	5.73E-02	antitoxin of the ChpBS toxin-antitoxin system
<i>ycbZ</i>	1.45	4.98E-15	putative peptidase
<i>ybgO</i>	-1.45	3.38E-02	putative fimbrial-like adhesin protein
<i>flgM</i>	1.45	4.06E-03	anti-sigma factor for FlhA (sigma 28)
<i>yjfl</i>	1.45	1.35E-01	conserved protein, DUF2170 family
<i>rluE</i>	1.45	1.31E-06	23S rRNA pseudouridine(2457) synthase
<i>exoX</i>	1.45	6.14E-11	exodeoxyribonuclease 10; DNA exonuclease X
<i>thrT</i>	-1.45	5.34E-14	tRNA
<i>ygeG</i>	1.45	2.79E-01	putative chaperone
<i>ydjX</i>	1.44	4.13E-02	inner membrane protein, TVP38/TMEM64 family
<i>bssR</i>	1.44	8.04E-07	repressor of biofilm formation by indole transport regulation
<i>yhdT</i>	-1.44	1.04E-01	conserved inner membrane protein
<i>fkpA</i>	-1.44	9.46E-13	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
<i>sgcR</i>	1.44	3.39E-03	KpLE2 phage-like element; predicted DNA-binding transcriptional regulator
<i>asnA</i>	-1.44	3.62E-03	asparagine synthetase A
<i>yfaS</i>	1.44	2.24E-03	pseudo
<i>yfcZ</i>	-1.44	1.81E-08	conserved protein, UPF0381 family
<i>xapB</i>	1.44	7.80E-04	xanthosine transporter
<i>vsr</i>	1.44	1.31E-04	DNA mismatch endonuclease of very short patch repair
<i>pqiB</i>	-1.44	5.71E-11	paraquat-inducible protein B
<i>ydjH</i>	1.44	4.94E-02	putative kinase
<i>bioD</i>	1.44	3.24E-10	dethiobiotin synthetase
<i>waaM</i>	-1.44	1.13E-11	lauryl-acyl carrier protein (ACP)-dependent acyltransferase
<i>thrW</i>	-1.44	4.97E-06	tRNA
<i>wecG</i>	-1.44	8.00E-07	UDP-N-acetyl-D-mannosaminuronic acid transferase
<i>bcsF</i>	1.44	9.84E-03	hypothetical protein
<i>hemD</i>	1.44	6.75E-12	uroporphyrinogen III synthase
<i>aspS</i>	1.44	2.44E-08	aspartyl-tRNA synthetase
<i>wza</i>	-1.44	3.43E-02	lipoprotein required for capsular polysaccharide translocation through the outer membrane
<i>fsaA</i>	-1.44	1.40E-03	fructose-6-phosphate aldolase 1
<i>yciE</i>	-1.44	1.20E-06	putative rubrerythrin/ferritin-like metal-binding protein
<i>hisJ</i>	-1.44	6.09E-13	histidine/lysine/arginine/ornithine transporter subunit
<i>mdtL</i>	-1.44	2.80E-02	multidrug efflux system protein
<i>wcaC</i>	1.44	1.11E-01	putative glycosyl transferase
<i>fdnH</i>	1.44	1.27E-01	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible
<i>cbrC</i>	-1.44	1.41E-03	conserved protein, UPF0167 family
<i>udp</i>	-1.44	4.22E-12	uridine phosphorylase
<i>gcl</i>	1.44	7.21E-03	glyoxylate carboligase
<i>cysM</i>	-1.44	2.07E-05	cysteine synthase B (O-acetylserine sulfhydrylase B)

<i>gutQ</i>	-1.44	4.74E-07	D-arabinose 5-phosphate isomerase
<i>napB</i>	-1.44	1.52E-01	nitrate reductase, small, cytochrome C550 subunit, periplasmic
<i>ydjE</i>	-1.44	2.92E-02	putative transporter
<i>higB</i>	-1.44	1.44E-02	mRNA interferase toxin of the HigB-HigA toxin-antitoxin system
<i>fliE</i>	1.44	2.98E-01	flagellar basal-body component
<i>gtrA</i>	-1.44	4.65E-09	CPS-53 (KpLE1) prophage; bactoprenol-linked glucose translocase (flippase)
<i>cbpA</i>	-1.43	2.49E-13	curved DNA-binding protein, DnaJ homologue that functions as a co-chaperone of DnaK
<i>minD</i>	-1.43	5.94E-15	membrane ATPase of the MinC-MinD-MinE system
<i>ybhG</i>	1.43	5.44E-05	putative membrane fusion protein (MFP) component of efflux pump, membrane anchor
<i>puuR</i>	-1.43	7.04E-05	DNA-binding transcriptional repressor for the puu divergon
<i>yiaA</i>	-1.43	1.22E-01	inner membrane protein, YiaAB family
<i>paaH</i>	1.43	1.22E-01	3-hydroxyadipyl-CoA dehydrogenase, NAD ⁺ -dependent
<i>yacL</i>	-1.43	2.14E-04	hypothetical protein
<i>rfbB</i>	-1.43	2.65E-12	dTDP-glucose 4,6 dehydratase, NAD(P)-binding
<i>add</i>	-1.43	2.81E-05	adenosine deaminase
<i>ybcL</i>	1.43	3.53E-03	DLP12 prophage; secreted protein, UPF0098 family
<i>oppB</i>	1.43	2.01E-02	oligopeptide transporter subunit
<i>fadH</i>	-1.43	1.06E-03	2,4-dienoyl-CoA reductase, NADH and FMN-linked
<i>yfaQ</i>	1.43	3.52E-02	tandem DUF2300 domain protein, function unknown
<i>amn</i>	1.43	1.52E-16	AMP nucleosidase
<i>yqiK</i>	-1.43	3.72E-02	PHB family membrane protein, function unknown
<i>bhsA</i>	1.43	1.80E-06	biofilm, cell surface and signaling protein
<i>anmK</i>	1.43	8.57E-09	anhydro-N-acetylmuramic acid kinase
<i>mglA</i>	-1.43	1.12E-05	fused methyl-galactoside transporter subunits of ABC superfamily: ATP-binding component
<i>glmS</i>	-1.43	1.56E-14	L-glutamine:D-fructose-6-phosphate aminotransferase
<i>rnr</i>	1.43	4.10E-09	exoribonuclease R, RNase R
<i>secY</i>	1.43	7.15E-06	preprotein translocase membrane subunit
<i>glyW</i>	-1.43	8.28E-06	tRNA
<i>psiE</i>	1.43	1.14E-04	phosphate starvation inducible protein
<i>ydiV</i>	-1.43	1.42E-08	anti-FlhD4C2 factor, inactive EAL family phosphodiesterase
<i>ohsC</i>	-1.43	4.26E-01	ncRNA
<i>sgcE</i>	1.43	1.40E-02	KpLE2 phage-like element; predicted epimerase
<i>yjgA</i>	-1.43	1.01E-09	conserved protein, ribosome-associated
<i>hflD</i>	1.43	5.61E-12	putative lysogenization regulator
<i>mukB</i>	1.43	2.60E-15	chromosome condensin MukBEF, ATPase and DNA-binding subunit
<i>yjbF</i>	1.43	1.91E-01	putative lipoprotein
<i>fliS</i>	1.43	2.60E-01	flagellar protein potentiates polymerization
<i>yeiS</i>	-1.43	4.44E-04	conserved protein, DUF2542 family
<i>fxsA</i>	-1.43	5.94E-05	suppressor of F exclusion of phage T7
<i>trg</i>	1.43	3.02E-04	methyl-accepting chemotaxis protein III, ribose and galactose sensor receptor
<i>ybhN</i>	-1.43	1.06E-04	conserved inner membrane protein
<i>mfd</i>	1.43	1.53E-15	transcription-repair coupling factor
<i>ugpE</i>	-1.42	9.98E-03	glycerol-3-phosphate transporter subunit

<i>yaaU</i>	1.42	2.90E-01	putative transporter
<i>napF</i>	-1.42	2.17E-01	ferredoxin-type protein, role in electron transfer to periplasmic nitrate reductase NapA
<i>wcaK</i>	1.42	1.60E-02	colanic acid biosynthesis protein
<i>yecH</i>	-1.42	8.96E-05	DUF2492 family protein, function unknown
<i>frdD</i>	-1.42	3.99E-05	fumarate reductase (anaerobic), membrane anchor subunit
<i>yegV</i>	1.42	2.20E-03	putative kinase
<i>yaiL</i>	-1.42	5.99E-06	hypothetical protein
<i>mpaA</i>	1.42	2.98E-10	murein peptide amidase A
<i>ycbK</i>	1.42	3.65E-13	hypothetical protein
<i>yjeO</i>	-1.42	1.69E-01	inner membrane protein
<i>yjhI</i>	1.42	1.66E-01	KpLE2 phage-like element; predicted DNA-binding transcriptional regulator
<i>smf</i>	1.42	2.89E-07	hypothetical protein
<i>recE</i>	1.42	1.24E-02	Rac prophage; exonuclease VIII, 5' -> 3' specific dsDNA exonuclease
<i>cfa</i>	1.42	1.64E-13	cyclopropane fatty acyl phospholipid synthase (unsaturated-phospholipid methyltransferase)
<i>wzyE</i>	-1.42	5.95E-06	putative Wzy protein involved in ECA polysaccharide chain elongation
<i>yjtD</i>	-1.42	1.07E-05	putative methyltransferase
<i>lysT</i>	-1.42	7.64E-05	tRNA
<i>sokB</i>	-1.42	1.54E-01	ncRNA
<i>yidI</i>	-1.42	2.19E-03	inner membrane protein
<i>yfdE</i>	-1.42	6.24E-03	putative CoA-transferase, NAD(P)-binding
<i>yagP</i>	1.42	3.91E-01	pseudo
<i>yafJ</i>	1.42	4.02E-13	putative amidotransferase
<i>pspF</i>	1.42	6.08E-06	DNA-binding transcriptional activator
<i>ttcC</i>	1.42	1.79E-02	pseudo
<i>dacB</i>	1.42	2.20E-13	D-alanyl-D-alanine carboxypeptidase
<i>kdpD</i>	1.42	3.07E-11	fused sensory histidine kinase with KdpE: signal sensing protein
<i>dsdC</i>	-1.42	8.95E-06	DNA-binding transcriptional dual regulator
<i>rpsQ</i>	1.42	4.28E-06	30S ribosomal subunit protein S17
<i>atoB</i>	1.42	6.12E-02	acetyl-CoA acetyltransferase
<i>rplC</i>	1.42	2.23E-07	50S ribosomal subunit protein L3
<i>yggR</i>	1.42	3.67E-01	putative pilus retraction ATPase
<i>recD</i>	1.42	1.18E-08	exonuclease V (RecBCD complex), alpha chain
<i>ybhA</i>	-1.42	1.85E-08	pyridoxal phosphate (PLP) phosphatase
<i>tufB</i>	-1.42	4.05E-09	protein chain elongation factor EF-Tu (duplicate of tufA)
<i>rne</i>	1.41	2.08E-12	fused ribonucleaseE: endoribonuclease/ RNA degradosome binding protein
<i>elfA</i>	-1.41	9.81E-03	putative fimbrial-like adhesin protein
<i>gapA</i>	1.41	1.33E-08	glyceraldehyde-3-phosphate dehydrogenase A
<i>ybjF</i>	1.41	6.95E-09	acyl-CoA esterase
<i>secE</i>	-1.41	3.48E-09	preprotein translocase membrane subunit
<i>adiY</i>	1.41	9.39E-02	DNA-binding transcriptional activator
<i>cysT</i>	-1.41	1.15E-04	tRNA
<i>pgaA</i>	-1.41	3.36E-04	biofilm adhesin polysaccharide PGA secretin; OM porin
<i>pfkA</i>	1.41	3.40E-15	6-phosphofructokinase I

<i>mhpA</i>	1.41	1.77E-01	3-(3-hydroxyphenyl)propionate hydroxylase
<i>thrL</i>	1.41	5.71E-04	thr operon leader peptide
<i>radA</i>	1.41	1.37E-09	DNA repair protein
<i>xanQ</i>	-1.41	4.25E-02	xanthine permease
<i>purL</i>	1.41	2.08E-12	phosphoribosylformyl-glycineamide synthetase
<i>spoT</i>	1.41	8.80E-15	(p)ppGpp synthetase II/ guanosine-3',5'-bis pyrophosphate 3'-pyrophosphohydrolase
<i>glnD</i>	1.41	1.24E-09	uridylyltransferase
<i>yhfW</i>	-1.41	2.52E-01	putative mutase
<i>pykA</i>	1.41	4.54E-11	pyruvate kinase II
<i>yajC</i>	-1.41	2.01E-13	SecYEG protein translocase auxillary subunit
<i>hyaF</i>	1.41	3.83E-02	protein involved in nickel incorporation into hydrogenase-1 proteins
<i>yecS</i>	1.41	8.43E-07	predicted transporter subunit: membrane component of ABC superfamily
<i>rsmG</i>	-1.41	8.10E-08	16S rRNA m(7)G527 methyltransferase; glucose-inhibited cell-division protein
<i>menA</i>	-1.41	4.23E-07	1,4-dihydroxy-2-naphthoate octaprenyltransferase
<i>rcdA</i>	-1.41	3.16E-03	putative DNA-binding transcriptional regulator
<i>fumB</i>	-1.41	2.87E-02	anaerobic class I fumarate hydratase (fumarase B)
<i>narG</i>	1.41	2.23E-03	nitrate reductase 1, alpha subunit
<i>paoD</i>	1.41	7.19E-02	moco insertion factor for PaoABC aldehyde oxidoreductase
<i>wzxE</i>	-1.41	1.01E-05	O-antigen translocase
<i>yfdT</i>	-1.41	4.92E-01	CPS-53 (KpLE1) prophage; putative protein
<i>paoB</i>	1.41	1.22E-01	PaoABC aldehyde oxidoreductase, FAD-containing subunit
<i>dcm</i>	1.41	1.90E-12	DNA cytosine methyltransferase
<i>yliE</i>	-1.41	8.08E-06	putative membrane-anchored cyclic-di-GMP phosphodiesterase
<i>chrR</i>	-1.41	2.73E-10	chromate reductase, Class I, flavoprotein
<i>ylbG</i>	1.41	2.61E-04	pseudo
<i>ycjT</i>	1.41	5.73E-02	putative hydrolase
<i>micF</i>	-1.41	2.91E-01	ncRNA
<i>mdaB</i>	-1.41	3.65E-07	NADPH quinone reductase
<i>nfrA</i>	1.41	6.34E-08	bacteriophage N4 receptor, outer membrane subunit
<i>ybaO</i>	1.41	1.02E-02	putative DNA-binding transcriptional regulator
<i>ybdJ</i>	-1.41	1.74E-03	putative inner membrane protein
<i>ulaA</i>	-1.41	1.57E-01	L-ascorbate-specific enzyme IIC component of PTS
<i>mdtM</i>	-1.41	1.77E-03	multidrug efflux system protein
<i>ftsW</i>	-1.41	1.14E-06	lipid II flippase; stabilizes FstZ ring during cell division
<i>fliT</i>	1.41	3.81E-01	putative chaperone
<i>gpmA</i>	1.41	3.40E-07	phosphoglyceromutase 1
<i>ampE</i>	-1.40	3.30E-08	putative inner membrane protein
<i>wecF</i>	-1.40	1.82E-09	TDP-Fuc4NAc:lipidIIFuc4NAc transferase
<i>yciX</i>	1.40	4.93E-06	hypothetical protein
<i>yobA</i>	-1.40	8.08E-10	hypothetical protein
<i>prmB</i>	1.40	7.21E-12	N5-glutamine methyltransferase
<i>ydgK</i>	-1.40	8.04E-10	inner membrane protein, DUF2569 family
<i>fnrS</i>	1.40	1.19E-02	ncRNA

<i>kdpA</i>	1.40	2.82E-01	potassium translocating ATPase, subunit A
<i>wzxB</i>	-1.40	1.25E-11	putative polisoprenol-linked O-antigen transporter
<i>hybD</i>	1.40	3.51E-04	maturation protease for hydrogenase 2
<i>pgm</i>	1.40	1.24E-13	phosphoglucomutase
<i>hsdS</i>	-1.40	1.24E-06	specificity determinant for hsdM and hsdR
<i>tnaC</i>	-1.40	5.36E-02	tryptophanase leader peptide
<i>dsdA</i>	1.40	2.72E-06	D-serine dehydratase
<i>talA</i>	1.40	8.60E-06	transaldolase A
<i>sodA</i>	-1.40	9.86E-06	superoxide dismutase, Mn
<i>mngB</i>	1.40	3.06E-05	alpha-mannosidase
<i>yhjA</i>	-1.40	2.66E-09	conserved protein, OsmC family
<i>acrR</i>	-1.40	4.77E-06	DNA-binding transcriptional repressor
<i>orn</i>	-1.40	6.05E-09	oligoribonuclease
<i>serA</i>	1.40	2.58E-06	D-3-phosphoglycerate dehydrogenase
<i>uxaB</i>	1.40	5.21E-04	altronate oxidoreductase, NAD-dependent
<i>ytjJ</i>	-1.40	3.67E-03	putative transcriptional regulator
<i>narP</i>	-1.40	5.57E-06	DNA-binding response regulator in two-component regulatory system with NarQ or NarX
<i>ygbE</i>	1.40	3.20E-06	DUF3561 family inner membrane protein
<i>rseC</i>	1.39	4.26E-07	RseC protein involved in reduction of the SoxR iron-sulfur cluster
<i>yneJ</i>	1.39	9.43E-06	putative DNA-binding transcriptional regulator
<i>yibI</i>	-1.39	1.26E-02	inner membrane protein, DUF3302 family
<i>ydcT</i>	1.39	8.91E-03	putative spermidine/putrescine transporter subunit
<i>yraI</i>	-1.39	4.08E-01	putative periplasmic pilin chaperone
<i>ydcO</i>	-1.39	1.28E-02	inner membrane protein, predicted transporter, function unknown
<i>yqfG</i>	1.39	4.02E-01	hypothetical protein
<i>glpB</i>	1.39	2.31E-01	sn-glycerol-3-phosphate dehydrogenase (anaerobic), membrane anchor subunit
<i>flhE</i>	1.39	4.15E-01	proton seal during flagellar secretion
<i>yjfiV</i>	1.39	1.69E-03	pseudo
<i>gspC</i>	-1.39	4.62E-02	general secretory pathway component, cryptic
<i>lsrA</i>	1.39	8.62E-02	autoinducer 2 import ATP-binding protein
<i>grxC</i>	-1.39	4.76E-07	glutaredoxin 3
<i>ycgI</i>	-1.39	1.23E-01	pseudo
<i>yjeV</i>	-1.39	1.11E-01	hypothetical protein
<i>yfdC</i>	-1.39	1.09E-04	putative inner membrane protein
<i>mokB</i>	1.39	1.15E-03	regulatory peptide
<i>nirD</i>	1.39	4.28E-01	nitrite reductase, NAD(P)H-binding, small subunit
<i>cvrA</i>	1.39	1.39E-07	putative cation/proton antiporter
<i>quuD</i>	-1.39	6.85E-02	DLP12 prophage; predicted antitermination protein
<i>yahJ</i>	1.39	1.56E-06	putative deaminase with metallo-dependent hydrolase domain
<i>hypC</i>	1.39	6.22E-01	protein required for maturation of hydrogenases 1 and 3
<i>yegL</i>	1.39	2.50E-01	hypothetical protein
<i>yrdB</i>	-1.39	1.14E-03	hypothetical protein
<i>yoeF</i>	-1.39	6.67E-02	pseudo

<i>narV</i>	-1.39	1.88E-02	nitrate reductase 2 (NRZ), gamma subunit
<i>yddE</i>	1.39	5.92E-08	conserved predicted enzyme, PhzC-PhzF family
<i>sgcA</i>	1.39	3.23E-02	KpLE2 phage-like element; predicted phosphotransferase enzyme IIA component
<i>hisS</i>	1.39	6.19E-12	histidyl tRNA synthetase
<i>hemC</i>	1.39	4.07E-07	hydroxymethylbilane synthase
<i>ynaI</i>	-1.39	3.01E-06	mechanosensitive channel protein, very small conductance
<i>rbsB</i>	-1.39	2.53E-05	D-ribose transporter subunit
<i>queD</i>	-1.39	5.43E-06	6-pyruvoyl tetrahydrobiopterin synthase (PTPS)
<i>ecpR</i>	-1.39	1.33E-02	putative regulator
<i>cydB</i>	1.38	3.40E-09	cytochrome d terminal oxidase, subunit II
<i>mnmE</i>	-1.38	4.53E-12	GTPase required for 5-methylaminomethyl-2-thiouridine modification at tRNA U34
<i>yeaI</i>	1.38	5.04E-02	putative membrane-anchored diguanylate cyclase
<i>curA</i>	-1.38	6.61E-04	curcumin/dihydrocurcumin reductase, NADPH-dependent
<i>ybhM</i>	-1.38	1.26E-02	inner membrane protein, UPF0005 family
<i>rnk</i>	-1.38	6.81E-08	regulator of nucleoside diphosphate kinase
<i>ycgV</i>	1.38	1.14E-06	putative adhesin
<i>apt</i>	-1.38	3.29E-09	adenine phosphoribosyltransferase
<i>xylF</i>	-1.38	6.67E-02	D-xylose transporter subunit
<i>yjhD</i>	1.38	9.69E-03	pseudo
<i>rtcA</i>	1.38	2.72E-03	RNA 3'-terminal phosphate cyclase
<i>yhcC</i>	1.38	1.13E-01	putative Fe-S oxidoreductase
<i>gatA</i>	-1.38	6.97E-08	galactitol-specific enzyme IIA component of PTS
<i>tyrT</i>	-1.38	5.44E-05	tRNA
<i>ytfL</i>	-1.38	2.96E-09	inner membrane protein, UPF0053 family
<i>yijO</i>	1.38	2.02E-03	putative DNA-binding transcriptional regulator
<i>cheA</i>	1.38	8.70E-02	i fused chemotactic sensory histidine kinase
<i>ccmD</i>	-1.38	2.93E-01	cytochrome c biogenesis protein
<i>yfgG</i>	1.38	6.92E-05	hypothetical protein
<i>intS</i>	-1.38	1.24E-05	CPS-53 (KpLE1) prophage; predicted prophage CPS-53 integrase
<i>trmA</i>	-1.38	1.47E-11	tRNA m(5)U54 methyltransferase, SAM-dependent
<i>fadB</i>	-1.38	7.36E-05	3-hydroxybutyryl-CoA epimerase/enoyl-CoA isomerase/enoyl-CoA hydratase
<i>gmd</i>	-1.38	1.18E-02	GDP-D-mannose dehydratase, NAD(P)-binding
<i>yibA</i>	-1.38	8.83E-04	putative lyase containing HEAT-repeat
<i>wecB</i>	-1.38	8.89E-08	UDP-N-acetyl glucosamine-2-epimerase
<i>yqeL</i>	1.38	4.57E-01	hypothetical protein
<i>yeiQ</i>	1.38	7.06E-07	putative D-mannonate oxidoreductase, NAD-dependent
<i>ygeK</i>	1.38	2.49E-01	pseudo
<i>ybbL</i>	-1.38	4.38E-05	putative transporter subunit: ATP-binding component of ABC superfamily
<i>rbsC</i>	-1.38	1.93E-05	D-ribose transporter subunit
<i>folA</i>	-1.38	2.29E-10	dihydrofolate reductase
<i>hisM</i>	-1.38	1.12E-05	histidine/lysine/arginine/ornithine transporter subunit
<i>yjiJ</i>	-1.38	2.40E-03	putative inner membrane protein
<i>yaiP</i>	-1.38	2.45E-02	putative glucosyltransferase

<i>kduD</i>	-1.38	1.51E-02	2-deoxy-D-gluconate 3-dehydrogenase
<i>cheB</i>	1.38	3.68E-01	fused chemotaxis regulator: protein-glutamate methylesterase
<i>yqiC</i>	-1.38	4.85E-07	hypothetical protein
<i>yqjH</i>	-1.38	1.47E-08	putative siderophore interacting protein
<i>cysI</i>	1.38	1.07E-08	sulfite reductase, beta subunit, NAD(P)-binding, heme-binding
<i>nth</i>	-1.38	2.65E-04	DNA glycosylase and apyrimidinic (AP) lyase (endonuclease III)
<i>yaiC</i>	-1.37	3.89E-02	diguanylate cyclase, cellulose regulator
<i>ycaK</i>	-1.37	2.47E-02	hypothetical protein
<i>fhuD</i>	-1.37	2.43E-05	iron-hydroxamate transporter subunit
<i>yghR</i>	1.37	3.98E-01	putative ATP-binding protein
<i>mepA</i>	1.37	3.00E-09	murein DD-endopeptidase
<i>pitB</i>	1.37	8.67E-02	phosphate transporter
<i>sgrR</i>	1.37	3.03E-04	transcriptional DNA-binding transcriptional activator of sgrS sRNA
<i>hybE</i>	1.37	6.99E-03	hydrogenase 2-specific chaperone
<i>grcA</i>	-1.37	1.43E-03	autonomous glycyl radical cofactor
<i>yfdQ</i>	1.37	2.53E-02	CPS-53 (KpLE1) prophage; putative protein
<i>hflK</i>	1.37	2.66E-12	modulator for HflB protease specific for phage lambda cII repressor
<i>epmA</i>	-1.37	8.37E-06	Elongation Factor P Lys34 lysyltransferase
<i>intF</i>	1.37	2.97E-12	CP4-6 prophage; predicted phage integrase
<i>yidD</i>	-1.37	1.28E-05	membrane protein insertion efficiency factor, inner membrane protein, UPF0161 family
<i>glcD</i>	1.37	4.48E-02	glycolate oxidase subunit, FAD-linked
<i>hsrA</i>	-1.37	4.76E-07	putative multidrug or homocysteine efflux system
<i>thiB</i>	-1.37	7.68E-03	thiamin transporter subunit
<i>yafD</i>	1.37	1.52E-11	hypothetical protein
<i>ais</i>	-1.37	3.64E-02	putative LPS core heptose(II)-phosphate phosphatase
<i>malT</i>	-1.37	3.67E-13	transcriptional activator for the mal regulon and maltotriose-ATP-binding protein
<i>sfsA</i>	-1.37	1.44E-06	putative DNA-binding transcriptional regulator
<i>rhtA</i>	-1.37	1.07E-02	threonine and homoserine efflux system
<i>garK</i>	1.37	3.33E-03	glycerate kinase I
<i>ydeN</i>	-1.37	5.91E-03	hypothetical protein
<i>xdhD</i>	1.37	6.59E-04	putative hypoxanthine oxidase, molybdopterin-binding/Fe-S binding
<i>nagD</i>	1.37	1.11E-11	UMP phosphatase
<i>yajR</i>	-1.37	1.17E-04	putative transporter
<i>lipB</i>	-1.37	3.96E-07	octanoyltransferase; octanoyl-[ACP]:protein N-octanoyltransferase
<i>ynfE</i>	1.37	1.33E-02	putative selenate reductase, periplasmic
<i>ybjE</i>	-1.37	3.14E-07	putative transporter
<i>oxc</i>	1.37	8.74E-03	oxalyl CoA decarboxylase, ThDP-dependent
<i>pauD</i>	1.37	1.37E-01	tRNA
<i>yeaN</i>	-1.37	3.18E-03	putative transporter
<i>araC</i>	1.37	7.51E-08	DNA-binding transcriptional dual regulator
<i>ydcD</i>	1.37	3.13E-02	hypothetical protein
<i>potD</i>	-1.37	1.82E-10	polyamine transporter subunit
<i>yjjM</i>	-1.37	2.71E-02	DNA-binding transcriptional activator for yjjMN; mutants fail to grow on L-galactonate

<i>emrK</i>	-1.37	1.87E-02	EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein component
<i>soxR</i>	1.37	1.70E-02	DNA-binding transcriptional dual regulator, Fe-S center for redox-sensing
<i>higA</i>	-1.37	2.43E-03	antitoxin of the HigB-HigA toxin-antitoxin system
<i>ptwF</i>	1.37	5.07E-02	tRNA
<i>yjfJ</i>	1.37	4.58E-01	conserved protein, PspA/IM30 family
<i>relE</i>	1.37	3.74E-08	Qin prophage; toxin of the RelE-RelB toxin-antitoxin system
<i>argP</i>	1.37	9.10E-11	DNA-binding transcriptional activator, replication initiation inhibitor
<i>yibG</i>	1.36	1.77E-01	hypothetical protein
<i>ycjV</i>	1.36	3.34E-01	pseudo
<i>yccB</i>	-1.36	1.49E-01	hypothetical protein
<i>mutL</i>	1.36	1.50E-11	methyl-directed mismatch repair protein
<i>ispG</i>	1.36	5.22E-11	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase
<i>insA</i>	1.36	6.04E-05	IS1 repressor TnpA
<i>yccF</i>	-1.36	1.26E-05	inner membrane protein, DUF307 family
<i>pgaB</i>	-1.36	3.77E-02	poly-beta-1,6-N-acetyl-D-glucosamine (PGA) N-deacetylase; deacetylase
<i>ykgR</i>	1.36	4.66E-01	hypothetical protein
<i>yneF</i>	1.36	9.67E-03	putative membrane-bound diguanylate cyclase
<i>edd</i>	-1.36	5.15E-06	6-phosphogluconate dehydratase
<i>bioB</i>	1.36	1.07E-06	biotin synthase
<i>secB</i>	-1.36	2.66E-10	protein export chaperone
<i>valY</i>	-1.36	7.21E-06	tRNA
<i>gltJ</i>	1.36	2.37E-06	glutamate, aspartate ABC transporter permease subunit
<i>msbA</i>	-1.36	5.04E-12	fused lipid transporter subunits of ABC superfamily
<i>ybiA</i>	1.36	2.09E-02	conserved protein, DUF1768 family
<i>trpS</i>	-1.36	4.97E-07	tryptophanyl-tRNA synthetase
<i>yibV</i>	1.36	4.61E-01	pseudo
<i>yggP</i>	1.36	1.10E-01	putative dehydrogenase
<i>rpsJ</i>	1.36	1.60E-05	30S ribosomal subunit protein S10
<i>sgcC</i>	1.36	5.44E-02	KpLE2 phage-like element; predicted phosphotransferase enzyme IIC component
<i>cobT</i>	1.36	2.88E-03	nicotinate-nucleotide--dimethylbenzimidazole phosphoribosyltransferase
<i>rrlG</i>	-1.36	2.03E-01	23S ribosomal RNA of rmG operon
<i>acul</i>	-1.36	7.35E-05	putative acryloyl-CoA reductase
<i>arnB</i>	-1.36	1.93E-05	uridine 5'-(beta-1-threo-pentapyranosyl-4-ulose diphosphate) aminotransferase
<i>ynfB</i>	1.36	2.43E-10	hypothetical protein
<i>yhbP</i>	1.36	3.13E-04	conserved protein, UPF0306 family
<i>recJ</i>	1.36	1.02E-10	ssDNA exonuclease, 5' --> 3'-specific
<i>dcuC</i>	1.36	7.72E-02	anaerobic C4-dicarboxylate transport
<i>rraB</i>	-1.36	2.93E-10	protein inhibitor of RNase E
<i>nudL</i>	1.36	8.46E-06	putative NUDIX hydrolase
<i>sdhE</i>	-1.36	5.66E-07	antitoxin of CptAB toxin-antitoxin pair
<i>rpmH</i>	-1.36	2.50E-05	50S ribosomal subunit protein L34
<i>tsf</i>	-1.36	9.09E-06	protein chain elongation factor EF-Ts
<i>ybiR</i>	-1.36	7.71E-05	putative transporter

<i>pssA</i>	-1.36	1.47E-11	phosphatidylserine synthase (CDP-diacylglycerol-serine O-phosphatidyltransferase)
<i>ynfM</i>	1.36	1.91E-06	putative arabinose efflux transporter
<i>yjhC</i>	1.36	8.27E-07	putative oxidoreductase
<i>gudD</i>	1.36	8.77E-03	(D)-glucarate dehydratase 1
<i>yfdL</i>	1.36	6.62E-01	pseudo
<i>pgi</i>	1.36	7.40E-10	glucosephosphate isomerase
<i>aroF</i>	-1.36	1.62E-06	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tyrosine-repressible
<i>ftnB</i>	-1.36	3.82E-07	ferritin B, probable ferrous iron reservoir
<i>yjeM</i>	-1.36	1.15E-02	putative transporter
<i>yebW</i>	-1.36	2.86E-06	hypothetical protein
<i>bglB</i>	1.36	2.41E-01	cryptic phospho-beta-glucosidase B
<i>ykgP</i>	1.36	6.56E-01	pseudo
<i>yfeD</i>	-1.36	2.00E-04	conserved protein, DUF1323 family; N-terminal HTH domain of the MerR superfamily
<i>narY</i>	1.36	5.82E-02	nitrate reductase 2 (NRZ), beta subunit
<i>cysU</i>	-1.36	8.91E-09	sulfate/thiosulfate ABC transporter permease
<i>yfhG</i>	1.36	6.89E-06	hypothetical protein
<i>ybhB</i>	-1.36	4.47E-09	kinase inhibitor homolog, UPF0098 family
<i>pcm</i>	1.36	5.37E-08	L-isoaspartate protein carboxymethyltransferase type II
<i>srlB</i>	1.36	4.16E-01	glucitol/sorbitol-specific enzyme IIA component of PTS
<i>yjgL</i>	-1.36	1.37E-03	hypothetical protein
<i>lsrC</i>	1.36	2.39E-01	autoinducer 2 import system permease protein
<i>eutB</i>	1.36	1.31E-03	ethanolamine ammonia-lyase, large subunit, heavy chain
<i>ydbK</i>	-1.36	3.30E-05	fused predicted pyruvate-flavodoxin oxidoreductase
<i>ybgJ</i>	1.36	4.63E-04	putative allophanate hydrolase, subunit 1
<i>srmB</i>	1.36	7.04E-10	ATP-dependent RNA helicase
<i>ymgD</i>	-1.36	1.20E-05	hypothetical protein
<i>cysJ</i>	1.36	1.20E-07	sulfite reductase, alpha subunit, flavoprotein
<i>mlc</i>	1.36	9.59E-05	global transcriptional repressor; autorepressor; required for anaerobic growth on glucosamin
<i>glmU</i>	-1.36	1.16E-08	NAG-1-phosphate uridyltransferase/glucosamine-1-phosphate acetyl transferase
<i>caiT</i>	1.36	3.18E-01	putative transporter
<i>ppk</i>	1.35	1.85E-11	polyphosphate kinase, component of RNA degradosome
<i>yeaR</i>	-1.35	5.17E-01	hypothetical protein
<i>ubiA</i>	-1.35	5.13E-07	p-hydroxybenzoate octaprenyltransferase
<i>yjjG</i>	1.35	2.94E-08	dUMP phosphatase
<i>mnmG</i>	-1.35	9.19E-07	5-methylaminomethyl-2-thiouridine modification at tRNA U34
<i>glpF</i>	-1.35	7.29E-02	glycerol facilitator
<i>ffh</i>	1.35	1.22E-10	Signal Recognition Particle (SRP) component with 4.5S RNA (ffs)
<i>yihA</i>	-1.35	4.47E-10	GTP-binding protein required for normal cell division
<i>mutM</i>	-1.35	6.38E-03	formamidopyrimidine/5-formyluracil/ 5-hydroxymethyluracil DNA glycosylase
<i>serS</i>	1.35	1.88E-08	seryl-tRNA synthetase, also charges selenocysteinyl-tRNA with serine
<i>rybB</i>	1.35	8.28E-02	ncRNA
<i>cvpA</i>	-1.35	1.02E-07	membrane protein required for colicin V production
<i>mcrC</i>	1.35	1.09E-04	5-methylcytosine-specific restriction enzyme McrBC, subunit McrC

<i>nusG</i>	-1.35	2.44E-11	transcription termination factor
<i>gudP</i>	1.35	3.82E-01	putative D-glucarate transporter
<i>ydjF</i>	-1.35	2.16E-06	putative DNA-binding transcriptional regulator
<i>ynfK</i>	1.35	1.54E-04	putative dethiobiotin synthetase
<i>yshB</i>	-1.35	2.21E-06	hypothetical protein
<i>yejK</i>	-1.35	1.94E-09	spermidine nucleoid-associated protein
<i>yddG</i>	-1.35	6.31E-06	aromatic amino acid exporter
<i>feaB</i>	1.35	7.64E-05	phenylacetaldehyde dehydrogenase
<i>ydiY</i>	1.35	3.75E-04	putative outer membrane protein, acid-inducible
<i>uidR</i>	-1.35	2.77E-08	DNA-binding transcriptional repressor
<i>thrU</i>	-1.35	8.04E-02	tRNA
<i>atpA</i>	1.35	1.31E-03	F1 sector of membrane-bound ATP synthase, alpha subunit
<i>bcp</i>	-1.35	8.90E-09	peroxiredoxin; thiol peroxidase, thioredoxin-dependent
<i>purE</i>	1.35	2.16E-10	N5-carboxyaminoimidazole ribonucleotide mutase
<i>aroM</i>	-1.35	5.26E-08	conserved protein, AroM family
<i>moaE</i>	-1.35	1.18E-04	molybdopterin synthase, large subunit
<i>eyeA</i>	1.35	4.90E-02	ncRNA
<i>clsC</i>	1.35	1.53E-05	stationary phase cardiolipin synthase 3
<i>cysQ</i>	-1.35	2.20E-08	PAPS (adenosine 3'-phosphate 5'-phosphosulfate) 3'(2'),5'-bisphosphate nucleotidase
<i>tdcC</i>	-1.35	1.32E-03	L-threonine/L-serine transporter
<i>dppF</i>	1.35	2.71E-07	dipeptide transporter
<i>ygiF</i>	1.35	6.73E-05	putative adenylate cyclase
<i>hcp</i>	1.35	2.95E-01	hybrid-cluster [4Fe-2S-2O] protein in anaerobic terminal reductases
<i>purH</i>	1.35	7.73E-09	fused IMP cyclohydrolase/phosphoribosylaminoimidazolecarboxamide formyltransferase
<i>pinE</i>	1.35	4.57E-01	e14 prophage; site-specific DNA recombinase
<i>fliL</i>	-1.35	4.85E-01	flagellar biosynthesis protein
<i>ycbB</i>	1.35	3.01E-10	murein L,D-transpeptidase
<i>glxK</i>	-1.35	5.03E-02	glycerate kinase II
<i>caiB</i>	1.35	3.49E-02	crotonobetainyl CoA:carnitine CoA transferase
<i>ddlA</i>	1.35	1.87E-06	D-alanine-D-alanine ligase A
<i>yhiJ</i>	-1.35	8.35E-03	hypothetical protein
<i>fkpB</i>	1.34	7.96E-07	FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)
<i>yhiN</i>	-1.34	3.21E-04	putative oxidoreductase with FAD/NAD(P)-binding domain
<i>yggT</i>	-1.34	5.48E-06	putative inner membrane protein
<i>torY</i>	1.34	3.46E-01	TMAO reductase III (TorYZ), cytochrome c-type subunit
<i>sthA</i>	1.34	5.35E-11	pyridine nucleotide transhydrogenase, soluble
<i>relA</i>	1.34	2.25E-06	(p)ppGpp synthetase I/GTP pyrophosphokinase
<i>dsbD</i>	1.34	1.06E-07	fused thiol:disulfide interchange protein: activator of DsbC/conserved protein
<i>yheS</i>	1.34	2.02E-09	fused predicted transporter subunits of ABC superfamily: ATP-binding components
<i>smtA</i>	1.34	3.24E-08	putative S-adenosyl-L-methionine-dependent methyltransferase
<i>insF1</i>	1.34	4.94E-01	IS3 transposase B
<i>hypF</i>	1.34	3.79E-03	carbamoyl phosphate phosphatase and maturation protein for [NiFe] hydrogenases
<i>fhuA</i>	1.34	1.74E-09	ferrichrome outer membrane transporter

<i>hflX</i>	1.34	8.47E-11	GTPase, stimulated by 50S subunit binding
<i>pyrF</i>	-1.34	7.29E-09	orotidine-5'-phosphate decarboxylase
<i>rsd</i>	-1.34	1.59E-05	stationary phase protein, binds sigma 70 RNA polymerase subunit
<i>tig</i>	-1.34	1.28E-10	peptidyl-prolyl cis/trans isomerase (trigger factor)
<i>ampG</i>	-1.34	5.93E-09	muropeptide transporter
<i>yoeB</i>	1.34	6.79E-04	toxin of the YoeB-YefM toxin-antitoxin system
<i>uhpA</i>	1.34	3.77E-04	DNA-binding response regulator in two-component regulatory system with UhpB
<i>yceJ</i>	-1.34	2.01E-03	putative cytochrome b561
<i>hisQ</i>	-1.34	1.43E-04	histidine/lysine/arginine/ornithine transporter permease subunit
<i>dgoR</i>	1.34	4.69E-05	putative DNA-binding transcriptional regulator
<i>metG</i>	1.34	8.56E-10	methionyl-tRNA synthetase
<i>yjfR</i>	1.34	4.86E-01	CP4-57 prophage; predicted DNA-binding transcriptional regulator
<i>yagB</i>	1.34	1.04E-04	pseudo
<i>yoaD</i>	1.34	7.95E-04	putative cyclic-di-GMP phosphodiesterase, regulator of cellulose production
<i>ybgF</i>	1.34	6.70E-11	periplasmic TolA-binding protein
<i>chbG</i>	1.34	8.53E-04	chito-oligosaccharide deacetylase
<i>yfgM</i>	1.34	3.38E-09	conserved protein, UPF0070 family
<i>dhaL</i>	1.34	2.09E-05	dihydroxyacetone kinase, C-terminal domain
<i>mltD</i>	-1.34	3.47E-09	putative membrane-bound lytic murein transglycosylase D
<i>mmuM</i>	1.34	2.03E-05	CP4-6 prophage; S-methylmethionine:homocysteine methyltransferase
<i>ybjP</i>	-1.34	8.88E-08	lipoprotein
<i>secG</i>	-1.34	3.35E-05	preprotein translocase membrane subunit
<i>gsiA</i>	1.34	9.74E-09	glutathione transporter ATP-binding protein, ABC superfamily
<i>yjjN</i>	1.34	5.88E-02	L-galactonate oxidoreductase
<i>frvB</i>	1.34	1.93E-01	fused predicted PTS enzymes: IIB component/IIC component
<i>yjcB</i>	1.34	2.39E-04	hypothetical protein
<i>perR</i>	-1.34	2.79E-02	CP4-6 prophage; predicted DNA-binding transcriptional regulator
<i>ydcS</i>	1.34	2.66E-05	polyhydroxybutyrate (PHB) synthase, ABC transporter periplasmic binding protein homolog
<i>pck</i>	1.34	3.96E-08	phosphoenolpyruvate carboxykinase
<i>acrF</i>	1.34	3.45E-04	multidrug efflux system protein
<i>rrlC</i>	1.34	6.15E-01	23S ribosomal RNA of <i>rrnC</i> operon
<i>valX</i>	-1.34	4.07E-05	tRNA
<i>ydbL</i>	-1.34	1.85E-02	hypothetical protein
<i>argK</i>	1.34	3.52E-01	membrane ATPase/protein kinase
<i>mepM</i>	1.34	3.32E-07	putative peptidase
<i>sgcQ</i>	1.34	6.69E-02	KpLE2 phage-like element; predicted nucleoside triphosphatase
<i>ykgH</i>	1.34	1.17E-01	putative inner membrane protein
<i>nfo</i>	1.34	2.03E-06	endonuclease IV with intrinsic 3'-5' exonuclease activity
<i>lsrK</i>	1.34	1.87E-03	autoinducer-2 (AI-2) kinase
<i>mukE</i>	1.34	4.00E-08	Chromosome condensin MukBEF, MukE localization factor
<i>yagM</i>	1.33	1.06E-01	CP4-6 prophage; putative protein
<i>ybjH</i>	-1.33	7.61E-03	hypothetical protein
<i>yjhV</i>	1.33	4.03E-01	pseudo

<i>ydfR</i>	-1.33	4.50E-01	Qin prophage; putative protein
<i>yhbE</i>	-1.33	1.82E-06	putative inner membrane permease
<i>yodD</i>	-1.33	4.91E-05	hypothetical protein
<i>hslJ</i>	1.33	2.31E-05	heat-inducible lipoprotein involved in novobiocin resistance
<i>yneE</i>	1.33	1.07E-04	putative inner membrane protein, bestrophin family
<i>ybiH</i>	1.33	3.25E-04	putative DNA-binding transcriptional regulator
<i>creD</i>	-1.33	1.35E-02	inner membrane protein
<i>yadN</i>	-1.33	3.91E-01	putative fimbrial-like adhesin protein
<i>caiD</i>	-1.33	3.91E-01	carnitiny-CoA dehydratase
<i>php</i>	1.33	3.61E-01	putative hydrolase
<i>otsB</i>	-1.33	1.59E-08	trehalose-6-phosphate phosphatase, biosynthetic
<i>sdhB</i>	-1.33	5.37E-08	succinate dehydrogenase, FeS subunit
<i>yfaA</i>	1.33	4.42E-02	DUF2138 family protein, function unknown
<i>matP</i>	-1.33	8.23E-06	Ter macrodomain organizer matS-binding protein
<i>plsY</i>	-1.33	8.88E-05	putative glycerol-3-phosphate acyltransferase
<i>rlmJ</i>	1.33	2.47E-04	23S rRNA m(6)A2030 methyltransferase, SAM-dependent
<i>bolA</i>	-1.33	3.63E-08	stationary-phase morphogene, repressor for mreB; also regulator for dacA, dacC, and ampC
<i>xylB</i>	-1.33	2.86E-02	xylulokinase
<i>maeB</i>	1.33	4.63E-06	fused malic enzyme predicted oxidoreductase/predicted phosphotransacetylase
<i>yqeA</i>	1.33	7.87E-03	putative amino acid kinase
<i>yddM</i>	1.33	5.15E-05	putative DNA-binding transcriptional regulator
<i>yahL</i>	-1.33	2.90E-01	hypothetical protein
<i>fryA</i>	1.33	5.25E-02	fused predicted PTS enzymes: Hpr component/enzyme I component/enzyme IIA component
<i>yaiV</i>	-1.33	4.61E-01	putative DNA-binding transcriptional regulator
<i>tktB</i>	1.33	7.41E-05	transketolase 2, thiamin-binding
<i>crr</i>	1.33	2.13E-09	glucose-specific enzyme IIA component of PTS
<i>yfcL</i>	-1.33	1.23E-04	hypothetical protein
<i>cpdB</i>	-1.33	3.30E-08	2':3'-cyclic-nucleotide 2'-phosphodiesterase
<i>rhsE</i>	1.33	3.30E-02	pseudo
<i>yjdK</i>	-1.33	8.77E-02	hypothetical protein
<i>iscA</i>	1.33	3.27E-07	FeS cluster assembly protein
<i>yfcI</i>	-1.33	1.11E-04	hypothetical protein
<i>csiE</i>	1.33	2.67E-04	stationary phase inducible protein
<i>sad</i>	1.33	6.11E-05	succinate semialdehyde dehydrogenase, NAD(P) ⁺ -dependent
<i>asnT</i>	-1.33	8.31E-03	tRNA
<i>treA</i>	-1.33	4.19E-04	periplasmic trehalase
<i>tar</i>	1.33	8.16E-02	methyl-accepting chemotaxis protein II
<i>rplQ</i>	1.33	5.02E-05	50S ribosomal subunit protein L17
<i>dacA</i>	-1.33	7.91E-11	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 5)
<i>cysN</i>	1.33	1.52E-06	sulfate adenylyltransferase, subunit 1
<i>recG</i>	1.33	1.62E-08	ATP-dependent DNA helicase
<i>sucC</i>	1.33	6.76E-04	succinyl-CoA synthetase, beta subunit
<i>ftsA</i>	-1.33	8.86E-07	ATP-binding cell division protein involved in recruitment of FtsK to Z ring

<i>ydcX</i>	-1.33	9.15E-03	conserved protein, DUF2566 family
<i>osmC</i>	-1.33	1.39E-07	lipoyl-dependent Cys-based peroxidase, hydroperoxide resistance
<i>sdsR</i>	-1.33	9.64E-02	ncRNA
<i>insJ</i>	-1.33	2.60E-02	IS150 transposase A
<i>rpsD</i>	1.33	3.48E-05	30S ribosomal subunit protein S4
<i>yfbM</i>	-1.32	1.89E-01	conserved protein, DUF1877 family
<i>yeiH</i>	-1.32	1.74E-03	inner membrane protein, UPF0324 family
<i>yeaP</i>	1.32	3.02E-05	diguanylate cyclase
<i>ytjP</i>	-1.32	3.46E-09	GGCT-like protein
<i>yjfN</i>	1.32	4.61E-03	hypothetical protein
<i>arnF</i>	-1.32	2.27E-01	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit
<i>ydeS</i>	1.32	2.27E-01	putative fimbrial-like adhesin protein
<i>csgA</i>	1.32	1.29E-02	curlin subunit, amyloid curli fibers, cryptic
<i>agal</i>	-1.32	2.32E-01	galactosamine-6-phosphate isomerase
<i>sibB</i>	1.32	6.49E-02	ncRNA
<i>ompT</i>	-1.32	9.14E-06	DLP12 prophage; outer membrane protease VII (outer membrane protein 3b)
<i>trmI</i>	-1.32	1.29E-07	tRNA m(7)G46 methyltransferase, SAM-dependent
<i>dcp</i>	1.32	1.27E-05	dipeptidyl carboxypeptidase II
<i>pfkB</i>	1.32	1.27E-09	6-phosphofructokinase II
<i>feaR</i>	-1.32	3.60E-04	DNA-binding transcriptional activator for <i>tynA</i> and <i>feaB</i>
<i>yjhU</i>	-1.32	4.14E-07	putative DNA-binding transcriptional regulator; KpLE2 phage-like element
<i>cbpM</i>	-1.32	6.39E-05	modulator of CbpA co-chaperone
<i>yigA</i>	1.32	6.71E-04	conserved protein, DUF484 family
<i>phnP</i>	1.32	1.37E-02	5-phospho-alpha-D-ribosyl 1,2-cyclic phosphate phosphodiesterase
<i>cyoE</i>	-1.32	1.83E-05	protoheme IX farnesyltransferase
<i>yrhC</i>	1.32	5.10E-01	pseudo
<i>chbF</i>	1.32	1.61E-02	phospho-chitobiase; general 6-phospho-beta-glucosidase activity
<i>nusA</i>	1.32	1.15E-06	transcription termination/antitermination L factor
<i>yhbJ</i>	1.32	8.15E-08	glmZ(sRNA)-inactivating NTPase, glucosamine-6-phosphate regulated
<i>intD</i>	1.32	2.46E-07	DLP12 prophage; predicted integrase
<i>yhdX</i>	1.32	2.12E-01	putative amino-acid transporter subunit
<i>proB</i>	1.32	7.01E-07	gamma-glutamate kinase
<i>prpR</i>	-1.32	9.36E-03	propionate catabolism operon regulatory protein
<i>yahB</i>	1.32	4.14E-03	putative DNA-binding transcriptional regulator
<i>nudK</i>	1.32	7.91E-05	GDP-mannose pyrophosphatase
<i>lplA</i>	1.32	2.99E-04	lipoate-protein ligase A
<i>folK</i>	1.32	1.58E-04	2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase
<i>elbB</i>	-1.32	1.60E-04	isoprenoid biosynthesis protein with amidotransferase-like domain
<i>xylA</i>	-1.32	1.40E-03	D-xylose isomerase
<i>yaeI</i>	1.32	1.44E-02	phosphodiesterase with model substrate bis-pNPP
<i>pawZ</i>	1.32	4.44E-01	tRNA
<i>ychO</i>	1.32	7.35E-05	putative invasin
<i>atpF</i>	-1.32	2.23E-03	F0 sector of membrane-bound ATP synthase, subunit b

<i>ybdH</i>	1.32	7.14E-06	putative oxidoreductase
<i>yjiN</i>	-1.32	1.63E-03	zinc-type alcohol dehydrogenase-like protein
<i>hyfF</i>	1.32	1.25E-01	hydrogenase 4, membrane subunit
<i>ydcF</i>	1.32	4.45E-07	conserved SAM-binding protein, DUF218 family
<i>insDI</i>	-1.32	5.13E-01	IS2 transposase TnpB
<i>yhaC</i>	-1.32	2.13E-01	hypothetical protein
<i>pinH</i>	1.32	7.01E-01	pseudo
<i>hybC</i>	1.32	9.91E-04	hydrogenase 2, large subunit
<i>dusA</i>	-1.32	7.68E-06	tRNA-dihydrouridine synthase A
<i>uacT</i>	1.32	5.97E-01	uric acid permease
<i>usg</i>	1.32	1.68E-03	putative semialdehyde dehydrogenase
<i>rplO</i>	1.32	1.81E-03	50S ribosomal subunit protein L15
<i>avtA</i>	1.32	1.51E-08	valine-pyruvate aminotransferase 1
<i>lacZ</i>	1.32	6.53E-02	beta-D-galactosidase
<i>rutR</i>	-1.31	3.21E-03	DNA-binding transcriptional repressor for rut operon
<i>alsA</i>	-1.31	2.95E-01	fused D-allose transporter subunits of ABC superfamily: ATP-binding components
<i>hyaC</i>	1.31	3.95E-01	hydrogenase 1, b-type cytochrome subunit
<i>yegT</i>	-1.31	4.75E-02	nucleoside transporter, low affinity
<i>lolC</i>	1.31	1.39E-06	lipoprotein-releasing system transmembrane protein
<i>glsB</i>	1.31	3.09E-04	glutaminase 2
<i>csrA</i>	-1.31	2.13E-08	pleiotropic regulatory protein for carbon source metabolism
<i>lpxH</i>	-1.31	2.88E-05	UDP-2,3-diacylglucosamine pyrophosphatase
<i>yicR</i>	-1.31	3.92E-06	conserved protein, UPF0758 family
<i>ompL</i>	-1.31	6.00E-01	outer membrane porin L
<i>thrA</i>	1.31	9.93E-04	fused aspartokinase I and homoserine dehydrogenase I
<i>manX</i>	-1.31	2.53E-07	fused mannose-specific PTS enzymes: IIA component/IIB component
<i>xseA</i>	1.31	6.96E-07	exonuclease VII, large subunit
<i>yjdF</i>	-1.31	9.89E-03	conserved inner membrane protein
<i>yfbS</i>	-1.31	1.71E-03	putative transporter
<i>cdh</i>	-1.31	7.41E-05	CDP-diacylglycerol phosphatidylhydrolase
<i>yehH</i>	1.31	4.83E-04	pseudo
<i>leuX</i>	-1.31	1.06E-01	tRNA
<i>gcvB</i>	-1.31	2.12E-05	ncRNA
<i>dcuS</i>	-1.31	6.32E-07	sensory histidine kinase in regulatory system with DcuR
<i>yadL</i>	-1.31	1.83E-01	putative fimbrial-like adhesin protein
<i>ligA</i>	-1.31	5.61E-09	DNA ligase, NAD(+)-dependent
<i>coaD</i>	-1.31	2.29E-05	pantetheine-phosphate adenylyltransferase
<i>ymgI</i>	-1.31	4.08E-01	hypothetical protein
<i>apaH</i>	1.31	1.14E-04	diadenosine tetraphosphatase
<i>yeaE</i>	-1.31	5.99E-05	aldo-keto reductase, methylglyoxal to acetol, NADPH-dependent
<i>ccmC</i>	-1.31	9.15E-03	heme exporter subunit
<i>cohE</i>	-1.31	1.10E-06	e14 prophage; repressor protein phage e14
<i>ynaK</i>	1.31	1.69E-01	Rac prophage; conserved protein

<i>yncI</i>	1.31	7.71E-02	pseudo
<i>frmR</i>	-1.31	4.09E-03	regulator protein that represses frmRAB operon
<i>ydcA</i>	-1.31	1.98E-04	hypothetical protein
<i>sppA</i>	1.31	1.56E-08	protease IV (signal peptide peptidase)
<i>yaiS</i>	1.31	5.04E-01	hypothetical protein
<i>yibQ</i>	1.31	3.29E-05	putative polysaccharide deacetylase
<i>fhuC</i>	-1.31	6.02E-04	iron-hydroxamate transporter subunit
<i>waaJ</i>	-1.31	2.05E-06	UDP-D-glucose:(galactosyl)lipopolysaccharide glucosyltransferase
<i>pheA</i>	-1.31	1.55E-04	fused chorismate mutase P/prephenate dehydratase
<i>agp</i>	-1.31	3.18E-05	glucose-1-phosphatase/inositol phosphatase
<i>yiiG</i>	-1.31	2.11E-01	conserved lipoprotein
<i>yfcA</i>	-1.31	1.46E-04	inner membrane protein, UPF0721 family
<i>yjbJ</i>	-1.31	1.73E-03	stress-induced protein, UPF0337 family
<i>mraY</i>	-1.31	8.16E-04	phospho-N-acetylmuramoyl-pentapeptide transferase
<i>yceD</i>	-1.31	1.09E-08	conserved protein, DUF177 family
<i>rrlH</i>	1.31	5.48E-01	23S ribosomal RNA of rrnH operon
<i>potI</i>	-1.31	4.38E-04	putrescine transporter subunit: membrane component of ABC superfamily
<i>yhhT</i>	-1.31	8.85E-03	inner membrane protein, predicted membrane permease, UPF0118 family
<i>speC</i>	-1.31	1.50E-06	ornithine decarboxylase, constitutive
<i>yaiA</i>	-1.31	2.64E-03	OxyR-regulated conserved protein
<i>mdtP</i>	1.31	3.78E-01	outer membrane factor of efflux pump
<i>eamB</i>	-1.30	1.47E-02	cysteine and O-acetylserine exporter
<i>lacI</i>	1.30	1.25E-05	DNA-binding transcriptional repressor
<i>nirC</i>	-1.30	5.35E-02	nitrite transporter
<i>kduI</i>	-1.30	2.08E-01	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase
<i>hyfR</i>	1.30	1.12E-01	DNA-binding transcriptional activator, formate sensing
<i>dapD</i>	-1.30	1.99E-09	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase
<i>ybgS</i>	-1.30	9.38E-05	hypothetical protein
<i>ppsR</i>	-1.30	7.53E-06	bifunctional regulatory protein: PEP synthase kinase and PEP synthase pyrophosphorylase
<i>rspA</i>	1.30	1.24E-01	bifunctional D-altronate/D-mannonate dehydratase
<i>lepA</i>	1.30	6.19E-08	back-translocating elongation factor EF4, GTPase
<i>yaaX</i>	-1.30	4.80E-03	hypothetical protein
<i>fsaB</i>	-1.30	2.95E-01	fructose-6-phosphate aldolase 2
<i>rpsM</i>	1.30	3.15E-05	30S ribosomal subunit protein S13
<i>eamA</i>	-1.30	1.30E-04	cysteine and O-acetyl-L-serine efflux system
<i>yfcJ</i>	-1.30	6.39E-03	putative arabinose efflux transporter
<i>alkA</i>	1.30	2.65E-02	3-methyl-adenine DNA glycosylase II
<i>rhuC</i>	-1.30	2.00E-05	23S rRNA pseudouridine(955,2504,2580) synthase
<i>yqgA</i>	-1.30	7.56E-02	putative inner membrane protein, DUF554 family
<i>waaF</i>	1.30	3.16E-07	ADP-heptose:LPS heptosyltransferase II
<i>fimA</i>	-1.30	5.12E-02	major type 1 subunit fimbrin (pilin)
<i>yceQ</i>	1.30	4.70E-01	hypothetical protein
<i>gspD</i>	-1.30	6.76E-02	general secretory pathway component, cryptic

<i>ybaQ</i>	-1.30	3.88E-07	putative DNA-binding transcriptional regulator
<i>yecM</i>	1.30	3.99E-05	putative metal-binding enzyme
<i>yehH</i>	-1.30	1.02E-05	putative inner membrane protein
<i>hypA</i>	1.30	5.23E-01	protein involved in nickel insertion into hydrogenases 3
<i>dcuR</i>	-1.30	6.95E-05	DNA-binding response regulator in two-component regulatory system with DcuS
<i>mltA</i>	-1.30	9.40E-07	membrane-bound lytic murein transglycosylase A
<i>ygeI</i>	1.30	4.70E-01	hypothetical protein
<i>yebJ</i>	1.30	3.00E-03	hypothetical protein
<i>uvrC</i>	1.30	1.32E-08	excinuclease UvrABC, endonuclease subunit
<i>ydiR</i>	1.30	1.41E-01	putative electron transfer flavoprotein, FAD-binding subunit
<i>ybcF</i>	1.30	4.24E-01	putative carbamate kinase
<i>rpmJ</i>	1.30	2.12E-05	50S ribosomal subunit protein L36
<i>otsA</i>	-1.30	5.15E-05	trehalose-6-phosphate synthase
<i>fdoI</i>	1.30	6.97E-03	formate dehydrogenase-O, cytochrome b556 subunit
<i>hycH</i>	1.30	1.19E-01	protein required for maturation of hydrogenase 3
<i>flgF</i>	1.30	3.63E-01	flagellar component of cell-proximal portion of basal-body rod
<i>dsbC</i>	1.30	4.30E-08	protein disulfide isomerase II
<i>ypfJ</i>	-1.30	1.03E-06	hypothetical protein
<i>ydiL</i>	-1.30	3.67E-01	hypothetical protein
<i>dcrB</i>	-1.30	5.71E-08	periplasmic protein, predicted lipoprotein
<i>yihO</i>	-1.30	1.21E-01	putative transporter
<i>mltC</i>	-1.30	3.58E-07	membrane-bound lytic murein transglycosylase C
<i>bglX</i>	-1.30	1.76E-07	beta-D-glucoside glucohydrolase, periplasmic
<i>grpE</i>	-1.30	1.86E-08	heat shock protein
<i>prlF</i>	-1.30	2.34E-05	antitoxin of the SohA(PrIF)-YhaV toxin-antitoxin system
<i>ytjR</i>	1.30	5.65E-02	putative sugar transporter subunit: ATP-binding component of ABC superfamily
<i>frmA</i>	-1.30	1.55E-06	alcohol dehydrogenase class III/glutathione-dependent formaldehyde dehydrogenase
<i>ydiB</i>	1.30	1.48E-01	quinat/shikimate 5-dehydrogenase, NAD(P)-binding
<i>opgD</i>	1.30	1.45E-07	osmoregulated periplasmic glucan (OPG) biosynthesis periplasmic protein
<i>panC</i>	1.30	6.40E-06	pantothenate synthetase
<i>eutG</i>	1.30	4.94E-01	ethanol dehydrogenase involved in ethanolamine utilization; aldehyde reductase
<i>rsmF</i>	1.30	2.93E-04	16S rRNA m(5)C1407 methyltransferase, SAM-dependent
<i>galM</i>	1.30	5.38E-07	galactose-1-epimerase (mutarotase)
<i>gfcC</i>	1.30	2.21E-01	hypothetical protein
<i>modE</i>	1.30	1.15E-04	DNA-binding transcriptional repressor for the molybdenum transport operon modABC
<i>acrD</i>	1.30	3.64E-03	aminoglycoside/multidrug efflux system
<i>kdsD</i>	-1.29	1.53E-07	D-arabinose 5-phosphate isomerase
<i>mliA</i>	-1.29	1.75E-06	ABC transporter maintaining OM lipid asymmetry, cytoplasmic STAS component
<i>yeaW</i>	-1.29	2.42E-01	putative 2Fe-2S cluster-containing protein
<i>yjiA</i>	1.29	9.22E-07	putative GTPase
<i>manZ</i>	-1.29	1.07E-06	mannose-specific enzyme IID component of PTS
<i>mliC</i>	-1.29	3.27E-07	ABC transporter maintaining OM lipid asymmetry, periplasmic binding protein
<i>chbB</i>	-1.29	3.19E-04	N,N'-diacetylchitobiose-specific enzyme IIB component of PTS

<i>ydiP</i>	1.29	8.60E-03	putative DNA-binding transcriptional regulator
<i>yqeC</i>	1.29	4.08E-01	hypothetical protein
<i>proC</i>	-1.29	1.16E-08	pyrroline-5-carboxylate reductase, NAD(P)-binding
<i>ykgS</i>	1.29	1.35E-01	pseudo
<i>ampC</i>	-1.29	5.32E-05	beta-lactamase/D-alanine carboxypeptidase
<i>yegS</i>	-1.29	6.92E-05	phosphatidylglycerol kinase, metal-dependent
<i>yhcE</i>	-1.29	1.63E-01	pseudo
<i>sibD</i>	1.29	6.67E-02	ncRNA
<i>yajQ</i>	-1.29	2.41E-08	phage Phi6 host factor, ATP/GTP binding protein
<i>puuB</i>	1.29	2.40E-01	gamma-Glu-putrescine oxidase, FAD/NAD(P)-binding
<i>yjhH</i>	1.29	2.31E-01	KpLE2 phage-like element; predicted lyase/synthase
<i>yohD</i>	-1.29	1.48E-03	inner membrane protein, DedA family
<i>pabA</i>	-1.29	2.80E-02	aminodeoxychorismate synthase, subunit II
<i>yddK</i>	1.29	5.43E-01	pseudo
<i>yicG</i>	-1.29	1.89E-01	inner membrane protein, UPF0126 family
<i>rodZ</i>	1.29	8.75E-07	cytoskeletal protein required for MreB assembly
<i>creA</i>	-1.29	5.97E-06	hypothetical protein
<i>rlmI</i>	-1.29	3.70E-05	23S rRNA m(5)C1962 methyltransferase, SAM-dependent
<i>ynaA</i>	1.29	6.02E-02	pseudo
<i>gadY</i>	-1.29	1.22E-01	ncRNA
<i>yjgB</i>	1.29	8.44E-07	putative alcohol dehydrogenase, Zn-dependent and NAD(P)-binding
<i>plsB</i>	1.29	1.25E-07	glycerol-3-phosphate O-acyltransferase
<i>cydA</i>	1.29	2.80E-04	cytochrome d terminal oxidase, subunit I
<i>kptA</i>	1.29	8.30E-02	RNA 2'-phosphotransferase
<i>insM</i>	1.29	2.04E-01	pseudo
<i>seqA</i>	1.29	5.06E-08	regulatory protein for replication initiation
<i>ydjA</i>	1.29	2.95E-03	putative oxidoreductase
<i>hfq</i>	-1.29	3.04E-06	global sRNA chaperone; HF-I, host factor for RNA phage Q beta replication
<i>aaeB</i>	1.29	3.08E-02	p-hydroxybenzoic acid efflux system component
<i>gnd</i>	-1.29	1.40E-06	6-phosphogluconate dehydrogenase, decarboxylating
<i>modB</i>	-1.29	3.83E-03	molybdate transporter subunit
<i>fbaB</i>	-1.29	3.77E-06	fructose-bisphosphate aldolase class I
<i>hcaE</i>	1.29	2.48E-03	3-phenylpropionate dioxygenase, large (alpha) subunit
<i>fabG</i>	-1.29	1.29E-08	3-oxoacyl-[acyl-carrier-protein] reductase
<i>pepE</i>	-1.29	6.89E-02	(alpha)-aspartyl dipeptidase
<i>mglB</i>	-1.29	2.04E-04	methyl-galactoside transporter subunit
<i>ascF</i>	1.29	2.40E-02	fused cellobiose/arbutin/salicin-specific PTS enzymes: IIB component/IC component
<i>yfeA</i>	-1.29	4.12E-07	putative diguanylate cyclase
<i>stfR</i>	1.29	3.80E-03	Rac prophage; predicted tail fiber protein
<i>rbn</i>	-1.29	2.09E-04	RNase BN, tRNA processing enzyme
<i>ynjD</i>	1.29	6.64E-03	putative transporter subunit: ATP-binding component of ABC superfamily
<i>ecpB</i>	1.29	2.61E-01	hypothetical protein
<i>mrcA</i>	-1.28	3.92E-07	fused penicillin-binding protein 1a: murein transglycosylase/murein transpeptidase

<i>intQ</i>	-1.28	1.30E-01	pseudo
<i>ribA</i>	-1.28	1.50E-05	GTP cyclohydrolase II
<i>ykgD</i>	-1.28	3.85E-02	putative DNA-binding transcriptional regulator
<i>ymfI</i>	-1.28	3.07E-06	e14 prophage; putative protein
<i>aspV</i>	-1.28	8.26E-02	tRNA
<i>ygfB</i>	1.28	9.93E-06	conserved protein, UPF0149 family
<i>insN</i>	1.28	5.94E-04	pseudo
<i>kch</i>	-1.28	2.52E-03	voltage-gated potassium channel
<i>nrfE</i>	1.28	3.55E-01	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfE
<i>ybeF</i>	-1.28	1.02E-01	putative DNA-binding transcriptional regulator
<i>yphF</i>	1.28	2.31E-01	putative sugar transporter subunit: periplasmic-binding component of ABC superfamily
<i>eutA</i>	1.28	3.34E-01	reactivating factor for ethanolamine ammonia lyase
<i>ybjS</i>	1.28	2.46E-05	putative NAD(P)H-binding oxidoreductase with NAD(P)-binding Rossmann-fold domain
<i>bcsG</i>	-1.28	4.44E-03	inner membrane protein, predicted endoglucanase, DUF3260 family
<i>ybcI</i>	1.28	2.97E-01	inner membrane protein, DUF457 family
<i>tdcF</i>	1.28	1.98E-01	putative reactive intermediate deaminase
<i>nikB</i>	-1.28	4.55E-01	nickel transporter subunit
<i>ybjL</i>	1.28	1.27E-06	putative transporter
<i>murR</i>	-1.28	1.06E-01	repressor for murPQ, MurNAc 6-P inducible
<i>ykgQ</i>	1.28	4.45E-01	pseudo
<i>flgG</i>	1.28	1.39E-01	flagellar component of cell-distal portion of basal-body rod
<i>ysaC</i>	-1.28	4.81E-01	pseudo
<i>mmuP</i>	1.28	3.84E-04	CP4-6 prophage; predicted S-methylmethionine transporter
<i>ybbD</i>	1.28	3.92E-01	pseudo
<i>rluF</i>	1.28	1.30E-05	23S rRNA pseudouridine(2604) synthase
<i>hybG</i>	1.28	7.09E-02	hydrogenase 2 accessory protein
<i>yhdZ</i>	-1.28	1.26E-01	putative amino-acid transporter subunit
<i>mr dB</i>	-1.28	1.21E-05	cell wall shape-determining protein
<i>rmf</i>	1.28	1.45E-03	ribosome modulation factor
<i>aspC</i>	1.28	2.91E-04	aspartate aminotransferase, PLP-dependent
<i>cobS</i>	-1.28	2.15E-01	cobalamin synthase
<i>gltP</i>	-1.28	1.25E-05	glutamate/aspartate:proton symporter
<i>ydjO</i>	-1.28	1.50E-01	hypothetical protein
<i>yifL</i>	1.28	5.48E-06	putative lipoprotein
<i>thiK</i>	1.28	2.39E-04	thiamin kinase
<i>yadK</i>	1.28	2.29E-01	putative fimbrial-like adhesin protein
<i>prpE</i>	1.28	2.04E-01	propionate--CoA ligase
<i>tilS</i>	1.28	3.45E-06	tRNA(Ile)-lysine synthetase
<i>hemY</i>	-1.28	9.50E-08	putative protoheme IX synthesis protein
<i>yceA</i>	-1.28	6.35E-05	putative rhodanese-related sulfurtransferase
<i>glnS</i>	1.28	4.61E-03	glutamyl-tRNA synthetase
<i>cysZ</i>	-1.28	2.70E-04	putative inner membrane protein
<i>zapB</i>	-1.28	3.70E-08	FtsZ stabilizer; septal ring assembly factor, stimulates cell division

<i>fadJ</i>	-1.28	4.34E-04	fused enoyl-CoA hydratase and epimerase and isomerase/3-hydroxyacyl-CoA dehydrogenase
<i>gspO</i>	-1.28	2.69E-01	bifunctional prepilin leader peptidase/ methylase
<i>smg</i>	1.28	2.73E-06	hypothetical protein
<i>truD</i>	1.28	9.16E-06	tRNA(Glu) pseudouridine(13) synthase
<i>dapE</i>	1.28	2.36E-05	N-succinyl-diaminopimelate deacylase
<i>pyrL</i>	-1.28	4.46E-02	pyrBI operon leader peptide
<i>tam</i>	1.28	1.69E-04	trans-aconitate methyltransferase
<i>rseA</i>	1.28	2.85E-05	anti-sigma factor
<i>ybbO</i>	1.28	4.78E-04	putative oxidoreductase with NAD(P)-binding Rossmann-fold domain
<i>yhcN</i>	-1.28	5.12E-03	hypothetical protein
<i>degP</i>	1.28	5.01E-05	serine endoprotease (protease Do), membrane-associated
<i>ydgA</i>	-1.28	8.80E-06	conserved protein, DUF945 family
<i>nuoL</i>	-1.28	5.51E-03	NADH:ubiquinone oxidoreductase, membrane subunit L
<i>yejL</i>	-1.28	1.21E-04	conserved protein, UPF0352 family
<i>ynjH</i>	-1.28	2.45E-02	conserved protein, DUF1496 family
<i>apbE</i>	-1.28	8.44E-03	putative thiamine biosynthesis lipoprotein
<i>proS</i>	-1.27	1.06E-07	prolyl-tRNA synthetase
<i>rstB</i>	1.27	2.86E-04	sensory histidine kinase in two-component regulatory system with RstA
<i>yecT</i>	-1.27	1.64E-01	hypothetical protein
<i>ispA</i>	1.27	1.19E-05	geranyltranstransferase
<i>frr</i>	1.27	1.00E-03	ribosome recycling factor
<i>yagK</i>	-1.27	1.90E-02	CP4-6 prophage; conserved protein
<i>queA</i>	-1.27	1.94E-05	S-adenosylmethionine:tRNA ribosyltransferase-isomerase
<i>fucA</i>	1.27	3.98E-01	L-fucose-1-phosphate aldolase
<i>yeiI</i>	1.27	4.45E-03	putative kinase
<i>flgD</i>	1.27	5.85E-01	flagellar hook assembly protein
<i>metR</i>	-1.27	2.39E-04	DNA-binding transcriptional activator, homocysteine-binding
<i>yrdD</i>	1.27	6.48E-07	putative DNA topoisomerase
<i>accA</i>	-1.27	9.16E-06	acetyl-CoA carboxylase, carboxytransferase, alpha subunit
<i>ydbJ</i>	-1.27	4.48E-05	putative lipoprotein, DUF333 family
<i>mhpE</i>	1.27	2.11E-01	4-hydroxy-2-oxovalerate/4-hydroxy-2-oxopentanoic acid aldolase, class I
<i>ygdG</i>	1.27	9.05E-03	Ssb-binding protein, misidentified as ExoIX
<i>ydcV</i>	1.27	8.85E-02	putative spermidine/putrescine transporter subunit
<i>clpX</i>	1.27	1.31E-06	ATPase and specificity subunit of ClpX-ClpP ATP-dependent serine protease
<i>pppA</i>	-1.27	4.65E-04	bifunctional prepilin leader peptidase/ methylase
<i>yhjY</i>	-1.27	1.62E-04	hypothetical protein
<i>kdgR</i>	-1.27	4.78E-06	DNA-binding transcriptional regulator f kdgK, kdgT, eda
<i>yhjY</i>	-1.27	2.46E-01	hypothetical protein
<i>caiE</i>	-1.27	2.28E-01	stimulator of CaiD and CaiB enzyme activities
<i>ghrA</i>	1.27	8.43E-07	glyoxylate/hydroxypyruvate reductase A
<i>rlpA</i>	1.27	1.23E-06	septal ring protein, suppressor of prc, minor lipoprotein
<i>yfcF</i>	-1.27	2.79E-04	glutathione S-transferase
<i>yeeN</i>	-1.27	3.58E-02	conserved protein, UPF0082 family

<i>amyA</i>	-1.27	1.46E-04	cytoplasmic alpha-amylase
<i>ypjN</i>	1.27	6.88E-03	putative membrane protein, UPF0370 family
<i>yfgH</i>	-1.27	2.33E-01	outer membrane integrity lipoprotein
<i>rrlA</i>	1.27	6.82E-01	23S ribosomal RNA of <i>rrnA</i> operon
<i>ulaF</i>	1.27	2.14E-01	L-ribulose 5-phosphate 4-epimerase
<i>uhpT</i>	-1.27	2.86E-01	hexose phosphate transporter
<i>yjiT</i>	-1.27	3.83E-04	pseudo
<i>tomB</i>	-1.27	8.26E-05	Hha toxicity attenuator; conjugation-related protein
<i>purF</i>	-1.27	1.11E-05	amidophosphoribosyltransferase
<i>yedY</i>	1.27	1.16E-03	membrane-anchored, periplasmic TMAO, DMSO reductase
<i>ycbL</i>	1.27	1.49E-05	putative metal-binding enzyme
<i>insH1</i>	-1.27	1.84E-01	IS5 transposase and trans-activator
<i>yphC</i>	1.27	8.18E-02	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>lolD</i>	1.27	1.81E-04	outer membrane-specific lipoprotein transporter subunit
<i>yjiP</i>	-1.27	2.12E-02	pseudo
<i>hiuH</i>	1.27	7.21E-02	hydroxyisourate hydrolase
<i>ydgD</i>	1.27	1.80E-05	putative peptidase
<i>qorB</i>	1.27	7.87E-03	NAD(P)H:quinone oxidoreductase
<i>gntX</i>	-1.27	5.57E-05	protein required for the utilization of DNA as a carbon source
<i>yajG</i>	-1.27	5.35E-04	putative lipoprotein
<i>slyD</i>	-1.27	6.18E-06	FKBP-type peptidyl prolyl cis-trans isomerase (rotamase)
<i>greA</i>	-1.27	2.85E-05	transcript cleavage factor
<i>wcaN</i>	-1.27	9.99E-07	putative regulatory subunit for GalU
<i>ydhI</i>	1.27	2.24E-02	putative inner membrane protein
<i>cyaA</i>	1.26	7.09E-08	adenylate cyclase
<i>narI</i>	-1.26	1.23E-01	nitrate reductase 1, gamma (cytochrome b(NR)) subunit
<i>gltD</i>	-1.26	1.46E-04	glutamate synthase, 4Fe-4S protein, small subunit
<i>mog</i>	-1.26	2.32E-03	molybdochelatase incorporating molybdenum into molybdopterin
<i>hmp</i>	-1.26	8.13E-04	fused nitric oxide dioxygenase/dihydropteridine reductase 2
<i>fadA</i>	-1.26	1.59E-02	3-ketoacyl-CoA thiolase (thiolase I)
<i>yqeK</i>	1.26	6.12E-01	hypothetical protein
<i>ssuB</i>	1.26	9.01E-02	alkanesulfonate transporter subunit
<i>ttdA</i>	-1.26	5.25E-01	L-tartrate dehydratase, alpha subunit
<i>parC</i>	1.26	6.17E-06	DNA topoisomerase IV, subunit A
<i>ydeH</i>	1.26	7.97E-03	diguanylate cyclase, required for <i>pgaD</i> induction
<i>pyrC</i>	1.26	2.82E-05	dihydro-orotase
<i>yjeI</i>	-1.26	2.79E-04	hypothetical protein
<i>rhaD</i>	1.26	6.15E-01	rhamnulose-1-phosphate aldolase
<i>ybjD</i>	1.26	3.06E-05	conserved protein with nucleoside triphosphate hydrolase domain
<i>yghS</i>	1.26	3.74E-01	putative ATP-binding protein
<i>ycfP</i>	-1.26	2.24E-05	hypothetical protein
<i>tusA</i>	-1.26	4.22E-03	sulfurtransferase required 2-thiolation step of <i>mmn(5)</i> -s(2)U34-tRNA synthesis
<i>rsmD</i>	-1.26	2.07E-03	16S rRNA m(2)G966 methyltransferase, SAM-dependent

<i>yebQ</i>	-1.26	1.42E-01	putative transporter
<i>pIsX</i>	-1.26	2.21E-06	putative phosphate acyltransferase
<i>argT</i>	-1.26	1.57E-05	lysine/arginine/ornithine transporter subunit
<i>cusF</i>	-1.26	2.95E-01	periplasmic copper- and silver-binding protein
<i>rsxA</i>	-1.26	1.70E-04	electron transport complex protein required for the reduction of SoxR
<i>cysP</i>	-1.26	6.08E-06	thiosulfate-binding protein
<i>dnaT</i>	1.26	1.01E-02	DNA biosynthesis protein (primosomal protein I)
<i>yeeL</i>	-1.26	1.85E-01	pseudo
<i>ydeM</i>	1.26	2.38E-01	hypothetical protein
<i>agaW</i>	-1.26	5.38E-01	pseudo
<i>mepH</i>	-1.26	2.06E-03	putative peptidase, C40 clan
<i>mreC</i>	1.26	1.56E-05	cell wall structural complex MreBCD transmembrane component MreC
<i>yidR</i>	1.26	1.32E-03	hypothetical protein
<i>aphA</i>	-1.26	3.38E-03	acid phosphatase/phosphotransferase, class B, non-specific
<i>ygcG</i>	1.26	3.33E-01	hypothetical protein
<i>ycgY</i>	1.26	2.08E-01	hypothetical protein
<i>ribF</i>	1.26	2.36E-06	bifunctional riboflavin kinase/FAD synthetase
<i>torS</i>	1.26	4.70E-02	hybrid sensory histidine kinase in two-component regulatory system with TorR
<i>ribC</i>	-1.26	4.45E-07	riboflavin synthase, alpha subunit
<i>yfdK</i>	1.26	1.45E-01	CPS-53 (KpLE1) prophage; conserved protein
<i>selD</i>	1.26	5.69E-04	selenophosphate synthase
<i>yafN</i>	1.26	2.52E-02	antitoxin of the YafO-YafN toxin-antitoxin system
<i>actP</i>	-1.26	1.14E-02	acetate transporter
<i>rssB</i>	1.26	2.83E-05	response regulator binding RpoS to initiate proteolysis by ClpXP
<i>pyrG</i>	1.26	8.45E-07	CTP synthetase
<i>ybeL</i>	-1.26	5.12E-05	conserved protein, DUF1451 family
<i>ybjT</i>	1.26	4.24E-05	conserved protein with NAD(P)-binding Rossmann-fold domain
<i>sdhA</i>	-1.26	1.11E-03	succinate dehydrogenase, flavoprotein subunit
<i>yhgE</i>	-1.26	2.13E-03	putative inner membrane protein
<i>mlaA</i>	-1.26	5.69E-07	ABC transporter maintaining OM lipid asymmetry, OM lipoprotein component
<i>cysG</i>	1.26	2.37E-04	1,3-dimethyluroporphyriongen III dehydrogenase/siroheme ferrochelatase
<i>rnd</i>	1.26	6.00E-06	ribonuclease D
<i>yrbL</i>	-1.26	3.72E-06	hypothetical protein
<i>waaS</i>	-1.26	1.52E-05	lipopolysaccharide core biosynthesis protein
<i>sstT</i>	1.26	4.24E-04	sodium:serine/threonine symporter
<i>ybhH</i>	-1.26	6.21E-01	hypothetical protein
<i>cpxR</i>	1.26	3.41E-07	DNA-binding response regulator in two-component regulatory system with CpxA
<i>yfeH</i>	1.26	4.99E-04	putative inner membrane protein
<i>ynfD</i>	1.26	6.03E-03	hypothetical protein
<i>znuB</i>	-1.26	1.96E-02	zinc transporter subunit: membrane component of ABC superfamily
<i>ycjW</i>	-1.26	5.62E-03	putative DNA-binding transcriptional regulator
<i>ihfB</i>	-1.26	2.21E-06	integration host factor (IHF), DNA-binding protein, beta subunit
<i>yeeY</i>	1.26	1.41E-02	putative DNA-binding transcriptional regulator

<i>dhaK</i>	1.25	9.05E-04	dihydroxyacetone kinase, PTS-dependent, dihydroxyacetone-binding subunit
<i>yifN</i>	-1.25	3.45E-04	pseudo
<i>mcbA</i>	1.25	4.04E-02	colanic acid mucoidy stimulation protein
<i>yjfZ</i>	-1.25	6.49E-02	hypothetical protein
<i>ompF</i>	-1.25	4.53E-04	outer membrane porin 1a (1a;b;F)
<i>rpiA</i>	-1.25	2.01E-06	ribose 5-phosphate isomerase, constitutive
<i>yoeA</i>	1.25	1.15E-02	pseudo
<i>ybaV</i>	-1.25	8.65E-02	conserved protein, ComEA homolog
<i>tusE</i>	-1.25	1.15E-04	sulfurtransferase required for 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis
<i>ygiR</i>	1.25	1.29E-04	putative NAD(P)-binding dehydrogenase
<i>osmF</i>	-1.25	4.21E-04	putative transporter subunit: periplasmic-binding component of ABC superfamily
<i>tsaE</i>	1.25	8.35E-04	tRNA(ANN) t(6)A37 threonylcarbamoyladenine modification protein
<i>yibS</i>	1.25	7.95E-01	pseudo
<i>yehN</i>	-1.25	3.42E-04	hypothetical protein
<i>ybgP</i>	-1.25	4.07E-01	putative periplasmic pilus chaperone
<i>fdoG</i>	1.25	3.34E-04	formate dehydrogenase-O, large subunit
<i>ydeI</i>	-1.25	2.97E-03	hypothetical protein
<i>rhdD</i>	1.25	9.73E-04	rhdD element protein
<i>dnaG</i>	1.25	6.46E-07	DNA primase
<i>cusC</i>	-1.25	4.71E-01	copper/silver efflux system, outer membrane component
<i>recF</i>	-1.25	2.35E-04	gap repair protein
<i>fdnI</i>	1.25	9.63E-02	formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible
<i>insB1</i>	1.25	1.49E-01	pseudo
<i>frlC</i>	1.25	3.30E-01	fructoselysine 3-epimerase
<i>yaiZ</i>	-1.25	2.65E-02	putative inner membrane protein, DUF2754 family
<i>rnpA</i>	-1.25	2.05E-03	protein C5 component of RNase P
<i>dusB</i>	-1.25	1.18E-05	tRNA-dihydrouridine synthase B
<i>ymjC</i>	1.25	2.39E-01	pseudo
<i>artI</i>	-1.25	3.74E-03	arginine transporter subunit
<i>hyuA</i>	1.25	3.69E-01	D-stereospecific phenylhydantoinase
<i>hycE</i>	1.25	3.81E-01	hydrogenase 3, large subunit
<i>glrR</i>	1.25	6.85E-04	response regulator regulating glmY sRNA with sensor protein GlrK
<i>ydbA</i>	1.25	8.82E-07	pseudo
<i>recQ</i>	1.25	1.13E-05	ATP-dependent DNA helicase
<i>eutD</i>	1.25	6.54E-01	phosphate acetyltransferase
<i>ada</i>	1.25	1.49E-02	fused DNA-binding transcriptional dual regulator/O6-methylguanine-DNA methyltransferase
<i>ymgF</i>	-1.25	2.38E-01	inner membrane division septum protein
<i>prfC</i>	-1.25	1.63E-05	peptide chain release factor RF-3
<i>hyfE</i>	1.25	6.83E-01	hydrogenase 4, membrane subunit
<i>rlmL</i>	1.25	4.81E-05	fused 23S rRNA m(2)G2445 and m(7)G2069 methyltransferase, SAM-dependent
<i>hyaE</i>	1.25	5.09E-01	putative HyaA chaperone
<i>ptrA</i>	1.25	2.24E-05	protease III
<i>frvR</i>	1.25	2.19E-01	putative frv operon regulator; contains a PTS EIIA domain

<i>yqeJ</i>	1.25	3.04E-01	hypothetical protein
<i>yeiL</i>	1.25	3.53E-01	DNA-binding transcriptional activator of stationary phase nitrogen survival
<i>yfcC</i>	1.25	2.02E-01	putative inner membrane protein
<i>fadK</i>	1.25	2.37E-01	short chain acyl-CoA synthetase, anaerobic
<i>rfbD</i>	-1.25	1.00E-04	dTDP-4-dehydrorhamnose reductase subunit of dTDP-L-rhamnose synthase
<i>creB</i>	-1.25	7.46E-03	DNA-binding response regulator in two-component regulatory system with CreC
<i>iraM</i>	1.25	8.68E-02	RpoS stabilizer during Mg starvation, anti-RssB factor
<i>glcB</i>	1.25	6.05E-05	malate synthase G
<i>parE</i>	1.25	1.59E-05	DNA topoisomerase IV, subunit B
<i>ybjG</i>	-1.25	5.95E-05	undecaprenyl pyrophosphate phosphatase
<i>yafP</i>	1.25	2.14E-01	putative acyltransferase with acyl-CoA N-acyltransferase domain
<i>purC</i>	-1.25	1.06E-03	phosphoribosylaminoimidazole-succinocarboxamide synthetase
<i>chpB</i>	1.25	2.22E-01	toxin of the ChpB-ChpS toxin-antitoxin system
<i>rnlA</i>	-1.25	5.97E-05	CP4-57 prophage; RNase LS
<i>atpD</i>	1.25	1.38E-03	F1 sector of membrane-bound ATP synthase, beta subunit
<i>ychJ</i>	-1.25	6.03E-05	conserved protein, UPF0225 family
<i>yadD</i>	-1.25	1.11E-01	putative transposase
<i>ygfM</i>	1.24	5.26E-01	putative oxidoreductase
<i>clcA</i>	-1.24	4.48E-05	H(+)/Cl(-) exchange transporter
<i>ygdQ</i>	1.24	3.53E-03	inner membrane protein, UPF0053 family
<i>fadL</i>	-1.24	8.46E-05	long-chain fatty acid outer membrane transporter
<i>rdlA</i>	-1.24	4.92E-02	ncRNA
<i>yfcQ</i>	1.24	5.14E-01	putative fimbrial-like adhesin protein
<i>ycbC</i>	-1.24	9.36E-03	conserved protein, DUF218 superfamily
<i>flgN</i>	1.24	1.21E-01	export chaperone for FlgK and FlgL
<i>acpP</i>	-1.24	2.78E-05	acyl carrier protein (ACP)
<i>ygcB</i>	-1.24	4.56E-02	R-loop helicase-annealase Cas3 needed for Cascade anti-viral activity
<i>yghF</i>	-1.24	1.12E-01	pseudo
<i>coaA</i>	-1.24	4.33E-06	pantothenate kinase
<i>aas</i>	-1.24	1.11E-05	2-acylglycerophospho-ethanolamine acyl transferase/acyl-acyl carrier protein synthetase
<i>ptsA</i>	1.24	5.20E-01	predicted PTS enzymes: Hpr component/enzyme I component/enzyme IIA component
<i>ygbF</i>	1.24	2.97E-01	putative ssRNA endonuclease Cas2, CRISPR adaptation protein
<i>symR</i>	-1.24	2.59E-01	ncRNA
<i>acpH</i>	1.24	5.81E-03	hypothetical protein
<i>mtn</i>	-1.24	1.11E-04	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
<i>moaA</i>	1.24	5.51E-05	molybdopterin biosynthesis protein A
<i>panD</i>	1.24	2.07E-05	aspartate 1-decarboxylase
<i>rlmN</i>	-1.24	4.66E-06	dual specificity 23S rRNA m(2)A2503, tRNA m(2)A37 methyltransferase
<i>rbsA</i>	-1.24	6.93E-03	fused D-ribose transporter subunits of ABC superfamily: ATP-binding components
<i>ypeC</i>	1.24	5.46E-02	hypothetical protein
<i>appB</i>	1.24	5.16E-02	cytochrome bd-II oxidase, subunit II
<i>pepA</i>	1.24	5.52E-06	multifunctional aminopeptidase A: a cyteinyglycinase, site-specific recombination factor
<i>artM</i>	-1.24	1.61E-02	arginine transporter subunit

<i>rplJ</i>	-1.24	2.37E-06	50S ribosomal subunit protein L10
<i>truC</i>	1.24	1.82E-02	tRNA(Ile1,Asp) pseudouridine(65) synthase
<i>ydiJ</i>	1.24	8.35E-05	putative FAD-linked oxidoreductase
<i>hldE</i>	-1.24	1.55E-04	fused heptose 7-phosphate kinase/heptose 1-phosphate adenylyltransferase
<i>trpR</i>	-1.24	3.53E-04	DNA-binding transcriptional repressor, tryptophan-binding
<i>aslB</i>	1.24	2.83E-01	putative regulator of arylsulfatase activity
<i>recO</i>	1.24	1.09E-03	gap repair protein
<i>proL</i>	-1.24	1.42E-01	tRNA
<i>dicF</i>	1.24	4.29E-01	ncRNA
<i>xanP</i>	-1.24	1.38E-05	xanthine permease
<i>yjdN</i>	1.24	4.46E-02	hypothetical protein
<i>ydcJ</i>	1.24	1.99E-02	putative metalloenzyme
<i>yifB</i>	-1.24	2.36E-01	putative bifunctional enzyme and transcriptional regulator
<i>yhcD</i>	-1.24	4.62E-03	putative outer membrane mbrial subunitusher protein
<i>quuQ</i>	1.24	1.33E-01	Qin prophage; predicted antitermination protein Q
<i>fliY</i>	-1.24	9.97E-03	cystine transporter subunit
<i>ylbF</i>	1.24	5.79E-01	hypothetical protein
<i>yajI</i>	-1.24	2.17E-02	putative lipoprotein
<i>betI</i>	1.24	4.39E-04	DNA-binding transcriptional repressor
<i>tpiA</i>	-1.24	1.56E-06	triosephosphate isomerase
<i>xerC</i>	1.24	1.20E-03	site-specific tyrosine recombinase
<i>uidC</i>	1.24	2.94E-01	putative outer membrane porin protein
<i>livJ</i>	-1.24	1.14E-01	leucine/isoleucine/valine transporter subunit
<i>trmJ</i>	1.24	2.00E-06	tRNA mC32,mU32 2'-O-methyltransferase, SAM-dependent
<i>tsgA</i>	-1.24	6.65E-04	putative transporter
<i>frwC</i>	-1.24	6.58E-01	putative enzyme IIC component of PTS
<i>hpf</i>	-1.24	7.58E-04	ribosome hibernation promoting factor HPF; stabilizes 70S dimers (100S)
<i>htpG</i>	-1.24	3.03E-04	protein refolding molecular co-chaperone Hsp90, Hsp70-dependent
<i>focA</i>	-1.24	3.02E-04	formate channel
<i>yrbG</i>	-1.24	1.06E-04	putative calcium/sodium:proton antiporter
<i>ykgB</i>	-1.24	1.09E-01	inner membrane protein, DUF417 family
<i>bax</i>	-1.24	8.79E-04	hypothetical protein
<i>cdd</i>	-1.24	6.77E-03	cytidine/deoxycytidine deaminase
<i>idnK</i>	-1.24	2.85E-01	D-gluconate kinase, thermosensitive
<i>yrdE</i>	-1.24	1.39E-01	pseudo
<i>ivy</i>	-1.24	7.41E-05	inhibitor of c-type lysozyme, periplasmic
<i>nuoK</i>	-1.24	1.69E-01	NADH:ubiquinone oxidoreductase, membrane subunit K
<i>hisA</i>	1.24	2.20E-03	phospho-L-ribosyl-formimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomeras
<i>flgH</i>	1.24	4.87E-01	flagellar protein of basal-body outer-membrane L ring
<i>ygaH</i>	-1.24	1.51E-03	putative L-valine exporter, norvaline resistance
<i>yqfE</i>	1.23	5.57E-01	pseudo
<i>renD</i>	-1.23	2.45E-01	pseudo
<i>yhjG</i>	-1.23	4.06E-04	Inner membrane protein, AsmA family

<i>ydfO</i>	-1.23	4.81E-01	Qin prophage; putative protein
<i>rarD</i>	-1.23	2.84E-02	putative chloramphenicol resistance permease
<i>uidB</i>	1.23	4.37E-01	glucuronide transporter
<i>yrdF</i>	-1.23	5.82E-01	pseudo
<i>cobC</i>	1.23	2.05E-02	putative alpha-ribazole-5'-P phosphatase
<i>ubiB</i>	1.23	2.17E-05	2-octaprenylphenol hydroxylase
<i>mall</i>	1.23	6.89E-02	transcriptional repressor of Mal regulon
<i>yfgC</i>	1.23	1.38E-04	periplasmic predicted metalloprotease, required for LoiP localization; TPR repeats
<i>aaeR</i>	1.23	2.83E-04	transcriptional regulator for aaeXAB operon
<i>yehY</i>	-1.23	5.09E-03	putative transporter subunit: membrane component of ABC superfamily
<i>ftsX</i>	-1.23	1.34E-05	putative transporter subunit: membrane component of ABC superfamily
<i>ttdT</i>	1.23	4.81E-01	L-tartrate/succinate antiporter
<i>fabA</i>	1.23	7.20E-05	beta-hydroxydecanoyl thioester dehydrase
<i>yfiE</i>	-1.23	5.35E-02	putative DNA-binding transcriptional regulator
<i>hcaT</i>	-1.23	1.30E-02	putative 3-phenylpropionic transporter
<i>napA</i>	1.23	7.80E-02	nitrate reductase, periplasmic, large subunit
<i>ylcI</i>	1.23	6.40E-01	hypothetical protein
<i>betT</i>	-1.23	1.46E-05	choline transporter of high affinity
<i>yjhF</i>	-1.23	1.51E-01	KpLE2 phage-like element; predicted transporter
<i>mrdA</i>	-1.23	9.21E-05	transpeptidase involved in peptidoglycan synthesis (penicillin-binding protein 2)
<i>hflC</i>	1.23	3.87E-05	modulator for HflB protease specific for phage lambda cII repressor
<i>ykfJ</i>	1.23	6.45E-01	pseudo
<i>nnr</i>	1.23	2.26E-05	NAD(P)H-hydrate repair enzyme; (S)-NAD(P)H-hydrate dehydratase
<i>yefH</i>	-1.23	1.53E-03	putative DNase
<i>efeB</i>	1.23	4.41E-03	deferrerochelate, periplasmic
<i>ygeY</i>	1.23	2.07E-01	putative peptidase
<i>fliF</i>	-1.23	6.83E-01	flagellar basal-body MS-ring and collar protein
<i>secA</i>	-1.23	2.31E-06	preprotein translocase subunit, ATPase
<i>yahC</i>	1.23	6.55E-01	putative inner membrane protein
<i>wecD</i>	-1.23	3.27E-02	TDP-fucosamine acetyltransferase
<i>yciU</i>	-1.23	2.91E-04	conserved protein, UPF0263 family
<i>ypeB</i>	-1.23	2.57E-01	hypothetical protein
<i>fimF</i>	-1.23	2.89E-01	minor component of type 1 fimbriae
<i>ymfD</i>	1.23	3.31E-02	e14 prophage; predicted SAM-dependent methyltransferase
<i>ybfL</i>	1.23	4.71E-01	pseudo
<i>yhcH</i>	1.23	3.85E-03	hypothetical protein
<i>sohB</i>	-1.23	2.90E-04	putative inner membrane peptidase; multicopy suppressor of htrA(degP)
<i>essD</i>	-1.23	4.07E-01	DLP12 prophage; predicted phage lysis protein
<i>hdfR</i>	1.23	2.00E-03	DNA-binding transcriptional regulator
<i>era</i>	1.23	8.92E-06	membrane-associated, 16S rRNA-binding GTPase
<i>napC</i>	-1.23	4.72E-02	quinol dehydrogenase, electron source for NapAB
<i>ygeX</i>	-1.23	4.81E-01	2,3-diaminopropionate ammonia lyase, PLP-dependent
<i>rtcB</i>	1.23	1.96E-02	hypothetical protein

<i>purK</i>	1.23	1.42E-03	N5-carboxyaminoimidazole ribonucleotide synthase
<i>gltA</i>	-1.23	4.68E-02	citrate synthase
<i>srlR</i>	-1.23	1.02E-02	DNA-binding transcriptional repressor
<i>holB</i>	1.23	1.21E-03	DNA polymerase III, delta prime subunit
<i>yecC</i>	1.23	1.67E-03	putative transporter subunit: ATP-binding component of ABC superfamily
<i>yeaM</i>	1.23	5.21E-03	putative DNA-binding transcriptional regulator
<i>zapC</i>	-1.23	2.56E-02	FtsZ stabilizer
<i>lpp</i>	-1.23	9.91E-04	murein lipoprotein
<i>rstA</i>	1.23	3.29E-04	multicopy suppressor of yjeE, yeaZ or ygiD deletion lethality, predicted response regulator
<i>ydcR</i>	1.23	1.48E-03	fused predicted DNA-binding transcriptional regulator/predicted amino transferase
<i>acrA</i>	-1.23	3.90E-05	multidrug efflux system
<i>ygiV</i>	-1.23	1.66E-01	inner membrane protein, Imp-YgiV family
<i>mntS</i>	1.23	1.57E-03	Mn(2)-response protein, MntR-repressed
<i>ygiS</i>	1.23	4.71E-01	putative oxidoreductase, 4Fe-4S ferredoxin-type subunit
<i>iscX</i>	-1.23	6.17E-04	Iron binding protein associated with IscS; putative molecular adaptor of IscS function
<i>tdcG</i>	1.23	1.28E-01	L-serine dehydratase 3
<i>yheO</i>	-1.23	9.93E-04	hypothetical protein
<i>idnT</i>	1.23	5.92E-02	L-idonate and D-gluconate transporter
<i>maeA</i>	-1.23	3.12E-04	malate dehydrogenase, (decarboxylating, NAD-requiring) (malic enzyme)
<i>pqiA</i>	-1.23	1.06E-03	paraquat-inducible membrane protein A
<i>yhbS</i>	-1.23	8.07E-04	putative acyltransferase with acyl-CoA N-acyltransferase domain
<i>lptD</i>	1.23	1.41E-05	LPS assembly OM complex LptDE, beta-barrel component
<i>murA</i>	-1.23	1.10E-05	UDP-N-acetylglucosamine 1-carboxyvinyltransferase
<i>rsxD</i>	-1.23	5.34E-03	electron transport complex protein required for the reduction of SoxR
<i>yehP</i>	1.23	6.71E-01	hypothetical protein
<i>cyoD</i>	-1.22	1.56E-03	cytochrome o ubiquinol oxidase subunit IV
<i>ygiC</i>	-1.22	2.49E-05	glutathionylspermidine synthase homolog
<i>ibaG</i>	-1.22	3.35E-04	acid stress protein; predicted transcriptional regulator, BofA family
<i>cheZ</i>	1.22	2.12E-01	chemotaxis regulator, protein phosphatase for CheY
<i>dhaM</i>	1.22	2.89E-03	fused predicted dihydroxyacetone-specific PTS enzymes: HPr component/EI component
<i>yghX</i>	1.22	1.03E-03	pseudo
<i>yfcE</i>	-1.22	4.61E-05	phosphodiesterase activity on bis-pNPP
<i>yniB</i>	-1.22	4.70E-05	putative inner membrane protein
<i>fimG</i>	-1.22	2.23E-01	minor component of type 1 fimbriae
<i>gfcB</i>	1.22	5.13E-01	putative outer membrane lipoprotein
<i>ydeQ</i>	1.22	2.61E-01	putative fimbrial-like adhesin protein
<i>gfcD</i>	1.22	1.83E-01	hypothetical protein
<i>recT</i>	1.22	1.33E-01	Rac prophage; recombination and repair protein
<i>arnD</i>	1.22	1.25E-01	undecaprenyl phosphate-alpha-L-ara4FN deformylase
<i>focB</i>	1.22	2.75E-01	putative formate transporter
<i>eptC</i>	-1.22	1.04E-04	putative LPS core phosphoethanolamine transferase
<i>mrr</i>	-1.22	1.68E-03	methylated adenine and cytosine restriction protein
<i>yhfG</i>	-1.22	1.07E-01	putative Fic-binding protein

<i>ybjX</i>	-1.22	1.23E-03	hypothetical protein
<i>torI</i>	-1.22	1.49E-02	response regulator inhibitor for tor operon
<i>yeeO</i>	1.22	5.72E-02	putative multidrug exporter, MATE family
<i>yihP</i>	1.22	4.26E-01	putative transporter
<i>flhB</i>	-1.22	6.61E-01	flagellin export apparatus, substrate specificity protein
<i>serB</i>	1.22	3.19E-03	3-phosphoserine phosphatase
<i>dusC</i>	-1.22	9.02E-02	tRNA-dihydrouridine synthase C
<i>manY</i>	-1.22	8.69E-04	mannose-specific enzyme IIC component of PTS
<i>lysU</i>	1.22	6.41E-05	lysine tRNA synthetase, inducible
<i>tyrS</i>	-1.22	1.35E-03	tyrosyl-tRNA synthetase
<i>mngR</i>	-1.22	7.09E-02	DNA-binding transcriptional dual regulator, fatty-acyl-binding
<i>ylaB</i>	-1.22	3.57E-03	putative membrane-anchored cyclic-di-GMP phosphodiesterase
<i>ybgI</i>	1.22	1.16E-02	conserved metal-binding protein, NIF3 family
<i>mnmA</i>	1.22	2.38E-04	tRNA(Gln,Lys,Glu) U34 2-thiouridylase, first step in mnm(5)-s(2)U34-tRNA synthesis
<i>hsdR</i>	1.22	1.32E-05	endonuclease R Type I restriction enzyme
<i>ydhT</i>	1.22	3.02E-01	hypothetical protein
<i>asnB</i>	1.22	2.86E-05	asparagine synthetase B
<i>cptA</i>	-1.22	4.32E-03	toxin of CptAB toxin-antitoxin pair
<i>lpxP</i>	1.22	8.60E-03	palmitoleoyl-acyl carrier protein (ACP)-dependent acyltransferase
<i>livG</i>	1.22	7.35E-03	leucine/isoleucine/valine transporter subunit
<i>tus</i>	1.22	4.02E-03	inhibitor of replication at Ter, DNA-binding protein
<i>ampH</i>	1.22	1.58E-04	penicillin-binding protein
<i>yjfK</i>	1.22	2.41E-04	CP4-57 prophage; conserved protein
<i>tsaD</i>	1.22	1.29E-04	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein
<i>ssb</i>	-1.22	1.48E-02	single-stranded DNA-binding protein
<i>cysB</i>	-1.22	1.62E-04	DNA-binding transcriptional dual regulator, O-acetyl-L-serine-binding
<i>cspG</i>	-1.22	7.70E-02	cold shock protein homolog, cold-inducible
<i>glrK</i>	1.22	1.38E-03	sensor protein kinase regulating glmY sRNA in two-component system
<i>dnaX</i>	1.22	1.91E-05	DNA polymerase III/DNA elongation factor III, tau and gamma subunits
<i>thiH</i>	1.22	2.91E-01	tyrosine lyase, involved in thiamin-thiazole moiety synthesis
<i>tmk</i>	1.22	1.27E-02	thymidylate kinase
<i>ygdB</i>	1.22	4.30E-01	conserved protein, DUF2509 family
<i>alaX</i>	-1.22	4.44E-02	tRNA
<i>rscB</i>	-1.22	1.16E-05	DNA-binding response regulator in two-component regulatory system with RcsC and YojN
<i>pgaD</i>	-1.22	1.95E-01	biofilm PGA synthase PgaCD, regulatory subunit
<i>ydcC</i>	1.22	4.07E-01	hypothetical protein
<i>omrB</i>	-1.22	2.52E-01	ncRNA
<i>yidE</i>	-1.22	1.05E-03	putative transporter
<i>ydaN</i>	1.22	3.91E-03	putative Zn(II) transporter
<i>argO</i>	-1.22	1.33E-02	arginine transporter
<i>iaaA</i>	1.22	2.86E-04	Isoaspartyl peptidase
<i>sbcB</i>	1.22	4.12E-04	exonuclease I
<i>ybgE</i>	1.22	7.32E-03	hypothetical protein

<i>nfi</i>	1.22	7.80E-04	endonuclease V; deoxyinosine 3' endonuclease
<i>folD</i>	1.22	6.79E-05	5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-THF cyclohydrolase
<i>nuoH</i>	-1.22	1.43E-02	NADH:ubiquinone oxidoreductase, membrane subunit H
<i>yqiI</i>	-1.22	2.78E-01	hypothetical protein
<i>lplT</i>	-1.22	1.90E-02	lysophospholipid transporter
<i>pbpC</i>	-1.22	1.36E-02	penicillin-binding protein PBP1C murein transglycosylase; inactive transpeptidase domain
<i>pdxY</i>	-1.22	6.63E-02	pyridoxamine kinase
<i>ydjY</i>	1.22	2.63E-01	hypothetical protein
<i>yjbE</i>	-1.22	5.62E-02	hypothetical protein
<i>sokC</i>	-1.22	7.87E-01	ncRNA
<i>psuT</i>	1.22	9.97E-02	putative nucleoside transporter
<i>yecE</i>	1.22	6.61E-03	conserved protein, UPF0759 family
<i>rfaH</i>	-1.22	3.60E-04	DNA-binding transcriptional antiterminator
<i>yidQ</i>	-1.22	1.77E-04	conserved outer membrane protein
<i>cheW</i>	1.22	2.78E-01	purine-binding chemotaxis protein
<i>yiaK</i>	-1.21	5.60E-01	2,3-diketo-L-gulonate reductase, NADH-dependent
<i>xseB</i>	1.21	3.26E-03	exonuclease VII small subunit
<i>plsC</i>	1.21	6.01E-04	1-acyl-sn-glycerol-3-phosphate acyltransferase
<i>yjjL</i>	-1.21	9.57E-02	L-galactonate transporter
<i>ydcN</i>	-1.21	9.08E-02	putative DNA-binding transcriptional regulator
<i>ydaV</i>	1.21	6.13E-01	Rac prophage; predicted DNA replication protein
<i>waaR</i>	-1.21	2.32E-04	UDP-D-galactose:(glucosyl)lipopolysaccharide- α -1,3-D-galactosyltransferase
<i>tmcA</i>	-1.21	9.12E-04	elongator methionine tRNA (ac4C34) acetyltransferase
<i>yedL</i>	1.21	1.43E-01	putative acyltransferase
<i>leuS</i>	1.21	1.17E-04	leucyl-tRNA synthetase
<i>gapC</i>	1.21	5.02E-02	pseudo
<i>ybiT</i>	-1.21	4.81E-05	fused predicted transporter subunits of ABC superfamily: ATP-binding components
<i>pdxH</i>	-1.21	9.90E-05	pyridoxine 5'-phosphate oxidase
<i>metH</i>	-1.21	8.69E-05	homocysteine-N5-methyltetrahydrofolate transmethylase, B12-dependent
<i>holD</i>	1.21	5.84E-03	DNA polymerase III, ψ subunit
<i>lysV</i>	-1.21	3.04E-01	tRNA
<i>rhlE</i>	1.21	2.07E-03	ATP-dependent RNA helicase
<i>livM</i>	1.21	1.62E-02	leucine/isoleucine/valine transporter subunit
<i>ygbN</i>	-1.21	1.46E-01	putative transporter
<i>csrB</i>	1.21	1.09E-01	ncRNA
<i>ryfA</i>	-1.21	2.02E-02	ncRNA
<i>hyaA</i>	1.21	5.77E-01	hydrogenase 1, small subunit
<i>yfbU</i>	1.21	9.12E-05	conserved protein, UPF0304 family
<i>rlmG</i>	-1.21	2.65E-02	23S rRNA m(2)G1835 methyltransferase, SAM-dependent
<i>yhjC</i>	1.21	1.85E-02	putative DNA-binding transcriptional regulator
<i>rplN</i>	1.21	5.69E-04	50S ribosomal subunit protein L14
<i>luxS</i>	-1.21	1.82E-04	S-ribosylhomocysteine lyase
<i>araF</i>	-1.21	1.33E-01	L-arabinose transporter subunit

<i>yjeH</i>	-1.21	7.95E-04	putative transporter
<i>glyX</i>	-1.21	4.61E-03	tRNA
<i>rlmB</i>	1.21	9.51E-04	23S rRNA mG2251 2'-O-ribose methyltransferase, SAM-dependent
<i>yecY</i>	1.21	2.97E-02	putative hydrolase
<i>ydfJ</i>	-1.21	2.27E-01	pseudo
<i>yfeO</i>	-1.21	4.37E-02	putative ion channel protein
<i>mntR</i>	-1.21	5.90E-03	DNA-binding transcriptional regulator of mntH
<i>argU</i>	-1.21	8.65E-02	tRNA
<i>yiaV</i>	-1.21	3.18E-01	membrane fusion protein (MFP) component of efflux pump, signal anchor
<i>gsiD</i>	-1.21	2.03E-03	glutathione transporter, permease component, ABC superfamily
<i>yecR</i>	-1.21	5.93E-01	lipoprotein, function unknown
<i>yajL</i>	-1.21	1.08E-03	oxidative-stress-resistance chaperone
<i>tdcA</i>	-1.21	4.79E-01	DNA-binding transcriptional activator
<i>folM</i>	1.21	7.44E-03	dihydropyrimidine reductase, NADPH-dependent; dihydrofolate reductase isozyme
<i>paaA</i>	1.21	5.99E-01	ring 1,2-phenylacetyl-CoA epoxidase subunit
<i>gmhA</i>	1.21	1.96E-04	D-sedoheptulose 7-phosphate isomerase
<i>malQ</i>	-1.21	1.20E-02	4- α -glucanotransferase (amylomaltase)
<i>deaD</i>	1.21	1.49E-03	ATP-dependent RNA helicase
<i>rfbC</i>	-1.21	2.71E-03	dTDP-4-deoxyrhamnose-3,5-epimerase
<i>arpB</i>	1.21	3.67E-01	pseudo
<i>trxA</i>	-1.21	6.64E-04	thioredoxin 1
<i>rimJ</i>	1.21	9.04E-04	ribosomal-protein-S5-alanine N-acetyltransferase
<i>glpK</i>	1.21	1.33E-02	glycerol kinase
<i>sixA</i>	-1.21	2.06E-03	phosphohistidine phosphatase
<i>sbcD</i>	1.21	2.65E-02	exonuclease, dsDNA, ATP-dependent
<i>gyrB</i>	-1.21	1.63E-04	DNA gyrase, subunit B
<i>intZ</i>	1.21	1.18E-03	CPZ-55 prophage; predicted integrase
<i>ybdG</i>	-1.21	1.78E-03	mechanosensitive channel protein, miniconductance
<i>yigM</i>	1.21	2.34E-02	putative inner membrane protein
<i>ydgH</i>	-1.21	1.30E-02	hypothetical protein
<i>ybiB</i>	-1.21	7.74E-04	putative family 3 glycosyltransferase
<i>grxB</i>	-1.21	3.30E-03	glutaredoxin 2 (Grx2)
<i>cydC</i>	1.21	2.41E-04	fused glutathione, cysteine exporter subunits of ABC superfamily
<i>ygiD</i>	1.21	8.75E-02	putative dioxygenase, LigB family
<i>feoB</i>	-1.21	1.71E-04	fused ferrous iron transporter, protein B: GTP-binding protein/membrane protein
<i>gltK</i>	1.21	9.18E-03	glutamate, aspartate ABC transporter permease subunit
<i>ppiB</i>	-1.21	6.81E-05	peptidyl-prolyl cis-trans isomerase B (rotamase B)
<i>inaA</i>	-1.21	1.86E-02	conserved protein, acid-induced
<i>mhpC</i>	1.21	5.53E-01	2-hydroxy-6-ketono-2,4-dienedioic acid hydrolase
<i>secF</i>	-1.21	3.87E-03	SecYEG protein translocase auxiliary subunit
<i>ygbI</i>	-1.21	2.40E-02	putative transcriptional regulator, DeoR family
<i>dbpA</i>	1.21	1.98E-02	ATP-dependent RNA helicase, specific for 23S rRNA
<i>gldA</i>	-1.21	5.76E-02	glycerol dehydrogenase, NAD

<i>ykfA</i>	-1.21	5.32E-02	CP4-6 prophage; predicted GTP-binding protein
<i>corA</i>	-1.21	2.02E-02	magnesium/nickel/cobalt transporter
<i>phnO</i>	1.21	1.49E-01	putative aminoalkylphosphonic acid N-acetyltransferase
<i>ung</i>	-1.21	1.55E-03	uracil-DNA-glycosylase
<i>Int</i>	-1.21	3.47E-04	apolipoprotein N-acyltransferase
<i>ybeR</i>	-1.21	8.84E-01	hypothetical protein
<i>ybbJ</i>	-1.20	5.82E-02	inner membrane protein that stimulates the ftsH htpX mutant suppressor activity of QmcA
<i>cheR</i>	1.20	5.31E-01	chemotaxis regulator, protein-glutamate methyltransferase
<i>rpsB</i>	-1.20	5.10E-02	30S ribosomal subunit protein S2
<i>preT</i>	-1.20	4.01E-01	dihydropyrimidine dehydrogenase, NADH-dependent, subunit N
<i>nagK</i>	1.20	1.39E-04	N-acetyl-D-glucosamine kinase
<i>yidL</i>	-1.20	1.09E-01	putative transcriptional regulator, AraC family
<i>xylE</i>	-1.20	2.02E-01	D-xylose transporter
<i>tatE</i>	-1.20	2.31E-02	TatABCE protein translocation system subunit
<i>qseB</i>	-1.20	1.15E-01	quorum sensing DNA-binding response regulator with QseC
<i>flgJ</i>	1.20	4.41E-01	muramidase
<i>ybcY</i>	1.20	8.60E-02	pseudo
<i>hsdM</i>	-1.20	1.72E-03	DNA methyltransferase M
<i>mlaF</i>	-1.20	6.46E-04	ABC transporter maintaining OM lipid asymmetry, ATP-binding protein
<i>hcr</i>	1.20	4.65E-01	HCP oxidoreductase, NADH-dependent
<i>hycI</i>	-1.20	1.79E-02	protease involved in processing C-terminal end of HycE
<i>yidP</i>	1.20	3.93E-01	putative DNA-binding transcriptional regulator
<i>nagE</i>	1.20	2.82E-03	fused N-acetyl glucosamine specific PTS enzyme: IIC, IIB, and IIA components
<i>btuD</i>	1.20	1.61E-02	vitamin B12 transporter subunit : ATP-binding component of ABC superfamily
<i>hldD</i>	1.20	2.45E-04	ADP-L-glycero-D-mannoheptose-6-epimerase, NAD(P)-binding
<i>sucD</i>	1.20	2.84E-02	succinyl-CoA synthetase, NAD(P)-binding, alpha subunit
<i>ynfA</i>	-1.20	1.61E-01	inner membrane protein, UPF0060 family
<i>frlR</i>	-1.20	6.16E-03	putative DNA-binding transcriptional regulator
<i>panF</i>	-1.20	1.44E-02	pantothenate:sodium symporter
<i>ybaP</i>	1.20	3.20E-03	conserved protein, TraB family
<i>aat</i>	1.20	3.50E-03	leucyl/phenylalanyl-tRNA-protein transferase
<i>ulaD</i>	1.20	2.69E-01	3-keto-L-gulonate 6-phosphate decarboxylase
<i>yeeD</i>	-1.20	8.03E-03	hypothetical protein
<i>yjff</i>	1.20	2.44E-01	putative sugar transporter subunit: membrane component of ABC superfamily
<i>yhdJ</i>	-1.20	2.06E-01	DNA adenine methyltransferase, SAM-dependent
<i>ynjF</i>	-1.20	7.11E-02	inner membrane protein, phosphatidylglycerophosphate synthase homolog
<i>dapF</i>	1.20	7.61E-04	diaminopimelate epimerase
<i>ppiA</i>	-1.20	2.49E-04	peptidyl-prolyl cis-trans isomerase A (rotamase A)
<i>yqaB</i>	1.20	9.61E-03	fructose-1-P and 6-phosphogluconate phosphatase
<i>lola</i>	1.20	6.38E-03	lipoprotein chaperone
<i>gshB</i>	-1.20	2.41E-03	glutathione synthetase
<i>polA</i>	1.20	1.57E-03	fused DNA polymerase I 5'->3' polymerase/3'->5' exonuclease/5'->3' exonuclease
<i>rsgA</i>	1.20	8.16E-04	ribosome small subunit-dependent GTPase A

<i>artQ</i>	-1.20	2.92E-02	arginine transporter subunit
<i>yffP</i>	1.20	2.61E-01	CPZ-55 prophage; putative protein
<i>waaB</i>	-1.20	5.52E-04	UDP-D-galactose:(glucosyl)lipopolysaccharide-1,6-D-galactosyltransferase
<i>yggE</i>	-1.20	4.47E-03	oxidative stress defense protein
<i>yciC</i>	-1.20	1.04E-03	inner membrane protein, UPF0259 family
<i>fabF</i>	-1.20	2.54E-04	3-oxoacyl-[acyl-carrier-protein] synthase II
<i>hisG</i>	1.20	5.88E-03	ATP phosphoribosyltransferase
<i>yhfU</i>	1.20	4.26E-01	hypothetical protein
<i>tesB</i>	-1.20	1.07E-03	acyl-CoA thioesterase II
<i>flgK</i>	1.20	1.46E-01	flagellar hook-filament junction protein 1
<i>hybA</i>	1.20	4.55E-01	hydrogenase 2 4Fe-4S ferredoxin-type component
<i>ydeP</i>	1.20	1.92E-02	putative oxidoreductase
<i>yejE</i>	-1.20	9.25E-02	microcin C transporter YejABEF, permease subunit; ABC family
<i>epmC</i>	-1.20	7.61E-02	Elongation Factor P Lys34 hydroxylase
<i>allB</i>	1.20	2.45E-01	allantoinase
<i>rnt</i>	1.20	1.11E-02	ribonuclease T (RNase T)
<i>ispF</i>	1.20	2.06E-02	2C-methyl-D-erythritol 2,4-cyclodiphosphate synthase
<i>nuoJ</i>	-1.20	5.67E-02	NADH:ubiquinone oxidoreductase, membrane subunit J
<i>pncC</i>	-1.20	5.81E-03	NMN amidohydrolase
<i>nfuA</i>	1.20	1.19E-03	Fe/S biogenesis protein; possible scaffold/chaperone for damaged Fe/S proteins
<i>mdlB</i>	-1.20	9.84E-02	fused predicted multidrug transporter subunits of ABC superfamily
<i>nupX</i>	-1.20	5.10E-01	nucleoside permease
<i>obgE</i>	-1.20	7.87E-02	GTPase involved in cell partitioning and DNA repair
<i>yfgI</i>	-1.20	2.61E-01	hypothetical protein
<i>trmH</i>	1.20	2.68E-02	tRNA mG18-2'-O-methyltransferase, SAM-dependent
<i>psrD</i>	1.19	1.09E-01	ncRNA
<i>ycfQ</i>	1.19	4.12E-03	repressor for bhsA(ycfR)
<i>intK</i>	-1.19	6.56E-01	pseudo
<i>trkH</i>	-1.19	6.13E-04	potassium transporter
<i>yehL</i>	-1.19	6.48E-01	putative transporter subunit: ATP-binding component of ABC superfamily
<i>yehU</i>	-1.19	1.96E-02	putative sensory kinase in two-component system with YehT, inner membrane protein
<i>marC</i>	-1.19	3.72E-03	inner membrane protein, UPF0056 family
<i>waaP</i>	-1.19	2.78E-03	kinase that phosphorylates core heptose of lipopolysaccharide
<i>yebT</i>	-1.19	1.90E-02	hypothetical protein
<i>ypdA</i>	1.19	1.36E-02	putative sensory kinase in two-component system with YpdB
<i>tfaP</i>	1.19	4.58E-01	e14 prophage; putative protein
<i>ycgG</i>	-1.19	2.09E-01	putative membrane-anchored cyclic-di-GMP phosphodiesterase
<i>tag</i>	-1.19	6.97E-03	3-methyl-adenine DNA glycosylase I, constitutive
<i>yhbO</i>	-1.19	2.97E-02	stress-resistance protein
<i>cadA</i>	1.19	3.15E-01	lysine decarboxylase, acid-inducible
<i>pstC</i>	-1.19	1.99E-02	phosphate transporter subunit
<i>murD</i>	-1.19	6.01E-03	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase
<i>murG</i>	-1.19	3.64E-02	N-acetylglucosaminyl transferase

<i>flxA</i>	-1.19	2.43E-01	Qin prophage; putative protein
<i>malP</i>	-1.19	9.49E-02	maltodextrin phosphorylase
<i>gatY</i>	-1.19	4.40E-04	D-tagatose 1,6-bisphosphate aldolase 2, catalytic subunit
<i>yjcF</i>	1.19	2.95E-01	pentapeptide repeat protein
<i>rpoE</i>	1.19	8.85E-04	RNA polymerase, sigma 24 (sigma E) factor
<i>hcaD</i>	1.19	1.77E-01	phenylpropionate dioxygenase, ferredoxin reductase subunit
<i>qmcA</i>	-1.19	3.08E-03	multicopy suppressor of <i>ftsH</i> <i>htpX</i> double mutant; membrane-anchored predicted protease
<i>nemR</i>	-1.19	1.95E-01	transcriptional repressor for the <i>nem</i> operon, NEM-inactivated
<i>rsxE</i>	-1.19	3.36E-02	NADH-quinone reductase required for the reduction of SoxR
<i>yccS</i>	-1.19	1.76E-03	inner membrane protein
<i>rpiR</i>	-1.19	6.29E-03	DNA-binding transcriptional repressor
<i>gspE</i>	-1.19	5.11E-01	general secretory pathway component, cryptic
<i>ratA</i>	1.19	9.30E-03	toxic UPF0083 family protein inhibitor of 70S ribosome formation
<i>sieB</i>	1.19	2.17E-01	Rac prophage; phage superinfection exclusion protein
<i>nhaR</i>	-1.19	2.87E-03	DNA-binding transcriptional activator
<i>fadD</i>	-1.19	9.58E-03	acyl-CoA synthetase (long-chain-fatty-acid--CoA ligase)
<i>oppF</i>	1.19	6.36E-02	oligopeptide transporter subunit
<i>fucR</i>	-1.19	1.09E-01	DNA-binding transcriptional activator
<i>waaC</i>	-1.19	2.45E-02	ADP-heptose:LPS heptosyl transferase I
<i>pheS</i>	1.19	3.11E-02	phenylalanine tRNA synthetase, alpha subunit
<i>ybdM</i>	-1.19	1.47E-01	hypothetical protein
<i>ynhG</i>	1.19	1.58E-03	murein L,D-transpeptidase
<i>ynhF</i>	1.19	1.35E-01	hypothetical protein
<i>yehK</i>	-1.19	7.24E-01	hypothetical protein
<i>ecpD</i>	-1.19	6.62E-02	putative receptor
<i>yfcO</i>	-1.19	2.46E-03	hypothetical protein
<i>epmB</i>	1.19	2.91E-03	EF-P-Lys34 lysylation protein; weak lysine 2,3-aminomutase
<i>aroG</i>	1.19	1.62E-04	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, phenylalanine repressible
<i>ydjI</i>	-1.19	6.02E-02	putative D-mannonate oxidoreductase, NAD-dependent
<i>dapA</i>	1.19	1.49E-04	dihydrodipicolinate synthase
<i>pdxA</i>	1.18	1.33E-03	4-hydroxy-L-threonine phosphate dehydrogenase, NAD-dependent
<i>ftsI</i>	-1.18	2.29E-02	transpeptidase involved in septal peptidoglycan synthesis (penicillin-binding protein 3)
<i>omrA</i>	-1.18	2.94E-01	ncRNA
<i>mcrA</i>	1.18	1.21E-01	e14 prophage; 5-methylcytosine-specific restriction endonuclease B
<i>tatD</i>	-1.18	3.65E-02	quality control of Tat-exported FeS proteins; Mg-dependent cytoplasmic DNase
<i>rpoH</i>	-1.18	1.19E-03	RNA polymerase, sigma 32 (sigma H) factor
<i>ynjF</i>	-1.18	6.48E-02	S- and N-oxide reductase, A subunit, periplasmic
<i>ybhP</i>	-1.18	1.86E-02	conserved protein, endo/exonuclease/phosphatase family PFAM PF03372
<i>ykgL</i>	1.18	4.08E-01	hypothetical protein
<i>ybcH</i>	-1.18	6.40E-02	hypothetical protein
<i>agaA</i>	-1.18	3.91E-01	pseudo
<i>lldR</i>	1.18	8.54E-02	dual role activator/repressor for <i>lldPRD</i> operon
<i>frlB</i>	1.18	4.14E-01	fructoselysine-6-P-deglycase

<i>rihC</i>	-1.18	1.05E-01	ribonucleoside hydrolase 3
<i>hscA</i>	1.18	7.00E-04	DnaK-like molecular chaperone specific for IscU
<i>yjbH</i>	-1.18	4.54E-02	putative porin
<i>rpe</i>	1.18	3.36E-03	D-ribulose-5-phosphate 3-epimerase
<i>dosC</i>	1.18	3.46E-02	diguanylate cyclase, cold- and stationary phase-induced oxygen-dependent biofilm regulator
<i>pldA</i>	-1.18	2.41E-03	outer membrane phospholipase A
<i>ycal</i>	-1.18	8.76E-02	inner membrane protein, ComEC family of competence proteins
<i>yghJ</i>	1.18	2.67E-04	putative inner membrane lipoprotein
<i>hypE</i>	-1.18	4.80E-02	carbamoyl dehydratase, hydrogenases 1,2,3 maturation protein
<i>alr</i>	1.18	1.22E-02	alanine racemase 1, PLP-binding, biosynthetic
<i>phnM</i>	1.18	8.10E-01	ribophosphonate triphosphate hydrolase
<i>rnhA</i>	-1.18	2.52E-02	ribonuclease HI, degrades RNA of DNA-RNA hybrids
<i>rpiB</i>	-1.18	3.63E-01	ribose 5-phosphate isomerase B/allose 6-phosphate isomerase
<i>ydjK</i>	1.18	5.75E-01	putative transporter
<i>yehD</i>	1.18	5.53E-01	putative fimbrial-like adhesin protein
<i>alsC</i>	1.18	6.02E-01	D-allose transporter subunit
<i>yafS</i>	-1.18	3.64E-02	putative S-adenosyl-L-methionine-dependent methyltransferase
<i>yagN</i>	1.18	1.27E-02	CP4-6 prophage; putative protein
<i>leuQ</i>	-1.18	7.71E-02	tRNA
<i>insII</i>	1.18	1.37E-01	IS30 transposase
<i>pyrH</i>	-1.18	5.39E-02	uridylate kinase
<i>yqjF</i>	-1.18	2.45E-01	putative quinol oxidase subunit
<i>insII</i>	1.18	5.77E-01	IS30 transposase
<i>ilvM</i>	-1.18	4.24E-01	acetolactate synthase II, small subunit
<i>csgC</i>	1.18	5.83E-01	curli assembly protein
<i>tusD</i>	-1.18	4.07E-02	sulfurtransferase for 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis
<i>yicI</i>	1.18	1.05E-01	putative alpha-glucosidase
<i>yfbK</i>	-1.18	4.71E-01	hypothetical protein
<i>pmrR</i>	1.18	1.24E-01	putative regulator of BasS activity, membrane protein
<i>csdA</i>	1.18	4.69E-03	cysteine sulfinatase desulfinate
<i>rsxB</i>	-1.18	1.93E-02	electron transport complex protein, iron-sulfur protein, required for the reduction of SoxR
<i>yigE</i>	-1.18	3.60E-01	putative protein, DUF2233 family
<i>clcB</i>	1.18	1.56E-01	H(+)/Cl(-) exchange transporter
<i>ycjP</i>	-1.18	7.52E-01	putative sugar transporter subunit: membrane component of ABC superfamily
<i>rna</i>	-1.18	2.48E-03	ribonuclease I
<i>fixB</i>	1.18	7.10E-01	putative electron transfer flavoprotein, EFTP adenine nucleotide-binding domain-like protein
<i>yagA</i>	1.18	7.36E-01	CP4-6 prophage; predicted DNA-binding transcriptional regulator
<i>motA</i>	1.18	7.08E-01	proton conductor component of flagella motor
<i>pstB</i>	-1.18	3.99E-03	phosphate transporter subunit
<i>insO</i>	-1.18	4.69E-02	pseudo
<i>cpxA</i>	1.18	4.97E-04	sensory histidine kinase in two-component regulatory system with CpxR
<i>hypD</i>	1.18	1.64E-01	protein required for maturation of hydrogenases
<i>ilvH</i>	-1.18	2.30E-02	acetolactate synthase III, thiamin-dependent, small subunit

<i>rppH</i>	1.18	5.62E-04	RNA pyrophosphohydrolase
<i>ypdB</i>	1.18	8.55E-03	putative response regulator in two-component system with YpdA
<i>yegI</i>	1.18	1.14E-01	hypothetical protein
<i>yaeQ</i>	1.18	2.72E-02	hypothetical protein
<i>rpsK</i>	1.18	5.61E-02	30S ribosomal subunit protein S11
<i>ycgN</i>	1.18	2.91E-03	UPF0153 family cysteine cluster protein, function unknown
<i>tadA</i>	-1.18	2.00E-02	tRNA-specific adenosine deaminase
<i>chiX</i>	-1.18	3.79E-01	ncRNA
<i>rspR</i>	1.18	1.23E-02	putative DNA-binding transcriptional regulator
<i>zraR</i>	1.18	1.88E-01	DNA-binding response regulator in two-component regulatory system with ZraS
<i>pncA</i>	-1.17	8.78E-03	nicotinamidase/pyrazinamidase
<i>yhaJ</i>	-1.17	4.80E-02	putative DNA-binding transcriptional regulator
<i>yedW</i>	-1.17	5.07E-02	putative DNA-binding response regulator in two-component system with YedV
<i>melA</i>	-1.17	1.45E-01	alpha-galactosidase, NAD(P)-binding
<i>ybfP</i>	1.17	2.69E-01	lipoprotein
<i>phoU</i>	-1.17	7.14E-02	negative regulator of PhoR/PhoB two-component regulator
<i>ygeF</i>	1.17	8.15E-01	pseudo
<i>acrE</i>	1.17	7.96E-01	cytoplasmic membrane lipoprotein
<i>opgH</i>	-1.17	1.74E-03	membrane glycosyltransferase
<i>rpoN</i>	1.17	1.10E-03	RNA polymerase, sigma 54 (sigma N) factor
<i>ymdB</i>	1.17	5.35E-02	O-acetyl-ADP-ribose deacetylase; RNase III inhibitor
<i>fau</i>	1.17	5.63E-02	conserved protein, 5-formyltetrahydrofolate cyclo-ligase family
<i>menB</i>	-1.17	1.62E-02	dihydroxynaphthoic acid synthetase
<i>ydcH</i>	-1.17	5.00E-02	DUF465 family protein, function unknown
<i>ykgJ</i>	-1.17	1.57E-01	UPF0153 cysteine cluster protein, function unknown
<i>ybfQ</i>	-1.17	7.26E-01	pseudo
<i>cysE</i>	1.17	1.23E-03	serine acetyltransferase
<i>rapA</i>	1.17	1.65E-03	RNA polymerase-associated helicase protein (ATPase and RNA polymerase recycling factor
<i>rluD</i>	-1.17	3.18E-03	23S rRNA pseudouridine(1911,1915,1917) synthase
<i>lomR</i>	1.17	5.48E-01	pseudo
<i>mocA</i>	-1.17	2.47E-01	CTP:molybdopterin cytidyltransferase
<i>hemX</i>	-1.17	4.03E-03	putative uroporphyrinogen III methyltransferase
<i>arnC</i>	-1.17	3.32E-01	undecaprenyl phosphate-L-Ara4FN transferase
<i>yhgN</i>	-1.17	9.05E-02	putative antibiotic transporter
<i>ydhP</i>	-1.17	4.61E-02	putative transporter
<i>ltaE</i>	1.17	6.99E-03	L-allo-threonine aldolase, PLP-dependent
<i>yiaG</i>	-1.17	3.37E-02	putative transcriptional regulator, HTH_CROC1 family
<i>yiaJ</i>	1.17	4.35E-02	DNA-binding transcriptional repressor of yiaK-S operon
<i>yibH</i>	-1.17	3.32E-01	hypothetical protein
<i>allS</i>	-1.17	5.26E-01	DNA-binding transcriptional activator of the allD operon
<i>rlmA</i>	-1.17	2.31E-02	23S rRNA m(1)G745 methyltransferase, SAM-dependent
<i>yhgF</i>	1.17	1.83E-02	putative transcriptional accessory protein
<i>yiaW</i>	-1.17	8.90E-01	inner membrane protein, DUF3302 family

<i>nadE</i>	1.17	9.74E-04	NAD synthetase, NH ₃ /glutamine-dependent
<i>ybhC</i>	-1.17	1.24E-03	acyl-CoA thioesterase, lipoprotein
<i>adiA</i>	1.17	3.07E-01	arginine decarboxylase
<i>osmB</i>	1.17	3.85E-02	lipoprotein
<i>ygeQ</i>	-1.17	4.63E-02	pseudo
<i>bcsA</i>	-1.17	1.47E-01	cellulose synthase, catalytic subunit
<i>ybfO</i>	1.17	3.82E-01	pseudo
<i>gatZ</i>	-1.17	1.18E-02	D-tagatose 1,6-bisphosphate aldolase 2, subunit
<i>yedI</i>	-1.17	1.38E-01	conserved inner membrane protein
<i>prpC</i>	1.17	8.47E-01	2-methylcitrate synthase
<i>ttcA</i>	-1.17	2.23E-03	tRNA 2-thiocytidine biosynthesis protein
<i>arfA</i>	-1.17	1.98E-01	alternate ribosome-rescue factor A
<i>envC</i>	1.17	1.54E-03	activator of AmiB,C murein hydrolases, septal ring factor
<i>yehW</i>	-1.17	6.13E-02	putative transporter subunit: membrane component of ABC superfamily
<i>racC</i>	1.17	8.72E-01	Rac prophage; putative protein
<i>cysH</i>	1.17	1.10E-01	3'-phosphoadenosine 5'-phosphosulfate reductase
<i>citT</i>	1.17	4.30E-01	citrate:succinate antiporter
<i>ybbY</i>	-1.17	3.70E-01	putative uracil/xanthine transporter
<i>pstA</i>	-1.17	2.96E-02	phosphate transporter subunit
<i>pphA</i>	-1.17	1.29E-01	serine/threonine-specific protein phosphatase 1
<i>ansB</i>	-1.17	2.19E-01	periplasmic L-asparaginase II
<i>smpB</i>	1.17	1.62E-02	trans-translation protein
<i>prmA</i>	-1.17	1.83E-02	methyltransferase for 50S ribosomal subunit protein L11
<i>arpA</i>	1.17	4.69E-01	ankyrin repeat protein
<i>thiC</i>	-1.17	3.24E-02	thiamin (pyrimidine moiety) biosynthesis protein
<i>ypeA</i>	-1.17	1.21E-01	putative acyltransferase with acyl-CoA N-acyltransferase domain
<i>rutG</i>	1.17	2.64E-01	pyrimidine permease
<i>btuB</i>	-1.17	2.07E-02	vitamin B12/cobalamin outer membrane transporter
<i>potH</i>	-1.17	1.13E-01	putrescine transporter subunit: membrane component of ABC superfamily
<i>infC</i>	-1.17	1.81E-03	protein chain initiation factor IF-3
<i>yceF</i>	-1.17	1.78E-03	Maf-like protein
<i>yggM</i>	-1.17	3.07E-01	hypothetical protein
<i>yehQ</i>	1.17	2.90E-01	pseudo
<i>mngA</i>	-1.17	8.30E-01	2-O-a-mannosyl-D-glycerate specific PTS enzymes: IIA/IIB /IIC
<i>cynR</i>	1.17	2.04E-01	transcriptional activator of cyn operon; autorepressor
<i>cmk</i>	-1.17	4.79E-03	cytidylate kinase
<i>rplK</i>	-1.17	2.95E-03	50S ribosomal subunit protein L11
<i>phr</i>	1.17	3.41E-02	deoxyribodipyrimidine photolyase, FAD-binding
<i>yaiX</i>	-1.17	4.67E-01	pseudo
<i>yehF</i>	-1.17	7.49E-04	catalase inhibitor protein; ATPase, K ⁺ -dependent, ribosome-associated
<i>glgA</i>	1.17	4.82E-02	glycogen synthase
<i>ybfG</i>	-1.17	5.16E-01	pseudo
<i>aslA</i>	-1.17	1.20E-01	acrylsulfatase-like enzyme

<i>yghG</i>	-1.17	1.33E-01	pilotin, required for secretin OM localization; verified lipoprotein
<i>oppA</i>	1.17	1.04E-02	oligopeptide transporter subunit
<i>yehB</i>	-1.17	3.93E-01	putative outer membrane protein
<i>yccA</i>	-1.16	4.45E-03	HflBKC-binding inner membrane protein, UPF0005 family
<i>kdgK</i>	-1.16	1.05E-02	ketodeoxygluconokinase
<i>pagP</i>	-1.16	2.61E-01	phospholipid:lipid A palmitoyltransferase
<i>appA</i>	1.16	6.49E-02	phosphoanhydride phosphorylase
<i>lolB</i>	1.16	1.21E-02	lipoprotein localization factor
<i>mazG</i>	-1.16	2.74E-02	nucleoside triphosphate pyrophosphohydrolase
<i>mobA</i>	1.16	8.14E-02	molybdopterin-guanine dinucleotide synthase
<i>yphG</i>	1.16	3.78E-01	hypothetical protein
<i>yiiM</i>	-1.16	3.00E-01	6-N-hydroxylaminopurine resistance protein
<i>ynbE</i>	-1.16	3.02E-01	lipoprotein
<i>cyaR</i>	1.16	7.35E-02	ncRNA
<i>ydgJ</i>	1.16	3.20E-02	putative oxidoreductase
<i>yhbT</i>	-1.16	2.81E-02	putative lipid carrier protein, COG3154 family
<i>rscF</i>	-1.16	1.54E-02	putative outer membrane protein, signal
<i>fldA</i>	-1.16	1.79E-02	flavodoxin 1
<i>srlD</i>	1.16	3.00E-01	sorbitol-6-phosphate dehydrogenase
<i>yibL</i>	-1.16	2.21E-02	conserved protein, ribosome-associated
<i>cysW</i>	-1.16	2.57E-03	sulfate/thiosulfate ABC transporter subunit
<i>yaeF</i>	-1.16	2.69E-01	putative lipoprotein
<i>opgG</i>	-1.16	2.07E-03	osmoregulated periplasmic glucan (OPG) biosynthesis periplasmic protein
<i>dedA</i>	-1.16	2.29E-02	conserved inner membrane protein
<i>hokB</i>	1.16	1.63E-01	toxic polypeptide, small
<i>zntA</i>	-1.16	3.54E-02	zinc, cobalt and lead efflux system
<i>rpoZ</i>	-1.16	4.22E-03	RNA polymerase, omega subunit
<i>lptF</i>	-1.16	9.00E-03	lipopolysaccharide export ABC permease of the LptBFGC export complex
<i>ybbA</i>	1.16	7.88E-02	putative transporter subunit: ATP-binding component of ABC superfamily
<i>moeB</i>	1.16	2.72E-02	molybdopterin synthase sulfurylase
<i>djlB</i>	1.16	6.17E-01	putative co-chaperone
<i>ybiW</i>	1.16	2.47E-01	putative pyruvate formate lyase
<i>ligT</i>	1.16	1.35E-01	2'-5' RNA ligase
<i>yggD</i>	1.16	1.69E-02	putative DNA-binding transcriptional regulator
<i>idnR</i>	1.16	9.44E-02	DNA-binding transcriptional repressor, 5-gluconate-binding
<i>yfbT</i>	1.16	4.34E-03	sugar phosphatase
<i>ycaN</i>	-1.16	6.92E-02	putative DNA-binding transcriptional regulator
<i>potB</i>	-1.16	9.85E-02	polyamine transporter subunit
<i>frdA</i>	-1.16	2.99E-02	fumarate reductase (anaerobic) catalytic and NAD/flavoprotein subunit
<i>envY</i>	1.16	4.27E-01	DNA-binding transcriptional activator of porin biosynthesis
<i>ldcA</i>	1.16	4.88E-02	murein tetrapeptide carboxypeptidase; LD-carboxypeptidase A
<i>rraA</i>	-1.16	7.71E-03	ribonuclease E (RNase E) inhibitor protein
<i>rnlB</i>	-1.16	7.09E-02	CP4-57 prophage; putative protein

<i>psiF</i>	-1.16	7.09E-02	conserved protein, PsiF family, pho regulon
<i>ybdN</i>	-1.16	5.10E-01	hypothetical protein
<i>fnr</i>	1.16	1.32E-03	DNA-binding transcriptional dual regulator, global regulator of anaerobic growth
<i>yjiC</i>	1.16	5.42E-01	hypothetical protein
<i>icd</i>	-1.16	5.13E-02	e14 prophage; isocitrate dehydrogenase, specific for NADP+
<i>rhmT</i>	1.16	6.27E-01	putative L-rhamnonate transporter
<i>hipA</i>	1.16	3.40E-02	EF-Tu kinase; serine protein kinase required for persister formation; toxin of HipAB TA pair
<i>deoD</i>	-1.16	6.83E-02	purine-nucleoside phosphorylase
<i>glpT</i>	-1.16	3.55E-01	sn-glycerol-3-phosphate transporter
<i>scpA</i>	1.16	4.55E-01	methylmalonyl-CoA mutase
<i>gutM</i>	1.16	6.40E-01	DNA-binding transcriptional activator of glucitol operon
<i>yfeC</i>	-1.16	9.73E-02	putative DNA-binding protein, DUF1323 family
<i>ybbP</i>	1.16	2.45E-02	putative ABC transporter permease
<i>aes</i>	-1.16	3.56E-01	acetyl esterase
<i>metJ</i>	-1.16	2.84E-02	DNA-binding transcriptional repressor, S-adenosylmethionine-binding
<i>ykgG</i>	-1.16	3.51E-01	putative transporter
<i>fdhF</i>	1.16	5.38E-02	formate dehydrogenase-H, selenopolypeptide subunit
<i>ytfQ</i>	1.16	1.16E-01	galactofuranose binding protein: periplasmic-binding component of ABC superfamily
<i>ynfG</i>	-1.16	4.51E-01	oxidoreductase, Fe-S subunit
<i>intB</i>	-1.16	4.22E-03	pseudo
<i>sxy</i>	-1.16	1.05E-01	required for expression of CRP-S-dependent promoters
<i>narK</i>	-1.16	4.81E-01	nitrate/nitrite transporter
<i>fliZ</i>	1.16	3.74E-01	RpoS antagonist; putative regulator of FlhA activity
<i>cysK</i>	-1.16	2.54E-03	cysteine synthase A, O-acetylserine sulphydrolase A subunit
<i>yfgF</i>	1.16	1.91E-01	cyclic-di-GMP phosphodiesterase, anaerobic
<i>rof</i>	-1.16	1.79E-02	modulator of Rho-dependent transcription termination
<i>yieK</i>	-1.16	4.70E-01	putative 6-phosphogluconolactonase
<i>yafO</i>	1.16	2.93E-01	mRNA interferase toxin of the YafO-YafN toxin-antitoxin system
<i>ygcS</i>	1.16	6.84E-01	putative transporter
<i>ycdU</i>	-1.16	6.29E-01	putative inner membrane protein
<i>erfK</i>	-1.16	9.46E-03	L,D-transpeptidase linking Lpp to murein
<i>bluR</i>	1.16	1.07E-02	repressor of blue light-responsive genes
<i>thiD</i>	1.16	4.15E-01	bifunctional hydroxy-methylpyrimidine kinase/ hydroxy-phosphomethylpyrimidine kinase
<i>pheV</i>	-1.16	3.98E-01	tRNA
<i>yjiV</i>	-1.16	8.51E-03	pseudo
<i>tamB</i>	1.16	3.45E-03	translocation and assembly module for autotransporter export, inner membrane subunit
<i>yhjX</i>	-1.16	3.73E-01	inner membrane protein, predicted oxalate-formate antiporter
<i>tdcB</i>	-1.16	8.18E-01	catabolic threonine dehydratase, PLP-dependent
<i>menE</i>	-1.16	2.95E-02	O-succinylbenzoate-CoA ligase
<i>yefM</i>	1.16	7.97E-02	antitoxin of the YoeB-YefM toxin-antitoxin system
<i>rplA</i>	-1.15	7.94E-03	50S ribosomal subunit protein L1
<i>yeeA</i>	-1.15	4.54E-02	inner membrane protein, FUSC family
<i>rplX</i>	1.15	3.13E-02	50S ribosomal subunit protein L24

<i>ompN</i>	1.15	5.14E-01	outer membrane pore protein N, non-specific
<i>waaG</i>	-1.15	1.24E-02	glucosyltransferase I
<i>glk</i>	1.15	6.33E-02	glucokinase
<i>ytjE</i>	-1.15	3.70E-01	iron-sulfur cluster repair protein RIC
<i>yegH</i>	-1.15	3.46E-02	inner membrane protein
<i>torZ</i>	1.15	1.67E-01	trimethylamine N-oxide reductase system III, catalytic subunit
<i>map</i>	-1.15	2.10E-03	methionine aminopeptidase
<i>yggN</i>	-1.15	1.68E-01	hypothetical protein
<i>ubiD</i>	1.15	8.50E-03	3-octaprenyl-4-hydroxybenzoate decarboxylase
<i>asnS</i>	1.15	2.57E-02	asparaginyl tRNA synthetase
<i>rnpB</i>	1.15	6.74E-02	ncRNA
<i>lptB</i>	1.15	1.92E-02	lipopolysaccharide export, ATP-binding protein of the LptBFGC export complex
<i>opgB</i>	-1.15	7.31E-03	phosphoglycerol transferases I and II
<i>yejO</i>	1.15	1.82E-02	pseudo
<i>yfcG</i>	-1.15	1.24E-01	GSH-dependent disulfide bond oxidoreductase
<i>mtlD</i>	1.15	4.10E-02	mannitol-1-phosphate dehydrogenase, NAD-dependent
<i>ybfB</i>	1.15	6.91E-01	putative membrane protein
<i>ynjE</i>	-1.15	1.30E-01	IscS specificity factor for molybdenum cofactor biosynthesis; rhodanese-like protein
<i>yaaY</i>	1.15	5.46E-01	hypothetical protein
<i>ccmA</i>	-1.15	2.32E-01	heme exporter subunit
<i>xylG</i>	1.15	3.32E-01	fused D-xylose transporter subunits of ABC superfamily: ATP-binding components
<i>ybjN</i>	1.15	4.78E-03	negative regulator of motility; multicopy suppressor of coaA(Ts)
<i>narW</i>	1.15	5.03E-01	nitrate reductase 2 (NRZ), delta subunit (assembly subunit)
<i>cpsB</i>	1.15	4.29E-01	mannose-1-phosphate guanylttransferase
<i>yqiB</i>	1.15	3.34E-02	DUF1249 protein YqiB
<i>yfgO</i>	-1.15	9.12E-02	putative inner membrane permease, UPF0118 family
<i>iclR</i>	-1.15	4.79E-03	DNA-binding transcriptional repressor
<i>metC</i>	1.15	9.74E-03	cystathionine beta-lyase, PLP-dependent
<i>ucpA</i>	-1.15	5.01E-02	furfural resistance protein, predicted short-chain oxidoreductase
<i>malX</i>	-1.15	3.43E-01	fused maltose and glucose-specific PTS enzymes: IIB component, IIC component
<i>dgkA</i>	-1.15	8.96E-03	diacylglycerol kinase
<i>sbcC</i>	1.15	1.22E-02	exonuclease, dsDNA, ATP-dependent
<i>yjfK</i>	-1.15	7.37E-01	conserved protein, DUF2491 family
<i>typA</i>	1.15	2.64E-03	GTP-binding protein
<i>feoA</i>	-1.15	6.07E-02	ferrous iron transporter, protein A
<i>clpP</i>	1.15	1.59E-02	proteolytic subunit of ClpA-ClpP and ClpX-ClpP ATP-dependent serine proteases
<i>arcB</i>	1.15	4.35E-02	aerobic respiration control sensor histidine protein kinase of ArcA
<i>ybeQ</i>	1.15	5.23E-01	hypothetical protein
<i>yafE</i>	1.15	1.35E-01	putative S-adenosyl-L-methionine-dependent methyltransferase
<i>visC</i>	1.15	2.51E-02	putative oxidoreductase with FAD/NAD(P)-binding domain
<i>yciB</i>	-1.15	1.78E-02	putative inner membrane protein
<i>kdgT</i>	-1.15	3.79E-01	2-keto-3-deoxy-D-gluconate transporter
<i>ppiD</i>	1.15	8.39E-03	periplasmic folding chaperone, has an inactive PPIase domain

<i>yhbQ</i>	-1.15	3.07E-01	conserved protein, GIY-YIG nuclease superfamily
<i>frlD</i>	1.15	4.16E-01	fructoselysine 6-kinase
<i>yahK</i>	-1.15	1.63E-02	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>yigI</i>	-1.15	3.68E-02	conserved protein, 4HBT family of thioesterases
<i>yigP</i>	1.15	7.67E-02	conserved protein, SCP2 family
<i>purU</i>	-1.15	1.58E-02	formyltetrahydrofolate hydrolase
<i>rprA</i>	1.15	7.41E-01	ncRNA
<i>yebS</i>	-1.15	2.98E-02	inner membrane protein
<i>alpA</i>	-1.15	6.25E-01	CP4-57 prophage; DNA-binding transcriptional activator
<i>sapA</i>	1.15	2.95E-02	antimicrobial peptide transport ABC transporter periplasmic binding protein
<i>ilvA</i>	1.15	5.21E-02	threonine deaminase
<i>atoS</i>	1.15	3.21E-01	sensory histidine kinase in two-component regulatory system with AtoC
<i>yggF</i>	1.15	7.28E-01	fructose 1,6 bisphosphatase isozyme
<i>yjdA</i>	1.15	1.23E-01	mutational suppressor of yhjH motility mutation; related to Dynamin GTPase
<i>yhfT</i>	-1.15	5.21E-01	putative inner membrane protein
<i>appC</i>	1.15	1.82E-01	cytochrome bd-II oxidase, subunit I
<i>dkgB</i>	-1.15	1.26E-01	2,5-diketo-D-gluconate reductase B
<i>uspE</i>	-1.15	3.24E-03	stress-induced protein
<i>rbsR</i>	-1.15	1.95E-01	DNA-binding transcriptional repressor of ribose metabolism
<i>potA</i>	1.15	2.22E-02	polyamine transporter subunit
<i>recR</i>	1.15	1.26E-02	gap repair protein
<i>npr</i>	1.15	1.13E-01	phosphohistidinoprotein-hexose phosphotransferase component of N-regulated PTS system
<i>ygfI</i>	1.15	2.98E-01	putative DNA-binding transcriptional regulator
<i>ybgT</i>	1.15	2.82E-01	hypothetical protein
<i>yqeF</i>	-1.15	2.00E-02	putative acyltransferase
<i>murP</i>	1.15	4.16E-01	N-acetylmuramic acid permease, EIIBC component, PTS system
<i>yegW</i>	1.15	2.19E-01	putative DNA-binding transcriptional regulator
<i>mtr</i>	-1.15	1.00E-01	tryptophan transporter of high affinity
<i>sodC</i>	-1.15	2.69E-02	superoxide dismutase, Cu, Zn, periplasmic
<i>yaeR</i>	1.15	1.01E-01	putative lyase
<i>cytR</i>	1.15	3.77E-02	DNA-binding transcriptional dual regulator
<i>ydhW</i>	1.15	4.61E-01	hypothetical protein
<i>paaJ</i>	1.15	1.93E-01	3-oxoadipyl-CoA/3-oxo-5,6-dehydrosuberil-CoA thiolase
<i>yceG</i>	1.15	3.83E-02	septation protein, ampicillin sensitivity
<i>gltB</i>	1.15	6.67E-02	glutamate synthase, large subunit
<i>yfcU</i>	1.15	2.65E-01	pseudo
<i>secM</i>	-1.15	1.34E-02	regulator of secA translation
<i>ryjB</i>	1.15	2.92E-01	ncRNA
<i>sseB</i>	1.15	7.11E-02	rhodanase-like enzyme, sulfur transfer from thiosulfate
<i>spf</i>	-1.15	7.09E-02	ncRNA
<i>tolC</i>	1.15	6.15E-03	transport channel
<i>yhhL</i>	-1.15	2.06E-01	conserved protein, DUF1145 family
<i>bglA</i>	-1.14	1.34E-02	6-phospho-beta-glucosidase A

<i>yjjU</i>	1.14	3.63E-01	putative phospholipase, patatin-like family
<i>glxR</i>	1.14	4.84E-01	tartronate semialdehyde reductase, NADH-dependent
<i>yafC</i>	-1.14	5.54E-02	putative DNA-binding transcriptional regulator
<i>pcnB</i>	1.14	1.23E-02	poly(A) polymerase
<i>ispH</i>	1.14	7.87E-03	4-hydroxy-3-methylbut-2-enyl diphosphate reductase, 4Fe-4S protein
<i>ybjQ</i>	-1.14	1.02E-02	conserved protein, UPF0145 family
<i>hslU</i>	1.14	3.92E-02	molecular chaperone and ATPase component of HslUV protease
<i>nhoA</i>	1.14	4.47E-01	N-hydroxyarylamine O-acetyltransferase
<i>yrhD</i>	-1.14	8.98E-01	hypothetical protein
<i>fimH</i>	-1.14	3.70E-01	minor component of type 1 fimbriae
<i>ygeV</i>	1.14	1.28E-01	putative DNA-binding transcriptional regulator
<i>fimD</i>	-1.14	4.07E-01	outer membrane usher protein, type 1 fimbrial synthesis
<i>yaiW</i>	1.14	2.20E-02	putative lipoprotein required for swarming phenotype
<i>sapB</i>	-1.14	1.75E-01	antimicrobial peptide transport ABC transporter permease
<i>flgA</i>	1.14	4.77E-01	assembly protein for flagellar basal-body periplasmic P ring
<i>ulaC</i>	1.14	7.06E-01	L-ascorbate-specific enzyme IIA component of PTS
<i>napG</i>	1.14	7.35E-01	ferredoxin-type protein essential for periplasmic nitrate reductase (NapAB)
<i>basR</i>	1.14	8.29E-02	DNA-binding response regulator in two-component regulatory system with BasS
<i>chaC</i>	-1.14	3.07E-02	cation transport regulator
<i>glgP</i>	-1.14	1.60E-02	glycogen phosphorylase
<i>casC</i>	-1.14	3.32E-01	CRISP RNA (crRNA) containing Cascade antiviral complex protein
<i>helD</i>	1.14	1.82E-02	DNA helicase IV
<i>ulaR</i>	-1.14	1.94E-01	transcriptional repressor for the L-ascorbate utilization (<i>ula</i>) divergon
<i>rhaR</i>	-1.14	6.31E-01	DNA-binding transcriptional activator for rhaSR, L-rhamnose-binding
<i>ybeM</i>	1.14	9.21E-02	pseudo
<i>phoP</i>	-1.14	9.12E-03	DNA-binding response regulator in two-component regulatory system with PhoQ
<i>yhdE</i>	1.14	3.69E-02	Maf-like protein
<i>sgcX</i>	-1.14	5.06E-01	KpLE2 phage-like element; predicted endoglucanase with Zn-dependent exopeptidase domain
<i>insF1</i>	1.14	7.98E-01	IS3 transposase B
<i>pdxK</i>	1.14	5.10E-03	pyridoxal-pyridoxamine kinase/hydroxymethylpyrimidine kinase
<i>yibN</i>	-1.14	9.92E-03	putative rhodanese-related sulfurtransferase
<i>uspC</i>	-1.14	1.50E-01	universal stress protein
<i>ycdX</i>	1.14	4.51E-02	alkaline phosphatase required for swarming
<i>prkB</i>	1.14	1.94E-02	putative phosphoribulokinase
<i>gcvA</i>	-1.14	2.88E-02	DNA-binding transcriptional dual regulator
<i>glpC</i>	1.14	6.11E-01	anaerobic sn-glycerol-3-phosphate dehydrogenase, C subunit, 4Fe-4S iron-sulfur cluster
<i>yhjE</i>	1.14	1.18E-01	inner membrane protein, predicted transporter
<i>gloB</i>	-1.14	3.12E-02	hydroxyacylglutathione hydrolase
<i>hscC</i>	1.14	4.55E-01	Hsp70 family chaperone Hsc62, binds to RpoD and inhibits transcription
<i>yeiW</i>	-1.14	7.04E-01	UPF0153 cysteine cluster protein, function unknown
<i>yjfl</i>	-1.14	9.06E-01	inner membrane protein, UPF0719 family
<i>mgsA</i>	-1.14	8.81E-03	methylglyoxal synthase
<i>livH</i>	1.14	7.19E-02	leucine/isoleucine/valine transporter subunit

<i>agaR</i>	-1.14	2.50E-02	DNA-binding transcriptional repressor of the aga regulon
<i>yqhC</i>	1.14	1.26E-01	transcriptional activator of yqhD
<i>phoB</i>	-1.14	7.10E-02	DNA-binding response regulator in two-component regulatory system with PhoR (or CreC)
<i>paaZ</i>	1.14	6.35E-01	fused oxepin-CoA hydrolase/3-oxo-5,6-dehydrosueryl-CoA semialdehyde dehydrogenase
<i>yciN</i>	-1.14	2.78E-02	DUF2498 protein YciN
<i>sclA</i>	1.14	3.48E-02	selenocysteine synthase
<i>ygbA</i>	-1.14	6.26E-01	hypothetical protein
<i>ascB</i>	1.14	1.38E-01	cryptic 6-phospho-beta-glucosidase
<i>hemE</i>	1.14	6.26E-03	uroporphyrinogen decarboxylase
<i>ygaZ</i>	-1.14	2.55E-02	putative L-valine exporter, norvaline resistance
<i>dxr</i>	1.14	5.96E-02	1-deoxy-D-xylulose 5-phosphate reductoisomerase
<i>yedQ</i>	1.14	3.33E-02	putative membrane-anchored diguanylate cyclase
<i>efeU</i>	-1.14	6.22E-02	pseudo
<i>ydfB</i>	-1.14	8.24E-01	Qin prophage; putative protein
<i>yeaK</i>	-1.14	1.10E-02	hypothetical protein
<i>dnaQ</i>	-1.14	1.72E-02	DNA polymerase III epsilon subunit
<i>yhhZ</i>	1.14	7.31E-01	hypothetical protein
<i>topA</i>	-1.14	1.72E-02	DNA topoisomerase I, omega subunit
<i>kbaY</i>	-1.14	9.17E-01	tagatose 6-phosphate aldolase 1, kbaY subunit
<i>casB</i>	-1.14	5.33E-01	CRISP RNA (crRNA) containing Cascade antiviral complex protein
<i>rrrQ</i>	-1.14	9.17E-01	Qin prophage; predicted lysozyme
<i>cysA</i>	1.14	1.10E-02	sulfate/thiosulfate transporter subunit
<i>yeaL</i>	-1.14	3.31E-01	putative inner membrane protein, UPF0756 family
<i>yicJ</i>	1.14	5.93E-01	putative transporter
<i>lepB</i>	-1.14	1.10E-02	leader peptidase (signal peptidase I)
<i>ycjQ</i>	1.14	6.65E-01	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>dcuD</i>	1.14	7.19E-01	putative transporter
<i>yjbQ</i>	1.14	3.54E-02	thiamin phosphate synthase
<i>ilvE</i>	-1.14	4.42E-02	branched-chain amino-acid aminotransferase
<i>zapD</i>	-1.14	4.28E-02	FtsZ stabilizer
<i>thiE</i>	-1.14	8.43E-01	thiamin phosphate synthase (thiamin phosphate pyrophosphorylase)
<i>murI</i>	-1.14	3.38E-02	glutamate racemase
<i>potE</i>	1.13	2.08E-01	putrescine/proton symporter: putrescine/ornithine antiporter
<i>yjcC</i>	-1.13	1.52E-01	putative membrane-anchored cyclic-di-GMP phosphodiesterase
<i>abrB</i>	-1.13	3.76E-01	regulator of aidB expression; inner membrane protein
<i>fabH</i>	-1.13	1.03E-01	3-oxoacyl-[acyl-carrier-protein] synthase III
<i>yjeT</i>	-1.13	6.49E-01	conserved protein, DUF2065 family
<i>ybjJ</i>	-1.13	1.13E-01	putative transporter
<i>yoaG</i>	-1.13	8.57E-01	hypothetical protein
<i>rpoS</i>	1.13	3.35E-01	RNA polymerase, sigma S (sigma 38) factor
<i>queG</i>	1.13	8.26E-02	epoxyqueuosine reductase, cobalamine-stimulated; queosine biosynthesis
<i>wcaM</i>	1.13	1.56E-01	colanic acid biosynthesis protein
<i>mnaT</i>	1.13	5.34E-02	methionine N-acyltransferase; L-amino acid N-acyltransferase

<i>ybdL</i>	1.13	8.28E-02	methionine aminotransferase, PLP-dependent
<i>carB</i>	-1.13	2.38E-01	carbamoyl-phosphate synthase large subunit
<i>yhgA</i>	-1.13	2.87E-01	putative transposase
<i>ykfB</i>	-1.13	1.87E-01	CP4-6 prophage; putative protein
<i>pgpB</i>	-1.13	5.63E-02	phosphatidylglycerophosphatase B
<i>yeaO</i>	-1.13	6.90E-02	hypothetical protein
<i>lpoB</i>	1.13	7.97E-02	outer membrane lipoprotein
<i>dsbA</i>	-1.13	3.49E-02	periplasmic protein disulfide isomerase I
<i>ybjI</i>	-1.13	6.37E-02	FMN and erythrose-4-P phosphatase
<i>ycjF</i>	1.13	1.25E-01	inner membrane protein, UPF0283 family
<i>bamC</i>	1.13	1.29E-02	lipoprotein required for OM biogenesis, in BamABCDE complex
<i>yadC</i>	-1.13	2.76E-01	putative fimbrial-like adhesin protein
<i>yhiL</i>	1.13	5.12E-01	pseudo
<i>hofM</i>	1.13	4.68E-01	protein required for the utilization of DNA as a carbon source
<i>paaX</i>	-1.13	5.17E-02	repressor of phenylacetic acid degradation paa operon, phenylacetyl-CoA inducer
<i>ydHs</i>	1.13	1.84E-01	conserved protein with FAD/NAD(P)-binding domain
<i>yaiE</i>	-1.13	3.44E-02	conserved protein, UPF0345 family
<i>rspB</i>	-1.13	4.01E-01	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>ydaT</i>	-1.13	6.15E-01	Rac prophage; putative protein
<i>bdcR</i>	-1.13	1.72E-01	transcriptional repressor for divergent bdcA
<i>fucO</i>	1.13	3.49E-01	L-1,2-propanediol oxidoreductase
<i>yibJ</i>	1.13	4.65E-01	pseudo
<i>yjiE</i>	1.13	1.50E-01	hypochlorite-responsive transcription factor
<i>bisC</i>	1.13	5.17E-02	biotin sulfoxide reductase
<i>yafQ</i>	-1.13	1.90E-01	translation inhibitor toxin of toxin-antitoxin pair YafQ/DinJ
<i>hrpB</i>	1.13	4.96E-02	putative ATP-dependent helicase
<i>mnmC</i>	1.13	4.06E-02	5-methylaminomethyl-2-thiouridine-forming enzyme methyltransferase
<i>iadA</i>	-1.13	4.89E-02	isoaspartyl dipeptidase
<i>yhaM</i>	1.13	2.63E-01	hypothetical protein
<i>ubiC</i>	1.13	7.70E-02	chorismate--pyruvate lyase
<i>rsuA</i>	-1.13	2.40E-02	16S rRNA pseudouridine(516) synthase
<i>ebgA</i>	1.13	5.22E-01	cryptic beta-D-galactosidase, alpha subunit
<i>ydiN</i>	-1.13	8.01E-01	inner membrane protein, predicted MFS superfamily transporter
<i>aaeA</i>	1.13	4.79E-01	p-hydroxybenzoic acid efflux system component
<i>mdtD</i>	-1.13	3.63E-01	putative arabinose efflux transporter
<i>brnQ</i>	1.13	1.86E-02	branched-chain amino acid transport system 2 carrier protein
<i>dnaB</i>	1.13	1.81E-02	replicative DNA helicase
<i>ghrB</i>	1.13	1.08E-02	glyoxylate/hydroxypyruvate reductase B
<i>wecC</i>	-1.13	1.15E-01	UDP-N-acetyl-D-mannosaminuronic acid dehydrogenase
<i>yahD</i>	-1.13	5.03E-01	ankyrin repeat protein
<i>ycbU</i>	-1.13	6.36E-01	putative fimbrial-like adhesin protein
<i>hinT</i>	-1.13	1.68E-02	purine nucleoside phosphoramidase, dadA activator protein
<i>psd</i>	1.13	1.56E-02	phosphatidylserine decarboxylase

<i>yhhX</i>	-1.13	2.58E-02	putative oxidoreductase with NAD(P)-binding Rossmann-fold domain
<i>selB</i>	1.13	5.07E-02	selenocysteinyl-tRNA-specific translation factor
<i>alx</i>	-1.13	1.89E-01	inner membrane protein, part of terminus
<i>gfcA</i>	1.13	5.45E-01	hypothetical protein
<i>gloA</i>	-1.13	2.13E-02	glyoxalase I, Ni-dependent
<i>yejG</i>	1.13	3.24E-02	hypothetical protein
<i>trmN</i>	-1.13	1.95E-01	tRNA ¹ (Val) (adenine(37)-N6)-methyltransferase
<i>mcaS</i>	1.13	6.63E-01	ncRNA
<i>ribE</i>	1.13	1.12E-02	riboflavin synthase beta chain
<i>deoR</i>	-1.13	2.17E-02	DNA-binding transcriptional repressor
<i>cbl</i>	-1.13	1.60E-01	DNA-binding transcriptional activator for the ssuEADCB and tauABCD operons
<i>arnE</i>	-1.13	6.67E-01	undecaprenyl phosphate-alpha-L-ara4N exporter; flippase ArnEF subunit
<i>gss</i>	1.13	3.13E-02	fused glutathionylspermidine amidase/glutathionylspermidine synthetase
<i>ascG</i>	-1.13	1.98E-01	DNA-binding transcriptional repressor
<i>gph</i>	1.13	5.51E-02	phosphoglycolate phosphatase
<i>ogrK</i>	-1.13	3.10E-01	positive regulator of P2 growth (insertion of P2 ogr gene into the chromosome)
<i>serV</i>	-1.13	2.39E-01	tRNA
<i>ygeR</i>	1.13	5.27E-02	putative lipoprotein involved in septation
<i>yfaD</i>	-1.13	3.76E-01	hypothetical protein
<i>menI</i>	-1.13	6.53E-02	acyl-CoA esterase
<i>mntP</i>	1.13	7.11E-01	putative Mn(2+) efflux pump, mntR-regulated
<i>agaD</i>	1.13	6.81E-01	N-acetylgalactosamine-specific enzyme IID component of PTS
<i>yihX</i>	-1.13	1.15E-01	alpha-D-Glucose-1-P phosphatase, anomer-specific
<i>yciQ</i>	-1.13	1.09E-01	putative inner membrane protein
<i>yebF</i>	-1.13	4.29E-02	extracellular Colicin M immunity family protein
<i>wcaE</i>	-1.13	5.67E-01	putative glycosyl transferase
<i>yoaH</i>	-1.13	1.80E-01	hypothetical protein
<i>rhcC</i>	-1.13	3.31E-01	rhcC element core protein RshC
<i>ylbH</i>	-1.12	6.63E-01	pseudo
<i>tusC</i>	1.12	2.25E-01	protein required for 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis
<i>nikD</i>	-1.12	7.54E-01	nickel transporter subunit
<i>thiI</i>	1.12	2.80E-02	tRNA s(4)U8 sulfurtransferase
<i>rsfS</i>	-1.12	7.57E-02	ribosomal silencing factor
<i>rlmM</i>	-1.12	3.24E-02	23S rRNA C2498 2'-O-ribose methyltransferase, SAM-dependent
<i>gstA</i>	-1.12	2.58E-02	glutathionine S-transferase
<i>truB</i>	-1.12	2.13E-02	tRNA pseudouridine(55) synthase
<i>ypdI</i>	-1.12	7.98E-01	putative lipoprotein involved in colanic acid biosynthesis
<i>yjfW</i>	-1.12	5.52E-01	CP4-57 prophage; predicted inner membrane protein
<i>yfeZ</i>	-1.12	3.43E-01	inner membrane protein
<i>yjjY</i>	-1.12	6.78E-01	hypothetical protein
<i>fsr</i>	-1.12	1.24E-01	putative fosmidomycin efflux system
<i>msrA</i>	-1.12	3.96E-02	methionine sulfoxide reductase A
<i>yagE</i>	-1.12	6.77E-01	2-keto-3-deoxy gluconate (KDG) aldolase; CP4-6 prophage

<i>pldB</i>	1.12	1.96E-02	lysophospholipase L2
<i>moeA</i>	1.12	1.07E-01	molybdopterin molybdenumtransferase; molybdopterin biosynthesis protein
<i>araG</i>	-1.12	4.00E-01	fused L-arabinose transporter subunits of ABC superfamily: ATP-binding components
<i>murJ</i>	-1.12	7.77E-02	putative peptidoglycan lipid II flippase required for murein synthesis
<i>glyV</i>	1.12	1.34E-01	tRNA
<i>ylcH</i>	1.12	6.79E-01	hypothetical protein, DLP12 prophage
<i>sfnH</i>	1.12	8.26E-01	putative fimbrial-like adhesin protein
<i>yecD</i>	1.12	5.73E-02	isochorismatase family protein
<i>elfC</i>	1.12	3.77E-01	putative outer membrane usher protein
<i>leuE</i>	-1.12	2.42E-01	neutral amino-acid efflux system
<i>proP</i>	-1.12	7.11E-02	proline/glycine betaine transporter
<i>cyoA</i>	-1.12	2.94E-02	cytochrome o ubiquinol oxidase subunit II
<i>yggS</i>	1.12	8.65E-02	putative enzyme, binds pyridoxal 5'-phosphate
<i>ulaG</i>	-1.12	5.34E-01	L-ascorbate 6-phosphate lactonase
<i>ade</i>	1.12	3.34E-01	cryptic adenine deaminase
<i>ybbN</i>	1.12	2.03E-02	DnaK co-chaperone, thioredoxin-like protein
<i>rcsD</i>	-1.12	4.21E-02	phosphotransfer intermediate protein in two-component regulatory system with RcsBC
<i>ydjG</i>	1.12	3.97E-01	alpha-Keto reductase, NADH-dependent; can use methylglyoxal as substrate
<i>clsA</i>	-1.12	2.00E-02	cardiolipin synthase I
<i>baeS</i>	-1.12	2.38E-01	sensory histidine kinase in two-component regulatory system with BaeR
<i>aroL</i>	-1.12	9.93E-02	shikimate kinase II
<i>yrfF</i>	-1.12	2.80E-02	inner membrane protein
<i>zitB</i>	-1.12	1.34E-01	zinc efflux system
<i>wecH</i>	-1.12	3.76E-01	O-acetyltransferase for enterobacterial common antigen (ECA)
<i>yjdP</i>	1.12	3.52E-01	hypothetical protein
<i>gfcE</i>	1.12	3.83E-01	lipoprotein required for formation of the O-antigen capsule
<i>ydiK</i>	-1.12	7.14E-02	inner membrane protein, UPF0118 family
<i>yieE</i>	-1.12	2.14E-01	putative phosphopantetheinyl transferase, COG2091 family
<i>aegA</i>	1.12	3.69E-01	fused predicted oxidoreductase: FeS binding subunit/NAD/FAD-binding subunit
<i>yfbV</i>	1.12	3.17E-02	inner membrane protein, UPF0208 family
<i>lsrR</i>	1.12	2.77E-01	lsr operon transcriptional repressor
<i>ompR</i>	1.12	3.44E-02	DNA-binding response regulator in two-component regulatory system with EnvZ
<i>yehT</i>	-1.12	2.61E-01	putative response regulator in two-component system with YehU
<i>yqjI</i>	1.12	5.33E-02	putative transcriptional regulator, PadR family
<i>yhcF</i>	-1.12	1.99E-01	putative transcriptional regulator
<i>alsK</i>	1.12	4.84E-01	D-allose kinase
<i>zwf</i>	1.12	1.78E-01	glucose-6-phosphate 1-dehydrogenase
<i>yicO</i>	1.12	6.80E-01	putative adenine permease
<i>cutC</i>	1.12	5.82E-02	copper homeostasis protein
<i>psrO</i>	1.12	9.25E-01	ncRNA
<i>prs</i>	-1.12	5.29E-02	phosphoribosylpyrophosphate synthase
<i>cusS</i>	-1.12	1.45E-01	sensory histidine kinase in two-component regulatory system with CusR, senses copper ions
<i>yffQ</i>	1.12	8.11E-01	CP4-57 prophage; putative protein

<i>zapA</i>	1.12	7.57E-02	FtsZ stabilizer
<i>dicA</i>	-1.12	1.18E-01	Qin prophage; predicted regulator for DicB
<i>rcnB</i>	1.12	1.25E-01	periplasmic modulator of Ni and Co efflux
<i>eptA</i>	1.12	2.00E-01	lipid A phosphoethanolamine transferase
<i>yjfP</i>	-1.12	4.38E-01	CP4-57 prophage; predicted GTP-binding protein
<i>eco</i>	1.12	1.74E-01	ecotin, a serine protease inhibitor
<i>oxyR</i>	1.12	4.00E-02	oxidative and nitrosative stress transcriptional regulator
<i>nuoE</i>	-1.12	1.11E-01	NADH:ubiquinone oxidoreductase, chain E
<i>yffN</i>	-1.12	8.15E-01	CPZ-55 prophage; putative protein
<i>ygdI</i>	-1.12	1.40E-01	putative lipoprotein
<i>pinR</i>	-1.12	7.35E-01	Rac prophage; predicted site-specific recombinase
<i>rhsB</i>	1.12	4.61E-01	rhsB element core protein RshB
<i>znuA</i>	-1.12	7.53E-02	zinc transporter subunit: periplasmic-binding component of ABC superfamily
<i>ftsY</i>	-1.12	5.99E-02	Signal Recognition Particle (SRP) receptor
<i>ftsB</i>	-1.12	8.14E-02	cell division protein
<i>wzzE</i>	-1.12	6.31E-02	Entobacterial Common Antigen (ECA) polysaccharide chain length modulation protein
<i>yciY</i>	1.12	1.32E-01	hypothetical protein
<i>ykgA</i>	-1.12	2.82E-01	pseudo
<i>yddW</i>	-1.12	1.14E-01	liprotein, glycosyl hydrolase homolog
<i>dtgC</i>	1.12	3.93E-01	dipeptide and tripeptide permease
<i>yidK</i>	1.12	7.21E-01	putative transporter
<i>cmoB</i>	1.12	1.37E-01	tRNA mo(5)U34 methyltransferase, SAM-dependent
<i>btuC</i>	-1.12	2.07E-01	vitamin B12 transporter subunit: membrane component of ABC superfamily
<i>araE</i>	-1.12	3.01E-01	arabinose transporter
<i>ygbK</i>	1.12	6.07E-01	hypothetical protein
<i>ydiM</i>	-1.12	8.01E-01	inner membrane protein, predicted transporter
<i>ycaO</i>	1.12	2.59E-02	ribosomal protein S12 methylthiotransferase accessory factor
<i>potG</i>	1.12	1.98E-01	putrescine transporter subunit: ATP-binding component of ABC superfamily
<i>nrdR</i>	1.12	1.13E-01	hypothetical protein
<i>ispE</i>	1.12	3.40E-02	4-diphosphocytidyl-2-C-methylerythritol kinase
<i>ydhU</i>	1.11	4.83E-01	putative cytochrome
<i>yobH</i>	-1.11	1.72E-01	hypothetical protein
<i>tsaB</i>	-1.11	8.13E-02	tRNA(ANN) t(6)A37 threonylcarbamoyladenine modification protein
<i>sdaC</i>	1.11	8.91E-02	putative serine transporter
<i>yihM</i>	-1.11	3.54E-01	putative sugar phosphate isomerase
<i>yafV</i>	1.11	1.49E-01	putative C-N hydrolase family amidase, NAD(P)-binding
<i>wbbJ</i>	-1.11	1.23E-01	putative lipopolysaccharide biosynthesis O-acetyl transferase
<i>pgrR</i>	-1.11	8.35E-02	putative DNA-binding transcriptional regulator
<i>cydD</i>	1.11	1.12E-01	fused glutathione, cysteine exporter subunits of ABC superfamily
<i>yhdP</i>	-1.11	7.72E-02	conserved membrane protein, predicted transporter
<i>tabA</i>	-1.11	1.96E-01	biofilm modulator regulated by toxins
<i>yrbN</i>	1.11	4.65E-01	hypothetical protein
<i>pgl</i>	-1.11	4.59E-02	6-phosphogluconolactonase

<i>intG</i>	1.11	8.70E-01	pseudo
<i>rtn</i>	-1.11	1.57E-01	resistance protein for phages lambda and N4, when overexpressed
<i>leuZ</i>	1.11	1.54E-01	tRNA
<i>eutH</i>	-1.11	6.49E-01	ethanolamine transporter
<i>mqsA</i>	1.11	1.02E-01	antitoxin for MqsR toxin; transcriptional repressor
<i>yojI</i>	1.11	5.02E-02	microcin J25 efflux pump, TolC-dependent
<i>pgsA</i>	1.11	6.25E-02	phosphatidylglycerophosphate synthetase
<i>rplI</i>	-1.11	1.51E-01	50S ribosomal subunit protein L9
<i>yrfG</i>	-1.11	1.22E-01	GMP/IMP nucleotidase
<i>sbmA</i>	1.11	1.32E-01	microcin B17 transporter
<i>yedD</i>	-1.11	8.08E-02	lipoprotein
<i>ygcQ</i>	1.11	6.48E-01	putative flavoprotein
<i>yegR</i>	-1.11	5.37E-01	hypothetical protein
<i>dgt</i>	1.11	7.21E-02	deoxyguanosine triphosphate triphosphohydrolase
<i>waaQ</i>	-1.11	7.88E-02	lipopolysaccharide core biosynthesis protein
<i>ratB</i>	1.11	1.62E-01	conserved protein, UPF0125 family
<i>aroC</i>	1.11	9.51E-02	chorismate synthase
<i>moaC</i>	-1.11	1.32E-01	molybdopterin biosynthesis, protein C
<i>ampD</i>	-1.11	1.24E-01	1,6-anhydro-N-acetylmuramyl-L-alanine amidase, Zn-dependent; murein amidase
<i>insX</i>	1.11	2.47E-01	pseudo
<i>nadD</i>	1.11	2.13E-01	nicotinic acid mononucleotide adenylyltransferase, NAD(P)-dependent
<i>rpoD</i>	1.11	5.54E-02	RNA polymerase, sigma 70 (sigma D) factor
<i>aroB</i>	-1.11	5.66E-02	3-dehydroquinate synthase
<i>yebV</i>	-1.11	2.02E-01	hypothetical protein
<i>yedP</i>	-1.11	9.30E-02	putative mannosyl-3-phosphoglycerate phosphatase
<i>yidX</i>	1.11	1.23E-01	putative lipoproteinC
<i>hybB</i>	1.11	6.92E-01	putative hydrogenase 2 cytochrome b type component
<i>yagI</i>	-1.11	1.63E-01	CP4-6 prophage; predicted DNA-binding transcriptional regulator
<i>ycgB</i>	-1.11	7.68E-02	hypothetical protein
<i>eutM</i>	-1.11	8.30E-01	putative carboxysome structural protein, ethanolamine utilization protein
<i>wecA</i>	-1.11	2.88E-02	UDP-GlcNAc:undecaprenylphosphate GlcNAc-1-phosphate transferase
<i>yigB</i>	1.11	1.42E-01	FMN phosphatase
<i>ygjQ</i>	1.11	7.68E-01	conserved protein, SanA family, DUF218 superfamily
<i>nadK</i>	1.11	5.84E-02	NAD kinase
<i>gspA</i>	-1.11	6.45E-01	general secretory pathway component, cryptic
<i>pnp</i>	1.11	9.87E-02	polynucleotide phosphorylase/polyadenylase
<i>ycdZ</i>	-1.11	2.16E-01	inner membrane protein, DUF1097 family
<i>pdxB</i>	1.11	3.97E-02	erythronate-4-phosphate dehydrogenase
<i>leuO</i>	-1.11	3.65E-01	DNA-binding transcriptional activator
<i>fucP</i>	1.11	7.94E-01	L-fucose transporter
<i>ypfH</i>	-1.11	2.15E-01	putative hydrolase
<i>syd</i>	-1.11	1.23E-01	secY-interacting protein
<i>yqiH</i>	1.11	6.24E-01	putative periplasmic pilin chaperone

<i>treC</i>	1.11	1.58E-01	trehalose-6-P hydrolase
<i>fabD</i>	-1.11	6.83E-02	malonyl-CoA-[acyl-carrier-protein] transacylase
<i>ybgQ</i>	1.11	8.13E-01	putative outer membrane protein
<i>rrlD</i>	-1.11	7.46E-01	23S ribosomal RNA of <i>rrnD</i> operon
<i>hemN</i>	-1.11	1.09E-01	coproporphyrinogen III oxidase, SAM and NAD(P)H dependent, oxygen-independent
<i>ydiZ</i>	-1.11	2.37E-01	hypothetical protein
<i>yajO</i>	-1.11	5.25E-02	2-carboxybenzaldehyde reductase
<i>rrsH</i>	-1.11	8.47E-01	16S ribosomal RNA of <i>rrnH</i> operon
<i>pth</i>	-1.11	1.02E-01	peptidyl-tRNA hydrolase
<i>gspI</i>	-1.11	9.23E-01	general secretory pathway component, cryptic
<i>alkB</i>	1.11	5.47E-01	oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions
<i>lafU</i>	1.11	6.65E-01	pseudo
<i>ybdF</i>	-1.11	2.23E-01	hypothetical protein
<i>yiaD</i>	-1.11	3.17E-01	multicopy suppressor of <i>bamB</i> ; outer membrane lipoprotein
<i>yoaF</i>	-1.11	3.65E-01	conserved outer membrane lipoprotein
<i>ybjO</i>	-1.11	2.82E-01	inner membrane protein, DUF2593 family
<i>yfgD</i>	1.11	9.02E-02	putative oxidoreductase
<i>proA</i>	1.11	4.15E-02	gamma-glutamylphosphate reductase
<i>yigZ</i>	1.11	2.42E-01	conserved protein, UPF0029 family
<i>ymfE</i>	-1.11	4.01E-01	e14 prophage; predicted inner membrane protein
<i>aroH</i>	1.11	6.46E-02	3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tryptophan repressible
<i>ylaC</i>	1.11	1.01E-01	inner membrane protein, DUF1449 family
<i>yqhH</i>	-1.11	8.08E-01	outer membrane lipoprotein, Lpp paralog
<i>yfcH</i>	1.11	4.53E-02	conserved protein with NAD(P)-binding Rossmann-fold domain
<i>ptsN</i>	1.11	7.54E-02	sugar-specific enzyme IIA component of PTS
<i>yrhB</i>	-1.11	5.81E-01	stable heat shock chaperone
<i>ybhR</i>	1.11	2.76E-01	putative transporter subunit: membrane component of ABC superfamily
<i>tyrR</i>	1.11	3.19E-02	DNA-binding transcriptional dual regulator, tyrosine-binding
<i>dxs</i>	-1.11	6.63E-02	1-deoxyxylulose-5-phosphate synthase, thiamine-requiring, FAD-requiring
<i>gsiB</i>	1.11	4.58E-02	glutathione periplasmic binding protein, ABC superfamily transporter
<i>htrE</i>	-1.11	4.55E-01	putative outer membrane usher protein
<i>yggI</i>	1.11	4.89E-01	hypothetical protein
<i>wecE</i>	-1.11	1.33E-01	TDP-4-oxo-6-deoxy-D-glucose transaminase
<i>ygaC</i>	-1.11	2.75E-01	hypothetical protein
<i>tdcD</i>	-1.11	6.08E-01	propionate kinase/acetate kinase C, anaerobic
<i>ftsQ</i>	-1.11	5.72E-02	divisome assembly protein, membrane anchored protein involved in growth of wall at septum
<i>prpB</i>	-1.11	7.86E-01	2-methylisocitrate lyase
<i>rutD</i>	1.11	9.37E-01	putative aminoacrylate hydrolase, reactive intermediate detoxification
<i>efeO</i>	1.11	1.59E-01	inactive ferrous ion transporter EfeUOB
<i>setB</i>	1.10	5.02E-01	lactose/glucose efflux system
<i>fimC</i>	-1.10	5.07E-01	periplasmic chaperone
<i>mgrR</i>	1.10	5.14E-01	ncRNA
<i>wcaI</i>	-1.10	7.35E-01	putative glycosyl transferase

<i>ravA</i>	-1.10	1.15E-01	fused predicted transcriptional regulator: sigma54 activator protein/conserved protein
<i>mhpR</i>	1.10	1.35E-01	DNA-binding transcriptional activator, 3HPP-binding
<i>moaD</i>	-1.10	4.66E-01	molybdopterin synthase, small subunit
<i>phoQ</i>	1.10	4.89E-02	sensory histidine kinase in two-component regulatory system with PhoP
<i>zipA</i>	-1.10	4.86E-02	FtsZ stabilizer
<i>ybhD</i>	-1.10	7.64E-01	putative DNA-binding transcriptional regulator
<i>miaB</i>	-1.10	8.10E-02	tRNA-i(6)A37 methylthiotransferase
<i>yehQ</i>	1.10	4.73E-01	putative inner membrane protein, SIRB family
<i>lolE</i>	1.10	5.72E-02	lipoprotein-releasing system transmembrane protein
<i>ynaJ</i>	-1.10	5.76E-02	putative inner membrane protein, DUF2534 family
<i>yqeG</i>	-1.10	3.76E-01	putative transporter
<i>ubiX</i>	-1.10	1.47E-01	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
<i>tehB</i>	1.10	1.01E-01	tellurite, selenium methyltransferase, SAM-dependent; tellurite, selenium resistance protein
<i>ytfI</i>	1.10	5.82E-01	hypothetical protein
<i>csdE</i>	1.10	2.15E-01	CsdA-binding activator; Fe-S protein
<i>yhhH</i>	1.10	7.32E-01	hypothetical protein
<i>ugpC</i>	-1.10	3.74E-01	glycerol-3-phosphate transporter subunit
<i>hns</i>	-1.10	8.30E-02	global DNA-binding transcriptional dual regulator H-NS
<i>nemA</i>	-1.10	1.43E-01	N-ethylmaleimide reductase, FMN-linked
<i>rimI</i>	1.10	1.74E-01	ribosomal-protein-S18-alanine N-acetyltransferase
<i>yphD</i>	-1.10	7.95E-01	putative sugar transporter subunit: membrane component of ABC superfamily
<i>speF</i>	-1.10	6.29E-01	ornithine decarboxylase isozyme, inducible
<i>rsmC</i>	-1.10	7.16E-02	16S rRNA m(2)G1207 methyltransferase, SAM-dependent
<i>arfB</i>	1.10	2.85E-01	alternative stalled-ribosome rescue factor B; peptidyl-tRNA hydrolase, ribosome-attached
<i>wbbK</i>	1.10	4.09E-02	lipopolysaccharide biosynthesis protein
<i>yhjK</i>	-1.10	9.94E-02	cyclic-di-GMP phosphodiesterase
<i>gpr</i>	-1.10	2.05E-01	L-glyceraldehyde 3-phosphate reductase
<i>rem</i>	-1.10	7.11E-01	Qin prophage; putative protein
<i>xylR</i>	1.10	2.19E-01	DNA-binding transcriptional activator, xylose-binding
<i>zupT</i>	-1.10	1.05E-01	zinc transporter
<i>tsaC</i>	-1.10	1.84E-01	tRNA(ANN) t(6)A37 threonylcarbamoyladenosine modification protein
<i>frvX</i>	1.10	6.54E-01	putative peptidase
<i>nupC</i>	-1.10	4.80E-02	nucleoside (except guanosine) transporter
<i>nrfB</i>	-1.10	8.15E-01	nitrite reductase, formate-dependent, penta-heme cytochrome c
<i>rhtB</i>	1.10	2.69E-01	homoserine, homoserine lactone and S-methyl-methionine efflux pump
<i>mppA</i>	-1.10	6.65E-02	murein tripeptide (L-ala-gamma-D-glutamyl-meso-DAP) transporter subunit
<i>yjbB</i>	-1.10	2.04E-01	putative Na ⁺ /Pi-cotransporter
<i>yraK</i>	-1.10	4.52E-01	putative fimbrial-like adhesin protein
<i>yebV</i>	1.10	8.10E-01	putative fimbrial-like adhesin protein
<i>pncB</i>	1.10	7.19E-02	nicotinate phosphoribosyltransferase
<i>argS</i>	-1.10	4.56E-02	arginyl-tRNA synthetase
<i>yidB</i>	-1.10	2.47E-01	conserved protein, DUF937 family
<i>yhdV</i>	1.10	5.04E-01	putative outer membrane protein

<i>ryjA</i>	1.10	5.01E-01	ncRNA
<i>yhbW</i>	1.10	7.22E-02	putative enzyme
<i>yraR</i>	-1.10	4.78E-01	putative nucleoside-diphosphate-sugar epimerase
<i>pmbA</i>	1.10	1.36E-01	putative peptidase required for the maturation and secretion of the antibiotic peptide MccB17
<i>csiR</i>	-1.10	2.11E-01	DNA-binding transcriptional repressor of <i>csiD</i>
<i>amiC</i>	1.10	8.20E-02	N-acetylmuramoyl-L-alanine amidase
<i>yagG</i>	1.10	6.59E-01	CP4-6 prophage; predicted sugar transporter
<i>zraS</i>	1.10	5.40E-01	sensory histidine kinase in two-component regulatory system with ZraR
<i>nuoG</i>	-1.10	2.21E-01	NADH:ubiquinone oxidoreductase, chain G
<i>yacH</i>	-1.10	6.10E-01	hypothetical protein
<i>mdtG</i>	-1.10	4.69E-01	putative drug efflux system
<i>xapA</i>	1.10	9.34E-01	purine nucleoside phosphorylase II
<i>yhfS</i>	1.10	6.42E-01	hypothetical protein
<i>marB</i>	1.10	4.14E-01	hypothetical protein
<i>yedV</i>	-1.10	3.64E-01	putative sensory kinase in two-component regulatory system with YedW
<i>ynbD</i>	1.10	6.42E-01	putative phosphatase inner membrane protein
<i>dsbE</i>	1.10	6.18E-01	periplasmic thioredoxin of cytochrome c-type biogenesis
<i>yehX</i>	-1.10	3.86E-01	putative transporter subunit: ATP-binding component of ABC superfamily
<i>ynfH</i>	-1.10	3.70E-01	oxidoreductase, membrane subunit
<i>yajD</i>	1.10	1.62E-01	conserved protein, HNH family
<i>astE</i>	-1.10	6.89E-01	succinylglutamate desuccinylase
<i>xylH</i>	-1.10	6.61E-01	D-xylose ABC transporter permease subunit
<i>nrdB</i>	1.10	7.88E-02	ribonucleoside-diphosphate reductase 1, beta subunit, ferritin-like protein
<i>kbl</i>	1.10	1.42E-01	glycine C-acetyltransferase
<i>alaE</i>	1.10	7.44E-01	alanine exporter, alanine-inducible, stress-responsive
<i>gnsA</i>	1.10	2.74E-01	multicopy suppressor of <i>secG</i> (Cs) and <i>fabA6</i> (Ts)
<i>dpiB</i>	1.10	3.75E-01	sensory histidine kinase in two-component regulatory system with <i>citB</i>
<i>wcaA</i>	-1.10	6.70E-01	putative glycosyl transferase
<i>pheT</i>	1.10	8.75E-02	phenylalanine tRNA synthetase, beta subunit
<i>hemL</i>	1.10	7.88E-02	glutamate-1-semialdehyde aminotransferase (aminomutase)
<i>yjfL</i>	1.10	1.18E-01	CP4-57 prophage; putative protein
<i>bcsE</i>	-1.10	1.11E-01	cellulose production protein
<i>yqeB</i>	1.10	5.47E-01	conserved protein with NAD(P)-binding Rossmann fold
<i>mdh</i>	-1.10	5.65E-02	malate dehydrogenase, NAD(P)-binding
<i>rlmF</i>	-1.10	3.26E-01	23S rRNA m(6)A1618 methyltransferase, SAM-dependent
<i>menC</i>	-1.10	3.03E-01	O-succinylbenzoyl-CoA synthase
<i>yihD</i>	1.10	1.75E-01	DUF1040 protein YihD
<i>mreB</i>	1.10	8.06E-02	cell wall structural complex MreBCD, actin-like component MreB
<i>rbsK</i>	-1.10	2.64E-01	ribokinase
<i>hisI</i>	-1.10	1.16E-01	fused phosphoribosyl-AMP cyclohydrolase/phosphoribosyl-ATP pyrophosphatase
<i>rimP</i>	1.10	1.56E-01	ribosome maturation factor for 30S subunits
<i>yggX</i>	-1.10	1.31E-01	protein that protects iron-sulfur proteins against oxidative damage
<i>waaN</i>	1.10	8.16E-02	myristoyl-acyl carrier protein (ACP)-dependent acyltransferase

<i>yghD</i>	1.10	6.90E-01	putative secretion pathway M-type protein, membrane anchored
<i>ybiP</i>	-1.10	3.07E-01	putative hydrolase, inner membrane
<i>nudJ</i>	1.10	2.59E-01	bifunctional thiamin pyrimidine pyrophosphate hydrolase/ thiamin pyrophosphate hydrolase
<i>xdhA</i>	1.10	5.09E-01	xanthine dehydrogenase, molybdenum binding subunit
<i>hspQ</i>	1.09	1.28E-01	heat shock protein involved in degradation of mutant DnaA
<i>yabP</i>	-1.09	1.22E-01	pseudo
<i>ves</i>	1.09	7.16E-01	hypothetical protein
<i>yjfS</i>	-1.09	8.17E-01	CP4-57 prophage; putative protein
<i>holE</i>	-1.09	2.71E-01	DNA polymerase III, theta subunit
<i>soxS</i>	-1.09	2.13E-01	DNA-binding transcriptional dual regulator
<i>hyfG</i>	1.09	5.46E-01	hydrogenase 4, subunit
<i>cusB</i>	1.09	6.54E-01	copper/silver efflux system, membrane fusion protein
<i>modC</i>	-1.09	4.05E-01	molybdate transporter subunit
<i>ybhS</i>	1.09	3.93E-01	putative transporter subunit: membrane component of ABC superfamily
<i>eutQ</i>	1.09	1.00E+00	hypothetical protein
<i>yjjQ</i>	-1.09	8.64E-01	DNA-binding transcriptional regulator
<i>yihI</i>	-1.09	8.97E-02	activator of Der GTPase
<i>btuE</i>	1.09	2.27E-01	glutathione peroxidase
<i>ypjA</i>	1.09	2.52E-01	adhesin-like autotransporter
<i>amiB</i>	1.09	9.07E-02	N-acetylmuramoyl-l-alanine amidase II
<i>nrjF</i>	-1.09	9.26E-01	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfF
<i>ihfA</i>	-1.09	9.28E-02	integration host factor (IHF), DNA-binding protein, alpha subunit
<i>yhhS</i>	1.09	3.08E-01	putative arabinose efflux transporter
<i>mutY</i>	-1.09	1.85E-01	adenine DNA glycosylase
<i>insP</i>	1.09	8.76E-01	pseudo
<i>hipB</i>	-1.09	5.13E-01	antitoxin of HipAB toxin-antitoxin system
<i>yagL</i>	-1.09	6.49E-01	CP4-6 prophage; DNA-binding protein
<i>yejM</i>	1.09	1.18E-01	putative hydrolase, inner membrane
<i>nirB</i>	1.09	4.89E-01	nitrite reductase, large subunit, NAD(P)H-binding
<i>proK</i>	1.09	6.59E-01	tRNA
<i>asnU</i>	-1.09	5.71E-01	tRNA
<i>chaB</i>	-1.09	2.53E-01	cation transport regulator
<i>thrC</i>	1.09	1.71E-01	threonine synthase
<i>rcnA</i>	1.09	5.42E-01	membrane protein conferring nickel and cobalt resistance
<i>ydjL</i>	-1.09	7.54E-01	putative oxidoreductase, Zn-dependent and NAD(P)-binding
<i>livK</i>	1.09	1.66E-01	leucine transporter subunit
<i>yffL</i>	1.09	4.09E-01	CPZ-55 prophage; putative protein
<i>fimZ</i>	1.09	7.74E-01	putative DNA-binding transcriptional regulator
<i>udk</i>	-1.09	1.71E-01	uridine/cytidine kinase
<i>ydeR</i>	1.09	8.06E-01	putative fimbrial-like adhesin protein
<i>yohO</i>	1.09	7.30E-01	hypothetical protein
<i>yjjJ</i>	1.09	2.62E-01	putative protein kinase
<i>acpT</i>	-1.09	2.38E-01	holo-(acyl carrier protein) synthase 2

<i>djlC</i>	1.09	4.27E-01	Hsc56 co-chaperone of HscC
<i>ftsZ</i>	-1.09	2.25E-01	GTP-binding tubulin-like cell division protein
<i>cysD</i>	1.09	2.15E-01	sulfate adenylyltransferase, subunit 2
<i>ybaL</i>	-1.09	1.18E-01	putative transporter with NAD(P)-binding Rossmann-fold domain
<i>ydfU</i>	1.09	9.27E-01	Qin prophage; putative protein
<i>ybfD</i>	-1.09	8.55E-01	hypothetical protein
<i>yfdV</i>	1.09	7.36E-01	putative transporter
<i>frc</i>	1.09	4.90E-01	formyl-CoA transferase, NAD(P)-binding
<i>yedS</i>	-1.09	2.95E-01	pseudo
<i>yqaA</i>	-1.09	1.61E-01	inner membrane protein, COG1238 family
<i>yncG</i>	1.09	3.83E-01	glutathione S-transferase homolog
<i>rep</i>	1.09	1.89E-01	DNA helicase and single-stranded DNA-dependent ATPase
<i>ycgM</i>	1.09	1.06E-01	putative isomerase/hydrolase
<i>yjiG</i>	-1.09	8.44E-01	inner membrane protein, SpmB family
<i>narL</i>	1.09	2.11E-01	DNA-binding response regulator in two-component regulatory system with NarX (or NarQ)
<i>bluF</i>	-1.09	2.62E-01	anti-repressor for YcgE, blue light-responsive
<i>tolB</i>	1.09	8.39E-02	periplasmic protein
<i>hslV</i>	1.09	3.11E-01	peptidase component of the HslUV protease
<i>nanC</i>	-1.09	7.66E-01	N-acetylmuramic acid outer membrane channel protein
<i>cpsG</i>	-1.09	6.97E-01	phosphomannomutase
<i>lptA</i>	1.09	1.00E-01	periplasmic LPS-binding protein
<i>ytjB</i>	1.09	3.96E-01	conserved membrane protein
<i>gdhA</i>	-1.09	1.89E-01	glutamate dehydrogenase, NADP-specific
<i>clsB</i>	-1.09	2.33E-01	cardiolipin synthase 2
<i>hicA</i>	1.09	5.94E-01	mRNA interferase toxin of the HicAB toxin-antitoxin system
<i>yccE</i>	-1.09	5.87E-01	hypothetical protein
<i>sroH</i>	1.09	5.73E-01	ncRNA
<i>yagJ</i>	-1.09	4.09E-01	pseudo
<i>cybC</i>	-1.09	3.03E-01	pseudo
<i>nfrB</i>	1.09	3.93E-01	bacteriophage N4 receptor, inner membrane subunit
<i>ykfI</i>	1.09	8.72E-01	CP4-6 prophage; toxin of the YkfI-YafW toxin-antitoxin system
<i>yhdU</i>	-1.09	6.36E-01	putative membrane protein
<i>ybfE</i>	-1.09	4.43E-01	conserved protein, LexA-regulated
<i>ygcE</i>	1.09	7.37E-01	putative kinase
<i>rhaT</i>	1.09	5.12E-01	L-rhamnose:proton symporter
<i>yjgM</i>	-1.09	3.25E-01	putative acetyltransferase
<i>patD</i>	-1.09	3.42E-01	gamma-aminobutyraldehyde dehydrogenase
<i>yjiP</i>	-1.09	5.13E-01	inner membrane protein, H-NS-repressed, DUF1212 family
<i>viaA</i>	-1.09	2.58E-01	putative von Willebrand factor containing protein
<i>dsdX</i>	1.09	6.45E-01	D-serine permease
<i>rluA</i>	-1.09	2.61E-01	dual 23S rRNA pseudouridine(746), tRNA pseudouridine(32) synthase, SAM-dependent
<i>rrsA</i>	-1.09	8.72E-01	16S ribosomal RNA of rrnA operon
<i>pal</i>	1.09	1.15E-01	peptidoglycan-associated outer membrane lipoprotein

<i>bcsZ</i>	-1.09	5.79E-01	endo-1,4-D-glucanase
<i>narX</i>	-1.09	1.44E-01	sensory histidine kinase in two-component regulatory system with NarL
<i>basS</i>	1.09	2.50E-01	sensory histidine kinase in two-component regulatory system with BasR
<i>yhhY</i>	-1.09	4.90E-01	putative acetyltransferase
<i>skp</i>	-1.09	9.65E-02	periplasmic chaperone
<i>rnc</i>	-1.09	1.06E-01	RNase III
<i>nikE</i>	1.09	8.14E-01	nickel transporter subunit
<i>yjfY</i>	1.09	4.97E-01	hypothetical protein
<i>folC</i>	1.09	2.55E-01	bifunctional folylpolyglutamate synthase/ dihydrofolate synthase
<i>fryC</i>	-1.09	8.62E-01	putative enzyme IIC component of PTS
<i>yjbT</i>	1.09	8.26E-01	hypothetical protein, no homologs
<i>gspM</i>	-1.09	7.94E-01	general secretory pathway component, cryptic
<i>purR</i>	1.09	1.30E-01	DNA-binding transcriptional repressor, hypoxanthine-binding
<i>yejB</i>	-1.09	4.89E-01	microcin C transporter YejABEF, permease subunit; ABC family
<i>mokC</i>	1.09	8.10E-01	regulatory protein for HokC, overlaps CDS of hokC
<i>nudF</i>	1.09	3.17E-01	ADP-ribose pyrophosphatase
<i>yedK</i>	1.08	4.74E-01	hypothetical protein
<i>emtA</i>	-1.08	2.12E-01	lytic murein endotransglycosylase E
<i>ccmH</i>	-1.08	3.18E-01	heme lyase, CcmH subunit
<i>chaA</i>	-1.08	1.44E-01	calcium/sodium:proton antiporter
<i>yjfM</i>	-1.08	9.37E-01	conserved protein, DUF1190 family
<i>araH</i>	-1.08	5.04E-01	fused L-arabinose transporter subunits of ABC superfamily: membrane components
<i>ydgl</i>	-1.08	4.91E-01	putative arginine/ornithine antiporter transporter
<i>hslO</i>	-1.08	1.53E-01	heat shock protein Hsp33
<i>caiC</i>	1.08	5.14E-01	putative crotonobetaine/carnitine-CoA ligase
<i>asmA</i>	1.08	1.03E-01	putative assembly protein
<i>nlpE</i>	1.08	2.19E-01	lipoprotein involved with copper homeostasis and adhesion
<i>ysaA</i>	1.08	5.85E-01	putative hydrogenase, 4Fe-4S ferredoxin-type component
<i>yieH</i>	-1.08	2.43E-01	phosphoenolpyruvate and 6-phosphogluconate phosphatase
<i>yacC</i>	1.08	3.60E-01	conserved protein, PulS_OutS family
<i>yggW</i>	1.08	1.96E-01	putative oxidoreductase, HemN family
<i>serT</i>	1.08	7.66E-01	tRNA
<i>napH</i>	1.08	8.67E-01	ferredoxin-type protein essential for periplasmic nitrate reductase (NapAB)
<i>ilvY</i>	-1.08	6.51E-01	DNA-binding transcriptional dual regulator
<i>yfhM</i>	-1.08	1.14E-01	hypothetical protein
<i>nikC</i>	-1.08	9.27E-01	nickel transporter subunit
<i>nikR</i>	-1.08	3.94E-01	DNA-binding transcriptional repressor, Ni-binding
<i>nagZ</i>	-1.08	2.58E-01	beta N-acetyl-glucosaminidase
<i>yegZ</i>	-1.08	7.39E-01	pseudo
<i>dmlR</i>	1.08	2.34E-01	DNA-binding transcriptional activator for dmlA
<i>infB</i>	1.08	2.31E-01	fused protein chain initiation factor 2, IF2: membrane protein/conserved protein
<i>poxB</i>	1.08	3.93E-01	pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FAD-binding
<i>ydeA</i>	-1.08	2.94E-01	arabinose efflux transporter, arabinose-inducible

<i>waaU</i>	-1.08	2.05E-01	lipopolysaccharide core biosynthesis
<i>yidG</i>	-1.08	7.01E-01	inner membrane protein
<i>yjgR</i>	1.08	3.51E-01	conserved protein, DUF853 family with NTPase fold
<i>fliC</i>	1.08	2.04E-01	flagellar filament structural protein (flagellin)
<i>azuC</i>	1.08	4.10E-01	hypothetical protein
<i>talB</i>	-1.08	2.43E-01	transaldolase B
<i>yqcA</i>	-1.08	3.18E-01	putative flavoprotein
<i>dmsD</i>	-1.08	2.88E-01	twin-arginine leader-binding protein for DmsA and TorA
<i>rhaS</i>	1.08	7.12E-01	DNA-binding transcriptional activator for rhaBAD and rhaT, L-rhamnose-binding
<i>rffH</i>	-1.08	3.44E-01	glucose-1-phosphate thymidyltransferase
<i>yehA</i>	1.08	8.59E-01	putative fimbrial-like adhesin protein
<i>mtfA</i>	1.08	1.84E-01	anti-repressor for DgsA(Mlc)
<i>tusB</i>	-1.08	3.99E-01	protein required for 2-thiolation step of mnm(5)-s(2)U34-tRNA synthesis
<i>glnP</i>	-1.08	1.42E-01	glutamine transporter subunit
<i>arsC</i>	-1.08	5.60E-01	arsenate reductase
<i>yhhM</i>	-1.08	3.07E-01	conserved protein, DUF2500 family
<i>ycgH</i>	1.08	3.71E-01	pseudo
<i>ycaL</i>	-1.08	5.11E-01	putative peptidase with chaperone function
<i>galE</i>	1.08	2.82E-01	UDP-galactose-4-epimerase
<i>puuE</i>	-1.08	7.42E-01	GABA aminotransferase, PLP-dependent
<i>yjjX</i>	-1.08	4.01E-01	inosine/xanthosine triphosphatase
<i>nuoF</i>	-1.08	3.27E-01	NADH:ubiquinone oxidoreductase, chain F
<i>gatR</i>	-1.08	2.43E-01	pseudo
<i>murC</i>	-1.08	2.47E-01	UDP-N-acetylmuramate:L-alanine ligase
<i>serC</i>	-1.08	1.26E-01	3-phosphoserine/phosphohydroxythreonine aminotransferase
<i>murB</i>	-1.08	1.73E-01	UDP-N-acetylenolpyruvoylglucosamine reductase, FAD-binding
<i>groS</i>	-1.08	2.38E-01	Cpn10 chaperonin GroES, small subunit of GroESL
<i>ydjZ</i>	1.08	6.25E-01	Inner membrane protein, TVP38/TMEM64 family
<i>cybB</i>	-1.08	1.33E-01	cytochrome b561
<i>trkG</i>	1.08	3.32E-01	Rac prophage; potassium transporter subunit
<i>menH</i>	1.08	6.45E-01	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase
<i>rimL</i>	1.08	2.03E-01	ribosomal-protein-L7/L12-serine acetyltransferase
<i>yiaC</i>	-1.08	4.51E-01	putative acyltransferase with acyl-CoA N-acyltransferase domain
<i>ycaQ</i>	1.08	4.91E-01	hypothetical protein
<i>chbR</i>	1.08	4.05E-01	repressor of chb operon for N,N'-diacetylchitobiose utilization
<i>yegD</i>	-1.08	3.25E-01	putative chaperone
<i>cutA</i>	1.08	4.07E-01	divalent-cation tolerance protein, copper sensitivity
<i>fixA</i>	1.08	8.67E-01	putative electron transfer flavoprotein subunit, required for anaerobic carnitine reduction
<i>rihA</i>	-1.08	4.14E-01	ribonucleoside hydrolase 1
<i>yeaJ</i>	-1.08	2.58E-01	putative diguanylate cyclase
<i>speG</i>	1.08	1.86E-01	spermidine N1-acetyltransferase
<i>yobD</i>	-1.08	3.91E-01	inner membrane protein, UPF0266 family
<i>bamE</i>	1.08	1.64E-01	lipoprotein component of BamABCDE OM biogenesis complex

<i>sseA</i>	-1.08	2.49E-01	3-mercaptopyruvate sulfurtransferase
<i>htpX</i>	1.08	1.70E-01	putative endopeptidase
<i>hycD</i>	-1.08	1.00E+00	hydrogenase 3, membrane subunit
<i>dnaN</i>	1.08	1.54E-01	DNA polymerase III, beta subunit
<i>rlmC</i>	1.08	5.02E-01	23S rRNA m(5)U747 methyltransferase, SAM-dependent
<i>nsrR</i>	-1.08	4.08E-01	nitric oxide-sensitive repressor for NO regulon
<i>hydN</i>	-1.08	8.25E-01	formate dehydrogenase-H, [4Fe-4S] ferredoxin subunit
<i>aspA</i>	-1.08	2.21E-01	aspartate ammonia-lyase
<i>yciO</i>	-1.08	1.49E-01	putative RNA binding protein
<i>marR</i>	1.08	6.09E-01	DNA-binding transcriptional repressor of multiple antibiotic resistance
<i>hyfI</i>	1.08	8.15E-01	hydrogenase 4, Fe-S subunit
<i>ubiF</i>	-1.08	4.87E-01	2-octaprenyl-3-methyl-6-methoxy-1,4-benzoquinol oxygenase
<i>rseP</i>	-1.08	1.55E-01	inner membrane zinc RIP metalloprotease; RpoE activator, by degrading RseA
<i>ygcP</i>	1.08	8.23E-01	putative anti-terminator regulatory protein
<i>ychA</i>	1.08	1.56E-01	hypothetical protein
<i>tatB</i>	1.08	2.93E-01	TatABCE protein translocation system subunit
<i>yijF</i>	1.08	8.68E-01	hypothetical protein
<i>yebO</i>	-1.07	2.01E-01	putative inner membrane protein
<i>idi</i>	1.07	4.51E-01	isopentenyl diphosphate isomerase
<i>ligB</i>	1.07	6.97E-01	DNA ligase, NAD(+)-dependent
<i>nlpI</i>	1.07	1.67E-01	lipoprotein involved in osmotic sensitivity and filamentation
<i>yqeH</i>	-1.07	6.99E-01	conserved protein with bipartite regulator domain
<i>xdhC</i>	-1.07	7.75E-01	xanthine dehydrogenase, Fe-S binding subunit
<i>thiM</i>	1.07	5.31E-01	hydroxyethylthiazole kinase
<i>gsiC</i>	-1.07	3.68E-01	glutathione transporter, permease component, ABC superfamily
<i>yffR</i>	-1.07	3.97E-01	CPZ-55 prophage; putative protein
<i>malZ</i>	1.07	3.62E-01	maltodextrin glucosidase
<i>yddH</i>	1.07	6.92E-01	hypothetical protein
<i>murE</i>	-1.07	2.39E-01	UDP-N-acetylmuramoyl-L-alanyl-D-glutamate:meso-diaminopimelate ligase
<i>ytfB</i>	-1.07	1.71E-01	putative cell envelope opacity-associated protein
<i>yibF</i>	-1.07	3.70E-01	glutathione S-transferase homolog
<i>rlmD</i>	1.07	2.96E-01	23S rRNA m(5)U1939 methyltransferase, SAM-dependent
<i>yqiJ</i>	-1.07	7.53E-01	inner membrane protein, DUF1449 family
<i>bamB</i>	1.07	2.34E-01	lipoprotein required for OM biogenesis, in BamABCDE complex
<i>mcrB</i>	-1.07	5.44E-01	5-methylcytosine-specific restriction enzyme McrBC, subunit McrB
<i>dpiA</i>	1.07	5.44E-01	DNA-binding response regulator in two-component regulatory system with citA
<i>ygiQ</i>	-1.07	2.19E-01	Radical SAM superfamily protein
<i>ecpE</i>	-1.07	6.35E-01	hypothetical protein
<i>ndh</i>	1.07	4.17E-01	respiratory NADH dehydrogenase 2/cupric reductase
<i>yebC</i>	1.07	2.08E-01	conserved protein, UPF0082 family
<i>bcsB</i>	-1.07	4.95E-01	regulator of cellulose synthase, cyclic di-GMP binding
<i>wzc</i>	-1.07	6.66E-01	protein-tyrosine kinase
<i>dinJ</i>	1.07	2.94E-01	antitoxin of YafQ-DinJ toxin-antitoxin system

<i>sanA</i>	1.07	4.75E-01	vancomycin high temperature exclusion protein
<i>ompA</i>	1.07	2.01E-01	outer membrane protein A (3a;II*;G;d)
<i>mtlR</i>	1.07	3.72E-01	mannitol operon repressor
<i>lfhA</i>	1.07	7.91E-01	pseudo
<i>ydcK</i>	1.07	2.84E-01	putative enzyme
<i>setA</i>	-1.07	5.89E-01	broad specificity sugar efflux system
<i>ykiA</i>	-1.07	4.83E-01	pseudo
<i>yciI</i>	-1.07	2.94E-01	putative enzyme
<i>chbA</i>	-1.07	8.20E-01	N,N'-diacetylchitobiose-specific enzyme IIA component of PTS
<i>alaW</i>	1.07	7.11E-01	tRNA
<i>rng</i>	-1.07	2.46E-01	ribonuclease G
<i>rrrD</i>	1.07	7.24E-01	DLP12 prophage; predicted lysozyme
<i>yfeW</i>	-1.07	7.41E-01	penicillin binding protein PBP4B; weak DD-carboxypeptidase activity
<i>yhhA</i>	-1.07	3.02E-01	conserved protein, DUF2756 family
<i>purT</i>	-1.07	5.12E-01	phosphoribosylglycinamide formyltransferase 2
<i>yacG</i>	-1.07	3.31E-01	DNA gyrase inhibitor
<i>wcaH</i>	1.07	8.82E-01	GDP-mannose mannosyl hydrolase
<i>ylbA</i>	1.07	4.54E-01	hypothetical protein
<i>fucK</i>	-1.07	5.91E-01	L-fuculokinase
<i>gmK</i>	-1.07	2.27E-01	guanylate kinase
<i>ycfT</i>	1.07	8.90E-01	inner membrane protein
<i>lldP</i>	1.07	4.61E-01	L-lactate permease
<i>ptrB</i>	-1.07	4.09E-01	protease II
<i>atpC</i>	1.07	2.95E-01	F1 sector of membrane-bound ATP synthase, epsilon subunit
<i>adiC</i>	1.07	8.05E-01	arginine:agmatine antiporter
<i>phoH</i>	-1.07	2.45E-01	conserved protein with nucleoside triphosphate hydrolase domain
<i>ecpC</i>	-1.07	6.72E-01	putative aromatic compound dioxygenase
<i>chiQ</i>	1.07	8.80E-01	putative lipoprotein induced by chitosugars
<i>ppx</i>	1.07	5.45E-01	exopolyphosphatase
<i>yjaB</i>	1.07	7.31E-01	putative acetyltransferase
<i>aroA</i>	-1.07	3.53E-01	5-enolpyruvylshikimate-3-phosphate synthetase
<i>murF</i>	1.07	3.50E-01	UDP-N-acetylmuramoyl-tripeptide:D-alanyl-D-alanine ligase
<i>mukF</i>	1.07	4.30E-01	chromosome condensin MukBEF, kleisin-like subunit, binds calcium
<i>ftsL</i>	1.07	3.39E-01	membrane bound cell division protein at septum containing leucine zipper motif
<i>ypdF</i>	-1.07	9.45E-01	Xaa-Pro aminopeptidase
<i>bglH</i>	1.07	8.39E-01	carbohydrate-specific outer membrane porin, cryptic
<i>wbbL</i>	1.07	2.86E-01	pseudo
<i>acpS</i>	-1.07	3.09E-01	holo-[acyl-carrier-protein] synthase 1
<i>ynjB</i>	1.07	4.82E-01	hypothetical protein
<i>yffB</i>	1.07	3.02E-01	putative reductase, function unknown, ArsC family; low abundance protein
<i>malY</i>	-1.07	4.50E-01	bifunctional beta-cystathionase, PLP-dependent/ regulator of maltose regulon
<i>yadG</i>	1.07	3.74E-01	putative transporter subunit: ATP-binding component of ABC superfamily
<i>yfeX</i>	-1.07	3.03E-01	porphyrinogen oxidase, cytoplasmic

<i>yhhI</i>	1.07	8.03E-01	putative transposase
<i>metQ</i>	1.07	2.51E-01	DL-methionine transporter subunit
<i>ulaE</i>	-1.07	8.69E-01	L-xylulose 5-phosphate 3-epimerase
<i>gspK</i>	-1.07	9.43E-01	general secretory pathway component, cryptic
<i>yihW</i>	1.07	3.62E-01	putative DNA-binding transcriptional regulator
<i>cspE</i>	1.07	3.74E-01	DNA-binding transcriptional repressor
<i>tamA</i>	1.07	1.99E-01	translocation and assembly module for autotransporter export, outer membrane subunit
<i>yadM</i>	-1.06	7.98E-01	putative fimbrial-like adhesin protein
<i>ygcU</i>	-1.06	6.87E-01	putative FAD containing dehydrogenase
<i>yfdP</i>	-1.06	8.90E-01	CPS-53 (KpLE1) prophage; putative protein
<i>panE</i>	-1.06	3.11E-01	2-dehydropantoate reductase, NADPH-specific
<i>tcdA</i>	-1.06	6.39E-01	sulfur acceptor for CsdA
<i>rssA</i>	-1.06	2.98E-01	putative phospholipase, patatin-like family
<i>yfaE</i>	-1.06	3.84E-01	ferredoxin involved with ribonucleotide reductase radical (Y*) cofactor maintenance
<i>ccmB</i>	-1.06	7.79E-01	heme exporter subunit
<i>flk</i>	-1.06	4.54E-01	putative flagella assembly protein
<i>trpD</i>	1.06	6.56E-01	fglutamine amidotransferase of anthranilate synthase/anthranilate phosphoribosyl transferase
<i>mltB</i>	-1.06	3.75E-01	membrane-bound lytic murein transglycosylase B
<i>gpsA</i>	-1.06	2.95E-01	glycerol-3-phosphate dehydrogenase (NAD ⁺)
<i>paoA</i>	1.06	7.83E-01	PaoABC aldehyde oxidoreductase, 2Fe-2S subunit
<i>glmY</i>	1.06	5.93E-01	ncRNA
<i>yjcE</i>	-1.06	3.33E-01	putative cation/proton antiporter
<i>yicN</i>	-1.06	6.45E-01	hypothetical protein
<i>rffG</i>	-1.06	4.60E-01	dTDP-glucose 4,6-dehydratase
<i>ybiO</i>	1.06	5.57E-01	mechanosensitive channel protein, intermediate conductance
<i>cyoB</i>	1.06	4.26E-01	cytochrome o ubiquinol oxidase subunit I
<i>hupB</i>	-1.06	2.90E-01	HU, DNA-binding transcriptional regulator, beta subunit
<i>allA</i>	-1.06	7.74E-01	ureidoglycolate hydrolase
<i>hicB</i>	1.06	4.04E-01	antitoxin for the HicAB toxin-antitoxin system
<i>gmhB</i>	-1.06	4.09E-01	D,D-heptose 1,7-bisphosphate phosphatase
<i>tdh</i>	1.06	3.63E-01	threonine 3-dehydrogenase, NAD(P)-binding
<i>insK</i>	-1.06	7.28E-01	IS150 transposase B
<i>yiiX</i>	1.06	4.97E-01	putative lipid binding hydrolase, DUF830 family, function unknown
<i>yegX</i>	1.06	7.22E-01	putative hydrolase
<i>dcuA</i>	1.06	2.67E-01	C4-dicarboxylate antiporter
<i>priB</i>	-1.06	4.88E-01	primosomal protein N
<i>yidF</i>	-1.06	7.33E-01	putative DNA-binding transcriptional regulator
<i>kefB</i>	1.06	4.53E-01	potassium:proton antiporter
<i>ybaE</i>	-1.06	7.18E-01	putative transporter subunit: periplasmic-binding component of ABC superfamily
<i>pdhR</i>	-1.06	3.74E-01	DNA-binding transcriptional dual regulator
<i>ygdR</i>	-1.06	3.95E-01	putative lipoprotein
<i>allR</i>	-1.06	3.09E-01	transcriptional repressor for allantoin and glyoxylate) operons; glyoxylate-induced
<i>lsrB</i>	1.06	7.39E-01	autoinducer 2-binding protein

<i>hofB</i>	-1.06	7.01E-01	conserved protein with nucleoside triphosphate hydrolase domain
<i>mioC</i>	1.06	4.06E-01	FMN-binding protein MioC
<i>gsk</i>	-1.06	2.69E-01	inosine/guanosine kinase
<i>speB</i>	1.06	3.58E-01	agmatinase
<i>lpxC</i>	1.06	2.86E-01	UDP-3-O-acyl N-acetylglucosamine deacetylase
<i>pgpA</i>	1.06	3.32E-01	phosphatidylglycerophosphatase A
<i>dacC</i>	1.06	2.91E-01	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6a)
<i>murQ</i>	-1.06	6.81E-01	N-acetylmuramic acid 6-phosphate (MurNAc-6-P) etherase
<i>yfaP</i>	1.06	8.47E-01	DUF2135 family protein, function unknown
<i>dcuB</i>	1.06	8.26E-01	C4-dicarboxylate transporter, anaerobic; DcuS co-sensor
<i>rhmA</i>	-1.06	8.34E-01	2-keto-3-deoxy-L-rhamnonate aldolase
<i>ybdO</i>	1.06	7.93E-01	putative DNA-binding transcriptional regulator
<i>garL</i>	1.06	8.57E-01	alpha-dehydro-beta-deoxy-D-glucarate aldolase
<i>yjgX</i>	1.06	5.31E-01	pseudo
<i>mdtA</i>	-1.06	5.27E-01	multidrug efflux system, subunit A
<i>tolR</i>	1.06	4.04E-01	membrane spanning protein in TolA-TolQ-TolR complex
<i>yffI</i>	1.06	8.12E-01	CP4-57 prophage; putative protein
<i>yjaH</i>	1.06	5.01E-01	hypothetical protein
<i>purM</i>	-1.06	3.33E-01	phosphoribosylaminoimidazole synthetase
<i>mdtH</i>	-1.06	8.60E-01	multidrug resistance efflux transporter
<i>garD</i>	1.06	6.60E-01	(D)-galactarate dehydrogenase
<i>yhdN</i>	-1.06	5.05E-01	conserved protein, DUF1992 family
<i>yeaX</i>	-1.06	7.55E-01	putative oxidoreductase
<i>glvG</i>	1.06	7.64E-01	pseudo
<i>greB</i>	1.06	5.14E-01	transcript cleavage factor
<i>surA</i>	1.06	2.67E-01	peptidyl-prolyl cis-trans isomerase (PPIase)
<i>guaB</i>	1.06	4.60E-01	IMP dehydrogenase
<i>menF</i>	-1.06	4.51E-01	isochorismate synthase 2
<i>mldD</i>	-1.06	5.04E-01	ABC transporter maintaining OM lipid asymmetry, anchored periplasmic binding protein
<i>ybcJ</i>	1.06	5.10E-01	ribosome-associated protein; predicted RNA-binding protein
<i>yabI</i>	1.06	5.14E-01	inner membrane protein, SNARE_assoc family
<i>arnA</i>	1.06	6.45E-01	fused UDP-L-Ara4N formyltransferase/UDP-GlcA C-4'-decarboxylase
<i>cmtA</i>	1.06	8.96E-01	putative fused mannitol-specific PTS enzymes: IIB component/IIC component
<i>thrS</i>	1.06	3.21E-01	threonyl-tRNA synthetase
<i>phoR</i>	-1.06	4.81E-01	sensory histidine kinase in two-component regulatory system with PhoB
<i>ybaB</i>	1.06	2.90E-01	hypothetical protein
<i>ddlB</i>	-1.06	3.00E-01	D-alanine:D-alanine ligase
<i>rsxC</i>	1.06	4.52E-01	electron transport complex protein required for the reduction of SoxR
<i>ygfQ</i>	1.06	7.11E-01	putative purine permease
<i>lpoA</i>	1.06	3.71E-01	hypothetical protein
<i>mreD</i>	1.06	5.13E-01	cell wall structural complex MreBCD transmembrane component MreD
<i>yijD</i>	1.06	4.55E-01	inner membrane protein, DUF1422 family
<i>yciS</i>	1.06	3.31E-01	DUF1049 family inner membrane protein, function unknown

<i>wzxC</i>	-1.06	8.76E-01	putative colanic acid exporter
<i>speA</i>	-1.06	3.18E-01	biosynthetic arginine decarboxylase, PLP-binding
<i>gltI</i>	-1.06	3.75E-01	glutamate, aspartate binding protein, periplasmic; part of GltJKLI ABC transporter
<i>insLI</i>	-1.06	7.95E-01	IS186 transposase
<i>sfmD</i>	-1.06	7.51E-01	putative outer membrane export usher protein
<i>gltX</i>	-1.06	3.77E-01	glutamyl-tRNA synthetase
<i>smrA</i>	-1.06	5.19E-01	DNA endonuclease
<i>yghU</i>	-1.06	3.58E-01	putative S-transferase
<i>ybaM</i>	-1.06	7.24E-01	hypothetical protein
<i>rpsR</i>	-1.06	5.55E-01	30S ribosomal subunit protein S18
<i>mdlA</i>	-1.06	6.45E-01	fused predicted multidrug transporter subunits of ABC superfamily
<i>uhpB</i>	1.06	6.23E-01	sensory histidine kinase in two-component regulatory system with UhpA
<i>gcd</i>	-1.06	4.81E-01	glucose dehydrogenase
<i>cof</i>	1.06	5.35E-01	thiamin pyrimidine pyrophosphate hydrolase; HMP-PP phosphatase
<i>kgtP</i>	-1.06	3.54E-01	alpha-ketoglutarate transporter
<i>nanS</i>	-1.06	7.37E-01	9-O-acetyl N-acetylneuraminic acid esterase
<i>flgL</i>	1.06	6.38E-01	flagellar hook-filament junction protein
<i>mobB</i>	-1.06	7.35E-01	molybdopterin-guanine dinucleotide biosynthesis protein B
<i>yjcH</i>	-1.06	7.92E-01	inner membrane protein, DUF485 family
<i>metT</i>	1.06	8.36E-01	tRNA
<i>ybdK</i>	-1.06	4.68E-01	weak gamma-glutamyl:cysteine ligase
<i>waaZ</i>	-1.06	4.16E-01	lipopolysaccharide core biosynthesis protein
<i>yjcZ</i>	-1.06	8.43E-01	mutational suppressor of yjhH motility mutation, function unknown
<i>mnmH</i>	-1.05	6.87E-01	tRNA 2-selenouridine synthase, selenophosphate-dependent
<i>rydB</i>	1.05	6.42E-01	ncRNA
<i>ompG</i>	1.05	9.40E-01	outer membrane porin G
<i>djlA</i>	1.05	4.16E-01	DnaJ-like protein, membrane anchored
<i>ygdH</i>	1.05	6.49E-01	conserved protein, UPF0717 family
<i>btuF</i>	-1.05	6.51E-01	vitamin B12 transporter subunit: periplasmic-binding component of ABC superfamily
<i>cueR</i>	-1.05	4.29E-01	DNA-binding transcriptional activator of copper-responsive regulon genes
<i>yaeP</i>	-1.05	3.83E-01	hypothetical protein
<i>ttdR</i>	-1.05	8.50E-01	transcriptional activator of ttdABT
<i>truA</i>	1.05	5.32E-01	tRNA pseudouridine(38-40) synthase
<i>ygeH</i>	1.05	8.39E-01	predicted transcriptional regulator
<i>lptC</i>	1.05	4.57E-01	lipopolysaccharide export, IM-tethered periplasmic protein of the LptBFGC export complex
<i>ydhC</i>	-1.05	5.85E-01	putative arabinose efflux transporter
<i>yafL</i>	1.05	7.63E-01	putative lipoprotein and C40 family peptidase
<i>ykgI</i>	1.05	7.79E-01	hypothetical protein
<i>rtcR</i>	1.05	8.75E-01	sigma 54-dependent transcriptional regulator of rtcBA expression
<i>arnT</i>	-1.05	6.58E-01	4-amino-4-deoxy-L-arabinose transferase
<i>casE</i>	1.05	7.26E-01	CRISPR RNA precursor cleavage enzyme
<i>mgrB</i>	1.05	5.21E-01	regulatory peptide for PhoPQ, feedback inhibition
<i>ymcE</i>	-1.05	1.00E+00	cold shock gene

<i>bcr</i>	-1.05	3.39E-01	bicyclomycin/cysteine/sulfonamide efflux transporter
<i>yjjW</i>	1.05	9.58E-01	putative pyruvate formate lyase activating enzyme
<i>yjbR</i>	-1.05	5.66E-01	hypothetical protein
<i>ryfD</i>	-1.05	8.74E-01	ncRNA
<i>yjaZ</i>	-1.05	6.64E-01	stationary phase growth adaptation protein
<i>lit</i>	1.05	7.95E-01	e14 prophage; cell death peptidase, inhibitor of T4 late gene expression
<i>modF</i>	-1.05	3.97E-01	fused molybdate transporter subunits of ABC superfamily: ATP-binding components
<i>tas</i>	-1.05	3.74E-01	putative oxidoreductase, NADP(H)-dependent aldo-keto reductase
<i>tff</i>	-1.05	6.54E-01	ncRNA
<i>roxA</i>	1.05	3.20E-01	cupin superfamily protein
<i>yebK</i>	1.05	4.38E-01	putative DNA-binding transcriptional regulator
<i>yhbU</i>	-1.05	9.05E-01	putative peptidase (collagenase-like)
<i>slyB</i>	-1.05	4.65E-01	outer membrane lipoprotein
<i>ybfC</i>	-1.05	7.70E-01	hypothetical protein
<i>lon</i>	1.05	4.12E-01	DNA-binding ATP-dependent protease La
<i>glvC</i>	1.05	9.40E-01	pseudo
<i>hofQ</i>	1.05	8.30E-01	protein required for the utilization of DNA as a carbon source; fimbrial transporter homolog
<i>ydcL</i>	1.05	4.60E-01	lipoprotein
<i>preA</i>	-1.05	7.91E-01	dihydropyrimidine dehydrogenase, NADH-dependent, subunit C
<i>yhcB</i>	1.05	3.83E-01	hypothetical protein
<i>yghQ</i>	-1.05	9.48E-01	putative inner membrane protein
<i>baeR</i>	1.05	5.24E-01	DNA-binding response regulator in two-component regulatory system with BaeS
<i>dtd</i>	-1.05	6.11E-01	D-tyr-tRNA(Tyr) deacylase
<i>mraZ</i>	-1.05	4.25E-01	RsmH methyltransferase inhibitor
<i>garR</i>	-1.05	8.09E-01	tartronate semialdehyde reductase
<i>ispB</i>	-1.05	3.71E-01	octaprenyl diphosphate synthase
<i>dam</i>	-1.05	4.05E-01	DNA adenine methyltransferase
<i>yfeY</i>	1.05	5.02E-01	RpoE-regulated lipoprotein
<i>ybfA</i>	-1.05	5.77E-01	hypothetical protein
<i>ydeT</i>	1.05	6.81E-01	pseudo
<i>hcaR</i>	-1.05	5.20E-01	DNA-binding transcriptional activator of 3-phenylpropionic acid catabolism
<i>gyrA</i>	1.05	4.57E-01	DNA gyrase (type II topoisomerase), subunit A
<i>ansA</i>	-1.05	4.12E-01	cytoplasmic L-asparaginase I
<i>kdsC</i>	-1.05	4.56E-01	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase
<i>yiaU</i>	1.05	7.01E-01	putative DNA-binding transcriptional regulator
<i>ydbH</i>	1.05	4.04E-01	hypothetical protein
<i>casA</i>	-1.05	8.43E-01	CRISP RNA (crRNA) containing Cascade antiviral complex protein
<i>rhsA</i>	1.05	8.36E-01	rhsA element core protein RshA
<i>yfbL</i>	-1.05	9.59E-01	putative peptidase
<i>yohK</i>	-1.05	7.09E-01	inner membrane protein, LrgB family
<i>rho</i>	1.05	4.13E-01	transcription termination factor
<i>ynfC</i>	-1.05	4.74E-01	lipoprotein, UPF0257 family
<i>yehS</i>	-1.05	5.56E-01	conserved protein, DUF1456 family

<i>ygaP</i>	-1.05	7.81E-01	putative inner membrane protein with hydrolase activity
<i>narZ</i>	-1.05	6.98E-01	nitrate reductase 2 (NRZ), alpha subunit
<i>yeiR</i>	1.05	5.73E-01	Zn-stimulated GTPase involved in zinc homeostasis
<i>yraP</i>	-1.05	4.82E-01	outer membrane lipoprotein
<i>ybaK</i>	1.05	4.71E-01	hypothetical protein
<i>purB</i>	1.05	3.94E-01	adenylosuccinate lyase
<i>lptG</i>	-1.05	4.12E-01	lipopolysaccharide export ABC permease of the LptBFGC export complex
<i>yjfC</i>	1.05	9.09E-01	glutathionylspermidine synthase homolog
<i>ycjD</i>	1.05	8.55E-01	hypothetical protein
<i>tesA</i>	1.05	6.33E-01	multifunctional acyl-CoA thioesterase I and protease I and lysophospholipase L1
<i>yedZ</i>	-1.05	6.72E-01	inner membrane heme subunit for periplasmic YedYZ reductase
<i>msrC</i>	-1.05	4.11E-01	free methionine-(R)-sulfoxide reductase
<i>lsrD</i>	-1.05	8.88E-01	autoinducer 2 import system permease protein
<i>idnD</i>	1.05	8.79E-01	L-idonate 5-dehydrogenase, NAD-binding
<i>dedD</i>	-1.05	4.16E-01	membrane-anchored periplasmic protein involved in septation
<i>thyA</i>	-1.05	4.03E-01	thymidylate synthetase
<i>yigL</i>	1.05	5.38E-01	putative hydrolase
<i>yniA</i>	1.05	5.02E-01	putative phosphotransferase/kinase
<i>ydfV</i>	1.04	9.44E-01	Qin prophage; putative protein
<i>prc</i>	1.04	4.17E-01	carboxy-terminal protease for penicillin-binding protein 3
<i>ybiS</i>	-1.04	4.56E-01	L,D-transpeptidase linking Lpp to murein
<i>gltL</i>	1.04	5.82E-01	glutamate, aspartate ABC transporter ATP-binding subunit
<i>yjcS</i>	-1.04	8.96E-01	conserved protein, metallo-beta-lactamase superfamily
<i>yaiO</i>	-1.04	7.94E-01	outer membrane protein
<i>rnb</i>	-1.04	4.11E-01	ribonuclease II
<i>ydaM</i>	-1.04	7.24E-01	diguanylate cyclase, csgD regulator
<i>purD</i>	1.04	5.15E-01	phosphoribosylglycinamide synthetase phosphoribosylamine-glycine ligase
<i>etk</i>	-1.04	5.52E-01	cryptic autophosphorylating protein tyrosine kinase Etk
<i>ynjI</i>	-1.04	8.05E-01	inner membrane protein
<i>yhaO</i>	1.04	8.47E-01	putative transporter
<i>dfp</i>	1.04	5.60E-01	f4'-phosphopantothenoylecysteine decarboxylase/phosphopantothenoylecysteine synthetase
<i>mazF</i>	-1.04	6.92E-01	mRNA interferase toxin, antitoxin is MazE
<i>yqhG</i>	-1.04	8.17E-01	hypothetical protein
<i>kdsA</i>	1.04	4.23E-01	3-deoxy-D-manno-octulosonate 8-phosphate synthase
<i>rhtC</i>	1.04	6.38E-01	threonine efflux pump
<i>serX</i>	-1.04	9.42E-01	tRNA
<i>yjfD</i>	-1.04	5.62E-01	inner membrane protein, UPF0053 family
<i>melR</i>	1.04	7.72E-01	DNA-binding transcriptional dual regulator
<i>minC</i>	1.04	4.81E-01	cell division inhibitor
<i>yieL</i>	-1.04	8.54E-01	putative xylanase
<i>mgtL</i>	1.04	6.51E-01	regulatory leader peptide for mgtA
<i>glpQ</i>	-1.04	4.94E-01	periplasmic glycerophosphodiester phosphodiesterase
<i>ycfS</i>	-1.04	4.86E-01	L,D-transpeptidase linking Lpp to murein

<i>setC</i>	1.04	8.86E-01	putative arabinose efflux transporter
<i>rbfA</i>	1.04	5.48E-01	30s ribosome binding factor
<i>selC</i>	-1.04	8.75E-01	tRNA
<i>yibW</i>	1.04	1.00E+00	pseudo
<i>mdtQ</i>	1.04	9.55E-01	pseudo
<i>glnQ</i>	1.04	5.34E-01	glutamine transporter subunit
<i>yjhG</i>	1.04	7.30E-01	KpLE2 phage-like element; predicted dehydratase
<i>bcsC</i>	1.04	5.66E-01	cellulose synthase subunit
<i>bdcA</i>	1.04	8.60E-01	c-di-GMP-binding biofilm dispersal mediator protein
<i>ymiB</i>	1.04	9.43E-01	hypothetical protein
<i>rttR</i>	-1.04	8.72E-01	ncRNA
<i>yidA</i>	1.04	5.39E-01	sugar phosphate phosphatase; substrates include erythrose 4-P and mannose 1-P phosphatase
<i>gluQ</i>	-1.04	6.38E-01	glutamyl-Q tRNA(Asp) synthetase
<i>pepB</i>	1.04	7.29E-01	aminopeptidase B
<i>ydcY</i>	-1.04	5.33E-01	hypothetical protein
<i>yjiR</i>	1.04	7.04E-01	fused predicted DNA-binding transcriptional regulator/predicted aminotransferase
<i>ruvC</i>	1.04	5.82E-01	component of RuvABC resolvase, endonuclease
<i>yhdY</i>	1.04	9.06E-01	putative amino-acid transporter subunit
<i>pdxJ</i>	-1.04	5.26E-01	pyridoxine 5'-phosphate synthase
<i>kefG</i>	-1.04	6.90E-01	potassium-efflux system ancillary protein for KefB, glutathione-regulated
<i>yihF</i>	-1.04	8.09E-01	conserved protein, DUF945 family
<i>ykgF</i>	-1.04	7.44E-01	putative electron transport protein with ferridoxin-like domain
<i>bamD</i>	-1.04	4.90E-01	lipoprotein required for OM biogenesis, in BamABCDE complex
<i>fimI</i>	-1.04	8.60E-01	fimbrial protein involved in type 1 pilus biosynthesis
<i>bglG</i>	1.04	9.50E-01	transcriptional antiterminator of the bgl operon
<i>yadE</i>	-1.04	7.11E-01	putative polysaccharide deacetylase lipoprotein
<i>diaA</i>	1.04	4.77E-01	DnaA initiator-associating factor for replication initiation
<i>ycbF</i>	1.04	8.23E-01	putative periplasmic pilini chaperone
<i>puuC</i>	-1.04	8.54E-01	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent
<i>yedR</i>	1.04	6.87E-01	inner membrane protein
<i>yoaJ</i>	-1.04	8.86E-01	expressed protein, membrane-associated
<i>ybhJ</i>	-1.04	8.98E-01	putative hydratase
<i>yiiF</i>	-1.04	8.59E-01	hypothetical protein
<i>nanR</i>	-1.04	5.59E-01	DNA-binding transcriptional repressor of the nan operon, induced by sialic acid
<i>pgpC</i>	-1.04	5.64E-01	hypothetical protein
<i>ypaA</i>	1.04	7.26E-01	hypothetical protein
<i>ispD</i>	1.04	6.43E-01	4-diphosphocytidyl-2C-methyl-D-erythritol synthase
<i>intA</i>	-1.04	5.43E-01	CP4-57 prophage; integrase
<i>ubiG</i>	-1.04	5.68E-01	3-demethylubiquinone-9 3-methyltransferase/ 2-octaprenyl-6-hydroxy phenol methylase
<i>adhP</i>	1.04	5.50E-01	ethanol-active dehydrogenase/acetaldehyde-active reductase
<i>ygbM</i>	1.04	8.46E-01	hypothetical protein
<i>ydcU</i>	1.04	8.48E-01	putative spermidine/putrescine transporter subunit
<i>ybhK</i>	-1.04	6.24E-01	putative transferase with NAD(P)-binding Rossmann-fold domain

<i>ydaS</i>	1.04	9.59E-01	Rac prophage; predicted DNA-binding transcriptional regulator
<i>cbrB</i>	1.04	8.72E-01	inner membrane protein, creBC regulon
<i>rrsD</i>	1.04	9.91E-01	16S ribosomal RNA of rrnD operon
<i>bglF</i>	1.04	1.00E+00	fused beta-glucoside-specific PTS enzymes: IIA component/IIB component/IIC component
<i>yhcM</i>	-1.04	5.84E-01	conserved protein with nucleoside triphosphate hydrolase domain
<i>psuG</i>	-1.04	1.00E+00	pseudouridine 5'-phosphate glycosidase
<i>mscM</i>	1.04	5.45E-01	mechanosensitive channel protein, miniconductance
<i>yedA</i>	-1.04	9.51E-01	amino acid exporter for phenylalanine, threonine
<i>macB</i>	1.04	7.26E-01	fused macrolide transporter subunits of ABC superfamily
<i>ybcM</i>	-1.04	6.58E-01	DLP12 prophage; predicted DNA-binding transcriptional regulator
<i>bglJ</i>	1.04	8.88E-01	bgl operon transcriptional activator
<i>rscC</i>	1.04	5.23E-01	hybrid sensory kinase in two-component regulatory system with RcsB and YojN
<i>emrD</i>	1.04	8.12E-01	multidrug efflux system protein
<i>yobB</i>	1.04	6.15E-01	hypothetical protein
<i>nikA</i>	-1.04	8.81E-01	nickel-binding, heme-binding periplasmic protein
<i>ftsN</i>	1.04	5.62E-01	essential cell division protein
<i>fdhD</i>	-1.04	6.58E-01	formate dehydrogenase formation protein
<i>cysS</i>	-1.04	5.21E-01	cysteinyI-tRNA synthetase
<i>wcaG</i>	-1.04	9.27E-01	GDP-fucose synthetase:GDP-4-dehydro-6-deoxy-D-mannose epimerase/reductase
<i>yjjA</i>	1.04	6.29E-01	hypothetical protein
<i>sucA</i>	-1.04	7.15E-01	2-oxoglutarate decarboxylase, thiamin-requiring
<i>elfG</i>	-1.04	8.46E-01	putative fimbrial-like adhesin protein
<i>ryeA</i>	1.04	6.67E-01	ncRNA
<i>fimE</i>	-1.04	8.45E-01	tyrosine recombinase/inversion of on/off regulator of fimA
<i>cmoA</i>	1.04	6.44E-01	tRNA cmo(5)U34 methyltransferase, SAM-dependent
<i>pepQ</i>	-1.03	6.15E-01	proline dipeptidase
<i>ygiB</i>	-1.03	6.21E-01	conserved protein, UPF0441 family
<i>endA</i>	1.03	8.93E-01	DNA-specific endonuclease I
<i>yjhY</i>	-1.03	6.49E-01	pseudo
<i>nadC</i>	1.03	5.87E-01	quinolinate phosphoribosyltransferase
<i>yghB</i>	1.03	6.43E-01	required, with yqjA, for membrane integrity; inner membrane protein
<i>yjC</i>	1.03	6.68E-01	phosphatase
<i>mdtC</i>	1.03	7.64E-01	multidrug efflux system, subunit C
<i>kdpC</i>	1.03	8.90E-01	potassium translocating ATPase, subunit C
<i>ygiI</i>	1.03	1.00E+00	putative transporter
<i>purN</i>	-1.03	5.65E-01	phosphoribosylglycinamide formyltransferase 1
<i>ldcC</i>	1.03	7.68E-01	lysine decarboxylase 2, constitutive
<i>yafY</i>	1.03	9.31E-01	lipoprotein, inner membrane; overproduction stimulates degP expression; CP4-6 prophage
<i>ydH</i>	-1.03	7.65E-01	inner membrane protein, DUF202 family
<i>ydhJ</i>	1.03	7.77E-01	putative membrane fusion protein (MFP) of YdhJK efflux pump
<i>ccmF</i>	-1.03	8.23E-01	heme lyase, CcmF subunit
<i>yadI</i>	1.03	8.25E-01	putative PTS Enzyme IIA
<i>lpxA</i>	1.03	5.46E-01	UDP-N-acetylglucosamine acetyltransferase

<i>fabZ</i>	1.03	5.83E-01	(3R)-hydroxymyristol acyl carrier protein dehydratase
<i>moaB</i>	-1.03	6.43E-01	molybdopterin biosynthesis protein B
<i>tehA</i>	1.03	7.70E-01	potassium-tellurite ethidium and proflavin transporter
<i>araJ</i>	1.03	7.08E-01	arabinose-inducible predicted transporter, MFS family
<i>znuC</i>	-1.03	7.18E-01	zinc transporter subunit: ATP-binding component of ABC superfamily
<i>yhhW</i>	-1.03	7.66E-01	quercetinase activity in vitro
<i>yjjV</i>	1.03	8.46E-01	putative DNase
<i>miaA</i>	-1.03	5.82E-01	delta(2)-isopentenylpyrophosphate tRNA-adenosine transferase
<i>waaY</i>	1.03	5.91E-01	lipopolysaccharide core biosynthesis protein
<i>metA</i>	1.03	6.90E-01	homoserine O-transsuccinylase
<i>fieF</i>	-1.03	5.85E-01	ferrous iron and zinc transporter
<i>yncD</i>	1.03	6.60E-01	putative iron outer membrane transporter
<i>coaE</i>	1.03	6.63E-01	dephospho-CoA kinase
<i>yeeX</i>	1.03	5.56E-01	conserved protein, UPF0265 family
<i>torR</i>	1.03	7.63E-01	DNA-binding response regulator in two-component regulatory system with TorS
<i>ydcP</i>	-1.03	6.41E-01	putative peptidase
<i>tldD</i>	-1.03	5.99E-01	putative peptidase
<i>aroP</i>	-1.03	6.55E-01	aromatic amino acid transporter
<i>ugpQ</i>	1.03	7.23E-01	glycerophosphodiester phosphodiesterase, cytosolic
<i>alsE</i>	-1.03	9.34E-01	allulose-6-phosphate 3-epimerase
<i>ygiP</i>	1.03	8.43E-01	putative metal dependent hydrolase
<i>qseC</i>	1.03	7.42E-01	quorum sensing sensory histidine kinase in two-component regulatory system with QseB
<i>gspL</i>	1.03	9.06E-01	general secretory pathway component, cryptic
<i>ycjR</i>	-1.03	9.01E-01	putative enzyme
<i>ybeX</i>	-1.03	5.83E-01	predicted ion transport
<i>torC</i>	-1.03	1.00E+00	trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit
<i>guaD</i>	1.03	7.95E-01	guanine deaminase
<i>yehE</i>	1.03	8.23E-01	putative inner membrane protein
<i>ypjC</i>	1.03	9.34E-01	pseudo
<i>hyfJ</i>	1.03	9.40E-01	putative processing element hydrogenase 4
<i>ykgE</i>	1.03	9.61E-01	putative oxidoreductase
<i>groL</i>	-1.03	6.82E-01	Cpn60 chaperonin GroEL, large subunit of GroESL
<i>rsmI</i>	-1.03	7.24E-01	16S rRNA C1402 2'-O-ribose methyltransferase, SAM-dependent
<i>yidJ</i>	-1.03	9.36E-01	putative sulfatase/phosphatase
<i>tatC</i>	-1.03	6.69E-01	TatABCE protein translocation system subunit
<i>yaiI</i>	1.03	7.99E-01	conserved protein, UPF0178 family, downregulated by beryllium
<i>yneK</i>	1.03	9.12E-01	hypothetical protein
<i>yejA</i>	-1.03	7.31E-01	microcin C transporter YejABEF, periplasmic binding protein; ABC family
<i>flgI</i>	-1.03	9.69E-01	putative flagellar basal body protein
<i>yjfU</i>	1.03	9.53E-01	pseudo
<i>pheU</i>	1.03	8.60E-01	tRNA
<i>sspA</i>	-1.03	6.32E-01	stringent starvation protein A
<i>secD</i>	-1.03	6.29E-01	SecYEG protein translocase auxillary subunit

<i>yfhR</i>	-1.03	9.63E-01	S9 peptidase family protein, function unknown
<i>artP</i>	-1.03	6.64E-01	arginine transporter subunit
<i>narQ</i>	-1.03	7.66E-01	sensory histidine kinase in two-component regulatory system with NarP (NarL)
<i>ybgC</i>	-1.03	6.73E-01	acyl-CoA thioesterase, involved in phospholipid metabolism
<i>potC</i>	-1.03	6.80E-01	polyamine transporter subunit
<i>yqiG</i>	1.03	8.60E-01	pseudo
<i>lpxD</i>	1.03	5.92E-01	UDP-3-O-(3-hydroxymyristoyl)-glucosamine N-acyltransferase
<i>yheV</i>	1.03	7.66E-01	hypothetical protein
<i>ybeD</i>	-1.03	6.32E-01	conserved protein, UPF0250 family
<i>fabR</i>	1.03	6.80E-01	DNA-binding transcriptional repressor
<i>dacD</i>	-1.03	8.80E-01	D-alanyl-D-alanine carboxypeptidase (penicillin-binding protein 6b)
<i>ycdY</i>	1.03	6.39E-01	YcdX chaperone, redox enzyme maturation protein (REMP) required for swarming
<i>nlpD</i>	1.03	8.08E-01	activator of AmiC murein hydrolase activity, lipoprotein
<i>nlpC</i>	-1.03	6.79E-01	putative peptidase, C40 clan, lipoprotein
<i>caiA</i>	-1.03	8.23E-01	crotonobetaine reductase subunit II, FAD-binding
<i>yadV</i>	1.03	1.00E+00	putative periplasmic pilin chaperone
<i>aer</i>	-1.03	8.10E-01	fused signal transducer for aerotaxis
<i>smrB</i>	1.03	7.52E-01	putative DNA endonuclease
<i>yoaI</i>	-1.03	1.00E+00	hypothetical protein
<i>gmr</i>	-1.03	6.89E-01	cyclic-di-GMP phosphodiesterase; csgD regulator; modulator of Rnase II stability
<i>rrsC</i>	1.03	1.00E+00	16S ribosomal RNA of rrnC operon
<i>proQ</i>	1.03	6.47E-01	RNA chaperone, probable regulator of ProP translation
<i>yhaK</i>	1.03	9.28E-01	redox-sensitive bicupin
<i>tolA</i>	1.03	6.73E-01	membrane anchored protein in TolA-TolQ-TolR complex
<i>ibpA</i>	-1.03	7.98E-01	heat shock chaperone
<i>yjdC</i>	1.03	6.56E-01	putative transcriptional regulator
<i>sapF</i>	-1.03	8.19E-01	antimicrobial peptide transport ABC system ATP-binding protein
<i>yfbN</i>	-1.03	9.03E-01	hypothetical protein
<i>yfeR</i>	1.03	8.31E-01	putative DNA-binding transcriptional regulator
<i>damX</i>	1.03	6.72E-01	cell division protein that binds to the septal ring
<i>yagF</i>	1.03	9.01E-01	CP4-6 prophage; predicted dehydratase
<i>yfeK</i>	1.03	8.74E-01	hypothetical protein
<i>rrsG</i>	-1.03	9.81E-01	16S ribosomal RNA of rrnG operon
<i>rihB</i>	1.03	1.00E+00	ribonucleoside hydrolase 2
<i>yejF</i>	1.03	8.25E-01	microcin C transporter, ATP-binding subunit; ABC family
<i>yhdW</i>	1.03	8.57E-01	pseudo
<i>marA</i>	1.03	8.22E-01	DNA-binding transcriptional dual activator of multiple antibiotic resistance
<i>dcd</i>	1.02	6.61E-01	2'-deoxycytidine 5'-triphosphate deaminase
<i>ygeW</i>	-1.02	1.00E+00	putative carbamoyltransferase
<i>mutH</i>	1.02	8.26E-01	methyl-directed mismatch repair protein
<i>ytfF</i>	-1.02	8.15E-01	inner membrane protein, DMT transporter family
<i>tfaS</i>	1.02	8.84E-01	pseudo
<i>yfiH</i>	1.02	7.50E-01	conserved protein, UPF0124 family

<i>yqfB</i>	-1.02	7.08E-01	conserved protein, UPF0267 family
<i>yjjK</i>	1.02	7.42E-01	fused predicted transporter subunits of ABC superfamily: ATP-binding components
<i>elaD</i>	-1.02	9.22E-01	protease, capable of cleaving an AMC-ubiquitin model substrate
<i>ydbC</i>	1.02	7.95E-01	putative oxidoreductase, NAD(P)-binding
<i>yeiG</i>	-1.02	7.06E-01	S-formylglutathione hydrolase
<i>mtlA</i>	-1.02	8.68E-01	fused mannitol-specific PTS enzymes: IIA components/IIB components/IIC components
<i>glgC</i>	1.02	7.52E-01	glucose-1-phosphate adenylyltransferase
<i>potF</i>	1.02	7.85E-01	putrescine transporter subunit: periplasmic-binding component of ABC superfamily
<i>etp</i>	1.02	9.47E-01	phosphotyrosine-protein phosphatase
<i>yggU</i>	-1.02	7.96E-01	conserved protein, UPF0235 family
<i>ypjD</i>	1.02	7.63E-01	putative inner membrane protein
<i>ompX</i>	-1.02	7.16E-01	outer membrane protein X
<i>mdtB</i>	1.02	8.24E-01	multidrug efflux system, subunit B
<i>yeaY</i>	1.02	7.31E-01	lipoprotein, RpoE-regulated, function unknown
<i>guaA</i>	1.02	7.60E-01	GMP synthetase (glutamine aminotransferase)
<i>cdaR</i>	-1.02	9.44E-01	DNA-binding transcriptional regulator for gar and gud operons; carbohydrate diacid regulator
<i>cobB</i>	1.02	7.67E-01	deacetylase of acs and cheY, chemotaxis regulator
<i>yciV</i>	1.02	7.74E-01	hypothetical protein
<i>yghE</i>	1.02	1.00E+00	pseudo
<i>cobU</i>	1.02	8.75E-01	bifunctional cobinamide kinase/ cobinamide phosphate guanylyltransferase
<i>mtgA</i>	1.02	8.91E-01	biosynthetic peptidoglycan transglycosylase
<i>cheY</i>	1.02	9.31E-01	chemotaxis regulator transmitting signal to flagellar motor component
<i>pabC</i>	1.02	8.33E-01	4-amino-4-deoxychorismate lyase
<i>trmL</i>	1.02	9.08E-01	tRNA Leu mC34,mU34 2'-O-methyltransferase, SAM-dependent
<i>yjiM</i>	-1.02	9.20E-01	putative 2-hydroxyglutaryl-CoA dehydratase
<i>pabB</i>	1.02	8.03E-01	aminodeoxychorismate synthase, subunit I
<i>yciM</i>	1.02	7.37E-01	TPR-repeats-containing protein
<i>ybdD</i>	1.02	8.36E-01	conserved protein, DUF466 family
<i>pptA</i>	1.02	8.43E-01	4-oxalocrotonate tautomerase
<i>mpl</i>	-1.02	7.76E-01	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase
<i>bamA</i>	1.02	7.11E-01	outer membrane protein assembly factor, forms pores; required for OM biogenesis
<i>pepT</i>	1.02	7.52E-01	peptidase T
<i>copA</i>	-1.02	8.30E-01	copper transporter
<i>valU</i>	-1.02	8.60E-01	tRNA
<i>chiA</i>	-1.02	8.15E-01	periplasmic endochitinase
<i>mhpT</i>	-1.02	9.45E-01	putative 3-hydroxyphenylpropionic transporter
<i>ycbX</i>	1.02	8.28E-01	putative 2Fe-2S cluster-containing protein; 6-N-hydroxylaminopurine resistance protein
<i>yoaK</i>	1.02	9.49E-01	expressed protein, membrane-associated
<i>srkA</i>	1.02	7.62E-01	Thr/Ser kinase implicated in Cpx stress response
<i>rrlE</i>	1.02	9.75E-01	23S ribosomal RNA of rrnE operon
<i>hyi</i>	1.02	9.51E-01	hydroxypyruvate isomerase
<i>ygeA</i>	-1.02	8.90E-01	conserved protein, Asp/Glu_racemase family
<i>treR</i>	1.02	8.47E-01	DNA-binding transcriptional repressor

<i>der</i>	1.02	7.38E-01	GTPase; multicopy suppressor of ftsJ
<i>ycfL</i>	-1.02	7.92E-01	hypothetical protein
<i>dhaR</i>	1.02	8.52E-01	DNA-binding transcription activator of the dhaKLM operon
<i>phnD</i>	-1.02	1.00E+00	phosphonate ABC transporter periplasmic binding protein
<i>mlaE</i>	-1.02	8.20E-01	ABC transporter maintaining OM lipid asymmetry, inner membrane permease protein
<i>ecnB</i>	-1.02	8.69E-01	entericidin B membrane lipoprotein
<i>yfbR</i>	-1.02	8.53E-01	5'-nucleotidase
<i>gspB</i>	-1.02	9.80E-01	part of gsp divergon involved in type II protein secretion
<i>yeaV</i>	1.02	1.00E+00	putative transporter
<i>nusB</i>	1.02	7.46E-01	transcription antitermination protein
<i>xapR</i>	-1.02	8.66E-01	DNA-binding transcriptional activator for for xapAB
<i>tqsA</i>	1.02	8.56E-01	pheromone AI-2 transporter
<i>racR</i>	1.02	8.24E-01	Rac prophage; predicted DNA-binding transcriptional regulator
<i>ybbC</i>	1.02	9.13E-01	hypothetical protein
<i>ygbT</i>	1.02	9.05E-01	multifunctional endonuclease CasI, CRISPR adaptation protein; DNA repair enzyme
<i>gstB</i>	-1.02	7.72E-01	glutathione S-transferase
<i>nudE</i>	-1.02	8.06E-01	adenosine nucleotide hydrolase; substrates include Ap3A, Ap2A, ADP-ribose, NADH
<i>srlA</i>	-1.02	1.00E+00	glucitol/sorbitol-specific enzyme IIC component of PTS
<i>sapD</i>	1.02	8.25E-01	antimicrobial peptide transport ABC system ATP-binding protein
<i>rdgB</i>	-1.02	8.15E-01	dITP/XTP pyrophosphatase
<i>barA</i>	1.02	7.93E-01	hybrid sensory histidine kinase, in two-component regulatory system with UvrY
<i>cusR</i>	1.02	8.90E-01	DNA-binding response regulator in two-component regulatory system with CusS
<i>nhaB</i>	1.02	7.82E-01	sodium:proton antiporter
<i>fdx</i>	-1.02	8.04E-01	[2Fe-2S] ferredoxin
<i>ygbJ</i>	1.02	1.00E+00	putative dehydrogenase, with NAD(P)-binding Rossmann-fold domain
<i>rob</i>	-1.02	8.38E-01	right oriC-binding transcriptional activator, AraC family
<i>birA</i>	1.02	8.52E-01	biotin-[acetylCoA carboxylase] holoenzyme synthetase
<i>dnaA</i>	1.02	7.65E-01	chromosomal replication initiator protein DnaA, DNA-binding transcriptional dual regulator
<i>nudG</i>	1.02	9.08E-01	CTP pyrophosphohydrolase
<i>uvrY</i>	1.02	7.95E-01	DNA-binding response regulator in two-component regulatory system with BarA
<i>yihY</i>	-1.02	8.27E-01	putative inner membrane protein
<i>atoE</i>	-1.02	1.00E+00	short chain fatty acid transporter
<i>ytfT</i>	1.02	1.00E+00	putative sugar transporter subunit: membrane component of ABC superfamily
<i>sfmF</i>	1.02	1.00E+00	putative fimbrial-like adhesin protein
<i>rsxG</i>	-1.02	9.15E-01	electron transport complex protein required for the reduction of SoxR
<i>yaiT</i>	-1.02	8.50E-01	pseudo
<i>yadH</i>	-1.02	8.48E-01	putative transporter subunit: membrane component of ABC superfamily
<i>ilvI</i>	1.02	8.43E-01	acetolactate synthase III, large subunit
<i>lgt</i>	-1.02	8.50E-01	phosphatidylglycerol-prolipoprotein diacylglycerol transferase
<i>priC</i>	-1.02	8.62E-01	primosomal replication protein N"
<i>livF</i>	1.02	8.77E-01	leucine/isoleucine/valine transporter subunit
<i>uup</i>	-1.02	7.89E-01	fused predicted transporter subunits of ABC superfamily: ATP-binding components
<i>apaG</i>	-1.02	8.23E-01	protein associated with Co ²⁺ and Mg ²⁺ efflux

<i>glgB</i>	-1.02	8.25E-01	1,4-alpha-glucan branching enzyme
<i>insG</i>	-1.02	8.89E-01	IS4 transposase
<i>dauA</i>	1.02	9.00E-01	C4-dicarboxylic acid transporter
<i>yjeN</i>	-1.02	1.00E+00	hypothetical protein
<i>ynjC</i>	1.02	9.43E-01	putative inner membrane ABC transporter permease, function unknown
<i>blr</i>	-1.02	8.66E-01	beta-lactam resistance membrane protein; divisome-associated protein
<i>pka</i>	-1.02	8.20E-01	protein lysine acetyltransferase
<i>lysR</i>	-1.02	9.27E-01	DNA-binding transcriptional dual regulator
<i>ycdI</i>	1.02	8.21E-01	putative DNA-binding transcriptional regulator
<i>thiL</i>	-1.02	9.17E-01	thiamin-monophosphate kinase
<i>yjjB</i>	1.02	9.34E-01	conserved inner membrane protein
<i>cusA</i>	1.02	9.71E-01	copper/silver efflux system, membrane component
<i>ydfC</i>	-1.02	9.63E-01	conserved protein, Qin prophage
<i>lipA</i>	1.02	8.11E-01	lipoate synthase
<i>gntR</i>	-1.02	8.28E-01	DNA-binding transcriptional repressor
<i>intR</i>	1.02	9.15E-01	Rac prophage; integrase
<i>ycdZ</i>	1.02	8.99E-01	inner membrane protein, DUF606 family
<i>acs</i>	-1.02	8.44E-01	acetyl-CoA synthetase
<i>ybcK</i>	1.02	9.84E-01	DLP12 prophage; predicted recombinase
<i>ymjA</i>	1.02	8.93E-01	hypothetical protein
<i>mug</i>	1.02	8.80E-01	G/U mismatch-specific DNA glycosylase; xanthine DNA glycosylase
<i>ybaA</i>	-1.01	9.38E-01	conserved protein, DUF1428 family
<i>pmrD</i>	-1.01	8.56E-01	inactive two-component system connector protein
<i>yiiQ</i>	-1.01	8.87E-01	hypothetical protein
<i>aroD</i>	1.01	8.43E-01	3-dehydroquinate dehydratase
<i>yhcG</i>	-1.01	9.25E-01	hypothetical protein
<i>exuT</i>	1.01	9.40E-01	hexuronate transporter
<i>hofC</i>	1.01	9.38E-01	assembly protein in type IV pilin biogenesis, transmembrane protein
<i>mrcB</i>	-1.01	8.20E-01	fused glycosyl transferase and transpeptidase
<i>cspF</i>	-1.01	1.00E+00	Qin prophage; cold shock protein
<i>glcG</i>	1.01	9.15E-01	hypothetical protein
<i>ymgJ</i>	1.01	1.00E+00	hypothetical protein
<i>yjbS</i>	1.01	1.00E+00	hypothetical protein
<i>menD</i>	1.01	8.93E-01	bifunctional 2-oxoglutarate decarboxylase/ SHCHC synthase
<i>queE</i>	-1.01	9.01E-01	7-carboxy-7-deazaguanine synthase; queosine biosynthesis
<i>gcvR</i>	-1.01	8.43E-01	DNA-binding transcriptional repressor, regulatory protein accessory to GcvA
<i>ypdE</i>	-1.01	1.00E+00	aminopeptidase
<i>yohJ</i>	1.01	9.84E-01	inner membrane protein, UPF0299 family
<i>gabP</i>	-1.01	9.15E-01	gamma-aminobutyrate transporter
<i>ydhB</i>	-1.01	9.37E-01	putative DNA-binding transcriptional regulator
<i>macA</i>	1.01	8.90E-01	macrolide transporter subunit, membrane fusion protein (MFP) component
<i>yeiE</i>	-1.01	8.88E-01	putative DNA-binding transcriptional regulator
<i>casD</i>	1.01	9.40E-01	CRISP RNA (crRNA) containing Cascade antiviral complex protein

<i>ymdA</i>	1.01	9.77E-01	hypothetical protein
<i>ldhA</i>	-1.01	9.11E-01	fermentative D-lactate dehydrogenase, NAD-dependent
<i>accC</i>	-1.01	9.15E-01	acetyl-CoA carboxylase, biotin carboxylase subunit
<i>yraN</i>	1.01	9.11E-01	conserved protein, UPF0102 family
<i>sspB</i>	-1.01	8.54E-01	ClpXP protease specificity enhancing factor
<i>yicH</i>	1.01	8.72E-01	hypothetical protein
<i>cedA</i>	1.01	9.62E-01	cell division modulator
<i>rlmH</i>	-1.01	8.86E-01	23S rRNA m(3)Psi1915 pseudouridine methyltransferase, SAM-dependent
<i>yfdF</i>	-1.01	9.72E-01	hypothetical protein
<i>yjhP</i>	-1.01	1.00E+00	KpLE2 phage-like element; predicted methyltransferase
<i>yohC</i>	-1.01	9.22E-01	inner membrane protein, Yip1 family
<i>nadR</i>	-1.01	8.79E-01	NMN adenylyltransferase, ribosylnicotinamide kinase, transcriptional repressor
<i>csrD</i>	1.01	8.56E-01	targeting factor for csrBC sRNA degradation
<i>tyrB</i>	1.01	8.71E-01	tyrosine aminotransferase, tyrosine-repressible, PLP-dependent
<i>yceK</i>	-1.01	1.00E+00	outer membrane integrity lipoprotein
<i>yphH</i>	-1.01	9.11E-01	putative DNA-binding transcriptional regulator
<i>yjaG</i>	1.01	8.79E-01	hypothetical protein
<i>accD</i>	1.01	8.45E-01	acetyl-CoA carboxylase, beta (carboxyltransferase) subunit
<i>zur</i>	1.01	9.25E-01	DNA-binding transcriptional repressor, Zn(II)-binding
<i>yedJ</i>	1.01	8.92E-01	putative hydrolase, HD superfamily
<i>tatA</i>	1.01	8.67E-01	TatABCE protein translocation system subunit
<i>uhpC</i>	1.01	9.70E-01	membrane protein regulates uhpT expression
<i>hemG</i>	-1.01	9.09E-01	protoporphyrin oxidase, flavoprotein
<i>mlrA</i>	-1.01	9.17E-01	DNA-binding transcriptional regulator
<i>accB</i>	1.01	9.24E-01	acetyl CoA carboxylase, BCCP subunit
<i>idnO</i>	-1.01	1.00E+00	5-keto-D-gluconate-5-reductase
<i>ubiE</i>	-1.01	9.07E-01	2-octaprenyl-6-methoxy-1,4-benzoquinone methylase/ SAM:2-DMK methyltransferase
<i>yfeS</i>	1.01	9.31E-01	hypothetical protein
<i>agaC</i>	1.01	1.00E+00	N-acetylgalactosamine-specific enzyme IIC component of PTS
<i>yidZ</i>	1.01	9.60E-01	putative DNA-binding transcriptional regulator
<i>rsmA</i>	-1.01	8.90E-01	16S rRNA m(6)A1518, m(6)A1519 dimethyltransferase, SAM-dependent
<i>nrfG</i>	-1.01	1.00E+00	heme lyase (NrfEFG) for insertion of heme into c552, subunit NrfG
<i>yiiD</i>	1.01	9.15E-01	putative acetyltransferase
<i>cysC</i>	1.01	9.19E-01	adenosine 5'-phosphosulfate kinase
<i>gshA</i>	1.01	8.99E-01	glutamate-cysteine ligase
<i>bioH</i>	1.01	9.51E-01	pimeloyl-ACP carboxylesterase
<i>yafK</i>	1.01	9.06E-01	hypothetical protein
<i>ycgL</i>	1.01	9.17E-01	hypothetical protein
<i>dnaE</i>	-1.01	8.98E-01	DNA polymerase III alpha subunit
<i>ydgC</i>	-1.01	9.67E-01	inner membrane protein, GlpM family
<i>fre</i>	-1.01	9.35E-01	NAD(P)H-flavin reductase
<i>ydhK</i>	1.01	9.77E-01	putative efflux protein (PET) component of YdhJK efflux pump
<i>hybO</i>	1.01	1.00E+00	hydrogenase 2, small subunit

<i>iap</i>	1.01	9.36E-01	aminopeptidase in alkaline phosphatase isozyme conversion
<i>yqeI</i>	-1.01	9.84E-01	putative transcriptional regulator
<i>yhfK</i>	1.01	9.37E-01	conserved inner membrane protein
<i>yjiY</i>	1.01	1.00E+00	putative inner membrane protein
<i>dmsC</i>	1.01	9.84E-01	dimethyl sulfoxide reductase, anaerobic, subunit C
<i>acrB</i>	1.01	9.22E-01	multidrug efflux system protein
<i>allC</i>	1.01	1.00E+00	allantoate amidohydrolase
<i>hyaD</i>	1.01	1.00E+00	hydrogenase 1 maturation protease
<i>mzrA</i>	1.01	9.76E-01	modulator of EnvZ/OmpR regulon
<i>queF</i>	-1.01	9.28E-01	7-cyano-7-deazaguanine reductase (NADPH-dependent)
<i>yffO</i>	1.01	1.00E+00	CPZ-55 prophage; putative protein
<i>nrfA</i>	1.01	1.00E+00	nitrite reductase, formate-dependent, cytochrome
<i>ydeJ</i>	1.01	9.81E-01	hypothetical protein
<i>lacA</i>	1.01	9.45E-01	thiogalactoside acetyltransferase
<i>envZ</i>	1.01	9.67E-01	sensory histidine kinase in two-component regulatory system with OmpR
<i>glcC</i>	1.01	9.66E-01	DNA-binding transcriptional dual regulator, glycolate-binding
<i>appY</i>	-1.01	9.61E-01	DNA-binding global transcriptional activator; DLP12 prophage
<i>ymfA</i>	1.01	1.00E+00	conserved inner membrane protein
<i>mqsR</i>	1.01	9.50E-01	GCU-specific mRNA interferase toxin of the MqsR-MqsA toxin-antitoxin system
<i>ccmE</i>	1.01	9.84E-01	periplasmic heme chaperone
<i>galR</i>	-1.01	9.72E-01	DNA-binding transcriptional repressor
<i>ebgR</i>	1.01	9.65E-01	DNA-binding transcriptional repressor
<i>amiD</i>	1.01	9.60E-01	1,6-anhydro-N-acetylmuramyl-L-alanine amidase, Zn-dependent; OM lipoprotein
<i>cspD</i>	1.01	9.47E-01	inhibitor of DNA replication, cold shock protein homolog
<i>ydhL</i>	-1.01	1.00E+00	hypothetical protein
<i>aldB</i>	-1.01	9.93E-01	aldehyde dehydrogenase B
<i>mazE</i>	-1.01	1.00E+00	antitoxin of the ChpA-ChpR toxin-antitoxin system
<i>sbmC</i>	1.01	9.69E-01	DNA gyrase inhibitor
<i>yheU</i>	-1.00	9.69E-01	hypothetical protein
<i>ydhF</i>	-1.00	9.55E-01	putative oxidoreductase
<i>zntR</i>	-1.00	9.84E-01	DNA-binding transcriptional activator in response to Zn(II)
<i>yegE</i>	1.00	9.70E-01	putative diguanylate cyclase, GGDEF domain signaling protein
<i>sdaB</i>	-1.00	9.85E-01	L-serine deaminase II
<i>creC</i>	-1.00	9.74E-01	sensory histidine kinase with CreB or PhoB, regulator of the CreBC regulon
<i>yccU</i>	-1.00	9.81E-01	putative CoA-binding protein
<i>rpsF</i>	-1.00	9.70E-01	30S ribosomal subunit protein S6
<i>tsaA</i>	-1.00	9.62E-01	tRNA-Thr(GGU) m(6)t(6)A37 methyltransferase, SAM-dependent
<i>rsmE</i>	1.00	1.00E+00	16S rRNA m(3)U1498 methyltransferase, SAM-dependent
<i>wbbI</i>	1.00	9.54E-01	d-Galf:alpha-d-Glc beta-1,6-galactofuranosyltransferase
<i>tolQ</i>	1.00	9.67E-01	membrane spanning protein in TolA-TolQ-TolR complex
<i>rsmH</i>	-1.00	9.63E-01	16S rRNA m(4)C1402 methyltransferase, SAM-dependent
<i>yggC</i>	-1.00	9.76E-01	conserved protein with nucleoside triphosphate hydrolase domain
<i>yecN</i>	-1.00	9.71E-01	inner membrane protein, MAPEG family

<i>fpr</i>	1.00	9.70E-01	ferredoxin-NADP reductase
<i>fliA</i>	1.00	1.00E+00	RNA polymerase, sigma 28 (sigma F) factor
<i>yfgJ</i>	1.00	9.79E-01	conserved protein, DUF1407 family
<i>rrlB</i>	1.00	1.00E+00	23S ribosomal RNA of <i>rrnB</i> operon
<i>panM</i>	-1.00	9.93E-01	PanD autocleavage accelerator, pantothenate synthesis
<i>ulaB</i>	-1.00	1.00E+00	L-ascorbate-specific enzyme IIB component of PTS
<i>yebB</i>	1.00	1.00E+00	conserved protein, DUF830 family
<i>yjcO</i>	1.00	9.82E-01	hypothetical protein
<i>dmsA</i>	-1.00	1.00E+00	dimethyl sulfoxide reductase, anaerobic, subunit A
<i>atpH</i>	1.00	9.85E-01	F1 sector of membrane-bound ATP synthase, delta subunit
<i>dgoT</i>	1.00	1.00E+00	D-galactonate transporter
<i>hslR</i>	1.00	9.86E-01	ribosome-associated heat shock protein Hsp15
<i>rayT</i>	1.00	1.00E+00	RAYT REP element-mobilizing transposase; TnpA(REP)
<i>glgX</i>	1.00	9.77E-01	glycogen debranching enzyme
<i>yheT</i>	-1.00	9.88E-01	putative hydrolase
<i>proY</i>	1.00	9.75E-01	proline-specific permease
<i>cycA</i>	1.00	9.76E-01	D-alanine/D-serine/glycine transporter
<i>yjhQ</i>	-1.00	1.00E+00	KpLE2 phage-like element; predicted acetyltransferase
<i>nudC</i>	1.00	9.76E-01	NADH pyrophosphatase
<i>fliR</i>	-1.00	1.00E+00	flagellar export pore protein
<i>torT</i>	-1.00	1.00E+00	periplasmic sensory protein associated with the TorRS two-component regulatory system
<i>yccT</i>	-1.00	9.93E-01	hypothetical protein
<i>yraJ</i>	1.00	1.00E+00	putative outer membrane protein
<i>fumC</i>	-1.00	9.98E-01	fumarate hydratase (fumarase C), aerobic Class II
<i>ynjA</i>	-1.00	9.91E-01	hypothetical protein
<i>yniC</i>	1.00	1.00E+00	2-deoxyglucose-6-P phosphatase
<i>yraH</i>	-1.00	1.00E+00	putative fimbrial-like adhesin protein
<i>hisF</i>	1.00	9.91E-01	imidazole glycerol phosphate synthase, catalytic subunit with HisH
<i>cyoC</i>	1.00	9.98E-01	cytochrome o ubiquinol oxidase subunit III
<i>lptE</i>	1.00	9.91E-01	LPS assembly OM complex LptDE, lipoprotein component
<i>glcF</i>	1.00	1.00E+00	glycolate oxidase 4Fe-4S iron-sulfur cluster subunit
<i>lldD</i>	1.00	1.00E+00	L-lactate dehydrogenase, FMN-linked
<i>yihU</i>	-1.00	1.00E+00	gamma-hydroxybutyrate dehydrogenase, NADH-dependent
<i>yqjA</i>	-1.00	1.00E+00	required, with <i>yghB</i> , for membrane integrity; inner membrane protein
<i>metY</i>	1.00	1.00E+00	tRNA
<i>manA</i>	1.00	1.00E+00	mannose-6-phosphate isomerase
<i>fadR</i>	1.00	1.00E+00	DNA-binding transcriptional dual regulator of fatty acid metabolism
<i>garP</i>	-1.00	1.00E+00	putative (D)-galactarate transporter
<i>dtpA</i>	-1.00	1.00E+00	dipeptide and tripeptide permease A
<i>mscK</i>	-1.00	1.00E+00	mechanosensitive channel protein, intermediate conductance, K ⁺ regulated
<i>ybgA</i>	1.00	1.00E+00	conserved protein, DUF1722 family
<i>ftsE</i>	-1.00	1.00E+00	putative transporter subunit: ATP-binding component of ABC superfamily
<i>cra</i>	1.00	1.00E+00	DNA-binding transcriptional repressor-activator for carbon metabolism

