

Supplementary Table 1

primer name	sequence (5' - 3')
Int upstream forward	TCACACTTCATTTCAAAAAAC
Int upstream reverse	ATTGTTTTAGTACCGAGCTCCTCAAAGTATGCTCTCATTTA
Int downstream forward	GCCATTTATTATTTCTTCCGCTAATTGCTAAATGTG
Int downstream reverse	GCTTTAAGTAGATTATCACTT
kanR forward	GAGCTCGGTACTAAAACAAT
kanR reverse	GAAGGAAATAATAAATGGC
Int seq forward	TGGATGACTGGCAATTTACA
Int seq reverse	CATCAATGGGACGTTGCAGT
16S RT forward	GGTAGTCCATGCCGTAAC
16S RT reverse	GAAGGCACCAATCCATCTC
hslJ RT forward	AACCCAGCCTTCAGCTA
hslJ RT reverse	GTCGCAACTGCTCCAAA
lolA RT forward	CGGAGCAACAAGCAACT
lolA RT reverse	TGCTGTGCAGACAAACC
rcnB RT forward	CAGCCAGGAGATCGTTTA
rcnB RT reverse	CGGTGGTGGAAAGTTGATAG
yjiM RT forward	GGTTTAGGTGCAGGTGTAG
yjiM RT reverse	CCCACCACAGATCCAATAC
cynT RT forward	ATAAATAAAGGGCTTCGATT
cynT RT reverse	CATCAAACCTTTCGGAAAGT

Supplementary Table 2

plasmid name	sequence inserted into BamHI site of pWH1266 (5' - 3')
pLnt	ACGCACTATTCATCTGATTTCGAGCTGTACATAAATGAGAGCATACTTTGAGCAGCTGTTAGGCAATTCCCGACAGCA AAAACAGCTTCCTTTTATTTTTCTTTTTTAATTCGCTATGTTCTGGCGCAATATTTAGTCTCGCTTTAGCACCTT ATTATTATTGGTGGATTGCGATTTTATCTCCAGCTCTGCTTTATGCCGTATTACATCGTCGCTCAGCCAAACAGGCA TTTATGCTGGGTTGGGCCTATGGGCTGGGATTATGGTTTGTCTGGGGCTTTCTGGCTTTATACTTCCATTCATGTATA TGCGGATACCAATGCCATTCTCAGTGTGTTGATGATTGCGATTATGGCACTGGTGATGGGCTTATTTACTGCCATCC AAACCTGGTTTTACCGCCGCTTTTTCCCGAAACGCCTTTAACTTTTGCGCCCATCTGGATTGTCTTTGAATGGGCA AAAACCTGGGTGTTTACAGGATTTCCGTGGTTATTTGCGGGTTATGCATTCACCGAGCGTTTTTTAGATCACTATGC ACCTTTGTTTGGTGTATTCGGTGTTCCTTTGTGGTTATTACCTTAGCTTGTGCTTTGGTTGAAATCATCAAAGGGC GTATTTTCTGGCTCATTCCATCGGGTCTGCTGCTGCTCGGTGCTTGGGGTGCATCCATTTACAATTTGTGCAACCC AAGAAAGCGCCTCCACTTTCTGTTTCATTAATTCAGGGCAATATTCCACAAGATTTAAATGGCTGACCGAATATCA ATTTAAAACGCTCATGATTTATGCCAATTTGACGCGTTCAGAATGGGGACGAGACCTGATTGTCTGGCCTGAATCTT CAATCCCAATGTTTCAAACCGATATTCAACCTTTTCTAGATGCCATGAACCAACAGGCAAAAAATCGAGGTTCCGGCA TGGGTCACCTGGCATTCCCTTATTGGGATGTTACAGGTTTCGCGGGAAGTGGGGACGCCACTCTATTATAATAGCATCAT GGCTTCTGGCGATAATTCTCAAGGCCTCTATAAAAAACAGCGTTTGGTTCCGTTTGGCGAATATATTCCGTTGTCTG GTCTATTAAGTTGGGTACTACCAGCGTTGCAAATGATCCGTCTATGAGTGGATTTAGTCAGGGATCAAATAATCAG AAACCGCTCATGATCAAAGGTCATCGACTTGCTGCTGCCATCTGTTATGAAGTGGCTTATCCAAACCTGACCAGACG CAACGCAGAAAATAGCGATTTTCTGGTTACGGTATCTAACGATGCTTGGTTTACGGGTACGGCTGGCCCAATGCAAC ATTTACAGATGGTGCAAATGCGGGCCAAAGAAAATGGACGCTGGTTTATCCGTGCCACCAATACTGGAGTGACTGCA TTTATTGATAGCCAAGGTCATATTGTGAAACAAGCACCTATTGATAAAGAAGCTGTTTTACGTGGCGACTTACCTGC AATGCAGGGTGAAACCTTATACACCCGTTTAAAGTGAAGTGGCCGATCTTACTGTTTTCGGTTCTATTGCTGATTCTGG GCTGGATCTATCGTCCACGTCAGGTCGATGTGTCATTTAAATCACGTCGCTAA

Supplementary Table 3**Greater than 5-fold increase**

gene number	fold change	p-value	homolog	localization	COG	function
ACIAD0040	184.72	0.0050		periplasm	unknown function	hypothetical protein
ACIAD0005	67.67	0.0022	<i>lacL</i>	cytoplasm	txn factor	DNA-binding transcriptional repressor
ACIAD0511	42.26	0.0043	<i>hslJ</i>		chaperone	heat shock protein
ACIAD2419	41.09	0.0043		inner membrane	unknown function	hypothetical protein
ACIAD0960	39.58	0.0018		cytoplasm	metabolism	succinate-semialdehyde dehydrogenase [NADP+] (GabD-like)
ACIAD1430	38.17	0.0012	<i>areC</i>	cytoplasm	metabolism	benzaldehyde dehydrogenase II
ACIAD0625	28.71	0.0023	<i>fimH</i>	outer membrane lipoprotein	protein secretion	minor fimbrial subunit, D-mannose specific adhesin
ACIAD0061	27.24	0.0080	<i>yfbL</i>	periplasm	unknown function	predicted peptidase
ACIAD2748	23.96	0.0033		cytoplasm	stress	peroxidase/hydrolase
ACIAD2081	23.09	0.0056		periplasm	transporter	periplasmic protein involved in nickel/cobalt export
ACIAD3290	23.00	0.0013		cytoplasm	metabolism	NADH-flavin reductase
ACIAD2009	21.19	0.0032	<i>murA</i>	cytoplasm	envelope	UDP-N-acetylglucosamine enolpyruvoyl transferase
ACIAD0328	20.69	0.0099	<i>ydgE</i>	cytoplasm	transporter	putative transport protein, major facilitator superfamily
ACIAD3646	20.53	0.0021		cytoplasm	protein modification	protease
ACIAD3384	17.04	0.0043		inner membrane	transporter	sulfate permease
ACIAD0041	16.85	0.0063		periplasm	unknown function	hypothetical protein
ACIAD1429	16.68	0.0039	<i>areB</i>	cytoplasm	metabolism	aryl-alcohol dehydrogenase

ACIAD3411	13.56	0.0026	<i>argP</i>	cytoplasm	txn factor	DNA-binding transcriptional dual regulator
ACIAD0620	13.23	0.0067	<i>rcnB</i>	periplasm	transporter	periplasmic protein involved in nickel/cobalt export
ACIAD3649	12.16	0.0027	<i>yfdL</i>		unknown function	hypothetical protein
ACIAD0062	10.88	0.0067	<i>nadC</i>	cytoplasm	nucleotide	nicotinate-nucleotide pyrophosphorylase
ACIAD2937	10.73	0.0067	<i>lolA</i>	periplasm	membrane protein	outer membrane lipoprotein carrier protein
ACIAD0310	10.11	0.0001	<i>yjiM</i>	periplasm	unknown function	hypothetical protein
ACIAD0150	9.84	0.0001	<i>ygiW</i>	outer membrane lipoprotein	stress	stress-induced protein
ACIAD3109	9.49	0.0039	<i>macA</i>	inner membrane	transporter	macrolide ABC transporter efflux pump subunit
ACIAD2124	8.87	0.0031		cytoplasm	metabolism	siderophore biosynthesis protein
ACIAD3110	8.28	0.0079	<i>macB</i>	inner membrane	transporter	macrolide ABC transporter ATP-binding/membrane protein
ACIAD2122	7.98	0.0080		inner membrane	transporter	MFS superfamily multidrug resistance protein
ACIAD0159	7.76	0.0012		cytoplasm	metabolism	glutathione S-transferase
ACIAD0145	7.59	0.0061	<i>rne</i>	outer membrane lipoprotein	nucleotide	ribonuclease E
ACIAD2476	7.49	0.0050	<i>yhhW</i>	cytoplasm	unknown function	pirin-like protein
ACIAD2668	7.37	0.0000	<i>ompF</i>	outer membrane	membrane protein	outer membrane protein F
ACIAD3111	7.31	0.0042		outer membrane	membrane protein	outer membrane protein precursor
ACIAD3529	7.19	0.0020	<i>nfrB</i>	periplasm	mobile elements	bacteriophage N4 receptor, inner membrane subunit
ACIAD0199	6.99	0.0084		cytoplasm	metabolism	nitrite reductase/ring-hydroxylating dioxygenase
ACIAD1315	6.98	0.0001	<i>rclA</i>	outer membrane lipoprotein	metabolism	predicted oxidoreductase with FAD/NAD(P)-binding domain
ACIAD3381	6.96	0.0018	<i>poxB</i>	cytoplasm	metabolism	pyruvate dehydrogenase (cytochrome)
ACIAD0711	6.93	0.0001	<i>ybeT</i>	outer membrane	membrane protein	conserved outer membrane protein

ACIAD1619	6.88	0.0073	<i>lpxL</i>	outer membrane	envelope	lauroyl acyltransferase
ACIAD1024	6.81	0.0053	<i>xdhA</i>	periplasm	nucleotide	xanthine dehydrogenase subunit
ACIAD3238	6.78	0.0032		cytoplasm	unknown function	hypothetical protein
ACIAD0647	6.76	0.0015		cytoplasm	metabolism	antioxidant protein
ACIAD3279	6.57	0.0043		periplasm	mobile elements	IS2 element protein
ACIAD2121	6.52	0.0072	<i>yidK</i>	cytoplasm	transporter	putative transport protein, sodium:solute symport family
ACIAD0204	6.36	0.0080		cytoplasm	nucleotide	cytidine and deoxycytidylate deaminase zinc-binding protein
ACIAD0810	6.04	0.0017	<i>lepB</i>	outer membrane lipoprotein	protein modification	leader peptidase (signal peptidase I)
ACIAD0027	5.84	0.0013	<i>rutA</i>	cytoplasm	nucleotide	pyrimidine oxygenase
ACIAD2819	5.80	0.0072		cytoplasm	metabolism	gluconolactonase
ACIAD2320	5.40	0.0000	<i>yidB</i>	cytoplasm	unknown function	hypothetical protein
ACIAD1226	5.38	0.0043	<i>yjhF</i>	inner membrane lipoprotein	transporter	putative transport protein, gluconate permease family
ACIAD0198	5.37	0.0011		outer membrane lipoprotein	membrane protein	surface lipoprotein
ACIAD3163	5.28	0.0071	<i>puuA</i>	outer membrane	metabolism	glutamate-putrescine ligase
ACIAD0039	5.26	0.0043	<i>argA</i>	cytoplasm	metabolism	N-acetylglutamate synthase
ACIAD1611	5.21	0.0084		cytoplasm	metabolism	acetyl-CoA synthetase/AMP-(fatty) acid ligase
ACIAD1446	5.20	0.0048	<i>catB</i>	cytoplasm	metabolism	muconate cycloisomerase I
ACIAD2759	5.05	0.0075		cytoplasm	txn factor	GntR family transcriptional regulator
ACIAD3408	5.02	0.0001		cytoplasm	nucleotide	DNA/RNA non-specific endonuclease G protein

Greater than 5-fold decrease

ACIAD0415	-1066.9	0.0024	<i>Int</i>	inner membrane	protein modification	apo-lipoprotein N-acyltransferase
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ACIAD0860	-11.54	0.0049	<i>aaeA</i>	outer membrane lipoprotein	transporter	hydroxylated, aromatic carboxylic acid exporter
ACIAD1272	-10.21	0.007	<i>cynT</i>	inner membrane lipoprotein	metabolism	carbonic anhydrase
ACIAD0189	-7.89	0.0074	<i>ebgA</i>	cytoplasm	metabolism	evolved beta-D-galactosidase, alpha subunit
ACIAD1487	-7.49	0.0041		outer membrane	membrane protein	outer membrane protein
ACIAD0387	-7.1	0.0031		outer membrane lipoprotein	protein secretion	type I secretion
ACIAD0940	-6.59	0.0053		outer membrane	protein secretion	hemagglutinin/hemolysin-related protein
ACIAD1488	-6.27	0.0018		inner membrane	transporter	protein secretion efflux ABC transporter ATP-binding protein
ACIAD1614	-6.12	0.0007		cytoplasm	metabolism	nitrile hydratase activator
ACIAD1776	-6.09	0.0011		cytoplasm	stress	general stress protein
ACIAD1489	-6.02	0.0019		inner membrane	transporter	protein secretion efflux system ABC transporter
ACIAD0336	-5.77	0.0099	<i>rluA</i>	outer membrane lipoprotein	translation	23S rRNA and tRNA pseudouridine synthase
ACIAD3677	-5.71	0.005	<i>yggE</i>	cytoplasm	unknown function	conserved protein
ACIAD0242	-5.63	0.008	<i>chlL</i>	cytoplasm	metabolism	magnesium chelatase
ACIAD1744	-5.58	0.0005	<i>aspA</i>	cytoplasm	metabolism	aspartate ammonia-lyase
ACIAD3338	-5.55	0.0011	<i>comP</i>	inner membrane	nucleotide	competence factor involved in DNA binding and uptake
ACIAD0939	-5.54	0.0017		outer membrane	protein secretion	hemolysin activator protein
ACIAD2843	-5.49	0.0043		periplasm	unknown function	hypothetical protein
ACIAD2482	-5.34	0.0014	<i>dusA</i>	cytoplasm	translation	tRNA-dihydrouridine synthase A
ACIAD2866	-5.31	0.0061		cytoplasm	protein secretion	hemagglutinin/hemolysin-related protein
ACIAD1651	-5.16	0.008	<i>pcaT</i>	inner membrane	transporter	major facilitator superfamily alpha-ketoglutarate permease
ACIAD0240	-5.1	0.0057	<i>chiP</i>	outer membrane	metabolism	chitobiose outer membrane channel