

Supplemental Table 1. List of genes that had more than 1.5-fold change in expression in *Escherichia coli* K12 associated with lettuce leaves.

Gene Number	Fold Change	Symbol	Function
<i>Amino acid biosynthesis</i>			
B4254	3.0	<i>argI</i>	ornithine carbamoyltransferase 1
B1748	2.7	<i>argD</i>	succinylornithine aminotransferase
B0674	2.6	<i>asnB</i>	asparagine synthetase B
B3213	2.3	<i>gltD</i>	glutamate synthase, small subunit
B3281	2.2	<i>aroE</i>	dehydroshikimate reductase
B3870	2.2	<i>glnA</i>	glutamine synthetase
<i>Biofilm</i>			
B0806	38.1	<i>ybiM</i> (<i>McbA</i>)	protein involved in colanic acid production
B1112	33.2	<i>ycfR</i> (<i>bhsA</i>)	protein involved in stress resistance and biofilm formation
B1060	3.6	<i>yceP</i>	biofilm formation regulatory protein
B1165	2.8	<i>ymgA</i>	protein involved in biofilm formation
<i>Biosynthesis of cofactors, prosthetic groups, and carriers</i>			
B3073	4.0	<i>ygiG</i>	putrescine--2-oxoglutarate aminotransferase
B2530	2.8	<i>IscS</i>	cysteine desulfurase
B3973	2.6	<i>birA</i>	biotin operon repressor
<i>Cell envelope</i>			
B1042	20.0	<i>csgA</i>	curlin major subunit, coiled surface structures, cryptic
B1041	14.3	<i>csgB</i>	minor curlin subunit precursor, nucleator for assembly of adhesive surface organelles
B1743	8.7	<i>spy</i>	periplasmic protein related to spheroblast formation
B1110	5.9	<i>ycfJ</i>	putative zinc peptidase
B1283	5.6	<i>osmB</i>	lipoprotein, osmotically inducible
B4045	5.3	<i>yibJ</i>	putative stress-response protein
B1806	3.2	<i>yeaY</i>	putative outer membrane lipoprotein
B0786	2.0	<i>ybhL</i>	putative transport protein
<i>Cellular processes</i>			
B1305	23.3	<i>pspB</i>	phage shock protein, putative inner membrane protein
B1304	21.5	<i>pspA</i>	phage shock protein, putative inner membrane protein
B1306	14.8	<i>pspC</i>	phage shock protein: activates phage shock- protein expression
B1307	13.3	<i>pspD</i>	phage shock protein mRNA interferase, toxin of the MqsR-YgiT
B3022	6.4	<i>ygiU</i>	toxin-antitoxin system
B1308	5.1	<i>pspE</i>	phage shock protein E
B1530	4.5	<i>marR</i>	repressor of mar operon toxin of the RelE-RelB toxin-antitoxin system and cofactor to enhance the repressor activity of RelB
B1563	4.1	<i>relE</i>	antitoxin of the RelE-RelB toxin-antitoxin system and DNA binding transcriptional repressor
B1564	3.9	<i>relB</i>	MqsA antitoxin of the MqsRA toxin-antitoxin system and DNA transcriptional repressor
B3021	3.7	<i>ygiT</i>	bacterioferritin-associated ferredoxin
B3337	3.4	<i>yheA</i>	bacterioferritin-associated ferredoxin
B1874	3.3	<i>cutC</i>	copper homeostasis protein

B4376	3.0	<i>osmY</i>	hyperosmotically inducible periplasmic protein
B4224	2.8	<i>chpS</i>	antitoxin ChpS; suppressor of inhibitory function of ChpB
B1897	2.6	<i>otsB</i>	trehalose-6-phosphate phosphatase
B0966	2.4	<i>HSpQ</i>	heat shock protein
B1531	2.4	<i>MarA</i>	transcriptional activator of defense systems
B0226	2.3	<i>dinJ</i>	damage-inducible protein J
B3183	2.3	<i>yhbZ</i>	GTPase involved in chromosome partitioning and ribosome assembly
B1020	2.1	<i>phoH</i>	phosphate starvation-inducible antitoxin of the YoeB-YefM toxin-antitoxin pair
B2017	2.0	<i>yefM</i>	
B3286	2.0	<i>smf_1</i>	rf, fragment 1
B1896	2.0	<i>otsA</i>	trehalose-6-phosphate synthase
<i>Central intermediary metabolism</i>			
B2752	3.8	<i>cysD</i>	sulfate adenylyltransferase subunit 2
B0384	3.5	<i>psiF</i>	induced by phosphate starvation
B2751	2.5	<i>cysN</i>	ATP-sulfurylase (ATP:sulfate adenylyltransferase), subunit 1
B2762	2.4	<i>cysH</i>	3'-phosphoadenosine 5'-phosphosulfate (PAPS) reductase
B2529	2.3	<i>iscU</i>	scaffold protein
B1684	2.3	<i>sufA</i>	iron-sulfur cluster assembly scaffold protein
B2764	2.2	<i>cysJ</i>	sulfite reductase (NADPH), flavoprotein beta subunit
B4106	2.1	<i>phnC</i>	ATP-binding component of phosphonate transport
B4214	2.0	<i>cysQ</i>	adenosine-3'(2'),5'-bisphosphate nucleotidase
<i>DNA metabolism</i>			
B1712	2.6	<i>himA</i>	integration host factor (IHF), alpha subunit
B3066	2.0	<i>dnaG</i>	DNA biosynthesis DNA primase
<i>Energy metabolism</i>			
B2582	13.1	<i>trxC</i>	putative thioredoxin-like protein
B0849	4.9	<i>grxA</i>	glutaredoxin1 redox coenzyme for glutathione-dependent ribonucleotide reductase
B0368	4.1	<i>tauD</i>	taurine dioxygenase, 2-oxoglutarate-dependent
B1416	3.8	<i>gapC_2</i>	glyceraldehyde 3-phosphate dehydrogenase C
B0608	3.6	<i>ybdR</i>	putative oxidoreductase
B4197	3.5	<i>ECs5173</i>	L-xylulose 5-phosphate 3-epimerase
B1747	3.3	<i>astA</i>	arginine N-succinyltransferase
B1417	3.3	<i>gapC</i>	glyceraldehyde-3-phosphate dehydrogenase
B1417	3.0	<i>gapC_1</i>	glyceraldehyde 3-phosphate dehydrogenase C
B2673	2.8	<i>nrdH</i>	glutaredoxin-like protein
B0898	2.8	<i>ycaD</i>	putative transport protein (MFS family)
B1678	2.7	<i>ynhG</i>	L,D-transpeptidase
B1478	2.4	<i>adhP</i>	alcohol dehydrogenase
B3494	2.4	<i>yhiO</i>	predicted universal stress (ethanol tolerance) protein B
B0333	2.3	<i>prpC</i>	putative citrate synthase
B1046	2.3	<i>ymdC</i>	putative synthase

B2696	2.2	<i>csrA</i>	carbon storage regulator, post-translational activator of flhDC expression, regulates biofilm formation, RNA-binding
B1476	2.1	<i>fdnI</i>	formate dehydrogenase-N, cytochrome B556(Fdn) gamma subunit, nitrate-inducible
B0146	2.1	<i>sfsA</i>	sugar fermentation stimulation protein A
<i>Fatty acid and phospholipid metabolism</i>			
B0221	2.7	<i>fadE</i>	putative acyl-CoA dehydrogenase
<i>Hypothetical proteins</i>			
B4199	48.2	<i>yjfY</i>	Predicted periplasmic protein, YhcN family, function unknown
B1259	21.7	<i>yciG</i>	hypothetical protein
B4050	15.2	<i>yjbO</i>	Effector of phage shock response; over expression reduces motility
B1005	14.6	<i>ycdF</i>	unknown CDS
B0389	9.5	<i>yaiA</i>	hypothetical
B1536	8.8	<i>ydeI</i>	Predicted secreted protein
B3238	8.2	<i>yhcN</i>	hypothetical protein
B1257	8.2	<i>yciE</i>	hypothetical
B2086	7.6	<i>yegS</i>	lipid kinase
B3448	7.5	<i>yhhA</i>	conserved protein
B0005	7.2	<i>yaaX</i>	hypothetical protein
B0753	6.9	<i>ybgS</i>	putative homeobox protein
B0802	6.6	<i>ybiJ</i>	Predicted periplasmic protein
B1195	6.0	<i>ymgE</i>	predicted inner membrane protein
B2135	5.8	<i>yohC</i>	hypothetical
B1953	4.2	<i>yodD</i>	hypothetical
B2672	4.0	<i>ygaM</i>	hypothetical protein
B0119	3.6	<i>ECs0123</i>	hypothetical
B3003	3.6	<i>yghA</i>	putative oxidoreductase
B2630	3.5	<i>yfiN</i>	CP4-57 prophage
B1758	3.5	<i>ECs2464</i>	putative cytochrome oxidase
B1431	3.4	<i>ydcL</i>	Novel verified lipoprotein
B3153	3.3	<i>yhbO</i>	Confers resistance to various stresses, chaperone homolog
B4107	3.3	<i>phnB</i>	hypothetical; PhnB protein
B2531	3.0	<i>IscR</i>	DNA-binding transcriptional regulator IscR
B1188	2.9	<i>ycgB</i>	putative sporulation protein
B3000	2.9	<i>yghY</i>	hypothetical protein; carboxymethylenebutenolidase
B2659	2.7	<i>csiD</i>	Carbon starvation induced gene, function unknown
B2353	2.7	<i>tfaS</i>	CPS-53 (KpLE1) prophage
B4217	2.6	<i>ytfK</i>	Hypothetical
B3866	2.6	<i>yihI</i>	conserved protein
B1836	2.6	<i>yebV</i>	hypothetical
B1100	2.6	<i>ycfH</i>	putative metallodependant hydrolase
B0057	2.5	<i>yabQ</i>	Hypothetical
B0516	2.5	<i>ylbB</i>	putative hydantoin utilization protein
B1490	2.5	<i>dosC</i>	hypothetical
B1837	2.5	<i>idi</i>	Isopentenyl diphosphate isomerase, isoprenoid biosynthesis; interconverts

			isopentenyl diphosphate (IPP) and dimethylallyl diphosphate (DMAPP)
B1164	2.4	<i>ycgZ</i>	Hypothetical
B3246	2.4	<i>yhdP</i>	hypothetical
B1958	2.4	<i>yedI</i>	putative transmembrane protein
B1298	2.3	<i>puuD</i>	putative amidotransferase subunit
B3598	2.3	<i>yibI</i>	predicted inner membrane protein
B0225	2.3	<i>yafQ</i>	Toxin of TA pair YafQ/DinJ, inhibitor of translation
B1649	2.3	<i>nemR</i>	hypothetical
B3184	2.3	<i>yhbE</i>	hypothetical
B3000	2.3	<i>yghY</i>	putative enzyme with alpha/beta-hydrolase domain
B1957	2.2	<i>yodC</i>	Hypothetical
B0446	2.2	<i>cof</i>	hypothetical
B2666	2.1	<i>ygaE</i>	hypothetical protein
B2809	2.1	<i>ygdI</i>	hypothetical
B1955	2.1	<i>yedP</i>	mannosyl-3-phosphoglycerate phosphatase
B3535	2.0	<i>yhjR</i>	hypothetical
B1952	2.0	<i>dsrB</i>	hypothetical protein; transcription is regulated by RpoS and DsrA RNA
B1436	2.0	<i>yncJ</i>	unknown CDS
<i>Mobile and extrachromosomal element functions</i>			
B1783	6.6	<i>yeaG</i>	Protein kinase
B1562	3.6	<i>hokD</i>	Qin prophage
B4209	3.6	<i>ytfE</i>	iron-sulfur cluster repair di-iron protein
B0456	3.4	<i>ybaA</i>	hypothetical
B2528	2.2	<i>iscA</i>	iron-sulfur cluster assembly protein
B0891	2.1	<i>lolA</i>	periplasmic chaperone, effects translocation of lipoproteins from inner membrane to outer
B0438	2.0	<i>clpX</i>	ATP-dependent specificity component of clpP serine protease, chaperone
B3932	2.0	<i>hslV</i>	heat shock protein hslVU, proteasome-related peptidase subunit
Protein fate			
Protein synthesis			
B1258	7.8	<i>yciF</i>	putative structural proteins
B4373	2.0	<i>rimI</i>	acyltransferase for 30S ribosomal subunit protein S18
<i>Purines, pyrimidines, nucleosides, and nucleotides</i>			
B0032	2.7	<i>carA</i>	carbamoyl-phosphate synthetase small subunit
B4246	2.1	<i>pyrL</i>	pyrBI operon leader peptide
B2028	2.1	<i>ugd</i>	UDP-glucose 6-dehydrogenase
B4245	2.0	<i>pyrB</i>	aspartate carbamoyltransferase, catalytic subunit
<i>Regulatory functions</i>			
B0803	3.4	<i>ybiI</i>	DksA-type zinc finger protein
B0435	3.2	<i>bolA</i>	putative regulator of murein genes
B0232	2.8	<i>yafN</i>	predicted toxin of the YafO-YafN toxin-antitoxin system
B0450	2.8	<i>glnK</i>	nitrogen regulatory protein P-II 2

B2573	2.6	<i>rpoE</i>	RNA polymerase, sigma-E factor
B0399	2.6	<i>PhoB</i>	Phosphorylated transcriptional dual regulator
B1040	2.6	<i>CsgD</i>	DNA-binding transcriptional regulator CsgD
B3555	2.5	<i>yiaG</i>	putative transcriptional regulator
B0453	2.5	<i>ybaY</i>	glycoprotein/polysaccharide metabolism
B1988	2.0	<i>nac</i>	nitrogen assimilation control protein
B0460	2.0	<i>hha</i>	haemolysin expression modulating protein
B2572	2.0	<i>rseA</i>	anti sigma E (sigma 24) factor, negative regulator
Transcription			
B3780	2.4	<i>rhlB</i>	putative ATP-dependent RNA helicase
B2567	2.3	<i>rnc</i>	RNase III
<i>Transport and binding proteins</i>			
B4002	8.8	<i>zraP/yjaI</i>	Zn-binding periplasmic protein
B0365	5.5	<i>tauA</i>	taurine transport protein (ABC superfamily, peri_bind)
B3728	5.0	<i>pstS</i>	high-affinity phosphate-specific transport system
B0366	4.7	<i>tauB</i>	taurine ATP-binding component of a transport system
B2425	3.5	<i>cysP</i>	thiosulfate binding protein
B0914	2.9	<i>msbA</i>	ATP-binding transport protein
B0461	2.6	<i>cusB</i>	membrane fusion protein of the CusCFBA copper efflux system
B0367	2.1	<i>tauC</i>	taurine transport system permease protein
B3006	2.0	<i>exbB</i>	uptake of enterobactin
B1710	2.0	<i>btuE</i>	putative glutathione peroxidase

Gene Number	Fold Change	Symbol	Function
<i>Amino acid biosynthesis</i>			
B2871	-3.8	<i>ygeX</i>	putative dehydratase
B0003	-2.3	<i>thrB</i>	homoserine kinase
B2878	-2.3	<i>ygfK</i>	putative oxidoreductase, Fe-S subunit
B2329	-2.2	<i>aroC</i>	chorismate synthase
<i>Biofilm</i>			
B0836	-6.1	<i>bssR</i>	biofilm formation regulatory protein BssR
<i>Biosynthesis of cofactors, prosthetic groups, and carriers</i>			
B1593	-2.8	<i>ynfK</i>	putative dithiobiotin synthetase
B3209	-2.1	<i>yhbL</i>	isoprenoid biosynthesis protein with amidotransferase-like domain
B3805	-2.0	<i>hemC</i>	hydroxymethylbilane synthase (porphobilinogen deaminase)
<i>Cell envelope</i>			
B1256	-24.5	<i>ompW</i>	OmpW, outer membrane protein
B4314	-13.2	<i>fimA</i>	major type 1 subunit fimbrin (pilin)
B3506	-11.9	<i>slp</i>	Slp outer membrane lipoprotein
B0957	-4.0	<i>ompA</i>	outer membrane protein 3a
B0087	-2.8	<i>mraY</i>	phospho-N-acetylmuramoyl-pentapeptide transferase
B4315	-2.3	<i>fimI</i>	fimbrial protein
B0091	-2.1	<i>murC</i>	UDP-N-acetyl-muramate:alanine ligase
B0092	-2.0	<i>ddlB</i>	D-alanine-D-alanine ligase B
B2742	-2.0	<i>nlpD</i>	lipoprotein
<i>Cellular processes</i>			
B1492	-14.0	<i>gadC</i>	acid sensitivity protein, putative transporter
B1656	-13.5	<i>sodB</i>	superoxide dismutase, iron
B0880	-6.9	<i>cspD</i>	cold shock protein
B3509	-6.5	<i>hdeB</i>	acid stress chaperone
B3510	-6.2	<i>hdeA</i>	Periplasmic chaperone of acid-denatured proteins; H-NS repressed
B2579	-6.0	<i>yfiD</i>	stress-induced alternate pyruvate formate-lyase subunit
B0607	-5.4	<i>uspG</i>	universal stress protein G
B1905	-5.0	<i>ftn</i>	cytoplasmic ferritin (an iron storage protein)
B3495	-4.6	<i>uspA</i>	universal stress protein
B0598	-4.5	<i>cstA</i>	carbon starvation protein
B3942	-4.5	<i>katG</i>	catalase
B3339	-4.2	<i>tufA</i>	protein chain elongation factor EF-Tu
B0990	-3.4	<i>cspG</i>	homolog of Salmonella cold shock protein
B3556	-3.4	<i>cspA</i>	cold shock protein 7.4, transcriptional activator of hns
B0095	-3.3	<i>ftsZ</i>	cell division
B3511	-2.9	<i>hdeD</i>	acid-resistance membrane protein
B1552	-2.9	<i>cspI</i>	Qin prophage, cold shock protein
B3928	-2.7	<i>yiiU</i>	cell division factor ZapB
B0094	-2.5	<i>ftsA</i>	Cell division protein FtsA
B1557	-2.4	<i>cspB</i>	Qin prophage; cold shock protein; predicted DNA-binding transcriptional regulator
B0093	-2.4	<i>ftsQ</i>	Cell division protein FtsQ
B1324	-2.4	<i>tpx</i>	thiol peroxidase
B3336	-2.2	<i>bfr</i>	bacterioferrin, an iron storage homoprotein

B1333	-2.1	<i>ydaA</i>	Stress-induced protein; UV-resistance; tandem Usp domains
B1175	-2.0	<i>minD</i>	cell division inhibitor, a membrane ATPase, activates minC
<i>Central intermediary metabolism</i>			
B3945	-7.1	<i>gldA</i>	glycerol dehydrogenase, (NAD)
B2095	-6.4	<i>gatZ</i>	putative tagatose 6-phosphate kinase 1
B2727	-2.9	<i>hypB</i>	guanine-nucleotide binding protein, functions as nickel donor for large subunit of hydrogenase 3
<i>DNA metabolism</i>			
B0440	-3.1	<i>hupB</i>	DNA-binding protein HU-beta, NS1 (HU-1)
Z2013	-2.3	<i>hns</i>	DNA-binding protein HLP-II (HU, BH2, HD, NS)
B4000	-2.1	<i>hupA</i>	DNA-binding protein HU-alpha (HU-2)
<i>Energy metabolism</i>			
B3708	-33.0	<i>tnaA</i>	tryptophanase
B3517	-17.4	<i>gadA</i>	glutamate decarboxylase isozyme
B0733	-15.7	<i>cydA</i>	cytochrome d terminal oxidase polypeptide subunit I
B2957	-15.4	<i>ansB</i>	periplasmic L-asparaginase II
B1064	-11.7	<i>grxB</i>	glutaredoxin 2
B2091	-10.7	<i>gatD</i>	galactitol-1-phosphate dehydrogenase
B0972	-10.4	<i>hyaA</i>	hydrogenase-1 small subunit
B0734	-9.0	<i>cydB</i>	cytochrome d terminal oxidase polypeptide subunit II
B1224	-8.8	<i>narG</i>	nitrate reductase 1, alpha subunit
B1226	-8.1	<i>narJ</i>	nitrate reductase 1, delta subunit, assembly function
B0485	-7.9	<i>ybaS</i>	putative glutaminase
B2904	-6.8	<i>gcvH</i>	glycine cleavage system H protein
B4154	-5.8	<i>frdA</i>	fumarate reductase, anaerobic, catalytic and NAD/flavoprotein subunit
B1225	-5.4	<i>narH</i>	nitrate reductase 1, Fe-S (beta) subunit
B4153	-5.0	<i>frdB</i>	FrdB
B2096	-4.8	<i>gatY</i>	tagatose 6-phosphate aldolase 2, subunit with GatZ
B0976	-4.6	<i>hyaE</i>	processing of HyaA and HyaB proteins
B0973	-4.5	<i>hyaB</i>	hydrogenase-1 large subunit
B2905	-4.5	<i>gcvT</i>	aminomethyltransferase
B0723	-4.5	<i>sdhA</i>	succinate dehydrogenase, flavoprotein subunit
B2096	-4.4	<i>gatY</i>	tagatose 6-phosphate aldolase 2, subunit with GatZ
B1002	-4.1	<i>agp</i>	periplasmic glucose-1-phosphatase
B0895	-3.8	<i>dmsB</i>	anaerobic dimethyl sulfoxide (DMSO) reductase, subunit B
B3403	-3.7	<i>pckA</i>	phosphoenolpyruvate carboxykinase
B0974	-3.6	<i>hyaC</i>	probable Ni/Fe-hydrogenase 1 b-type cytochrome subunit
B3049	-3.5	<i>glgS</i>	glycogen biosynthesis, rpoS dependent
B1603	-3.5	<i>pntA</i>	pyridine nucleotide transhydrogenase alpha subunit
B4014	-3.4	<i>aceB</i>	malate synthase A
B1136	-3.4	<i>icd</i>	isocitrate dehydrogenase
B4139	-3.3	<i>aspA</i>	aspartate ammonia-lyase
B2800	-3.3	<i>fucA</i>	L-fuculose-1-phosphate aldolase
B4152	-3.2	<i>frdC</i>	fumarate reductase, anaerobic, membrane anchor polypeptide
B0116	-3.2	<i>lpdA</i>	dihydrolipoamide dehydrogenase, FAD/NAD(P)-binding,

			component of the 2-oxoglutarate dehydrogenase and the pyruvate dehydrogenase complexes
B3893	-3.1	<i>fdoH</i>	formate dehydrogenase-O iron-sulfur subunit
B2097	-3.1	<i>fbaB</i>	fructose-bisphosphate aldolase class I
B0722	-3.0	<i>sdhD</i>	succinate dehydrogenase hydrophobic subunit
B4015	-3.0	<i>aceA</i>	isocitrate lyase
B2997	-2.9	<i>hybO</i>	hydrogenase 2 small subunit
B0756	-2.9	<i>galM</i>	galactose-1-epimerase (mutarotase)
B3733	-2.8	<i>atpG</i>	F-type H ⁺ -transporting ATPase subunit gamma
B3236	-2.8	<i>mdh</i>	malate dehydrogenase
B4071	-2.7	<i>nrfB</i>	formate-dependent nitrite reductase NrfB
B3236	-2.7	<i>mdh</i>	malate dehydrogenase
B1276	-2.7	<i>acnA</i>	aconitate hydratase 1
B1589	-2.6	<i>ynfG</i>	putative dimethyl sulfoxide reductase, Fe-S subunit
B3894	-2.6	<i>fdoG</i>	formate dehydrogenase-O major subunit
B1588	-2.6	<i>ynfF</i>	putative dimethyl sulfoxide reductase, major subunit
B1587	-2.6	<i>ynfE</i>	putative oxidoreductase major subunit
			part of glycogen operon, a glycosyl hydrolase, debranching enzyme
B3431	-2.6	<i>glgX</i>	
B2277	-2.6	<i>nuoM</i>	NADH dehydrogenase I chain M
B0727	-2.6	<i>sucB</i>	dihydrolipoamide succinyltransferase
B0729	-2.6	<i>sucD</i>	succinyl-CoA synthetase alpha subunit
B3617	-2.5	<i>kbl</i>	2-amino-3-ketobutyrate CoA ligase
B0894	-2.5	<i>dmsA</i>	anaerobic dimethyl sulfoxide reductase subunit A
B3430	-2.5	<i>glgC</i>	glucose-1-phosphate adenylyltransferase
B2133	-2.5	<i>dld</i>	D-lactate dehydrogenase
B2799	-2.5	<i>fucO</i>	L-1,2-propanediol oxidoreductase
B0724	-2.5	<i>sdhB</i>	succinate dehydrogenase, iron sulfur protein
B2870	-2.4	<i>ygeW</i>	putative carbamoyl transferase
			fumarate reductase, anaerobic, membrane anchor
B4151	-2.4	<i>frdD</i>	polypeptide
B3429	-2.4	<i>glgA</i>	glycogen synthase
B1854	-2.4	<i>pykA</i>	pyruvate kinase II, glucose stimulated
B0721	-2.3	<i>sdhC</i>	succinate dehydrogenase
B2286	-2.2	<i>nuoC</i>	NADH dehydrogenase I chain C, D
B0897	-2.2	<i>ycaC</i>	putative cysteine hydrolase
B2996	-2.2	<i>hybA</i>	hydrogenase-2 small subunit
B2995	-2.2	<i>hybB</i>	probable cytochrome Ni/Fe component of hydrogenase-2
B3049	-2.2	<i>glgS</i>	glycogen biosynthesis, rpoS dependent
B0728	-2.2	<i>sucC</i>	succinyl-CoA synthetase beta subunit
B2284	-2.1	<i>nuoF</i>	NADH dehydrogenase I chain F
B0977	-2.1	<i>hyaF</i>	nickel incorporation into hydrogenase-1 proteins
B1590	-2.1	<i>ynfH</i>	putative DMSO reductase anchor subunit
B3892	-2.1	<i>fdol</i>	formate dehydrogenase cytochrome B556 (FDO) subunit
B2288	-2.0	<i>nuoA</i>	NADH dehydrogenase I chain A
B2279	-2.0	<i>nuoK</i>	NADH dehydrogenase I chain K
B1227	-2.0	<i>narI</i>	nitrate reductase 1, cytochrome b(NR), gamma subunit
B4079	-2.0	<i>fdhF</i>	formate dehydrogenase
B2282	-2.0	<i>nuoH</i>	NADH dehydrogenase I chain H
B2935	-2.0	<i>tktA</i>	transketolase 1 isozyme
B0726	-2.0	<i>sucA</i>	2-oxoglutarate dehydrogenase decarboxylase component

<i>Fatty acid and phospholipid metabolism</i>			
B2426	-4.2	<i>ucpA</i>	short chain dehydrogenase
B1199	-2.6	<i>dhaL</i>	putative dihydroxyacetone kinase (EC 2.7.1.2)
B2323	-2.5	<i>fabB</i>	3-oxoacyl-[acyl-carrier-protein] synthase I
B1093	-2.2	<i>fabG</i>	3-ketoacyl-(acyl-carrier-protein) reductase
B1288	-2.0	<i>fabI</i>	enoyl-[acyl-carrier-protein] reductase (NADH)
<i>Hypothetical proteins</i>			
B1376	-9.4	<i>ynaF</i>	nucleotide binding filament protein
B3207	-4.5	<i>yrbL</i>	hypothetical
B2146	-4.5	<i>yeiT</i>	putative oxidoreductase
B1667	-4.1	<i>ydhR</i>	Lipid A biosynthesis, KDO2-lipid IVA palmitoleoyl-ACP acyltransferase; cold temperature inducible
B1777	-3.4	<i>yeaC</i>	hypothetical
B1420	-3.4	<i>mokB</i>	hypothetical
B4380	-3.4	<i>yjiI</i>	hypothetical
B4330	-3.1	<i>yjiH</i>	hypothetical
B3024	-2.6	<i>ygiW</i>	Secreted protein, function unknown
B3929	-2.6	<i>menG</i>	menaquinone biosynthesis, unknown
B0442	-2.5	<i>ybaV</i>	Competence protein ComEA homolog, function unknown
B3011	-2.5	<i>yqhD</i>	putative oxidoreductase
B1000	-2.5	<i>cbpA</i>	curved DNA-binding protein
B0097	-2.4	<i>yacA</i>	Secretion monitor controlling secA expression
B2909	-2.4	<i>ygfB</i>	hypothetical
B1765	-2.3	<i>ydiA</i>	hypothetical
ECS2704	-2.3	<i>ECs2704</i>	hypothetical
B2880	-2.3	<i>ygfM</i>	Methionine sulfoxide reductase A; specific for S diastereoisomers
B4187	-2.3	<i>aidB</i>	putative acyl coenzyme A dehydrogenase
B1541	-2.3	<i>ydfZ</i>	hypothetical
B2584	-2.3	<i>yfiQ</i>	fused predicted acyl-CoA synthetase: NAD(P)-binding subunit, ATP-binding subunit
B2343	-2.2	<i>yfcZ</i>	hypothetical
B2532	-2.2	<i>trmJ</i>	putative ATP synthase beta subunit
B4329	-2.2	<i>yjiG</i>	hypothetical
B1426	-2.2	<i>ydcH</i>	hypothetical
B1108	-2.2	<i>ycfP</i>	putative hydrolase
B3803	-2.1	<i>hemX</i>	uroporphyrinogen III methylase
B2795	-2.1	<i>ygdH</i>	hypothetical
B4179	-2.1	<i>rnr</i>	hypothetical
B2876	-2.1	<i>yqeC</i>	hypothetical
B2897	-2.0	<i>ygfY</i>	hypothetical
B0488	-2.0	<i>ybbJ</i>	Stimulates ftsH htpX mutant suppressor activity of QmcA
B1067	-2.0	<i>yceH</i>	hypothetical
<i>Mobile and extrachromosomal element functions</i>			
B2449	-2.2	<i>yffR</i>	CPZ-55 prophage
B2192	-2.1	<i>trs5_8</i>	IS5 transposase and trans-activator
<i>Protein fate</i>			
B1967	-7.2	<i>hchA</i>	chaperone protein HchA
B4143	-7.2	<i>mopA</i>	GroEL, chaperone Hsp60, peptide-dependent ATPase, heat shock protein
B0975	-5.1	<i>hyaD</i>	processing of HyaA and HyaB proteins

B0014	-3.4	<i>dnaK</i>	molecular chaperone DnaK
B1778	-3.3	<i>msrB</i>	methionine sulfoxide reductase B
B2908	-3.2	<i>pepP</i>	proline aminopeptidase P II
B2726	-3.0	<i>hypA</i>	guanine-nucleotide-binding protein in formate-hydrogenlyase system, functions as nickel donor for HycE of hydrogenlyase 3
B3103	-2.7	<i>yhaH</i>	putative cytochrome
B3300	-2.7	<i>prlA</i>	preprotein translocase, membrane component, transport across inner membrane (General Secretory Pathway)
B2872	-2.6	<i>ygeY</i>	putative deacetylase
B0932	-2.2	<i>pepN</i>	aminopeptidase N
B4142	-2.2	<i>mopB</i>	GroES, 10 Kd chaperone binds to Hsp60 in pres. Mg-ATP, suppressing its ATPase activity
B2728	-2.1	<i>hypC</i>	pleiotrophic effects on 3 hydrogenase isozymes
<i>Protein synthesis</i>			
B0953	-4.8	<i>rmf</i>	ribosome modulation factor
B3305	-4.0	<i>rplF</i>	50S ribosomal subunit protein L6
B4129	-3.8	<i>lysU</i>	lysine tRNA synthetase, inducible
B3304	-3.1	<i>rplR</i>	50S ribosomal subunit protein L18
B3299	-3.0	<i>rpmJ</i>	50S ribosomal subunit protein L36
B0865	-3.0	<i>ybjP</i>	putative lipoprotein
B3306	-2.8	<i>rpsH</i>	30S ribosomal subunit protein S8
B2607	-2.8	<i>trmD</i>	tRNA (guanine-7-)-methyltransferase
B3301	-2.5	<i>rplO</i>	50S ribosomal subunit protein L15
B3303	-2.5	<i>rpsE</i>	30S ribosomal subunit protein S5
B3340	-2.5	<i>fusA</i>	GTP-binding protein chain elongation factor EF-G
B2606	-2.4	<i>rplS</i>	50S ribosomal subunit protein L19
B1480	-2.4	<i>rpsV</i>	30S ribosomal subunit protein S22
B3302	-2.3	<i>rpmD</i>	50S ribosomal subunit protein L30
B3308	-2.3	<i>rplE</i>	50S ribosomal subunit protein L5
B3307	-2.2	<i>RpsN</i>	30S ribosomal subunit protein S14
B2292	-2.0	<i>yfbS</i>	putative transport protein
B3309	-2.0	<i>rplX</i>	50S ribosomal subunit protein L24
<i>Purines, pyrimidines, nucleosides, and nucleotides</i>			
B2147	-4.3	<i>yeiA</i>	putative dihydropyrimidine dehydrogenase, FMN-linked
B4177	-3.1	<i>purA</i>	adenylosuccinate synthetase
<i>Regulatory functions</i>			
B2597	-5.7	<i>raiA</i>	ribosome-associated inhibitor A
B4062	-4.9	<i>soxS</i>	regulation of superoxide response regulon
B3357	-3.1	<i>crp</i>	cyclic AMP receptor protein
B0999	-2.9	<i>yccD</i>	Modulator of CbpA co-chaperone activity
B0812	-2.9	<i>dps</i>	global regulator, starvation conditions
B2090	-2.4	<i>gatR_2</i>	split galactitol utilization operon repressor, fragment 2
B0487	-2.3	<i>cueR</i>	putative transcriptional regulator
B3461	-2.2	<i>rpoH</i>	RNA polymerase, sigma(32) factor
B2898	-2.2	<i>ygfZ</i>	Hda suppressor; also involved in methylthio modification at 2-methylthio-6-iodoadenosine in tRNA; mutants grow slowly, especially at low temperature; slow growth is suppressed by MnmE; binds folate
B3912	-2.0	<i>cpxR</i>	response regulator in two-component regulatory system with CpxA, regulates expression of stress-related genes (OmpR family)

Transport and binding proteins

B2094	-13.7	<i>gatA</i>	PTS family enzyme IIA, galactitol-specific
B2092	-13.1	<i>gatC</i>	PTS system galactitol-specific enzyme IIC
B2093	-10.3	<i>gatB</i>	PTS family enzyme IIB, galactitol-specific
B3751	-9.6	<i>rbsB</i>	D-ribose periplasmic binding protein
B2215	-7.1	<i>ompC</i>	OmpC outer membrane porin C
B0904	-3.7	<i>focA</i>	probable formate transporter (formate channel 1)
B0486	-3.3	<i>ybaT</i>	putative amino acid/amine transport protein
B0553	-2.5	<i>nmpC</i>	DLP12 prophage
B1818	-2.5	<i>manY</i>	PTS enzyme IIC, mannose-specific
B3161	-2.4	<i>mtr</i>	tryptophan-specific transport protein
B0019	-2.2	<i>nhaA</i>	Na ⁺ /H antiporter, pH dependent
B0484	-2.1	<i>copA</i>	Cu(I)-translocation P-type ATPase
B3093	-2.1	<i>exuT</i>	hexuronate transport protein (MFS family)
