



SNP	548883	T→G	T141(AAC→CCC)	ppib	b0525	G	G	G	peptidyl prolyl cis-trans isomerase B (rotamase B)
SNP	550576	T→C	N918(AAC→AGC)	cvyB	b0526	G	G	G	cytosine deaminase
SNP	569031	A→C	L70F(TTA→TTC)	quidD	b0551	C	C	C	DLF12 prophage; predicted antitermination protein
SNP	572708	A→C	K771(AAA→ACA)	rrdD	b0555	C	C	C	DLF12 prophage; predicted lysoczyme
SNP	576479	T→G	pseudogene (1867/44 nt)	aaad	b4634	-	-	-	DLF12 prophage; predicted tail fiber assembly protein (pseudogene)/Phase or Prophage Related
SNP	576921	T→G	pseudogene (702/744 nt)	aaad	b4634	-	-	-	DLF12 prophage; predicted tail fiber assembly protein (pseudogene)/Phase or Prophage Related
SNP	578302	T→G	intergenic (+376/245)	ftaf/afpp	b0565/b0564	-	-	-	pseudogene; DUF12 prophage/Phase or Prophage Related/DNA-binding globulin transcriptional activator; DUF12 prophage
SNP	579576	A→C	T246(AAC→AAC)	ompt	b0565	C	C	C	DLF12 prophage; outer membrane protease VII (outer membrane protein 3b)
SNP	580908	A→C	intergenic (409/15)	ompt/paubD	b0565/b4635	C	C	C	DLF12 prophage; outer membrane protease VII (outer membrane protein 3b)/RNA-OTHER
SNP	590201	A→G	Y378(TAC→CAC)	curR	b0571	G	G	G	DNA-binding response regulator in two-component regulatory system with CusC
SNP	590646	A→C	intergenic (+164/22)	curC	b0572	G	G	G	copper/silver efflux system; outer membrane component
SNP	598592	T→G	E313(AAG→GCG)	musM	b0577	G	G	G	mechanosensitive channel protein, miniconductance
DEL	600982	Δ1bp	coding (84/249 nt)	ybcJ	b0580	Δ1bp	Δ1bp	Δ1bp	predicted inner membrane protein
SNP	601099	C→T	intergenic (364/329)	yskY/ydkb	b0580/b0581	T	T	T	predicted membrane protein/weak gamma glutamylcysteine ligase
SNP	606469	T→G	K238(AAA→CAA)	fcpA	b0584	G	G	G	iron-entrobactin outer membrane transporter
SNP	614728	A→C	F113C(TT→TGT)	fcpC	b0588	-	-	-	iron-entrobactin transporter subunit
SNP	616689	T→C	I333(TAC→GTC)	fcpD	b0590	-	-	-	iron-entrobactin transporter subunit
SNP	618132	T→C	W323(TGG→GCG)	ens5	b0591	C	C	C	entrobactin exporter; iron-regulated
SNP	626219	A→C	V209(GTT→GCT)	ybmX	b0601	C	C	C	conserved protein
SNP	632821	T→G	K207(AAA→CAA)	dsuG	b0604	G	G	G	thio/diulfate interchange protein, periplasmic
SNP	642780	A→G	V414(GTC→GCC)	cxk	b0614	G	G	G	apo-citrate lyase phosphoribosyl-dephospho-CoA transferase
SNP	644173	A→G	A208(ACT→GCC)	ene	b0616	G	G	G	citrate lyase, citryl-ACP lyase (beta) subunit
SNP	647509	A→C	T374(AAC→GCT)	dsb	b0619	G	G	G	sensory histidine kinase in two-component regulatory system with c8B
SNP	649988	T→G	I283(ATT→ACT)	dcuC	b0621	-	-	-	anaerobic C4-dicarboxylate transport
SNP	650732	C→T	G255(GCC→GAC)	dcuE	b0622	-	-	-	anaerobic C4-dicarboxylate transport
SNP	650825	A→G	F41(TTC→CTC)	dcuC	b0621	-	-	-	anaerobic C4-dicarboxylate transport
SNP	655195	A→G	S195(TCC→CCC)	ybeF	b0629	G	G	G	predicted DNA-binding transcriptional regulator
SNP	658673	C→T	D596(GAC→GAC)	daaA	b0632	T	T	T	D-allyl-D-alanine carbonyltransferase (penicillin-binding protein 5)
SNP	665284	T→G	NS27(AAC→ACC)	nadD	b0639	G	G	G	nicotinic acid mononucleotide adenyltransferase, NAD(P)-dependent
SNP	666711	A→C	D821(GAT→GAG)	lptE	b0641	C	C	C	LPS assembly OM complex LptE, lipoprotein component
SNP	676859	A→C	H314(AAC→GAC)	hscC	b0650	G	G	G	Hsp70 family chaperone Hsc62; binds to RpoD and inhibits transcription
SNP	677325	A→G	V512(GTG→GGC)	hscC	b0650	G	G	G	Hsp70 family chaperone Hsc62; binds to RpoD and inhibits transcription
INS	685462	+CAC	coding (280/1539 nt)	int	b0657	-	-	+CAC	apoptoprotein N acetyltransferase
DEL	696274	Δ1bp	intergenic (136/24)	fldA/ybfE	b0676	Δ1bp	Δ1bp	Δ1bp	DNA-binding transcriptional regulator; repressor of N-acetylglucosamine
SNP	706447	A→G	intergenic (114/24)	fldA/ybfE	b0684/b0685	G	G	G	flavodoxin I/LexA-regulated conserved protein
SNP	710995	A→C	pseudogene (469/651 nt)	yBg	b0691	-	-	-	pseudogene
SNP	711869	A→G	pseudogene (197/255 nt)	ybfE	b0692	-	-	-	putrescine/putrescine symporter; putrescine/ornithine antiporter
SNP	712265	T→G	L289(TAC→GCT)	potE	b0692	G	G	G	putrescine/putrescine symporter; putrescine/ornithine antiporter
SNP	723250	A→C	S171(TAC→GCT)	kdpA	b0698	C	C	C	potassium translocating ATPase, subunit A
SNP	730296	T→C	pseudogene (1311/1434 nt)	ybfE	b0711	-	-	-	pseudogene; rfs-like
SNP	730480	T→C	pseudogene (1395/1434 nt)	ybfD	b0703	-	-	-	pseudogene; rfs-like
SNP	730627	A→G	T38A(ACT→GCT)	ybcJ	b0704	G	G	G	predicted protein
DEL	730631	Δ1bp	coding (116/670 nt)	ybcJ	b0704	-	-	-	Δ1bp
SNP	731439	T→C	pseudogene (129/255 nt)	ybfQ	b4514	C	C	C	pseudogene; H repeat associated protein
SNP	734949	A→C	K178(AAA→AAG)	phr	b0708	-	-	-	deoxyriboflavin photolyase, FAD-binding
SNP	735117	C→T	S322(AAC→AAT)	phr	b0708	-	-	-	deoxyriboflavin photolyase, FAD-binding
SNP	735632	A→C	L420(TAC→CTC)	phr	b0708	-	-	-	deoxyriboflavin photolyase, FAD-binding
SNP	738564	A→C	intergenic (124/24)	ybfE	b0711	-	-	-	predicted enzyme subunit
SNP	749576	A→C	intergenic (242/467)	glx/ybcH	b0720/b0721	C	C	C	citrate synthase/succinate dehydrogenase, membrane subunit; binds cytochrome b556
SNP	749952	A→C	intergenic (618/91)	glx/ybcH	b0720/b0721	-	-	-	citrate synthase/succinate dehydrogenase, membrane subunit; binds cytochrome b556
SNP	753344	A→C	E304(AAC→GAC)	sdhB	b0724	G	G	G	succinate dehydrogenase, membrane subunit; binds cytochrome b556
SNP	752576	T→G	Y80(TAT→GAT)	sdhB	b0724	G	G	G	succinate dehydrogenase, Fe/S subunit
SNP	755678	T→G	S703(TCT→GCT)	suaA	b0726	-	-	-	2-oxoglutarate decarboxylase, thiamin requiring
SNP	756150	A→G	intergenic (140/24)	suaA	b0726	-	-	-	2-oxoglutarate decarboxylase, thiamin requiring
SNP	761532	A→C	E228(AAG→ACA)	mngA	b0731	-	-	-	fused 2-O-alpha-mannosyl-D-glycerate specific P15 enzymes: IIA component/IIA component/IIIC component
SNP	762940	A→C	N338(AAT→CAT)	mngB	b0732	-	-	-	alpha-mannosidase
SNP	763656	A→C	E212(AAC→GAC)	mngB	b0732	-	-	-	alpha-mannosidase
SNP	766030	G→A	intergenic (+553/294)	mngB/cyD4	b0732/b0733	A	A	A	alpha-mannosidase/cytochrome d terminal oxidase, subunit I
SNP	772416	A→G	P350F(CAC→CCG)	toaA	b0739	-	-	-	membrane anchored protein in ToxA/ToL/ToK complex
SNP	773181	T→C	Y240(TAC→CAC)	ybfF	b0742	C	C	C	periplasmic ToxB binding protein
SNP	778914	A→G	V258A(GTG→GGC)	zifB	b0752	G	G	G	zinc efflux system
SNP	784908	A→C	F250V(TTC→GTC)	galk	b0757	-	-	-	galactokinase
DEL	787967	Δ44bp	coding (645/644/473 nt)	modE	b0761	G	Δ44bp	G	predicted malylate transporter subunits of ABC superfamily; ATP-binding components
SNP	789065	A→G	V148A(GTC→GCC)	modE	b0761	G	G	G	DNA-binding transcriptional repressor for the molybdenum transport operon modABC
SNP	793151	T→G	intergenic (54/101)	ybfA/ygfJ	b0766/b0767	-	-	-	pyruvate kinase
SNP	797400	T→G	I404(TAT→GAT)	ybfA/ygfJ	b0766/b0767	-	-	-	predicted transporter
SNP	800831	T→G	intergenic (+201/438)	ybfJ/ybcH	b0771/b0772	-	-	-	predicted hydratase/acyl-CoA thioesterase, lipoprotein
SNP	802773	T→G	intergenic (1977/103)	ybcZ/cj	b0772/plamid_gene01	-	-	-	acyl-CoA thioesterase, lipoprotein/phage lambda repressor protein C1
SNP	802776	T→G	intergenic (1977/103)	ybcZ/cj	b0772/plamid_gene01	-	-	-	acyl-CoA thioesterase, lipoprotein/phage lambda repressor protein C1
SNP	802784	A→C	intergenic (988/90)	ybcZ/cj	b0772/plamid_gene01	C	-	-	acyl-CoA thioesterase, lipoprotein/phage lambda repressor protein C1
SNP	804461	A→C	L1424(TTA→TTG)	teaA	plamid_gene02	-	-	-	TeaA protein
SNP	809604	T→G	I333(AAC→GAC)	bioF	b0776	T	T	T	8-aminopurine nucleoside synthase
SNP	820597	C→T	L167(LTC→CTC)	ybfD	b0789	T	T	T	cardiolipin synthase 2
SNP	839156	C→T	G264D(GGC→GAC)	glp	b0805	T	T	T	ATP-dependent DNA helicase
SNP	845401	A→G	G486G(TGG→GGC)	glpP	b0810	G	G	G	catechololate siderophore receptor FII
SNP	845656	T→G	intergenic (126/157)	glpP/dsp	b0811/b0812	G	G	G	glutamine transporter subunit
SNP	847475	A→C	intergenic (139/140)	dps/rhaA	b0812/b0813	C	C	C	glutamine transporter subunit/Fe-binding and storage protein
SNP	847609	A→C	intergenic (1273/26)	dps/rhaA	b0812/b0813	C	C	C	Fe-binding and storage protein/threonine and homoserine efflux system
DEL	848657	Δ1bp	coding (166/188 nt)	rhaA	b0813	-	-	-	Δ1bp
SNP	848886	T→C	D146G(GAT→GGT)	rhaA	b0813	-	-	-	threonine and homoserine efflux system
SNP	854868	A→C	K153G(AAG→GAG)	ybtI	b0820	-	-	-	fused predicted transporter subunits of ABC superfamily; ATP-binding components
SNP	855117	T→G	F321(TTC→GTT)	ybtI	b0820	-	-	-	fused predicted transporter subunits of ABC superfamily; ATP-binding components
SNP	857557	T→G	intergenic (71/81)	ybfJ/ybfV	b0821/b0822	-	-	-	predicted protein/sugar phosphatase; preference for fructose-1-P, ribose-5-P and glucose-6-P
SNP	858301	A→C	L511(TTT→CTG)	ybfV	b0822	-	-	-	sugar phosphatase; preference for fructose-1-P, ribose-5-P and glucose-6-P
SNP	865116	T→G	L108(LCT→GCT)	iaaA	b0828	G	G	G	isoaspartyl methyltransferase
DEL	865532	Δ1bp	coding (540/968 nt)	iaaA	b0828	-	-	-	Δ1bp
DEL	866840	Δ1bp	coding (1004/1980 nt)	gIA	b0829	-	-	-	Δ1bp
SNP	878630	C→T	D288(TCC→GCT)	yfi	b0837	T	T	T	isoaspartyl methyltransferase
SNP	889240	A→C	S344(TCG→GCG)	deoR	b0840	-	-	-	DNA-binding transcriptional repressor
SNP	890165	T→G	intergenic (677/93)	grnA/ybcJ	b0849/b0850	G	G	G	glutaredoxin 1, redox coenzyme for ribonucleotide reductase (HnrL1)/conserved protein, DUF1448 family
INS	896700	+G	coding (614/296 nt)	potH	b0856	+G	+G	+G	putrescine transporter subunit; membrane component of ABC superfamily
SNP	897170	T→G	H76Q(TAC→CAG)	rlnD	b0859	-	-	-	23S rRNA M5/J74 methytransferase
INS	899264	+C	intergenic (364/227)	arlY/arlM	b0860/b0861	+C	+C	+C	arginine binding protein, periplasmic/arginine transporter subunit
SNP	902668	C→T	G140C(GCC→GAC)	yfp	b0866	-	-	-	lipoprotein
SNP	910583	C→T	L299I(TCC→CTA)	ybtI	b0869	-	-	-	conserved protein with NAD(P) binding Rossmann-fold domain
SNP	916006	A→C	S379(AAG→GAG)	ybfD	b0876	-	-	-	conserved protein with nucleoside triphosphate hydrolase domain
SNP	918295	T→G	I333(GTA→GCA)	ybfD	b0876	-	-	-	conserved protein with nucleoside triphosphate hydrolase domain
SNP	919606	T→G	F370Q(TTT→TGT)	ybfD	b0876	-	-	-	conserved protein with nucleoside triphosphate hydrolase domain
SNP	920818	T→G	L616R(TCC→GGG)	ybfD	b0879	-	-	-	conserved protein with nucleoside triphosphate hydrolase domain
INS	924217	+GG	noncoding (80/88 nt)	serW	b0883	+GG	+GG	+GG	HNAI-ser
SNP	926113	T→G	E503(AAG→ACA)	cytC	b0886	-	-	-	fused glutathione, cysteine exporter subunits of ABC superfamily; membrane component/ATP-binding component
SNP	932383	A→C	I382(AAG→GAG)	ftxK	b0895	-	-	-	DNA translocase at septal ring sorting daughter chromosomes
SNP	934653	A→C	Q765F(GAC→CCG)	ftxK	b0890	C	C	C	DNA translocase at septal ring sorting daughter chromosomes
SNP	940138	T→G	V252G(GTG→GGG)	dmsA	b0894	-	-	-	dimethyl sulfoxide reductase, anaerobic, subunit A
SNP	942250	A→C	I382(AAG→GAG)	dmsA	b0895	-	-	-	dimethyl sulfoxide reductase, anaerobic, subunit B
SNP	949011	C→T	W165(TGG→TGA)	pflA	b0902	T	T	T	pyruvate formate lyase activating enzyme 1
SNP	958465	T→C	intergenic (122/44)	araY/ackA	b0908/b0909	-	-	-	5-enolpyruvylshikimate-3-phosphate synthetase/predicted peptide with chaperone function
SNP	963846	A→C	I293(TAT→GAT)	rnl	b0913	-	-	-	inner membrane protein, ComC family competence protein
SNP	978757	A→C	E1338A(GAA→GCA)	ruk8	b0924	C	C	C	chromosome condensation MukBEF, ATPase and DNA-binding subunit
SNP	982288	T→G	Y220(TAC→GAC)	ybcL	b0927	G	G	G	predicted metal-binding enzyme
SNP	992195	T→G	T39V(TAC→GAC)	ybcL	b0933	G	G	G	alkanesulfonate transporter subunit
SNP	992821	C→T	G146G(GGC→GAC)	ssuC	b0934	T	T	T	putative alkane sulfonate transporter subunit
SNP	996575	A→G	T95A(AAC→GAC)	eHA	b0938	G	G	G	predicted fibrin-like adhesion protein
SNP	997449	A→C	I178A(GTC→GTC)	eibD	b0939	G	G	G	predicted periplasmic zinc chaperone
SNP	998745	A→C	K38Q(AAA→CAA)	eifC	b0940	C	C	C	predicted outer membrane usher protein
DEL	999441	Δ1bp	coding (180/260 nt)	eifC	b0940	-	-	-	Δ1bp
SNP	999611	T→G	L246(TTC→G						

SNP	1228892	A-C	intergenic ( 73/300)	hvi/umuD	b1182/b1183	-	-	-	C	hemolysin E/DNA polymerase V, subunit D
SNP	1231222	C-T	intergenic ( 225/111)	fadR	b1187	-	-	-	T	DNA-binding transcriptional regulator of fatty acid metabolism
SNP	1238020	T-G	Z39M(ATT-ATG)	dadX	b1190	G	G	-	T	alanine racemase 2, P,KP-binding
SNP	1238656	T-G	intergenic ( 282/104)	dadX/cvra	b1190/b1191	G	G	G	G	alanine racemase 2, P,KP-binding/predicted cation/proton antiporter
SNP	1241889	T-A	intergenic ( 165/124)	emaA	b1192	G	G	-	C	lysine methyltransferase/glyoxylate E
SNP	1245317	T-C	Y162(CAT-ATG)	traA	b1197	C	C	-	C	periplasmic trehalase
DEL	1245247	del	coding (121/2888 nt)	ycfY	b1202	-	-	-	del	predicted adhesin
SNP	1255771	T-G	Y165(AAA-ACA)	ycfH	b1203	-	-	-	G	ATPase, 1 $\alpha$ -dependent, ribosome-associated
SNP	1257846	A-C	Y452(GTT-GTG)	ychM	b1206	-	-	-	C	predicted transporter
SNP	1261873	A-G	Y348(GTG-GGG)	lobB	b1209	G	G	G	G	DM lipoprotein required for localization of lipoproteins
SNP	1265109	C-T	intergenic ( 113/125)	prnMC	b1212	-	-	-	C	N $\epsilon$ -glutamine methyltransferase, modifies release factors RF-1 and RF-2
SNP	1269694	T-G	Y105(GTT-GTG)	kdsA	b1215	-	-	-	T	3-deoxy-D-manno-oxulosonate 8-phosphate synthase
SNP	1271447	A-G	intergenic ( 104/235)	narX/narK	b1222/b1223	G	G	G	G	senary histidine kinase in two-component regulatory system with NarX/nitrate/nitrite transporter
SNP	1286621	A-G	F116(CAT-ATG)	narX	b1227	-	-	-	G	nitrate reductase 1, gamma lytic/oxoiron-NADH subunit
SNP	1287485	T-G	intergenic ( 127/185)	ychI/rnsA	b1233/b1234	G	G	G	G	conserved protein, UPF0225 family/predicted phospholipase, patatin-like family
SNP	1288515	A-G	G282(GGA-GGG)	rnsA	b1234	G	G	G	G	predicted phospholipase, patatin-like family
SNP	1294614	A-G	S649(TTC-ATC)	adhE	b1241	-	-	-	G	fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deacetylase
MOB	1297920	-	intergenic ( 250/485)	ychE/oppA	b1242/b1243	MOB	MOB	MOB	MOB	predicted inner membrane protein/oligopeptide transporter subunit
SNP	1300779	T-G	Y544(CAT-ATG)	oppD	b1246	G	G	G	G	oligopeptide transporter subunit
SNP	1307560	T-G	intergenic ( 255/115)	kyfY/kyfI	b1250/b1251	-	-	-	G	voltage-gated potassium channel/predicted enzyme
SNP	1308206	C-T	intergenic ( 139/109)	ychI/tonB	b1251/b1252	-	-	-	T	predicted enzyme/membrane spanning protein in TonB-EcbA-EcbD transport complex
SNP	1312256	T-G	K1291(AAA-ACA)	trpB	b1261	-	-	-	G	tryptophan synthase, beta subunit
SNP	1324479	A-C	intergenic ( 144/238)	ycfX/tonB	b1271/b1272	C	C	C	C	predicted oxoacyl (acyl carrier protein) reductase, EmrKY-ToxC system/predicted inner membrane peptidase; multiplicity suppressor of htrA(dspF)
SNP	1324880	A-C	D454(GAC-ATC)	sonB	b1272	-	-	-	C	predicted inner membrane peptidase; multiplicity suppressor of htrA(dspF)
SNP	1331356	A-G	A232(GAC-ATC)	cyrB	b1275	G	G	G	G	DNA-binding transcriptional dual regulator, O $_2$ acetyl-L-serine-binding
SNP	1332406	A-G	E71(GAA-GAG)	ymnA	b4522	G	G	G	G	hypothetical protein
SNP	1333942	T-G	intergenic ( 258/115)	ycfX/cvraA	b4523/b1276	G	G	G	G	hypothetical protein/acetonate hydratase 1
SNP	1333708	A-G	T188(GAC-GGG)	pyz	b1281	-	-	-	G	uridine-5' phosphate decarboxylase
SNP	1344040	A-C	F331(TTT-ATG)	ribB	b1286	-	-	-	C	ribonuclease II
SNP	1347469	A-G	G199(GGT-ATC)	fabI	b1288	G	G	G	G	enoyl-acyl-carrier-protein reductase, NADH-dependent
SNP	1352400	C-T	intergenic ( 175/129)	saabB	b1293	-	-	-	T	inner-membrane peptidase transport ABC transporter permease
SNP	1352489	A-G	L701(TTA-CTA)	sapB	b1293	G	G	G	G	antimicrobial peptide transport ABC transporter permease
SNP	1353599	T-G	T339(ATT-ATC)	puuP	b1296	-	-	-	G	putrescine importer
SNP	1362329	A-G	Y186(GAT-GAG)	puaf	b1303	-	-	-	G	DNA-binding transcriptional activator
SNP	1364845	A-C	intergenic ( 15/70)	pspD/pspE	b1307/b1308	-	-	-	C	periplasmic inner membrane phase-shock protein/hiosphatase:cyanide sulfurtransferase (rhodanese)
SNP	1370497	T-C	L179(TTC-ATC)	ycfJ	b1311	-	-	-	C	predicted sugar transporter subunit: membrane component of ABC superfamily
SNP	1371075	A-G	intergenic ( 125/112)	ycfS	b1315	-	-	-	G	predicted oxidoreductase, NADH-binding
SNP	1374443	A-G	D125(GAC-GGG)	ycfS	b1315	G	G	G	G	predicted oxidoreductase, NADH-binding
SNP	1375927	A-C	E273(GAA-GCA)	ycfT	b1316	C	C	C	C	predicted hydrolase
SNP	1377798	A-G	D420(GAA-GAG)	ycfU	b1317	G	G	G	G	beta-phosphoglucomutase
SNP	1377995	A-G	T208(AAC-GCC)	ycfU	b1317	G	G	G	G	beta-phosphoglucomutase
SNP	1378982	T-G	psuedogene (916/1082 nt)	ycfV	b4524	G	G	G	G	psuedogene; putative ATP-binding component of a transport system
SNP	1395654	A-C	psuedogene (958/1217 nt)	psuB	b1333	C	C	C	C	stress-induced protein
DEL	1397205	del	coding (258/516 nt)	egt	b1335	del	del	del	del	O-6-alkylguanine-DNA-cytosine protein methyltransferase
DEL	1397947	del	coding (1053/1527 nt)	agf	b1336	del	del	del	del	p-aminobenzoate glutamate transporter; membrane protein
SNP	1398320	C-T	intergenic ( 176/121)	abpB	b1337	-	-	-	T	p-aminobenzoate glutamate hydratase, B subunit
SNP	1402449	T-G	F161(TTT-ATG)	abpR	b1339	-	-	-	G	predicted DNA-binding transcriptional regulator of abgA8 operon
SNP	1412493	A-G	intergenic ( 265/151)	ycfW/ocacB	b1355/b1356	-	-	-	G	Rac phage; pseudogene; tail protein homology/Phage or Phage Related
SNP	1420156	A-G	psuedogene (230/612 nt)	ydaW	b1361	G	G	G	G	Rac phage; pseudogene, DNA-binding protein homology/Phage or Phage Related
SNP	1420474	T-G	psuedogene (548/612 nt)	ydaW	b1361	-	-	-	G	Rac phage; pseudogene, DNA-binding protein homology/Phage or Phage Related
SNP	1424284	A-G	psuedogene (755/2029 nt)	sttA	b1368	-	-	-	G	Rac phage; pseudogene; tail protein homology/Phage or Phage Related; putative alpha helix protein
SNP	1424664	A-G	S1305(TCA-ATC)	ydaR	b1372	G	G	G	G	Rac phage; predicted tail fiber protein
SNP	1431355	T-C	G326(GAA-GGG)	ydaE	b1375	-	-	-	C	cold shock protein, function unknown, Rac phage
SNP	1431605	A-G	D534(GAC-GGC)	ydaE	b1378	-	-	-	C	fused predicted pyruvate:flavoindoxyl oxidoreductase; conserved protein/conserved protein/P45 binding protein
SNP	1435081	A-G	Y977(GTA-GCA)	ybaK	b1378	G	G	G	G	fused predicted pyruvate:flavoindoxyl oxidoreductase; conserved protein/conserved protein/P45 binding protein
SNP	1442776	A-C	N834(AAT-ATC)	ydbH	b1381	-	-	-	C	predicted protein
SNP	1448971	T-G	G633(GAA-GAG)	paaf	b1387	-	-	-	G	fused coenzyme CoA hydrolase 3-oxo-5,6-dihydroxyheptyl-CoA semialdehyde dehydrogenase
SNP	1451520	A-G	A344(GCA-GGG)	paaf	b1388	G	G	G	G	ring 1,2-phenylacetyl-CoA epoxidase subunit
SNP	1456187	A-C	D238(GAC-GCC)	paaf	b1394	-	-	-	C	1,2-epoxyphenylacetyl-CoA isomerase, coenzyme CoA-forming
SNP	1456626	A-G	D564(GCA-GGG)	paaf	b1398	-	-	-	G	phenylacetyl-CoA ligase
SNP	1460162	T-C	V271(GTT-GCT)	paaf	b1398	C	C	C	C	phenylacetyl-CoA ligase
SNP	1462172	A-G	Y159(CAT-ATC)	paaf	b1400	G	G	G	G	predicted heparidase repeat acetyltransferase
SNP	1464382	T-G	intergenic ( 172/8622 nt)	ybaA	b4492	-	-	-	G	psuedogene, autoantiserum homolog; interrupted by IS2 and IS30
SNP	1464932	A-G	psuedogene (3775/8622 nt)	ybaA	b4492	G	G	G	G	psuedogene, autoantiserum homolog; interrupted by IS2 and IS30
SNP	1467912	T-G	psuedogene (5295/8622 nt)	ybaA	b4492	-	-	-	C	psuedogene, autoantiserum homolog; interrupted by IS2 and IS30
DEL	1471356	del	coding (90/861 nt)	ydcC	b1406	del	del	del	del	psuedogene, autoantiserum homolog; interrupted by IS2 and IS30
INS	1472082	+	coding (636/861 nt)	ydcC	b1406	+	+	+	+	predicted oxidoreductase, NAD(P) binding
SNP	1474106	A-G	E246(GAG-GGG)	ydbD	b1407	G	G	G	G	predicted PF12071 family periplasmic methylglyoxyl resistance protein
SNP	1474985	A-G	Y995(TAC-ATC)	ydbD	b1407	-	-	-	G	predicted PF12071 family periplasmic methylglyoxyl resistance protein
SNP	1475255	A-C	N137(AAC-ATC)	ybaA	b1408	C	C	C	C	inner membrane protein
SNP	1477986	A-G	K541(AAA-9AAG)	ybaC	b1410	G	G	G	G	predicted hydrolase
SNP	1478764	T-G	E384(MAT-ATC)	ybaD	b1410	G	G	G	G	predicted phosphatase inner membrane protein
SNP	1482635	A-G	S7885(TCA-ATC)	hraA	b1413	G	G	G	G	predicted ATP-dependent helicase
SNP	1484704	A-G	N815(AAT-ATC)	ydcF	b1414	-	-	-	C	conserved S4M-binding protein, DUf218 superfamily
SNP	1484935	A-G	T359(AAC-GGG)	ydcF	b1414	G	G	G	G	conserved S4M-binding protein, DUf218 superfamily
SNP	1487284	A-C	psuedogene (656/1001 nt)	gafC	b4493	C	C	C	C	psuedogene, GAP dehydrogenase; glyceraldehyde 3-phosphate dehydrogenase (second fragment)
SNP	1490554	C-T	intergenic ( 122/518)	gafC	b1421	-	-	-	T	methylophilin-like protein; galactose sensor receptor
SNP	1503442	A-G	L151(CAT-ATG)	ydcN	b1434	G	G	G	G	predicted DNA-binding transcriptional regulator
SNP	1504765	T-G	N153(AAT-ATG)	ydcN	b1435	G	G	G	G	predicted peritase
SNP	1507111	A-C	A154(AAC-GCC)	hcrB	b1438	C	C	C	C	antitoxin for the HcrA toxin-antitoxin system; mutational suppressor of null pscE lethality
SNP	1507804	T-G	D192(GAT-GAG)	ydbR	b1439	G	G	G	G	predicted iron outer membrane transporter
SNP	1513831	A-G	H438(GAC-GGC)	pry	b1444	G	G	G	G	gamma-aminobutyraldehyde dehydrogenase
SNP	1517724	A-G	T96(AAA-9AAG)	mydA	b1450	G	G	G	G	colicin acid and toxin gene transcriptional regulator, MspR-controlled
SNP	1518425	T-G	M623(ATG-CGT)	yndC	b1451	-	-	-	G	predicted iron outer membrane transporter
SNP	1519937	G-A	Q119(TCA-ATA)	yndC	b1451	-	-	-	A	predicted iron outer membrane transporter
SNP	1521024	C-T	H176(AAC-ATC)	yneF	b1452	-	-	-	T	ATP-binding protein, periplasmic, function unknown
SNP	1530682	A-G	W687(TGC-CCG)	ydbH	b1462	-	-	-	C	conserved protein
SNP	1531365	A-G	T306(GAC-CCC)	nhoA	b1463	C	C	C	C	N-hydroxyvaline O-acetyltransferase
SNP	1533829	A-G	S966(TTT-ATC)	narZ	b1468	-	-	-	C	nitrate reductase 2 (NrdZ), alpha subunit
SNP	1540400	T-C	N119(AAC-ATC)	ydgE	b1473	-	-	-	C	aromatic amino acid exporter
SNP	1540850	A-G	S740(GAG-GGG)	hmg	b1474	G	G	G	G	formate dehydrogenase-N, alpha subunit, nitrate-inducible
SNP	1541022	A-G	F618(GAT-GAG)	fdhH	b1475	-	-	-	G	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible
SNP	1542112	A-G	I217(AAT-ATC)	fdhI	b1476	-	-	-	G	formate dehydrogenase-N, cytochrome B556 (gamma) subunit, nitrate-inducible
SNP	1552123	A-C	intergenic ( 24/78)	sra/bdm	b1480/b1481	-	-	-	C	Stationary phase-induced ribosome-associate protein/biofilm-dependent modulation protein
SNP	1555419	A-G	F971(TTC-ATG)	ycfE	b1487	-	-	-	C	D-3 $\alpha$ -D-3 transporter subunit
SNP	1560916	T-G	K682(GAT-CAG)	douP	b1489	-	-	-	G	oxygen sensor, c-di-GMP phosphodiesterase, heme-regulated; cold- and stationary phase-induced bifilm regulator
SNP	1574236	A-G	F174(GTC-ATC)	ydbH	b1499	-	-	-	G	predicted porin protein
SNP	1581849	T-G	intergenic ( 139/13)	ydcN/ydcO	b1490/b1499	G	G	G	G	conserved protein/transcriptional activator for mdxE
SNP	1585974	T-G	intergenic ( 61/14)	ydcO/yafA	b1499/b1500	G	G	G	G	transcriptional activator for mdxE/Two component system connector membrane protein, EvgSA to PhoDP
SNP	1585945	A-G	E470(GAA-9AAG)	safA	b1500	-	-	-	G	Two component system connector membrane protein, EvgSA to PhoDP
SNP	1581952	C-T	Y587(CTG-ATC)	ydcP	b1501	T	T	T	T	predicted oxidoreductase
SNP	1582480	A-G	V088(GTA-GCA)	ydcP	b1501	G	G	G	G	predicted oxidoreductase
SNP	1583800	A-G	intergenic ( 183/234)	ydcQ/ydcQc	b1501/b1502	G	G	G	G	predicted oxidoreductase, Zn-dependent and NAD(P)-binding
SNP	1584759	T-G	N688(AAT-ATC)	ydcQ	b1502	-	-	-	G	predicted fibrillar-like adhesin protein
INS	1588606	+	psuedogene (422/1149 nt)	ydcT	b1505	-	-	-	+	psuedogene; putative outer membrane protein
SNP	1587507	T-G	psuedogene (1216/283 nt)	yneE	b1506	-	-	-	G	psuedogene, iron formate
SNP	1588882	A-G	I184(TTT-ATC)	hpaB	b1507	G	G	G	G	serine protein kinase required for perister formation; toxin of HpaAB toxin-antitoxin system
INS	1591350	+	psuedogene (386/1422 nt)	yneO	b4996	+	+	+	+	psuedogene, A16a homolog
INS	1591474	+	psuedogene (3839/1422 nt)	yneO	b4996	+	+	+	+	psuedogene, A16a homolog
INS	1594532	+	psuedogene (781/5422 nt)	yneO	b4996	+	+	+	+	psuedogene, A16a homolog
DEL	1595561	del	intergenic ( 249/280)	yneO/hcrK	b4996/b1511	del	del	del	del	psuedogene, A16a homolog/autolysin 2 (A1-2) kinase
SNP	1600620	T-G	luc	luc	b1514	G	G	G	G	Autolysin 2 import system permease protein
SNP	1600698	G-A	A218(GGG-GCA)	luc	b1514	A	A	A	A	Autolysin 2 import system permease protein
SNP	1612034	A-T	D210(GAT-ATC)	yneI	b1526	-	-	-	T	predicted DNA-binding transcriptional regulator
SNP	1613536	T-G	H176(GAT-ATC)	yneE	b1527	-	-	-	G	predicted protein
SNP	1614602	A-C	I1171(ATT-CTT)	ydaE	b1528	-	-	-	G	predicted arabinose transporter
SNP	1615469	T-G	*221(TAA-ATC)	marC	b1529	-	-	-	G	inner membrane protein, UPF056 family
SNP	1615987	T-G	L377(CAT-ATC)	ydcE	b1534	-	-	-	G	predicted transporter
SNP	1619149	T-G	S188A(TGC-GCC)	ydcE	b1534	-	-	-	G	predicted transporter
SNP	1619347	T-C	V807(GAT-GCA)	ydcE	b1534	-	-	-	C	predicted transporter
SNP	1621129	T-C	H484(GAT-ATC)	dcp	b1538	-	-	-	G	predicted carboxypeptidase II
SNP	1624215	T-G	E131(GAA-GCA)	dcp	b1538	G	G	G	G	predicted carboxypeptidase II
SNP	1624481	T-G	E420(GAA-9AAG)	dcp	b1538	-	-	-	G	predicted carboxypeptidase II
SNP	1628531	A-C	psuedogene (2154/2183 nt)	ydcI	b4600	-	-	-	G	psuedogene, MFS transporter family; interrupted by Qin phage; Phage or Phage Related; putative transport protein
SNP	1631929	T-G	psuedogene (16136/21							

SNP	181135	A->G	L170L(TA->CTG)	ylfX	b1750	-	G	G	inner membrane protein, TPV38/TEM64 family	
SNP	181216	A->G	L537G(GC->GCA)	top8	b1763	-	G	A	DNA topoisomerase II	
SNP	1844040	G->A	A49V(GCG->GTG)	top8	b1763	-	A	A	DNA topoisomerase II	
SNP	1846150	T->G	F38C(TTC->ATC)	sppA	b1766	-	-	G	protease IV (signal peptide peptidase)	
SNP	1846297	A->C	K397T(GTC->ATC)	sppA	b1766	-	-	C	protease IV (signal peptide peptidase)	
SNP	1848645	T->G	CL178A(TGT->TGG)	pnxA	b1768	-	-	G	nicotinamide/syrazinamide	
SNP	1852050	A->C	intergenic (7-1146)	ydf/ydfG	b1770/b1771	-	G	C	predicted DNA-binding transcriptional regulator/alpha-keto reductase, NADH-dependent; can use methylglyoxal as substrate	
DEL	1851140	del	intergenic (117-117)	ydfG	b1771	-	-	A	alpha-keto reductase, NADH-dependent; can use methylglyoxal as substrate	
SNP	1858237	T->G	T107T(ACA->ACC)	ydlJ	b1776	-	-	G	predicted oxidoreductase, 2n-dependent and NAD(P) binding	
SNP	1858732	A->C	intergenic (1378-195)	ydf/ydfC	b1776/b1777	-	-	C	predicted oxidoreductase, 2n-dependent and NAD(P) binding/conserved protein	
SNP	1861178	A->C	G86A(AAG->AAC)	yead	b1780	-	-	C	conserved protein	
SNP	1866788	T->C	P203R(CCT->CCC)	yeah	b1784	-	-	C	conserved protein	
SNP	1869262	A->G	A249A(GCA->GCG)	yeah	b1784	-	-	G	conserved protein	
SNP	1869829	T->C	S122T(TCC->GCC)	yeal	b1786	-	-	C	predicted diguanylate cyclase	
SNP	1870384	T->C	G378G(GGT->GGC)	yeal	b1786	-	-	C	predicted diguanylate cyclase	
SNP	187397	T->C	G282G(GCA->GGG)	yea2	b1795	-	-	C	conserved protein, UPF010 family	
DEL	187580	del	intergenic (1001-848)	yea2/yea2b	b1795/b1796	-	-	A	conserved protein, UPF010 family/predicted protein	
SNP	1878940	G->A	S31L(CA->TTA)	dmrIR	b1799	-	A	A	DNA-binding transcriptional activator for dnmA	
SNP	1882494	A->C	G142P(CAG->CCG)	yeaK	b1809	-	-	C	predicted oxidoreductase	
SNP	1882491	A->C	H292Q(CAT->CAG)	faed	b1805	-	-	C	acyl-CoA synthetase (long-chain-fatty acid-CoA ligase)	
SNP	1889517	A->C	T889Y(TG->CGG)	yoaA	b1808	-	-	C	conserved protein with nucleoside triphosphatase domain	
SNP	1889428	T->G	D138A(GAT->GAG)	padB	b1812	-	-	G	aminooxychlorimide synthase, subunit I	
SNP	1895005	T->G	T277T(ACT->AGC)	sdaA	b1814	-	-	C	conserved protein	
SNP	1895029	T->C	G285G(GGT->GGC)	sdaA	b1814	-	-	C	L-serine deaminase I	
SNP	1902937	T->G	L429G(TAT->GCT)	asbB	b1815	-	-	G	predicted phosphohydroxylase	
SNP	1900124	T->G	D262E(GAT->GAG)	manX	b1817	-	-	G	fused mannose-specific PTS enzymes: IIA component/IIb component	
SNP	1903684	T->G	H021P(CAT->CCT)	rhmA	b1822	-	G	G	23S rRNA m1G745 methyltransferase	
SNP	1915096	T->G	Y649G(TAC->TGC)	prc	b1830	-	-	C	carboxy-terminal protease for penicillin-binding protein 3	
SNP	1911879	A->C	S55A(TTC->GCT)	prc	b1830	-	-	C	carboxy-terminal protease for penicillin-binding protein 3	
SNP	1912744	T->G	K60A(GAG->CAG)	proQ	b1831	-	-	G	RNA chaperone, probable regulator of ProP transcription	
SNP	1915668	A->G	G195G(GCT->GAT)	yeaG	b1833	-	-	G	inner membrane protein	
SNP	1921917	G->A	A89V(GCC->GTC)	yobA	b1841	-	A	A	conserved protein	
SNP	1921192	T->G	N178A(AAT->AAG)	yobB	b1843	-	-	G	conserved protein	
SNP	1924460	A->C	coding (136/1085 nt)	iroB	b1845	-	-	C	protease II	
SNP	1927255	T->C	T314A(TGT->GCT)	yedB	b1847	-	-	C	secreted protein	
SNP	1930411	A->C	V473G(TGT->GTC)	yefE	b1851	-	-	C	6-phosphogluconate dehydratase	
INS	1931703	A->G	coding (2161/227)	zwf/yeaX	b1852/b1853	-	+A	+A	glucose-6-phosphate dehydrogenase/predicted DNA-binding transcriptional regulator	
SNP	1946028	A->C	F570T(TTT->TGT)	aspS	b1866	-	-	C	aspartyl-tRNA synthetase	
SNP	1967415	T->C	D205G(GAT->GGT)	tap	b1885	-	-	C	methyl-accepting protein IV	
SNP	1970746	A->G	N68A(TAA->AAG)	chvE	b1887	-	-	G	putine-binding, serine-threonine protein	
SNP	1974425	T->G	intergenic (1150/65)	motA/Ihbc	b1890/b1891	-	-	G	proton conductor component of flagellar motor/DNA-binding transcriptional dual regulator with FliD	
SNP	1974973	T->G	E320A(GAA->GAC)	Rhc	b1891	-	-	G	DNA-binding transcriptional dual regulator with FliD	
SNP	1978940	A->C	S243T(TAC->ACC)	otcB	b1897	-	-	G	trehalose-6-phosphate phosphatase, biosynthetic	
SNP	1981009	A->C	F115L(TTT->TGT)	araF	b1901	-	-	C	L-arabinose transporter subunit	
SNP	1988377	A->C	V156G(GTA->GGA)	yeaA	b1908	-	-	C	conserved protein, UPF010 family	
SNP	1988988	A->C	G23W(TTT->GTT)	pgaA	b1912	-	-	C	phosphoglycylphosphatase synthetase	
SNP	1993737	G->A	A233(GCC->GTC)	doyD	b1919	-	-	A	D-cysteine desulfurase, PLP-dependent	
INS	1995872	A->G	coding (133/1087 nt)	iroB	b1919	-	-	G	D-cysteine desulfurase, PLP-dependent	
SNP	2000983	T->G	intergenic (1151/113)	fliC/RD	b1923/b1924	-	-	G	flagellar filament structural protein (flagellin)/flagellar filament capping protein	
SNP	2003443	T->C	G186G(TGT->GGC)	amyA	b1927	-	-	C	cytoplasmic alpha-amylase	
SNP	2003442	A->C	E33A(GAT->GCA)	yeaE	b1929	-	-	C	predicted inner membrane protein	
SNP	2011359	T->G	S303A(TCC->GCC)	fliF	b1938	-	-	C	flagellar basal-body MS-ring and collar protein	
SNP	2021267	A->C	K263A(AAA->CAA)	rcaA	b1951	-	-	C	DNA-binding transcriptional activator, co-regulator with RcaB	
SNP	2025425	A->C	predicted DNA-binding response regulator in two-component system with YeeV	yeaM	b1969	-	-	C	predicted DNA-binding response regulator in two-component system with YeeV	
SNP	2040809	A->C	intergenic (28/166)	serJ/nstA	b1975/b1976	-	-	C	HNA-Ser/anti-repressor for Dga(Mlc)	
SNP	2040805	A->C	K7N(AAA->AAG)	mfaA	b1976	-	-	C	anti-repressor for Dga(Mlc)	
SNP	2045139	G->A	G99A(GAA->GAA)	yeaI	b1978	-	-	A	probable aspartyl-tRNA synthetase	
SNP	2050932	A->C	R229I(GCA->GCC)	shaA	b1981	-	-	C	shikimate transporter	
INS	205648	A	coding (277/1488 nt)	yeoD	b1985	-	-	+A	predicted multidrug exporter, MATE family	
SNP	2056768	A->G	G130G(GAT->GAT)	nae	b1988	-	-	G	DNA-binding transcriptional dual regulator of nitrogen assimilation	
SNP	2059202	T->C	intergenic (45/282)	naa/sunV	b1988/b1989	-	-	G	DNA-binding transcriptional dual regulator of nitrogen assimilation/rRNA-Aus	
SNP	2061222	T->G	intergenic (234/67)	cobU/yeeh	b1993/b4639	-	-	G	bifunctional cobamide kinase; cobamide nucleotide guanylyltransferase/pseudogene	
SNP	2061647	A->C	coding (133/1087 nt)	iroB	b1995	-	-	G	INS transposase and trans-activator	
SNP	2065634	T->C	pseudogene (10/15 nt)	yeaH	b4641	-	-	C	conserved protein	
SNP	2067572	A->C	intergenic (89/127)	yeaY/yeaA	b4641/b4582	-	-	C	pseudogene, CP4-44 putative phage remnant/Phase or Prophage Related; interrupted by G2 and C-terminal deletion	
SNP	2069096	T->G	intergenic (187/3870 nt)	yepF	b1999/b2000	-	-	G	CP4-44 prophage; predicted disrupted hemin or colicin receptor/Phase or Prophage Related; interrupted by G2 and C-terminal deletion	
SNP	2068605	A->G	intergenic (1709/158)	yepY/ru	b1999/b2000	-	-	G	pseudogene, CP4-44 prophage; predicted GTP-binding protein/Phase or Prophage Related; putative histone/CP4-44 prophage; antigen 43 [Ag43] phase-variable biofilm formation autoantiseroprotein	
SNP	2068623	A->C	intergenic (180/140)	yeaY/ru	b1999/b2000	-	-	C	pseudogene, CP4-44 prophage; predicted GTP-binding protein/Phase or Prophage Related; putative histone/CP4-44 prophage; antigen 43 [Ag43] phase-variable biofilm formation autoantiseroprotein	
SNP	2070255	G->A	intergenic (17/10)	ru	b2000	-	-	C	CP4-44 prophage; antigen 43 [Ag43] phase-variable biofilm formation autoantiseroprotein	
SNP	2071386	T->C	L875Y(TGC->CCG)	ru	b2000	-	-	C	CP4-44 prophage; antigen 43 [Ag43] phase-variable biofilm formation autoantiseroprotein	
SNP	2074834	T->G	S45Y(TCT->TCG)	cbaA	b2005	-	-	G	CP4-44 prophage; toxin of the YeeV-YeeU toxin-antitoxin system	
SNP	2078125	C->T	E212A(TAT->AAT)	slmC	b2009	-	-	G	DNA gyrase inhibitor	
SNP	2078915	A->G	intergenic (129/190)	slmC/tadC	b2009/b2010	-	-	G	DNA gyrase inhibitor	
SNP	2080569	A->C	G285G(GGT->GGC)	scbA	b2011	-	-	C	exonuclease I	
SNP	2080987	T->G	I836A(TAT->ATG)	scbB	b2011	-	-	G	exonuclease I	
SNP	2082583	A->C	V566G(TGT->GGT)	yeeE	b2013	-	-	C	inner membrane protein, UPF0384 family	
SNP	2091702	C->T	coding (133/1087 nt)	iroB	b2122	-	-	C	6-phosphogluconate dehydratase, catalytic subunit with HsdH	
SNP	2098120	T->C	T125A(GCC->GCC)	gnd	b2029	-	-	C	6-phosphogluconate dehydratase, decarboxylating	
SNP	2100961	A->C	F288T(TTC->TTC)	wbbK	b2032	-	-	C	lipopolysaccharide biosynthesis protein	
SNP	2102589	A->C	G28A(TAT->GAT)	galT	b2034	-	-	C	GalT/alpha-galactose-1,3-galactosyltransferase	
SNP	2106136	A->C	S25A(TTC->GCT)	rfaX	b2037	-	-	C	predicted polyprenol-linked O-antigen transporter	
SNP	2108715	G->A	F164T(TTC->TTT)	rhd	b2040	-	-	A	dTDP-4-dehydroxyflavonone reductase subunit, NAD(P) binding; of dTDP-L-rhamnose synthase	
SNP	2110055	T->G	intergenic (162/419)	rfaK/rfaF	b2041/b2042	-	-	G	INS-glucose-6-phosphate dehydrogenase, NAD(P) binding/putative regulatory subunit for GalT	
SNP	2112335	T->C	I262M(ATA->ATG)	wcaM	b2043	-	-	C	colanic acid biosynthesis protein	
SNP	2117860	G->A	P979G(CCG->TCG)	wcaI	b2047	-	-	A	A	predicted UDP-glucose lipid carrier transferase
SNP	2121496	T->G	S176A(GCC->GCC)	rmlB	b2049	-	-	G	mannose-1-phosphate guanylyltransferase	
SNP	2121270	T->C	E59E(GAA->GAG)	gmm	b2051	-	-	C	GDP-mannose mannosyl hydrolase	
SNP	2121514	T->G	E142A(GAA->GCA)	gmd	b2053	-	-	C	GDP-D-mannose dehydratase, NAD(P) binding	
SNP	2121746	A->G	L203W(GAT->GAT)	wcaD	b2056	-	-	C	predicted colanic acid polymerase	
SNP	2131306	A->C	L617T(A-TGA)	wab	b2061	-	-	C	protein-tyrosine phosphatase	
SNP	2141463	T->G	E102A(GTA->GCA)	waa	b2062	-	-	G	protein required for capsular polysaccharide translocation through the outer membrane	
SNP	2141516	A->G	Y67C(TAC->ACC)	yeeE	b2067	-	-	C	predicted diguanylate cyclase, GGCC domain-signaling protein	
SNP	2141970	T->C	G80G(GCA->GGG)	yefB	b2070	-	-	C	conserved protein	
SNP	2154510	A->G	Y67C(TAC->ACC)	mehB	b2075	-	-	G	multidrug efflux system, subunit B	
SNP	2155204	G->A	S196A(TCC->ACC)	mehC	b2075	-	-	G	multidrug efflux system, subunit B	
SNP	2161750	A->C	K287Q(AAA->AAG)	yeeQ	b2081	-	-	C	predicted peptidase	
SNP	2164117	T->G	V61G(TGT->GAG)	yeeR	b2086	-	-	G	phosphatidylglycerol kinase, metal-dependent	
SNP	2171819	A->C	intergenic (749/21)	galT/pepA	b2093/b2094	-	-	C	galactosyl-specific enzyme IIb component of PIS/galactol-specific enzyme IIA component of PTS	
SNP	2181925	A->C	C201T(TGT->GCT)	rhm	b2104	-	-	C	hydroxyethylthioalazine kinase	
SNP	2181517	A->C	E138A(GAG->GAG)	rfaH	b2106	-	-	C	membrane protein conferring nickel and cobalt resistance	
SNP	2181980	A->C	intergenic (124/195)	rcaA/rcaN	b2106/b2107	-	-	C	membrane protein conferring nickel and cobalt resistance/periplasmic modulator of Ni and Co efflux	
SNP	2186163	A->G	S688T(TGC->CCG)	yeeH	b2109	-	-	G	predicted outer membrane protein	
SNP	2191048	A->C	Y85D(GAT->GAT)	yeeH/yeaH	b2109/b2118	-	-	C	predicted outer membrane protein	
SNP	2201803	A->C	intergenic (290/137)	yeeH/yeaH	b4541/b2119	-	-	C	predicted protein/predicted transporter subunit: ATP-binding component of ABC superfamily	
SNP	2204143	T->G	L409V(TTA->GTA)	yeeM	b2120	-	-	C	predicted protein	
SNP	2208813	A->C	pseudogene (1806/4605 nt)	yeeD	b2122	-	-	C	pseudogene	
DEL	2211558	del	coding (311/1686 nt)	yeeHJ	b2126	-	-	A	predicted sensory kinase in two-component system with YeeT, inner membrane protein	
SNP	2211580	A->C	L97V(TTA->GTA)	yeeHJ	b2126	-	-	C	predicted sensory kinase in two-component system with YeeT, inner membrane protein	
SNP	2215612	T->G	K153A(GAT->GAT)	yeeV	b2130	-	-	C	predicted transporter subunit/membrane protein component of ABC superfamily	
SNP	2218755	C->T	M153A(TGC->ATC)	bgjX	b2132	-	-	T	T	beta-D-glucose glycohydrolase, periplasmic
SNP	2221388	A->C	L122A(TAT->ACT)	yeeD	b2136	-	-	C	inner membrane protein, DnaE family	
SNP	2221789	A->C	T33A(TAT->GCT)	yeeK	b2142	-	-	C	inner membrane protein, UspF family	
SNP	2237615	A->C	intergenic (43/237)	mgjB/gaIs	b2150/b2151	-	-	C	methylgalactoside transporter subunit/DNA-binding transcriptional repressor	
SNP	2250989	A->G	R167R(GGT->GGC)	nuxP	b2161	-	-	G	nucleoside pyrophosphatase	
SNP	2261795	A->C	E146A(GCA->GCA)	rfaB	b2162	-	-	G	ribonucleoside diphosphate 2	
SNP	2251694	A->C	F288C(TTC->TGC)	psuT	b2164	-	-	-	C	predicted nucleoside transporter
SNP	2252137	T->G	E152A(GAA->GCA)	psuG	b2165	-	-	-	C	pseudouridine 5-phosphate glycohydrolase
SNP	2266795	A->C	S45U(AGT->AGC)	ipdA	b2172	-	-	-	C	Predicted D-mannose oxidoreductase, NAD-dependent
SNP	2267280	T->C	S45U(AGT->AGC)	ipdA	b2172	-	-	C	Lipid A 1-diphosphate synthase; undecaprenyl pyrophosphate/lipid A 1-phosphate phosphotransferase	
SNP	2271870	T->G	I550M(ATI->ATG)	yeeH	b2178	-	-	-	C	microsome C transporter YeeH/ABE8; permease subunit; ABC family
SNP	2272328	A->C	L340A(TAT->GAT)	bor	b2182	-	-	C	biochemical pathway efflux system	
SNP	2279134	T->G	F427T(TTC->GTC)	yeeH	b2184	-	-	-	C	predicted ATP-dependent DNA or RNA helicase
SNP	2279561	A->C	E580A(GAA->GCA)	yeeH	b2186	-	-	-	C	predicted ATP-dependent DNA or RNA helicase
SNP	2280501	T->G	R224P(CAG->CCG)	yeeK	b2186	-	-	-	C	nucleoside-associated protein
SNP	2282031	T->G	V144V(GTT->GTC)	yeeH	b2188	-	-	G	G	predicted hydrolyase, inner membrane
SNP	2284021	A->C	L150P(TAT->GAT)	ccsB	b2201	-				

SNP	251483	T-C	ET3H(GAA→GAG)	xapR	b2405	C	C	C	DNA-binding transcriptional activator for xapB		
SNP	251481	A-C	1261(AAT→ACT)	xapB	b2407	-	-	-	purine nucleoside phosphorylase I		
SNP	251516	A-C	F196G(TTC→TGC)	xapA	b2407	C	C	C	purine nucleoside phosphorylase II		
SNP	252160	G-A	intergenic (158/191)	xapA/yfeN	b2407/b2408	-	A	A	purine nucleoside phosphorylase II/hypredicted outer membrane protein		
SNP	252168	C-T	CG2(DNA→GAG)	yfeT	-	-	-	-	predicted DNA-binding transcriptional regulator		
SNP	2524006	C-T	E25E(GAG→GAA)	yfeR	b2409	T	T	T	predicted DNA-binding transcriptional regulator		
SNP	2527108	A-G	V98A(GTG→GGC)	lgaI	b2411	-	G	G	DNA ligase, NAD(+)-dependent		
SNP	2528348	A-C	D211A(TTG→TGT)	cysZ	b2413	-	C	C	predicted inner membrane protein		
SNP	2531986	A-C	N233H(AAC→CAC)	ptg	b2416	-	-	-	PEP-protein phosphotransferase of PTS system (enzyme I)		
SNP	2531448	A-C	H114L(TC→CTC)	crn	b2417	-	-	-	glucose-specific enzyme IIA component of PTS		
SNP	2531700	A-C	N817A(GAC→GCA)	cysA	b2422	G	G	G	sulfate/thiosulfate transporter subunit		
SNP	2537771	T-C	T80A(ACG→GGC)	cysA	b2422	-	-	-	sulfate/thiosulfate transporter subunit		
SNP	2549646	A-C	S275(TCA→TCC)	ama	b2435	-	-	-	N-acetylmethyl-L-alanine amidase I		
SNP	2553952	T-G	E117G(GAC→GAG)	eucC	b2440	G	C	C	ethanolamine mono-lyase, small subunit (light chain)		
SNP	2559630	A-C	D99A(GAT→GCT)	yfD	b2446	-	-	-	CP2.55 prophage; predicted protein		
DEL	2560940	Δ	coding (125/378 nt)	yfR2	b2448	-	Δ	Δ	CP2.55 prophage; predicted protein		
SNP	2561075	T-G	V97G(TGC→GGC)	yfR2	b2448	-	-	-	CP2.55 prophage; predicted protein		
SNP	2563735	T-G	D334A(GAC→GCC)	eucG	b2453	G	G	G	ethanol dehydrogenase involved in ethanolamine utilization; aldehyde reductase, converts acetaldehyde to ethanol		
SNP	2570396	A-C	V65G(GTC→GGC)	eucD	b2458	-	-	-	phosphate acetyltransferase		
SNP	2573023	T-G	K30A(AA→CAA)	eucS	b2462	G	G	G	predicted carboxymethyl structural protein with predicted role in ethanol utilization		
SNP	2573620	T-C	E61G(ACA→GGA)	mseB	b2463	C	C	C	fused malic enzyme predicted oxidoreductase/predicted phosphotransferase		
SNP	2573821	A-C	F58A(TTT→TTG)	mseB	b2463	-	-	-	fused malic enzyme predicted oxidoreductase/predicted phosphotransferase		
SNP	2574776	A-C	E27G(GAA→GCA)	mseB	b2463	-	-	-	fused malic enzyme predicted oxidoreductase/predicted phosphotransferase		
SNP	2575334	A-C	V23G(GTT→GGT)	mseB	b2463	-	-	-	fused malic enzyme predicted oxidoreductase/predicted phosphotransferase		
SNP	2575953	T-G	S23Y(TTC→ACC)	talA	b2464	-	-	-	transaldolase A		
SNP	2580907	T-C	T615A(ACC→GCC)	aegA	b2468	C	C	C	fused predicted oxidoreductase: Fe5 binding subunit/NAD/FAD binding subunit		
SNP	2582838	T-C	intergenic (89/267)	aegA/narX	b2468/b2469	C	C	C	fused predicted oxidoreductase: Fe5 binding subunit/NAD/FAD binding subunit/sensory histidine kinase in two-component regulatory system with NarP (NarI)		
SNP	2583761	A-C	intergenic (141/488)	acdY/yfj	b2470/b2466	-	-	-	CP2.55 prophage; predicted protein		
SNP	2583837	T-G	intergenic (277/104)	yfRm/yfB	b4606/b2471	G	G	G	hypothetical protein/predicted reductase, function unknown, ArsC family; low abundance protein		
SNP	2596158	T-C	D276G(GAC→GGC)	dapA	b2478	C	C	C	dihydrodipicolinate synthase		
SNP	2597350	G-A	N103A(GAG→GTA)	hyb	b2482	-	-	-	hydrogenase 4, membrane subunit		
SNP	2602181	T-G	M416H(ATG→AGG)	hyfD	b2484	-	-	-	hydrogenase 4, membrane subunit		
SNP	2603666	T-C	S63P(TTC→CCC)	hyfE	b2485	C	C	C	hydrogenase 4, membrane subunit		
SNP	2606470	T-G	E117G(GAC→GAG)	hyfF	b2486	G	C	C	hydrogenase 4, membrane subunit		
SNP	2607424	A-G	T134A(ACC→GCC)	hyfH	b2488	G	G	G	hydrogenase 4, Fe-S subunit		
SNP	2609518	A-C	Q132P(ACA→CCA)	hyr	b2491	-	-	-	DNA-binding transcriptional activator, formate sensing		
SNP	2609524	G-A	Y134A(GAG→GTA)	hyr	b2491	-	-	-	DNA-binding transcriptional activator, formate sensing		
SNP	2609938	T-G	L272H(CTT→CGT)	hyr	b2491	-	-	-	DNA-binding transcriptional activator, formate sensing		
SNP	2614609	T-G	I326A(TAC→CTC)	uraA	b2497	-	-	-	G	uracil permease	
SNP	2616594	T-G	H244C(ACC→GCC)	uraA	b2497	-	-	-	G	uracil permease	
SNP	2618851	A-C	E106A(GAA→GCA)	purM	b2499	-	-	-	-	phosphoribosylaminimidazole synthetase	
DEL	2620170	Δ	intergenic (174/38)	purN/ppk	b2500/b2501	-	Δ	Δ	phosphoribosylglycylamide formyltransferase 1/polyphosphate kinase, component of RNA degradingosome		
DEL	2636377	Δ	coding (213/611 nt)	yfM	b2513	-	Δ	Δ	conserved protein; fliP/9070 family		
SNP	2648602	C-T	D30M(GAT→AAT)	yfM	b2520	T	T	T	conserved protein		
SNP	2649382	T-G	N44H(ACC→CAC)	yfM	b2520	G	G	G	conserved protein		
SNP	2649889	A-G	R184C(ACC→GCC)	ssa	b2521	-	-	-	3-mercaptopyruvate sulfurtransferase		
SNP	2650280	G-A	R188H(CGC→CAC)	ssa	b2521	-	-	-	3-mercaptopyruvate sulfurtransferase		
SNP	2651952	A-G	Y206T(ATT→GTT)	hcrT	b2522	-	Δ	Δ	glutathione-like enzyme; sulfur transfer from acetyl-CoA synthetase		
SNP	2655486	T-G	intergenic (133/131)	iscR/hmj	b2531/b2532	C	C	C	DNA-binding transcriptional repressor/rRNA mC32/mL32 methyltransferase, SAM-dependent		
SNP	2660550	T-C	intergenic (3/116)	trmJ/subJ	b2532/b2533	C	C	C	rRNA mC32/mL32 methyltransferase, SAM-dependent/inositol monophosphatase		
DEL	2664800	Δ	coding (271/140 nt)	hcr	b2536	-	-	-	predicted 3-glyoxylate transporter		
SNP	2673775	A-G	V92A(GTG→GGC)	yfD	b2546	G	G	G	predicted sugar transporter subunit; membrane component of ABC superfamily		
SNP	2681724	A-C	A338A(GTC→GGC)	glaY	b2551	-	-	-	C	serine hydroxymethyltransferase	
SNP	2682517	T-C	intergenic (181/142)	glaY/nmp	b2551/b2552	-	-	-	C	serine hydroxymethyltransferase/fused nitric oxide dioxygenase/dihydropyridine reductase 2	
SNP	2686660	A-C	L248H(TGC→GGC)	yfG	b2555	-	-	-	-	conserved protein	
SNP	2687787	T-C	E397E(GAA→GAG)	gfrK	b2556	-	-	-	-	C	Sensor protein kinase regulating glrK rRNA in two-component system with response regulator GRR
SNP	2688707	T-G	intergenic (145/113)	gfrK/purL	b2556/b2557	-	-	-	-	C	Sensor protein kinase regulating glrK rRNA in two-component system with response regulator GRR/phosphoribosylformylglycinamide synthetase
SNP	2692434	A-C	Y112D(TAC→GAC)	purL	b2557	-	-	-	-	C	phosphoribosylformylglycinamide synthetase
SNP	2692713	T-G	intergenic (146/128)	yfH/ashB	b2562/b4687	-	-	-	-	G	predicted 4Fe-4S cluster-containing protein/outer membrane protein
SNP	2703390	T-G	E120A(GAG→GTA)	lgaA	b2569	-	-	-	-	C	beta-translucanase/flagellin factor/H4, CTXase
SNP	2705362	A-C	L206V(ATT→GTG)	rseB	b2571	-	-	-	-	C	anti-sigma E factor, binds RseA
SNP	2705731	A-G	V93A(GTG→GGC)	rseB	b2571	-	-	-	-	G	anti-sigma E factor, binds RseA
SNP	2708908	T-G	L419A(TTC→GTC)	naeB	b2574	-	-	-	-	C	quinolinate synthase 1, separate oxidase (B protein) subunit
SNP	2712108	T-C	Y146G(TAT→TGT)	yfE	b2577	C	C	C	predicted DNA-binding transcriptional regulator		
SNP	2717705	G-A	intergenic (137/273)	yfU/yng	b2579/b2580	A	A	A	A	autonomous glycol radical cofactor/uracil DNA glycosylase	
DEL	2719041	Δ	coding (71/203 nt)	yfF	b2581	-	-	-	-	Δ	predicted methyltransferase
SNP	2715822	T-G	intergenic (170/137)	yfI/trxC	b2581/b2582	-	-	-	-	G	predicted methyltransferase/thioredoxin 2
SNP	2718105	C-T	S30L(CTA→TTA)	yfQ	b2584	T	T	T	T	T	inhibiting acetyltransferase for acetyl-CoA synthetase
SNP	2718198	A-T	E184A(TGC→GGC)	yfQ	b2584	-	-	-	-	Δ	inhibiting acetyltransferase for acetyl-CoA synthetase
SNP	2734184	T-G	intergenic (177/194)	bamD/raA	b2595/b2597	G	G	G	G	lipoprotein required for OME biosynthesis, in BamABCD complex/cold shock protein associated with 30S ribosomal subunit	
SNP	2734310	A-C	intergenic (120/148)	bamD/raA	b2595/b2597	C	C	C	C	lipoprotein required for OME biosynthesis, in BamABCD complex/cold shock protein associated with 30S ribosomal subunit	
SNP	2734362	T-G	H238T(CAT→TAT)	tyrA	b2600	A	A	A	A	MOB	fused chorismate mutase 1/zephrinate dehydrogenase
MOB	2736031	Δ	coding (208/77 nt)	yfL	b2602	-	-	-	-	Δ	lipoprotein
SNP	2736631	A-C	N9H(AAT→CAT)	ripN	b2604	C	C	C	C	C	probable inner membrane diguanylate cyclase
SNP	2741372	T-G	K80Q(AAA→CAA)	rpsP	b2609	-	-	-	-	G	30S ribosomal subunit protein S16
SNP	2741449	A-G	intergenic (114/100)	ffb	b2610	-	-	-	-	C	Signal Recognition Particle (SRP) component with 4.5S RNA (fts)
SNP	2747156	A-T	I372H(TAC→TTC)	yfT	b4461	T	T	T	T	T	inner membrane protein, LPP0503 family
SNP	2751219	T-C	intergenic (163/164)	smfB/mntA	b2620/b2622	-	-	-	-	A	trans-translation protein/CP4.5 prophage; integrase
SNP	2751472	G-A	E188G(GGG→GGG)	yfK	b2627	-	-	-	-	A	CP4.5 prophage; conserved protein
SNP	2758791	T-G	E658D(GAA→GAG)	yfK	b2627	-	-	-	-	A	CP4.5 prophage; conserved protein
SNP	2760012	T-C	CG215G(GGA→GGG)	yfK	b2627	-	-	-	-	C	CP4.5 prophage; conserved protein
INS	2763011	-C	intergenic (131/131)	yfM/mntA	b2629/b2630	-	-	-	-	-	CP4.5 prophage; predicted protein/CP4.5 prophage; RNase LS
SNP	2764735	T-C	intergenic (156/199)	ribJ/yfP	b2631/b2632	C	C	C	C	CP4.5 prophage; predicted protein/CP4.5 prophage; predicted GTP-binding protein	
SNP	2767825	T-C	F105Y(TTC→CTC)	yarK	b2635	C	C	C	C	CP4.5 prophage; predicted inner membrane protein	
SNP	2772154	A-C	E181A(GAC→GCA)	yfW	b2642	C	C	C	C	CP4.5 prophage; predicted inner membrane protein	
SNP	2774538	A-C	E67A(GAA→GCA)	yfZ	b2645	C	C	C	C	CP4.5 prophage; antitoxin of the YnfP-YnfN toxin-antitoxin system	
SNP	2775602	T-C	E1450G(GAG→GGG)	yfA	b2647	-	-	-	-	C	adhesin-like autotransporter
SNP	2776150	C-T	intergenic (106/77 nt)	yfA	b2647	-	-	-	-	T	adhesin-like autotransporter
SNP	2781140	T-C	pseudogene (1096/1378 nt)	ypjC	b2650	-	-	-	-	-	pseudogene
SNP	2782113	A-G	pseudogene (1237/1374 nt)	ypjC	b2650	-	-	-	-	G	pseudogene
SNP	2786050	A-G	intergenic (117/118 nt)	yedQ/cdb	b4462/b2659	-	-	-	-	G	predicted protein; putative enzyme/Carbon starvation induced gene
SNP	2787500	A-C	K333T(AAA→ACA)	gabD	b2661	C	C	C	C	C	succinate semialdehyde dehydrogenase I, NADP-dependent
INS	2791387	-A	intergenic (146/160)	gabT/gabP	b2662/b2663	-	-	-	-	A	4-aminobutyrate aminotransferase, PEP-dependent/gamma-aminobutyrate transporter
DEL	2793580	C-T	E188G(GGG→GGC)	gabF	b2663	T	T	T	T	T	gamma-aminobutyrate transporter
SNP	2793648	G-A	D24D(AGC→GAT)	stpA	b2669	-	-	-	-	Δ	DNA binding protein, nucleoid-associated
DEL	2797835	Δ	coding (147/140/141 nt)	nrdE	b2674	-	-	-	-	Δ	Flavodoxin required for N-fixid cluster assembly
SNP	2800564	-T	intergenic (195/210 nt)	nrdE	b2675	-	-	-	-	-	Flavodoxin required for N-fixid cluster assembly
SNP	2800871	C-T	T89H(CTC→ATT)	nrdF	b2676	T	T	T	T	T	ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like protein
SNP	2800874	T-C	V50N(GAT→AGC)	nrdF	b2676	C	C	C	C	C	ribonucleoside-diphosphate reductase 2, beta subunit, ferritin-like protein
SNP	2803831	G-A	V200N(CTC→ATC)	prwW	b2678	A	A	A	A	A	glycine betaine transporter subunit
SNP	2805636	T-G	pseudogene (97/1178 nt)	ygaY	b2681	-	-	-	-	-	predicted transporter (pseudogene)/putative transporter; Not classified; putative transport protein
SNP	2805944	A-C	intergenic (105/178 nt)	ygaY	b2681	-	-	-	-	G	predicted transporter (lipoprotein)/putative transporter; Not classified; putative transport protein
SNP	2808822	G-A	AS8T(GCA→ACA)	errA	b2685	-	-	-	-	A	multidrug efflux system
SNP	2809301	T-C	R237P(TGC→ATC)	errA	b2685	-	-	-	-	C	multidrug efflux system
SNP	2809398	T-C	A33A(GCC→GGC)	errB	b2686	-	-	-	-	G	multidrug efflux system
SNP	2820868	A-G	S42S(TCT→TCC)	recA	b2699	G	G	G	G	G	DNA strand exchange and recombination protein with protease and nuclease activity
SNP	2821688	A-C	intergenic (118/127)	ygdD/mfb	b2700/b2701	-	-	-	-	C	conserved protein/membrane-bound lytic murein transglycosylase B
SNP	2821807	A-G	intergenic (125/294)	mfb	b2701	-	-	-	-	-	membrane-bound lytic murein transglycosylase B
SNP	2822501	T-G	P100P(ACA→CCC)	mfb	b2701	-	-	-	-	G	membrane-bound lytic murein transglycosylase B
SNP	2822404	A-C	Q50P(CAG→CCG)	srfA	b2702	-	-	-	-	C	glutathionyl-specific enzyme IIC component of PTS
SNP	2824379	T-G	D22A(TTC→GGC)	srfE	b2703	-	-	-	-	G	glutathionyl-specific enzyme IIB component of PTS
INS	2828916	-T	coding (598/1515 nt)	norR	b2709	-	-	-	-	-	Anaerobic nitric oxide reductase DNA-binding transcriptional activator
SNP	2830696	A-C	Q73H(ACA→CAC)	ascF	b2715	C	C	C	C	C	fused cellobiose/arbutin/salicyl-specific PTS enzymes: IIB component/C component
SNP	2831111	A-C	intergenic (106/77 nt)	ascF	b2715	-	-	-	-	-	fused cellobiose/arbutin/salicyl-specific PTS enzymes: IIB component/C component
SNP	2841829	A-C	C50S(GTC→GGC)	hyfF	b2720	-	-	-	-	-	formate hydroxylase complex inner-sulfur protein
SNP	2842483	G-A	S42S(TCT→TCC)	hyeE	b2721	-	-	-	-	A	hydrogenase 3, large subunit
SNP	2846205	T-G	E137A(GTC→GGC)	hyeB	b2724	-	-	-	-	A	hydrogenase 3, S subunit
SNP	2847230	G-A	G144*(CAA→TAA)	hyaA	b2725	A	A	A	A	A	regulator of the transcriptional regulator FHA
INS	2852408	-T	coding (84/2079 nt)	rhaA	b2731	-	-	-	-	-	DNA-binding transcriptional activator
SNP	2853150	T-C	R65A(GAT→GCA)	rhaA	b2731	-	-	-	-	-	DNA-binding transcriptional activator
SNP	2854737	A-C	D100Q(GAC→GGC)	ppbB	b2734	-	-	-	-	G	serine/threonine-specific protein phosphatase 2
SNP	2858626	T-G	L178H(CTC→GCA)	trbD	b2736	-	-	-	-	-	predicted dehydrogenase, with NAD(P)+ binding Rossmann fold domain
SNP	2862739	C-T	intergenic (149/14)	glnA/ygdP	b2741/b2742	-	-	-	-	-	RNA polymerase, sigma 5 (sigma 38) factor/tyrosine Amino acid N-acetyltransferase
SNP	2865559	T-G	D142A(GAT→GCA)	yruJ	b2745	-	-	-	-	-	r

SNP	3109393	T-C	D1380(GAC-GGG)	ygdH	b2968	-	C	C	predicted secretion pathway M type protein, membrane anchored
DEL	3109393	del	coding (648/660 nt)	ygdH	b4466	-	-	del	predicted inner membrane lipoprotein
SNP	3113101	T-G	K231Q(AAA-CAA)	yjHJ	b4466	G	G	G	predicted inner membrane lipoprotein
SNP	3113148	A-C	L331I(TTA-GTA)	glfF	b4467	-	-	-	glyoxylate oxidase 4Fe-4S iron-sulfur cluster subunit
SNP	3120099	T-G	L331I(TTA-GTA)	glfE	b4468	-	-	-	glyoxylate oxidase FAD binding subunit
SNP	3121566	A-C	L379V(TTA-GTA)	glcD	b2979	C	C	C	glyoxylate oxidase subunit, FAD-linked
SNP	3122161	T-C	D176I(GAC-GGG)	glcD	b2979	C	C	C	glyoxylate oxidase subunit, FAD-linked
SNP	3122822	T-C	intergenic (1327/1258)	glcE	b2982/b2980	C	C	C	glyoxylate oxidase subunit, FAD-linked/DNA-binding transcriptional dual regulator, glycylate-binding
SNP	3123969	T-G	intergenic (456/511)	inhA/ygdH	b2982/b2983	G	G	G	ISS transposase and trans-activator/predicted inner membrane protein
SNP	3130248	A-C	F208I(TTC-TGC)	piB	b2987	C	C	C	phosphate transporter
SNP	3131618	T-C	L684K(GAC-TGC)	hyrC	b2994	-	-	-	hydrogenase 2, large subunit
SNP	3137339	C-T	Q110Q(CAG-CAA)	hyrC	b2994	T	T	T	hydrogenase 2, large subunit
SNP	3139053	C-T	G2170(GCC-GAC)	hyrA	b2996	-	-	-	hydrogenase 2 4Fe-4S ferredoxin type component
SNP	3144163	T-C	intergenic (1341/170)	ygdH/ygdA	b3002/b3003	C	C	C	predicted inner membrane protein, UPPF14 family/predicted oxidoreductase
INS	3151580	+A	coding (278/828 nt)	dkgA	b3012	-	+A	+A	2,5-diketo-D-glucuronate reductase A
SNP	3151953	T-G	S62N(GAC-TGC)	yjQ	b4469	G	G	G	conserved protein
SNP	3151917	A-G	S35T(TTC)	yjQ	b4469	G	G	G	conserved protein
SNP	3151972	T-G	K47N(AAA-AGA)	parC	b3019	G	G	G	DNA topoisomerase IV, subunit A
DEL	3171283	del	penicillinase (407/408/631 nt)	nuoF	b3034	-	-	del	ADP-ribose pyrophosphatase
SNP	3171549	A-G	E162I(GAA-AGA)	yjB	b3037	G	G	G	conserved protein, UPPF463 family
SNP	3175601	A-G	E167I(GAA-AGA)	yjC	b3038	G	G	G	Glutathionylperoxidase synthase homolog
SNP	3182999	T-C	penicillinase (2257/2803 nt)	yjB	b3046	-	-	-	penicillinase; outer membrane usher homology;putative membrane; Not classified, putative membrane protein
SNP	3191212	T-G	H737I(TAT-TCT)	glE	b3053	-	-	-	fused deoxyribose/transferase/adenyltransferase for glutamine synthetase
SNP	3191449	A-C	M66H(ATG-AGG)	yjF	b3054	C	C	C	predicted adenylate cyclase
SNP	3191487	A-G	F120L(TTC-TCT)	baeA	b3057	G	G	G	undecylsuccinyl pyrophosphate phosphatase
SNP	3213986	A-G	H92V(ATC-GTC)	ebgA	b3076	G	G	G	cryptic beta-D-galactosidase, alpha subunit
SNP	3222766	T-G	W96G(GC-GGG)	yjJ	b3079	G	G	G	conserved protein
SNP	3223936	A-G	V207I(GTC-TGC)	rimD	b3084	G	G	G	23S rRNA-mG1835 methyltransferase, SAM dependent
SNP	3230227	A-G	V110N(GTG-GGG)	rimG	b3084	G	G	G	23S rRNA-mG1835 methyltransferase, SAM dependent
SNP	3231161	A-C	intergenic (181/59)	ygpY/yjQ	b3085/b3086	-	-	-	predicted metal dependent hydrolase/conserved protein, SaaA family, DUF218 superfamily
SNP	3232284	A-G	Y124I(TAT-AGG)	mitD	b3088/b3089	G	G	G	inner membrane protein, part of ferredoxin/sodium/cerium/brethione symporter
INS	3235657	+G	coding (1034/1245 nt)	sstI	b3089	-	+G	+G	sodium/sulfur/brethione symporter
SNP	3239868	T-G	K152Q(AAA-CAA)	uxcX	b3092	-	-	-	urate ionomerase
SNP	3239902	T-G	intergenic (1271/80)	uxcX/uxcT	b3092/b3093	G	G	G	urate ionomerase/uracinate dehydrogenase transporter
SNP	3240480	C-T	H233I(CAT-TAT)	exuT	b3093	T	T	T	neuramate transporter
SNP	3242437	T-G	intergenic (129/161)	exuR/yjgA	b3094/b3095	G	G	G	DNA-binding transcriptional repressor/required, with yjgH, for membrane integrity; inner membrane protein
SNP	3248708	G-A	L162I(TAT-TCT)	yjE	b3105	A	A	A	N-acetylglucosamine-specific enzyme IIc component of PFS
SNP	3250447	A-C	D295I(GAT-GAG)	yjAM	b4470	C	C	C	conserved protein
SNP	3252618	T-C	S25G(GAG-AGG)	yjAD	b3110	C	C	C	predicted transporter
SNP	3252704	A-G	intergenic (414/131)	tsfC/tdcR	b4471/b3113	G	G	G	L-serine dehydratase/transcriptional regulator
SNP	3260526	G-A	G61G(GCC-GGT)	tdcB	b3117	A	A	A	catabolic threonine dehydratase, PLP-dependent
SNP	3261351	T-G	E132A(GAA-AGA)	tdcA	b3118	-	-	-	DNA-binding transcriptional activator
SNP	3261513	A-G	E140K(AAG-AGC)	yjAC	b3121	-	-	-	predicted protein
SNP	3273798	G-A	G63G(GCC-AGC)	kbzA	b3132	A	A	A	tagatase 6-phosphate aldolase 1, kbzA subunit
SNP	3275409	A-G	penicillinase (89/402 nt)	agwV	b3134	-	-	-	N-acetylglucosamine-specific enzyme IIc component of PFS, fragment (pseudogene)/enzyme; Central intermediary metabolism: Amino sugars; PFS system N: acetylglucosamine-specific; IC component 2
INS	3279140	+T	coding (1012/1245 nt)	mir	b3141	+C	+C	+C	ribonuclease G
SNP	3284888	A-G	N332I(AAC-AGC)	yjAJ	b3144	G	G	G	predicted outer membrane protein
SNP	3285056	A-G	L162I(TAT-TCT)	yjB	b3147	G	G	G	conserved protein
SNP	3285808	G-A	T243I(ACC-AACA)	lpoA	b3147	A	A	A	conserved protein
SNP	3292049	A-C	D657I(GAT-TGC)	lpoA	b3147	-	-	-	conserved protein
SNP	3292041	A-C	L162I(TAT-TCT)	yjB	b3147	C	C	C	conserved protein
SNP	3296484	A-C	Y107I(TAT-TCT)	yjBU	b3158	-	-	-	predicted nucleotide diphosphate-sugar epimerase
SNP	3296797	C-T	R211I(GCC-TGC)	yjBU	b3158	-	-	-	predicted peptidase (collagenase-like)
INS	3299466	+G	coding (622/866 nt)	mir	b3161	+C	+C	+C	ribonuclease G
SNP	3306409	A-C	intergenic (454/104)	rpsD/truB	b3165/b3166	C	C	C	30S ribosomal subunit protein S15/rRNA U55 pseudouridine synthase
SNP	3311826	A-C	V127I(GTT-GTG)	nuaA	b3169	-	-	-	transcription termination/antitermination L factor
SNP	3312112	T-G	intergenic (151/205)	metV/yjgG	b3171/b3172	G	G	G	N-6-methyllysine/lysine/lysine synthase
SNP	3327245	C-T	K376G(AAG-AAA)	yjBE	b3184	T	T	T	predicted inner membrane permease
INS	3327354	+C	coding (622/866 nt)	yjBE	b3184	+C	+C	+C	predicted inner membrane permease
SNP	3334004	T-G	intergenic (126/88)	npr/yjBL	b3206/b3207	G	G	G	ADP-ribose transferase/DNA ligase III asymmetry, periplasmic binding protein
SNP	3334136	A-G	T69A(GCC-GCC)	yjDL	b3207	G	G	G	phosphohistidinol-protein-hexose phosphotransferase component of N-regulated PFS system (NprI)/predicted protein
SNP	3334365	A-G	intergenic (206/264)	elbC/yjFB	b3210/b3210	G	G	G	ADP-ribose transferase
SNP	3347961	A-C	I257I(AAC-AGC)	yjCC	b3211	-	-	-	predicted Fe-S oxidoreductase
SNP	3354764	T-G	intergenic (146/28)	gfr/yjCA	b3216/b3215	-	-	-	periplasmic protein/predicted periplasmic chaperone protein
SNP	3361468	T-C	L321I(GAT-TGC)	yjAC	b3220	-	-	-	conserved protein
SNP	3366075	A-G	Y894I(TAT-CAAT)	nanT	b3224	G	G	G	salicylic acid transporter
SNP	3368703	T-G	E136A(GAA-AGA)	nanR	b3226	-	-	-	DNA-binding transcriptional repressor of the nan operon, induced by salicylic acid
SNP	3370841	T-C	K324I(GAT-TGC)	dczA	b3227	C	C	C	predicted transporter
SNP	3372027	A-G	V25A(TCC-GCC)	ssaA	b3229	G	G	G	stringent starvation protein A
INS	3373939	+C	coding (738/1128 nt)	yjHM	b3232	+C	+C	+C	conserved protein with nucleoside triphosphate hydrolase domain
SNP	3374164	T-G	L321I(GAT-TGC)	yjAC	b3232	-	-	-	conserved protein with nucleoside triphosphate hydrolase domain
SNP	3377881	A-C	V334I(GTA-GTC)	degS	b3235	C	C	C	serine endoprotease, periplasmic
SNP	3381338	A-G	intergenic (151/205)	aaeB	b3240	C	C	C	p-hydroxybenzoic acid efflux system component
SNP	3381585	A-C	N428I(AAT-AAAG)	aaeB	b3240	-	-	-	p-hydroxybenzoic acid efflux system component
SNP	3382653	G-A	I72I(TCC-TAT)	aaeB	b3240	A	A	A	p-hydroxybenzoic acid efflux system component
SNP	3382854	A-G	L162I(TAT-TCT)	yjB	b3242	-	-	-	membrane protein, efflux system
SNP	3384290	T-G	S31A(TCC-GGC)	yjER	b3243	-	-	-	transcriptional regulator for aaexA operon
SNP	3389386	A-G	L469V(TTC-TGC)	aaeP	b4472	-	-	-	conserved membrane protein, predicted transporter
SNP	3392139	C-T	G113G(GCC-AGC)	rrb	b3247	T	T	T	ribonuclease G
SNP	3394215	G-A	G148I(GCC-GGC)	mreC	b3250	A	A	A	cell wall structural complex MreBCD transmembrane component MreC
SNP	3395576	G-A	G64G(GCC-TGC)	mreB	b3251	-	-	-	cell wall structural complex MreBCD, actin-like component MreB
SNP	3396971	A-G	L59I(TAT-AGG)	carD	b3252	-	-	-	trypsin-like factor for the utilization of DNA as a carbon source; fibroblast assembly protein homolog
SNP	3398286	T-G	Y41I(TAT-AGG)	yjDH	b3253	-	-	-	predicted oxidoreductase, Zn-dependent and NAD(P) <sup>+</sup> binding
SNP	3410172	T-G	N54I(AAC-AGC)	achF	b3266	-	-	-	multidrug efflux system protein
SNP	3413036	A-G	intergenic (126/164)	acdA/yjvH	b3266/b3267	G	G	G	multidrug efflux system protein/predicted outer membrane protein
SNP	3424146	T-G	D77E(GAT-GAG)	yjDA	b3279	-	-	-	conserved protein
SNP	3424518	G-A	D340I(GAC-AGT)	yjBB	b3280	A	A	A	conserved protein
SNP	3431613	A-C	Y190I(TAT-TCT)	tSA	b3290	C	C	C	NAD <sup>+</sup> -binding component of Trk potassium transporter
SNP	3439597	T-G	I105I(ATC-TCT)	rpsE	b3303	G	G	G	30S ribosomal subunit protein S6
SNP	3440574	A-C	F83V(TTC-TGC)	rpfF	b3305	-	-	-	50S ribosomal subunit protein L6
SNP	3441750	T-G	K340Q(AAG-ACA)	rpfP	b3313	-	-	-	50S ribosomal subunit protein L16
SNP	3443119	T-G	E82A(GAA-AGA)	rpsC	b3314	-	-	-	30S ribosomal subunit protein S3
SNP	3445353	T-C	R182N(AAG-AGG)	gspA	b3323	C	C	C	general secretory pathway component, cryptic
SNP	3452854	T-G	Y82E(GAT-TGC)	gspD	b3325	-	-	-	general secretory pathway component, cryptic
SNP	3454848	T-G	L182R(TTC-TGC)	gspK	b3332	-	-	-	general secretory pathway component, cryptic
SNP	3468689	T-G	intergenic (486/491)	rpsM	b3341/b3342	G	G	G	30S ribosomal subunit protein S17/30S ribosomal subunit protein S12
INS	3471121	+G	coding (131/166)	yjvD/yjgA	b3346/b3347	+A	+A	+A	conserved protein/Hsp70-type peptidyl-prolyl-cis-trans isomerase (rotamase)
SNP	3474149	A-C	L380R(TTA-AGA)	kefB	b3350	-	-	-	potassium/proton antiporter
SNP	3477182	A-G	H495G(GAC-AGG)	yjHE	b3352	G	G	G	fused predicted transporter-subunits of ABC superfamily: ATP-binding components
SNP	3479173	T-C	Q471I(TTC-TCT)	prfB	b3355	C	C	C	predicted phosphotransferase
SNP	3488333	T-G	L162I(TAT-TCT)	tgaA	b3364	-	-	-	predicted transporter
SNP	3490228	T-G	intergenic (131/166)	nicC	b3366	-	-	-	nucleic acid transporter
SNP	3491530	T-C	G285G(GGT-GGC)	cydG	b3368	-	-	-	fused siroheme synthase L3-dimethylporphyrinogen III dehydrogenase and siroheme ferrochelatase/porphyrinogen methyltransferase
SNP	3491929	A-C	I214I(ATC-TCT)	fiaA	b3370	-	-	-	predicted fructosyltransferase protein
SNP	3501214	A-G	G302I(GAT-TGC)	yjHT	b3377	-	-	-	predicted inner membrane protein
SNP	3501443	T-C	T351(AAC-GCC)	yjHW	b3380	C	C	C	predicted mutase
INS	3508568	+T	coding (502/739 nt)	gph	b3385	+T	+T	+T	phosphoglycolate phosphatase
SNP	3509291	T-G	L150I(TCC-AGC)	rpe	b3386	-	-	-	D-ribulose 5-phosphate 3-epimerase
SNP	3511163	T-G	E275A(GAG-GCC)	damX	b3388	-	-	-	cell division protein that binds to the septal ring
SNP	3511892	A-C	intergenic (148/253)	arxK/hofQ	b3390/b3391	-	-	-	shikimate kinase (lysozyme required for the utilization of DNA as a carbon source; fibroblast transporter homolog)
SNP	3514445	G-A	L59I(TAT-AGG)	carD	b3394	-	-	-	trypsin-like factor for the utilization of DNA as a carbon source; fibroblast assembly protein homolog
SNP	3518251	A-C	Y242I(TAT-AGG)	arxK	b3396	-	-	-	fused penicillin-binding protein 1a: murein transglycosylase/murein transpeptidase
SNP	3527886	A-C	D131A(GAC-TGC)	yjFG	b3399	C	C	C	GMPT/IMP nucleosidase
SNP	3529056	A-G	K137I(AAC-AGC)	hnr	b4000	-	-	-	ribosome-associated heat shock protein Hsp15
SNP	3538927	A-C	L200V(TTG-GTG)	bioH	b3412	-	-	-	pimelyl-ACP carboxylesterase
SNP	3542440	T-G	F40I(TTC-TGC)	gntI	b3415	G	G	G	glucanate transporter, high-affinity GNT I system
DEL	3544567	del	coding (284/288 nt)	madA	b3416	-	-	del	alpha-1,4-glucanase (amyloamylase)
SNP	3545251	C-T	A63T(GAA-ACA)	malP	b3417	T	T	T	maltoedextrin phosphorylase

SNP	3747299	T→G	I210(ATC→AGC)	yjru	b3585	-	G	G	predicted DNA binding transcriptional regulator
SNP	3748037	T→G	I186(AAC→AAC)	yjue	b3586	-	G	G	membrane fusion protein (MFP) component of efflux pump, signal anchor
SNP	3750715	T→G	E159(AAG→GCA)	aldB	b3588	G	G	G	aldehyde dehydrogenase 8
SNP	3751021	G→A	A571(GCG→GTG)	aldB	b3588	A	A	A	aldehyde dehydrogenase 8
SNP	3753880	G→A	R175(GCC→GCT)	sea	b3591	A	A	A	homocysteine synthase
SNP	3756832	A→G	intergenic (-198/-30)	yifB/rhA	b3592/b3593	-	-	-	glutathione S-transferase homolog/rhA element core protein RchA
SNP	3756939	G→A	V261(GTG→GTA)	rhaA	b3593	-	-	A	rha element core protein RhaA
SNP	3759462	C→T	R376(GCC→GCT)	rhaA	b3593	-	-	T	rha element core protein RhaA
SNP	3761079	A→C	K22Q(AAA→CAA)	yjba	b3594	-	-	C	Predicted lysine containing HEAT-repeat
INS	3761710	→A	coding (89/874 nt)	yjba	b3594	→A	→A	→A	predicted lysine containing HEAT-repeat
INS	3763961	T→G	pseudogene (852/868 nt)	yjba	b3594	-	-	-	pseudogene, rhk-link
DEL	3787453	Δ1bp	intergenic (-224/+51)	k21/yjbb	b3617/b3618	Δ1bp	Δ1bp	Δ1bp	glycine C-acetyltransferase/conserved protein, pfa09612 family
SNP	3789372	T→C	G236(GGT→GGC)	rhd	b3619	-	-	C	ADP-1-glycero-D-mannohexose-6-epimerase, NAD(P)-binding
SNP	3792857	T→G	intergenic (-94/67)	rfa	b3622	G	G	G	O-antigen ligase
DEL	3794503	Δ1bp	coding (372/852 nt)	rfaZ	b3624	Δ1bp	Δ1bp	Δ1bp	lipopolysaccharide core biosynthesis protein
DEL	3794939	Δ1bp	intergenic (-65/+6)	rfaZ/rfaY	b3624/b3625	Δ1bp	Δ1bp	Δ1bp	lipopolysaccharide core biosynthesis protein/lipopolysaccharide core biosynthesis protein
SNP	3797435	G→A	F101(TCT→CTT)	rfa	b3627	A	A	A	UDP-D-galactose-4-epimerase/lipopolysaccharide-alpha-1,3-D-galactosyltransferase
SNP	3803400	T→G	T61(TAT→ACG)	waaA	b3633	-	-	G	3-deoxy-D-manno-oxalulosonic acid transferase (KDO transferase)
SNP	3803439	T→C	Y108(TAT→CAT)	waaA	b3633	-	-	G	3-deoxy-D-manno-oxalulosonic acid transferase (KDO transferase)
SNP	3804104	T→C	Y06(AATC→AGCC)	waaB	b3633	C	C	C	3-deoxy-D-manno-oxalulosonic acid transferase (KDO transferase)
SNP	3806416	T→G	intergenic (-64/+153)	rpmB/yjrc	b3637/b3638	G	G	G	50S ribosomal subunit protein L28/conserved protein, LUF0758 family, rna30c
SNP	3808793	T→G	S62A(TAC→GCA)	trmH	b3651	-	-	C	rRNA mG18-2'-O-methyltransferase, SAM-dependent
SNP	3818671	A→C	E160(AAG→GCA)	yjch	b3651	-	-	G	conserved protein
SNP	3828249	T→G	M327(ATG→AAG)	yjch	b3655	-	-	G	conserved protein
SNP	3829206	A→G	G234(GGT→GGC)	yjcl	b3657	-	-	C	predicted transporter
SNP	3833075	T→G	I50(MAT→ATC)	yjcl	b3660	G	G	G	predicted inner membrane protein
INS	3834115	→C	coding (557/819 nt)	rjpa	b3661	→C	→C	→C	cytoplasmic membrane lipoprotein-28
SNP	3838311	T→C	T113(AAC→AGC)	yjef	b3664	-	-	C	Probable adenine permease
SNP	3847072	A→C	S31A(TCT→GCT)	lrvB	b3671	-	-	C	acetylacetyl synthase I, large subunit
SNP	3854112	T→G	H228(TAC→ACC)	yjik	b3679	-	-	G	predicted transporter
SNP	3854704	A→C	S31A(TCT→GCT)	yjik	b3679	-	-	C	predicted transporter
DEL	3861805	Δ12bp	coding (282-296/414 nt)	lbpA	b3687	Δ12bp	Δ12bp	Δ12bp	heat shock chaperone
SNP	3865044	A→C	R330(GAG→GAC)	chrA	b3900	C	C	C	predicted oxidoreductase with FAD/NAD(P)+ binding domain
SNP	3866323	T→C	E128(AAG→AGC)	dgpD	b4478	-	-	C	galactonate dehydrogenase
SNP	3873372	A→C	C476(GTG→GGT)	gyrB	b3699	-	-	C	DNA gyrase, subunit B
SNP	3880070	T→G	F106(TTT→TGT)	yjdc	b3705	G	G	G	membrane protein insertase
SNP	3880828	T→C	S124(TCC→GCT)	yjef	b3712	G	G	G	predicted phosphoenolpyruvate transferase, COG2091 family
SNP	3882220	T→C	I54(VATC→GTC)	bgjB	b3721	-	-	C	cryptic phospho-beta-glucosidase 8
SNP	3890979	A→C	A189(ATC→AGC)	bgjF	b3722	-	-	C	fused beta-glucuronidase-specific P15 enzyme, IIA component/IIB component/II component
SNP	3900760	T→G	K324(AAG→GAG)	bgjG	b3723	G	G	G	transcriptional antiterminal of the bgj operon
DEL	3901102	Δ1bp	coding (144/837 nt)	bgjG	b3723	Δ1bp	Δ1bp	Δ1bp	transcriptional antiterminal of the bgj operon
SNP	3905177	T→G	K342(AAG→GAG)	p05	b3728	G	G	G	periplasmic phosphatase binding protein, high-affinity
SNP	3917319	G→A	E058(GCC→GCT)	atpD	b3733	-	-	G	F1 sector of membrane-bound ATP synthase, gamma subunit
SNP	3918403	T→G	K175(AAA→CAA)	atpA	b3734	-	-	G	F1 sector of membrane-bound ATP synthase, alpha subunit
SNP	3919594	A→C	G86(AAG→AGG)	atpE	b3737	C	C	C	F0 sector of membrane-bound ATP synthase, subunit c
SNP	3917799	T→G	K175(AAA→CAA)	atpE	b3737	-	-	C	F0 sector of membrane-bound ATP synthase, subunit c
SNP	3918820	G→A	H489(TAC→ATC)	mmgM	b3741	A	A	A	5-methylmethyl-2-thiouridine modification of tRNA L34
SNP	3921391	A→C	E128(AAG→AGC)	vacJ	b3745	-	-	G	predicted vacA toxin factor containing protein
SNP	3924359	T→G	A122(AAG→AGC)	kup	b3747	-	-	G	potassium transporter
SNP	3929269	T→G	S272(TAT→GCT)	rbaA	b3749	G	G	G	fused D-ribose transporter subunits of ABC superfamily-ATP-binding domains
SNP	3932002	C→T	intergenic (-121/12)	rbaM/rbaR	b3750/b3753	-	-	G	rhamnulose/DNA-binding transcriptional repressor of ribose metabolism
SNP	3943677	T→G	H324(TAT→GCT)	yjfb	b3765	-	-	G	predicted bifunctional enzyme and transcriptional regulator
SNP	3974622	T→G	I288(ATT→ATG)	yjfk	b3795	-	-	G	predicted transporter
INS	3975574	→C	coding (17/67 nt)	hcrT	b3798	→C	→C	→C	HcrA-toxin
SNP	3978282	A→C	K216(AG→AGC)	asfB	b3800	C	C	C	predicted regulator of arylsulfatase activity
SNP	3987462	A→G	E378(AAG→GAG)	cyaA	b3806	G	G	G	adenylate cyclase
SNP	3988852	A→C	E115(GTT→GAT)	hcrG/yjrc	b3807/b4558	-	-	C	iron-dependent inhibitor of iron-sulfur cluster formation; frataxin; iron-binding and oxidizing protein/predicted lipoprotein
SNP	3994657	A→G	N665(AAC→AGC)	uvrD	b3813	G	G	G	DNA-dependent ATPase I and helicase II
SNP	4013819	A→G	N185(AAG→GCA)	tafB	b3838	-	-	G	TafA/B-C protein translocation system subunit
SNP	4015933	A→C	K195(TTA→TGA)	tafA	b3845	-	-	G	TafA/B-C protein translocation system subunit
SNP	4020661	A→C	Y539(TAT→TAG)	fabB	b3846	C	C	C	fused 3-hydroxybutyryl CoA epimerase/delta(3)-cis-delta(2)-trans-enoil-CoA isomerase/enoil-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase
SNP	4020798	A→C	C494(GTC→GGC)	fabB	b3846	-	-	C	fused 3-hydroxybutyryl CoA epimerase/delta(3)-cis-delta(2)-trans-enoil-CoA isomerase/enoil-CoA hydratase/3-hydroxyacyl-CoA dehydrogenase
SNP	4023388	A→C	E128(AAG→AGC)	fabB	b3846	-	-	C	predicted ven-Wilbraux-like factor containing protein
SNP	4032075	T→G	intergenic (-113/+137)	rfaM/rnbB	b3855/b3856	-	-	G	5S ribosomal RNA of rna operon/molybdopterin-guanine dinucleotide biosynthesis protein B
SNP	4032078	C→G	intergenic (-136/+134)	rfaM/rnbB	b3855/b3856	-	-	G	5S ribosomal RNA of rna operon/molybdopterin-guanine dinucleotide biosynthesis protein B
SNP	4034985	A→C	G239(AAG→AGC)	rfaA	b3859	A	A	A	The/For kinase implicated in Gcp stress response
SNP	4047175	T→G	K157(AAA→AAC)	glnL	b3869	G	G	G	sensory histidine kinase in two-component regulatory system with GlnG
SNP	4049160	T→G	H11(ATT→CTT)	glnA	b3870	-	-	G	glutamine synthetase
SNP	4052764	T→C	K134(AAG→AGC)	yjfp	b3877	-	-	G	alpha-glucosidase
SNP	4060515	T→G	H23P(TAT→CCT)	yjhg	b3878	-	-	G	alpha-glucosidase
SNP	4064861	A→C	H62(TTT→TGT)	yjhu	b3882	-	-	C	gamma-hydroxyglutarate dehydrogenase, NADH-dependent
SNP	4067129	A→G	E076(GCC→GCT)	yjix	b3885	-	-	G	ADP-D-glucose-1-P phosphatase, gamma subunit
SNP	4077011	T→G	K100(AAG→GAG)	fdsG	b3894	G	G	G	formate dehydrogenase-O, large subunit
SNP	4077797	A→C	E128(AAG→AGC)	fdsH	b3895	-	-	G	formate dehydrogenase-O, large subunit
SNP	4079297	A→C	E130(GAA→GAC)	yjig	b3896	C	C	C	conserved lipoprotein
SNP	4089027	C→T	intergenic (-27/15)	rhaB/rhaS	b3904/b3905	T	T	T	rhamnulose/DNA-binding transcriptional activator for rhaBAD and rhaT, r-hamnose binding
SNP	4092214	A→C	E155(ATC→GCT)	katG/yjhm	b3909/b3910	G	G	G	2-oxo-3-deoxy-glucuronate transporter/6-hydroxymethylamine resistance protein
SNP	4094417	A→C	N97(TAT→GCT)	yjlm	b3910	-	-	G	6-N-hydroxymethylamine resistance protein
SNP	4098999	A→G	T109(AAC→GCA)	fler	b3915	G	G	G	ferrous iron and zinc transporter
SNP	4099314	C→T	E155(ATC→GCT)	yjla	b3916	T	T	T	6-phosphofructokinase
SNP	4100334	T→G	G65(GGT→GGG)	slp	b3917	G	G	G	sulfate transporter subunit
SNP	4101001	A→C	K288(AAG→GCA)	yjrb	b3917	-	-	C	sulfate transporter subunit
SNP	4101822	A→C	L186(ATC→AGC)	cdh	b3918	-	-	G	CDH-diacylglycerol phosphatidylhydrolase
SNP	4105206	A→G	S191(AGT→AGC)	hru	b3924	G	G	G	ferredoxin-NADP reductase
SNP	4111928	T→G	I176(TAT→CTC)	flrJ	b3931	-	-	G	molecular chaperone and ATPase component of HslU protease
SNP	4115160	A→C	T145(GTA→GGG)	yjif	b3937	-	-	G	conserved protein, DUF839 family
SNP	4122884	A→C	G858(CAG→CCG)	metL	b3940	C	C	C	fused aspartyltransferase II, homoserine dehydrogenase II
SNP	4126417	A→C	E426(AAG→GCA)	katG	b3942	C	C	C	catalase-peroxidase III, heme b containing
SNP	4127051	A→C	Y513(TTA→TGA)	katG	b3942	-	-	C	catalase-peroxidase III, heme b containing
SNP	4133096	A→G	G144(GGT→GGC)	ptaA	b3947	-	-	G	fused predicted P15 enzymes: Hpr component/enzyme I component/enzyme IIA component
SNP	4133584	C→T	T87(AAG→AGC)	ptaA	b3947	T	T	T	fused predicted P15 enzymes: Hpr component/enzyme I component/enzyme IIA component
SNP	4142096	A→C	E170(GTC→GGC)	ppc	b3956	G	G	G	phosphoenolpyruvate carboxylase
SNP	4144876	G→A	intergenic (-472/+126)	ppc/argE	b3956/b3957	-	-	A	phosphoenolpyruvate carboxylase/acetylthiolase decarboxylase
SNP	4151277	T→G	N274(AAT→CAT)	strA	b3962	-	-	G	pyridine nucleotide transhydrogenase, soluble
SNP	4170146	A→G	E133(ATC→GCT)	rpk	b3983	-	-	G	50S ribosomal subunit protein L11
SNP	4174834	A→C	N762(AAG→CAC)	rpoB	b3987	-	-	C	RNA polymerase, beta subunit
SNP	4181776	C→T	E58(AAG→AAG)	thgE	b3991	-	-	T	thiamin biosynthesis ThgM complex subunit
SNP	4184302	A→C	E194(GTC→GGC)	thfF	b3992	C	C	C	adenylate transferase, modifies ThS C-terminus
SNP	4187235	G→A	G576(GCC→GGT)	thc	b3994	A	A	A	thiamin (pyrimidine moiety) biosynthesis protein
SNP	4189591	A→C	T180(TAT→ATC)	hcrE	b3997	-	-	G	uroporphyrinogen decarboxylase
INS	4191485	→C	intergenic (-155/-132)	hcrE/yjhpA	b3999/b4000	→C	→C	→C	conserved protein/HLA-DNA-binding transcriptional regulator, alpha subunit
SNP	4191334	A→C	I85(LAT→CTT)	zraS	b4003	G	G	G	senary histidine kinase in two-component regulatory system with ZraR
SNP	4208719	C→T	E128(AAG→AGC)	aceA	b4015	-	-	C	isocitrate lyase
SNP	4208793	A→G	T127(AAC→AGC)	aceA	b4015	G	G	G	isocitrate lyase
SNP	4211725	G→A	H23H(CAT→CAT)	arpA	b4017	A	A	A	ankyrin repeat protein
SNP	4212197	A→G	E128(AAG→AGC)	hcr	b4018	-	-	G	DNA-binding transcriptional repressor
SNP	4217666	A→C	K823Q(AAA→CAA)	metM	b4019	-	-	G	homocysteine-N5-methyltetrahydrofolate transmethyase, B12-dependent
SNP	4231360	A→G	G676(GGT→GGC)	yjie	b4021	G	G	G	D-xylulose transporter
SNP	4231747	A→C	intergenic (-221/343)	metM/flaMk	b4020/b4035	-	-	G	maltose transporter subunit/fused maltose transport subunit, ATP-binding component of ABC superfamily/regulatory protein
SNP	4241410	A→C	pseudogene (1402/1581 nt)	yjbl	b4028	C	C	C	pseudogene, pentapeptide repeat-related
SNP	4243819	A→G	H81C(CAT→GCT)	ubcC	b4039	G	G	G	chorismate-pyruvate lyase
SNP	4248144	A→C	I81(LAT→CTT)	qjgA	b4042	-	-	G	diacylglycerol kinase
SNP	4251758	A→C	H41(AAT→ATC)	yjbl	b4047	C	C	C	predicted protein
SNP	4252062	G→A	V151(GTT→ATT)	dxaA	b4049	A	A	A	rRNA-dihydrouridine synthase A
SNP	4264967	A→C	intergenic (-189/253)	yjif/yjgA	b4101/b4055	-	-	G	hypothetical protein/acid phosphatase/phosphotransferase, class B, non-specific
SNP	4264513	T→G	E222(AAG→GAG)	uvrA	b4058	-	-	G	ATPase and DNA damage recognition protein of nucleotide excision repair endonuclease UvrABC
SNP	4265066	A→C	S38A(TC→GCT)	uvrA	b4058	-	-	G	ATPase and DNA damage recognition protein of nucleotide excision repair endonuclease UvrABC
SNP	4269860	T→C	G132(GCC→GCT)	yjef	b4071	-	-	C	nucleotide reductase, formate-dependent, penta-heme cytochrome c
SNP	4284426	A→C	I520(ATG→CTT)	nrfE	b4074	-	-	C	heme lyase (NrfE/G) for insertion of heme into C52, subunit NrfE
SNP	4284605	T→G	Y870(TAC→GAC)	gfp	b4077	-	-	C	glutamate/aspartate proton symporter
INS	4287186	→C	intergenic (-1686/+56)	gfp/yjFD	b4077/b4078	-	-	C	glutamate/aspartate proton symporter/conserved protein
SNP	4288716	T→C	T633(AAC→AGC)	fdhF	b4079	C	C	C	formate dehydrogenase-H, selenium-dependent subunit
SNP	4299378	A→C	F145(TCC→TCC)	metN	b4082	-	-	C	membrane fusion protein of efflux pump
SNP	4299800	T→C	T392(AAG→GAG)	atpC	b4086	-	-	G	carbon subunit
SNP	4309087	G→A	L39F(TTC→TTC)	phnL	b4096	A	A	A	carbon phosphorus lyase complex subunit
SNP	4309541	A→C	E127(AAG→AGC)	phnB	b4097	G	G	G	carbon phosphorus lyase complex subunit
SNP	4311361	C→T	W156(TGG→TGA)	yjfn	b4102	-	-	T	predicted DNA-binding transcriptional regulator of phosphonate uptake and biodegradation
SNP	4316707	A→C	M114(AAG→AGG)	phnF	b4107	C	C	C	conserved protein
SNP	4320551	A→G	I687(TAT→ATC)	yjfm	b4109	G	G	G	multisubunit suppressor of yjhl motility mutation, function unknown; related to Dynamis GTPase
SNP	4323286	A→C	D537E(TG→GAG)	epiA	b4114	-	-	C	predicted metal dependent hydrolase
SNP	4326479	A→C	C140(GTC→GGC)	epiA	b4114	-	-	C	predicted metal dependent hydrolase

SNP	4460510	A→G	YS27(CAC→TGC)	mgfA	b4242	G	G	G	magnesium transporter
SNP	4460506	T→C	S395(ACT→AGC)	ygiJ	b4251	-	-	C	predicted transcriptional regulator
SNP	4461380	A→C	NSH(AAT→CAT)	tabA	b4252	-	-	C	biofilm modulator regulated by toxins
SNP	4466471	T→G	F102(TTT→GTT)	tabA	b4252	G	G	G	biofilm modulator regulated by toxins
SNP	4466522	C→T	intergenic (+12/-111)	tabA/ygiJ	b4252/b4253	T	T	T	biofilm modulator regulated by toxins/predicted protein
SNP	4467331	A→C	K197(QAAA→CAA)	ygiJ	b4253	C	C	C	predicted protein
SNP	4468167	T→G	F475(TTT→TTG)	ygiJ	b4253	G	G	G	predicted protein
SNP	4470236	C→T	G110(GGG→GAG)	ygiM	b4256	T	T	T	predicted acetyltransferase
INS	4471270	+T	pseudogene (262/1223 nt)	ygiN	b4257	+T	+T	+T	inner membrane protein, DUF898 family
SNP	4472728	A→G	V472A(GTT→GCT)	vais	b4258	G	G	G	valyl-tRNA synthetase
SNP	4473369	A→G	R338(GCT→GGC)	vais	b4258	G	G	G	valyl-tRNA synthetase
SNP	4475570	A→G	F64(TTC→CTC)	hoiC	b4259	G	G	G	DNA polymerase III, chi subunit
SNP	4476334	T→G	Y280(TAT→GAT)	lptF	b4261	G	G	G	lipopolysaccharide export ABC permease of the LptBFG export complex
SNP	4481872	C→T	E154(GAA→AAA)	ygiB	b4269	T	T	T	predicted alcohol dehydrogenase, Zn-dependent and NAD(P) <sup>+</sup> binding
SNP	4489280	A→C	intergenic (+135/-297)	intB/nsiC	b4271/b4272	C	C	C	pseudogene, integrase homology/S, phage, Tr; Phage-related functions and prophages; KpLE2 phage-like element; P4-like integrase/52 repressor TnpA
SNP	4489560	T→C	intergenic (+135/-17)	intB/nsiC	b4271/b4272	-	-	-	pseudogene, integrase homology/S, phage, Tr; Phage-related functions and prophages; KpLE2 phage-like element; P4-like integrase/52 repressor TnpA
SNP	4492542	A→C	R365(GAG→GAGC)	ygiF	b4277	-	-	C	KpLE2 phage-like element; predicted protein
SNP	4494004	T→G	K245(QAAA→CAA)	insG	b4278	G	G	G	IS4 transposase
SNP	4500526	T→C	pseudogene (2022/2597 nt)	insD	b4283	-	-	C	pseudogene, IS911 transposase B/S, phage, Tr; Transposon-related functions; extrachromosomal; transposon related
SNP	4500447	A→G	V334(GTG→GGG)	FecA	b4291	G	G	G	KpLE2 phage-like element; ferric citrate outer membrane transporter
SNP	4509156	A→G	F129(LTT→ACT)	fectI	b4293	-	-	G	KpLE2 phage-like element; RNA polymerase, sigma 19 factor
SNP	4511257	A→C	N23K(IAT→AAG)	yjiF	b4296	C	C	C	KpLE2 phage-like element; predicted transporter
SNP	4524212	T→G	NS91(AAC→CAC)	yjiP	b4306	-	-	G	KpLE2 phage-like element; predicted methyltransferase
SNP	4525478	A→G	intergenic (+120/-373)	yjiV/yjiZ	b4566/b4657	-	-	G	conserved protein/pseudogene, rimK paralog, C-terminal fragment
SNP	4531018	A→C	intergenic (+122/-1244)	nanC/rimB	b4511/b4512	-	-	C	N-acetylneuraminic acid outer membrane channel protein/tyrosine recombinase/inversion of on/off regulator of fimA
SNP	4541752	G→A	C271(TTC→TAC)	uxuA	b4322	A	A	A	mannonate hydrolase
INS	4548065	+T	intergenic (+440/-232)	yjiC/irad	b4325/b4326	+T	+T	+T	predicted protein/RpoS stabilizer after DNA damage, anti-RsaB factor
SNP	4555513	T→G	T149(GCA→CCA)	yjiL	b4334	G	G	G	predicted ATPase, activator of (R)-hydroxyglutaryl-CoA dehydratase
SNP	4568662	A→C	Y211(TAT→GAT)	mcrC	b4345	-	-	C	5-methylcytosine-specific restriction enzyme McrBC, subunit McrC
SNP	4569079	A→C	Y720(TAC→GAC)	mcrC	b4345	-	-	C	5-methylcytosine-specific restriction enzyme McrBC, subunit McrC
SNP	4572549	A→C	Y402(TAT→GAT)	hds	b4348	-	-	C	specificity determinant for hsdM and hsdR
SNP	4573472	T→C	Q249(CAG→CGG)	hdsM	b4349	C	C	C	DNA methyltransferase M
SNP	4573999	A→G	V356A(GTG→GGC)	hdsR	b4350	G	G	G	endonuclease R Type I restriction enzyme
SNP	4578383	G→A	G210(GGG→AGG)	mrr	b4351	A	A	A	methylated adenine and cytosine restriction protein
SNP	4582270	A→G	V105A(GTG→GGC)	yjiY	b4354	G	G	G	predicted inner membrane protein
SNP	4588884	T→G	N474H(AAC→CAC)	oppB	b4359	-	-	G	phosphoglycerol transferases I and II
INS	4597390	+G	noncoding (80/87 nt)	leuV	b4368	+G	+G	+G	tRNA-Leu
INS	4597511	+G	noncoding (80/87 nt)	leuP	b4369	+G	+G	+G	tRNA-Leu
SNP	4602463	T→G	intergenic (+154/-239)	prfC/omvY	b4376/b4376	-	-	C	peptide chain release factor RF-3/periplasmic protein
SNP	4602309	A→C	K194(QAAA→CAA)	omvY	b4376	-	-	C	periplasmic protein
SNP	4605501	A→G	E171E(GAA→GAG)	yjiV	b4378	G	G	G	predicted Dnaase
SNP	4606045	A→G	L208S(TTG→TGG)	yjiW	b4379	G	G	G	predicted pyruvate formate lyase activating enzyme
SNP	4606057	A→C	854(EAT→AGT)	yjiW	b4379	-	-	C	predicted pyruvate formate lyase activating enzyme
SNP	4606903	G→A	G489(GGC→GGT)	yjiI	b4380	A	A	A	conserved protein
SNP	4608045	A→C	S70(GAG→GGC)	deoC	b4381	-	-	C	2-deoxyribose 5-phosphate aldolase, NAD(P) <sup>+</sup> linked
SNP	4609744	A→C	D28A(GAG→GGC)	deoA	b4382	C	C	C	thymidine phosphorylase
SNP	4611163	A→C	Y86S(TAC→TCC)	deoB	b4383	-	-	C	phosphopentomutase
SNP	4611935	C→T	I343(ATC→ATT)	deoB	b4383	T	T	T	phosphopentomutase
SNP	4624699	A→C	G117G(GGT→GGG)	yjiX	b4394	-	-	C	inosine/kanthosine triphosphatase
SNP	4629068	A→G	T357A(ACC→GCC)	creC	b4399	G	G	G	sensory histidine kinase in two-component regulatory system with CreB or PhoB, regulator of the CreBC regulon
SNP	4632851	A→G	G202(QCA→CAG)	yjiD	b4403	G	G	G	predicted tRNA methyltransferase