

Table S2. Mutational spectrum of *Escherichia coli* evolving populations under genetic drift.

kind	position	mutation	annotation	gene	locus	description
DEL	330	330bp	intergenic (-) hcr	hcrA	0002/b0002	hcr operon leader peptide/fused aspartokinase I and homoserine dehydrogenase I
SNP	22796 G_A	G1365(GGT_1he5	G1365(GGT_1he5	00026	00026	isoacyl tRNA synthetase
SNP	33671 G_A	G952(GDGC_carB	G952(GDGC_carB	00033	00033	carbamoyl phosphate synthase large subunit
DEL	3412	13bp	intergenic (-) carK/carI	carK/carI	00033/b0033	carbamoyl phosphate synthase large subunit/DNA-binding transcriptional activator
SNP	41251 A_G	H277(HCAT_caiT	H277(HCAT_caiT	00040	00040	predicted transporter
SNP	47130 A_G	M442(VATG_yaaU	M442(VATG_yaaU	00045	00045	predicted transporter
SNP	49456 G_G	M633(AAC_1heC	M633(AAC_1heC	00047	00047	potassium proton antiporter
SNP	5181 A_G	T199(TGCA_sdhB	T199(TGCA_sdhB	00051	00051	IES-RNA dimethylallyltransferase, SAM-dependent
SNP	54597 C_T	V361(GGT_AT_sua	V361(GGT_AT_sua	00053	00053	peptidyl-prolyl cis-trans isomerase (PPIase)
SNP	56877 T_T	G782(GGT_C1pD	G782(GGT_C1pD	00054	00054	LPS assembly OM complex LptDE, beta-barrel component
SNP	60621 G_A	R179(GGT_1shP	R179(GGT_1shP	00055	00055	fused thiamin transporter subunits of ABC superfamily; membrane components
SNP	69622 C_T	L681(CTG_CT1hP	L681(CTG_CT1hP	00067	00067	fused thiamin transporter subunits of ABC superfamily; membrane components
SNP	70218 A_G	L2351(TTG_C1hB	L2351(TTG_C1hB	00068	00068	thiamin transporter subunit
SNP	97061 C_C	G465(GGT_murC	G465(GGT_murC	00091	00091	UDP-N-acetylmuramate-L-alanine ligase
SNP	115546 A_G	Y208(TAT_TampE	Y208(TAT_TampE	00111	00111	predicted inner membrane protein
SNP	121896 G_A	A1871(GCT_aceF	A1871(GCT_aceF	00115	00115	pyruvate dehydrogenase, dihydrolipoyltransacylase component E2
SNP	124735 A_G	D394(GAC_lpd	D394(GAC_lpd	00116	00116	liponamide dehydrogenase, E3 component is part of three enzyme complexes
SNP	129203 A_G	F700(GAA_sdhB	F700(GAA_sdhB	00118	00118	bifunctional aconitate hydratase 2/2-methylsuccinate dehydratase
SNP	129595 G_A	AB311(GCG_sdhB	AB311(GCG_sdhB	00118	00118	bifunctional aconitate hydratase 2/2-methylsuccinate dehydratase
SNP	134429 T_T	intergenic (-) cueO/gcd	cueO/gcd	00123/b0124	00123/b0124	multicopper oxidase (laccase)/glucose dehydrogenase
SNP	135262 C_T	S338(WGC_1he	S338(WGC_1he	00124	00124	glucose dehydrogenase
SNP	144358 C_T	V9V(GTG_G1panC	V9V(GTG_G1panC	00133	00133	panthothenate synthetase
SNP	163295 C_G	P57A(CCT_G1fluA	P57A(CCT_G1fluA	00150	00150	ferriochrome outer membrane transporter
SNP	170068 G_A	A153(WGC_1hemL	A153(WGC_1hemL	00154	00154	glutamate 1-semialdehyde aminotransferase (aminomutase)
SNP	174551 C_T	G780(GGC_C1m	G780(GGC_C1m	00159	00159	5'-methylthioadenosine/S-adenosylhomocysteine nucleosidase
SNP	181933 C_T	Q278(QCAG_glnD	Q278(QCAG_glnD	00167	00167	uridylyltransferase
SNP	183623 C_T	G244(GGC_glnD	G244(GGC_glnD	00167	00167	uridylyltransferase
SNP	184133 C_T	G544(GGC_glnD	G544(GGC_glnD	00167	00167	uridylyltransferase
SNP	184868 A_G	V94V(GTT_G map	V94V(GTT_G map	00168	00168	methionine aminopeptidase
SNP	185151 A_G	intergenic (-) map/psb	map/psb	00168/b0166	00168/b0166	methionine aminopeptidase/30S ribosomal subunit protein S2
SNP	187673 T_T	G586(GGC_1sp	G586(GGC_1sp	00171	00171	uridylylase
SNP	202373 A_G	G335(AAA_dnaE	G335(AAA_dnaE	00184	00184	DNA polymerase III alpha subunit
SNP	207997 A_G	Q8Q(CAA_C1sH	Q8Q(CAA_C1sH	00188	00188	tRNA(Ile)-lysidine synthetase
SNP	213157 C_T	G4183(GGT_1proS	G4183(GGT_1proS	00194	00194	prolyl-tRNA synthetase
INS	229727	INAME1	coding (653) fadB	00212	00212	hydroxyglutathione hydrolase
DEL	23807	1bp	coding (900) fadE	00221	00221	acyl coenzyme A dehydrogenase
SNP	238824 G_A	G41(GGT_C1fadE	G41(GGT_C1fadE	00221	00221	acyl coenzyme A dehydrogenase
SNP	242002 C_T	F129(WGC_1he	F129(WGC_1he	00227	00227	predicted lipoprotein and C40 family peptidase
SNP	251688 G_A	L231(CTG_CT gpt	L231(CTG_CT gpt	00238	00238	guanine-hypoxanthine phosphoribosyltransferase
INS	257855	INAME1	intergenic (-) thrW/kfN	00244/b462	00244/b462	RNA Thp/pseudogene, yda family
SNP	279871 C_T	R620(WGC_ynfP	R620(WGC_ynfP	00269	00269	CN4-G-prophage; predicted dehydratase
SNP	302400 A_G	R600(AAC_1yngK	R600(AAC_1yngK	00281	00281	predicted aromatic compound dihydrogenase
INS	304918	INAME1	intergenic (-) matC/matB	00292/b0293	00292/b0293	predicted protein/cryptic Mat fibrillin gene
INS	311442	INAME1	pseudogene ynfA	00300	00300	pseudogene, Arac family/putative regulator; Not classified; putative ARAC-type regulatory protein
SNP	313511 C_T	intergenic (-) ynfK/yngK	ynfK/yngK	00300/b0300	00300/b0300	predicted protein/putative pyridine nucleoside-disulfide oxidoreductase
DEL	316425	1bp	intergenic (-) ynfK/yngK	00300/b0300	00300/b0300	predicted DNA-binding transcriptional regulator/predicted oxidoreductase
SNP	321440 G_A	I179(ATC_A1beta	I179(ATC_A1beta	00311	00311	choline dehydrogenase, a flavoprotein
SNP	322283 T_T	V467(WGC_1heB	V467(WGC_1heB	00312	00312	betaine aldehyde dehydrogenase, NAD-dependent
SNP	325685 C_T	V452(WTC_1betT	V452(WTC_1betT	00314	00314	choline transporter of high affinity
SNP	326005 C_T	A559(WGC_1betT	A559(WGC_1betT	00314	00314	choline transporter of high affinity
SNP	32676 G_G	intergenic (-) betT/yahA	betT/yahA	00314/b0315	00314/b0315	choline transporter of high affinity/(-)-di-GMP-specific phosphodiesterase
SNP	329731 C_T	S332(TTG_1he	S332(TTG_1he	00317	00317	predicted inner membrane protein
SNP	329922 C_T	intergenic (-) yahC/yahD	yahC/yahD	00317/b0318	00317/b0318	predicted inner membrane protein/ankyrin repeat protein
SNP	336428 G_G	D146(GAC_yahU	D146(GAC_yahU	00324	00324	predicted deaminase with metallo-dependent hydrolase domain
SNP	336731 C_T	F136(WGC_1he	F136(WGC_1he	00325	00325	predicted deaminase with metallo-dependent hydrolase domain
SNP	338189 C_T	Q147(CAA_yahK	Q147(CAA_yahK	00325	00325	predicted oxidoreductase, Zn-dependent and NAD(P)-binding
SNP	338824 A_T	intergenic (-) yahK/yahL	yahK/yahL	00325/b0326	00325/b0326	predicted oxidoreductase, Zn-dependent and NAD(P)-binding/predicted protein
DEL	362709	2bp	coding (578) ynfM	00326	00326	DNA-binding transcriptional activator, 3HPP-binding
SNP	365730 G_A	L386(WGT_1mhB	L386(WGT_1mhB	00348	00348	1,2-dihydroxyphenylpropanoate 1,2-dioxygenase
INS	374879	INAME1	intergenic (-) frmK/yaiO	00357/b0358	00357/b0358	regulator protein that represses frmAB operon/outer membrane protein
SNP	375276 G_G	V1454(WGC_1he	V1454(WGC_1he	00358	00358	outer membrane protein
SNP	382118 C_T	F298(WGC_1he	F298(WGC_1he	00358	00358	outer membrane protein
SNP	388155 A_G	pseudogene ynfA	ynfA	04580	04580	predicted protein/putative structure; Not classified; putative flagellin structural protein; interrupted by 53
SNP	388300 A_G	pseudogene ynfA	ynfA	04580	04580	predicted protein/putative structure; Not classified; putative flagellin structural protein; interrupted by 53
SNP	391712 G_G	L591(WGC_1he	L591(WGC_1he	00377	00377	protein B17 transporter
SNP	395048 A_G	V248(WTA_d4A	V248(WTA_d4A	00381	00381	D-alanine-D-alanine ligase A
SNP	398444 T_C	S995(AGT_A1psf	S995(AGT_A1psf	00384	00384	conserved protein, Puf family, pho regulon
DEL	402275	1bp	intergenic (-) ynfA/aroM	00388/b0396	00388/b0396	predicted protein/conserved protein, AroM family; regulated by aroK
SNP	402400 A_G	N655(AAC_A1aroM	N655(AAC_A1aroM	00390	00390	conserved protein, AroM family; regulated by aroK
SNP	416097 A_G	N825(AAC_A1proY	N825(AAC_A1proY	00402	00402	proline-specific permease
SNP	423013 C_T	T156(ACT_A1sed	T156(ACT_A1sed	00408	00408	SecYEG protein translocase auxiliary subunit
SNP	425019 C_T	R235(WGC_1he	R235(WGC_1he	00411	00411	SecYEG protein translocase auxiliary subunit
SNP	426515 T_C	K122(AAA_1tsx	K122(AAA_1tsx	00411	00411	nucleoside channel, receptor of phage T6 and colicin K
SNP	434536 G_A	I170(ATC_A1dks	I170(ATC_A1dks	00420	00420	1-deoxyxylulose-5-phosphate synthase, thiamine-requiring, FAD-requiring
SNP	434579 T_C	T156(WGC_1he	T156(WGC_1he	00420	00420	1-deoxyxylulose-5-phosphate synthase, thiamine-requiring, FAD-requiring
SNP	441822 C_T	G2515(WGT_1cyoE	G2515(WGT_1cyoE	00428	00428	prothrome IX farnesyltransferase
SNP	442461 G_A	L381(CTG_TT cyoE	L381(CTG_TT cyoE	00428	00428	prothrome IX farnesyltransferase
SNP	442724 G_G	G481(WGC_1cyoD	G481(WGC_1cyoD	00429	00429	cytochrome c ubiquinol oxidase subunit IV
SNP	442731 G_G	L594(CTG_TT cyoD	L594(CTG_TT cyoD	00429	00429	cytochrome c ubiquinol oxidase subunit IV
SNP	453184 T_C	F298(WTT_C1cpX	F298(WTT_C1cpX	00438	00438	ATPase and specificity subunit of CtpX-CtpA ATP-dependent serine protease
INS	453600	INAME1	intergenic (-) ctpX/lon	00438/b0438	00438/b0438	ATPase and specificity subunit of CtpX-CtpA ATP-dependent serine protease/DNA-binding ATP-dependent protease La
SNP	476519 A_G	F393(WTC_1he	F393(WTC_1he	00463	00463	multidrug efflux system protein
SNP	478405 A_G	L289(CTG_1he	L289(CTG_1he	00463	00463	multidrug efflux system protein
SNP	479413 A_G	R358(WGC_1acrA	R358(WGC_1acrA	00463	00463	multidrug efflux system protein
SNP	495884 A_G	D296(WGC_1pk	D296(WGC_1pk	00477	00477	inositol/guanosine kinase
SNP	496125 A_G	F778(WTA_1pk	F778(WTA_1pk	00477	00477	inositol/guanosine kinase
SNP	497791 C_T	A105A(GCG_ybaL	A105A(GCG_ybaL	00478	00478	predicted transporter with NAD(P)-binding Rossmann-fold domain
SNP	499630 C_T	intergenic (-) ftr/ynfA	ftr/ynfA	00479/b0480	00479/b0480	predicted fosmidomycin efflux system/bifunctional UDP-sugar hydrolase/5'-nucleosidase
SNP	502629 C_T	D90(WGC_1he	D90(WGC_1he	00484	00484	copper transporter subunit
SNP	507905 C_T	R155(WGC_ybaT	R155(WGC_ybaT	00486	00486	predicted transporter
SNP	509491 C_C	V796(WTC_1he	V796(WTC_1he	00488	00488	inner membrane protein that stimulates the fliH hcr mutant suppressor activity of OmcA
SNP	510773 T_C	S241(CTG_1he	S241(CTG_1he	00490/b0490	00490/b0490	multisubunit protease with histH double mutant; membrane-anchored predicted of protein with C-terminal cytoplasmic PHB domain/predicted transporter subunit; ATP-binding component of ABC superfamily
SNP	511679 C_T	A77(WGC_1ybaM	A77(WGC_1ybaM	00491	00491	inner membrane protein, LIP00014 family
SNP	512387 T_C	T254A(ACG_ybaN	T254A(ACG_ybaN	00492	00492	DnaK co-chaperone, thioredoxin-like protein
SNP	514124 A_G	V704(WTC_1he	V704(WTC_1he	00494	00494	multifunctional acyl-CoA thioesterase I and protease I and liposphospholipase L1
SNP	517281 C_T	A690(WGC_1he	A690(WGC_1he	00496	00496	predicted ABC transporter permease
INS	518073	INAME1	intergenic (-) ybbP/rhdD	00496/b0493	00496/b0493	predicted ABC transporter permease/rhdD element protein
SNP	520270 T_G	N7155(AAC_rhdD	N7155(AAC_rhdD	00497	00497	rhdD element protein
SNP	520701 C_T	G881(WGC_rhdD	G881(WGC_rhdD	00497	00497	rhdD element protein
SNP	528954 C_T	AS8V(WGC_Gcd	AS8V(WGC_Gcd	00507	00507	glyoxylate carboxylase
SNP	531649 A_G	T661(WTA_MprR	T661(WTA_MprR	00509	00509	tartronate semialdehyde reductase, NADH-dependent
SNP	535730 G_A	G934(CTG_1he	G934(CTG_1he	00513	00513	predicted urea/L-arginine transporter
SNP	544297 C_T	Q359(WGC_1he	Q359(WGC_1he	00522	00522	were a pseudo gene - frameshift fused
SNP	545709 A_G	A135A(GCA_ybcF	A135A(GCA_ybcF	00521	00521	predicted carbamate kinase
SNP	548437 C_T	G665(WGT_A1pH	G665(WGT_A1pH	00524	00524	UDP-2,3-diacylglycerol pyrophosphatase
SNP	552061 C_T	R086(WGC_1he	R086(WGC_1he	00529	00529	uridine 5,10-methylene-tetrahydrofolate dehydrogenase/ 5,10-methylene-tetrahydrofolate cyclohydrolase
SNP	553139 A_G	Y21(CTAT_1he	Y21(CTAT_1he	00530	00530	predicted fibrin-like adhesion protein
INS	557533	-	coding (326) rfmI	00533	00533	predicted fibrin-like adhesion protein
SNP	570818 A_G	intergenic (-) ynfM	ynfM	00533	00533	DLP12 membrane protein/outer membrane porin (pseudogene)is, phage, Tn, Phage or Prophage Related; outer membrane porin protein; locus of qsr prophage
INS	573118	-	coding (187) rfpD	00556	00556	DLP12 prophage; predicted murein endopeptidase
SNP	575940 A_G	T81A(CTG_1he	T81A(CTG_1he	00560	00560	DLP12 prophage; DNA packaging protein
SNP	588914 C_T	L241(CTG_1he	L241(CTG_1he	00570	00570	sensory histidine kinase in two-component regulatory system with CuxR, senses copper ions
SNP	597621 A_G	A136A(GCG_1he	A136A(GCG_1he	00576	00576	phenylalanine transporter
SNP	599924 A_G	F123A(CTG_C1hB	F123A(CTG_C1hB	00578	00578	dihydropteridine reductase, NAD(P)H-dependent, oxygen-insensitive
SNP	612804 A_G	E1262(GAG_1he	E1262(GAG_1he	00586	00586	enterobactin synthase multienzyme complex component, ATP-dependent
SNP	613013 C_C	intergenic (-) ynfE/pepT	ynfE/pepT	00586/b0586	00586/b0586	enterobactin synthase multienzyme complex component, ATP-dependent/regulator of length of O-antigen component of lipopolysaccharide chains
SNP	620311 C_T	A194(WGC_1he	A194(WGC_1he	00593	00593	isochloraninate synthase 1
SNP	624775 G_G	K6E(AAA_GA csaA	K6E(AAA_GA csaA	00598	00598	carbon starvation protein
SNP	625804 A_G	T340A(ACC_1he	T340A(ACC_1he	00598	00598	carbon starvation protein
SNP	629843 G_A	R134(CTG_1he	R134(CTG_1he	00601	00601	conserved protein
SNP	632802 T_T	G213E(GGC_1he	G213E(GGC_1he	00604	00604	thiol-disulfide interchange protein, periplasmic
SNP	640013 C_T	G479(WGC_1he	G479(WGC_1he	00612	00612	citrate/succinate antiporter
SNP	655538 A_G	R144(WGC_1he	R144(WGC_1he	00619	00619	predicted DNA-binding transcriptional regulator
SNP	661116 G_A	L224(CTG_TT mrdB	L224(CTG_TT mrdB	00634	00634	cell wall shape-determining protein
SNP	669772 C_T	intergenic (-) ynfU/ynfV</				

SNP	963258_C_T	P1725(CCG_ycal	b0913	inner membrane protein, ComEC family of competence proteins
SNP	962146_C_T	R248(CCT_Cvba)	b0927	predicted metal-binding enzyme
INS	987463_INAME1	intergenic (-1:545)gncb	b0930/b0933	isoparganinyl tRNA synthetase/isocitinate phosphoribosyltransferase
SNP	997267_C_T	A118(VGCA_eId	b0939	predicted periplasmic pilin chaperone
INS	1002578_INAME1	coding (207)/yfcP	b0944	predicted periplasmic pilin chaperone
INS	1003105_INAME1	intergenic (-1:145)pyrD	b0946/b0945	predicted periplasmic pilin chaperone/dihydro-orotate oxidase, FMN-linked
SNP	1011629_C_T	P4025(CCG_pqa)	b0950	paraquat-inducible membrane protein A
SNP	1016788_C_T	intergenic (-1:23)matP	b0955/b0955	predicted peptidase/Ter macromodular organizer mats-binding protein
SNP	1017462_C_T	intergenic (-1:10)maA	b0955	Ter macromodular organizer mats-binding protein/outer membrane protein A (3a)1 st ,Gsd
SNP	1018428_G_A	T171(ACC_AcompA	b0957	outer membrane protein A (3a)1 st ,Gsd
SNP	1019952_A_G	E130E(GAA_say	b0959	required for expression of CRP-S-dependent promoters
INS	1029211_INAME1	intergenic (-1:164)ycyca	b0969/b0973	suflutrantransferase required for 3-thiolation step of mnmS5-s12J34-rRNA synthesis/HMBKC-binding inner membrane protein, UPF0005 family
SNP	1031030_G_A	G164(GCG_hyaK	b0972	hydrogenase 1, large subunit
SNP	1031983_A_G	N1025(AAC_hyaB	b0973	hydrogenase 1, large subunit
INS	1051935_INAME1	coding (2639)torS	b0993	hybrid sensory histidine kinase in two-component regulatory system with TorR
SNP	1052262_C_T	P744(GCC_torS	b0993	hybrid sensory histidine kinase in two-component regulatory system with TorR
SNP	1053187_G_A	P4633(CCC_torS	b0993	hybrid sensory histidine kinase in two-component regulatory system with TorR
SNP	1054999_C_T	A109(VGCC_torT	b0994	periplasmic sensory protein associated with the TorRS two-component regulatory system
SNP	1055025_C_T	S114(LCA_torT	b0994	periplasmic sensory protein associated with the TorRS two-component regulatory system
SNP	1055609_A_G	N1345(AAC_torC	b0996	trimethylamine N-oxide (TMAO) reductase I, cytochrome c-type subunit
SNP	1063315_T_C	S2855(AGT_ycyC	b1001	predicted protein
INS	1070707_C_C	coding (3159)hnbH	b1011	ureidobicyclic amidohydrolase
SNP	1074670_A_G	F780(UTC_CpudA	b1014	fused DNA-binding transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase
SNP	1076351_G_A	G319(GCG_puaA	b1014	fused DNA-binding transcriptional regulator/proline dehydrogenase/pyrroline-5-carboxylate dehydrogenase
INS	1095636_INAME1	intergenic (-1:ycyD)serX	b1029/b1032	predicted inner membrane protein/rRNA-Ser
INS	1095938_INAME1	monocoding (5)serX	b1032	rRNA-Ser
SNP	1113240_C_T	V226(GTC_rmtD	b1053	predicted drug efflux system
SNP	1118656_G_A	A119(VGCC_suaA	b1059	N-methyltryptophan oxidase, FAD-binding
SNP	1118825_C_T	A531(GCT_A_suaA	b1059	N-methyltryptophan oxidase, FAD-binding
SNP	1119121_T_C	intergenic (-1:160)hbaS	b1059/b1060	N-methyltryptophan oxidase, FAD-binding/biofilm regulator
SNP	1133524_A_G	Q1248(CAG_flgG	b1078	flagellar component of cell-distal portion of basal-body rod
SNP	1134511_A_G	T1754(ACC_flgH	b1079	flagellar protein of basal-body outer-membrane r-ring
SNP	1139032_C_T	G188(GCC_flgE	b1083	flagellar hook-flare-2 C-methylerythritol kinase
SNP	1140309_C_T	L828(ITTG_rme	b1084	fused ribonuclease E, endoribonuclease/RNA-binding protein/RNA deprossome binding protein
SNP	1155924_G_A	E2411(GAA_ycyH	b1100	predicted DNase
SNP	1160526_C_T	E306(GCC_ycyH	b1103	putative nucleoside phosphoramide_sdaA activator protein
SNP	1165117_G_A	G184(GCC_nhd	b1109	respiratory NADH dehydrogenase 2/cypric reductase
SNP	1166159_A_G	T424(AGC_ycyC	b1110	predicted protein
SNP	1170555_C_G	V624(GTA_mfd	b1114	transcription-repair coupling factor
SNP	1170569_C_T	G169(AGC_ycyC	b1114	transcription-repair coupling factor
SNP	1175012_T_C	A387(AGC_tolC	b1116	lipoprotein-releasing system transmembrane protein
SNP	1184344_C_T	T164(AGC_pgpT	b1127	peptidase T
SNP	1186732_C_T	A177(GCC_ycyE	b1129	sensory histidine kinase in two-component regulatory system with PhoP
SNP	1196751_C_T	intergenic (-1:ymf)lit	b1138/b1135e14	prphage; predicted inner membrane protein/e14 prphage; cell death peptidase, inhibitor of 14 late gene expression
SNP	1206652_G_A	W371(TGG_t1aP	b1155	e14 prphage; predicted protein
SNP	1210565_C_G	intergenic (-1:19)hlyVegS	b1160/b1161	HlyB stabilizing HlyG-stabilator, anti-RhoB factor/predicted protein
INS	1219781_A_G	pseudogene yegH	b4491	Probable pseudogene; putative ATP-binding component of a transport system
SNP	1221510_T_C	N270(AAT_Gymg	b4593	hypothetical protein
DEL	1222403_1bp	intergenic (-1:ycg)hmlT	b4622/b1176	pseudogene/cell division topological specificity factor
SNP	1225808_C_T	E365(AGC_galg	b1179	predicted protein
INS	1226193_INAME1	coding (55)2:ycg	b1179	conserved protein
SNP	1228996_C_T	intergenic (-1:116)rumD	b1182/b1181	Hemolysin E/DNA polymerase V, subunit D
SNP	1233366_G_A	L20(CTC_ATCsdb	b1187	DNA-binding transcriptional dual regulator of fatty acid metabolism
SNP	1233622_C_T	A87(GCC_c1aR	b1187	DNA-binding transcriptional dual regulator of fatty acid metabolism
SNP	1237720_C_T	G425(GGC_dadA	b1189	D-amino acid dehydrogenase
SNP	1241502_G_A	S291(GTC_C1aA	b1192	L-D-carboxypeptidase A
SNP	1241889_T_C	E596(GCT_DemaA	b1193	HlyC mucin endoribonuclease/lysostaphin E
SNP	1247581_A_G	M201(ATG_dhaI	b1199	dihydroxyacetone kinase, C-terminal domain
SNP	1252983_A_G	G465(GCG_ycgV	b1202	predicted adhesin
SNP	1251097_C_T	E192(GCC_C1aE	b1202	diphosphophoryl-2-C-methylerythritol kinase
SNP	1276147_A_G	intergenic (-1:narX/narK	b1222/b1223	sensory histidine kinase in two-component regulatory system with NarI/nitrate/nitrite transporter
SNP	1292111_A_G	A46V(GCC_C1ns	b1237	global DNA-binding transcriptional dual regulator H-Ns
SNP	1294614_A_G	S946(GCC_C1ns	b1237	global DNA-binding transcriptional dual regulator H-Ns
MOB	1297920	intergenic (-1:ycb)oppA	b1242/b1242	predicted inner membrane protein/oligopeptide transporter subunit
SNP	1299279_A_G	H291(CAC_oppA	b1243	oligopeptide transporter subunit
SNP	1300229_C_T	F591(TTT_TT_oppB	b1244	oligopeptide transporter subunit
SNP	1300959_A_G	T294(AGC_oppB	b1244	oligopeptide transporter subunit
DEL	1311722_1bp	coding (477)ompW	b1256	outer membrane protein W
SNP	1321140_C_T	S1981(CTC_ycyJ	b1266	conserved protein
SNP	1323772_C_T	H609(AGC_ycyC	b1268	predicted inner membrane protein
DEL	1325931_1bp	coding (408)ycyK	b1271	predicted oxoacyl-(acyl carrier protein) reductase, EmrKv-TotC-binding
SNP	1331993_C_T	R105(GCC_ycyB	b1275	DNA-binding transcriptional dual regulator, O-acetyl-L-serine-binding
SNP	1332055_C_G	A292(GCC_ycyB	b1275	DNA-binding transcriptional dual regulator, O-acetyl-L-serine-binding
SNP	1333412_C_T	P191(CCG_CscaA	b1276	aconitate hydratase 1
SNP	1336698_T_C	V484(GTC_gpgB	b1278	phosphatidylglycerophosphatase B
SNP	1339571_G_A	G142(GCC_pyrF	b1281	orotidine-5-phosphate decarboxylase
SNP	1343643_A_G	E195(GCC_eme	b1285	cyclic-di-GMP phosphodiesterase; csgD regulator; modulator of RseII stability
SNP	1346180_A_G	intergenic (-1:rmB)yciW	b1286/b1287	ribonuclease II/predicted oxidoreductase
SNP	1347525_A_G	V247(VGT_f1aB1	b1288	enoyl-(acyl-carrier-protein) reductase, NADH-dependent
SNP	1350926_G_A	E192(GCC_puqD	b1298	gamma-Glu-GABA hydrolase
SNP	1361292_C_T	R442'(VGA_puqC	b1300	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent
SNP	1370435_A_G	intergenic (-1:ycjN)ycjQ	b1310/b1311	predicted sugar transporter subunit; periplasmic-binding component of ABC superfamily/predicted sugar transporter subunit; membrane component of ABC superfamily
SNP	1371109_C_T	A221(VGCC_ycjQ	b1311	predicted sugar transporter subunit; membrane component of ABC superfamily
INS	1389979_INAME1	coding (183)ymzF	b1318	predicted DNA-binding transcriptional regulator
DEL	1416324_1bp	coding (428)sieB	b1353	Rac prphage; phage superinfection exclusion protein
DEL	1418882_A_G	N180(DAAT_ycaJ	b1359	Rac prphage; conserved protein
DEL	1423213_1bp	intergenic (-1:136)ymaA	b1360/b1360	Phage-related/Rac prphage-Phage or Phophage Related/Rac prphage; pseudogene, tail protein homology/Phage or Phophage Related; putative alpha helix protein
DEL	1429333_2bp	coding (3059)hfr	b1372	Rac prphage; predicted tail fiber protein
SNP	1436053_A_G	A653(VGCC_ydbK	b1378	fused predicted pyruvate-flavodoxin oxidoreductase; conserved protein/conserved protein/FeS binding protein
SNP	1437213_C_T	A653(VGCC_ydbK	b1378	fused predicted pyruvate-flavodoxin oxidoreductase; conserved protein/conserved protein/FeS binding protein
SNP	1449937_A_G	V311(AGT_paaZ	b1387	fused oxepin-CoA hydrolase/3-oxo-5,6-dehydrooxepin-CoA semialdehyde dehydrogenase
INS	1450172_C_C	coding (697)paaz	b1387	fused oxepin-CoA hydrolase/3-oxo-5,6-dehydrooxepin-CoA semialdehyde dehydrogenase
SNP	1451320_A_G	A544(GCA_paaA	b1388	ring 1,2-ephenylacetyl-CoA epoxidase subunit
SNP	1463351_A_G	pseudogene ydbA	b4492	pseudogene, autotransporter homolog; interrupted by IS2 and IS30
SNP	1466392_A_G	pseudogene ydbA	b4492	pseudogene, autotransporter homolog; interrupted by IS2 and IS30
SNP	1467666_G_A	pseudogene ydbA	b4492	pseudogene, autotransporter homolog; interrupted by IS2 and IS30
SNP	1473605_C_T	G143(CAA_ynfC	b1417	predicted PF0971 family periplasmic methylglyoxal resistance protein
SNP	1477986_A_G	K541(KAA_ynbC	b1410	predicted hydrolase
SNP	1479185_A_G	E388(GAA_ynbD	b1411	predicted phosphatase inner membrane protein
SNP	1490152_C_T	V191(GTT_C1ns	b1440	polyhydroxybutyrate (PHB) synthase, ABC transporter periplasmic binding protein homolog
SNP	1519144_A_G	E286(GCC_ynfU	b1442	predicted spermidine/putrescine transporter subunit
SNP	1520319_A_G	intergenic (-1:yncD)yncE	b1451/b1452	predicted iron outer membrane transporter/ATP-binding protein, periplasmic, function unknown
SNP	1536022_A_G	C262(TGT_Tnaary	b1467	nitrate reductase 2 (Nrd2), beta subunit
SNP	1548013_C_A	E1120(GCC_eme	b1475	formate dehydrogenase-N, Fe-S (beta) subunit, nitrate-inducible
SNP	1548324_T_C	V213(AGT_fldH	b1475	malate dehydrogenase, (decarboxylating, NAD-requiring) (malic enzyme)
INS	1552874_INAME1	coding (223)maeA	b1479	D-D-glucosylidase system, ATP-binding component
SNP	1555148_C_T	E209(GTC_ynfD	b1484	D-D-glucosylidase system, ATP-binding component
SNP	1558083_T_C	intergenic (-1:ddpB)ddpA	b1486/b1487	D-ala-D-ala transporter subunit/D-ala-D-ala transporter subunit
SNP	1560900_G_A	R718(CGC_cddpX	b1488	D-ala-D-ala dipeptidase, Zn-dependent
SNP	1570185_C_T	S748(CTC_pggG	b1494	predicted peptidase
SNP	1574310_A_G	T244(CTC_cdbB	b1495	predicted protein
SNP	1579291_T_C	T1544(ACC_ycdN	b1498	conserved protein
SNP	1581112_G_A	V254(GTT_C_sufA	b1500	'Two component system connector membrane protein, EvgSA to PhoQP
SNP	1582188_C_T	V920(GTC_ycyE	b1501	predicted oxidoreductase
SNP	1582490_A_G	V4084(GTA_ydeP	b1501	predicted oxidoreductase
DEL	1591931_1bp	pseudogene ynfO	b4696	pseudogene, Aida homolog
INS	1591974_C_C	pseudogene ynfO	b4696	pseudogene, Aida homolog
DEL	1594533_1bp	pseudogene ynfO	b4696	pseudogene, Aida homolog
SNP	1601583_A_G	N1045(AAC_hsdR	b1515	autoluciferase 2 import system permease protein
SNP	1604084_G_A	A247(GCT_ynfR	b1517	putative autoluciferase-2 (A1-2) aldolase
DEL	1615024_1bp	coding (171)ycyK	b1524	predicted arabinose transporter
SNP	1616154_T_C	intergenic (-1:mar)marR	b1529/b1530	inner membrane protein, UPF0056 family/DNA-binding transcriptional repressor of multiple antibiotic resistance
INS	1621575_INAME1	coding (149)ycyE	b1536	conserved protein
SNP	1629659_T_C	pseudogene ynfJ	b4600	pseudogene, MFS transporter family; interrupted by Qln prphage-Phage or Phophage Related; putative transporter protein
SNP	1631282_C_T	pseudogene ynfJ	b4600	pseudogene, MFS transporter family; interrupted by Qln prphage-Phage or Phophage Related; putative transporter protein
SNP	1634635_A_G	pseudogene ynfJ	b4600	pseudogene, MFS transporter family; interrupted by Qln prphage-Phage or Phophage Related; putative transporter protein
SNP	1645797_A_G	pseudogene ynfJ	b4600	pseudogene, MFS transporter family; interrupted by Qln prphage-Phage or Phophage Related; putative transporter protein
SNP	1646535_T_C	pseudogene ynfJ	b4600	pseudogene, MFS transporter family; interrupted by Qln prphage-Phage or Phophage Related; putative transporter protein
SNP	1656457_T_C	A388(VGCA_ynfE	b1587	probable selenate reductase, periplasmic
SNP	1657346_G_A	G618(GCC_ynfE	b1587	probable selenate reductase, periplasmic
SNP	1664401_C_T	V213(AGT_holM	b1606	predicted DNA-binding transcriptional regulator
SNP	1678839_T_C	V213(AGT_holM	b1606	dihydroneopterin reductase, NADPH-dependent; dihydrofolate reductase isozyme
SNP	1685476_T_C	A431(GCA_sLumA	b1612	lumarate hydratase (lumarase A), aerobic Class I
SNP	1687953_G_A	G293(GCC_ynfD	b1614	conserved protein, DUF945 family
SNP	1700311_T_C	V285(AGT_ald	b1623	adenosine deaminase
SNP	1705030_T_C	V296(AGT_rsaC	b1629	electron transport complex protein required for the reduction of SoxR; predicted membrane-associated NADH oxidoreductase
DEL	1711543_1bp	intergenic (-1:dlpA)gsta	b1634/b1635	peptide and tripeptide permease A/glutathione S-transferase
SNP	1711547_A_G	intergenic (-1:dlpA)gsta	b1634/b1635	peptide and tripeptide permease A/glutathione S-transferase
SNP	1713748_T_C	T234(AAC_tyrS	b1637	tyrosyl-tRNA synthetase
DEL	1719838_2bp	coding (493)ycyK	b1645	Efflux protein family (PET) component of predicted ynfK efflux pump
SNP	1720701_C_C	N472(ATC_ynfK	b1645	Efflux protein family (PET) component of predicted ynfK efflux pump
SNP	1721498_A_G	V128(AGT_sodC	b1646	superoxide dismutase, Cu, Zn
SNP	1727141_C_T	I2771(ATC_A1hr	b1653	predicted ATP-dependent heliase
SNP	1727315_C_T	N389(GCC_thr	b1653	predicted ATP-dependent heliase
SNP	1727882_C_T	V524(AGT_thr	b1653	predicted ATP-dependent heliase
SNP	1738104_T_C	R323(CGT_ynfC	b1660	predicted transporter
SNP	1749958_C_T	V360(GTT_ynfH	b1673	predicted oxidoreductase
SNP	1751343_C_T	A130(GCC_ynfH	b1673	predicted 4Fe-4S ferroxidase-type protein
SNP	1756085_G_A	intergenic (-1:ymh)ufE	b1678/b1675	murein LD-transpeptidase/sulfur acceptor protein
SNP	1759563_C_C	T594(AGC_sufC	b1682	component of SufBCD complex; ATP-binding component of ABC superfamily
SNP	1762081_C_T	E540(GCA_ynfJ	b1687	predicted FAD-linked oxidoreductase
INS	1765660_INAME1	coding (251)ycyJ	b1687	predicted FAD-linked oxidoreductase
INS	1781742_INAME1	coding (1487)fadK	b1701	short chain acyl-CoA synthetase, anaerobic
SNP	1782401_A_G	P846(GCC_sppA	b1702	phosphoenolpyruvate synthase
SNP	1786410_A_G	intergenic (-1:2)hcbA	b1714/b1715	beta-lactamase RNA synthetase, alpha subunit/phenylalanyl-tRNA synthetase operon leader peptide
SNP	1799034_G_A	Y254(ATC_Thrs	b1719	threonyl-tRNA synthetase
INS	1803261_C_C	coding (48)7ydf	b1722	predicted outer membrane protein, acid-inducible
SNP	1803810_C_T	A128(ATC_ynfN	b1729	predicted transporter
SNP	1810636_T_C	intergenic (-1:ycdJ)cedA	b1730/b1733	predicted protein/cell division modulator
INS	1811038_INAME1	intergenic (-1:cedA)katt	b1731/b1731	cell division modulator/Catalase HPI, heme d-containing
INS	1830430_C_C	coding (778)hbaA	b1749	exonuclease III
SNP	1831135_A_G	L170(LCA_CyxD	b1750	inner membrane protein, TPV38/TMEM64 family
SNP	1855003_C_T	intergenic (-1:ycjJ)ycjJ	b1773/b1777	predicted aldolase/predicted oxidoreductase, Zn-dependent and NAD(P)-binding
SNP	1862451_C_T	G173(GCG_ycyE	b1781	aldo-keto reductase, methylglyoxal to acetol, NADPH-dependent
SNP	1862765_A_G	A181(GCC_ycyE	b1784	conserved protein
SNP	1870836_G_A	R130(CCG_CycaK	b1787	conserved protein
DEL	1876580_1bp	intergenic (-1:yeaD)yeaG	b1795/b1795	conserved protein, UPF0410 family/predicted protein
SNP	1879613_T_C	intergenic (-1:emf)dmA	b1799/b1800	DNA-binding transcriptional repressor for dmxA/D-malate oxidase, NAD-dependent; probable tartrate dehydrogenase
SNP	1893901_T_C	G555(GGT_dmiA	b1800	D-malate oxidase, NAD-dependent; probable tartrate dehydrogenase
SNP	1897961_A_G	T1851(CAA_dmiA	b1800	D-malate oxidase, NAD-dependent; probable tartrate dehydrogenase
SNP	1881133_T_C	F286(CTC_ycyW	b1801	predicted transporter
SNP	1890484_A_G	intergenic (-1:yoaA)yoaB	b1808/b1808	conserved protein with nucleoside triphosphate hydrolase domain/conserved protein, UPF0076 family
SNP	1898950_G_A	intergenic (-1:yoaF)manX	b1816/b1811	fused predicted membrane protein/conserved protein/fused mannose-specific PTS enzymes: IIA component/IIIB component

SNP	1907902_A_G	P134P(CCA_yybQ	B1828	predicted transporter
SNP	1925235_T_C	H279(CAC_rfbB	B1845	protease II
INS	1933749_INAMET	intergenic (-)Fwf/yebK	B1852/B1853	glucose-6-phosphate 1-dehydrogenase/predicted DNA-binding transcriptional regulator
SNP	1935745_T_C	I291I(ATT_A1)pykA	B1854	pyruvate kinase II
SNP	1944629_A_G	intergenic (-)rcuY/yebC	B1863/B1864	component of RuvABC resolvase, endonuclease/conserved protein, UPF0082 family
SNP	1952001_T_C	D239N(GAT_ars5	B1872	trimethylamine N-oxide reductase system III, catalytic subunit
SNP	1958042_G_A	D239N(GAT_ars5	B1876	arginyl-tRNA synthetase
SNP	1967415_T_C	D265(GAT_tap	B1885	methyl-accepting protein IV
SNP	1979731_T_C	D265(GAT_tap	B1885/B1886	trimethylamine N-oxide reductase system III, catalytic subunit
INS	1982739_C	coding (614)/araF	B1901	L-arabinose transporter subunit
SNP	1991403_T_C	G154(GGA_uvrC	B1913	exonuclease UvrABC, endonuclease subunit
SNP	2000981_A_G	pseudogene hfg	B1936	predicted defective phage integrase (pseudogene)
SNP	2029470_T_C	M223I(ATG_hchA	B1961	DNA cytosine methyltransferase
SNP	2033727_G_A	F104I(TTC_ChuH	B1967	Glyoxalase III and Hsp31 molecular chaperone
SNP	2036489_T_C	I1413(ATC_yeeI	B1970	hydroxyisourate hydrolase
SNP	2044601_T_C	Q231E*(CAA_yeeI	B1978	probable adhesin
SNP	2049107_C_T	A307(GCC_shiA	B1981	shikimate transporter
SNP	2051785_G_A	noncoding (3)aurW	B1984	RNA-Ase
SNP	2052522_C_G	G130(GGT_nac	B1988	DNA-binding transcriptional dual regulator of nitrogen assimilation
SNP	2058768_A_G	G130(GGT_nac	B1988/B1989	putative autotransporter and trans-activator
SNP	2063416_G_A	intergenic (-)yeeH/inhH	B2029	glucose 1-phosphate thymidyltransferase
DEL	2064578_35590bp	pseudogene [yeeE]_wbbJ	B2460	[D45]-cb-42 genes(-)b-38-[yeeE], yeeH, yeeA, imd, insD, yeeF, flu, yeeE, yeeI, yeeU, cbaA, yeeW, yeeD, yeeX, yeeA, slmC, dacD, sbcB, yeeD, yeeE, plaI, yeeV, yeeZ, yeeM, hisL, hisG, hisD, hisC, hisH, hisI, hisJ, cld, ugd, gnd, hisI, [wbbJ]/(-)
SNP	2107575_T_C	T298I(AC_rfbA	B2029	glucose 1-phosphate thymidyltransferase
SNP	2109133_T_C	S261G(AGC_rfbB	B2041	dTPD-glucose 4,6 dehydratase, NAD(P)-binding
SNP	2117469_T_C	Y437I(TAC_twaI	B2047	predicted UDP-glucose lipid carrier transferase
SNP	2142340_C_G	A027(AGC_yegE	B2067	predicted diguanylate cyclase, GGDEF domain signaling protein
SNP	2144679_G_A	T29M(AGC_araA	B2068	3-methyl-adenine DNA glycosylase II
SNP	2156727_C_T	T343M(AGC_mtdC	B2076	multidrug efflux system, subunit C
SNP	2160284_T_C	V50I(GTA_yneG	B2086	phosphatidylyserine kinase, metal-dependent
INS	2183802_INAMET	intergenic (-)rcrR/rcrA	B2105/B2106	DNA-binding transcriptional repressor of rcaM/membrane protein conferring nickel and cobalt resistance
SNP	2183833_T_C	F151(TTC_CT_rcaN	B2106	membrane protein conferring nickel and cobalt resistance
SNP	2183899_T_C	intergenic (-)rcrM/rcrB	B2106/B2107	membrane protein conferring nickel and cobalt resistance/periplasmic modulator of Ni and Co efflux
SNP	2192413_C_T	L3043(GA_TmetE	B2116	predicted HRA synthetase
SNP	2199926_T_A	D808(GAT_yeeH	B2118	conserved protein
DEL	2208780_13bp	coding (837)/yehR	B2123	lipoprotein, DUF1307 family
SNP	2209982_G_A	coding (53)/yehT	B2125	predicted response regulator in two-component system with YehU
SNP	2213732_A_G	H300H(CAT_yehX	B2129	predicted transporter subunit: ATP-binding component of ABC superfamily
SNP	2221259_G_A	T279H(AC_A_pfbG	B2134	D-alanyl-D-alanine endopeptidase
SNP	2227264_G_A	F166(GCC_tduc	B2140	RNA-dihydrouridine synthase C
SNP	2230162_G_A	G230(GGC_rfbA	B2158	vancomycin high level resistance exclusion protein; mutants have a defective envelope more permeable to vancomycin at 42 degrees
SNP	2247282_T_C	S1145(AGT_yjeH	B2158	inner membrane protein, UPF0324 family
INS	2262740_INAMET	coding (663)/yixT	B2174	Lipid A 1-diphosphate synthase, undecaprenyl pyrophosphate-lipid A 1-phosphate phosphotransferase
SNP	2269332_G_A	D940(GAT_rts	B2176	pseudogene, auto transporter for phages lambda and N4, when overexpressed
DEL	2284189_13bp	pseudogene yjeJ	B2190	pseudogene, auto transporter outer membrane homology/putative transport; Not classified; putative ATP-binding component of a transport system
INS	2285778_C	pseudogene yjeD	B2190	pseudogene, auto transporter outer membrane homology/putative transport; Not classified; putative ATP-binding component of a transport system
SNP	2288024_C_G	R1212I(TAC_yjeK	B2190	DNA-binding transcriptional regulator in two-component regulatory system with NaG or NaX
SNP	2302099_T_C	intergenic (-)ecoA/mqp	B2209/B2212	ecocin, a serine protease inhibitor/malate dehydrogenase, FAD/NAD(P)-binding domain
SNP	2302212_C_G	intergenic (-)ecoA/mqp	B2209/B2212	ecocin, a serine protease inhibitor/malate dehydrogenase, FAD/NAD(P)-binding domain
SNP	2307536_G_A	R32C(CGT_T1nda	B2213	fused DNA-binding transcriptional dual regulator/DG-methylguanine-DNA methyltransferase
SNP	2312629_G_A	D940(GAT_rts	B2216	phosphotransfer intermediate protein in two-component regulatory system with RbCdc
SNP	2322417_T_C	G146(GGT_atoC	B2223	short chain fatty acid transporter
DEL	2323419_13bp	coding (871)/rsbB	B2224	acetyl-CoA acetyltransferase
SNP	2323880_G_A	D238H(AGC_rfbG	B2450	pseudogene, UPF0592 family, putative membrane protein
SNP	2344780_T_C	RS8H(CGC_C_rhbD	B2235	ribonucleoside-diphosphate reductase 1, beta subunit, ferritin-like protein
SNP	2349724_A_G	intergenic (-)gfp7/gfpA	B2240/B2241	long-glycerol-3-phosphate transporter/long-glycerol-3-phosphate dehydrogenase (anaerobic), large subunit, FAD/NAD(P)-binding
SNP	2353189_G_A	Y149H(TAT_gbcG	B2243	anaerobic long-glycerol-3-phosphate dehydrogenase, C subunit, 4Fe-4S iron-sulfur cluster
SNP	2354624_T_C	R356I(AGC_amb	B2253	undecyl-5-beta-1-thiopyranose phosphoryl-4-oxo-diphosphate aminotransferase, PLP-dependent
INS	2356208_C	coding (914)/amcC	B2254	undecaprenyl phosphate 1-Ara4FN transferase
DEL	2368387_13bp	coding (497)/yibJ	B2271	predicted peptidase
SNP	2404881_A_G	R133H(AC_GabaA	B2290	valine-pyruvate aminotransferase 2
SNP	2409979_C_T	K126K(AAG_yfbV	B2295	inner membrane protein, UPF0208 family
INS	2424382_INAMET	coding (647)/yagT	B2310	lysine/arginine/ornithine transporter subunit
SNP	2429982_G_A	R176C(TAC_T1c0C	B2315	functional thiolglyoxylate synthase/dihydrofolate synthase
SNP	2436224_C_T	G374E(GGG_yfJ	B2322	predicted transporter
SNP	2440141_T_C	V253A(GTT_mmmC	B2324	fused 5-methylaminopyruvate 2-thiouridine-forming enzyme methyltransferase and FAD-dependent demodification enzyme
SNP	2443940_G_A	A253P(GCC_ancC	B2329	chromatinase
SNP	2447892_G_A	A136A(GCC_yfca	B2334	predicted fibrin-like adhesin protein
INS	2448797_C	coding (12/5)/yfrR	B2335	predicted fibrin-like adhesin protein
SNP	2449289_T_C	N915I(AC_A_yheR	B2336	predicted periplasmic pilus chaperone
SNP	2452974_INAMET	intergenic (-)yhbA/yhbA	B2339/B2342	predicted fibrin-like adhesin protein/phosphohistidine phosphatase
SNP	2453556_T_C	N100I(AAT_G_fadI	B2341	fused enoyl-CoA hydratase and epimerase and isomerase/3-hydroxyacyl-CoA dehydrogenase
SNP	2459885_T_C	intergenic (-)fadI/yfbF	B2344/B2345	long-chain fatty acid outer membrane transporter/predicted protein
SNP	2460214_C_G	intergenic (-)fadI/yfbF	B2344/B2345	long-chain fatty acid outer membrane transporter/predicted protein
SNP	2464599_G_A	A369I(GCT_gtrS	B2352	serine-specific glucosyl transferase, CP5-53 [KpLE1] prophage
SNP	2484105_A_G	L836I(TTA_tvvgS	B2370	hybrid sensory histidine kinase in two-component regulatory system with EvgA
SNP	2484157_T_C	S843I(TCC_cvgS	B2370	hybrid sensory histidine kinase in two-component regulatory system with EvgA
SNP	2489626_G_A	R139I(GCC_yjeE	B2380	predicted sensory kinase in two-component system with YjeB
SNP	2498924_C_T	Q191*(CAG_yjeP	B2382	predicted DNA-binding protein
SNP	2502349_G_A	R141H(CGT_yjeP	B2384	aminopeptidase
SNP	2509159_G_A	A246(GCC_mtmH	B2392	manganese/divalent cation transporter
SNP	2513360_T_C	H566H(CAC_yjeA	B2395	predicted diguanylate cyclase
SNP	2514376_T_C	L271I(TCA_C_yjeA	B2395	predicted diguanylate cyclase
SNP	2517177_T_C	K240H(AAG_gjR	B2400	glutaryl-RNA synthetase
SNP	2523314_T_C	P246P(CCA_yjeB	B2409	predicted DNA-binding transcriptional regulator
SNP	2529347_A_G	M221A(ATG_yjeZ	B2413	predicted inner membrane protein
SNP	2541500_G_A	G116(GGC_yjeA	B2426	predicted short-chain oxidoreductase
SNP	2542111_C_G	S231I(TCC_CmurB	B2427	Repressor for murPD, MurKac, P-9 inducible
SNP	2544645_T_C	M250I(ATG_murP	B2429	N-acetylmuramic acid permease, EIIBC component, PTS system
SNP	2547423_C_G	A116(GCC_yjeX	B2431	deferrioxalate, cytoplasmic
INS	2557383_INAMET	intergenic (-)yhbZ/yhbZ	B2442/B2444	CP2-55 prophage; predicted integrase/CP2-55 prophage; predicted protein
INS	2557533_C	coding (53/6)/yflL	B2443	CP2-55 prophage; predicted protein
SNP	2567072_C_T	D164N(GAT_eutI	B2454	predicted chaperonin, ethanolamine utilization protein
SNP	2574154_G_A	I483I(ATI_A_maeB	B2463	fused malic enzyme predicted oxidoreductase/predicted phosphotransacetylase
SNP	2582713_C_T	L305I(TCC_tcrD	B2470	aminoglycoside/multidrug efflux system
SNP	2586958_G_A	V714M(GTG_acrD	B2470	aminoglycoside/multidrug efflux system
SNP	2598478_T_C	C182I(TGT_T1hYhA	B2481	hydrogenase 4, 4Fe-4S subunit
INS	2599234_C	coding (155)/yhbB	B2482	hydrogenase 4, membrane subunit
SNP	2603666_T_C	S61P(TCC_CyHfE	B2485	hydrogenase 4, membrane subunit
SNP	2607424_G_A	T13A(ACC_G_yhH	B2488	hydrogenase 4, Fe-S subunit
SNP	2609979_G_A	I270M(TAT_yhbR	B2491	DNA-binding transcriptional activator, formate sensing
SNP	2610593_T_C	D490D(GAT_hyR	B2491	DNA-binding transcriptional activator, formate sensing
SNP	2618379_A_G	intergenic (-)zupp/purM	B2498/B2499	phosphoribosyltransferase/phosphoribosylaminoimidazole synthetase
SNP	2624882_C_T	G394(GGT_yjeF	B2503	cyclic-di-GMP phosphodiesterase, anaerobic
SNP	2628064_G_A	N172A(GCC_yjeI	B2506	conserved protein
SNP	2630795_G_A	A167P(GCC_guaB	B2508	IMOP dehydrogenase
DEL	2632452_13bp	coding (632)/bamB	B2512	lipoprotein required for OM biogenesis, in BamABCD complex
SNP	2641836_G_A	R85C(GCC_T1c0B	B2518	multifunctional nucleoside diphosphate kinase and apyrimidinic endonuclease and 3'-phosphodiesterase
SNP	2655740_C_T	R140R(CGG_hisA	B2526	DnaK-like molecular chaperone specific for tsclJ
SNP	2662132_C_T	G173G(GCC_yhbR	B2534	S9 septilase family protein, function unknown
SNP	2671662_G_A	S284I(TCC_T1yph	B2544	conserved protein
SNP	2681542_G_A	A397I(GCC_yjeA	B2551	serine hydroxymethyltransferase
SNP	2704762_T_C	G880(GGA_cseC	B2570	RseC protein involved in reduction of the SoxR iron-sulfur cluster
SNP	2718105_C_T	S310I(TCA_T1qI	B2584	inhibiting acetyltransferase for acetyl-CoA synthetase
SNP	2719711_T_C	G454(GCT_yfjQ	B2584	inhibiting acetyltransferase for acetyl-CoA synthetase
INS	2731759_INAMET	coding (500)/yihH	B2593	conserved protein, UPF0124 family
MOB	2734342	intergenic (-)bamD/raa	B2595/B2599	lipoprotein required for OM biogenesis, in BamABCD complex/cold shock protein associated with 30S ribosomal subunit
SNP	2738375_G_A	I197I(GCT_A1adp	B2601/B2602	D-erythro-D-xylose phosphoryl-3-phosphate synthase, lysine-repressible/lipoprotein
SNP	2747094_A_G	W351*(TGG_yjD	B4461	inner membrane protein, UPF0583 family
SNP	2758344_T_C	C48H(TGT_CyJfI	B2625	CP4-57 prophage; predicted protein
SNP	2765091_A_G	C53H(TGT_T1yph	B2625	CP4-57 prophage; predicted GTP-binding protein
SNP	2768023_A_G	intergenic (-)yhbI/yhbI	B2627/B2628	CP4-57 prophage; predicted protein/CP4-57 prophage; conserved protein; Phage or Prophage Related
SNP	2775384_T_C	N1523D(AAC_yjJ	B2647	adhesin-like autotransporter
SNP	2776150_T_C	G1267(GGG_yjeA	B2647	adhesin-like autotransporter
SNP	2784975_G_A	pseudogene yjeM	B2662	predicted protein; putative enzyme
SNP	2789141_G_A	A215A(GCC_gaH0	B2661	succinate-semialdehyde dehydrogenase I, NADP-dependent
SNP	2790102_C_T	G48G(GCC_gaB1	B2662	4-aminobutyrate aminotransferase, PLP-dependent
SNP	2790579_G_A	P207P(GCC_gaB1	B2662	4-aminobutyrate aminotransferase, PLP-dependent
SNP	2797905_T_C	intergenic (-)ygaM/nraH	B2672/B2673	predicted protein/Hydrogen donor for hsdE electron transport system; glutaredoxin-like protein
SNP	2805944_A_G	pseudogene ygaY	B2681	predicted transporter (pseudogene); putative transport; Not classified; putative transport protein
SNP	2816785_G_A	G817(GCC_ahaS	B2697	alanyl-tRNA synthetase
SNP	2820864_G_A	S426I(TCC_mraA	B2699	DNA strand exchange and recombination protein with protease and nuclease activity
INS	2822302_C	coding (499)/mibB	B2701	membrane-bound lytic murein transglycosylase B
SNP	2831790_A_G	T219A(ACC_murW	B2711	NADH flavin:ubiquinone oxidoreductase
SNP	2840540_T_C	G49Y(GCC_T1c0B	B2718	protein required for maturation of hydrogenase 3
SNP	2842426_C_T	G424S(GCC_hyE	B2721	hydrogenase 3, large subunit
SNP	2842823_G_A	A291A(GCC_hyE	B2721	hydrogenase 3, large subunit
SNP	2850095_G_A	A246I(GCC_hyD	B2729	protein required for maturation of hydrogenases
SNP	2850570_G_A	H171I(TGG_T1yph	B2730	carbamoyl dehydratase, hydrogenases 1, 2, 3 maturation protein
SNP	2880050_T_C	H57V(ATT_GyxB	B2761	Cas3 predicted helicase needed for Cascade anti-viral activity
SNP	2887104_G_A	H178I(ACC_C_ued	B2765	6-pyruvoyl tetrahydropteridine synthase (PTPS)
SNP	2896522_G_A	A418I(GCC_yjeE	B2775	inner membrane protein, predicted transporter
SNP	2900205_T_C	intergenic (-)tque/yqcG	B2777/B2781	carboxy-7-deazaadenine synthase; queosine biosynthesis/expressed protein
SNP	2908424_T_C	H419H(CAC_rimC	B2785	23S rRNA m5U1939 methyltransferase, SAM-dependent
SNP	2915521_C_T	I197I(GCT_A1adp	B2789	predicted D-glucurate transporter
INS	2923099_INAMET	coding (152)/sdcC	B2796	predicted serine transporter
SNP	2923910_T_C	S335P(TCC_C_sdcC	B2796	predicted serine transporter
SNP	2923397_G_A	A361I(GCT_huK	B2803	L-fucosylase
SNP	2924943_A_G	H399I(CGC_mba	B2813	membrane-bound lytic murein transglycosylase A
INS	2942350_C	noncoding (f)metV	B2816	RNA-Met
SNP	2942666_G_A	V292A(GTC_rod	B2819	exonuclease V (RecBCD complex), alpha chain
SNP	2954593_C_T	H258I(GCC_recC	B2822	exonuclease V (RecBCD complex), gamma chain
SNP	2956636_G_A	L158I(CTG_TrecC	B2822	exonuclease V (RecBCD complex), gamma chain
INS	2957165_C	coding (278)/ppdC	B2823	predicted protein
SNP	2959882_G_A	F245I(TTC_T1yph	B2828	phosphatidylyserine-oxalophosphoethanol diacylglycerol transferase
SNP	2956449_G_A	H175G(GG_mdbS	B2832	inner membrane protein, UPF0503 family
SNP	2974608_T_C	A303A(GCT_hyR	B2839	DNA-binding transcriptional dual regulator
SNP	2979758_G_A	R172I(GCT_yjeF	B2844	predicted acyltransferase
SNP	2987213_G_A	D153N(GAT_ygeH	B2852	predicted transcriptional regulator
INS	2994352_INAMET	coding (177)/ygeR	B2865	novel lipoprotein, function unknown
INS	2994428_C	coding (101)/ygeR	B2865	novel lipoprotein, function unknown
SNP	3003503_G_A	H49I(CAT_T1yph	B2872	predicted peptidase
SNP	3003001_T_C	G153G(GGT_yjeY	B2872	predicted peptidase
INS	3009627_INAMET	intergenic (-)yqcC/mocA	B2876/B2877	conserved protein/CTP:molybdopterine cytidyltransferase
SNP	3012684_G_A	E442I(GAC_yjR	B2878	predicted oxidoreductase, Fe-S subunit
SNP	3013889_A_G	H71I(ATG_yjK	B2878	predicted oxidoreductase, Fe-S subunit
SNP	3023044_G_A	M415I(ATG_yjQ	B4464	predicted purine permease
SNP	3023578_T_C	L381I(TTA_T1yph	B2886	predicted oxidoreductase, 4Fe-4S ferredoxin-type subunit
SNP	3023900_G_A	F571I(GCC_yjeE	B2887	fused predicted oxidoreductase, Fe-S subunit/nucleoside-binding subunit
SNP	3030670_G_A	R98*(CGA_T1yph	B2891	peptide chain release factor RF-2
SNP	3051424_C_T	P169S(CCT_fau	B2912	conserved protein, 5-formyltetrahydrofolate cyclo-ligase family
SNP	3052912_G_A	T131I(CAT_araA	B2914	ribose-5-phosphate isomerase, constitutive
SNP	3071788_G_A	A116A(GCC_yggP	B4465	predicted dehydrogenase
SNP	3078743_T_A	D616E(GAT_spaA	B2938	biosynthetic arginine decarboxylase, PLP-binding

SNP	3081809_C_T	A142(VGCA_mexk	b2942	S-adenosylmethionine synthetase
SNP	3092128_C_A	G745(GGC_A_yggf	b2953	conserved protease, UPF0235 family
SNP	3093341_C_C	S220(GAGT_vgkM	b2956	conserved protein
DEL	3095712_1bp	coding (591)_yggN	b2958	predicted protein
SNP	3096674_C_C	N470(AAC_C_yg8t	b2959	conserved protein, DUF469 family
SNP	3096917_A_G	B187(NCGT_rmti	b2960	RNA methyltransferase, SAM-dependent
SNP	3104125_G_G	intergenic (-)speC/vgga	b2965/b2966	formin-like decarboxylase, constitutive/predicted inner membrane protein, DUF554 family
SNP	3105091_C_C	noncoding (6)phvV	b2967	RNA-Phe
SNP	3115501_C_G	R248(CGCT_rhga	b2975	glycylate transporter
SNP	3116307_A_G	intergenic (-)gkA/gldB	b2975/b2976	glycolate transporter/malate synthase G
SNP	3117751_C_T	N2455(AAT_gldB	b2976	malate synthase G
SNP	3124197_C_C	pseudogene yhcD	b2981	pseudogene, DNA-binding transcriptional regulator homology
SNP	3128873_C_A	G224(GGC_C_yhhV	b2986	predicted ATP-binding protein
INS	3129030_rNAME?	coding (221)_yghT	b2986	predicted ATP-binding protein
SNP	3129245_G_A	E1464(GAA_yghT	b2986	predicted ATP-binding protein
SNP	3129816_A_G	V224(GT_C_yhb	b2987	phosphate transporter
SNP	3139861_A_G	R360R(CGT_hybO	b2997	hydrogenase 2, small subunit
SNP	3140914_T	HQ9(CAT_C_hybO	b2997	hydrogenase 2, small subunit
SNP	3152015_C_C	R248(CGCT_rhga	b3012	2,5-diketide-D-glucuronate reductase A
SNP	3160152_G_A	N167N(AAC_pacC	b3019	DNA topoisomerase IV, subunit A
INS	3170470_-C	coding (216)_yqIA	b3031	acyl CoA esterase in vitro
DEL	3172183_1bp	pseudogene nudF	b3034	ADP-ribose pyrophosphatase
SNP	3176821_C_C	ARSN(GCA_C_ygdD	b3029	predicted diogenase, LigB family
SNP	3177383_A_G	MS2(VATG_csuPT	b3040	zinc transporter
INS	3179794_-C	coding (275)_yqIC	b3042	conserved protein
SNP	3182657_A_G	pseudogene yqgD	b3046	pseudogene; outer membrane usher homology/putative membrane; Not classified; putative membrane protein
SNP	3186448_G_A	Q58*(CAG_T_gq5	b3049	predicted glycogen synthesis protein
DEL	3188029_1bp	coding (486)_yqIK	b3051	PHB family membrane protein, function unknown
SNP	3189036_rNAME?	coding (1493)_yqK	b3051	PHB family membrane protein, function unknown
SNP	3195785_C_T	intergenic (-)y8F/vgM	b3054/b3055	predicted adenylate cyclase/adenylate domain protein
SNP	3202668_A_C	intergenic (-)ttdB/ttdT	b3062/b3061	tartrate dehydratase, beta subunit/L-tartrate/succinate antiporter
SNP	3223480_C_T	R334(CGC_yjgJ	b3079	conserved protein
SNP	3229918_A_G	G224(GTC_rtmD	b3084	2,3-diketide methyltransferase, SAM-dependent
SNP	3245842_G_A	G475(GGT_A_yqIG	b3102	predicted S-transferase
SNP	3245900_G_A	S675(AGC_A_tdcF	b3113	predicted L-PSF (mRNA) endoribonuclease
INS	3246019_rNAME?	coding (807)_yqG	b3118	DNA-binding transcriptional activator
SNP	3266929_A_G	V168A(GTC_garR	b3125	tartronate semialdehyde reductase
SNP	3270982_A_G	V341(GTC_garD	b3128	(D) galactarate dehydrogenase
SNP	3273798_G_A	G618(GTC_A_hzb	b3132	tagatase 6-phosphate aldolase 1, kbzA subunit
SNP	3275573_C_C	coding (178)_yqH	b3132	N-acetylglucosamine-6-phosphate epimerase, IC component of PTS, fragment (pseudogene); enzyme; Central intermediary metabolism: Amino sugars; PTS system N-acetylglucosamine-specific IC component 2
SNP	3281518_G_A	R190N(CGC_agal	b3141	galactosamine 6-phosphate isomerase
SNP	3285656_G_A	T721(ACG_yjai	b3144	predicted outer membrane protein
SNP	3291072_A_G	G224(GTC_rtmD	b3149	DNA-iniator-associating factor for replication initiation
SNP	3295666_C_T	L971(CTG_CT_yhbT	b3157	predicted lipid carrier protein, COG3154 family
SNP	3304538_G_A	S4620(CTC_tmp	b3164	polynucleotide phosphorylase/polyadenylase
SNP	3313735_C_C	T147(AAC_C_yqG	b3172	argininosuccinate synthetase
SNP	3320512_C_T	D235(GAC_fmH	b3178	protease, ATP-dependent zinc-metallo
INS	3323489_rNAME?	intergenic (-)s greA/dacB	b3181/b3182	transcript cleavage factor/D-alanyl-D-alanine carboxypeptidase
DEL	3323918_1bp	coding (276)_dacB	b3182	D-alanyl-D-alanine carboxypeptidase
SNP	3327245_C_C	K57(KAG_A_yhE	b3185	predicted inner membrane permease
SNP	3330157_G_A	R340(CGT_murA	b3189	UDP-N-acetylglucosamine 1- carboxyvinyltransferase
INS	3331348_rNAME?	coding (136)_yrbA	b3190	predicted DNA-binding transcriptional regulator, Boka family
SNP	3331774_rNAME?	coding (162)_mlaB	b3191	ABC transporter maintaining OM lipid asymmetry, cytoplasmic; STAS component
DEL	3331775_1bp	coding (162)_mlaB	b3191	ABC transporter maintaining OM lipid asymmetry, cytoplasmic; STAS component
INS	3331775_rNAME?	coding (162)_mlaB	b3191	ABC transporter maintaining OM lipid asymmetry, cytoplasmic; STAS component
SNP	3332238_G_A	Y128(ATA_t_mic	b3192	ABC transporter maintaining OM lipid asymmetry, periplasmic binding protein
SNP	3333211_C_C	AB8(GGC_C_yheV	b3196	predicted calcium/iodium/proton antiporter
SNP	3341793_A_G	intergenic (-)ptsN/yhbJ	b3204/b3205	sugar-specific enzyme IIA component of PTS(glmZ)RNA-inactivating NTPase, glucosamine-6-phosphate regulated
SNP	3342953_C_C	intergenic (-)npr/yrbL	b3206/b3207	phosphohistidinol-protein-hexose phosphotransferase component of N-regulated PTS system (Npr)/predicted protein
INS	3344817_rNAME?	coding (143)_yhb	b3207	predicted biosynthesis protein with amidotransferase-like domain
SNP	3351556_G_A	G7185(GGC_gldB	b3212	glutamate synthase, large subunit
SNP	3362330_G_A	intergenic (-)yhcF/yhcG	b3219/b3220	predicted transcriptional regulator/conserved protein
SNP	3363113_C_G	V212(GTC_yhcG	b3220	conserved protein
SNP	3363602_G_A	A366T(GCC_yhcG	b3220	conserved protein
SNP	3366232_G_A	R341(GCC_nanT	b3226	siatic acid transporter
SNP	3368618_A_G	G184(GGT_nanT	b3226	DNA-binding transcriptional repressor of the nan operon, induced by siatic acid
INS	3373919_C_C	coding (197)_yhbM	b3232	conserved protein with nucleoside triphosphate hydrolase domain
SNP	3379896_C_C	intergenic (-)argR/yhN	b3237/b3238	DNA-binding transcriptional dual regulator, L- arginine-binding/conserved protein
SNP	3381013_C_C	E619(GAA_aaeB	b3240	p-hydroxybenzoic acid efflux system component
SNP	3384682_C_C	intergenic (-)yhb	b3243	transcriptional regulator for aaeKAB operon
SNP	3391730_T_C	Y248(CTAC_rmg	b3247	ribonuclease G
SNP	3394215_A_G	G148(GGC_rmcC	b3250	cell wall structural complex MreBCD transmembrane component MreC
SNP	3397191_1bp	coding (143)_yhb	b3252	targeting factor for csiBC sRNA degradation
SNP	3397802_A_G	S71P(TCC_C_csd	b3252	targeting factor for csiBC sRNA degradation
SNP	3411569_G_A	G619Q(CAG_acrF	b3266	multidrug efflux system protein
SNP	3424214_C_T	I1007(ATT_A_yrdA	b3279	conserved protein
SNP	3435540_G_A	T57(KAC_AT_yqk	b3285	RNA polymerase, alpha subunit
SNP	3442286_T_C	G540(CAA_CrpIX	b3309	SOS ribosomal subunit protein L24
SNP	3449533_C_C	R182(RAG_a_gpa	b3323	general secretory pathway component, cryptic
SNP	3450913_G_G	L232(ATA_T_gpc	b3324	general secretory pathway component, cryptic
SNP	3451477_G_C	A141P(GCC_gspD	b3325	general secretory pathway component, cryptic
SUB	3451477_1bp_CC	coding (421)_gspD	b3325	general secretory pathway component, cryptic
SNP	3455114_C_C	W138R(TGG_gspG	b3328	pseudogenin, cryptic, general secretion pathway
INS	3474001_G_A	A18N(GCC_C_yheV	b4551	predicted protein
SNP	3476289_G_A	G1076(GGG_yheS	b3352	fused predicted transporter subunits of ABC superfamily-ATP-binding components
SNP	3487921_G_A	D816(GAT_C_FIC	b4474	fructoseylase 3-epimerase
SNP	3497813_C_C	T394(CTC_C_csd	b3374	fructoseylase 6-kinase
SNP	3514908_T_C	D1595(GAT_hufQ	b3391	protein required for the utilization of DNA as a carbon source; fibrillar transporter homolog
SNP	3548440_G_A	A226T(GCC_mnM	b3418	DNA-binding transcriptional activator for the mal regulon and maltotriose-ATP-binding protein
SNP	3548311_G_C	N472(AAC_C_yqG	b3422	sigma 54-dependent transcriptional regulator of ricBA expression
INS	3564762_-C	coding (1238)_yqK	b3431	glycogen branching enzyme
SNP	3592026_T_C	Y72(CTAT_T_civK	b3458	leucine transporter subunit
SNP	3606305_C_C	A103A(GAC_yhH	b3473	inner membrane protein, predicted transporter
SNP	3606217_G_A	T56(KAC_AT_yqk	b3473	inner membrane protein, predicted transporter
SNP	3612020_T_C	L1095(ITA_T_niK	b3479	nickel transporter subunit
INS	3630694_rNAME?	intergenic (-)yhm/yhn	b3491/b3492	inner membrane protein, DUF1323 family/predicted oxidoreductase with FAD(NAD(P))-binding domain
SNP	3645699_rNAME?	intergenic (-)yhb	b3505	predicted protein
SNP	3649664_T_C	L101P(CTC_C_dcr	b3507	predicted DNA-binding transcriptional regulator
SNP	3659590_C_C	intergenic (-)gadA/gadX	b3515/b3516	transcriptional activator of gadA and gadBC in absence of GaoX/DNA-binding transcriptional dual regulator
SNP	3660491_A_G	intergenic (-)gadP/gadZ	b3515/b3516	DNA-binding transcriptional dual regulator/glutamate decarboxylase A, PL-dependent
INS	3663217_C_C	coding (651)_yJIA	b3518	predicted cytochrome C peroxidase
SNP	3663565_T_C	A101A(GCA_yhJA	b3518	predicted cytochrome C peroxidase
SNP	3663701_C_C	E566(GAA_G_yhJA	b3518	predicted cytochrome C peroxidase
SNP	3663563_C_T	A161A(GCC_ref	b3519	cytoplasmic esterase
SNP	3677959_G_A	T561(ACC_M_dctA	b3528	C4-dicarboxylic acid, oxalate and citrate transporter
SNP	3685330_A_G	S639(CTC_yrbC	b3532	regulator of cellulose synthase, cyclic di-GMP binding
SNP	3689213_A_G	Y128(ATA_T_gpc	b3532	cellulose synthase, catalytic subunit
SNP	3694595_T_C	intergenic (-)bcg/dtdD	b3538/b445	inner membrane protein, predicted endoglucanase, DUF3260 family/toxic polypeptide, small
SNP	3696739_G_A	P270L(CCG_dppP	b3540	dipeptide transporter
SNP	3701088_A_G	W438R(TGG_dppC	b3544	dipeptide transporter
SNP	3713008_C_C	intergenic (-)dhrV/yaf	b3553/b3554	gamma-hydroxybutyrate reductase B/conserved protein
SNP	3738106_T_C	V232A(GTG_yiak	b3575	2,3-diketide-L-gulonate reductase, NADH-dependent
SNP	3742796_G_A	G345(GGC_yiK	b3580	L-xylose kinase
SNP	3751210_rNAME?	coding (695)_yrbA	b3594	predicted lyase containing HEAT-repeat
SNP	3763826_A_G	pseudogene yibW	b4651	pseudogene, rhaA-linked
SNP	3780719_G_A	N2615(AAC_gpmM	b3612	phosphoglycerate mutase III, cofactor-independent
SNP	3786661_C_C	D210(GAAC_hsl	b3617	glycine C-acetyltransferase
SNP	3791415_G_A	G253G(GGG_rfaC	b3621	ADP-heptose-LPS heptosyl transferase I
SNP	3798000_T_C	L272(CTA_C_rfaB	b3628	UDP-D-galactose:glucosyl(1)populosaccharide-1, 6-D galactosyltransferase
SNP	3801476_C_T	M90N(ATA_A_rag	b3631	glucosyltransferase I
SNP	3802400_C_C	T136(GAC_A_rfaQ	b3632	trypoglyosaccharide core biosynthesis protein
SNP	3804104_T_C	V296A(GTC_waaA	b3633	3-deoxy-D-manno-oxulosonic acid transferase (KDO transferase)
SNP	3820271_G_C	M128N(ATA_rmcG	b3652	ATP-dependent DNA helicase
SNP	3827887_C_C	H514(GTC_rmcI	b3652	predicted alpha-glucosidase
SNP	3847963_C_T	intergenic (-)yhbL/ttdB	b3672/b416	Hsp68 operon leader peptide/lexA-regulated toxic peptide involved in persister formation; membrane peptide that decreases proton motive force and ATP levels
SNP	3873773_G_A	S342T(CTC_T_yrbP	b3699	DNA gyrase, subunit B
SNP	3881801_G_A	R236(CTC_C_rmcH	b3707	hyphoplasman leader peptide
SNP	3888115_C_T	L225(CTG_T_hzJ	b3711	predicted DNA-binding transcriptional regulator
SNP	3892611_G_A	G143E(GGA_cbrB	b3716	inner membrane protein, creBC regulon
SNP	3893912_C_C	K34E(AAG_C_yieK	b3718	predicted 6-phosphoglucomutase
SNP	3904573_G_A	I168(ATA_C_yieK	b3727	phosphate transporter subunit
SNP	3919976_C_T	L112L(CTG_C_mmmG	b3741	S-methylamionomethyl-2-thiouridine modification at tRNA U34
SNP	3921055_C_T	E27K(GAA_A_micC	b3742	FMN-binding protein MicC
INS	3926212_rNAME?	coding (238)_hup	b3747	potassium transporter
SNP	3938090_C_T	intergenic (-)mrcG/glu	b3756/b3755	ribosomal RNA of rmc operon/tRNA-Glu
SNP	3951956_C_T	V209V(GTG_hvY	b3773	DNA-binding transcriptional dual regulator
SNP	3953451_C_T	G286R(GGC_dppC	b3774	keton-acid reductoisomerase, NAD(P) binding
SNP	3954807_G_A	G130V(GGC_wzE	b3785	Enterobacterial Common Antigen (ECA) polysaccharide chain length modulation protein
SNP	3972122_C_T	G389G(GGC_wzE	b3792	O-antigen transferase
SNP	3972451_C_T	H83N(CTC_C_HTF	b4481	TDP-FucNAc:lipidII-FucNAc transferase
SNP	3982862_C_T	L161L(CTG_T_hemX	b3803	predicted uracilphosphorylase III methyltransferase
SNP	3985036_C_C	A137T(GTC_hemC	b3805	hydroxymethylbilane synthase
INS	4002416_-C	intergenic (-)hrcQ/rhcT	b3822/b3823	ATP-dependent DNA gyrase/threonine efflux pump
SNP	40210915_C_G	T87A(GC_AC_ygpP	b3834	conserved protein, SCF2 family
SNP	4042354_C_T	intergenic (-)yhbA/yhbI	b3865/b3866	GTP-binding protein required for normal cell division/activator of Der GTPase
DEL	4051578_1bp	intergenic (-)ytpA/yhbI	b3871/b3872	GTP-binding protein/predicted DNA-binding transcriptional regulator
SNP	4060606_C_C	intergenic (-)ytdQ/yhbR	b3871/b3872	alpha-glucosidase/predicted aldose-1-epimerase
SNP	4062363_C_T	W222*(TTC_yhbT	b3881	predicted aldolase
SNP	4064595_A_G	S95P(TCC_C_yihU	b3882	gamma-hydroxybutyrate dehydrogenase, NADH-dependent
SNP	4088183_C_C	D191(GCAC_rhaB	b3904	hamulokinase
SNP	4107591_C_C	A54V(GTC_C_ygpD	b3923	stress-induced protein
SNP	4106697_T_C	A63A(GCA_G_ygpX	b3925	fructose 1,6-bisphosphatase II
SNP	4112687_C_T	A123T(CTC_huJ	b3931	molecular chaperone and ATPase component of HspU/Protein
SNP	4120186_C_C	T731(ACT_A_methB	b3939	cystathionine gamma-synthase, PLP-dependent
SNP	4137048_C_C	D831(ATC_A_hfD	b3951	predicted formate acetyltransferase 2 (pyruvate lyase II)
SNP	4148762_G_A	T203A(ACG_argH	b3960	argininosuccinate lyase
SNP	4166153_A_G	R60R(CTG_C_oaaB	b3974	paritiothate kinase
SNP	4211113_T_G	noncoding (5)_ybv	b4008	RNA-Glu
SNP	4207574_C_T	A264V(GCC_aceB	b4019	malate synthase A
SNP	4225208_C_C	M409V(ATG_rgi	b4025	glycosephosphate isomerase
SNP	4234883_G_A	A500V(GCC_mafF	b4033	maltose transporter subunit
SNP	4243819_A_G	H3R(CAC_CG_ubiC	b4039	chorismate-pyruvate lyase
SNP	4260633_C_T	intergenic (-)yib5/aphA	b4621/b4055	hypothetical protein/acid phosphatase/phosphotransferase, class B, non-specific
SNP	4265154_C_A	GR6(GGC_Gr_vra	b4058	ATPase and DNA damage recognition protein of nucleotide excision repair excinuclease UvrABC
INS	4292049_rNAME?	intergenic (-)yrbK/yidC	b4063/b4064	DNA-binding transcriptional dual regulator, Fe-C center for redox-sensing/predicted permease
SNP	4275252_C_T	A319A(GGC_aacP	b4067	acetate transporter
SNP	4280860_C_C	Y104N(CTC_rnfB	b4071	nitrite reductase, formate-dependent, penta-heme cytochrome c
SNP	4281388_C_T	G56(GGC_rnfC	b4072	formate-dependent nitrite reductase, 4Fe-4S subunit
SNP	4283239_G_A	R124H(GCC_nrfE	b4074	heme lyase (NrfE)G for insertion of heme into c552, subunit NrfE
INS	4287886_rNAME?	intergenic (-)yrbP/yidC	b4077/b4078	glutamate/aspartate proton symporter/conserved protein
SNP	42882715_C_C	T532R(CTC_rnfH	b4079	formate dehydrogenase-H, selenopolypeptide subunit
SNP	4289091_A_G	W528R(TGG_rnfH	b4079	formate dehydrogenase-H, selenopolypeptide subunit
SNP	4325404_A_G	V488A(GTT_espA	b4114	predicted metal dependent hydrolase

DEL	4325457_1bp	coding (1440) epfA	b4114	predicted metal dependent hydrolase
SNP	4349100_A_G	L2751ATC_A_adaA	b4211	lyxine decarboxylase, acid-inducible
SNP	4355497_G_A	G2846GGC_dsdD	b4136	fused thiol:disulfide interchange protein; activator of DsbC/conserved protein
SNP	4358824_C_T	A270AGCG_aspA	b4139	aspartate ammonia-lyase
SNP	4373280_A_G	R748(GGT_C)trdA	b4154	fumarate reductase (anaerobic) catalytic and NAD/flavo-protein subunit
SNP	4374714_C_T	R256GGT_vjyA	b4155	EF-P-lysinyl-lysine ligase
SNP	4398757_A_G	L266(LTTA_T)mir	b4179	exoribonuclease R, RNase R
SNP	4400788_A_G	r70W(ATT_GT)rimB	b4180	23S rRNA (Gm2251)-methyltransferase
SNP	4411014_C_T	intergenic (-)idgA/dubA	b4150/b4191	L-ascorbate 6-phosphate lactonase/L-ascorbate-specific enzyme IIC component of PTS
SNP	4413069_C_T	A19V(GCA_G)uacA	b4195	L-ascorbate-specific enzyme IA component of PTS
SNP	4419228_A_G	pseudogene yfA	b4205	pseudogene, related to transcriptional regulators
SNP	4423612_A_G	G658(CAC_C)yhH	b4212	predicted transcriptional regulator, HcIIr-type, DUF24 family
SNP	4438800_A_G	V961(VCTA_v)hN	b4221	large conserved protein, DUF450 family
DEL	4447073_1bp	intergenic (-)fbp/nplI	b4232/b4233	fructose-1,6-bisphosphatase I/UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl-meso-diaminopimelate lyase
SNP	4448855_T_G	N106T(AAC_C)vjyA	b4234	conserved protein, ribosome-associated
INS	4471270_#NAME?	pseudogene vjgM	b4257	inner membrane protein, DUF658 family
SNP	4473728_A_G	V472A(GTT_v)alsI	b4258	valyl-tRNA synthetase
SNP	4474935_C_T	G705(GGC_A)valS	b4258	valyl-tRNA synthetase
SNP	4482671_C_T	S387(NAG_C)nitT	b4265	L-lysine and D-glucamate transporter
SNP	4491422_C_C	pseudogene vjgX	b4575	KpLE2 phage-like element; predicted protein, C-ter fragment (pseudogene)
SNP	4503345_C_T	L125(LITG_T)ecdD	b4288	KpLE2 phage-like element; iron-dicitrate transporter subunit
SNP	4512640_C_T	G229(GGG_v)hF	b4296	KpLE2 phage-like element; predicted transporter
SNP	4513876_C_T	G508(GGG_v)hG	b4297	KpLE2 phage-like element; predicted dehydratase
SNP	4523281_G_A	intergenic (-)sgcX/yjyH	b4305/b4356	KpLE2 phage-like element; predicted endoglucanase with Zn-dependent exopeptidase domain/pseudogene, novel zinc finger family
SNP	4528939_C_C	intergenic (-)nanS/nanM	b4309/b4310	9-O-acetyl-N-acetylneuraminic acid esterase/N-acetylneuraminic acid mutarotase
INS	4541716_#NAME?	coding (886) gntP	b4321	fructuronate transporter
DEL	4544240_1bp	coding (351) uxuB	b4323	D-mannonate oxidoreductase, NAD-dependent
INS	4548065_#NAME?	intergenic (-)yjiK/radD	b4325/b4326	predicted protein/Rps stabilizer after DNA damage, anti-RssB factor
SNP	4550091_A_G	L3551(ATT_A)vjyM	b4335	predicted 2-hydroxyglutaryl-CoA dehydratase
SNP	4564710_C_T	pseudogene yjT	b4342	pseudogene
SNP	4564845_C_T	pseudogene yjT	b4342	pseudogene
SNP	4569673_T_G	P323P(CCG_m)crB	b4346	5-methylcytosine-specific restriction enzyme McrBC subunit McrB
SNP	4578853_G_A	G3015(GGC_m)rr	b4351	methylated adenine and cytosine restriction protein
SNP	4580254_A_G	Y44H(ATT_C)vjyX	b4353	conserved protein
SNP	4590564_A_G	intergenic (-)opgB/yjyA	b4359/b4366	phosphoglycerol transferases I and II/conserved protein
SNP	4590910_C_C	intergenic (-)opgB/yjyA	b4359/b4366	phosphoglycerol transferases I and II/conserved protein
INS	4597390_#NAME?	noncoding (8)leuP	b4368	tRNA-Leu
INS	4597511_#NAME?	noncoding (8)leuP	b4369	tRNA-Leu
INS	4597626_#NAME?	noncoding (8)leuQ	b4370	tRNA-Leu
DEL	4597627_1bp	noncoding (7)leuQ	b4370	tRNA-Leu
SNP	4600543_C_T	H158H(CAC_v)jyG	b4374	dUMP phosphatase
INS	4600633_+C	intergenic (+)yjiG/prfC	b4374/b4375	dUMP phosphatase/peptide chain release factor RF-3
SNP	4601280_T_C	V191(VTAT_T)prfC	b4375	peptide chain release factor RF-3
SNP	4606903_G_A	G489G(GGC_v)jyI	b4380	conserved protein
SNP	4612348_A_G	K54K(AAA_A)deoD	b4384	purine-nucleoside phosphorylase
SNP	4612459_C_T	S915(TCC_TC)deoD	b4384	purine-nucleoside phosphorylase
SNP	4613568_C_T	R166*(CGA_v)jyI	b4385	HipA family protein
SNP	4614026_A_G	G318Q(CAA_v)jyI	b4385	HipA family protein
SNP	4614061_T_C	V330A(IGT_v)jyI	b4385	HipA family protein
SNP	4615538_C_T	G1865(GGC_m)B	b4387	conserved membrane protein
SNP	4621836_C_T	intergenic (-)yjiK/alt	b4391/b4392	fused predicted transporter subunits of ABC superfamily; ATP-binding components/lytic murein transglycosylase, soluble
SNP	4623593_C_T	S528S(AGC_v)ilt	b4392	lytic murein transglycosylase, soluble
SNP	4629474_A_G	intergenic (+)creC/creD	b4399/b4400	xylose isomerase in two-component regulatory system with CreB or PhoB, regulator of the CreC regulon/inner membrane protein
INS	4630868_#NAME?	intergenic (+)creC/arcA	b4400/b4401	inner membrane protein/DNA-binding response regulator in two-component regulatory system with ArcB or CpxA