

Table T3.1 (SCV, isolate 1)

position	mutation	freq	annotation	gene	description
66457	C→A	100%	V32F (GTT→TTT)	<i>araD</i> ←	L-ribulose-5-phosphate 4-epimerase
97880	C→T	100%	S265F (TCC→TTC)	<i>murD</i> →	UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase
167632	C→A	100%	P50Q (CCG→CAG)	<i>fhuA</i> →	ferrichrome outer membrane transporter
274547	A→G	100%	intergenic (-206/-2)	<i>insH</i> ← / → <i>mmuP</i>	IS5 transposase and trans-activator/S-methylmethionine transporter
274731	Δ97,240 bp	100%		[<i>mmuP</i>]- [<i>mhpD</i>]	90 genes [<i>mmuP</i>], <i>mmuM</i> , <i>afuC</i> , <i>afuB</i> , <i>insB</i> , <i>insA</i> , <i>ykgN</i> , <i>yagB</i> , <i>yagA</i> , <i>yagE</i> , <i>yagF</i> , <i>yagG</i> , <i>yagH</i> , <i>yagI</i> , <i>argF</i> , <i>insB</i> , <i>insA</i> , <i>yagJ</i> , <i>yagK</i> , <i>yagL</i> , <i>yagM</i> , <i>yagN</i> , <i>intF</i> , <i>yagP</i> , <i>yagQ</i> , <i>yagR</i> , <i>yagS</i> , <i>yagT</i> , <i>yagU</i> , <i>ykgJ</i> , <i>yagV</i> , <i>yagW</i> , <i>yagX</i> , <i>yagY</i> , <i>yagZ</i> , <i>ykgK</i> , <i>ykgL</i> , <i>Y75_p4288</i> , <i>Y75_p4289</i> , <i>eaeH</i> , <i>insE</i> , <i>insF</i> , <i>ykgA</i> , <i>ykgB</i> , <i>ykgI</i> , <i>ykgC</i> , <i>ykgD</i> , <i>ykgE</i> , <i>ykgF</i> , <i>ykgG</i> , <i>ykgH</i> ,

position	mutation	freq	annotation	gene	description
					<i>betA, betB, betI, betT, yahA, yahB, yahC, yahD, yahE, yahF, yahG, yahH, yahI, yahJ, yahK, yahL, yahM, yahN, yahO, prpR, prpB, prpC, prpD, prpE, codB, codA, cynR, cynT, cynS, cynX, lacA, lacY, lacZ, lacI, mhpR, mhpA, mhpB, mhpC, [mhpD]</i>
547694	A→G	100%	intergenic (+123/-1156)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
547831	+G	100%	intergenic (+260/-1019)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
556858	A→T	100%	L36Q (CTG→CAG)	<i>fold</i> ←	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase
569996	G→C	100%	intergenic (+345/-120)	<i>ybcK</i> → / → <i>ybcL</i>	recombinase/kinase inhibitor
654214	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>

position	mutation	freq	annotation	gene	description
749354	C→A	100%	P17P (CCG→CCT)	<i>ybgO</i> ←	fimbrial-like adhesin protein
758440	C→A	100%	F110L (TTC→TTA)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
887234	C→A	100%	A176A (GCG→GCT)	<i>ybjJ</i> ←	transporter
987574	G→T	100%	intergenic (-170/+433)	<i>ompF</i> ← / ← <i>asnS</i>	outer membrane porin 1a (Ia;b;F)/aspara ginyl tRNA synthetase
1093686	T→C	100%	V130A (GTA→GCA)	<i>ycdT</i> →	diguanylate cyclase
1097580	C→T	20.7%	intergenic (+329/+226)	<i>ycdU</i> → / ← <i>serX</i>	inner membrane protein/tRNA- Ser
1170573	C→T	100%	intergenic (-164/-77)	<i>ycfQ</i> ← / → <i>ycfR</i>	DNA-binding transcriptional regulator/hypot hetical protein
1301041	Δ1,336 bp	100%		<i>insC-insD</i>	<i>insC</i> , <i>insD</i>
1318876	G→A	100%	P21S (CCT→TCT)	<i>trpA</i> ←	tryptophan synthase subunit alpha
1413639	Δ23,060 bp	100%		<i>[ydaO]-ynaE</i>	30 genes <i>[ydaO], intR,</i> <i>ydaQ, ydaC,</i> <i>lar, recT, recE,</i> <i>racC, ydaE,</i> <i>kil, sieB, ydaF,</i> <i>ydaG, racR,</i> <i>ydaS, ydaT,</i> <i>ydaU, ydaV,</i> <i>ydaW, rzpR,</i> <i>rzoR, trkG,</i> <i>ynaK, ydaY,</i> <i>ynaA, insH,</i> <i>stfR, tfaR,</i> <i>pinR, ynaE</i>
1483588	G→A	100%	L322L (CTG→CTA)	<i>ynbD</i> →	phosphatase, inner

position	mutation	freq	annotation	gene	description
					membrane protein
1496775	Δ1 bp	100%	coding (11/924 nt)	<i>ydcl</i> ←	DNA-binding transcriptional regulator
1615814	C→A	100%	D202Y (GAC→TAC)	<i>yneI</i> ←	aldehyde dehydrogenase
1669599	Δ1 bp	100%	coding (680/1221 nt)	<i>dgsA</i> ←	DNA-binding transcriptional repressor
1724327	Δ3 bp	12.6%	coding (493-495/2013 nt)	<i>ydhK</i> →	inner membrane protein
1844073	G→A	100%	intergenic (-224/-12)	<i>ynjH</i> ← / → <i>gdhA</i>	hypothetical protein/glutamate dehydrogenase, NADP-specific
1918872	T→A	100%	S301T (TCC→ACC)	<i>yebS</i> →	inner membrane protein
1973476	G→A	100%	L310L (CTC→CTT)	<i>tar</i> ←	methyl-accepting chemotaxis protein II
2005401	C→T	100%	E115K (GAA→AAA)	<i>fliC</i> ←	flagellar filament structural protein
2170094	C→A	100%	intergenic (-437/+32)	<i>ogrK</i> ← / ← <i>yegR</i>	DNA-binding transcriptional regulator/hypothetical protein
2320795	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
2406075	C→T	100%	V51I (GTT→ATT)	<i>nuoF</i> ←	NADH:ubiquinone oxidoreductase, chain F
2416102	G→A	100%	L233L (CTG→TTG)	<i>yfbS</i> ←	transporter
2538628	C→T	100%	T258T (ACC→ACT)	<i>cysK</i> →	cysteine synthase A, O-acetylserine sulfhydrylase A

position	mutation	freq	annotation	gene	description
					subunit
2865228	A→G	3.8%	L288P (CTG→CCG)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2865274	+46 bp	76.7%	coding (817/876 nt)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2865278	+92 bp	61.6%	coding (813/876 nt)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2866111	A→G	100%	intergenic (-21/+159)	<i>rpoS</i> ← / ← <i>nlpD</i>	RNA polymerase, sigma S (sigma 38) factor/outer membrane lipoprotein
3003330	G→A	100%	L371L (CTC→CTT)	<i>ygeV</i> ←	DNA-binding transcriptional regulator
3049815	G→T	100%	R387S (CGC→AGC)	<i>visC</i> ←	oxidoreductase
3397813	C→G	100%	D141H (GAT→CAT)	<i>yhdE</i> ←	hypothetical protein
3449851	G→A	100%	A494V (GCG→GTG)	<i>rpoC</i> ←	RNA polymerase, beta prime subunit
3742936	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
3746911	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
3750122	Δ1 bp	96.8%	coding (365/1416 nt)	<i>tnaA</i> ←	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
3750123	C→T	3.2%	G122S (GGC→AGC)	<i>tnaA</i> ←	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
3750591	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
3898657	C→G	100%	L259V	<i>yiaJ</i> →	DNA-binding

position	mutation	freq	annotation	gene	description
			(CTG→GTG)		transcriptional repressor
3958123	Δ34 bp	100%	coding (1156-1189/1287 nt)	<i>dctA</i> →	C4-dicarboxylic acid, orotate and citrate transporter
4090749	A→T	100%	Q135L (CAG→CTG)	<i>malQ</i> →	4-alpha-glucanotransferase
4165991	A→C	100%	K43T (AAA→ACA)	<i>rpsL</i> →	30S ribosomal protein S12
4310363	Δ1,199 bp	100%		<i>insH</i> –[<i>alsK</i>]	<i>insH</i> , [<i>alsK</i>]
4371271	Δ2 bp	100%	intergenic (-6/+299)	<i>dcuA</i> ← / ← <i>aspA</i>	C4-dicarboxylate antiporter/aspartate ammonia-lyase
4546535	T→A	100%	intergenic (+296/-182)	<i>fimB</i> → / → <i>fimE</i>	tyrosine recombinase/inversion of on/off regulator of <i>fimA</i> /tyrosine recombinase/inversion of on/off regulator of <i>fimA</i>

Table 3.2 (SCV, isolate 2)

position	mutation	freq	annotation	gene	description
66457	C→A	100%	V32F (GTT→TTT)	<i>AraD</i> ←	L-ribulose-5-phosphate 4-epimerase
97880	C→T	100%	S265F (TCC→TTC)	<i>murD</i> →	UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase
104633	A→C	1.8%	I218L (ATC→CTC)	<i>ftsA</i> →	ATP-binding cell division protein involved in recruitment of FtsK to Z ring
167632	C→A	100%	P50Q	<i>fhuA</i> →	ferrichrome

position	mutation	freq	annotation	gene	description
			(CCG→CAG)		outer membrane transporter
274547	A→G	100%	intergenic (-206/-2)	<i>insH</i> ← / → <i>mmuP</i>	IS5 transposase and trans-activator/S-methylmethionine transporter
274733	Δ97,240 bp	100%		[<i>mmuP</i>]- [<i>mhpD</i>]	90 genes [<i>mmuP</i>], <i>mmuM</i> , <i>afuC</i> , <i>afuB</i> , <i>insB</i> , <i>insA</i> , <i>ykgN</i> , <i>yagB</i> , <i>yagA</i> , <i>yagE</i> , <i>yagF</i> , <i>yagG</i> , <i>yagH</i> , <i>yagI</i> , <i>argF</i> , <i>insB</i> , <i>insA</i> , <i>yagJ</i> , <i>yagK</i> , <i>yagL</i> , <i>yagM</i> , <i>yagN</i> , <i>intF</i> , <i>yagP</i> , <i>yagQ</i> , <i>yagR</i> , <i>yagS</i> , <i>yagT</i> , <i>yagU</i> , <i>ykgJ</i> , <i>yagV</i> , <i>yagW</i> , <i>yagX</i> , <i>yagY</i> , <i>yagZ</i> , <i>ykgK</i> , <i>ykgL</i> , <i>Y75_p4288</i> , <i>Y75_p4289</i> , <i>eaeH</i> , <i>insE</i> , <i>insF</i> , <i>ykgA</i> , <i>ykgB</i> , <i>ykgI</i> , <i>ykgC</i> , <i>ykgD</i> , <i>ykgE</i> , <i>ykgF</i> , <i>ykgG</i> , <i>ykgH</i> , <i>betA</i> , <i>betB</i> , <i>betI</i> , <i>betT</i> , <i>yahA</i> , <i>yahB</i> , <i>yahC</i> , <i>yahD</i> , <i>yahE</i> , <i>yahF</i> , <i>yahG</i> , <i>yahH</i> , <i>yahI</i> , <i>yahJ</i> , <i>yahK</i> , <i>yahL</i> , <i>yahM</i> , <i>yahN</i> , <i>yahO</i> , <i>prpR</i> ,

position	mutation	freq	annotation	gene	description
					<i>prpB, prpC, prpD, prpE, codB, codA, cynR, cynT, cynS, cynX, lacA, lacY, lacZ, lacI, mhpR, mhpA, mhpB, mhpC, [mhpD]</i>
547694	A→G	100%	intergenic (+123/-1156)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
547831	+G	100%	intergenic (+260/-1019)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
556858	A→T	100%	L36Q (CTG→CAG)	<i>fold</i> ←	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase
569996	G→C	100%	intergenic (+345/-120)	<i>ybcK</i> → / → <i>ybcL</i>	recombinase/kinase inhibitor
654214	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
749354	C→A	100%	P17P (CCG→CCT)	<i>ybgO</i> ←	fimbrial-like adhesin protein
758440	C→A	100%	F110L (TTC→TTA)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
887234	C→A	100%	A176A (GCG→GCT)	<i>ybjJ</i> ←	transporter
987574	G→T	100%	intergenic	<i>ompF</i> ← / ←	outer

position	mutation	freq	annotation	gene	description
			(-170/+433)	<i>asnS</i>	membrane porin 1a (Ia;b;F)/asparaginyl tRNA synthetase
1093686	T→C	100%	V130A (GTA→GCA)	<i>ycdT</i> →	diguanylate cyclase
1097580	C→T	23.7%	intergenic (+329/+226)	<i>ycdU</i> → / ← <i>serX</i>	inner membrane protein/tRNA-Ser
1170573	C→T	100%	intergenic (-164/-77)	<i>ycfQ</i> ← / → <i>ycfR</i>	DNA-binding transcriptional regulator/hypothetical protein
1301041	Δ1,336 bp	100%		<i>insC-insD</i>	<i>insC, insD</i>
1318876	G→A	100%	P21S (CCT→TCT)	<i>trpA</i> ←	tryptophan synthase subunit alpha
1413639	Δ23,060 bp	100%		<i>[ydaO]-ynaE</i>	30 genes <i>[ydaO], intR, ydaQ, ydaC, lar, recT, recE, racC, ydaE, kil, sieB, ydaF, ydaG, racR, ydaS, ydaT, ydaU, ydaV, ydaW, rzpR, rzoR, trkG, ynaK, ydaY, ynaA, insH, stfR, tfaR, pinR, ynaE</i>
1483588	G→A	100%	L322L (CTG→CTA)	<i>ynbD</i> →	phosphatase, inner membrane protein
1496775	Δ1 bp	100%	coding (11/924 nt)	<i>ydcl</i> ←	DNA-binding transcriptional regulator
1615814	C→A	100%	D202Y (GAC→TAC)	<i>yneI</i> ←	aldehyde dehydrogenase
1669599	Δ1 bp	100%	coding	<i>dgsA</i> ←	DNA-binding

position	mutation	freq	annotation	gene	description
			(680/1221 nt)		transcriptional repressor
1844073	G→A	100%	intergenic (-224/-12)	<i>ynjH</i> ← / → <i>gdhA</i>	hypothetical protein/glutamate dehydrogenase, NADP-specific
1918872	T→A	100%	S301T (TCC→ACC)	<i>yebS</i> →	inner membrane protein
1973476	G→A	100%	L310L (CTC→CTT)	<i>tar</i> ←	methyl-accepting chemotaxis protein II
2005401	C→T	100%	E115K (GAA→AAA)	<i>fliC</i> ←	flagellar filament structural protein
2170094	C→A	100%	intergenic (-437/+32)	<i>ogrK</i> ← / ← <i>yegR</i>	DNA-binding transcriptional regulator/hypothetical protein
2178210	A→C	3.0%	intergenic (+179/+183)	<i>insH</i> → / ← <i>gatZ</i>	IS5 element protein/D-tagatose 1,6-bisphosphate aldolase 2, subunit
2320795	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
2406075	C→T	100%	V51I (GTT→ATT)	<i>nuoF</i> ←	NADH:ubiquinone oxidoreductase, chain F
2416102	G→A	100%	L233L (CTG→TTG)	<i>yfbS</i> ←	transporter
2538628	C→T	100%	T258T (ACC→ACT)	<i>cysK</i> →	cysteine synthase A, O-acetylserine sulfhydrylase A subunit
2865228	A→G	2.5%	L288P (CTG→CCG)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor

position	mutation	freq	annotation	gene	description
2865274	+46 bp	76.2%	coding (817/876 nt)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2865278	+92 bp	57.6%	coding (813/876 nt)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2866111	A→G	100%	intergenic (-21/+159)	<i>rpoS</i> ← / ← <i>nlpD</i>	RNA polymerase, sigma S (sigma 38) factor/outer membrane lipoprotein
3003330	G→A	100%	L371L (CTC→CTT)	<i>ygeV</i> ←	DNA-binding transcriptional regulator
3049815	G→T	100%	R387S (CGC→AGC)	<i>visC</i> ←	oxidoreductase
3397813	C→G	100%	D141H (GAT→CAT)	<i>yhdE</i> ←	hypothetical protein
3449851	G→A	100%	A494V (GCG→GTG)	<i>rpoC</i> ←	RNA polymerase, beta prime subunit
3742936	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
3746911	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
3750122	Δ1 bp	100%	coding (365/1416 nt)	<i>tnaA</i> ←	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
3750591	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
3898657	C→G	100%	L259V (CTG→GTG)	<i>yiaJ</i> →	DNA-binding transcriptional repressor
3958123	Δ34 bp	100%	coding (1156-1189/1287 nt)	<i>dctA</i> →	C4-dicarboxylic acid, orotate and citrate transporter
4090749	A→T	100%	Q135L (CAG→CTG)	<i>malQ</i> →	4-alpha-glucanotransferase
4165991	A→C	100%	K43T	<i>rpsL</i> →	30S ribosomal

position	mutation	freq	annotation	gene	description
			(AAA→ACA)		protein S12
4310363	Δ1,199 bp	100%		<i>insH</i> –[<i>alsK</i>]	<i>insH</i> , [<i>alsK</i>]
4371271	Δ2 bp	100%	intergenic (-6/+299)	<i>dcuA</i> ← / ← <i>aspA</i>	C4-dicarboxylate antiporter/aspartate ammonia-lyase
4519481	T→C	4.6%	D626G (GAT→GGT)	<i>fecA</i> ←	ferric citrate outer membrane transporter
4546535	T→A	100%	intergenic (+296/-182)	<i>fimB</i> → / → <i>fimE</i>	tyrosine recombinase/in version of on/off regulator of <i>fimA</i> /tyrosine recombinase/in version of on/off regulator of <i>fimA</i>

Table 3.3 (LCV, isolate 1)

position	mutation	freq	annotation	gene	description
66457	C → A	100%	V32F (GTT → TTT)	<i>araD</i> ←	L-ribulose-5-phosphate 4-epimerase
97880	C → T	100%	S265F (TCC → TTC)	<i>murD</i> →	UDP-N-acetyl muramoyl-L-alanine:D-glutamate ligase
167632	C → A	100%	P50Q (CCG → CAG)	<i>fhuA</i> →	ferrichrome outer membrane transporter
274547	A → G	100%	intergenic (-206/-2)	<i>insH</i> ← / → <i>mmuP</i>	IS5 transposase and trans-activator/ S-methylmethionine transporter
274733	Δ97,240 bp	100%		[<i>mmuP</i>]– [<i>mhpD</i>]	90 genes [<i>mmuP</i>],

					<i>mmuM, afuC, afuB, insB, insA, ykgN, yagB, yagA, yagE, yagF, yagG, yagH, yagI, argF, insB, insA, yagJ, yagK, yagL, yagM, yagN, intF, yagP, yagQ, yagR, yagS, yagT, yagU, ykgJ, yagV, yagW, yagX, yagY, yagZ, ykgK, ykgL, Y75_p4288, Y75_p4289, eaeH, insE, insF, ykgA, ykgB, ykgI, ykgC, ykgD, ykgE, ykgF, ykgG, ykgH, betA, betB, betI, betT, yahA, yahB, yahC, yahD, yahE, yahF, yahG, yahH, yahI, yahJ, yahK, yahL, yahM, yahN, yahO, prpR, prpB, prpC, prpD, prpE, codB, codA, cynR, cynT, cynS, cynX, lacA, lacY, lacZ, lacI, mhpR, mhpA, mhpB, mhpC, [mhpD]</i>
547694	A → G	100%	intergenic (+123/-1156)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold

					domain/hypothetical protein
547831	+G	100%	intergenic (+260/-1019)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
556858	A → T	100%	L36Q (CTG → CAG)	<i>folD</i> ←	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase /5,10-methylene-tetrahydrofolate cyclohydrolase
569996	G → C	100%	intergenic (+345/-120)	<i>ybcK</i> → / → <i>ybcL</i>	recombinase/kinase inhibitor
654214	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
749354	C → A	100%	P17P (CCG → CCT)	<i>ybgO</i> ←	fimbrial-like adhesin protein
758440	C → A	100%	F110L (TTC → TTA)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
758562	T → A	100%	L151H (CTC → CAC)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
887234	C → A	100%	A176A (GCG → GCT)	<i>ybjJ</i> ←	transporter
987574	G → T	100%	intergenic (-170/+433)	<i>ompF</i> ← / ← <i>asnS</i>	outer membrane porin 1a (Ia;b;F)/asparaginyl tRNA synthetase
1093686	T → C	100%	V130A (GTA → GCA)	<i>ycdT</i> →	diguanylate cyclase
1097580	C → T	19.1%	intergenic (+329/+226)	<i>ycdU</i> → / ← <i>serX</i>	inner membrane protein/tRNA-Ser
1170573	C → T	100%	intergenic (-164/-77)	<i>ycfQ</i> ← / → <i>ycfR</i>	DNA-binding transcriptional regulator/hypothetical protein

1197797	C → T	100%	H366H (CAC → CAT)	<i>icd</i> →	isocitrate dehydrogenase , -specific for NADP+
1301041	Δ1,336 bp	100%		<i>insC-insD</i>	<i>insC, insD</i>
1318876	G → A	100%	P21S (CCT → TCT)	<i>trpA</i> ←	tryptophan synthase subunit alpha
1413639	Δ23,060 bp	100%		<i>[ydaO]-ynaE</i>	30 genes <i>[ydaO], intR,</i> <i>ydaQ, ydaC,</i> <i>lar, recT, recE,</i> <i>racC, ydaE,</i> <i>kil, sieB, ydaF,</i> <i>ydaG, racR,</i> <i>ydaS, ydaT,</i> <i>ydaU, ydaV,</i> <i>ydaW, rzpR,</i> <i>rzoR, trkG,</i> <i>ynaK, ydaY,</i> <i>ynaA, insH,</i> <i>stfR, tfaR,</i> <i>pinR, ynaE</i>
1483588	G → A	100%	L322L (CTG → CTA)	<i>ynbD</i> →	phosphatase, inner membrane protein
1496775	Δ1 bp	100%	coding (11/924 nt)	<i>ydcI</i> ←	DNA-binding transcriptional regulator
1555625	G → A	100%	intergenic (-73/+61)	<i>adhP</i> ← / ← <i>sfcA</i>	alcohol dehydrogenase , 1-propanol preferring/mala te dehydrogenase , NAD-requiring
1615814	C → A	100%	D202Y (GAC → TAC)	<i>yneI</i> ←	aldehyde dehydrogenase
1669599	Δ1 bp	100%	coding (680/1221 nt)	<i>dgsA</i> ←	DNA-binding transcriptional repressor
1844073	G → A	100%	intergenic (-224/-12)	<i>ynjH</i> ← / → <i>gdhA</i>	hypothetical protein/glutam ate dehydrogenase ,

					NADP-specific
1918872	T → A	100%	S301T (TCC → ACC)	<i>yebS</i> →	inner membrane protein
1973476	G → A	100%	L310L (CTC → CTT)	<i>tar</i> ←	methyl-accepting chemotaxis protein II
2005401	C → T	100%	E115K (GAA → AAA)	<i>fliC</i> ←	flagellar filament structural protein
2170094	C → A	100%	intergenic (-437/+32)	<i>ogrK</i> ← / ← <i>yegR</i>	DNA-binding transcriptional regulator/hypothetical protein
2320795	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
2406075	C → T	100%	V51I (GTT → ATT)	<i>nuoF</i> ←	NADH:ubiquinone oxidoreductase, chain F
2416102	G → A	100%	L233L (CTG → TTG)	<i>yfbS</i> ←	transporter
2538628	C → T	100%	T258T (ACC → ACT)	<i>cysK</i> →	cysteine synthase A, O-acetylserine sulfhydrylase A subunit
2866111	A → G	100%	intergenic (-21/+159)	<i>rpoS</i> ← / ← <i>nlpD</i>	RNA polymerase, sigma S (sigma 38) factor/outer membrane lipoprotein
3003330	G → A	100%	L371L (CTC → CTT)	<i>ygeV</i> ←	DNA-binding transcriptional regulator
3049815	G → T	100%	R387S (CGC → AGC)	<i>visC</i> ←	oxidoreductase
3397813	C → G	100%	D141H (GAT → CAT)	<i>yhdE</i> ←	hypothetical protein
3406254	Δ3 bp	12.3%	coding (483-485/1350 nt)	<i>accC</i> →	acetyl-CoA carboxylase, biotin carboxylase subunit

3742936	Δ 1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
3746911	Δ 1,199 bp	100%		<i>insH</i>	<i>insH</i>
3750122	Δ 1 bp	95.0%	coding (365/1416 nt)	<i>tnaA</i> ←	tryptophanase/ L-cysteine desulfhydrase, PLP-dependent
3750123	C → T	4.6%	G122S (GGC → AGC)	<i>tnaA</i> ←	tryptophanase/ L-cysteine desulfhydrase, PLP-dependent
3898657	C → G	100%	L259V (CTG → GTG)	<i>yiaJ</i> →	DNA-binding transcriptional repressor
3958123	Δ 34 bp	100%	coding (1156-1189/1287 nt)	<i>dctA</i> →	C4-dicarboxylic acid, orotate and citrate transporter
4090749	A → T	100%	Q135L (CAG → CTG)	<i>malQ</i> →	4-alpha-glucan otransferase
4165991	A → C	100%	K43T (AAA → ACA)	<i>rpsL</i> →	30S ribosomal protein S12
4310363	Δ 1,199 bp	100%		<i>insH-[alsK]</i>	<i>insH, [alsK]</i>
4371271	Δ 2 bp	100%	intergenic (-6/+299)	<i>dcuA</i> ← / ← <i>aspA</i>	C4-dicarboxylate antiporter/aspartate ammonia-lyase
4546535	T → A	100%	intergenic (+296/-182)	<i>fimB</i> → / → <i>fimE</i>	tyrosine recombinase/in version of on/off regulator of <i>fimA</i> /tyrosine recombinase/in version of on/off regulator of <i>fimA</i>

Table 3.4 (LCV, isolate2)

position	mutation	freq	annotation	gene	description
66457	C → A	100%	V32F (GTT → TTT)	<i>araD</i> ←	L-ribulose-5-phosphate 4-epimerase
97880	C → T	100%	S265F	<i>murD</i> →	UDP-N-acetyl

			(TCC → TTC)		muramoyl-L-alanine:D-glutamate ligase
167632	C → A	100%	P50Q (CCG → CAG)	<i>fhuA</i> →	ferrichrome outer membrane transporter
274547	A → G	100%	intergenic (-206/-2)	<i>insH</i> ← / → <i>mmuP</i>	IS5 transposase and trans-activator/S-methylmethionine transporter
274733	Δ97,240 bp	100%		[<i>mmuP</i>]- [<i>mhpD</i>]	90 genes [<i>mmuP</i>], <i>mmuM</i> , <i>afuC</i> , <i>afuB</i> , <i>insB</i> , <i>insA</i> , <i>ykgN</i> , <i>yagB</i> , <i>yagA</i> , <i>yagE</i> , <i>yagF</i> , <i>yagG</i> , <i>yagH</i> , <i>yagI</i> , <i>argF</i> , <i>insB</i> , <i>insA</i> , <i>yagJ</i> , <i>yagK</i> , <i>yagL</i> , <i>yagM</i> , <i>yagN</i> , <i>intF</i> , <i>yagP</i> , <i>yagQ</i> , <i>yagR</i> , <i>yagS</i> , <i>yagT</i> , <i>yagU</i> , <i>ykgJ</i> , <i>yagV</i> , <i>yagW</i> , <i>yagX</i> , <i>yagY</i> , <i>yagZ</i> , <i>ykgK</i> , <i>ykgL</i> , <i>Y75_p4288</i> , <i>Y75_p4289</i> , <i>eaeH</i> , <i>insE</i> , <i>insF</i> , <i>ykgA</i> , <i>ykgB</i> , <i>ykgI</i> , <i>ykgC</i> , <i>ykgD</i> , <i>ykgE</i> , <i>ykgF</i> , <i>ykgG</i> , <i>ykgH</i> , <i>betA</i> , <i>betB</i> , <i>betI</i> , <i>betT</i> , <i>yahA</i> , <i>yahB</i> , <i>yahC</i> , <i>yahD</i> , <i>yahE</i> , <i>yahF</i> , <i>yahG</i> , <i>yahH</i> , <i>yahI</i> , <i>yahJ</i> , <i>yahK</i> , <i>yahL</i> , <i>yahM</i> , <i>yahN</i> ,

					<i>yahO, prpR, prpB, prpC, prpD, prpE, codB, codA, cynR, cynT, cynS, cynX, lacA, lacY, lacZ, lacI, mhpR, mhpA, mhpB, mhpC, [mhpD]</i>
547694	A → G	100%	intergenic (+123/-1156)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
547831	+G	100%	intergenic (+260/-1019)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
556858	A → T	100%	L36Q (CTG → CAG)	<i>fold</i> ←	bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase /5,10-methylene-tetrahydrofolate cyclohydrolase
569996	G → C	100%	intergenic (+345/-120)	<i>ybcK</i> → / → <i>ybcL</i>	recombinase/kinase inhibitor
749354	C → A	100%	P17P (CCG → CCT)	<i>ybgO</i> ←	fimbrial-like adhesin protein
758440	C → A	100%	F110L (TTC → TTA)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
758562	T → A	100%	L151H (CTC → CAC)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
887234	C → A	100%	A176A (GCG → GCT)	<i>ybjJ</i> ←	transporter
987574	G → T	100%	intergenic (-170/+433)	<i>ompF</i> ← / ← <i>asnS</i>	outer membrane

					porin 1a (Ia;b;F)/asparaginyl tRNA synthetase
1093686	T → C	100%	V130A (GTA → GCA)	<i>ycdT</i> →	diguanylate cyclase
1097580	C → T	18.8%	intergenic (+329/+226)	<i>ycdU</i> → / ← <i>serX</i>	inner membrane protein/tRNA-Ser
1170573	C → T	100%	intergenic (-164/-77)	<i>ycfQ</i> ← / → <i>ycfR</i>	DNA-binding transcriptional regulator/hypothetical protein
1197797	C → T	100%	H366H (CAC → CAT)	<i>icd</i> →	isocitrate dehydrogenase, -specific for NADP+
1301041	Δ1,336 bp	100%		<i>insC-insD</i>	<i>insC, insD</i>
1318876	G → A	100%	P21S (CCT → TCT)	<i>trpA</i> ←	tryptophan synthase subunit alpha
1413639	Δ23,060 bp	100%		<i>[ydaO]-ynaE</i>	30 genes <i>[ydaO], intR, ydaQ, ydaC, lar, recT, recE, racC, ydaE, kil, sieB, ydaF, ydaG, racR, ydaS, ydaT, ydaU, ydaV, ydaW, rzpR, rzoR, trkG, ynaK, ydaY, ynaA, insH, stfR, tfaR, pinR, ynaE</i>
1483588	G → A	100%	L322L (CTG → CTA)	<i>ynbD</i> →	phosphatase, inner membrane protein
1496775	Δ1 bp	100%	coding (11/924 nt)	<i>ydcI</i> ←	DNA-binding transcriptional regulator
1555625	G → A	100%	intergenic (-73/+61)	<i>adhP</i> ← / ← <i>sfcA</i>	alcohol dehydrogenase, 1-propanol

					preferring/malate dehydrogenase, NAD-requiring
1615814	C → A	100%	D202Y (GAC → TAC)	<i>yneI</i> ←	aldehyde dehydrogenase
1669599	Δ1 bp	100%	coding (680/1221 nt)	<i>dgsA</i> ←	DNA-binding transcriptional repressor
1844073	G → A	100%	intergenic (-224/-12)	<i>ynjH</i> ← / → <i>gdhA</i>	hypothetical protein/glutamate dehydrogenase, NADP-specific
1907281	C → A	1.9%	intergenic (+308/-121)	<i>yobD</i> → / → <i>yebN</i>	inner membrane protein/inner membrane protein
1918872	T → A	100%	S301T (TCC → ACC)	<i>yebS</i> →	inner membrane protein
1973476	G → A	100%	L310L (CTC → CTT)	<i>tar</i> ←	methyl-accepting chemotaxis protein II
2005401	C → T	100%	E115K (GAA → AAA)	<i>fliC</i> ←	flagellar filament structural protein
2170094	C → A	100%	intergenic (-437/+32)	<i>ogrK</i> ← / ← <i>yegR</i>	DNA-binding transcriptional regulator/hypothetical protein
2320795	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
2406075	C → T	100%	V51I (GTT → ATT)	<i>nuoF</i> ←	NADH:ubiquinone oxidoreductase, chain F
2416102	G → A	100%	L233L (CTG → TTG)	<i>yfbS</i> ←	transporter
2538628	C → T	100%	T258T (ACC → ACT)	<i>cysK</i> →	cysteine synthase A, O-acetylserine sulfhydrylase A subunit

2866111	A → G	100%	intergenic (-21/+159)	<i>rpoS</i> ← / ← <i>nlpD</i>	RNA polymerase, sigma S (sigma 38) factor/outer membrane lipoprotein
3003330	G → A	100%	L371L (CTC → CTT)	<i>ygeV</i> ←	DNA-binding transcriptional regulator
3049815	G → T	100%	R387S (CGC → AGC)	<i>visC</i> ←	oxidoreductase
3397813	C → G	100%	D141H (GAT → CAT)	<i>yhdE</i> ←	hypothetical protein
3742936	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
3750122	Δ1 bp	100%	coding (365/1416 nt)	<i>tnaA</i> ←	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
3750591	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
3898657	C → G	100%	L259V (CTG → GTG)	<i>yiaJ</i> →	DNA-binding transcriptional repressor
3958123	Δ34 bp	100%	coding (1156-1189/1287 nt)	<i>dctA</i> →	C4-dicarboxylic acid, orotate and citrate transporter
4090749	A → T	100%	Q135L (CAG → CTG)	<i>malQ</i> →	4-alpha-glucanotransferase
4165991	A → C	100%	K43T (AAA → ACA)	<i>rpsL</i> →	30S ribosomal protein S12
4310363	Δ1,199 bp	100%		<i>insH-[alsK]</i>	<i>insH, [alsK]</i>
4353540	T → C	1.1%	intergenic (-118/+453)	<i>dcuB</i> ← / ← <i>dcuR</i>	C4-dicarboxylate antiporter/DNA-binding response regulator in two-component regulatory system with DcuS
4371271	Δ2 bp	100%	intergenic (-6/+299)	<i>dcuA</i> ← / ← <i>aspA</i>	C4-dicarboxylate antiporter/aspartate

					ammonia-lyase
4546535	T → A	100%	intergenic (+296/-182)	<i>fimB</i> → / → <i>fimE</i>	tyrosine recombinase/in version of on/off regulator of <i>fimA</i> /tyrosine recombinase/in version of on/off regulator of <i>fimA</i>

Table 3.5 (Mixed population)

position	mutation	freq	annotation	gene	description
66457	C → A	100%	V32F (GTT → TTT)	<i>araD</i> ←	L-ribulose-5-p hosphate 4-epimerase
97880	C → T	100%	S265F (TCC → TTC)	<i>murD</i> →	UDP-N-acetyl muramoyl-L-al anine:D-gluta mate ligase
167632	C → A	100%	P50Q (CCG → CAG)	<i>fhuA</i> →	ferrichrome outer membrane transporter
274547	A → G	100%	intergenic (-206/-2)	<i>insH</i> ← / → <i>mmuP</i>	IS5 transposase and trans-activator/ S-methylmethi onine transporter
274733	Δ97,240 bp	100%		[<i>mmuP</i>]- [<i>mhpD</i>]	90 genes [<i>mmuP</i>], <i>mmuM</i> , <i>afuC</i> , <i>afuB</i> , <i>insB</i> , <i>insA</i> , <i>ykgN</i> , <i>yagB</i> , <i>yagA</i> , <i>yagE</i> , <i>yagF</i> , <i>yagG</i> , <i>yagH</i> , <i>yagI</i> , <i>argF</i> , <i>insB</i> , <i>insA</i> , <i>yagJ</i> , <i>yagK</i> , <i>yagL</i> , <i>yagM</i> , <i>yagN</i> , <i>intF</i> , <i>yagP</i> , <i>yagQ</i> , <i>yagR</i> , <i>yagS</i> ,

					<p>yagT, yagU, ykgJ, yagV, yagW, yagX, yagY, yagZ, ykgK, ykgL, Y75_p4288, Y75_p4289, eaeH, insE, insF, ykgA, ykgB, ykgI, ykgC, ykgD, ykgE, ykgF, ykgG, ykgH, betA, betB, betI, betT, yahA, yahB, yahC, yahD, yahE, yahF, yahG, yahH, yahI, yahJ, yahK, yahL, yahM, yahN, yahO, prpR, prpB, prpC, prpD, prpE, codB, codA, cynR, cynT, cynS, cynX, lacA, lacY, lacZ, lacI, mhpR, mhpA, mhpB, mhpC, [mhpD]</p>
547694	A → G	100%	intergenic (+123/-1156)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
547831	+G	100%	intergenic (+260/-1019)	<i>fdrA</i> → / → <i>ylbF</i>	acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein
556858	A → T	100%	L36Q (CTG → CAG)	<i>folD</i> ←	bifunctional 5,10-methylene-tetrahydrofolate

					dehydrogenase /5,10-methylene-tetrahydrofolate cyclohydrolase
569996	G → C	100%	intergenic (+345/-120)	<i>ybcK</i> → / → <i>ybcL</i>	recombinase/kinase inhibitor
654214	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
749354	C → A	100%	P17P (CCG → CCT)	<i>ybgO</i> ←	fimbrial-like adhesin protein
758440	C → A	44.7%	F110L (TTC → TTA)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
758562	T → A	5.2%	L151H (CTC → CAC)	<i>sdhB</i> →	succinate dehydrogenase, FeS subunit
887234	C → A	100%	A176A (GCG → GCT)	<i>ybjJ</i> ←	transporter
987574	G → T	100%	intergenic (-170/+433)	<i>ompF</i> ← / ← <i>asnS</i>	outer membrane porin 1a (Ia;b;F)/asparaginyl tRNA synthetase
1093686	T → C	100%	V130A (GTA → GCA)	<i>ycdT</i> →	diguanylate cyclase
1097580	C → T	18.4%	intergenic (+329/+226)	<i>ycdU</i> → / ← <i>serX</i>	inner membrane protein/tRNA-Ser
1170573	C → T	100%	intergenic (-164/-77)	<i>ycfQ</i> ← / → <i>ycfR</i>	DNA-binding transcriptional regulator/hypothetical protein
1197797	C → T	3.2%	H366H (CAC → CAT)	<i>icd</i> →	isocitrate dehydrogenase, -specific for NADP+
1197809	C → T	2.7%	T370T (ACC → ACT)	<i>icd</i> →	isocitrate dehydrogenase, -specific for NADP+
1197822	T → C	2.6%	L375L (TTA → CTA)	<i>icd</i> →	isocitrate dehydrogenase, -specific for NADP+

1197824	A → G	2.6%	L375L (TTA → TTG)	<i>icd</i> →	isocitrate dehydrogenase, -specific for NADP+
1197857	G → C	1.4%	A386A (GCG → GCC)	<i>icd</i> →	isocitrate dehydrogenase, -specific for NADP+
1301041	Δ1,336 bp	100%		<i>insC-insD</i>	<i>insC, insD</i>
1306963	C → T	5.1%	P166S (CCG → TCG)	<i>oppD</i> →	oligopeptide transporter subunit
1318876	G → A	100%	P21S (CCT → TCT)	<i>trpA</i> ←	tryptophan synthase subunit alpha
1413639	Δ23,060 bp	100%		<i>[ydaO]-ynaE</i>	30 genes <i>[ydaO], intR, ydaQ, ydaC, lar, recT, recE, racC, ydaE, kil, sieB, ydaF, ydaG, racR, ydaS, ydaT, ydaU, ydaV, ydaW, rzpR, rzoR, trkG, ynaK, ydaY, ynaA, insH, stfR, tfaR, pinR, ynaE</i>
1483588	G → A	100%	L322L (CTG → CTA)	<i>ynbD</i> →	phosphatase, inner membrane protein
1496775	Δ1 bp	100%	coding (11/924 nt)	<i>ydcI</i> ←	DNA-binding transcriptional regulator
1555625	G → A	4.6%	intergenic (-73/+61)	<i>adhP</i> ← / ← <i>sfcA</i>	alcohol dehydrogenase, 1-propanol preferring/malate dehydrogenase, NAD-requiring
1615814	C → A	100%	D202Y (GAC → TAC)	<i>yneI</i> ←	aldehyde dehydrogenase

1669599	Δ1 bp	100%	coding (680/1221 nt)	<i>dgsA</i> ←	DNA-binding transcriptional repressor
1844073	G → A	100%	intergenic (-224/-12)	<i>ynjH</i> ← / → <i>gdhA</i>	hypothetical protein/glutam ate dehydrogenase , NADP-specific
1918872	T → A	100%	S301T (TCC → ACC)	<i>yebS</i> →	inner membrane protein
1973476	G → A	100%	L310L (CTC → CTT)	<i>tar</i> ←	methyl-accepti ng chemotaxis protein II
2005401	C → T	100%	E115K (GAA → AAA)	<i>fliC</i> ←	flagellar filament structural protein
2170094	C → A	100%	intergenic (-437/+32)	<i>ogrK</i> ← / ← <i>yegR</i>	DNA-binding transcriptional regulator/hypot hetical protein
2320795	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
2406075	C → T	100%	V51I (GTT → ATT)	<i>nuoF</i> ←	NADH:ubiquin one oxidoreductase , chain F
2416102	G → A	100%	L233L (CTG → TTG)	<i>yfbS</i> ←	transporter
2538628	C → T	100%	T258T (ACC → ACT)	<i>cysK</i> →	cysteine synthase A, O-acetylserine sulfhydrylase A subunit
2733780	T → A	11.3%	E296D (GAA → GAT)	<i>rluD</i> ←	23S rRNA pseudouridine synthase
2865228	A → G	5.1%	L288P (CTG → CCG)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2865274	+46 bp	21.5%	coding (817/876 nt)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor

2865278	+92 bp	8.9%	coding (813/876 nt)	<i>rpoS</i> ←	RNA polymerase, sigma S (sigma 38) factor
2866111	A → G	100%	intergenic (-21/+159)	<i>rpoS</i> ← / ← <i>nlpD</i>	RNA polymerase, sigma S (sigma 38) factor/outer membrane lipoprotein
3003330	G → A	100%	L371L (CTC → CTT)	<i>ygeV</i> ←	DNA-binding transcriptional regulator
3049815	G → T	100%	R387S (CGC → AGC)	<i>visC</i> ←	oxidoreductase
3397813	C → G	100%	D141H (GAT → CAT)	<i>yhdE</i> ←	hypothetical protein
3449851	G → A	13.6%	A494V (GCG → GTG)	<i>rpoC</i> ←	RNA polymerase, beta prime subunit
3450056	C → A	22.3%	A426S (GCA → TCA)	<i>rpoC</i> ←	RNA polymerase, beta prime subunit
3742936	Δ1,336 bp	100%		<i>insD-insC</i>	<i>insD, insC</i>
3746911	Δ1,199 bp	100%		<i>insH</i>	<i>insH</i>
3750122	Δ1 bp	97.5%	coding (365/1416 nt)	<i>tnaA</i> ←	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
3750123	C → T	2.5%	G122S (GGC → AGC)	<i>tnaA</i> ←	tryptophanase/L-cysteine desulfhydrase, PLP-dependent
3898657	C → G	100%	L259V (CTG → GTG)	<i>viaJ</i> →	DNA-binding transcriptional repressor
3958123	Δ34 bp	99.6%	coding (1156-1189/1287 nt)	<i>dctA</i> →	C4-dicarboxylic acid, orotate and citrate transporter
4090749	A → T	100%	Q135L (CAG → CTG)	<i>malQ</i> →	4-alpha-glucanotransferase
4165991	A → C	100%	K43T	<i>rpsL</i> →	30S ribosomal

			(AAA → ACA)		protein S12
4200197	A → G	36.1%	K271E (AAA → GAA)	<i>rpoA</i> →	RNA polymerase subunit alpha
4310363	Δ1,199 bp	100%		<i>insH</i> –[<i>alsK</i>]	<i>insH</i> , [<i>alsK</i>]
4346527	C → G	3.9%	intergenic (-221/-62)	<i>melR</i> ← / → <i>melA</i>	DNA-binding transcriptional dual regulator/alpha-galactosidase
4346883	T → A	3.3%	F99I (TTC → ATC)	<i>melA</i> →	alpha-galactosidase
4347339	C → T	2.8%	R251C (CGC → TGC)	<i>melA</i> →	alpha-galactosidase
4371271	Δ2 bp	100%	intergenic (-6/+299)	<i>dcuA</i> ← / ← <i>aspA</i>	C4-dicarboxylate antiporter/aspartate ammonia-lyase
4371461	T → C	2.4%	intergenic (-196/+110)	<i>dcuA</i> ← / ← <i>aspA</i>	C4-dicarboxylate antiporter/aspartate ammonia-lyase
4546535	T → A	100%	intergenic (+296/-182)	<i>fimB</i> → / → <i>fimE</i>	tyrosine recombinase/inversion of on/off regulator of <i>fimA</i> /tyrosine recombinase/inversion of on/off regulator of <i>fimA</i>