

| | Position | Mutation | Annotation | Gene | Function |
|----|----------|------------|----------------------------|-----------------|--|
| 1 | 66457 | C→A | V32F (GTT→TTT) | araD ← | L-ribulose-5-phosphate 4-epimerase |
| 2 | 97880 | C→T | S265F (TCC→TTC) | murD → | UDP-N-acetylmuramoyl-L-alanine:D-glutamate ligase |
| 3 | 167632 | C→A | P50Q (CCG→CAG) | fhuA → | ferrichrome outer membrane transporter |
| 4 | 274547 | A→G | intergenic (-206/-2) | insH ← / → mmuP | ISS transposase and trans-activator/S-methylmethionine transporter |
| 5 | 274733 | Δ97,240 bp | | [mmuP]-[mhpD] | 90 genes: [mmuP], 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, betL, 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][mmuP], 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, betL, 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] |
| 6 | 547694 | A→G | intergenic (+123/-1156) | fdrA → / → ylbF | acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein |
| 7 | 547831 | +G | intergenic (+260/-1019) | fdrA → / → ylbF | acyl-CoA synthetase with NAD(P)-binding Rossmann-fold domain/hypothetical protein |
| 8 | 556858 | A→T | L36Q (CTG→CAG) | folD ← | bifunctional 5,10-methylene-tetrahydrofolate dehydrogenase/5,10-methylene-tetrahydrofolate cyclohydrolase |
| 9 | 569996 | G→C | intergenic (+345/-120) | ybcK → / → ybcL | recombinase/kinase inhibitor |
| 10 | 654214 | Δ1,199 bp | | insH | insH |
| 11 | 749354 | C→A | P17P (CCG→CCT) | ybgO ← | fimbrial-like adhesin protein |
| 12 | 758440 | C→A | F110L (TTC→TTA) | sdhB → | succinate dehydrogenase, FeS subunit |
| 13 | 887234 | C→A | A176A (GCG→GCT) | ybjJ ← | transporter |
| 14 | 987574 | G→T | intergenic (-170/+433) | ompF ← / ← asnS | outer membrane porin 1a (la;b;F)/asparaginyl tRNA synthetase |
| 15 | 1093686 | T→C | V130A (GTA→GCA) | ycdT → | diguanylate cyclase |
| 16 | 1170573 | C→T | intergenic (-164/-77) | ycfQ ← / → ycfR | DNA-binding transcriptional regulator/hypothetical protein |
| 17 | 1301041 | Δ1,336 bp | | insC-insD | insC, insD |
| 18 | 1318876 | G→A | P21S (CCT→TCT) | trpA ← | tryptophan synthase subunit alpha |
| 19 | 1413639 | Δ23,060 bp | | [ydaO]-ynaE | 30 genes: [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[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 |
| 20 | 1483588 | G→A | L322L (CTG→CTA) | ynbD → | phosphatase, inner membrane protein |
| 21 | 1496775 | Δ1 bp | coding (11/924 nt) | ydcI ← | DNA-binding transcriptional regulator |
| 22 | 1615814 | C→A | D202Y (GAC→TAC) | yneI ← | aldehyde dehydrogenase |
| 23 | 1669599 | Δ1 bp | coding (680/1221 nt) | dgsA ← | DNA-binding transcriptional repressor |
| 24 | 1844073 | G→A | intergenic (-224/-12) | ynjH ← / → gdhA | hypothetical protein/glutamate dehydrogenase, NADP-specific |
| 25 | 1918872 | T→A | S301T (TCC→ACC) | yebS → | inner membrane protein |
| 26 | 1973476 | G→A | L310L (CTC→CTT) | tar ← | methyl-accepting chemotaxis protein II |
| 27 | 2005401 | C→T | E115K (GAA→AAA) | fliC ← | flagellar filament structural protein |
| 28 | 2170094 | C→A | intergenic (-437/+32) | ogrK ← / ← yegR | DNA-binding transcriptional regulator/hypothetical protein |
| 29 | 2320795 | Δ1,336 bp | | insD-insC | insD, insC |
| 30 | 2406075 | C→T | V51I (GTT→ATT) | nuoF ← | NADH:ubiquinone oxidoreductase, chain F |
| 31 | 2416102 | G→A | L233L (CTG→TTG) | yfbS ← | transporter |
| 32 | 2538628 | C→T | T258T (ACC→ACT) | cysK → | cysteine synthase A, O-acetylserine sulfhydrylase A subunit |
| 33 | 2865274 | +46 bp | coding (817/876 nt) | rpoS ← | RNA polymerase, sigma S (sigma 38) factor |
| 34 | 2866111 | A→G | intergenic (-21/+159) | rpoS ← / ← nlpD | RNA polymerase, sigma S (sigma 38) factor/outer membrane lipoprotein |
| 35 | 3003330 | G→A | L371L (CTC→CTT) | ygeV ← | DNA-binding transcriptional regulator |
| 36 | 3049815 | G→T | R387S (CGC→AGC) | visC ← | oxidoreductase |
| 37 | 3397813 | C→G | D141H (GAT→CAT) | yhdE ← | hypothetical protein |
| 38 | 3742936 | Δ1,336 bp | | insD-insC | insD, insC |
| 39 | 3746911 | Δ1,199 bp | | insH | insH |
| 40 | 3750122 | Δ1 bp | coding (365/1416 nt) | tnaA ← | tryptophanase/L-cysteine desulfhydrase, PLP-dependent |
| 41 | 3898657 | C→G | L259V (CTG→GTG) | yiaJ → | DNA-binding transcriptional repressor |
| 42 | 3958123 | Δ34 bp | coding (1156-1189/1287 nt) | dctA → | C4-dicarboxylic acid, orotate and citrate transporter |
| 43 | 4090749 | A→T | Q135L (CAG→CTG) | malQ → | 4-alpha-glucanotransferase |
| 44 | 4165991 | A→C | K43T (AAA→ACA) | rpsL → | 30S ribosomal protein S12 |
| 45 | 4310363 | Δ1,199 bp | | insH-[alsK] | insH, [alsK] |
| 46 | 4371271 | Δ2 bp | intergenic (-6/+299) | dcuA ← / ← aspA | C4-dicarboxylate antiporter/aspartate ammonia-lyase |
| 47 | 4546535 | T→A | intergenic (+296/-182) | fimB → / → fimE | tyrosine recombinase/inversion of on/off regulator of fimA/tyrosine recombinase/inversion of on/off regulator of fimA |