

Table S6. Polymorphisms and fixed mutations in an *E. coli* evolving population under mild genetic drift effect

Genome position	Mutation	Individuals kind	Gene	Description
34,112 Δ1 bp		6.40% intergenic (-74/-188)	<i>carB</i>	→ carbon-β-phosphate synthase large subunit/DNA-binding transcriptional activator
45,078 C		100% A300V (GCC→GTC)	<i>fixC</i>	→ predicted oxidoreductase with FAD/NAD(P)-binding domain
83,967 C→T		100% S61L (TCA→TIA)	<i>cre</i>	→ DNA-binding transcriptional repressor-activator for carbon metabolism
94,792 C→T		5.10% A249V (GCA→GTA)	<i>ftsW</i>	→ Lipid II flippase; integral membrane protein involved in stabilizing FtsZ ring during cell division
103,188 +T		100% intergenic (+70/-229)	<i>lpxC</i>	→ UDP-3-O-acyl N-acetylglucosamine deacetylase/regulator of sac translocation
115,381 +G		2.60% coding (458/855 nt)	<i>ampE</i>	→ predicted inner membrane protein
125,879 A→G		4.10% V342A (GTC→GCC)	<i>yachI</i>	→ predicted protein
134,998 T→C		5.60% N624S (AAC→AGC)	<i>gcd</i>	→ glucose dehydrogenase
143,452 A→G		7.90% D281G (GAC→GAC)	<i>yadD</i>	→ predicted transposase
162,606 G→A		2.60% R145H (CGT→CAT)	<i>mrcB</i>	→ fused glycosyl transferase and transpeptidase
221,872 A→G		3.70% noncoding (471/2904 nt)	<i>rriH</i>	→ 23S ribosomal RNA of rriH operon
256,437 Δ1 bp		4.60% coding (68/1254 nt)	<i>proA</i>	→ gamma-glutamylphosphate reductase
263,342 G→A		2.10% S162S (AGC→AGT)	<i>ykfA</i>	→ CP4-6 prophage; predicted GTP-binding protein
302,914 +C		100% coding (1286/2526 nt)	<i>yagX</i>	→ predicted aromatic compound dioxygenase
305,276 G→A		100% S88L (TCA→TAA)	<i>matB</i>	→ cryptic Mat fibrillin gene
332,612 C→T		66.00% T323M (AGC→ATG)	<i>yahF</i>	→ predicted acyl-CoA synthetase with NAD(P)-binding domain and succinyl-CoA synthetase domain
354,567 Δ1 bp		4.70% coding (212/471 nt)	<i>cynS</i>	→ cyanate aminohydrolase
374,880 Δ1 bp		48.00% intergenic (-132/+56)	<i>fmrR</i>	→ regulator protein that represses fmrRAB operon/outer membrane protein
374,881 Δ1 bp		5.80% intergenic (-133/+55)	<i>fmrR</i>	→ regulator protein that represses fmrRAB operon/outer membrane protein
382,904 G→A		3.20% E81E (GAG→GAA)	<i>tauD</i>	→ tauroxanthine 2,2-oxoglutarate-dependent
421,890 G→A		2.30% G296D (GGC→GAC)	<i>tgt</i>	→ tRNA-guanine transglycosylase
428,446 A→G		6.20% Y36C (TAC→TGC)	<i>nbD</i>	→ fused diaminohydroxyphosphoribosylaminopyrimidine deaminase and 5-amino-6-(5-phosphoribosylamino) uracil reductase
441,376 G→A		4.70% A53V (GCC→GTC)	<i>yajR</i>	→ predicted transporter
446,939 A→G		14.30% *492Q (TAA→CAA)	<i>ampG</i>	→ muropeptide transporter
459,067 C→T		46.30% V88V (GTC→GTI)	<i>ybaV</i>	→ conserved protein, ComEA homolog
464,431 Δ1 bp		2.90% coding (607/1686 nt)	<i>mdtA</i>	→ fused predicted multidrug transporter subunits of ABC superfamily: ATP-binding components
506,924 +C		21.10% coding (605/798 nt)	<i>usbZ</i>	→ bifunctional UDP-glucose 4-epimerase/nucleotidase
518,073 +T		100% intergenic (+378/-54)	<i>ybbP</i>	→ predicted ABC transporter permease/rhsD element protein
532,746 C→T		10.40% A83V (GCG→GTG)	<i>ybbW</i>	→ predicted allantoin transporter
538,167 T→C		2.00% Y249C (TAT→TGT)	<i>yibA</i>	→ conserved protein
539,430 A→G		100% S243S (AGT→AGC)	<i>allC</i>	→ allantoin amidohydrolase
539,932 A→G		100% V76A (GTT→GCT)	<i>allC</i>	→ allantoin amidohydrolase
556,086 Δ1 bp		2.30% coding (1524/2604 nt)	<i>sfmD</i>	→ predicted outer membrane export usher protein
566,913 T→C		100% R198R (CGT→CGC)	<i>ybcM</i>	→ DLP12 prophage; predicted DNA-binding transcriptional regulator
566,924 +C		21.10% coding (605/798 nt)	<i>ybcM</i>	→ DLP12 prophage; predicted DNA-binding transcriptional regulator
624,845 G→A		100% G29E (GGC→GAC)	<i>cbtA</i>	→ carbon starvation protein
652,106 A→G		5.50% intergenic (+123/-52)	<i>papP</i>	→ phospholipid/lipid A palmitoyltransferase/DNA-binding transcriptional repressor
655,155 Δ1 bp		2.50% intergenic (-73/+136)	<i>lipA</i>	→ lipotease/predicted DNA-binding transcriptional regulator
686,553 Δ1 bp		2.50% coding (98/879 nt)	<i>ybeX</i>	→ predicted ion transport
692,983 A→G		2.10% V354A (GTG→GGC)	<i>asnB</i>	→ asparagine synthetase B
697,752 A→G		5.10% P242P (CCT→CCG)	<i>nagB</i>	→ glucosamine-6-phosphate deaminase
704,595 A→G		100% T466A (ACC→GCC)	<i>chiP</i>	→ chitinopurine, uptake of chitosugars
710,510 C→T		4.80% S78L (TGA→TAA)	<i>yjpfP</i>	→ lipoprotein
730,003 A→G		100% pseudogene (918/1434 nt)	<i>yojO</i>	→ pseudogene, rps-like
736,011 Δ1 bp		2.20% coding (1412/1482 nt)	<i>dtpD</i>	→ dipeptide and tripeptide permease D
825,134 A→G		2.40% F182L (TTC→CTC)	<i>ybhS</i>	→ predicted transporter subunit: membrane component of ABC superfamily
873,149 C→T		2.70% T582T (ACC→ACT)	<i>yliE</i>	→ predicted cyclic-di-GMP phosphodiesterase, inner membrane protein
909,164 G→A		5.60% S104P (TCC→TTC)	<i>poxB</i>	→ pyruvate dehydrogenase (pyruvate oxidase), thiamin-dependent, FAD-binding
919,281 A→G		100% E170E (GAA→GAG)	<i>macB</i>	→ fused macrolide transporter subunits of ABC superfamily: ATP-binding component/membrane component
962,053 A→G		6.30% N545S (AAC→AGC)	<i>rpsA</i>	→ 30S ribosomal subunit protein S1
975,763 A→G		2.80% N338S (AAC→AGC)	<i>mukB</i>	→ chromosome condensin MukBEF, ATPase and DNA-binding subunit
980,270 Δ1 bp		100% coding (799/1848 nt)	<i>yccb</i>	→ murein L,D-transpeptidase
980,270 +C		3.40% coding (309/1142 nt)	<i>aspC</i>	→ aspartate aminotransferase, PLP-dependent
985,426 Δ1 bp		5.30% intergenic (-19/+584)	<i>ompF</i>	→ outer membrane porin 1a (Ia/F)/asparaginyl tRNA synthetase
1,000,642 +G		19.40% coding (411/1071 nt)	<i>elfG</i>	→ predicted fibrillar-like adhesion protein
1,002,578 +G		7.30% coding (207/711 nt)	<i>ycbF</i>	→ predicted periplasmic pilin chaperone
1,007,074 A→G		3.00% Q269R (CAA→CGA)	<i>rmlL</i>	→ 23S rRNA mG2445 methyltransferase, SAM-dependent
1,017,394 Δ1 bp		4.20% intergenic (-32/+44)	<i>matP</i>	→ Ter macromodular organizer matS-binding protein/outer membrane protein A (3a1)*;G;D
1,027,406 T→C		13.00% N330S (AAT→AGT)	<i>rmlI</i>	→ 23S rRNA m(5)C1962 methyltransferase, SAM-dependent
1,064,599 +A		4.00% coding (590/1242 nt)	<i>agg</i>	→ glucose-1-phosphatase/nostol phosphatase
1,064,599 +C		4.00% coding (590/1242 nt)	<i>agg</i>	→ glucose-1-phosphatase/nostol phosphatase
1,080,375 C→T		4.80% pseudogene (392/627 nt)	<i>efeU</i>	→ ferrous iron permease (pseudogene)
1,087,096 T→G		2.50% N396T (AAC→ACC)	<i>pgaB</i>	→ biofilm adhesin polysaccharide PGA export lipoprotein with a polysaccharide deacetylase activity needed for export
1,087,350 Δ1 bp		100% coding (933/2019 nt)	<i>pgaB</i>	→ biofilm adhesin polysaccharide PGA export lipoprotein with a polysaccharide deacetylase activity needed for export
1,103,366 Δ1 bp		1.70% intergenic (+39/-20)	<i>csfA</i>	→ curlin subunit, amyloid curl fibers, cryptic/curl assembly protein
1,104,841 Δ1 bp		2.60% coding (122/1482 nt)	<i>ymdC</i>	→ predicted hydrolase
1,124,216 A→G		100% Y77C (TAC→TGC)	<i>rimJ</i>	→ ribosomal-protein-S5-alanine N-acetyltransferase
1,146,270 T→C		9.30% P69P (CCT→CCG)	<i>pixX</i>	→ probable phosphate acyltransferase
1,166,483 Δ1 bp		1.80% coding (448/528 nt)	<i>yctI</i>	→ predicted protein
1,171,205 A→G		3.90% V19A (GTC→GCT)	<i>ycpC</i>	→ repressor for bhsA(yjcR)
1,172,430 Δ1 bp		100% intergenic (-41/+87)	<i>mif</i>	→ transcription-repair coupling factor/inner membrane protein
1,189,968 A→G		2.80% R148R (CGT→CGC)	<i>purB</i>	→ adenylosuccinate lyase
1,203,259 Δ1 bp		4.00% pseudogene (665/1368 nt)	<i>oweE</i>	→ pseudogene, lambda replication protein O homolog; CPS-53/KPLE1 prophage; Phage or Prophage Related
1,210,277 A→C		14.70% I51S (ATC→AGC)	<i>iraM</i>	→ RpoS stabilizer during Mg starvation, anti-RssB factor
1,214,628 G→A		100% D46N (GAT→AAT)	<i>ymgA</i>	→ connector protein for RcsB regulation of biofilm
1,249,884 G→A		3.90% A132T (GCT→AGC)	<i>dhaR</i>	→ DNA-binding transcription activator of the dhaKLM operon
1,252,302 A→G		2.40% G692G (GCT→GGC)	<i>yogV</i>	→ predicted adhesin
1,252,893 +C		3.00% coding (1385/2868 nt)	<i>yogV</i>	→ predicted adhesin
1,254,337 C→T		1.90% R14H (CGT→CAT)	<i>yogV</i>	→ predicted adhesin
1,267,766 Δ1 bp		17.80% intergenic (-66/+362)	<i>ldrA</i>	→ toxic polypeptide, small/toxic polypeptide, small
1,274,249 A→G		18.60% S2S (AGT→AGC)	<i>narL</i>	→ DNA-binding response regulator in two-component regulatory system with NarX (or NarX)
1,294,680 C→T		30.70% A623T (GCA→ACA)	<i>adhE</i>	→ fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
1,294,800 A→G		10.10% F583L (TTC→CTC)	<i>adhE</i>	→ fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
1,295,249 A→G		18.00% V433A (GTT→GCT)	<i>adhE</i>	→ fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
1,295,433 A→G		45.50% Y372H (ACG→ACC)	<i>adhE</i>	→ fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
1,295,998 T→C		2.40% T217A (ACT→GCT)	<i>adhE</i>	→ fused acetaldehyde-CoA dehydrogenase/iron-dependent alcohol dehydrogenase/pyruvate-formate lyase deactivase
1,327,920 IS5 (+) (+4) bp		100% intergenic (+250/+485)	<i>chb</i>	→ predicted inner membrane protein/oligopeptide transporter subunit
1,308,563 A→G		7.30% K83K (AAA→AAG)	<i>tonB</i>	→ membrane spanning protein in TonB-ExbB-ExbD transport complex
1,333,625 A→T		2.60% K190L (AAA→ATA)	<i>acnA</i>	→ aconitate hydratase 1
1,336,353 Δ1 bp		2.60% coding (34/591 nt)	<i>nbA</i>	→ GTP cyclohydrolase II
1,336,354 Δ1 bp		2.60% coding (33/591 nt)	<i>nbA</i>	→ GTP cyclohydrolase II
1,348,415 +G		5.50% intergenic (-150/+218)	<i>fabI</i>	→ enoyl-[acyl-carrier-protein] reductase, NADH-dependent/conserved protein
1,352,793 G→A		3.50% A515V (GCC→GTC)	<i>sapA</i>	→ antimicrobial peptide transport ABC transporter periplasmic binding protein
1,353,750 G→A		3.80% A196V (GCC→GTC)	<i>sapA</i>	→ antimicrobial peptide transport ABC transporter periplasmic binding protein
1,367,261 +T		3.00% intergenic (+32/-181)	<i>pspE</i>	→ thiosulfate cyanide sulfurtransferase (rhodanese)/predicted glucosyltransferase
1,367,262 Δ1 bp		5.10% intergenic (+33/-180)	<i>pspE</i>	→ thiosulfate cyanide sulfurtransferase (rhodanese)/predicted glucosyltransferase
1,377,856 A→G		100% T195A (ACC→GCC)	<i>ycjU</i>	→ beta-phosphoglucomutase
1,388,677 C→T		12.90% A135T (GCC→ACC)	<i>ycjY</i>	→ predicted hydrolase
1,392,081 G→T		16.20% intergenic (+15/+36)	<i>mppA</i>	→ murein tripeptide (L-alanine-gamma-D-glutamyl-meso-DAP) transporter subunit/MscS family inner membrane protein
1,396,692 G→A		4.30% Q21* (CAG→TAG)	<i>fmr</i>	→ DNA-binding transcriptional dual regulator, global regulator of anaerobic growth
1,397,205 Δ1 bp		2.90% coding (258/516 nt)	<i>ogt</i>	→ O-6-alkylguanine-DNA,cysteine-protein methyltransferase
1,400,464 A→G		100% R6R (CGT→CGC)	<i>abgB</i>	→ p-aminobenzoyl-glutamate hydrolase, B subunit
1,416,669 +C		6.50% coding (525/858 nt)	<i>ydbU</i>	→ Rac prophage; conserved protein
1,428,060 A→G		4.50% T596A (ACT→GCT)	<i>sfrR</i>	→ Rac prophage; predicted tail fiber protein
1,429,120 Δ1 bp		2.70% coding (2846/3363 nt)	<i>sfrR</i>	→ Rac prophage; predicted tail fiber protein
1,432,066 Δ1 bp		5.30% intergenic (-616/+115)	<i>ynaE</i>	→ cold shock protein, function unknown, Rac prophage/pseudogene, prophage Rac integration site ttcA duplication; Phage or Prophage Related
1,443,974 A→G		2.40% L179P (CTG→CCG)	<i>feaR</i>	→ DNA-binding transcriptional activator for tynA and feaB
1,472,335 +C		3.30% intergenic (+28/-35)	<i>ybcC</i>	→ predicted oxidoreductase, NAD(P)-binding/predicted PF10971 family periplasmic methylglyoxal resistance protein
1,483,712 T→C		2.40% R1142R (CGT→CGC)	<i>hrpA</i>	→ predicted ATP-dependent helicase
1,517,957 A→G		100% Q157R (CAA→CAA)	<i>mcuR</i>	→ colanic acid and biofilm gene transcriptional regulator, MqsR-controlled
1,521,372 C→T		3.20% N280N (AAG→AAT)	<i>ycnC</i>	→ ATP-binding protein, periplasmic, function unknown
1,537,360 T→C		100% S819S (TCA→TCC)	<i>nazF</i>	→ nitrate reductase 2 (NR2), alpha subunit
1,546,080 A→G		100% N289S (AAC→AGC)	<i>ftnG</i>	→ formate dehydrogenase-N, alpha subunit, nitrate-inducible
1,584,892 Δ1 bp		4.00% coding (69/915 nt)	<i>ydeQ</i>	→ predicted fibrillar-like adhesion protein
1,588,542 C→T		10.10% E287E (GAG→GAA)	<i>hipA</i>	→ serine protein kinase required for persister formation; toxin of HipAB toxin-antitoxin system
1,591,350 +C		10.30% pseudogene (3963/3975 nt)	<i>rlyeO</i>	→ pseudogene, AidA homolog
1,591,351 Δ1 bp		4.30% pseudogene (3962/3975 nt)	<i>rlyeO</i>	→ pseudogene, AidA homolog
1,591,474 +C		8.30% pseudogene (3839/3975 nt)	<i>rlyeO</i>	→ pseudogene, AidA homolog
1,594,532 +C		5.00% pseudogene (781/3975 nt)	<i>rlyeO</i>	→ pseudogene, AidA homolog
1,598,677 Δ1 bp		3.30% intergenic (-210/-39)	<i>lsrR</i>	→ lsr operon transcriptional repressor/Autoinducer 2 import ATP-binding protein
1,684,382 A→G		2.50% G407G (GGC→GGC)	<i>fumA</i>	→ fumarate hydratase (fumarate A), aerobic Class I
1,711,543 Δ1 bp		100% intergenic (+47/-59)	<i>dtpA</i>	→ dipeptide and tripeptide permease Aglutathione S-transferase
1,731,522 +T		3.80% intergenic (-196/-207)	<i>grxD</i>	→ glutaredoxin-4/predicted peptidase, C40 clan
1,736,700 C→T		7.10% R108R (CGG→CGA)	<i>ydhB</i>	→ predicted DNA-binding transcriptional regulator
1,766,697 Δ1 bp		2.80% coding (399/1113 nt)	<i>ydiK</i>	→ inner membrane protein, UPF0118 family
1,775,491 T→C		63.80% C357C (TGT→TGC)	<i>ydiO</i>	→ predicted acyl-CoA dehydrogenase
1,796,172 T→C		11.40% intergenic (-5/+279)	<i>pheS</i>	→ phenylalanine tRNA synthetase, alpha subunit/phenylalanyl-tRNA synthetase operon leader peptide
1,805,182 Δ1 bp		3.80% coding (162/861 nt)	<i>ynaI</i>	→ predicted phosphotransferase/kinase
1,815,768 +C		5.50% intergenic (-43/+62)	<i>chbF</i>	→ phospho-chitobiose; general 6-phospho-beta-glucosidase activity/Repressor, chb operon for N,N'-diacetylchitobiose utilization

1,832,193 G-A  
1,854,456 +C  
1,866,170 +G  
1,899,185 C-T  
1,911,715 C-A  
1,922,176 A-G  
1,933,749 +A  
1,942,886 A-G  
1,946,737 Δ1 bp  
1,946,738 Δ1 bp  
1,960,440 Δ1 bp  
1,963,408 T-C  
1,974,753 A-G  
1,975,658 +G  
2,046,754 A-G  
2,055,782 T-C  
2,062,965 +C  
2,067,482 +G  
2,105,881 A-G  
2,106,695 A-G  
2,186,176 +C  
2,196,354 G-T  
2,197,907 +G  
2,197,907 +A  
2,223,832 C-T  
2,230,704 Δ1 bp  
2,236,692 Δ1 bp  
2,274,969 C-T  
2,283,254 G-A  
2,306,078 T-A  
2,316,275 A-G  
2,368,640 +C  
2,368,640 +A  
2,418,153 G-A  
2,460,104 +C  
2,479,121 Δ1 bp  
2,480,693 +A  
2,514,988 T-C  
2,561,005 Δ1 bp  
2,561,006 Δ1 bp  
2,561,014 C-T  
2,598,024 A-G  
2,612,192 A-G  
2,625,155 A-G  
2,650,487 C-T  
2,661,742 T-C  
2,661,978 G-T  
2,662,022 Δ1 bp  
2,677,863 T-C  
2,677,864 G-A  
2,712,880 G-A  
2,731,759 +C  
2,734,342 IS1 (+) +8 bp  
2,737,330 +G  
2,756,552 Δ1 bp  
2,758,567 T-C  
2,768,588 G-A  
2,774,389 Δ1 bp  
2,807,977 A-G  
2,815,563 Δ1 bp  
2,861,341 A-G  
2,867,739 G-A  
2,872,618 +C  
2,878,908 G-A  
2,909,428 T-C  
2,908,616 Δ1 bp  
2,908,760 A-G  
2,941,247 Δ1 bp  
2,984,222 T-C  
2,998,152 +G  
2,999,210 +C  
2,999,700 T-C  
3,004,979 T-C  
3,022,589 T-C  
3,025,014 A-T  
3,042,722 G-A  
3,095,711 +C  
3,104,125 A-G  
3,114,771 A-G  
3,120,093 Δ1 bp  
3,120,094 Δ1 bp  
3,123,862 G-A  
3,136,536 C-T  
3,153,678 Δ1 bp  
3,159,661 A-G  
3,183,493 A-G  
3,186,115 +A  
3,188,759 G-A  
3,192,418 C-G  
3,249,438 A-G  
3,212,940 C-T  
3,216,198 T-C  
3,262,760 T-C  
3,299,486 +C  
3,309,669 C-T  
3,316,099 T-C  
3,342,775 G-A  
3,346,233 G-A  
3,349,579 T-C  
3,370,569 +G  
3,392,252 G-A  
3,406,122 Δ1 bp  
3,406,123 Δ1 bp  
3,406,124 Δ1 bp  
3,406,125 Δ1 bp  
3,411,319 C-T  
3,427,668 +C  
3,432,306 T-C  
3,451,478 Δ1 bp  
3,471,744 T-C  
3,543,623 C-T  
3,545,374 C-T  
3,548,610 Δ1 bp  
3,571,562 G-A  
3,579,523 C-A  
3,600,138 Δ1 bp  
3,608,549 T-C  
3,634,552 Δ1 bp  
3,655,686 T-C  
3,664,698 Δ1 bp  
3,672,140 A-G  
3,685,449 T-C  
3,710,670 G-C  
3,764,113 G-T  
3,797,366 T-A  
3,793,369 T-C  
3,810,479 Δ1 bp  
3,810,557 +C  
3,837,297 T-C  
3,879,160 +T  
3,883,353 G-T

25.60% R54H (CGC→CAC)  
100% coding (539/837 nt)  
5.00% intergenic (-103/-10)  
3.50% intergenic (-375/-154)  
42.60% L198I (CTC→CTI)  
23.20% STP (TCC→CCC)  
100% intergenic (-210/-127)  
7.60% intergenic (-6/+3)  
2.90% coding (1010/1773 nt)  
2.90% coding (1009/1773 nt)  
41.50% coding (1835/2079 nt)  
4.40% intergenic (-167/+209)  
3.90% C106R (TGC→ATC)  
9.50% intergenic (-237/+84)  
16.50% K153K (AAA→AAQ)  
24.10% Y378C (TAC→TGC)  
2.30% coding (24/546 nt)  
5.00% intergenic (-78/-12)  
3.10% L310L (TTG→CTG)  
100% G38G (GGT→GGC)  
3.50% coding (1959/2481 nt)  
2.80% pseudogene (1832/2022 nt)  
3.40% coding (405/3633 nt)  
3.40% coding (405/3633 nt)  
4.10% V221V (GTG→GTA)  
3.40% coding (603/720 nt)  
2.90% coding (881/999 nt)  
2.60% I482I (ATC→ATT)  
41.80% A97A (GCC→GCT)  
3.10% D163V (GAT→GTT)  
2.30% T469A (ATC→ATC)  
3.20% coding (609/1653 nt)  
3.20% coding (609/1653 nt)  
3.00% W103\* (TGG→TGA)  
11.30% intergenic (+234/-132)  
2.60% coding (280/1539 nt)  
3.40% intergenic (-238/-286)  
4.90% V23V (GTA→GTE)  
2.50% coding (190/378 nt)  
2.60% coding (191/378 nt)  
2.40% P67S (CCG→ICG)  
10.10% E108G (GAA→GGA)  
31.20% V305A (GTT→GCT)  
7.40% V336V (GTT→GTC)  
39.10% P257L (CCA→CTA)  
100% G43G (GGT→GGC)  
2.60% T122T (ACC→ACT)  
4.00% coding (409/855 nt)  
6.10% S703G (AGC→GGC) †  
6.10% A702A (GCC→GCT) †  
7.80% A61A (CGC→GCA)  
14.30% coding (500/732 nt)  
100% intergenic (+245/-29)  
2.60% coding (1035/1071 nt)  
5.50% coding (344/1410 nt)  
14.20% intergenic (+170/+8)  
15.80% G73R (GGG→AGG)  
2.10% coding (51/318 nt)  
3.00% intergenic (+74/-17)  
17.00% intergenic (-65/+134)  
5.40% L297P (CTC→CQC)  
20.20% T93I (ACA→ATA)  
12.90% intergenic (+321/+630)  
4.00% intergenic (-91/+324)  
19.70% T19A (ATG→CCG)  
3.00% coding (1064/1302 nt)  
7.70% S310S (AGT→AGC)  
2.60% coding (611/1098 nt)  
33.80% S50S (AGT→AGC)  
15.40% coding (860/879 nt)  
2.30% coding (1256/1779 nt)  
2.60% T256A (ATC→ATC)  
100% I91I (ATT→ATG)  
3.80% V267A (GTA→GCA)  
3.20% D199E (GAT→GAA)  
3.60% N333N (AAC→AAT)  
5.10% coding (592/720 nt)  
62.30% intergenic (-291/-206)  
10.90% G396G (GGT→GGC)  
5.50% coding (48/1224 nt)  
5.50% coding (45/1224 nt)  
4.50% pseudogene (833/1173 nt)  
4.40% G378E (GGG→GAG)  
6.00% coding (2148/2220 nt)  
3.40% M331T (ATG→ACG)  
5.70% pseudogene (1393/2445 nt)  
2.70% coding (804/1065 nt)  
8.00% A406T (GCC→ACC)  
3.80% G635A (GAT→GCT)  
4.00% Y871C (C→G)  
7.50% T734A (CCG→GCG)  
4.30% V18A (GTA→GCA)  
2.30% V76A (GTC→GCC)  
44.90% coding (1012/1245 nt)  
3.40% M342I (ATG→ATA)  
100% A65A (GCA→GCE)  
7.50% A44T (GCT→ACT)  
42.60% S491S (AGC→ACT)  
100% L59L (TTA→CTA)  
15.60% coding (102/11368 nt)  
3.30% P75L (CCG→CTG)  
1.80% coding (172/297 nt)  
1.80% coding (173/297 nt)  
1.80% coding (174/297 nt)  
1.80% coding (175/297 nt)  
2.50% S538F (TCC→TIC)  
2.60% coding (573/1125 nt)  
44.70% V370A (GTT→GCT)  
3.40% coding (422/1953 nt)  
4.30% K119R (AAA→AGA)  
100% A376A (GCG→GCA)  
3.40% D594N (GAC→AAC)  
4.00% coding (848/2706 nt)  
12.20% G39G (GGC→GGI)  
4.90% R29S (GCG→AGC)  
2.30% coding (153/360 nt)  
5.30% V68A (GIG→GCG)  
4.90% intergenic (-152/-239)  
2.50% L198P (CTG→CCG)  
3.50% coding (428/1650 nt)  
5.70% V297A (GTT→GCT)  
100% D613G (GAC→GEC)  
3.00% A117G (GCG→GEG)  
1.90% intergenic (+129/+30)  
2.40% intergenic (-137/+138)  
100% T208A (CAA→GCA)  
3.30% intergenic (-33/+62)  
25.00% coding (671/687 nt)  
2.90% T391A (ACC→GCC)  
7.30% intergenic (+6/-11)  
2.10% intergenic (+166/-55)

yjzJ → Inner membrane protein, TVP38/TMEM64 family  
yjiI → predicted aldolase  
yeeG → protein kinase, function unknown; autokinase/conserved protein  
yoeF → fused predicted mannose protein/conserved mannose-specific PTS enzymes: IIA component/IIB component  
prc → carboxy-terminal protease for penicillin-binding protein 3  
yobA → conserved protein  
zwf → glucose-6-phosphate 1-dehydrogenase/predicted DNA-binding transcriptional regulator  
ruvB → ATP-dependent DNA helicase, component of RuvABC resolvosome/component of RuvABC resolvosome, regulatory subunit  
aspS → aspartyl-tRNA synthetase  
aspS → aspartyl-tRNA synthetase  
flhA → predicted flagellar export pore protein  
flhB → flagellin export apparatus, substrate specificity protein/chemotaxis regulator, protein phosphatase for CheY  
flhC → DNA-binding transcriptional dual regulator with FlhD  
flhD → DNA-binding transcriptional dual regulator with FlhC/IS1 transposase B  
yeeJ → probable adhesin  
yeeO → predicted multidrug exporter, MATE family  
cobU → bifunctional cobinamide kinase/ cobinamide phosphate guanylyltransferase  
insC → IS2 repressor TnpA/CP4-44 prophage; predicted disrupted hemin or colicin receptor; Phage or Prophage Related; interrupted by IS2 and C-terminal deletion  
rfbX → predicted polysprenol-linked O-antigen transporter  
rfbX → predicted polysprenol-linked O-antigen transporter  
yehB → predicted outer membrane protein  
pseudogene; molybdate metabolism regulator, first fragment; molybdate metabolism regulator, second fragment 2  
yehI → conserved protein  
yehI → conserved protein  
yohF → predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain  
sanA → vancomycin high temperature exclusion protein; mutants have a defective envelope more permeable to vancomycin at 42 degrees  
mgfB → methyl-galactoside transporter subunit  
yefF → microcin C transporter, ATP-binding subunit; ABC family  
ccmC → heme exporter subunit  
alkB → oxidative demethylase of N1-methyladenine or N3-methylcytosine DNA lesions  
yjaA → α-glycerol 3-phosphate dehydrogenase (anaerobic), large subunit, FAD/NAD(P)-binding  
arnT → 4-amino-4-deoxy-L-arabinose transferase  
arnT → 4-amino-4-deoxy-L-arabinose transferase  
yfcG → GSH-dependent disulfide bond oxidoreductase  
fadL → long-chain fatty acid outer membrane transporter/predicted protein  
emrY → predicted multidrug efflux system  
emrK → EmrKY-TolC multidrug resistance efflux pump, membrane fusion protein component/DNA-binding response regulator in two-component regulatory system with EvgS  
yfaA → predicted diguanylate cyclase  
yfgQ → CPZ-55 prophage; predicted protein  
yfgQ → CPZ-55 prophage; predicted protein  
yfgQ → CPZ-55 prophage; predicted protein  
bcp → thiol peroxidase, thioredoxin-dependent  
yfgO → predicted inner membrane permease, UPF0118 family  
yfgP → cyclic-di-GMP phosphodiesterase, anaerobic  
sseA → 3-mercaptopyruvate sulfurtransferase  
yhrR → S9 peptidase family protein, function unknown  
yhrR → S9 peptidase family protein, function unknown  
yhrR → S9 peptidase family protein, function unknown  
yphG → conserved protein  
yphG → conserved protein  
eamB → cysteine and O-acetylserine exporter  
yfhH → conserved protein, UPF0124 family  
bamD → lipoprotein required for OM biogenesis, in BamABCDE complex/cold shock protein associated with 30S ribosomal subunit  
aroF → 3-deoxy-D-arabino-heptulosonate-7-phosphate synthase, tyrosine-repressible  
yjiI → CP4-57 prophage; predicted protein  
yjiJ → CP4-57 prophage; predicted protein  
yjiJ → CP4-57 prophage; predicted protein  
yjiZ → CP4-57 prophage; antitoxin of the YjiF-YjiZ toxin-antitoxin system  
ygaH → probable L-valine exporter, norvaline resistance/DNA-binding transcriptional repressor of microcin B17 synthesis and multidrug efflux  
argY → tRNA-ArgRNA-Arg  
rpoS → RNA polymerase, sigma S (sigma 38) factor  
ygeE → conserved inner membrane protein  
iap → I-aminopeptidase in alkaline phosphatase isozyme conversion/probable ssRNA endonuclease, CRISP-associated protein  
casA → CRISPR RNA (crRNA) containing Cascade antiviral complex protein/Cas3 predicted helicase needed for Cascade anti-viral activity  
ygcB → Cas3 predicted helicase needed for Cascade anti-viral activity  
rimC → 23S rRNA m5(U)1939 methyltransferase, SAM-dependent  
rimC → 23S rRNA m5(U)1939 methyltransferase, SAM-dependent  
mftA → membrane-bound lytic murein transglycosylase A  
yqeJ → predicted protein  
xdhB → xanthine dehydrogenase, FAD-binding subunit  
ygeV → predicted DNA-binding transcriptional regulator  
ygeV → predicted DNA-binding transcriptional regulator  
hyaA → D-steroid-specific phenylhydantoinase  
ygdG → predicted purine permease  
ygtT → fused predicted oxidoreductase: Fe-S subunit/nucleotide-binding subunit  
gcvP → glycine decarboxylase, PLP-dependent, subunit (protein P) of glycine cleavage complex  
yggN → predicted protein  
speC → ornithine decarboxylase, constitutive/predicted inner membrane protein, DUF554 family  
glcA → glycolate transporter  
glcF → glycolate oxidase 4Fe-4S iron-sulfur cluster subunit  
glcF → glycolate oxidase 4Fe-4S iron-sulfur cluster subunit  
yphO → pseudogene, DNA-binding transcriptional regulator homology  
hybC → hydrogenase 2, large subunit  
ygiQ → conserved protein  
parC → DNA topoisomerase IV, subunit A  
pseudogene; outer membrane usher homology; putative membrane; Not classified; putative membrane protein  
yqiI → conserved protein  
yqjK → PHB family membrane protein, function unknown  
gluE → fused deadenyltransferase/adenylyltransferase for glutamine synthetase  
rpoD → RNA polymerase, sigma 70 (sigma D) factor  
yer → fused signal transducer for aerotaxis sensory component/methyl accepting chemotaxis component  
ehgR → DNA-binding transcriptional repressor  
yhaB → predicted protein  
mtr → tryptophan transporter of high affinity  
infB → fused protein chain initiation factor 2, IF2: membrane protein/conserved protein  
yhbX → predicted hydrolase, inner membrane  
npr → phosphohistidinophenyl-hexose phosphotransferase component of N-regulated PTS system (Npr)  
arcB → aerobic respiration control sensor histidine protein kinase, cognate to two-component response regulators ArcA and RssB  
yhb → glutamate synthase, large subunit  
dcdU → predicted transporter  
mg → ribonuclease G  
fis → global DNA-binding transcriptional dual regulator  
acrF → multidrug efflux system protein  
smf → conserved protein  
trkA → NAD-binding component of Trk potassium transporter  
gspD → general secretory pathway component, cryptic  
fkpA → FKBP-type peptidyl-prolyl cis-trans isomerase (rotamase)  
malQ → 4-alpha-glucanotransferase (amylomaltase)  
malP → maltodextrin phosphorylase  
malT → DNA-binding transcriptional activator for the mal regulon and maltotriose-ATP-binding protein  
gntU → gluconate transporter, low affinity GNT 1 system  
yhbY → predicted protein  
yhhM → conserved protein, DUF2500 family  
nikA → Nickel-binding, heme-binding periplasmic protein  
uspB → universal stress (ethanol tolerance) protein B/universal stress global response regulator  
mdtF → anaerobic multidrug efflux transporter, ArcA-regulated  
treF → cytoplasmic trehalase  
yhgG → Inner membrane protein, AsmA family  
regulator of cellulose synthase, cyclic di-GMP binding  
bcsB → biotin sulfite oxidoreductase  
yhwY → pseudogene, tRNA-linked/hypothetical protein, no homologs  
ybi → glycine C-acetyltransferase/conserved protein, pfam09612 family  
wauU → lipopolysaccharide core biosynthesis  
pyrE → orotate phosphoribosyltransferase/defective ribonuclease PH  
rph → defective ribonuclease PH  
yicO → Probable adenine permease  
rpmH → 50S ribosomal subunit protein L34/protein C5 component of RNase P  
tnaC → tryptophanase leader peptide/tryptophanase-L-cysteine desulfhydrase, PLP-dependent

3,900,309 Δ1 bp  
 3,960,228 Δ1 bp  
 4,003,806 +A  
 4,004,074 A→G  
 4,037,965 A→G  
 4,094,124 A→G  
 4,113,515 C→T  
 4,124,006 Δ1 bp  
 4,156,496 C→T  
 4,175,120 T→C  
 4,188,448 A→G  
 4,190,927 A→G  
 4,225,439 Δ1 bp  
 4,294,406 Δ1 bp  
 4,297,686 +CG  
 4,303,503 Δ1 bp  
 4,313,141 G→A  
 4,330,536 T→C  
 4,381,847 T→C  
 4,401,351 Δ1 bp  
 4,402,611 T→C  
 4,447,338 Δ1 bp  
 4,453,646 C→G  
 4,453,651 C→G  
 4,457,492 C→T  
 4,457,497 G→A  
 4,457,498 G→A  
 4,464,733 G→A  
 4,471,270 +T  
 4,471,954 G→A  
 4,479,877 +C  
 4,500,691 G→A  
 4,548,065 +T  
 4,594,767 G→C  
 4,597,511 +G  
 4,597,626 +G  
 4,605,748 A→G  
 4,605,807 T→C  
 4,631,366 C→T

3.40% intergenic (-34/+100)  
 13.50% coding (81/1266 nt)  
 3.10% intergenic (-69/-42)  
 4.10% D76G (GAC→GCG)  
 100% intergenic (-57/-307)  
 100% intergenic (+145/-4)  
 2.10% intergenic (-3/+171)  
 2.70% coding (85/891 nt)  
 18.10% R518C (CGT→TGT)  
 11.80% V857A (GTG→GCG)  
 2.30% Q80Q (CAA→CAG)  
 5.60% T40A (ACC→GCC)  
 2.10% coding (376/1650 nt)  
 3.60% coding (1538/1608 nt)  
 100% intergenic (+586/+56)  
 22.40% coding (795/891 nt)  
 6.60% C196C (TGC→TGT)  
 4.20% N431S (AAC→AGC)  
 3.50% E274E (GAA→GAG)  
 10.50% intergenic (+39/-88)  
 4.80% S2P (TCT→GCT)  
 4.50% coding (248/1374 nt)  
 2.20% E107D (GAG→GAC)  
 2.50% V106L (GTC→CTC)  
 15.40% intergenic (-6/+113)  
 26.80% intergenic (-11/+108)  
 7.70% intergenic (-12/+107)  
 2.20% V209V (GTC→GTT)  
 100% pseudogene (262/291 nt)  
 6.60% pseudogene (550/927 nt)  
 5.20% coding (1492/1503 nt)  
 100% pseudogene (378/543 nt)  
 96.80% intergenic (-440/-232)  
 2.20% intergenic (-605/-14)  
 4.60% noncoding (80/87 nt)  
 6.40% noncoding (80/87 nt)  
 19.70% intergenic (+184/+236)  
 20.60% intergenic (+243/+177)  
 10.60% G62D (GGC→GAC)

*bglF* ← / fused beta-glucoside-specific PTS enzymes: IIA component/IIB component/IIC component/transcriptional antiterminator of the *bgl* operon  
*rhlB* ← ATP-dependent RNA helicase  
*rhlB* ← homoserine, homoserine lactone and S-methyl- methionine efflux pump/lysophospholipase L2  
*plbB* → lysophospholipase L2  
*yjhG* → inner membrane protein. Predicted acyltransferase/fused DNA polymerase [5'→3' polymerase/3'→5' exonuclease/5'→3' exonuclease  
*kdgT* → /2-keto-3-deoxy-D-gluconate transporter/6-N-hydroxylaminopurine resistance protein  
*hslV* → / peptidase component of the HslUV protease/essential cell division protein  
*metF* → 5,10-methylenetetrahydrofolate reductase  
*btuB* → vitamin B12/cobalamin outer membrane transporter  
*rpoB* → RNA polymerase, beta subunit  
*nudC* → NADH pyrophosphatase  
*yjaG* → conserved protein  
*pgj* → glucosylphosphate isomerase  
*nrfE* → heme lyase (NrfEG) for insertion of heme into c552. subunit NrfE  
*glpP* → / glutamate/aspartate:proton symporter/conserved protein  
*rpiR* ← DNA-binding transcriptional repressor  
*phnF* ← predicted DNA-binding transcriptional regulator of phosphonate uptake and biodegradation  
*adiA* ← arginine decarboxylase  
*rsqA* ← ribosome small subunit-dependent GTPase A  
*rmbB* → / 23S rRNA (Gm2251)-methyltransferase/conserved protein, DUF2170 family  
*yjfk* → conserved protein, DUF2491 family  
*mpi* → UDP-N-acetylmuramate-L-alanyl-gamma-D-glutamyl- meso-diaminopimelate ligase  
*nrpD* ← anaerobic ribonucleoside-triphosphate reductase  
*nrpD* ← anaerobic ribonucleoside-triphosphate reductase  
*treB* ← / fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component/DNA-binding transcriptional repressor  
*treB* ← / fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component/DNA-binding transcriptional repressor  
*treB* ← / fused trehalose(maltose)-specific PTS enzyme: IIB component/IIC component/DNA-binding transcriptional repressor  
*yjgl* ← predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain  
*yjgN* → inner membrane protein, DUF898 family  
*yjgN* → inner membrane protein, DUF898 family  
*yjgR* ← conserved protein, DUF853 family with NTPase fold  
*insO* → pseudogene, IS911 transposase B:IS, phage, Tn; Transposon-related functions; extrachromosomal; transposon related  
*yjIC* ← predicted protein/RpoS stabilizer after DNA damage, anti-RssB factor  
*yjIP* ← inner membrane protein, H-NS-repressed, DUF1212 family/DNA-binding transcriptional regulator  
*leuP* ← tRNA-Leu  
*leuQ* ← tRNA-Leu  
*yjV* → / predicted DNase/predicted pyruvate formate lyase activating enzyme  
*yjV* → / predicted DNase/predicted pyruvate formate lyase activating enzyme  
*arcA* ← DNA-binding response regulator in two-component regulatory system with ArcB or CpxA