

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
yjiG → 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
rsmB → / 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
yjiI ← predicted oxidoreductase with NAD(P)-binding Rossmann-fold domain
yjiN → inner membrane protein, DUF898 family
yjiN → inner membrane protein, DUF898 family
yjiR ← 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
yjiV → / predicted DNase/predicted pyruvate formate lyase activating enzyme
yjiV → / predicted DNase/predicted pyruvate formate lyase activating enzyme
arcA ← DNA-binding response regulator in two-component regulatory system with ArcB or CpxA