Genome position	Mutation	Annotation	Gene
37,281	$C \rightarrow A$	A798A (GC <u>C</u> →GC <u>A</u>)	carB
112,876	(T) _{5→6}	coding	secA
242,025	Δ21,535 bp	between ISI	ECB_00212- phoE
248,651	$C \rightarrow A$	H180N	lpcA
539,643	$G \rightarrow T$	pseudogene	ybcD
539,649	$C \rightarrow T$	pseudogene	vbcD
539,661	$G \rightarrow C$	pseudogene	ybcD
539,664	$C \rightarrow T$	pseudogene	ybcD
539,670	$T\rightarrow C$	pseudogene	ybcD
539,673	C→A	pseudogene	ybcD
539,679	A→G	pseudogene	ybcD
539,681	+T	pseudogene	ybcD
539,686	2 bp→A	pseudogene	ybcD
539,694	C→T	pseudogene	ybcD
539.698	C→A	pseudogene	ybcD
539,721	A→C	pseudogene	ybcD
539,827	T→G	pseudogene	ybcD
539,879	G→T	intergenic	ybcD / renD
539,891	A→G	intergenic	ybcD / renD
539,893	A→C	intergenic	ybcD / renD
539,907	G→C	intergenic	ybcD / renD
539,915	T→C	intergenic	ybcD / renD
549,746	C→T	R57R (CGC→CGT)	ybcT renD
549,764	A→G	A63A ($GCA \rightarrow GCG$)	ybcT
549,767	G→C	L64L (CTG→CTC)	ybcT
549,772	A→C	E66A (GAA \rightarrow GCA)	ybcT
787,879	Δ12,090 bp	LOUA (GAA 7GCA)	ECB_00726- ECB_00739
1,003,024	C→A	D351Y ($\underline{G}AC \rightarrow \underline{T}AC$)	ompF
1,003,277	A→C	F266L (TTT→TTG)	ompF
1,117,882	G→A	intergenic	csgD / csgB
1,230,063	(T) _{8→9}	pseudogene	hlyE
1,893,290	A→C	L35* $(T\underline{T}A \rightarrow T\underline{G}A)$	prc
2,103,918	(CCAG) _{7→8}	coding	ECB 01992
2,183,354	A→G	E91E (GAA→GAG)	cdd
3,023,945	Δ777 bp		insB-22- ECB_02825
3,481,793	$A \rightarrow T$	I37F (ATC→TTC)	malT
3,482,495	Δ20 bp	coding	malT
3,482,706	25 bp duplication*	coding	malT
3,734,067	Δ1 bp	coding	gumD
3,736,304	Δ4,894 bp	IS1-mediated	waaC-waaT
4,141,100	G→T	R58L (CGT→CTT)	yijC