Table S1. Sequence differences between *E. coli* K-12 strains W3110-D8 and W3110-D13 compared to that of the *E.coli* K-12 reference genome, NC_007779.1 .*

Position (bp)	Gene	Mutation	Type of Coding Effect	Codon Change		
					D8-W	**D13-W**
547,694	**fdrA → / → ylbF**	A→G	INTERGENIC	intergenic (+123/-1156)	1	1
547,831	**fdrA → / → ylbF**	+G	INTERGENIC INSERTION	intergenic (+260/-1019)	1	1
556,858	**folD ←**	A→T	MISSENSE	(CTG→CAG) L36Q	1	1
654,214	**insH**	Δ1,199 bp	DELETION		1	1
987,574	**ompF ← / ← asnS**	G→T	INTERGENIC	intergenic (-170/+433)	1	1
1,093,686	**ycdT →**	T→C	MISSENSE	(GTA→GCA) V130A	1	1
1,197,797	**icd →**	C→T	SILENT	(CAC→CAT) H366H	1	1
1,197,809	**icd →**	C→T	MISSENSE	(ACC→ACT) T370T	1	1
1,197,822	**icd →**	T→C	MISSENSE	(TTA→CTG) L375M	1	1
1,197,824	**icd →**	A→G	MISSENSE	(TTA→CTG) L375M	1	1
1,197,854	**icd →**	C→T	SILENT	(AAC→AAT) N385N	1	1
1,197,857	**icd →**	G→C	SILENT	(GCG→GCC) A386A	1	1
1,197,860	**icd →**	A→ G	SILENT	(AAA→AAG) K387K	2	1
1,197,869	**icd →**	C→T	SILENT	(ACC→ACT) T390T	2	1
1,197,881	**icd →**	G→A	SILENT	(GAG→GAA) E394E	2	1
1,519,222	**ydcX →**	G→T	SILENT	(GTG→GTT) V40V	1	1
1,669,599	**dgsA ←**	Δ1 bp	DELETION	coding (680/1221 nt)	1	1
1,979,957	**flhD ← / ← insH**	G→T	INTERGENIC	intergenic (-37/+398)	1	1
2,005,401	**fliC ←**	C→T	MISSENSE	(GAA→AAA) E115K	1	1
2,176,983	**insH**	Δ1,199 bp	DELETION		1	1
2,245,455	**yeiB ←**	A→G	MISSENSE	(TCG→CCG) S283P	1	1
2,320,795	**insD–insC**	Δ1,336 bp	DELETION		2	1
2,866,111	**rpoS ← / ← nlpD**	A→G	INTERGENIC	intergenic (-21/+159)	1	1
3,261,134	**insH–[tdcD]**	Δ1,199 bp	DELETION		1	2
3,268,825	**yhaC →**	A→G	MISSENSE	(ACA→GCA) T186A	1	1
3,742,936	**insD–insC**	Δ1,336 bp	DELETION		1	1
3,746,911	**insH**	Δ1,199 bp	DELETION		1	1
3,750,591	**insH**	Δ1,199 bp	DELETION		1	2
3,958,123	**dctA →**	Δ34 bp	DELETION	coding (1156-1189/1287 nt)	1	1
4,310,363	**insH–[alsK]**	Δ1,199 bp	DELETION		2	1
4,371,271	**dcuA ← / ← aspA**	Δ2 bp	DELETION	intergenic (-6/+299)	2	1
4,371,272	**dcuA ← / ← aspA**	Δ1 bp	DELETION	intergenic (-7/+299)	1	2

*Predicted differences in the two laboratory stock strains resequenced for this study—W3110-D8 (D8-W) as the strain ancestral to the adapted populations; W3110-D13 (D13-W) as another resequenced W3110 strain. The breseq pipeline was used to align sequences to the reference genome, NC_007779.1 . A “1” indicates a confirmed coding effect by breseq and visual genome alignment with IGV (Broad Institute); a “2” indicates a region of low genomic coverage with a possible coding effect.