

Gene	Codon	W3110	55989	HUSEC041	LB226692	Protein function
mutT	89	CGC (R)	AGC (S)	AGC (S)	AGC (S)	8-oxo-(d)GTP hydrolase
mutS	337	GGG (G)	GAG (E)	GAG (E)	GAG (E)	Methyl-directed mismatch repair
mutL	83	CTG (L)	CAG (Q)	CAG (Q)	CAG (Q)	Methyl-directed mismatch repair
	389	CCC (L)	as W3110	as W3110	as W3110*	
	418	TTA (L)	CCA (P)	CCA (P)	CCA (P)	
uvrD		wt	as W3110	as W3110	as W3110	Helicase II, nucleotide excision repair
mutD	222	ATT (I)	CTT (L)	CTT (L)	CTT (L)	Subunit of DNA polymerase III
	233	CAG (Q)	GAG (E)	GAG (E)	GAG (E)	
mutY	217	GCG (A)	TCG (S)	TCG (S)	TCG (S)	Adenine glycosylase, mismatch repair
	272	CAG (Q)	CAT (H)	CAT (H)	CAT (H)	
mutM	94	GAT (D)	GAA (E)	GAA (E)	GAA (E)	DNA glycosylase in base excision repair
dam		wt	as W3110	as W3110	as W3110	DNA adenine methylase

Supplementary Table S2. Putative mutations in the coding regions of genes for DNA maintenance and repair in the outbreak O104:H4 strain in comparison to 55989, HUSEC041 and W3110. The genome sequences of the outbreak strain (LB226692) as well as its close relatives 55989 and HUSEC041 show a number of common amino acid variations in several known mutator genes in comparison to W3110. The reported genome sequence of LB226692 also features a deletion of one nucleotide in codon 389 of *mutL* (the last C in a row of 6 Cs; indicated by * in the table), suggesting a translational frameshift. However, resequencing this DNA region from a PCR fragment showed this variation to be a sequencing error.