

TABLE S3. Mutations found in mutator genes in ancestral Escherich strain isolates and prediction of their functional effect

Genes	Gene products	Mutations at the protein level*					Predictions of functional effect			Frequency of the observed allele in Uniprot
		NCTC86_Meric	NCTC86	CIP61.11	ATCC4157	DSM301	SIFT	PolyPhen-2	PROVEAN	
<i>dnaQ (mutD)</i>	ε subunit of DNA polymerase III	-	-	-	-	-				
<i>polC (dnaE)</i>	α subunit of DNA polymerase III	-	-	-	-	-				
<i>polA</i>	DNA polymerase I	-	-	-	-	-				
<i>mutT</i>	Nucleoside triphosphatase	Frameshift (truncated)	Frameshift (truncated)	Frameshift (truncated)	Frameshift (truncated)	Frameshift (truncated)				
<i>dam</i>	DNA adenine methyltransferase	P141T	P141T	P141T	P141T	P141T	0.08	Probably damaging (0.990)	Deleterious (-7.836)	0/106
<i>mutS</i>	DNA mismatch repair protein MutS	V785I	V785I	V785I	V785I	V785I	0.02	Possibly damaging (0.790)	Neutral (-0.818)	0/233
<i>mutL</i>	DNA mismatch repair protein MutL	68delL 69delA	68delL 69delA	68delL 69delA	68delL 69delA	68delL 69delA				
<i>mutH</i>	Endonuclease	-	-	-	-	-				
<i>uvrD</i>	DNA helicase II	E152V	E152V	E152V	E152V	E152V	0.00	Benign (0.167)	Deleterious (-5.393)	0/132
<i>mutY</i>	DNA glycosylase	A217S A280S	A217S A280S	A217S A280S	A217S A280S	A217S A280S	0.70 0.80	Benign (0.000)	Neutral (-0.028)	72/104
<i>mutM</i>	DNA glycosylase	S98N T127A	S98N T127A	S98N T127A	S98N T127A	S98N T127A	0.67 1.00	Benign (0.000)	Neutral (-0.459)	19/217
<i>miaA</i>	Transferase	-	-	-	N163H	N163H	0.08	Probably damaging (1.000)	Deleterious (-4.47)	0/216
<i>sodA</i>	Superoxide dismutases	-	-	-	-	-				
<i>sodB</i>	Superoxide dismutases	-	-	-	V71A	V71A	0.46	Possibly damaging (0.899)	Deleterious (-3.522)	0/71
<i>oxyR</i>	Regulatory protein	-	-	-	-	-				
<i>nth</i>	Glycosylase and abasic-lyase activity	-	-	-	-	-				
<i>nei</i>	Glycosylase and abasic-lyase activity	-	-	-	-	-				
<i>xthA</i>	Nuclease	-	-	-	-	-				
<i>nfo</i>	Nuclease	-	-	-	-	-				
<i>ung</i>	Uracil glycosylase	-	-	-	-	-				
<i>vsr</i>	Endonuclease	A2V S45D E128A	A2V S45D E128A	A2V S45D E128A	A2V S45D E128A	A2V S45D E128A	0.26 0.75 0.00 (low confidence)	Possibly damaging (0.562)	Neutral (-1.537)	17/95
<i>ada</i>	Methyltransferase	-	-	-	-	-				
<i>ogt</i>	Methyltransferase	-	-	-	-	-				
<i>recA</i>	DNA-binding protein	-	-	-	-	-				
		A8T	A8T	A8T	A8T	A8T	0.00 (low confidence)	Benign (0.000)	Neutral (-0.127)	19/247
		A109T	A109T	A109T	A109T	A109T	0.33	Benign (0.000)	Neutral (-0.645)	210/247
<i>recG</i>	DNA helicase	R282H E347K A362S H476R	R282H E347K A362S H476R	R282H E347K A362S H476R	R282H E347K A362S H476R	R282H E347K A362S H476R	0.07 0.75 0.31 0.54	Benign (0.000)	Neutral (-0.027)	36/247
<i>hns</i>	DNA-binding protein	-	-	-	-	-				
<i>topB (mutR)</i>	DNA topoisomerase III	-	-	L474V	-	-	0.54	Benign (0.000)	Neutral (-0.392)	1/254
<i>ssb</i>	Single-stranded DNA-binding protein	-	-	-	-	-				

*Mutations predicted to be deleterious at the protein level at least with two of the three softwares and absent in Uniprot database are highlighted in red