

Supporting Information

1,3-Butadiene-induced adenine DNA adducts
are genotoxic but only weakly mutagenic when
replicated in *Escherichia coli* of various repair
and replication backgrounds

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Table S1. Error rate of the conserved sequence surrounding the site of interest (site N in Figure 2 and this table) in the control genome in wild-type cells (HK81) of the AlkB/DinB experiment. The expected sequence of the 21 bases encompassing the site of interest is 5'-ACGAAGACCTNGGCGTCCAAT-3' where N is the site of interest at position 6260. The average error rate from the three biological replicates at each of the 21 sites is presented along with the standard deviation.

Position	Expected base	Average error rate	SD
6250	A	0.19%	0.04%
6251	C	0.17%	0.04%
6252	G	0.19%	0.06%
6253	A	0.20%	0.08%
6254	A	0.57%	0.19%
6255	G	0.31%	0.10%
6256	A	0.28%	0.17%
6257	C	0.14%	0.03%
6258	C	0.20%	0.02%
6259	T	0.26%	0.08%
6260	N	0.71%	0.18%
6261	G	0.36%	0.09%
6262	G	0.35%	0.10%
6263	C	0.33%	0.10%
6264	G	0.42%	0.05%
6265	T	0.20%	0.07%
6266	C	0.52%	0.15%
6267	C	0.58%	0.08%
6268	A	0.13%	0.05%
6269	A	0.10%	0.03%
6270	T	0.10%	0.03%

Table S2. Error rate of the conserved sequence surrounding the site of interest (site N in Figure 2 and this table) in the control genome in wild-type cells (AB1157) of the MutM/MutY experiment. The expected sequence of the 21 bases encompassing the site of interest is 5'-ACGAAGACCTNGGCGTCCAAT-3' where N is the site of interest at position 6260. The average error rate from the three biological replicates at each of the 21 sites is presented along with the standard deviation.

Position	Expected base	Average error rate	SD
6250	A	0.11%	0.02%
6251	C	0.15%	0.01%
6252	G	0.12%	0.02%
6253	A	0.07%	0.04%
6254	A	0.10%	0.01%
6255	G	0.16%	0.02%
6256	A	0.30%	0.09%
6257	C	0.15%	0.06%
6258	C	0.20%	0.07%
6259	T	0.34%	0.03%
6260	N	1.31%	0.08%
6261	G	0.15%	0.04%
6262	G	0.15%	0.02%
6263	C	0.14%	0.06%
6264	G	0.17%	0.01%
6265	T	0.19%	0.02%
6266	C	0.11%	0.03%
6267	C	0.09%	0.02%
6268	A	0.08%	0.01%
6269	A	0.08%	0.05%
6270	T	0.06%	0.01%

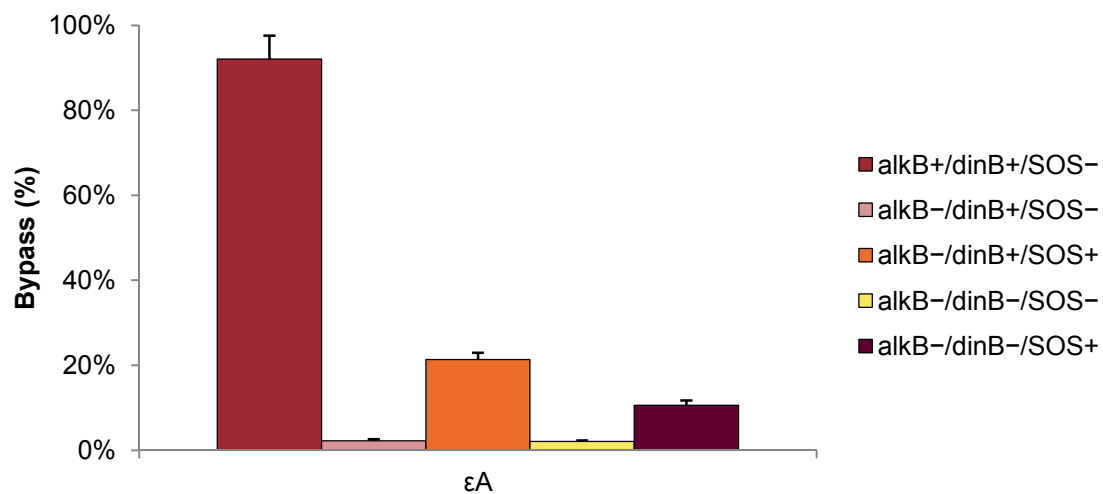


Figure S1. Lesion bypass efficiency of ϵ A in the five conditions with various AlkB, DinB and SOS-induction statuses. Error bars represent one SD (N = 3).

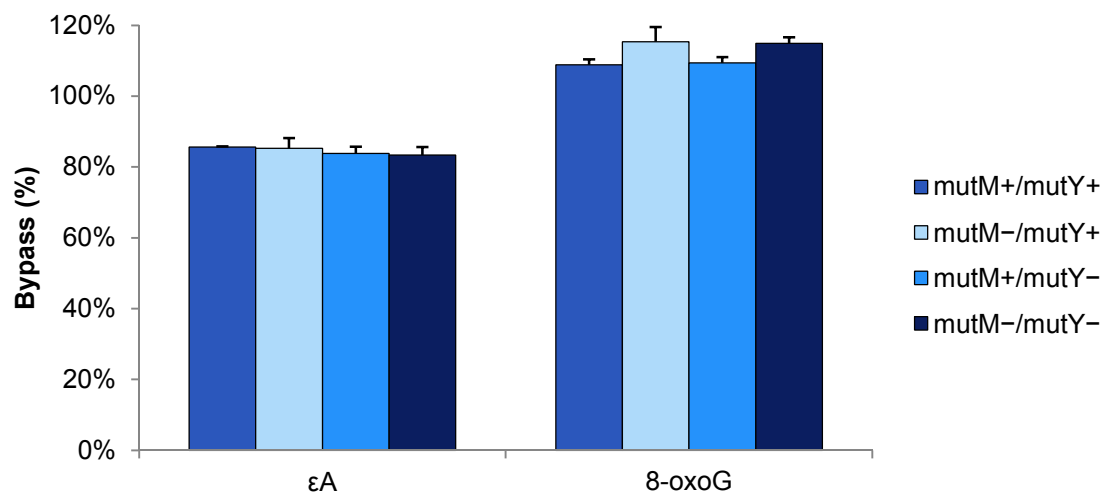


Figure S2. Lesion bypass efficiency of ϵ A and 8-oxoG in the four cell strains with various MutM and MutY statuses. Error bars represent one SD (N = 3).

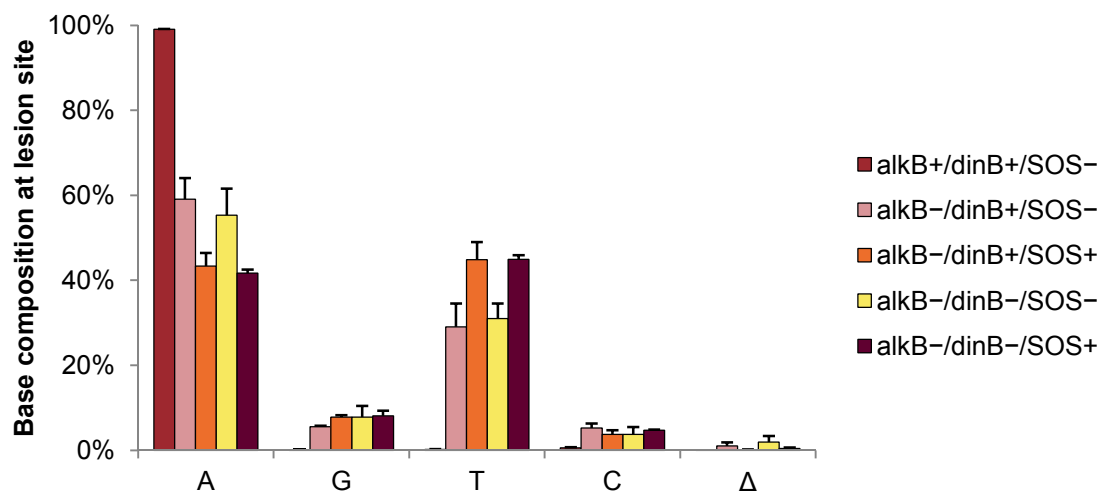


Figure S3. Mutation frequency and specificity of ϵ A in the five conditions with various AlkB, DinB and SOS-induction statuses. A, G, T and C indicate the possible bases present at the lesion site (site N of Figure 2) after *in vivo* replication, and Δ denotes the occurrence of deletions at the lesion site. Error bars represent one SD (N = 3).

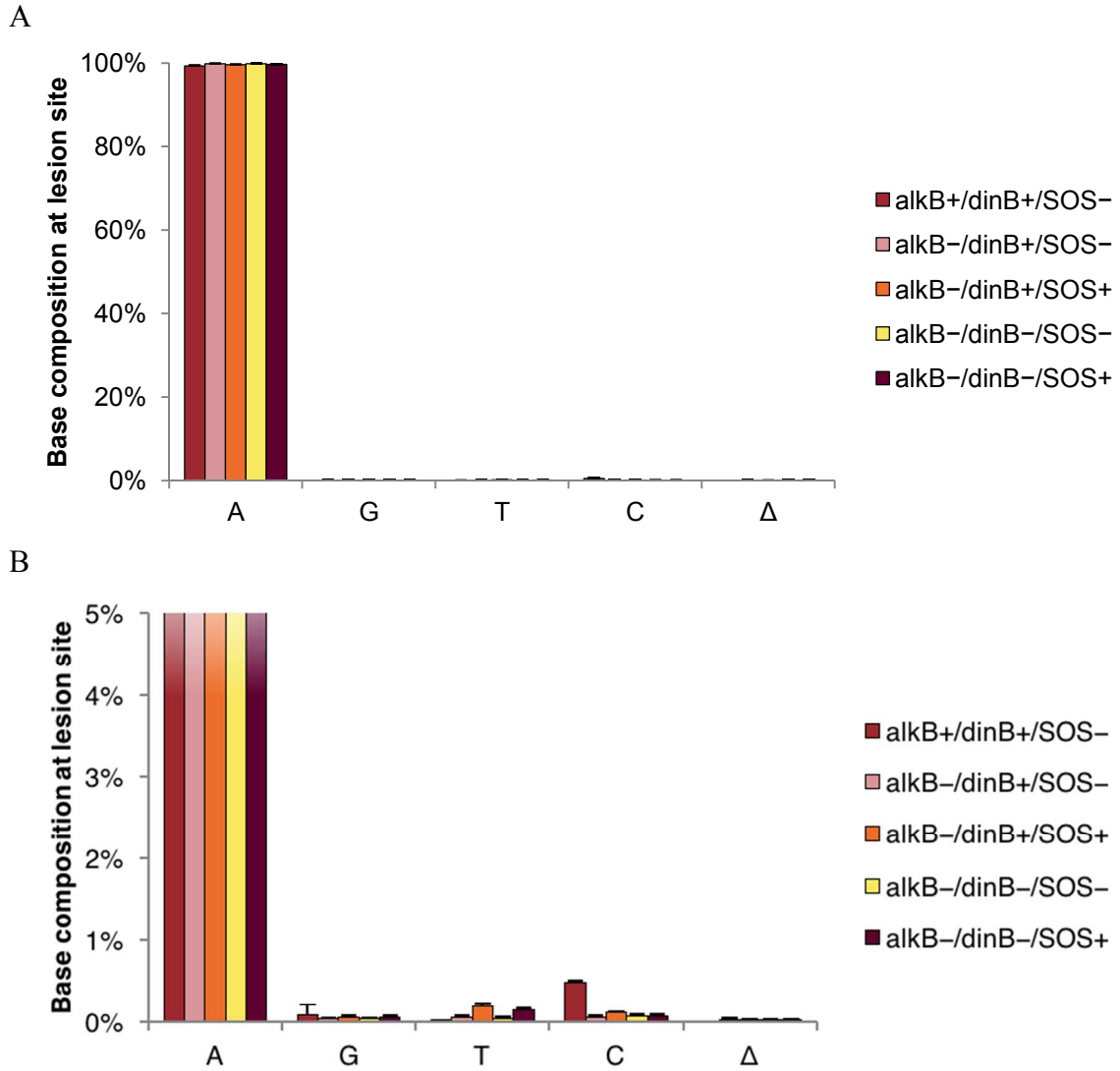


Figure S4. Mutation frequency and specificity of the negative control (A) in the five conditions with various AlkB, DinB and SOS-induction statuses. *A*, the complete chart with the y-axis ranging from 0 to 100%. *B*, the y-axis is enlarged to show low frequency events. A, G, T and C indicate the possible bases present at the lesion site (site N of Figure 2) after *in vivo* replication, and Δ denotes the occurrence of deletions at the lesion site. Error bars represent one SD (N = 3).

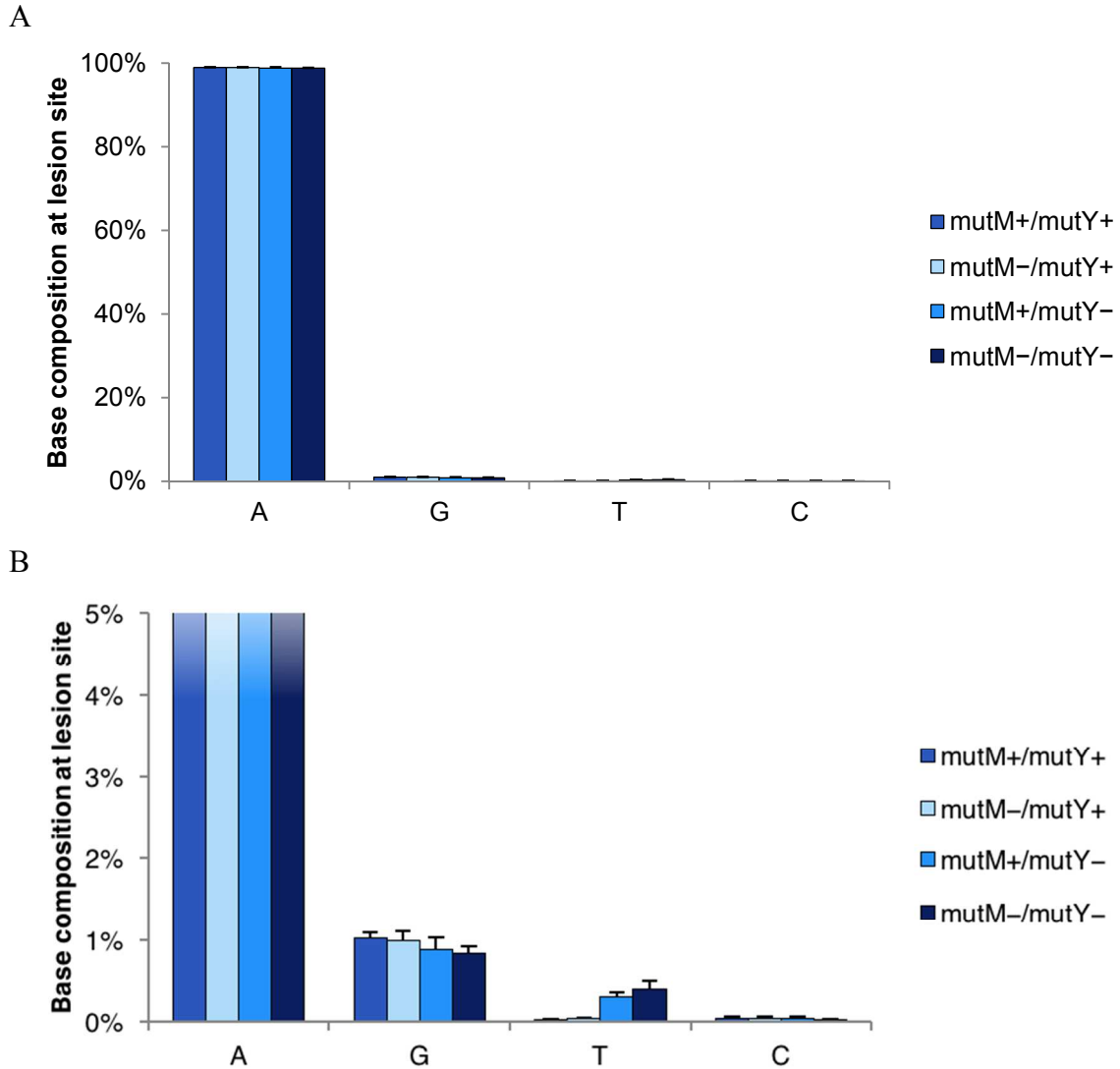


Figure S5. Mutation frequency and specificity of the negative control (A) in the four cell strains with various MutM and MutY statuses. *A*, the complete chart with the y-axis ranging from 0 to 100%. *B*, the y-axis is enlarged to show low frequency events. A, G, T and C indicate the possible bases present at the lesion site (site N of Figure 2) after *in vivo* replication. Error bars represent one SD (N = 3).

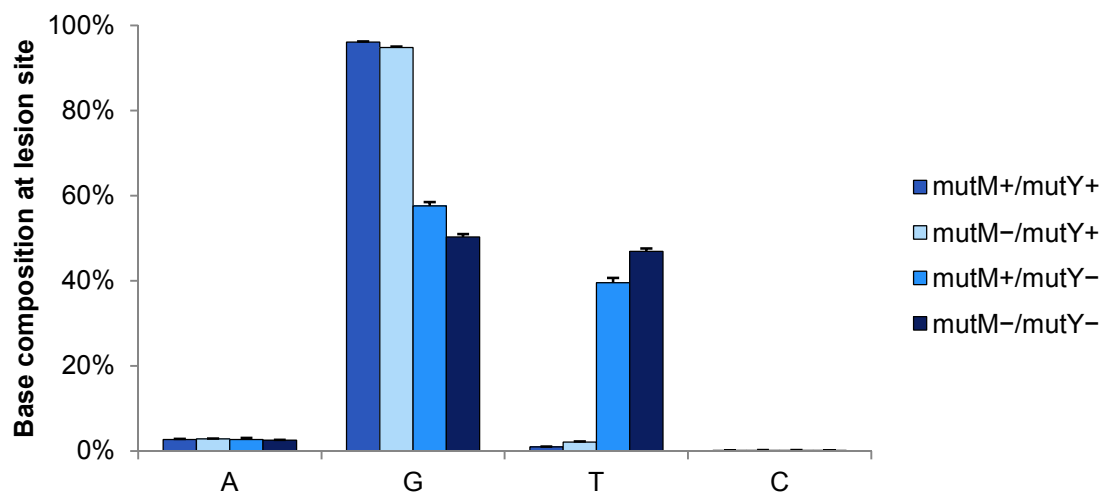


Figure S6. Mutation frequency and specificity of 8-oxoG in the four cell strains with various MutM and MutY statuses. A, G, T and C indicate the possible bases present at the lesion site (site N of Figure 2) after *in vivo* replication. Error bars represent one SD (N = 3). Deletion mutation was not included here because this lesion is not known to cause deletions.