

Supplemental Table S1:
p-values of genotypic comparisons for SDSA + LTR annealing repair events

Figure 3A

Genotype	<i>wild type</i>	<i>helq</i>	<i>blm</i>	<i>helq blm</i>	
<i>wild type</i>	X	< 0.0001	< 0.0001	< 0.0001	
<i>helq</i>	X	X	> 0.99	0.55	
<i>blm</i>	X	X	X	0.04	
<i>helq blm</i>	X	X	X	X	

Figure 4A

Genotype	<i>wild type</i>	<i>fancm</i>	<i>blm</i>	<i>blm fancm</i>	
<i>wild type</i>	X	< 0.0001	< 0.0001	< 0.0001	
<i>fancm</i>	X	X	0.005	0.10	
<i>blm</i>	X	X	X	0.96	
<i>blm fancm</i>	X	X	X	X	

Figure 5A

Genotype	<i>wild type</i>	<i>helq</i>	<i>fancm</i>	<i>helq fancm</i>	
<i>wild type</i>	X	<0.0001	<0.0001	<0.0001	
<i>helq</i>	X	X	0.20	0.18	
<i>fancm</i>	X	X	X	0.99	
<i>helq fancm</i>	X	X	X	X	

p-values were calculated with the Kruskal-Wallis test with Dunn's multiple comparisons, using GraphPad Prism 9 software. Comparisons with $p < 0.05$ are highlighted in yellow.

**Supplemental Table S2:
p-values of genotypic comparisons for aborted SDSA repair events**

Figure 3B

Genotype	<i>wild type</i>	<i>helq</i>	<i>blm</i>	<i>helq blm</i>	
<i>wild type</i>	X	< 0.0001	< 0.0001	< 0.0001	
<i>helq</i>	X	X	0.006	0.19	
<i>blm</i>	X	X	X	> 0.99	
<i>helq blm</i>	X	X	X	X	

Figure 4B

Genotype	<i>wild type</i>	<i>fancm</i>	<i>blm</i>	<i>blm fancm</i>	
<i>wild type</i>	X	0.25	< 0.0001	0.0001	
<i>fancm</i>	X	X	< 0.001	0.0083	
<i>blm</i>	X	X	X	0.89	
<i>blm fancm</i>	X	X	X	X	

Figure 5B

Genotype	<i>wild type</i>	<i>helq</i>	<i>fancm</i>	<i>helq fancm</i>	
<i>wild type</i>	X	< 0.0001	0.63	0.005	
<i>helq</i>	X	X	< 0.0001	0.48	
<i>fancm</i>	X	X	X	0.03	
<i>helq fancm</i>	X	X	X	X	

p-values were calculated with the Kruskal-Wallis test with Dunn's multiple comparisons, using GraphPad Prism 9 software. Comparisons with $p < 0.05$ are highlighted in yellow.

**Supplemental Table S3:
p-values of genotypic comparisons for repair synthesis tract lengths**

Figure 3C

Genotypic comparison	Minimum number of base pairs synthesized				
	5	250	1000	2400	4600
<i>wild type / helq</i>	0.29	0.14	0.0002	0.0042	0.0004
<i>wild type / blm</i>	0.0012	0.0023	< 0.0001	< 0.0001	0.033
<i>helq / blm</i>	0.044	0.14	0.23	0.0015	0.210
<i>helq / helq,blm</i>	< 0.0001	< 0.0001	< 0.0001	< 0.0001	0.68
<i>blm / helq,blm</i>	0.0004	< 0.0001	0.0001	0.026	0.097

Figure 4C

Genotypic comparison	Minimum number of base pairs synthesized				
	5	250	1000	2400	4600
<i>wild type / fancm</i>	0.11	0.12	0.038	0.15	0.13
<i>wild type / blm</i>	0.064	N.D.	< 0.0001	< 0.0001	0.011
<i>fancm / blm</i>	1.0	N.D.	0.098	0.0026	0.43
<i>fancm / blm,fancm</i>	1.0	0.13	0.0069	0.0068	1.0
<i>blm / blm,fancm</i>	1.0	N.D.	0.21	1.0	1.0

Figure 5C

Genotypic comparison	Minimum number of base pairs synthesized				
	5	250	1000	2400	4600
<i>wild type / fancm</i>	0.11	0.12	0.038	0.15	0.13
<i>wild type / helq</i>	0.29	0.14	0.0002	0.0042	0.0004
<i>fancm / helq</i>	0.58	0.81	0.40	0.41	0.23
<i>helq / helq,fancm</i>	0.80	< 0.0001	< 0.0001	< 0.0001	0.26
<i>fancm / helq,fancm</i>	0.79	0.0019	< 0.0001	< 0.0001	0.025

Two-tailed p-values were calculated with Fisher's exact test, using GraphPad Prism 9 software. N.D. = no data. Comparisons with p<0.05 are highlighted in yellow.