Supporting Information

Izhar et al. 10.1073/pnas.1216894110

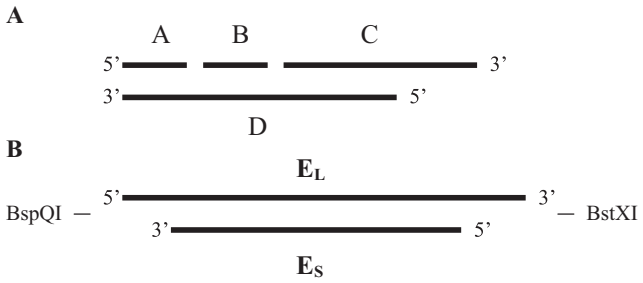


Fig. S1. Construction of double-stranded oligonucleotides carrying the core lesion sequence used for the construction of the lesion shuttle vectors and controls. (*A*) Oligonucleotide B containing a site-specific benzo[*a*]pyrene-guanine (BP-G) or TT 6–4 photoproduct (PP) adduct was extended by ligating oligonucleotides A and C to its 5′ and 3′ ends, respectively, using oligonucleotide D as a scaffold. (*B*) Extended oligonucleotides E_L and E_S were annealed to form a short DNA duplex with 5′ BspQI and 3′ BstXI compatible overhangs, which was then ligated to the 4,321-bp BspQI-BstXI–digested fragment of plasmid pLSV5, whose construction is described in *Materials and Methods*.

Table S1. Tolerance efficiency and sequence signature of two-staggered BP-G adducts integrated into human chromosomes

Event type	DNA damage tolerance product	No. isolates	%
1 Accurate TLS	5′GT**G**AC----------CGTAT 3′ 3′CACTG----------GCATA 5′	68	76%
	5′GTCAC----------CGCAT 3′ 3′CAGTG----------GC**G**TA 5′		
2 Mutagenic TLS	5′GT**T**AC----------CGTAT 3′ 3′CAATG----------GCATA 5′	6	6%
	5′GT**A**AC----------CGTAT 3′ 3′CATTG----------GCATA 5′		
	5′GTCAC----------CGAAT 3′ 3′CAGTG----------GC**T**TA 5′		
3 HDR	5′GT**C**AC----------CGTAT 3′ 3′CAGTG----------GC**A**TA 5′	16	18%
Total no. isolates:		90	

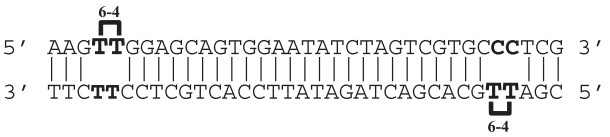
Human XP12RO xeroderma pigmentosum group A (XPA) cells were stably transformed with the lesion shuttle vector pLSV5(BP-GstaggBP-G) that carries two BP-G lesions in a staggered conformation with opposing G or T, respectively. Shown are sequences obtained from amplified genomic DNA of individual colonies after integration and long-term propagation. The nucleotides at the lesion's position are marked with boldface type. HDR, homology-dependent repair; TLS, translesion DNA synthesis.

Table S2. Relative colony yield of cells after genomic integration of the two-staggered BP-G adducts lesion shuttle vector pLSV5(BP-GstaggBP-G)

	No. colonies per dish		
Shuttle vector	Exp. 1	Exp. 2	Exp. 3
Control	144	162	159
pLSV5(BP-GstaggBP-G)	120	191	193
Relative colony yield (RCY), %	83	118	121
Average RCY, %		107 ± 17	

Relative colony yield was calculated as the ratio of the number of colonies obtained in pLSV5(BP-GstaggBP-G) to a control vector without BP-G adducts (pBCs) transfections. Shown is an average value of three independent experiments.

Table S3. Tolerance efficiency and sequence signature of two-staggered TT 6–4 photoproducts integrated into human chromosomes



	Event type	DNA damage tolerance product	No. isolates	%
1	Accurate TLS	5′AAG**TT**GGA———–TGCCCT 3′ 3′TTCAACCT——— ACGTTA 5′ 5′AAGAAGGA———–TGCAAT 3′ 3′TTCTTCCT———–ACG**TT**A 5′	18	40
2	Mutagenic TLS	5′AA**TTT**GGA———–TGCCCT 3′ 3′TTAAACCT———–ACGGGA 5′ 5′AA**TTC**GGA———–TGCCCT 3′ 3′TTAAGCCT———–ACGGGA 5′ 5′AA**TTA**GGA———–TGCCCT 3′ 3′TTAATCCT———–ACGGGA 5′	22	48
3	HDR	5′AAG**AA**GGA———–TGCCCT 3′ 3′TTCTTCCT———–ACG**GG**A 5′	5	11
Total no. isolates:			45	

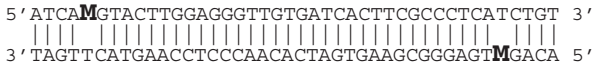
Human XP12RO XPA cells were stably transformed with pLSV56-4TTstagg that carries two 6–4TT lesions in a staggered conformation with opposing TT or CC, respectively. Shown are sequences obtained from amplified genomic DNA of individual colonies after integration and long-term propagation. The nucleotides at the lesion's position and/or neighboring bases are in boldface type.

Table S4. Relative colony yield of cells after genomic integration of the two-staggered 6-4TT adducts lesion shuttle vector pLSV5(6-4stagg6-4)

Shuttle vector	No. colonies per dish		
Control	187	190	90
pLSV5(6-4Stagg6-4)	176	184	96
Relative colony yield (RCY), %	94	97	107
Average RCY, %		99 ± 5	

Relative colony yield was calculated as the ratio of the number of colonies obtained with pLSV5(6-4stagg6-4) to pC6-4s (control with no lesions). Shown is an average value of three independent experiments.

Table S5. Tolerance efficiency and sequence signature of two-staggered trimethylene lesions integrated into human chromosomes



	Event type	DNA damage tolerance product	No. isolates	Fraction,%
1	HDR	5′ATCA**A**G----------CATCTGT 3′ 3′TAGTTC----------GT**A**GACA 5′	29	76%
2	TLS	8 5′ATCAAG----------CAGCTGT 3′ 3′TAGTTC----------GT**C**GACA 5′ 1 5′ATCA**T**G----------CATCTGT 3′ 3′TAGTAC----------GTAGACA 5′	9	24%
Total No. isolates:			38	

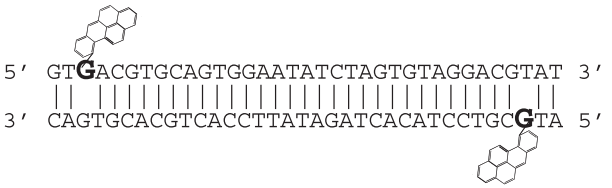
Human XP12RO XPA cells were stably transformed with pLSV5(M3staggM3) that carries two trimethylene (M3) lesions in staggered conformation. Shown are sequences obtained from amplified genomic DNA of individual colonies after integration and long-term propagation. The nucleotides present at the lesion's position are in boldface type.

Table S6. Relative colony yield of cells after genomic integration of the two-staggered M3 adducts lesion shuttle vector pLSV5(M3staggM3)

Shuttle vector	No. colonies per dish		
Control	131	129	126
pLSV5(M3staggM3seq2)	63	77	44
Relative colony yield (RCY), %	48	60	35
Average RCY, %		48 ± 10	

Relative colony yield was calculated as the ratio of the number of colonies obtained with pLSV5(M3staggM3) to a control vector without M3 adducts (pCMs). Shown is an average value of five independent experiments.

Table S7. Sequence signature of two-staggered BP-G adducts integrated into human chromosomes in cells in which expression of *REV3L*, the gene encoding the catalytic subunit of DNA polymerase zeta, was knocked down



Event type	DNA damage tolerance product	No. isolates (%) siControl	No. isolates (%) si*REV3L*
1. Accurate TLS		27 (67.5)	35 (81.4)
	5′GT**G**AC————--CGTAT 3′		
	3′CACTG————--GCATA 5′		
	5′GTCAC————--CGCAT 3′		
	3′CAGTG————--GC**G**TA 5′		
2. Mutagenic TLS		3 (7.5) (7)	1 (2.3)
	5′GT**T**AC————--CGTAT 3′		
	3′CAATG————--GCATA 5′		
	5′GT**A**AC————--CGTAT 3′		
	3′CATTG————--GCATA 5′		
	5′GTCAC————--CGAAT 3′		
	3′CAGTG————--GC**T**TA 5′		
	5′GT**C**AC————--CGTAT 3′		
	3′CAGTG————--GC**A**TA 5′		
Total no. isolates		40	43

Human XP12RO XPA cells were treated with a control siRNA or siRNA against *REV3L* and with a boost treatment 24 h later. After 48 additional hours cells were stably transformed with pLSV5(BP-GstaggBP-G) that carries two BP-G lesions in a staggered conformation with opposing G or T, respectively. Shown are sequences obtained from amplified genomic DNA of individual colonies after integration and long-term propagation. The nucleotides at the lesion's position are marked with boldface type.

Table S8. Chromosomal DNA sequence at the integration site of the lesion shuttle vector pLSV5(BP-GstaggBP-G)

Event no.	Chromosomal location	Chromosome: *attR*	*Vector*	Chromosome: *attL*
1	19q13.31	CCCAGTACCATCAGAAGGACCCTGGTGAC***CACCCGCACC GCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCGG***TCTCATTCTTCACCACTGT GGGATCCCATAGAAGTCAGG
2	19q13.31	CCCAGTACCATCAGAAGGACCCTGGTGAC***CACCCGC ACCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCGG***TCTCATTCTTCACCAC TGTGGGATCCCATAGAAGTCAGG
3	19q13.31	AGAATGAGACCACGG***AGGGCACGCCCTGGCACCCGCA CCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGG***TCACCAGGGT CCTTCTGATGGTACTGGGGACACCTG
4	19q13.31	CCCAGTACCATCAGAAGGACCCTGGTG***ACCCGCACCG CGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCC***TATTCCGTGGTCTCATTCTT CACCACTGTGGGATCCCA
5	19q13.31	ATCCCCTGACTTCTATGGGATCCCACAGTGGTGAAGA ATGAGACCA***CGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA***GGGGTC ACCAGGGTCCTTCTGATGGTACTGGGGA
6	19q13.31	AGGTGTCCCCAGTACCATCAGAAGGACCCTGG***CGCAC CGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCGG***TCATTCTTCACCAC TGTGGGATCCCATAGAAGTCAGGGGA
7	19q13.31	TGAACATCCCCTGACTTCTATG***GCCCTGGCACCCGCA CCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCC***TTCTGATG GTACTGGGGACACCTGATCCCAT
8	19q13.31	ATCCCCTGACTTCTATGGGATCCCACAGTGGTGAAG AATGAGACCA***CGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA***GG GGTCACCAGGGTCCTTCTGATGGTACTGGGGACACCTGATCC
9	19q13.31	ATCCCCTGACTTCTATGGGATCCCACAGTGGTGAAG AATGAGACCA***CGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGA***GGGGT CACCAGGGTCCTTCTGATGGTACTGGGGACACCTGATCC
10	19q13.31	ATGAGACCACGGAATACCAAGGA***CCCTGGCACCC GCACCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGG****TCACCAGGGTCCTTC TGATGGTACTGGGGA*
11	19q13.31	TCCTGAACATCCCCTGACTTCTATGGGATCCCACAGT GGTGAAGAATGAGACCA***CGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA*** GGGGTCACCAGGGTCCTTCTGATGGTACTGGGGACACCTGATCC
12	2p11.1	TTTGAAACACTCTTTTTGTAGTATATGGAAGTGGA CAT***TTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA*** GACAGAAGCATTCTCAGAAGCTTCATTGGGATGTTTCAATTGAAGTCACA
13	2q23.2	AAGACATAGGACCATGAAGAT***CCAGGGCACGCCCTG GCACCCGCACCGCG GCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAG***ACCTAATTAAACTAAAGAGCTTCTGCACN ACTAAAGAAACTATCA
14	6P21.1	ATATATAGTTCCATGGA***GGCACCCGCACCGC GGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGC CCAATGG***CATTTGTTCTGTAAAATGCATATAAA
15	9p13.2	TTGGAATATAGGTGCTGGATAAA***CCCTGGCACCCGCA CCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA***GGTGCA ATTCCATCATTGAACAGATGGGGAGGCTGAGACT
16	9p21.2	AACATCATCAGATAAATAATTAAGTCAAAGTAC CTGGAAATTAA***CCGCACCGNGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGG***GTAAGAACTAGGAG ACCCTTAACATTTCCCAGGGCAATACACATGGTAAA
17	8p22	TACAGCAATAAGTACTTGGGTTT***CCCTGGCACCCGCAC CGCGGCTTCGAGACCG***	***Vector***	***TGGCAGACTTGGGTGTGAACAGATATTTCTGGTTTCCATGTTCTTTA***
18	8p22	AACGCGGGCCAGAGTTTTAGAAAATGGTAT***CCCGCAC CGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA***CCCCA AGTCTCCTCTCACTAGACTCCCCCC
19	8p22	CATTGCGTCATGGCTTAAAATCTCCA***TGGCACCCGCA CCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGC***GTCCAAGTA CTTATTGCTGTATTTGAAACCACC
20	5q14.3	GGGTAAATAGTTTTCTGTGGTGGCAT***TGGCACCCGCAC CGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCG***CCCCTTCTCCAGCTCTAG TGAAATTTAAGGGCCTACCTTAT
21	4q35.2	GGGTTAGGGTTAGGGTTAGGGTTAGGGTTAGGGT GAGGT***ACCCGCACCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA***GGTGAGGG TGAGGGTGAGGGTGAGGGTTAGGGTTAGGGGTTA
22	4q35.1	CTCTGACCCCACAGTAGCATCTAGGAT***TGGCACCCGCACC GCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGCCCA***CACGCCC AGTGGGCATAATACAGTGCTCTTTTAGCTCTGCCATTCGCAGA

Table S8. Cont.

Event no.	Chromosomal location	Chromosome: *attR*	*Vector*	Chromosome: *attL*
23	7p14.1	CTGAAAAACCCTAAAGTATTCTAGG***AGGGCA*** ***CGCCCTGGCACCCGCACCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGAGC***T AAACTGTCTTCCATTTCAGTTTTGAATCAGTATTGTTACACTCAAACC
24	10q22.1	TCTTGGAGAACGACCATGGATTCTCATAAG***CG*** ***CCCTGGCACCCGCACCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCC***ACTCCA ATTGCAGCTGCTGTACCAGATGTGGTTTCATTGCCTCA
25	20p13	GGGAAAGCAGACAGACCATGGGGTGGC***CCCGCA*** ***CCGCGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCC***AGGATCCCCATGGCCG GGGGGCTCACTGACT
26	3p23	GTCTGTCCAAAGATCCAGTAAACATCCACCT CTATTTTCTTT***CGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGA GCC***CTATGGCATTATTTTAAAACAATTAATTGCTTATTCTCTC
27	1q41	TGTATGTTTATTAAATTTATTTTTTTAAATCC TCATTTTTTAACCAATCCG***CGGCTTCGAGACCG***	***Vector***	***GACCAGATGGGTGAGGTGGAGTACGCGCCCGGGGA GCCC***GAGGAAAATGATCATTTTAGTTTCATAATATTCAACAAG
28	13q13.3	AAGTCAAGAT AATGGTTAAA GGCTTTGAAG AG TATCTTTG***CG***	***Vector***	***GACCAGATGG***CTAGGAAGAATTGGTGGGTGCAGAG AAAGGAGAAATGGAAGGAGGGATGAGCCTTACATG
29	4p13	TACACATCCTGGACCATGAA GAAAGGTAGAC***CTGC*** ***AGATCTGNGATCTCATACAGAACTTAT****	***	****GTTTCGAGGGCGAGAGCTTCCCGGT*** ATATCTTTGCTTTCCCCAGAT CCTGCCAGCCTGACTCCTT
30	12q22	CCAGACGCGTCCGGGGCGCCGCTC***GCACCCGCCGAC*** ***GCCGTCGCACGTCCCGTGCTCAC****	***	****GTGACCGTCGAGAACCCGCTGANGCTGCCCCGCGTCTC***CTCCCAG GACCTTATGTAACCCAGCGTCGGCAGCAAG
31	Xq22.3	CCAGTTTCTTCAACAAAAAAATTGCAAAAATAAAAAG GAACAAGG***AGAACTTATAAGATTCCC****	***	****CGTTCATCATGATGGACCAGATGGGTG***ATAGATTAAATGAGGCATT AAAGACATATCAACCAAATGTAACC

Human XP12RO XPA cells were stably transformed with pLSV5(BP-GstaggBP-G) that carries two BP-G lesions in a staggered conformation. Individual colonies carrying the integrated plasmid were propagated for 21 d, after which the integrated plasmids were rescued and subjected to DNA sequence analysis of the vector–chromosome junctions. *attR* and *attL* are pseudo *att* sites, which are hallmarks of ϕC31 integrase-mediated integration. Several random integrations were detected too (marked by asterisks). The authentic *attP* site is 5′-GCCCCAACTGGGGTAACCTTTGAGTTCTCTCAGTTGGGGG-3′ (the *attL* and *attR* sites are underlined).

*Random integration.

Table S9. Signature of chromosomal DNA damage tolerance of a single TT 6–4 PP
5′ CAAGTTGGAGC
3′ GTTCTTCCTCG

No.	Event type	DNA damage tolerant product	No. isolates	Fraction, %
1	Accurate TLS			
		5′ CAAGTTGGAGC 3′ GTTCAACCTCG	13	12
2	Mutagenic TLS			38
			40	
		5′ CAA***T***TTGGAGC 3′ GTT***A***AACCTCG	19	
		5′ CAA***T***T***C***GGAG 3′ GTT***A***A***G***CCTC	4	
		5′ CAA***T***T***A***GGAGC 3′ GTT***A***A***T***CCTCG	3	
		5′ CAAG***C***TGGAGC 3′ GTTC***G***ACCTCG	3	
		5′ CAAG***TA***TGGAGC 3′ GTTC***AT***ACCTCG	2	
		5′ CAA***C***T***C***GGAGC 3′ GTT***G***A***G***CCTCG	2	
		5′ CAAGTT***G***GGAGC 3′ GTTCAA***C***CCTCG	1	
		5′ CAA***AAA***GGAGC 3′ GTT***TTT***CCTCG	1	
		5′ CAA**AAAA**GAGC 3′ GTT***TTTT***CTCG	1	
		5′ CAAG***G***TGGAGC 3′ GTTC***C***ACCTCG	1	
		5′ CAA***T***TTGGA***A***GC 3′ GTTAAACCT***T***CG	1	
		5′ CA_GTT***G***GGAGC 3′ GT_CAA***C***CCTCG	1	
		5′ CAA***T***T***A***TGGAGC 3′ GTT***A***A***T***ACCTCG		
3	Replication/HDR			
		5′ CAAGAAGGAGC 3′ GTTCTTCCTCG	53	50
Total no. isolates:			106	100

Human XP12RO XPA cells were stably transformed with pLSV5(TT6-4) that carries a single TT 6–4 PP lesion with opposing TT. Shown are sequences obtained from amplified genomic DNA of individual colonies after integration and long-term propagation. The nucleotides at the location of the original lesion are underlined. The mutations are in boldface type and italics.

Table S10. Oligonucleotides used for construction of pLSV5(BP-GstaggBP-G), pLSV5(BP-G), and pLSV5BCs vectors

	Sequence	bp
Long		
$1A_L$	GCTCGATCTGAC	12
$1B_L$	GTTCGT (**G**) ACGTG	12
$1C_L$	CAGTGGAATATCTAGTGTAGGACGTATGCTCCTTGAACGCACCG	44
$1D_L$	CGTCCTACACTAGATATTCCACTGCACGTCACGAACGTCAGATCGAG	47
$1E_L$	GCTCGATCTGACGTTCGT (**G**) ACGTGCAGTGGAATATCTAGTGTAGGACGTATGCTCCTTGAACGCACCG	68
$1F_L$	GCTCGATCTGACGTTCGTGACGTGCAGTGGAATATCTAGTGTAGGACGTATGCTCCTTGAACGCACCG	68
Short		
$1A_S$	GCGTTCAAGGAG	12
$1B_S$	CAT (**G**) CGTCCTAC	12
$1C_S$	ACTAGATATTCCACTGCACGTGACGAACGTCAGATCG	37
$1D_S$	CACGTGCAGTGGAATATCTAGTGTAGGACGCATGCTCCTTGAACG	45
$1E_S$	GCGTTCAAGGAGCAT (**G**) CGTCCTACACTAGATATTCCACTGCACGTGACGAACGTCAGATCG	61
$1F_S$	GCGTTCAAGGAGCATGCGTCCTACACTAGATATTCCACTGCACGTGACGAACGTCAGATCG	61

Shown are the oligonucleotides used to construct the duplex oligonucleotides carrying the core lesion sequences for building the lesion shuttle vectors carrying BP-G lesions and their controls. The underlined G represents the BP-G adduct. The outline of the construction is shown in Fig. S1 and described in *Materials and Methods*.

Table S11. Oligonucleotides used for construction of pLSV5(TT6-4staggTT6-4) and pV5TTCs vectors

	Sequence	bp
Long		
$2A_L$	GCTCGATCTGAC	12
$2B_L$	GCAAG (**TT**) GGAG	11
$2C_L$	CAGTGGAATATCTAGTCGTGCCCTCGCACTCCTTGAACGCACCG	44
$2D_L$	GCGAGGGCACGACTAGATATTCCACTGCTCCAACTTGCGTCAGATCGAGC	50
$2E_L$	GCTCGATCTGACGCAAG (**TT**) GGAGCAGTGGAATATCTAGTCGTGCCCTCGCACTCCTTGAACGCACCG	67
$2F_L$	GCTCGATCTGACGCAAGTTGGAGCAGTGGAATATCTAGTCGTGCCCTCGCACTCCTTGAACGCACCG	67
Short		
$2A_S$	GCGTTCAAGGAG	12
$2B_S$	TGCGA (**TT**) GCACG	12
$2C_S$	ACTAGATATTCCACTGCTCCTTCTTGCGTCAGATCG	36
$2D_S$	GAAGGAGCAGTGGAATATCTAGTCGTGCAATCGCACTCCTTGAACGC	49
$2E_S$	GCGTTCAAGGAGTGCGA (**TT**) GCACGACTAGATATTCCACTGCTCCTTCTTGCGTCAGATCG	60
$2F_S$	GCGTTCAAGGAGTGCGATTGCACGACTAGATATTCCACTGCTCCTTCTTGCGTCAGATCG	60

Shown are the oligonucleotides used to construct the duplex oligonucleotides carrying the core lesion sequences for building the lesion shuttle vector carrying TT 6–4 PP lesions and their controls. The underlined TT represents the 6–4 PP. The outline of the construction is shown in Fig. S1 and described in *Materials and Methods*.

Table S12. Oligonucleotides used for construction of pLSV5(M3staggM3), pLSV5(M3oppM3), and pV5MCs vectors

	Sequence	bp
Long		
3E1	GCTGCTCTCCATCAA**M**TACTTGGAGGGTTGTGATCACTTCGCCCTCAGCTGTGTTGTGGCGGACCG	66
3E2	GCTGCTCTCCATCA**M**GTACTTGGAGGGTTGTGATCACTTCGCCCTCATCTGTGTTGTGGCGGACCG	66
3F	GCTGCTCTCCATCAAGTACTTGGAGGGTTGTGATCACTTCGCCCTCAGCTGTGTTGTGGCGGACCG	66
Short		
3E	CCGCCACAACACAG**M**TGAGGGCGAAGTGATCACAACCCTCCAAGTACTTGATGGAGAGC	59
3F	CCGCCACAACACAGCTGAGGGCGAAGTGATCACAACCCTCCAAGTACTTGATGGAGAGC	59

Shown are the oligonucleotides used to construct the duplex oligonucleotides carrying the core lesion sequences for building the lesion shuttle vectors carrying M3 lesions and their controls. The underlined M represents the M3 lesion. The outline of the construction is shown in Fig. S1 and described in *Materials and Methods*.