Tsaalbi-Shtylik et al., http://www.jem.org/cgi/content/full/jem.20140817/DC1

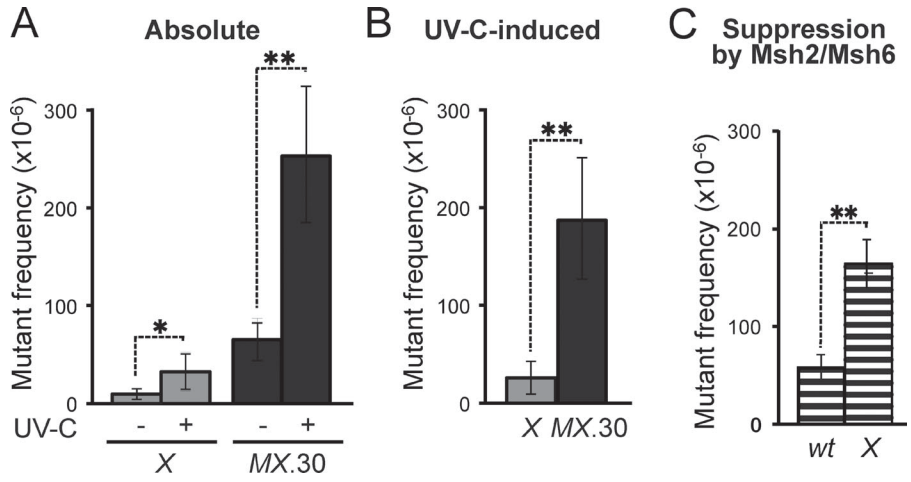

Figure S1. **Msh2/Msh6-dependent suppression of the mutagenicity of UV-C.** (A) Mutant frequencies in isogenic ES cell lines after mock treatment or after low-dose UV-C (0.75 J/m^2). The Msh6$^{-/-}$Xpa$^{-/-}$ line used here was line 30. Bars represent averages of three independent experiments. See Fig. 1 for results using an independently derived Msh6$^{-/-}$Xpa$^{-/-}$ clone (line 4). (B) UV-C–induced mutagenesis in Msh6$^{-/-}$ and in Msh6$^{-/-}$Xpa$^{-/-}$ line 30 cells. (C) Msh2/Msh6-dependent suppression of induced mutagenesis in NER–proficient cells (WT; derived from Fig. 2 C) and in NER-deficient cells (X; Xpa$^{-/-}$ and Msh6$^{-/-}$Xpa2$^{-/-}$ line 30).

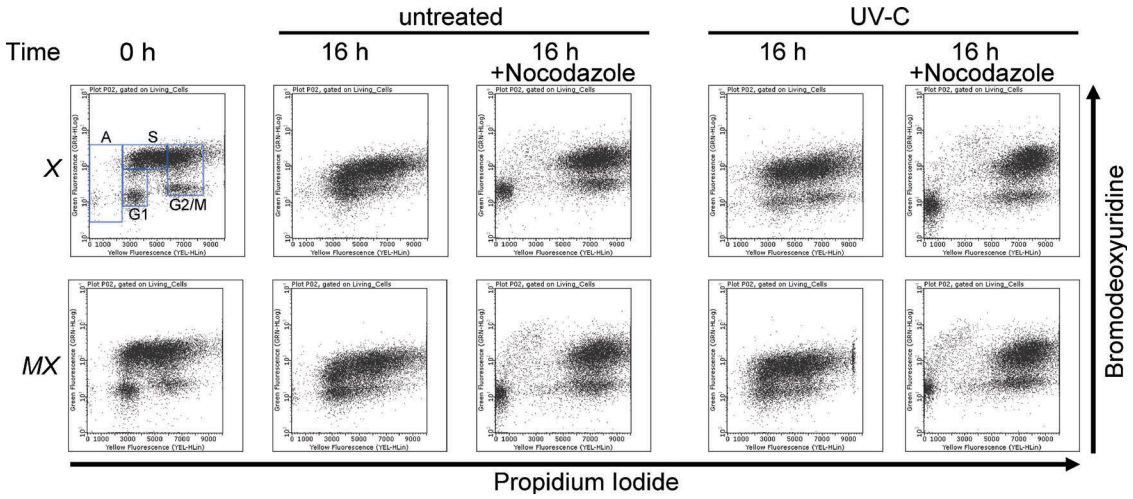

Figure S2. **Accumulation of UV-C exposed ES cell lines at mitosis after nocodazole-treatment.** ES cells were treated with 0.75 J/m2 UV-C or mock treated and replicating cells were pulse-labeled with BrdU, followed by the addition of Nocodazole. At 16 h after UV-C treatment, cells were fixed and stained for DNA content (using Propidium Iodide) and for BrdU and analyzed by bivariate FACS. A, sub-G1 fraction, G1, G1 phase, S, S phase, G2, and G2/M phases. 10,000 cells were analyzed per data point.

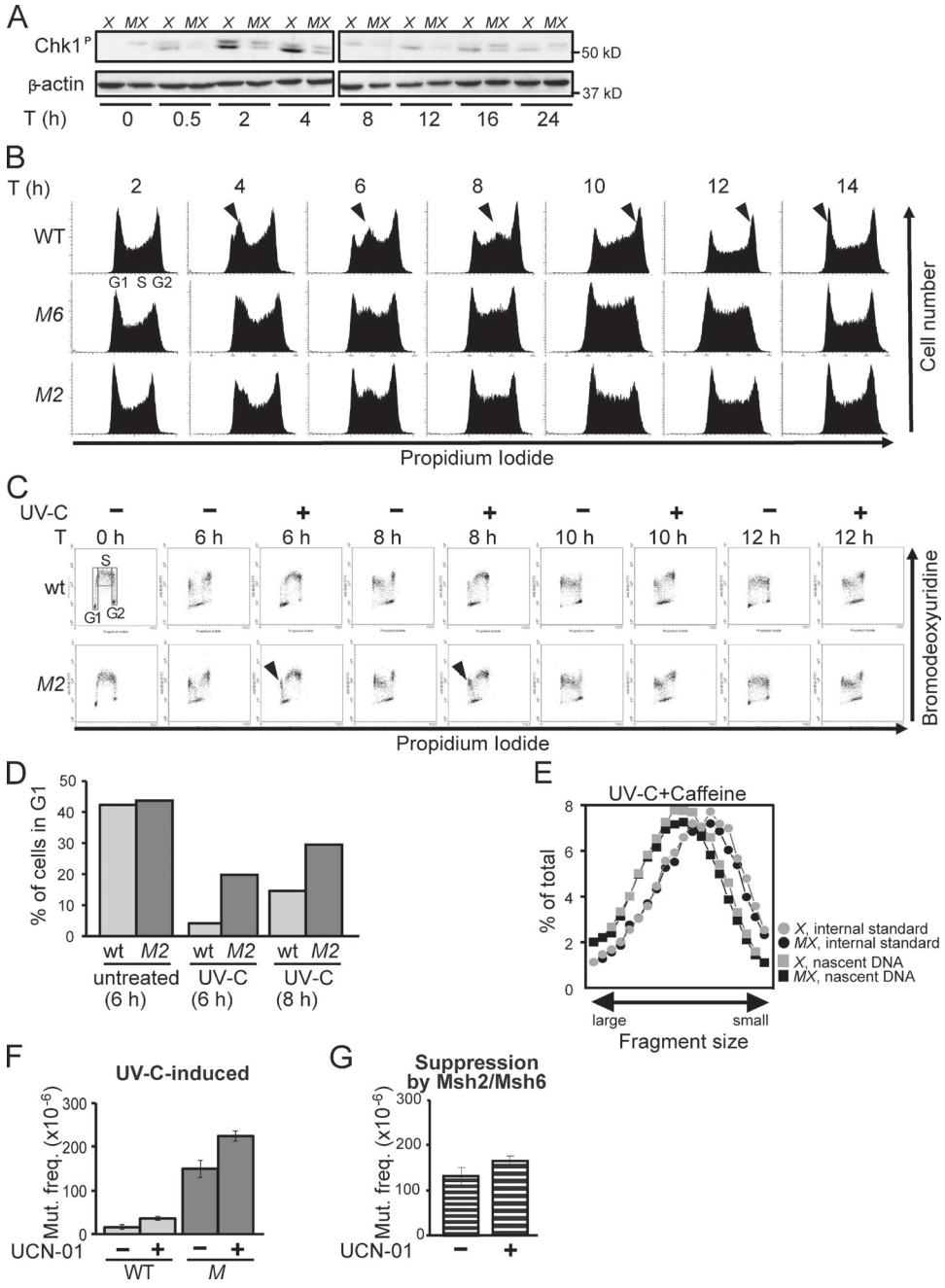

Figure S3. **Msh2/Msh6-dependent DNA damage signaling and induction of cell cycle checkpoints.** (A) Kinetics of phosphorylation of Chk1 in response to UV-C light (0.75 J/m^2). b-actin, loading control. X, Xpa$^{-/-}$, MX, Msh6$^{-/-}$Xpa$^{-/-}$ line 4. Shown is a representative experiment of three independent experiments. See Fig. 4 A for one independent experiment. (B) Cell cycle responses of WT, Msh6$^{-/-}$ (M6), and Msh2$^{-/-}$ (M2) ES cell lines to UV-C exposure (2 J/m^2). After exposure, cells were fixed at the indicated times and analyzed for DNA content (propidium iodide staining) by flow cytometry. Arrowheads indicate delayed progression of damaged WT cells, compared with the Msh2- or Msh6-deficient cells. 10,000 cells were analyzed per data point. Shown is a representative experiment of three independent experiments. (C) Bivariate cell cycle profiles after UV-C exposure (2 J/m^2) of WT and Msh2$^{-/-}$ (M2) ES cells. Replicating cells were pulse-labeled with BrdU immediately after exposure. Cells were fixed at the indicated times and analyzed for DNA and BrdU content (propidium iodide staining and immunostaining, respectively) by flow cytometry. Arrowheads indicate the increased reappearance of BrdU-positive Msh2$^{-/-}$ ES cells at G1, compared with WT controls. 10,000 cells were analyzed per data point. Shown is a representative experiment of three independent experiments. (D) Quantification of WT and Msh2$^{-/-}$ (M2) cells at G1, at 6 and 8 h after treatment with 2 J/m^2 UV, derived from C. (E) Maturation of nascent strands, 4 h after UV-C treatment (0.75 J/m^2) of ES cells, cultured in the presence of the Atr inhibitor caffeine (5 mM). Circles, internal standards ([14C] label, representing intra-CPD fragments). Squares, nascent strands ([3H] label). (F) Frequencies of UV-C (2 J/m^2)-induced Hprt mutants in WT and Msh6$^{-/-}$ (M) ES cells, cultured in the absence and in the presence of UCN-01 (300 nM). Bars represent averages of three independent experiments. (G) Suppression of induced mutations by post-TLS repair, cultured in the absence and in the presence of UCN201 after UV-C exposure, were derived from Fig. S3F.

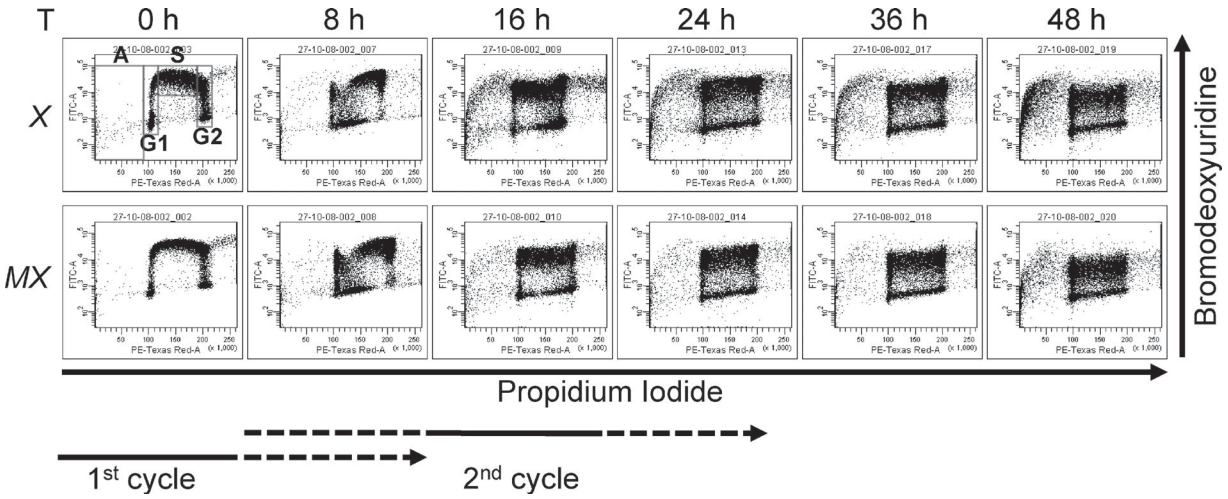

Figure S4. **Msh2/Msh6-dependent induction of delayed apoptosis in response to low-dose UV-C.** Bivariate flow cytometry of $Xpa^{-/-}$ (X) and Msh62/ $2Xpa^{-/-}$ (MX) ES cells after exposure to 0.75 J/m^2 UV-C. Immediately after treatment, replicating cells were pulse labeled with BrdU. Cells were analyzed for DNA content (propidium iodide staining) and for levels of incorporated BrdU. A, sub-G1 fraction; G1, G1 phase; S, S phase, G2/M phase. 10,000 cells were analyzed per data point.

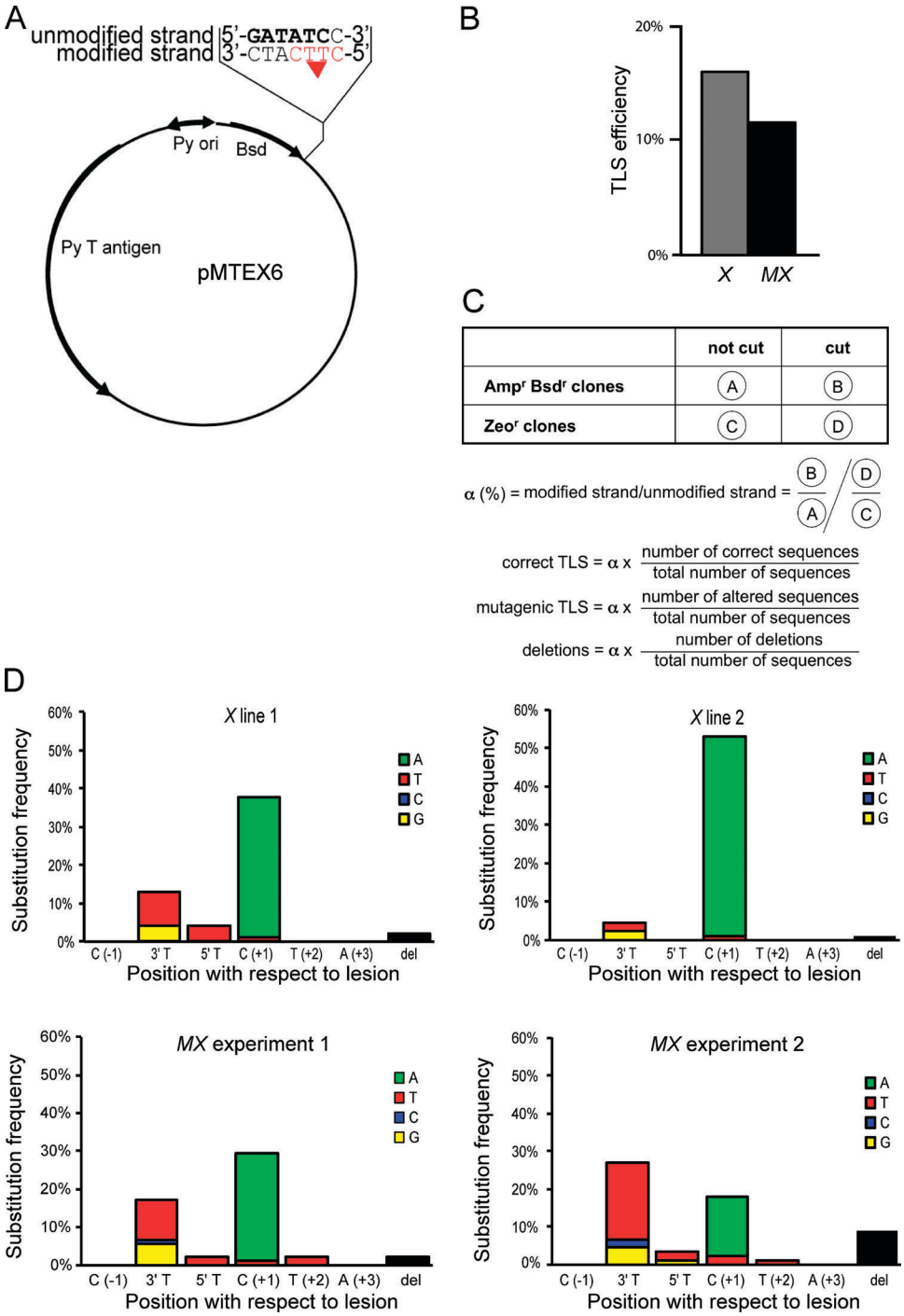

Figure S5. **Normal frequency but increased mutagenicity of TLS at a defined (624)TT in Msh2/Msh6-deficient cells.** X, Xpa$^{-/-}$, MX, Msh6$^{-/-}$Xpa$^{-/-}$. (A) Replicating plasmid pMTEX6 carrying a site-specific (624)TT photolesion (red triangle). Bold, disrupted EcoRV site. Red sequence, mismatched tetramer, enabling to distinguish both strands after replication. Py ori, mouse Polyoma virus replication origin. Py T antigen, mouse Polyoma virus large T antigen, required for replication origin function. Bsd, Blasticidin resistance cassette. (B) Relative efficiency of TLS at a site-specific (6–4)TT photolesion in MEF lines. X, MEFs deficient for the core NER gene Xpc, MX, MEFs deficient for Xpc and Msh2. Two Xpc$^{-/-}$ lines (top) and one Msh6$^{-/-}$Xpc$^{-/-}$ line (bottom) were used. (C) Calculation of frequencies of mutagenic and nonmutagenic TLS. (D) Quantification of mutations at, and adjacent to, the site-specific (624)TT photolesion in replicated plasmids rescued, from transfected MEFs. X, MEFs deficient for the key NER gene Xpc (two independent lines), MX, MEFs deficient for Xpc and Msh2 (one line, two independent experiments). The frequency of substitutions opposite the 39, T of the (6–4)TT photolesion was significantly ($P = 0.0012$) increased in the Msh2-deficient cells. Del, deletions of ≤4 nucleotides. The relatively high frequency of substitutions at the +1 position in both genotypes represents an artifact of the assay as these substitutions are not observed in the genomic mutation spectra (Table S1).

Table S1. **Mutation spectra at genomic *Hprt* in ES cells**

***Xpa*$^{-/-}$ ES cells (*n* = 127 substitutions, from in total two experiments), 0.75 J/m^2 UV-C**

position	mutation	strand[1]	5′ → 3′ target	amino acid change	# of mutants
Transitions at dipyrimidine sites					
113	GC>AT	NTS	TTC(C)TCA	Pro>Leu	1
145	GC>AT	NTS	AGA(C)TTG	Leu>Phe	1
146	AT>GC	NTS	GAC(T)TGC	Leu>Pro	1
151	GC>AT	NTS	GCT(C)GAG	Arg>stop	1
203	AT>GC	NTS	TGC(T)CAA	Leu>Pro	1
208	GC>AT	TS	AAG(G)GGG	Gly>Arg	4
209	GC>AT	TS	AGG(G)GGG	Gly>Glu	3
217	AT>GC	TS	TAT(A)AGT	Lys>Glu	1
325	GC>AT	NTS	GAT(C)AGT	Gln>stop	2
400	GC>AT	TS	GTT(G)AAG	Glu>Lys	13
419	GC>AT	TS	CTG(G)TAA	Gly>Asp	1
464	GC>AT	NTS	GCC(C)CAA	Pro>Leu	1
508	GC>AT	NTS	TCT(C)GAA	Arg>stop	3
527	GC>AT	NTS	GGC(C)AGA	Pro>Leu	1
538	GC>AT	TS	GTT(G)GAT	Gly>Arg	4
539	GC>AT	TS	TTG(G)ATT	Gly>Glu	2
544	GC>AT	TS	TTT(G)AAA	Glu>Lys	7
545	AT>GC	TS	TTG(A)AAT	Glu>Gly	1
568	GC>AT	TS	GTT(G)GAT	Gly>Arg	4
569	GC>AT	TS	TTG(G)ATA	Gly>Glu	4
580	GC>AT	TS	CTT(G)ACT	Asp>Asn	2
589	GC>AT	TS	AAT(G)AGT	Glu>Lys	1
599	GC>AT	TS	TCA(G)GGA	Arg>Lys	5
601	GC>AT	TS	AGG(G)ATT	Asp>Asn	1
635	GC>AT	TS	CTG(G)AAA	Gly>Glu	2
Transversions at dipyrimidine sites					
96	GC>TA	TS	TTT(G)GAA	Leu>Phe	1
100	AT>TA	TS	GAA(A)AAG	Lys>stop	1
125	AT>TA	NTS	TGA(T)TAT	Ile>Asn	1
133	AT>TA	TS	GAC(A)GGA	Arg>Trp	1
149	GC>TA	NTS	TTG(C)TCG	Ala>Asp	1
205	AT>TA	TS	CTC(A)AGG	Lys>stop	1
208	GC>CG	TS	AAG(G)GGG	Gly>Arg	1
271	AT>TA	TS	GAT(A)GAT	Arg>stop	1
475	AT>TA	TS	GTT(A)AGG	Lys>stop	1
486	GC>TA	NTS	AAG(C)TTG	Ser>Arg	1
548	AT>TA	NTS	AAA(T)TCC	Val>Asp	1
551	GC>TA	NTS	TTC(C)AGA	Pro>Gln	1
606	GC>TA	TS	TTT(G)AAT	Leu>Phe	1
623	AT>TA	NTS	TCA(T)TAG	Ile>Asn	1
631	AT>TA	TS	GAA(A)CTG	Thr>Ser	1
635	GC>TA	TS	CTG(G)AAA	Gly>Val	1
640	GC>TA	TS	AAA(G)CCA	Ala>Ser	2
Tandem mutations					
118	GC>AT	TS	CAT(GG)ACT	Gly>Lys	5
119	GC>AT	TS			
207	GC>AT	TS	CAA(GG)GGG	Gly>Arg	2
208	GC>AT	TS			

[1]TS, transcribed DNA strand; NTS, non-transcribed DNA strand; NA, not applicable.

Table S1. **Mutation spectra at genomic *Hprt* in ES cells** *(Continued)*

***Xpa*$^{-/-}$ ES cells (*n* = 127 substitutions, from in total two experiments), 0.75 J/m^2 UV-C**					
208	GC>AT	TS	AAG(GG)GGG	Gly>Lys	2
209	GC>AT	TS			
209	GC>AT	TS	AGG(GG)GGC	Gly>Glu	1
210	GC>AT	TS			
211	GC>TA	TS	GGG(GG)CTA	Gly>Tyr	1
212	GC>AT	TS			
418	GC>AT	TS	ACT(GG)TAA	Gly>Asn	2
419	GC>AT	TS			
495	GC>TA	TS	GGT(GA)AAA	Lys>stop	1
496	AT>TA	TS			
499	AT>TA	TS	AAA(AG)GAC	Arg>stop	1
500	GC>AT	TS			
538	GC>AT	TS	GTT(GG)ATT	Val>Lys	1
539	GC>AT	TS			
568	GC>AT	TS	GTT(GG)ATA	Gly>Lys	2
569	GC>AT	TS			
600	GC>AT	TS	CAG(GG)ATT	Asp>Asn	4
601	GC>AT	TS			
600	GC>CG	TS	CAG(GGA)TTT	Asp>Ile	1
601	GC>AT	TS			
602	AT>TA	TS			
Multiple independent mutations					
34	GC>TA +C	TS	AGC(G)(+C)ATG		1
113	GC>AT	NTS	TTC(C)T(-C)ATG		1
115	-C				
202	GC>AT	NTS	GTG(C)T(C)AAG	Leu>Phe	2
204	GC>AT	NTS			
380	GC>AT	TS	CTG(G)A(A)AGA	Gly>Glu	1
382	AT>GC	TS		Lys>Glu	
403	GC>AT	TS	GAA(G)A(T)ATA	Asp>Lys	1
405	AT>TA	NTS			
580	GC>AT	TS	CTT(G)A(C)TAT	Asp>Lys	1
582	GC>TA	NTS			
589	GC>TA	TS	AAT(G)A(G)TAC	Glu>stop	1
591	GC>AT	TS			
Insertions					
511	+T		GAA(+T)GTG		1
625	+T		TTA(+T)GTG		1
Deletions					
47	-G		CAG(-G)TTA		1

[1]TS, transcribed DNA strand; NTS, non-transcribed DNA strand; NA, not applicable.

Table S1. **Mutation spectra at genomic *Hprt* in ES cells** *(Continued)*

***Xpa*$^{-/-}$ ES cells (*n* = 127 substitutions, from in total two experiments), 0.75 J/m^2 UV-C**

Transversions at non-dipyrimidine sites				
1	AT>TA	(A)TGC	Met>Leu	3
2	AT>GC	A(T)GCC	Met>Thr	1
84	AT>CG	TTA(T)GCC	Tyr>stop	1
397	GC>TA	ATT(G)TTG	Val>Phe	1
Multiple independent mutations				
199	GC>TA	TGT(G)T(G)CTC	Val>Phe	1
201	GC>TA			
Insertions				
631	+T	AAA(+T)CTG		1
Deletions				
533-553	21bp			1

Msh6$^{-/-}$*Xpa*$^{-/-}$ ES cell line 4 (*n* = 141 substitutions, from in total two experiments) 0.75 J/m^2 UV-C

position	mutation	strand	5′ → 3′ target	amino acid change	# of mutants
Transitions at dipyrimidine sites					
40	GC>AT	TS	GAT(G)AAC	Glu>Lys	1
113	GC>AT	NTS	TTC(C)TCA	Pro>Leu	5
118	GC>AT	TS	CAT(G)GAC	Gly>Arg	2
122	AT>GC	NTS	GAC(T)GAT	Leu>Pro	1
139	GC>AT	TS	ACT(G)AAA	Glu>Lys	3
149	GC>AT	NTS	TTG(C)TCG	Ala>Val	1
196	AT>GC	NTS	CTC(T)GTG	Cys>Arg	1
209	GC>AT	TS	AGG(G)GGG	Gly>Glu	1
212	GC>AT	TS	GGG(G)CTA	Gly>Asp	6
233	AT>GC	NTS	ACC(T)GCT	Leu>Pro	1
254	AT>GC	NTS	CAC(T)GAA	Leu>Pro	1
374	AT>GC	NTS	CTT(T)AAC	Leu>Ser	1
400	GC>AT	TS	GTT(G)AAG	Glu>Lys	9
403	GC>AT	TS	GAA(G)ATA	Asp>Asn	1
418	GC>AT	TS	ACT(G)GTA	Gly>Ser	2
508	GC>AT	NTS	TCT(C)GAA	Arg>stop	1
526	GC>AT	NTS	AGG(C)CAG	Pro>Ser	1
533	AT>GC	NTS	ACT(T)TGT	Phe>Ser	1
538	GC>AT	TS	GTT(G)GAT	Gly>Arg	1
539	GC>AT	TS	TTG(G)ATT	Gly>Glu	4
541	AT>GC	NTS	GGA(T)TTG	Phe>Leu	1
544	GC>AT	TS	TTT(G)AAA	Glu>Lyss	7
550	GC>AT	NTS	ATT(C)CAG	Pro>Ser	1
551	GC>AT	NTS	TTC(C)AGA	Pro>Leu	2
568	GC>AT	TS	GTT(G)GAT	Gly>Arg	1
580	GC>AT	TS	CTT(G)ACT	Asp>Asn	1
589	GC>AT	TS	AAT(G)AGT	Glu>Lys	10
599	GC>AT	TS	TCA(G)GGA	Arg>Lys	5
601	GC>AT	TS	AGG(G)ATT	Asp>Asn	2
605	AT>GC	NTS	ATT(T)GAA	Leu>Ser	1
635	GC>AT	TS	CTG(G)AAA	Gly>Glu	3
655	AT>GC	NTS	GCC(T)AAG	stop>Gln	1
Transversions at dipyrimidine sites					

[1]TS, transcribed DNA strand; NTS, non-transcribed DNA strand; NA, not applicable.

Table S1. **Mutation spectra at genomic *Hprt* in ES cells** *(Continued)*

***Xpa*$^{-/-}$ ES cells (*n* = 127 substitutions, from in total two experiments), 0.75 J/m^2 UV-C**					
101	AT>TA	TS	AAA(A)AGT	Lys>Ile	1
118	GC>TA	TS	CAT(G)GAC	Gly>stop	1
125	AT>CG	NTS	TGA(T)TAT	Ile>Ser	3
140	AT>TA	TS	CTG(A)AAG	Glu>Val	1
222	GC>TA	NTS	GTT(C)TTT	Phe>Leu	1
296	AT>CG	NTS	ATT(T)TAT	Phe>Cys	1
391	AT>TA	NTS	GTC(T)TGA	Leu>Met	1
395	AT>TA	NTS	TGA(T)TGT	Ile>Asn	1
498	AT>TA	TS	GAA(A)AGG	Lys>Asn	1
544	GC>TA	TS	TTT(G)AAA	Glu>stop	1
548	AT>CG	NTS	AAA(T)TCC	Ile>Ser	1
581	AT>CG	TS	TTG(A)CTA	Asp>Ala	1
583	AT>TA	NTS	GAC(T)ATA	Tyr>Asn	2
594	GC>CG	NTS	GTA(C)TTC	Tyr>stop	1
606	GC>TA	TS	TTT(G)AAT	Leu>Phe	1
Tandem mutations					
46	GC>AT	TS	CCA(GG)TTA	Gly>Asn	2
47	GC>AT	TS			
109	AT>GC	no dimer	TTT(AT)TCC	Ile>Gly	1
110	AT>CG	NTS			
112	GC>AT	NTS	ATT(CC)TCA	Pro>Phe	1
113	GC>AT	NTS			
118	GC>AT	TS	CAT(GG)ACT	Gly>Lys	3
119	GC>AT	TS			
124	AT>TA	TS	CTG(AT)TAT	Ile>Tyr	1
125	AT>TA	NTS			
207	GC>AT	TS	CAA(GG)GGG	Gly>Arg	1
208	GC>AT	TS			
208	GC>AT	TS	AAG(GG)GGG	Gly>Lys	3
209	GC>AT	TS			
209	GC>AT	TS	AGG(GG)GGC	Gly>Glu	4
210	GC>AT	TS			
400	GC>AT	TS	GTT(GA)AGA	Glu>Arg	1
401	AT>GC	TS			
418	GC>AT	TS	ACT(GG)TAA	Gly>Asn	2
419	GC>AT	TS			
463	GC>TA	NTS	AGC(CC)CAA	Pro>Ile	1
464	GC>AT	NTS			
538	GC>AT	TS	GTT(GG)ATT	Gly>Lys	2
539	GC>AT	TS			
568	GC>AT	TS	GTT(GG)ATA	Gly>Lys	2
569	GC>AT	TS			
598	AT>GC	TS	TTC(AG)GGA	Arg>Glu	1

[1]TS, transcribed DNA strand; NTS, non-transcribed DNA strand; NA, not applicable.

Table S1. **Mutation spectra at genomic *Hprt* in ES cells** *(Continued)*

***Xpa*$^{-/-}$ ES cells (*n* = 127 substitutions, from in total two experiments), 0.75 J/m^2 UV-C**					
599	GC>AT	TS			
599	GC>AT	TS	TCA(GG)GAT	Arg>Lys	1
600	GC>AT	TS			
600	GC>AT	TS	CAG(GG)ATT	Asp>Asn	1
601	GC>AT	TS			
Multiple Independent mutations					
69	AT>TA	no dimer	TTG(T)ATA	Cys>stop	1
79	GC>AT	NTS	AAT(C)ATT	His>Tyr	
103	GC>TA	TS	AAA(G)TGT	Val>Leu	1
112	GC>AT	NTS	ATT(C)CTC	Pro>Ser	
179	AT>TA	no dimer	GCC(A)T(C)ACA	His>Leu	1
181	GC>AT	NTS	GCC(A)T(C)ACA	His>Tyr	
209	insertion		GGG(+A)GGG		1
213	GC>AT	NTS	GGG(C)T(A)TAA		
215	AT>TA	no dimer	GGG(C)T(A)TAA		
400	GC>AT	TS	GTT(G)A(A)GAT	Glu>Lys	1
402	AT>GC	TS	GTT(G)A(A)GAT		
471	GC>AT	TS	AAT(G)GTT	Met>Ile	1
482	GC>CG	no dimer	TTG(C)AAG	Ala>Gly	
553	insertion		CCA(+T)GAC		1
554	AT>CG	TS	CAG(AC)AAG		
555	GC>TA	no dimer	CAG(AC)AAG		
558	GC>TA	TS	CAA(G)TTT		
Insertions					
207-212	+G	TS	GGGGGG		1
Transitions at non-dipyrimidine sites					
3	GC>AT		AT(G)CCG	Met>Ile	1
197	GC>AT		TCT(G)TGT	Cys>Tyr	1
521	AT>GC		GAT(A)CAG	Tyr>stop	1
Transversions at non-dipyrimidine sites					
109	AT>TA		TTT(A)TTC	Ile>Phe	2
197	GC>CG		TCT(G)TGT	Cys>Tyr	1
572	AT>CG		GAT(A)TGC	Tyr>Ser	1
Tandem mutations					
571	AT>TA		GGA(TA)TGC	Tyr>Ser	1
572	AT>GC				
Spontaneous substitutions in *Msh6*$^{-/-}$*Xpa*$^{-/-}$ ES cell line 4, from in total two experiments (*n* = 30)					
position	mutation	strand	5′ → 3′ target	amino acid change	#of mutants
Transitions at dipyrimidines sites					
149	GC>AT	NA	TTG(C)TCG	Ala>Val	3
212	GC>AT	NA	GGG(G)CTA	Gly>Asp	12
233	AT>GC	NA	ACC(T)GCT	Leu>Pro	1

[1]TS, transcribed DNA strand; NTS, non-transcribed DNA strand; NA, not applicable.

Table S1. **Mutation spectra at genomic *Hprt* in ES cells** *(Continued)*

***Xpa*$^{-/-}$ ES cells (*n* = 127 substitutions, from in total two experiments), 0.75 J/m^2 UV-C**					
440	AT>GC	NA	TGC(T)TTC	Leu>Pro	1
491	AT>GC	NA	TGC(T)GGT	Leu>Pro	1
526	GC>AT	NA	AGG(C)CAG	Pro>Ser	1
563	AT>GC	NA	TTG(T)TGT	Val>Ala	1
589	GC>AT	NA	AAT(G)AGT	Glu>Lys	3
Transversions at dipyrimidines sites					
125	AT>CG	NA	TGA(T)TAT	Ile>Ser	1
223	AT>CG	NA	TTC(T)TTG	Phe>Val	2
293	AT>TA	NA	TAG(A)TTT	Asp>Val	1
Transitions at non-dipyrimidine sites					
148	GC>AT	NA	CTT(G)CTC	Ala>Thr	1
617	GC>AT	NA	TTT(G)TGT	Cys>Tyr	2

[1]TS, transcribed DNA strand; NTS, non-transcribed DNA strand; NA, not applicable.

Table S2. **Mutations induced at a site-specific (6-4)TT embedded within a replicating plasmid.**

				***Xpc* (line 1, exp. 1)**		***Xpc* (line 2, exp. 2)**		***Msh2Xpc* (exp.1)**		***Msh2Xpc* (exp. 2)**	
TLS events				87	98.9%	93	98.9%	88	100%	89	100.0%
Correct TLS											
5′-TT	→		5′-TT	36	40.9%	45	47.9%	46	52.3%	42	47.2%
Mutagenic TLS				50	56.8%	46	48.9%	40	45.5%	39	43.8%
5′-TT	→		5′-TA	0	0.0%	5	5.3%	5	5.7%	15	16.9%
5′-TT	→		5′-TC	4	4.5%	2	2.1%	5	5.7%	4	4.5%
5′-TT	→		5′-TG	0	0.0%	0	0.0%	1	1.1%	1	1.1%
5′-TT	→		5′-AT	0	0.0%	4	4.3%	1	1.1%	2	2.2%
5′-TT	→		5′-CT	0	0.0%	0	0.0%	0	0.0%	1	1.1%
5′-TT	→		5′-GT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TT	→		5′-AA	0	0.0%	0	0.0%	1	1.1%	0	0.0%
5′-TT	→		5′-AC	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TT	→		5′-CA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TT	→		5′-CC	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TT	→		5′-GC	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→		5′-TTT	43	48.9%	29	30.9%	21	23.9%	10	11.2%
5′-CTT	→		5′-ATT	1	1.1%	1	1.1%	1	1.1%	1	1.1%
5′-CTT	→		5′-GTT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→		5′-TAT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→		5′-TTA	2	2.3%	3	3.2%	3	3.4%	2	2.2%
5′-CTT	→		5′-TTC	0	0.0%	2	2.1%	0	0.0%	0	0.0%
5′-CTT	→		5′-TTG	0	0.0%	0	0.0%	0	0.0%	1	1.1%
5′-CTT	→		5′-TAA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→		5′-AAT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→		5′-AAA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→		5′-ATA	0	0.0%	0	0.0%	0	0.0%	1	1.1%
5′-CTT	→		5′-ATC	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTT	→		5′-ACTT	0	0.0%	0	0.0%	1	1.1%	0	0.0%
5′-TCTT	→		5′-ACTA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTT	→		5′-ATTT	0	0.0%	0	0.0%	1	1.1%	1	1.1%
5′-TCTT	→		5′-ATAT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTT	→		5′-AAAC	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTT	→		5′-ATTA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTT	→		5′-CTTA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-ATCTT	→		5′-TTCTT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
deletion				1	1.1%	2	2.1%	2	2.3%	8	9.0%
5′-TT	→	5′-A		0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TT	→	5′-C		0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTT	→	5′-TT		1	1.1%	1	1.1%	1	1.1%	1	1.1%
5′-CTT	→		5′-TA	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TTC	→		5′-TT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTT	→		5′-CTT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-ATCTT	→		5′-TCTT	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTTC	→		5′-CC	0	0.0%	1	1.1%	0	0.0%	4	4.5%
5′-CTTC	→		5′-C	0	0.0%	0	0.0%	1	1.1%	1	1.1%
5′-CTTCA	→		5′-CC	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-CTTCA	→		5′-C	0	0.0%	0	0.0%	0	0.0%	0	0.0%
5′-TCTTC	→		5′-T	0	0.0%	0	0.0%	0	0.0%	1	1.1%
5′-TCTTC	→		5′-C	0	0.0%	0	0.0%	0	0.0%	1	1.1%
insertion				0	0.0%	0	0.0%	0	0.0%	0	0.0%
large deletion /insertion			1	1	1.1%	1	1.1%	0	0.0%	0	0.0%
sum				88	100%	94	100%	88	100%	89	100%