

Figure S1. Distribution of repair events per replicate (single male). Each male (replicate) from the $P\{w^a\}$ assay was categorized according to the distribution of repair events observed in his progeny and the data are displayed as a percentage of all males assayed in each genotype. Red indicates red-eyed progeny were observed; yellow indicates yellow-eyed progeny; both indicates red- and yellow-eyed progeny; and no repair indicates no red or yellow-eyed progeny were observed in the progeny of every male.



Figure S2. Distribution of *P*{*wlw*} **events in wild type and Marcal1 mutants after molecular analysis.** A) Distribution of molecularly analyzed events from collected red-eyed progeny as a percentage of total red analyzed events (listed below genotype). Mutated cut site: amplified band (primer set wlw_cut, Table S3) was not cut with *I-Scel*; indel at cut site: band was smaller or larger than predicted; intact cut site: band was cut with *I-Scel*; deletion of linker region: no amplification with primer set. B) Distribution of molecularly analyzed events (listed below genotype). Upstream FRT: only FRT associated with upstream *mini-w* amplified (primer set, Table S3) (categorized as annealed events); upstream FRT verified EJ: larger or smaller than predicted products from whole construct amplification (categorized as EJ events); downstream FRT: only downstream FRT amplified (verified to be in the upstream locus, removed from final data set); both FRTs: both amplified (categorized as EJ events); no FRTs: no amplification (categorized as EJ events).

Mutagen	Dosage	Biological replicates	Unexposed progeny	Exposed progeny
Methyl methanesulfonate	3.23 mM	16	2864	1397
Nitrogen mustard	0.2 mM	22	3828	3131
Hydroxyurea	100 mM	22	3964	1841
Etoposide	10 mM	9	1098	876
Camptothecin	0.05 mM	26	3432	2233
Ionizing radiation	2000 rads (20 Gy)	19	2196	1395

Table S1. Dosage and sample sizes of mutagen exposure experiment. *Marcal1* null mutants were treated with each mutagen in separate experiments as described in Materials and Methods. Biological replicates refers to individual vials assayed, each containing a single male (ratios of *wt:mutant* survival were calculated per vial). Progeny counts are the aggregated total number of flies scored for each mutagen.



Description	Primer 1	Primer 2
5 bp right side	CCGCGGCCGCGGACCACCTTATGTTA TTT	GCCTTGCTTCTTCCACACAGCGTG
0.9 Kb right side	CCCTCGCAGCGTACTATTGAT	AGATGGGTGTTTGCTGCCTCCG
2.4 Kb right side	GAGCGAGATGGCCATATGGCTG	CGTTGTTTGCACGTCTCGCTCG
4.6 Kb right side (into <i>copia</i>)	GGACTGGGCCCATAACCTGTTG	GAGCGACACATACCGGCG
5 bp left side	CCGCGGCCGCGGACCACCTTATGTTA TTT	ACCATTGCAAGCTACATAGCTGAC
2 Kb left side	GACTGTGCGTTAGGTCCTGT	CGTTTCGTAGTTGCTCTTTCGC
5.2 Kb left side (all <i>w</i> exons into <i>copia</i>)	TGCCAGAGAGCAAGTTCAGA	GAGGTCATCCTGCTGGACAT

Table S2. *P*{*w*^a} **primers.** Diagram above table depicts PCR products. Sizes represent synthesis from break end, not PCR product size. The null *white* (*w*) gene in the $ywP\{w^a\}$ genotype is a partial deletion of the 5' end of *w* leaving the 3' end intact. The left side of the construct above is identical to the 3' end of *w*; therefore, all PCRs of the left end must be anchored in the *P*-element ends or in *copia* to prevent amplification of the background copy of *w*.



Table S3. *P*{*wlw*} primers. Diagram above table depicts PCR products. The wlw_cut primer set was used to amplify the *I*-Scel cut site in red-eyed repair events. The X97 primer set was used to assess annealing via SSA in white-eyed repair events. The upstream product is 480 bp whereas the downstream product is 369 bp. Presence of only the upstream product represents correct annealing via SSA; presence of both indicates EJ that abolishes *mini-white* function; the presence of only the downstream product was rare and verified to be in the upstream location using the Pin 5 and X97 primer 2 set. These events are interpreted as SSA with small deletions in the X97 region. Lack of amplification with the X97 primer set indicates EJ.