Supporting Information

10.1073/pnas.0812715106

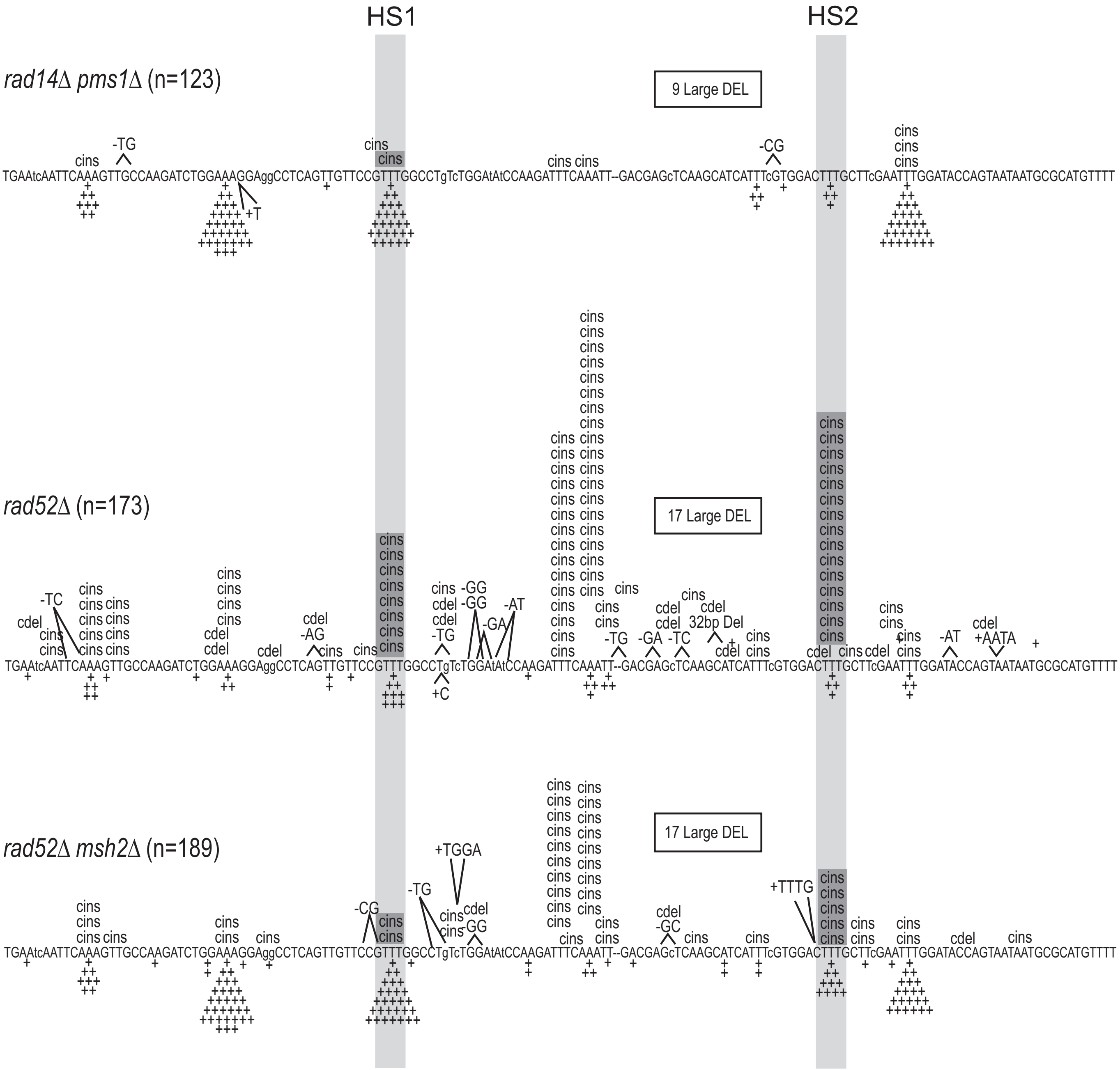

Fig. S1. *lys2ΔA746-NR* reversion spectra in repair-defective backgrounds. The sequence of the ≈150-bp reversion window is shown. The site of the 1-nt deletion that defines the allele is indicated by a dash and additional changes from the WT sequence are in lowercase. Simple insertions are indicated by ''+'' below the sequence and other mutation types are indicated above the sequence. The positions of HS1 and HS2 are indicated by light gray shading; complex insertions (''cins'') at these positions are shaded dark gray. ''Large DEL'' refers to 95-nt deletions with endpoints in 10-nt direct repeats; ''cdel'' corresponds to −2 events associated with nearby base substitutions. The number (''n'') of independent revertants sequenced from each background is indicated.

Table S1. Yeast strains

Strain	Relevant repair genotype	Construction
SJR1472	*msh2Δ::hisG-URA3-hisG*	OST of SJR1467 with AatII/XbaI−digested GC1914 (1)
SJR2645	*rad14Δ::kan*	OST of SJR1467 with PCR fragment amplified from pFA6a−kanMX6 (2)
SJR2672	*rad14Δ::kan msh2Δ::hisG-URA3-hisG*	OST of SJR2645 with AatII/XbaI−digested GC1914 (1)
SJR2733	*rad52Δ::kan*	OST of SJR1467 with PCR fragment amplified from pFA6a−kanMX6 (2)
SJR2734	*msh2Δ::hisG-URA3-hisG rad52Δ::kan*	OST of SJR1472 with PCR fragment amplified from pFA6a−kanMX6 (2)
SJR2773	*rad14Δ::kan pms1Δ::hyg*	OST of SJR2645 with PCR fragment amplified from hphMX4 (3)
SJR2778	*rad14Δ::kan rad52Δ::hyg*	OST of SJR2645 with PCR fragment amplified from hphMX4 (3)
SJR2779	*rad14Δ::kan msh2Δ::hisG-URA3-hisG rad52Δ::hyg*	OST of SJR2672 with PCR fragment amplified from hphMX4 (3)
SJR2808	*rad14Δ::kan pms1-G128A,I854M*	Sequential TST of SJR2645 with pSR760 [*pms1-I854M* allele (4)] and pYI−pms1−128 [*pms1-G128A* allele (5)]

OST, 1-step allele transplacement; TST, 2-step allele transplacement. All strains were derived from SJR1467 (*MATα ade2-101*$_{oc}$ *his3Δ 200 ura3Δ Nco lys2Δ A746-NR*) by transformation.

1. Greene CN, Jinks-Robertson S (1997) Frameshift intermediates in homopolymer runs are removed efficiently by yeast mismatch repair proteins. *Mol Cell Biol* 17:2844–2850.
2. Longtine MS, et al. (1998) Additional modules for versatile and economical PCR−based gene deletion and modification in *Saccharomyces cerevisiae*. *Yeast* 14:953–961.
3. Goldstein AL, McCusker JH (1999) Three new dominant drug resistance cassettes for gene disruption in *Saccharomyces cerevisiae*. *Yeast* 15:1541–1553.
4. Welz-Voegele C, et al. (2002) Alleles of the yeast *PMS1* mismatch-repair gene that differentially affect recombination- and replication-related processes. *Genetics* 162:1131–1145.
5. Tran PT, Liskay M (2000) Functional studies on the candidate ATPase domains of *Saccharomyces cerevisiae* MutLα. *Mol Cell Biol* 20:6390–6398.

Table S2. Distributions of hotspot 1 complex events in different strain backgrounds

Hotspot 1 position										Number of events										
	C	C	G	***T***	***T***	***T***	G	**G**	C	WT	*msh2*Δ	*rad14*Δ	*rad14*Δ *msh2*Δ	*rad14*Δ *rad52*Δ	*rad14*Δ *rad52*Δ *msh2*Δ	*rad14*Δ *pms1*Δ	*rad14*Δ *pms1-GA,IM*	*rad52*Δ	*rad52*Δ *msh2*Δ	Total
	–	–	–		+		–	T	–	2		11		3	3		1	1		21
	–	–	C		+		–	T	–			8		2	1	1	1	1		14
	–	–	C		+		–	–	–	1					2			2	1	6
	–	–	–		+		T	–	–					2	1		1		1	5
	–	–	–		+		–	A	–			3		1						4
	–	–	T		+		–	T	–			1					1	1		3
	T	–	T		+		–	–	–					1	1					2
	–	–	–		+		A	–	–					2						2
	–	–	–		+		T	T	–					2			1			3
	–	–	C		+		–	C	–			1								1
	T	G	T		+		–	–	–					1						1
	–	–	T		+		–	–	–									1		1
*	–	–	C		+		–	–	–					1						1
	–	–	A		+		–	–	–						1					1
	–	A	–		+		–	–	–						1					1
	–	–	–		+		–	A	T						1					1
	T	–	–		+		–	–	G								1			1
	–	–	–		+		T	A	–									1		1
	–	–	–		+		T	–	G									1		1
Total										3	0	24	0	15	11	1	6	8	2	70

The 3T run where the selected frameshift occurs is italicized and bold; the G where base substitutions most frequently occur is bold and underlined. A base substitution outside of the core hotspot sequence is indicated by an asterisk. *pms1-GA,IM*=*pms1-G128A,1854M.*

Table S3. Distributions of hotspot 2 complex events in different strain backgrounds

Hotspot 2 position										Number of events										
	G	A	C	***T***	***T***	***T***	**G**	C	T	WT	*msh2Δ*	*rad14Δ*	*rad14Δ msh2Δ*	*rad14Δ rad52Δ*	*rad14Δ rad52Δ msh2Δ*	*rad14Δ pms1Δ*	*rad14Δ pms1-GA,IM*	*rad52Δ*	*rad52Δ msh2Δ*	Total
	–	–	–		+		T	–	–	1		7		11	5		1	9	3	37
	–	–	T		+		T	–	–			2		3	1			1		7
	–	–	–		+		–	T	–					1	1		1	1		4
	–	–	–		+		A	–	–			2							1	3
	–	G	T		+		A	–	–			1					1			2
	–	–	–		+		C	–	–					1				1		2
	–	–	T		+		–	–	–						1				1	2
	–	–	A		+		T	–	–					1				1		2
*	–	–	A		+		T	–	–			1								1
*	–	–	A		+		–	–	–				1							1
	–	G	T		+		–	T	–					1						1
	–	–	–		+		T	A	–					1						1
*	–	G	T		+		A	A	–					1						1
*	–	–	A		+		T	–	C					1						1
	–	G	–		+		T	–	–					1						1
	–	–	A		+		–	–	–					1						1
	–	–	–		+		T	T	–					1						1
	–	–	T		+		–	T	–						1					1
	–	T	T		+		T	–	–						1					1
	–	G	T		+		T	–	–									1		1
	–	–	–		+		T	–	C									1		1
Total										1	0	13	1	24	10	0	3	15	5	72

The 3T run where the selected frameshift occurs is italicized and bold; the G where base substitutions most frequently occur is bold and underlined. A base substitution outside the core hotspot sequence is indicated by an asterisk.