Supporting Information

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SI Materials and Methods

In order to determine the viability of cells on selective plates lacking tryptophan, strains GCY2506 and GCY2512 containing both a G148T and *LYS2* mutation (Table S11) were transformed with LYS2TCARev (Table S12), which corrects the *LYS2* mutation, following the procedure in *Materials and Methods*. For a given transformation, equal aliquots were plated on several synthetic dextrose-Trp-Lys plates and on the specified day, 500 μL of 0.45% Trp was added to a plate. No growth was observed before Trp addition, and only cells transformed with the LYS2TCARev oligo were able to grow after Trp addition.

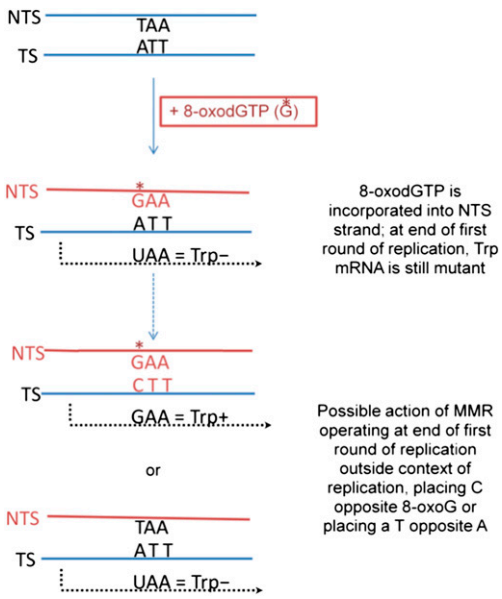

Fig. S1. Model for transformation of *trp5* G148T strains with 8-oxodGTP. TAA is the nontranscribed strand sequence of the mutant glutamic acid codon that must be mutated to GAA to give Trp^+ revertants in the G148T strains. At the end of the first round of replication, any transcribed RNA will be Trp^-. Mismatch repair (MMR) correction operating outside the context of the replication fork after the first round of replication could result in a C being placed opposite the 8-oxoG, giving rise to Trp^+ mRNA.

Table S1. Data for Fig. 3: Transformation of *wt* and *msh6* strains with transcribed strand (TS) and nontranscribed strand (NTS) oligos

Experiment	Strain	MMR genotype	Trp oligo	No. Trp^+ in 25 mL 45 min	No. Trp^+ in 25 mL 2 h	% Trp at 45 min	SD	Replication strand
1	GCY2506	*wt*	NTS	2,643	7,010	37.7		Lagging
2	GCY2506	*wt*	NTS	3,678	7,323	50.2		Lagging
3	GCY2506	*wt*	NTS	2,588	5,058	51.2		Lagging
						46	7.5	
1	GCY2512	*msh6*	NTS	790	31,890	2.5		Lagging
2	GCY2512	*msh6*	NTS	1,630	31,750	5.1		Lagging
3	GCY2512	*msh6*	NTS	380	10,470	3.6		Lagging
						3.7	1.3	
1	GCY2506	*wt*	TS	213	415	51.2		Leading
2	GCY2506	*wt*	TS	360	570	63.2		Leading
3	GCY2506	*wt*	TS	600	1,170	51.3		Leading
4	GCY2506	*wt*	TS	70	190	36.8		Leading
						50.6	10.8	
1	GCY2512	*msh6*	TS	12,003	13,843	86.7		Leading
2	GCY2512	*msh6*	TS	10,030	12,800	78.4		Leading
3	GCY2512	*msh6*	TS	24,620	28,350	86.8		Leading
4	GCY2512	*msh6*	TS	19,520	22,070	88.4		Leading
						85.1	4.6	

Shown is the number of revertants in a 25-mL culture, plated after a recovery time of 45 min or 2 h. The mean and SD are given for each set of experiments.

Table S2. Data for *trp5* G148T gene in inverted orientation (G148T R): Transformation of *wt* and *msh6* strains with TS and NTS oligos

Experiment	Strain	MMR genotype	Trp oligo	No. Trp^+ in 25 mL 45 min	No. Trp^+ in 25 mL 2 h	% Trp at 45 min	SD	Replication strand
1	GCY2251	*wt*	NTS	730	1,310	55.7		Leading
2	GCY2251	*wt*	NTS	145	983	14.8		Leading
3	GCY2251	*wt*	NTS	640	820	78.0		Leading
4	GCY2251	*wt*	NTS	160	250	64.0		Leading
5	GCY2251	*wt*	NTS	530	630	84.1		Leading
6	GCY2251	*wt*	NTS	610	910	67.0		Leading
						61	24.6	
1	GCY2344	*msh6*	NTS	20	810	2.5		Leading
2	GCY2140	*msh6*	NTS	190	4,440	4.3		Leading
3	GCY2140	*msh6*	NTS	110	8,715	1.3		Leading
4	GCY2140	*msh6*	NTS	340	11,500	3.0		Leading
						2.7	1.2	
1	GCY2251	*wt*	TS	380	668	56.9		Lagging
2	GCY2251	*wt*	TS	230	530	43.4		Lagging
3	GCY2251	*wt*	TS	440	700	62.9		Lagging
4	GCY2251	*wt*	TS	340	640	53.1		Lagging
						54.1	8.2	
1	GCY2344	*msh6*	TS	22,120	29,690	74.5		Lagging
2	GCY2344	*msh6*	TS	43,590	44,070	98.9		Lagging
3	GCY2344	*msh6*	TS	31,580	38,460	82.1		Lagging
4	GCY2140	*msh6*	TS	64,080	74,870	85.6		Lagging
5	GCY2140	*msh6*	TS	97,320	101,250	96.1		Lagging
						87.4	10.1	

Shown is the number of revertants in a 25-mL culture, plated after a recovery time of 45 min or 2 h. The mean and SD are given for each set of experiments.

Table S3. Data for Fig. 4*B* in *trp5* G148T F strains: Transformation by 8-oxodGTP

			No. of revertants from 25-mL culture on the indicated day						
MMR genotype	Strain	Recovery time	3	5	7	9	11	13	15
wt	GCY2506	15 min	285	584	1,009	1,134	1,144	1,144	1,144
		2 h	3,806	4,136	4,266	4,276	4,296	4,296	4,296
wt	GCY1862	15 min	95	345	593	805	1,028	1,030	1,030
		2 h	1,655	1,868	1,945	1,988	1,988	1,995	1,995
wt	GCY1862	15 min	130	271	363	419	432	449	462
		2 h	1,258	2,030	2,068	2,090	2,118	2,118	2,118
wt	GCY1862	15 min	45	95	150	163	188	218	218
		2 h	398	498	528	540	548	548	548
msh6	GCY2512	15 min	5	15	15	15	15	25	25
		2 h	3,686	3,846	3,966	3,966	3,966	3,966	3,966
msh6	GCY2036	15 min	0	3	3	8	15	15	15
		2 h	1,113	1,315	1,330	1,353	1,353	1,353	1,353
msh6	GCY2036	15 min	2	5	10	12	15	17	17
		2 h	2,053	2,543	2,550	2,550	2,558	2,558	2,558
msh6	GCY2036	15 min	8	10	10	13	13	13	13
		2 h	333	418	445	450	450	450	450

Table S4. Table S3 data expressed as percentages

			Percent of 2-h final number for each day						
MMR genotype	Strain	Recovery time	3	5	7	9	11	13	15
wt	GCY2506	15 min	7	14	23	26	27	27	27
		2 h	89	96	99	100	100	100	100
wt	GCY1826	15 min	5	17	30	40	52	52	52
		2 h	83	94	97	100	100	100	100
wt	GCY1826	15 min	6	13	17	20	20	21	22
		2 h	59	96	98	99	100	100	100
wt	GCY1826	15 min	8	17	27	30	34	40	40
		2 h	73	91	96	99	100	100	100
msh6	GCY2512	15 min	0	0	0	0	0	1	1
		2 h	93	97	100	100	100	100	100
msh6	GCY2036	15 min	0	0	0	1	1	1	1
		2 h	82	97	98	100	100	100	100
msh6	GCY2036	15 min	0	0	0	0	1	1	1
		2 h	80	99	100	100	100	100	100
msh6	GCY2036	15 min	2	2	2	3	3	3	3
		2 h	74	93	99	100	100	100	100

Table S5. Summary of Tables S3 and S4

	Average and SD for percentage data on each day													
	3		5		7		9		11		13		15	
wt 15 min	7		14		23		26		27		27		27	
	5		17		30		40		52		52		52	
	6		13		17		20		20		21		22	
	8		17		27		30		34		40		40	
Avg/SD	6.4	1.4	15	2.4	24	5.5	29	8.6	33	13	35	14	35	13
wt 2 h	89		96		99		100		100		100		100	
	83		94		97		100		100		100		100	
	59		96		98		99		100		100		100	
	73		91		96		99		100		100		100	
Avg/SD	76	13	94	2.5	98	1.2	99	0.6	100	0.0	100	0.0	100	0.0
msh6 15 min	0		0		0		0		0		1		1	
	0		0		0		1		1		1		1	
	0		0		0		0		1		1		1	
	2		2		2		3		3		3		3	
Avg/SD	0.5	0.9	0.8	1.0	0.8	0.9	1.1	1.2	1.2	1.1	1.3	1.1	1.3	1.1
msh6 2h	93		97		100		100		100		100		100	
	82		97		98		100		100		100		100	
	80		99		100		100		100		100		100	
	74		93		99		100		100		100		100	
Avg/SD	82	7.9	97	2.7	99	0.8	100	0.2	100	0.0	100	0.0	100	0.0

The averages and SDs are plotted in Fig. 4*B*.

Table S6. Data for transformation by 8-oxodGTP in *trp5* G148T R strains

			No. of revertants from 25-mL culture on the indicated day						
MMR genotype	Strain	Recovery time	3	5	7	9	11	13	15
wt	GCY2251	15 min	65	140	148	163	183	183	183
		2 h	1,029	1,099	1,159	1,159	1,179	1,179	1.179
wt	GCY1718	15 min	35	80	133	160	200	240	265
		2 h	425	500	515	545	550	555	560
wt	GCY1718	15 min	17	27	43	55	67	80	108
		2 h	193	265	285	303	325	343	348
wt	GCY1718	15 min	20	30	40	45	48	48	48
		2 h	115	145	160	168	168	168	168
msh6	GCY2344	15 min	0	5	5	5	5	5	5
		2 h	1,089	1,119	1,239	1,239	1,239	1,239	1.239

Table S7. Table S6 data expressed as percentages

			Percent of 2-h final number for each day						
MMR genotype	Strain	Recovery time	3	5	7	9	11	13	15
wt	GCY2251	15 min	6	12	13	14	16	16	16
		2 h	87	93	98	98	100	100	100
wt	GCY1718	15 min	6	14	24	29	36	43	47
		2 h	76	89	92	97	100	100	100
wt	GCY1718	15 min	5	8	12	16	19	23	31
		2 h	55	76	82	87	100	100	100
wt	GCY1718	15 min	12	18	24	27	29	29	29
		2 h	68	86	95	100	100	100	100
msh6	GCY2344	15 min	0	0	0	0	0	0	0
		2 h	88	90	100	100	100	100	100

Table S8. Summary of data in Tables S6 and S7

	Average and SD for percentage data on each day													
	3		5		7		9		11		13		15	
wt 15 min	6		12		13		14		16		16		16	
	6		14		24		29		36		43		47	
	5		8		12		16		19		23		31	
	12		18		24		27		29		29		29	
Avg/SD	7.1	3.2	12.9	4.2	18.1	6.5	21.2	7.5	24.8	9.1	27.5	11.6	30.6	13.1
wt 2,h	87		93		98		98		100		100		100	
	76		89		92		97		100		100		100	
	55		76		82		87		100		100		100	
	68		86		95		100		100		100		100	
Avg/SD	71.8	13.3	86.2	7.3	91.9	7.1	95.7	5.8	100.0	0.0	100.0	0.0	100.0	0.0

Table S9. Viability of cells on plates

	Revertants appearing after indicated number of days before adding Trp		
MMR genotype*	3	6 (% of 3 d)	9 (% of 3 d)
wt	1,552	1,044 (67)	724 (47)
msh6	1,909	1,119 (59)	764 (40)

*See *SI Materials and Methods*.

Table S10. Effect of MMR on C-T vs. G-A mismatch

Strain no.	MMR genotype	Oligo	Mispair created	Replication strand for oligo	Average Trp$^+$ revertants with 2-h recovery time	SD of average	Independent experiments	*msh6*/*wt* Revertants
GCY2506	*wt*	TS	C-T	Leading	590	520	4	
GCY2251	*wt*	TS	C-T	Lagging	630	70	4	
GCY2251	*wt*	NTS	G-A	Leading	820	360	6	
GCY2506	*wt*	NTS	G-A	Lagging	6500	1,200	3	
GCY2512	*msh6*	TS	C-T	Leading	19,000	7,300	4	32
GCY2140, GCY2344	*msh6*	TS	C-T	Lagging	58,000	30,000	5	92
GCY2344	*msh6*	NTS	G-A	Leading	6,400	4,700	4	8
GCY2512	*msh6*	NTS	G-A	Lagging	25,000	12,000	3	4

The average number of total Trp$^+$ revertants in both *trp5* G148T F and R strains after a long recovery time is shown, and the number of revertants in *msh6* compared with wild-type strains is given.

Table S11. Yeast strains

Strain	*trp5* mutation and orientation	MMR genotype
GCY1718	G148T R	*wt*
GCY1862	G148T F	*wt*
GCY2036	G148T F	*msh6Δ::kan*
GCY2140	G148T R	*msh6Δ::kan*
GCY2251	G148T R	*wt*
GCY2344	G148T R	*msh6Δ::loxP*
GCY2512	G148T F	*msh6Δ::kan*
GCY2506	G148T F	*wt*

All strains are derivatives of *Saccharomyces cerevisiae* GCY1487 (SJR828a) (*MATα his3Δ200 ura3-52 leu2Δ1*) (1). In addition, GCY2506, GCY2251, GCY2512, and GCY2344 contained a *LYS2* mutation (beginning at nucleotide position 1264 TCT to TGA). All *msh6* deletions were created by one-step disruption with PCR-generated fragments. The *msh6Δ::kan* deletion was made from a PCR fragment generated from the collection of yeast gene deletions (2). For the *msh6Δ::loxP* deletion, the PCR fragment was from a strain in which *MSH6* had been disrupted by a loxP-kanMX-loxP fragment that was subsequently excised by Cre expression (3).

1. Williams T-M, Fabbri RM, Reeves JW, Crouse GF (2005) A new reversion assay for measuring all possible base pair substitutions in *Saccharomyces cerevisiae*. *Genetics* 170:1423–1426.
2. Winzeler EA, et al. (1999) Functional characterization of the *S. cerevisiae* genome by gene deletion and parallel analysis. *Science* 285:901–906.
3. Güldener U, Heck S, Fielder T, Beinhauer J, Hegemann JH (1996) A new efficient gene disruption cassette for repeated use in budding yeast. *Nucleic Acids Res* 24:2519–2524.

Table S12. Oligo sequences

Oligo	Sequence
NTS	ATGGTGGTGTAGATATCATCGAATTGGGTATGCCCTTCTC
TS	GAGAAGGGCATACCCAATTCGATGATATCTACACCACCAT
LYS2TCARev	CCAACCCTATCTTTCACATCAGGTTCCGAAGGTATTCCTA