

Table S1. Polymorphisms between ry^{531} and ry^{606} .

Position	ry^{531}	ry^{606}
-2657	C	T
-2010	G	C
-1316	C	T
-1061	A	T
-1029	T	-
-996	G	T
-937	A	T
-910	G	A
-698	A	T
-685	GGGT	----
-679	A	G
-668	A	T
-667	G	A
-636	A	C
-468	G	A
-44	T	C
467	C	T
736	A	G
767	A	G
777	A	G
1153	C	T
1596	G	T
2653	T	G
2957	T	C
3148	C	T
3312	A	G
3529	T	C
3557	G	A
3703	T	A
3723	C	A
4415	A	C
4739	C	A
4777	G	C

This table lists the polymorphisms between ry^{531} and ry^{606} used in this study. Positions are relative to an *EcoRI* site in the coding region {for additional information, see Blanton, 2005 #2600}. The ry^{606} mutation is at -468 (bold), and the ry^{531} is at 3312 (bold).

Table S2. Allele-specific PCR primers and conditions.

Position	Allele	Forward Primer	Reverse Primer	Mg ⁺⁺ (mM)	Annealing (°C)	Time (sec)
-2657	606	CCAAGTAATCCTGGCATgGTt	AGCAAACAACGAGGCTTCAC	3.0	56	45
-1316	606	GCGTGTCTTTCTTAAaGTt	CCGGATGCAGACGCGTTT	3.0	59	30
-468	606	GCTGTGCGGAACGAAGTaGGa	GAGTGGTCTTCCGAAAGTGG	3.0	64	30
-468	606	TGTCTAACTCGGTTTTGG	CGCATCCGCCTTCCGCAtAtt	3.5	59	30
-44	606	TGGTGCACCTGCCAATCGCG	ATCGGTCTCCGCATCGGTgCCg	3.5	67	30
1596	606	GCACCGGCTATCGACCCATT	AAAGTGTGATCCGCCTGaGa	2.5	58	60
1596	531	GCACCGGCTATCGACCCATT	AAAGTGTGATCCGCCTGaGc	2.5	58	60
2957	606	GGCGAGTGTGGGATCCaATc	GCTCTCCAGCTTAGTTTA	2.5	58	60
2957	531	GGCGAGTGTGGGATCCaATt	GCTCTCCAGCTTAGTTTA	2.5	58	60
2957	606	AGCTCAAGTCCTATTTCCCG	AGTACGGCCATTCCGTgCAg	2.5	56	45
2957	531	AGCTCAAGTCCTATTTCCCG	AGTACGGCCATTCCGTgCAa	2.5	56	45
3312	606	CGAGGGAGCATTcATGCAaGg	GCTCTCCAGCTTAGTTTA	3.0	58	30
3312	531	CGAGGGAGCATTcATGcGGa	GCTCTCCAGCTTAGTTTA	3.0	58	30
3312	606	GATTGCTTGAAGCAGTCGAG	CCAAAGTGAACAGTCCAaAGc	3.0	58	30
3312	531	GATTGCTTGAAGCAGTCGAG	CCAAAGTGAACAGTCCAaAGt	3.0	58	30
3557	606	CATTGCAGCTGCTCGCaAGa	GGGCGCACTGTAATTGAATCG	3.5	64	45
3557	531	CATTGCAGCTGCTCGCaAGg	GGGCGCACTGTAATTGAATCG	3.5	64	45
4415	606	AATCCGGCTATTGACATTGG	GGGCTTGGCAATTTCCGaAg	2.5	58	60
4415	531	AATCCGGCTATTGACATTGG	GGGCTTGGCAATTTCCGaAt	2.5	58	60

This table lists primers used in allele-specific PCR. Specificity is provided by one primer in each pair; this primer has a 3' nucleotide (lowercase) that matches the allele of one chromosome (ry^{606} or ry^{531}), and an additional nucleotide (lowercase) that is mismatched for both chromosomes. All PCR reactions included an initial denaturing step (five min. at 94 °C), followed by 30 cycles of 30 seconds at 94 °C, 30 seconds at the annealing temperature specified, and the specified number of seconds at 72 °C. Reactions contained the specified concentration of Mg⁺⁺, and 0.5 µl of fly prep in a 20 µl volume. Bold positions indicate locations of ry^{606} and ry^{531} mutations. For sites with a position <0, only a ry^{606} -specific PCR is done, because a ry^{531} -specific PCR would amplify the ry^{506} chromosome.

Table S3. Repair of different types of heterologies.

Heterology	PMS	Events	% PMS
A/A or T/T	8	61	13.1
G/A or C/T	11	58	19.0
G/T or C/A	38	184	20.7
indel	0	26	0.0

This table lists the total number of occurrences of PMS among NCOs and COs from *Msh6* mutants for sites definitely included in a recombination event (gray bars in Figures 2 and 3). Because we cannot determine on which chromosome recombination was initiated, there are two possible mismatches for each site, except for the two insertion/deletion loops (indels). Two-sided p values by Fisher's exact test are significant only for G/A or C/T versus indel and for G/T or C/A versus indel; however, estimations of repair frequencies from these data are imprecise. In the DSBR model, some gene conversion occurs without formation of hDNA (*e.g.*, bottom left chromatid in Figure 4); this leads to an underestimation of repair frequency. Conversely, when the outer-most heterologies are repaired to give restoration, we cannot tell that the site was included in the recombination event; this leads to an overestimation of PMS frequency. Furthermore, within each class of base-base mismatch, there are sites at which we never observed PMS (Figures 2 and 3).