

Table S1. Variation in recombination rate between transformants.

Genotype	C β 2/C β 2 His $^+$ homologous recombination rate ($\times 10^{-6}$)	C β 2/C β 2-ns His $^+$ divergent recombination rate ($\times 10^{-6}$)	Fold variation (σ^*)	
			Homologous	Divergent
wild-type (total)	0.52	0.027	1.03	1.18
wild-type transformant A	0.52	0.028		
wild-type transformant B	0.50	0.022		
<i>pol30-8</i> (total)	0.74	0.026	1.33	1.36
<i>pol30-8</i> transformant A	1.05	0.031		
<i>pol30-8</i> transformant B	0.91	0.037		
<i>pol30-8</i> transformant C	0.58	0.021		
<i>sir2Δ</i> (total)	2.12	0.050	1.15	1.48
<i>sir2Δ</i> transformant A	2.11	0.046		
<i>sir2Δ</i> transformant B	1.54	0.049		
<i>sir2Δ</i> transformant C	2.01	0.033		
<i>sir2Δ</i> transformant D	1.92	0.084		
<i>sir2Δ msh2Δ</i> (total)	4.87	3.58	1.23	1.19
<i>sir2Δ msh2Δ</i> transformant A	4.13	3.37		
<i>sir2Δ msh2Δ</i> transformant B	6.25	4.70		
<i>sir2Δ msh2Δ</i> transformant C	5.16	3.39		
<i>hst3Δ hst4Δ</i> (total)	11.3	4.53	2.08	1.48
<i>hst3Δ hst4Δ</i> transformant A	5.41	6.32		
<i>hst3Δ hst4Δ</i> transformant B	10.3	3.19		
<i>hst3Δ hst4Δ</i> transformant C	23.4	4.94		
<i>hst3Δ hst4Δ</i> transformant D		2.72		

Two to four independent transformants (arbitrarily labeled A to D) were analyzed for each genotype (Materials and Methods). Total recombination rates were obtained from Table 2. σ^* is the multiplicative standard deviation; it is calculated from the standard deviation of the logs of the rates (Limpert E, Stahel WA, Abbt M (2001) Log-normal distributions across the sciences: Keys and clues. BioScience 51: 341-352). Assuming a log-normal distribution, 68% of the samples are expected to lie between μ/σ^* to $\sigma^*\mu$.