Supporting information for Yao *et al.* (April 16, 2002) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.082562199.

Table 2. Rate of recombination within the *a1-sh2* interval

	No. recombinants[*]				
Year	Clsh	clrd	Total	Population Size	cM[†]
1992[‡]	28	47	75	67,000	0.11 ± 0.01
1993	46	54	100	182,000	0.055 ± 0.005
Total [§]	74	101	175	249,000	0.070 ± 0.005

Clsh: colored shrunken kernels; clrd: colorless round kernels.

[*] Based on corrected numbers from Table 1.

[†] Genetic distances were calculated as follows: cM = (no. of recombinants /population size) X 100.

[‡] These data have been extended from those of Civardi *et al* (1).

[§] A homogeneity χ^2 test indicated that there was a significant difference in the rates of recombination between these two years. However, because no differences were found between the distributions of the recombination breakpoints, data were combined across years to calculate recombination rates and genetic distances.

Reference:

1. Civardi, L., Xia, Y. J., Edwards, K. J., Schnable, P. S. & Nikolau, B. J. (1994) *Proc. Natl. Acad. Sci. USA* **91,** 8268-8272.