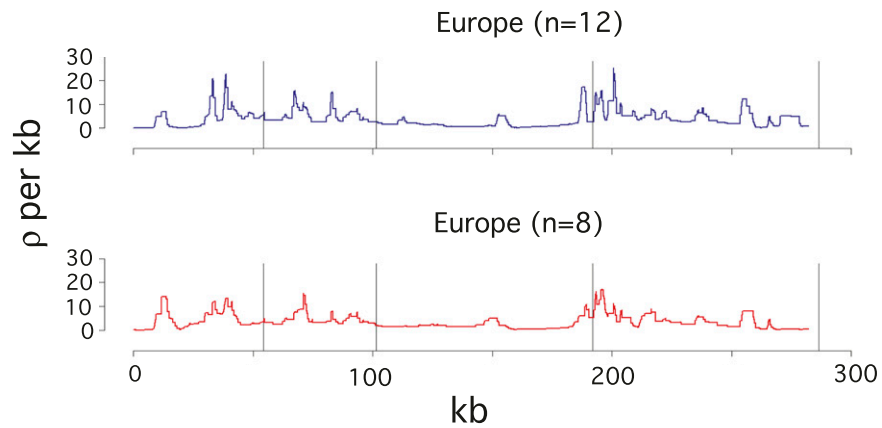
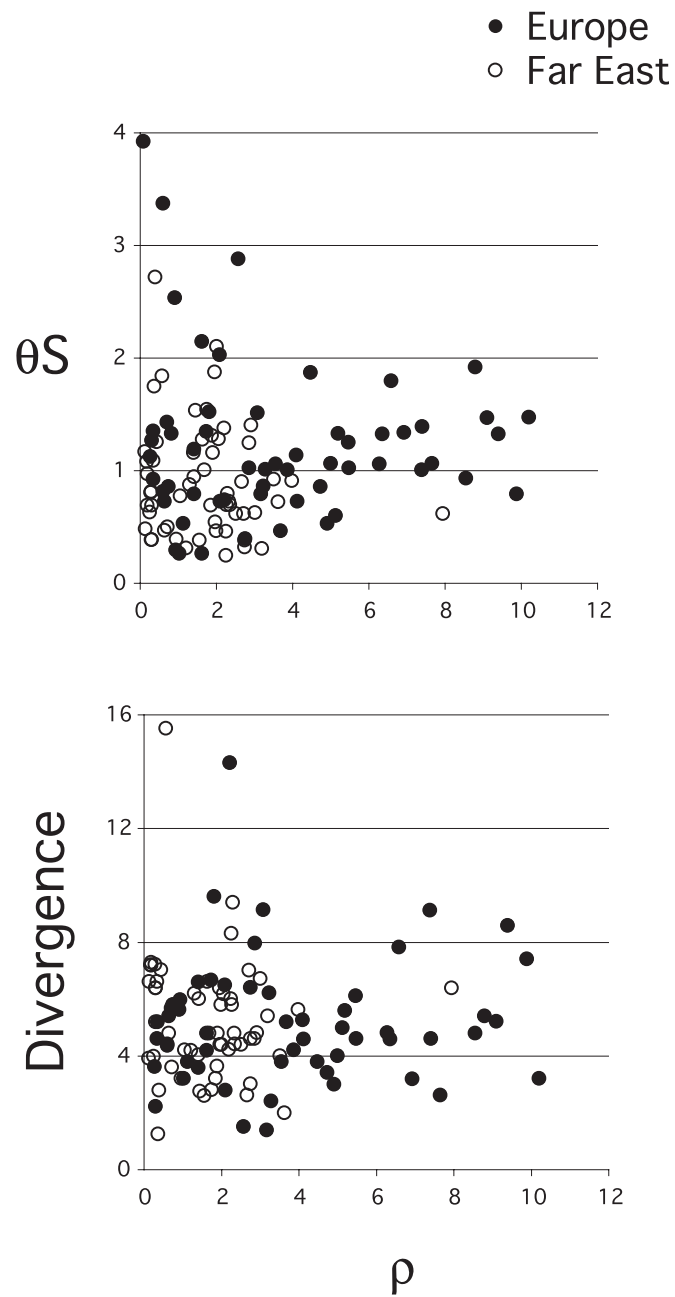


# Supporting Information

Tsai et al. 10.1073/pnas.0908774107



**Fig. S1.** The pattern of recombination along the chromosome is preserved, even when the sample size in Europe is reduced from 12 to only 8 strains, similar to the sample size in the Far East population.



**Fig. S2.** Nucleotide diversity  $\theta_S$  and divergence from common ancestor plotted as a function of the population recombination parameter  $\rho$  (Morgans/kb) for Europe (closed) and Far East (open); points are values from nonoverlapping 5-kb windows (both correlations are nonsignificant; Kendall's  $\tau$ ,  $P > 0.40$ ).

**Table S1. Distribution of SNPs and haplotype blocks in chromosome III of *Saccharomyces paradoxus***

	<i>n</i>	No. sites*	No. SNPs <sup>†</sup>	No. blocks	Block length (kb; SE, max)	No. SNPs per block (SE)
Europe	12	230,106	464	110	2.2 (0.2, 9.6)	5.4 (0.4)
	8 <sup>‡</sup>	242,501	377	89	2.6 (0.3, 11.2)	5.9 (0.6)
Far East	8	213,559	232	47	6.3 (0.9, 21.8)	6.6 (0.7)

Total length of the alignment is 286,935 bp; *n* is for number of chromosome sequences analyzed.

\*Only sites with no missing data in any of the strains are analyzed.

<sup>†</sup>Nonsingleton SNPs only.

<sup>‡</sup>Eight sequences chosen at random from the European population.

**Table S2. Summary statistics for genes and intergenes along chromosome III of *Saccharomyces paradoxus***

	<i>n</i>	Europe $\rho$ (Morgans/kb) (SE)	<i>n</i>	Far East $\rho$ (Morgans/kb) (SE)
Genes	140	3.9 (0.28)	141	2.0 (0.14)
Intergenes	141	4.0 (0.33)	141	1.9 (0.14)
5' in at least one end	105	4.5 (0.42)	105	2.0 (0.17)
5' - 5'	35	4.2 (0.71)	36	1.9 (0.25)
5'-3' and 3'-5'	69	4.6 (0.52)	69	2.1 (0.22)
3'-3'	36	2.7 (0.40)	36	1.6 (0.18)

**Table S3. Measures of autocorrelation for 56 nonoverlapping 5-kb windows along chromosome III of *S. paradoxus***

	Europe		Far East	
	<i>r</i>	<i>P</i> value	<i>r</i>	<i>P</i> value
Recombination rate ( $\rho$ )	0.48	0.0003	0.51	0.0001
GC content	0.23	0.08	0.25	0.06
$\theta_s$	0.06	0.63	-0.007	0.96
$\theta_\pi$	0.07	0.59	0.02	0.87
Divergence	-0.007	0.96	0.10	0.47