Table S1. Genome-wide estimates of the migration parameter M under a symmetric island model, as inferred from F_{ST}.

Population pair	Mean F_{ST} [a]	$\widehat{M}$ [b]	$(5, 95)$th percentiles for $\widehat{M}$
M vs. N.A.	0.96	0.07	(0, 0.48)
M vs. S	0.84	0.31	(0, 1.52)
M vs. W.A.	0.97	0.05	(0, 0.32)
M vs. W/E	0.93	0.13	(0, 0.57)
N.A. vs. S	0.69	0.70	$(0, \infty)$
N.A. vs. W.A.	0.98	0.04	(0, 0.13)
N.A. vs. W/E	0.90	0.18	(0, 0.93)
S vs. W.A.	0.79	0.41	(0, 2.40)
S vs. W/E	0.82	0.35	(0, 1.45)
W.A. vs. W/E	0.91	0.15	(0, 0.64)

Each row reports estimated population differentiation and migration parameter values for one pair of yeast populations.

[a] In a given gene window, F_{ST} is calculated as one minus the ratio of within- to between-population diversity, as given by the mean number of pairwise sequence differences. Mean F_{ST} is the mean of this value across genes, weighted by length.

[b] A point estimate of the migration parameter M in a symmetric five-island model, inferred from mean F_{ST} and using a theoretical prediction of the relationship between M and F_{ST} (see MATERIALS & METHODS). Also given are percentiles for this estimate, inferred from the distribution of F_{ST} across genes.