Supplemental Materials for: Evolution of Drift Robustness in Small Populations of Digital Organisms

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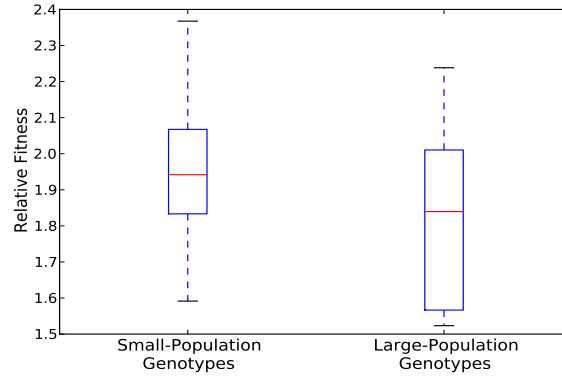Michigan State University, East Lansing, MI 48824

Figure S1: The fitness of the small-population and large-population genotypes relative to the ancestor. Red lines are medians, edges of the box are first and third quartile, whiskers are at most 1.5 times the relevant quartile, and the plus signs are outliers.
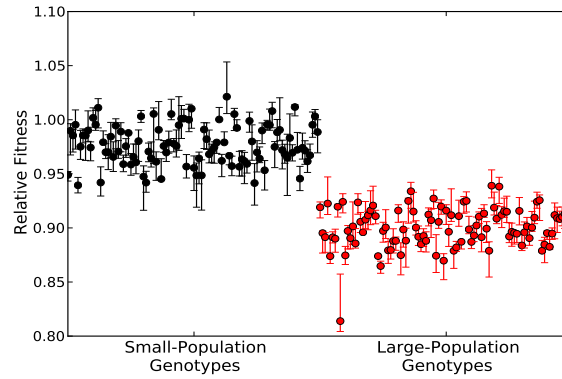

Figure S2: Results from the drift robustness test performed for 10^4 generations. Genotypes tested were the same as in Fig. 1. Black (red) markers are for small-population (large-population) genotypes. Test population size was 50 individuals. Circles represent the median value of 10 replicates for one genotype; error bars are 1st and 3rd quartile.
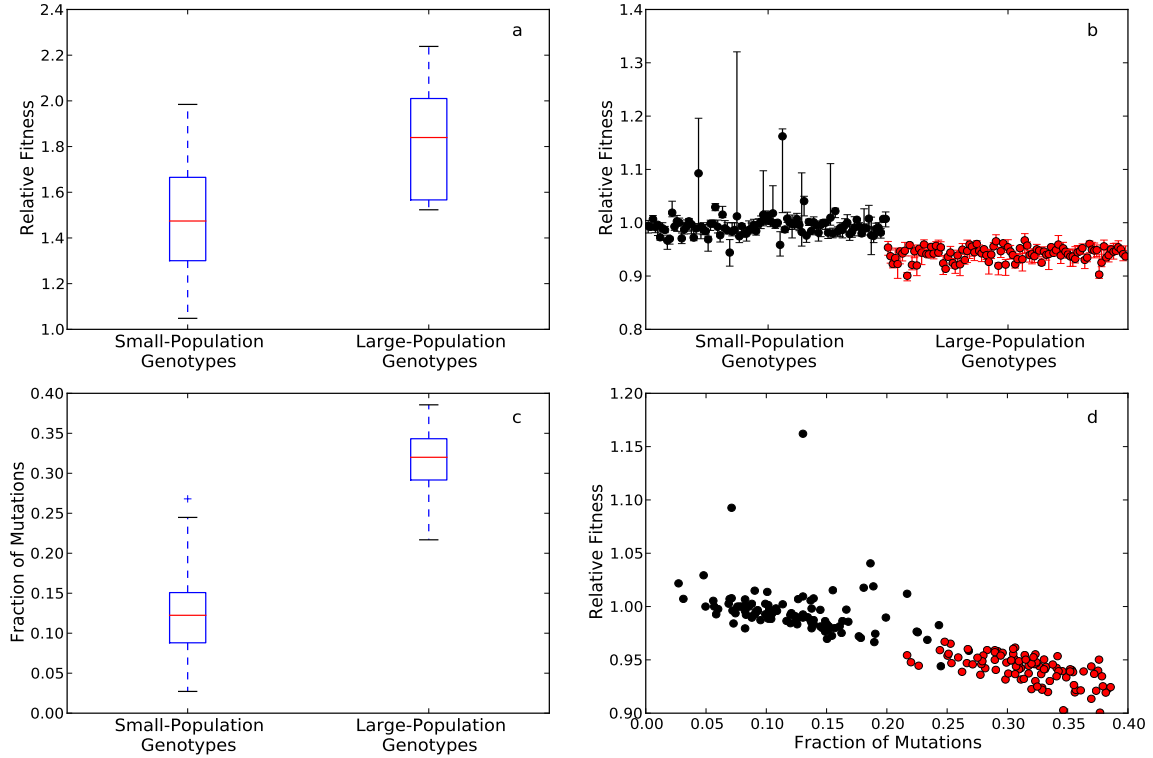
Figure S3: Evolution of drift robustness when small and large populations evolved for an equal number of generations. Data for large populations same as in main text and Fig. S1. Black (red) represents small-population (large-population) genotypes. a) The fitness of the small-population and large-population genotypes relative to the ancestor. Figure description same as Fig. S1. b) Results from the drift robustness test. Figure description same as Fig. 1a. c) Fraction of mutations that had a small deleterious effect. Figure description same as Fig. 3a. d) Relationship between fitness change in the drift robustness test and the fraction of small-effect deleterious mutations. Figure description same as Fig. 3b.
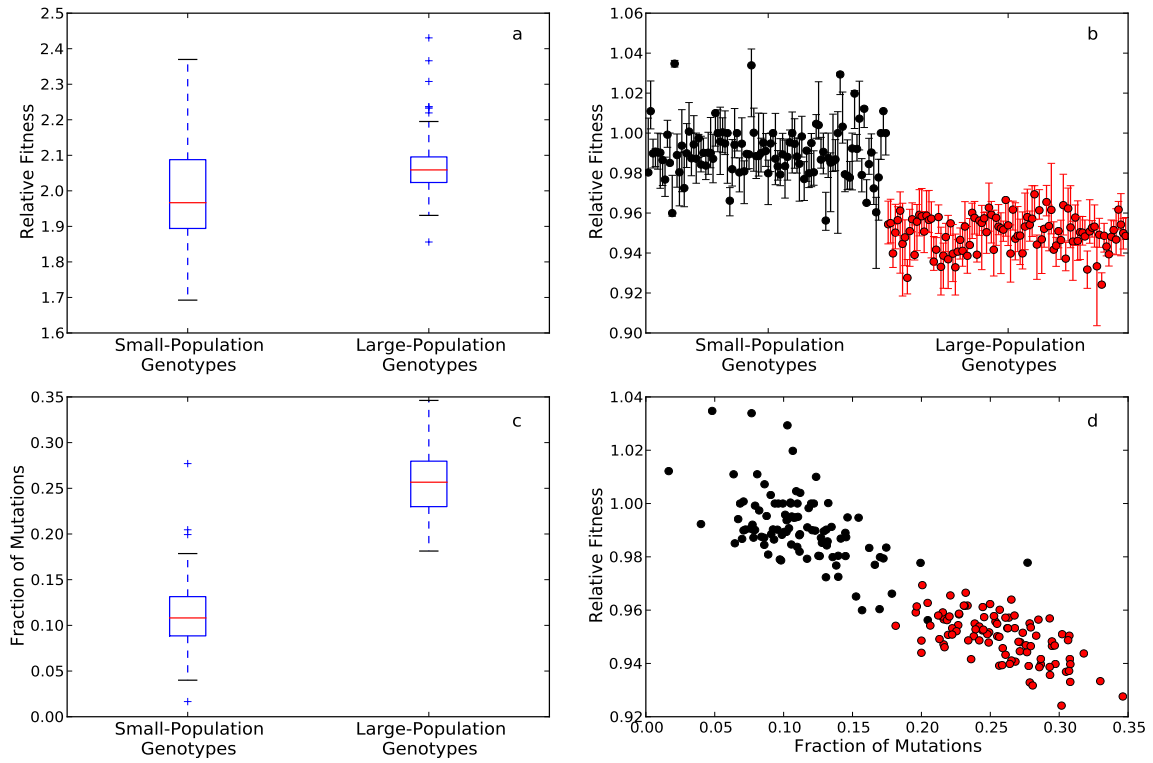
Figure S4: Evolution of drift robustness when genome size could evolve during the experiments. Figure descriptions same as in Fig. S3
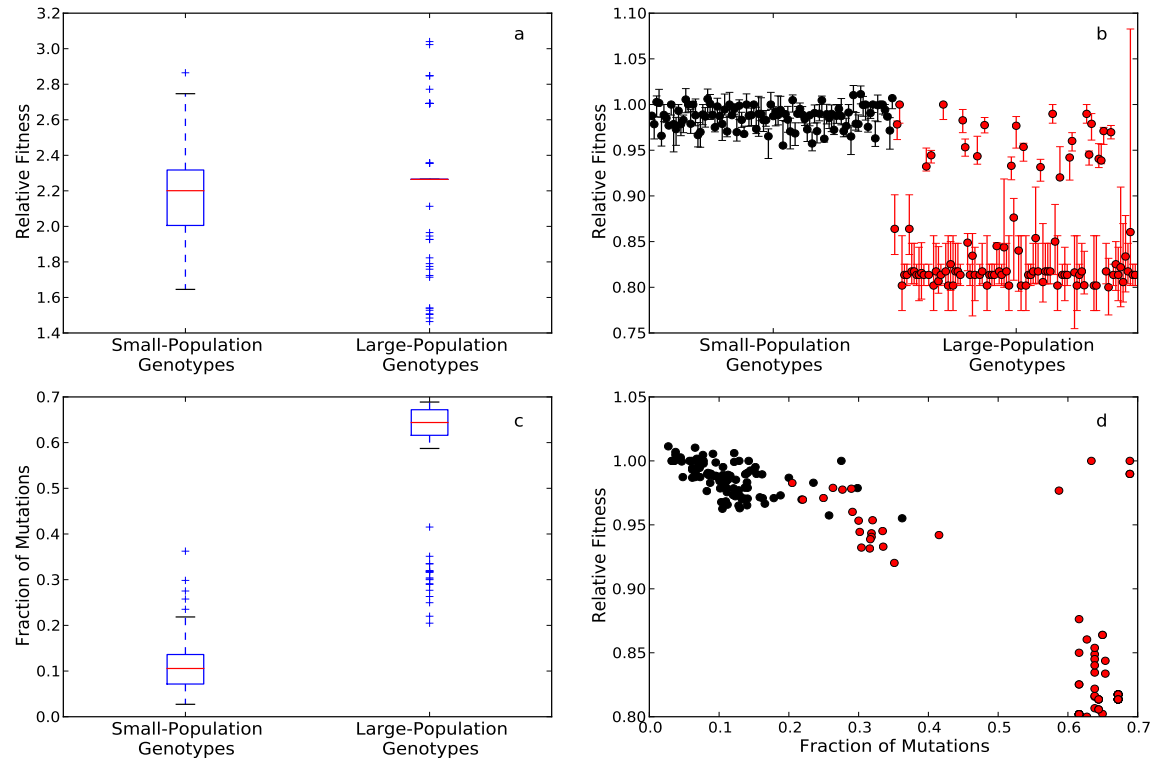
Figure S5: Evolution of drift robustness when reproduction was sexual. Figure descriptions same as in Fig. S3
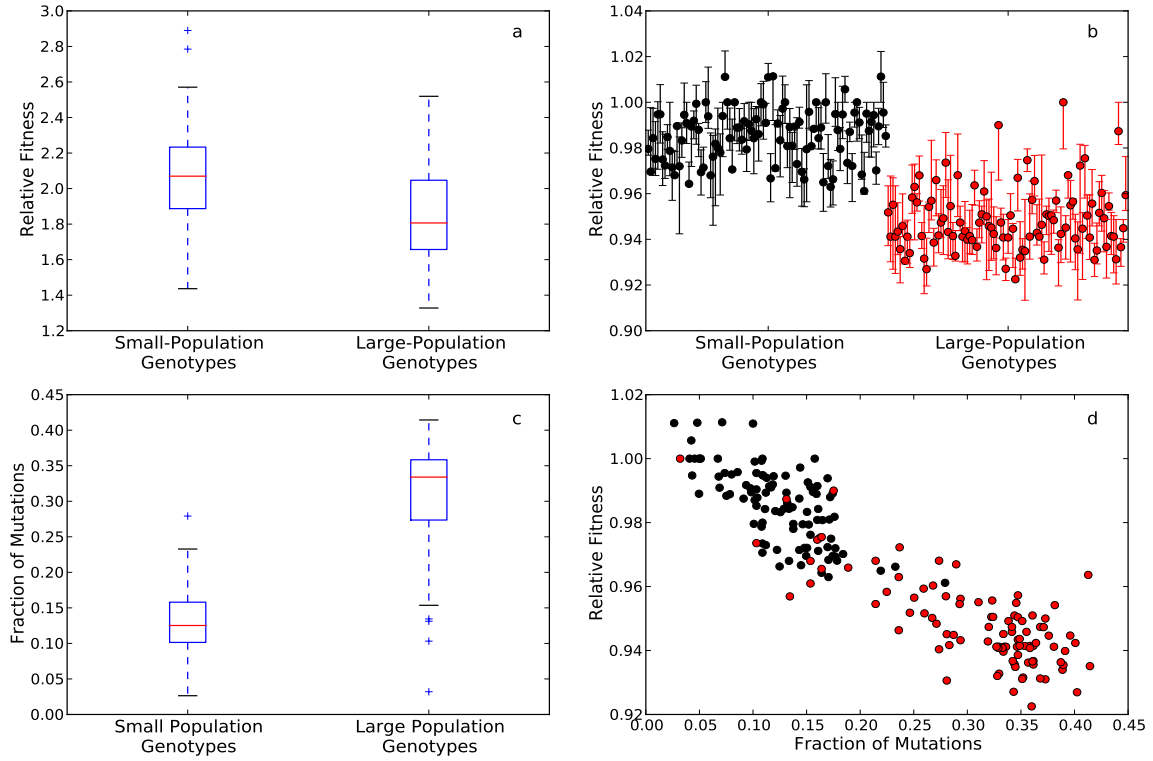
Figure S6: Evolution of drift robustness when the genomic mutation rate was 10^{-2}/generation/genome (an order of magnitude lower than the main experiments). Figure descriptions same as in Fig. S3
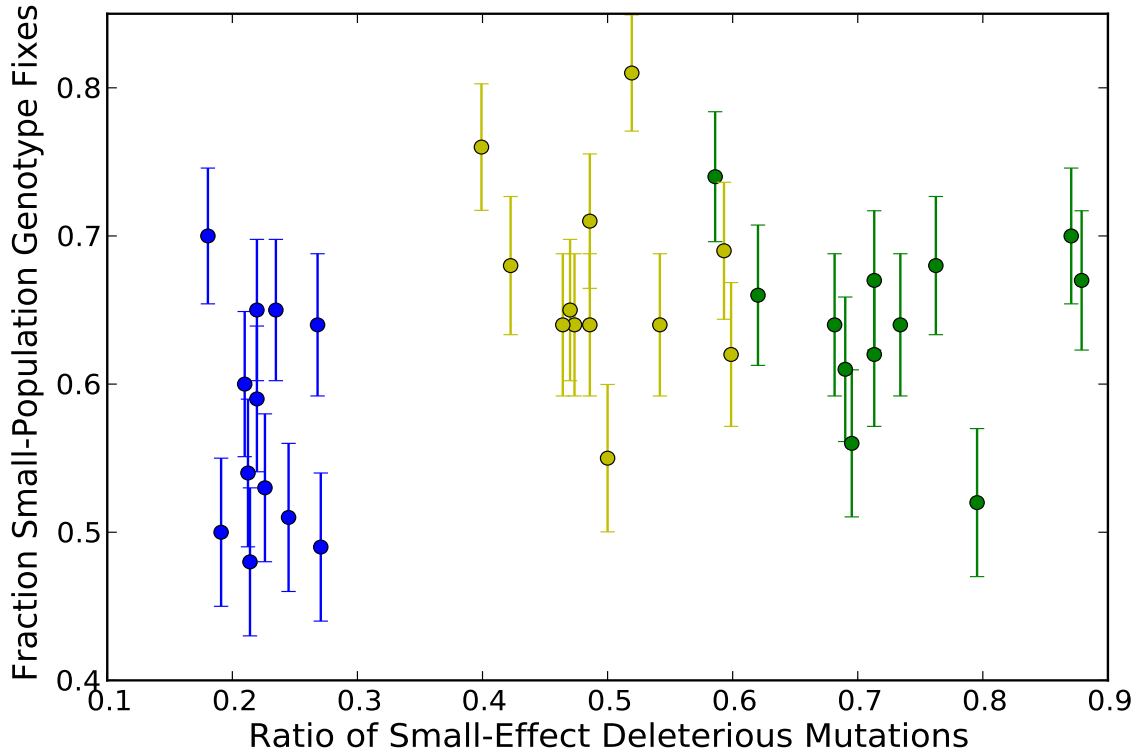
Figure S7: Relationship between mutational effects and competition experiment outcomes. Blue, yellow, and green represent the three small-population genotypes. Each marker is the fraction of competitions (out of 100) where the small-population genotype fixed versus one large-population genotype as a function of the ratio of the fraction of small-effect deleterious mutations in the small-population genotype to the fraction of small-effect deleterious mutations in the large-population genotype. Error bars are 95% confidence intervals of the mean.

Table 1: Correlations for each small-population genotype in the competition experiments

Color	Correlation to small-effect deleterious mutations
Green	$r = -0.11, p < 0.74$
Yellow	$r = -0.20, p < 0.53$
Blue	$r = -0.14, p < 0.57$