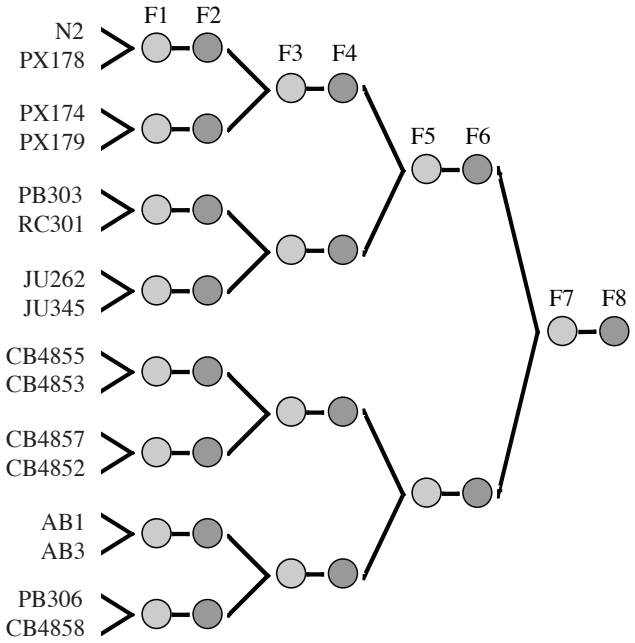
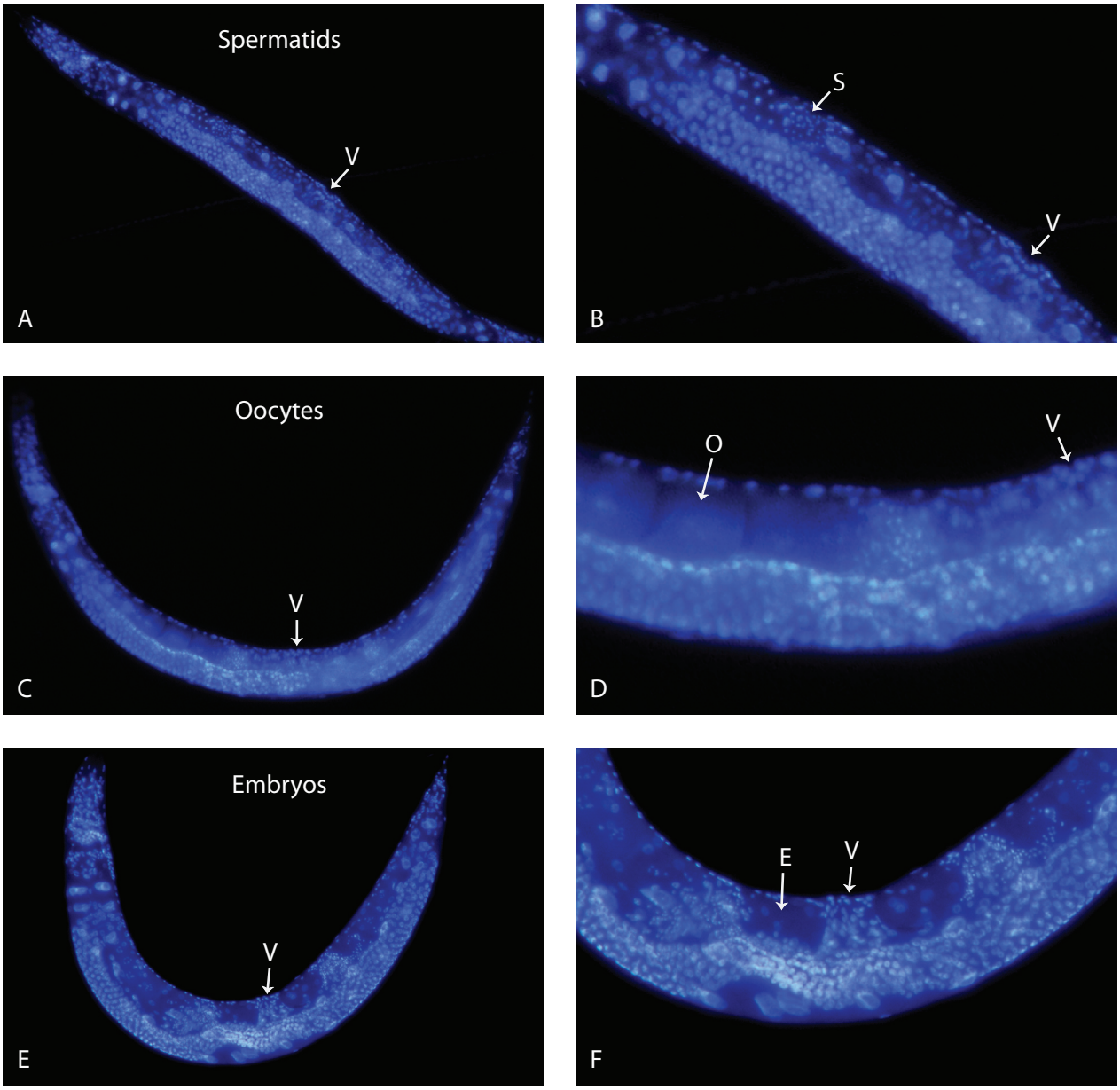


Supplementary Figure 1. Crossing design used to derive heterogeneous the ancestral population. To produce the F1 generation pairs of parental strains were reciprocally mated in a ratio of three males to one hermaphrodite (this ratio was used throughout the crosses). F1 individuals from each pair were then divided among five plates to give equal representation of males and hermaphrodites from the bi-directional crosses. These individuals (40 per plate/ 200 per line) were allowed to randomly mate for one generation to produce the F2 generation. Pairs of F2 lines were then reciprocally mated (80 total parental worms) to generate the F3 lines. F3 individuals from each pair of bi-directional crosses were partitioned among replicate plates as above (40 per plate/ 400 per line). This process was repeated for an additional two rounds of crosses and population expansions, increasing both the number of worms crossed (200, 400) and the number of worms allowed to reproduce in the following generation (800, 20000) in each round. Crosses proceeded synchronously through generation F7 and yielded a single outcrossed population from the original 16 strains. Following the final population expansion, the offspring of 20,000 worms reared on 20 (100 mm) plates were combined, grown for one generation, and then frozen; these worms serve as the ancestral populations (generation 0) in our experiments. *Caenorhabditis elegans* strain number is indicated on the far left. Generation number is indicated above each circle. Light circles represent populations resulting from pair-wise crosses and dark circles from random mating in the previous generation. Subsequent genomic analysis has revealed that PX174 is identical to RC301 and PX178 is not different from PX179 (E. Anderson, pers. Comm.).



Supplementary Figure 2. Representative developmental stages of *C. elegans*. DAPI stained *C. elegans* hermaphrodites (anterior to left) illustrating the presence of A, B) **S**permatids; C, D) **O**ocytes; E, F) **E**mbryos. The **V**ulva of each worm is labeled to assist with orientation.

Supplementary Table 1. Estimates of effective population size.

We sought to create a lower bound on the effective population size generated by variation in offspring production per individual per generation. To do this we used the actual offspring production values obtained in our fitness estimates and used them as a proxy for variation in offspring number among individuals within each line. Offspring production on day three of reproduction per individual was normalized by the total day three offspring production for all individuals within the sample and then multiplied by 7,500 in order to calculate the fraction of the total number of individuals transferred each generation in the experimental evolution protocol that would be expected to be generated for each individual. These values were then used to calculate the expected mean and variance in offspring production within a line, which in turn were used to calculate the expected effective population size (N_e) for a self-fertilizing diploid population (c.f., Caballero 1994 Heredity 73:657-679, Eq. 14):

$$N_e = \frac{N\mu - 1}{\mu - 1 + \sigma^2/\mu},$$

where N is the census population size (set at 7,500), μ is the average offspring contribution, and σ^2 is the variance in offspring production. These values are lower bounds with respect to the potential effects of outcrossing versus self-fertilization, although it is possible that other demographic factors could also perturb the effective population size to some extent. However, the effective population sizes are large enough such that even fairly substantial variation in these estimates would not be expected to yield qualitative effects on the response to selection.

Line	Generation	N_e
Ancestor	0	4428
A	6	5859
	24	6146
	47	4410
B	6	5932
	24	5587
	47	6711
C	6	6019
	24	4142
	47	6644
D	6	6723
	24	5460
	47	6047
F	6	6591
	24	5515
	47	5712