

78 File S3 Results based on total length of the genealogy

In the main text, we use average pairwise coalescence times to assess genetic diversity. Here we show the corresponding
80 results for the average total length of the genealogy G_{total} , a measure related to the number of segregating sites or the
number of alleles in a sample. To measure the proportion of variation maintained, we divided G_{total} by $4k_0 \cdot \sum_{i=1}^{2n_s-1} \frac{1}{i}$,
82 the expected total length of the sample genealogy if all lineages would have been sampled in the source population
(Wakeley 2009, p. 76). The results (Figure S3 and S4) were qualitatively similar to the results based on average pairwise
84 coalescence times (see Figures 5 and 6), except that the proportion of variation maintained more slowly approached one
with increasing founder population size.

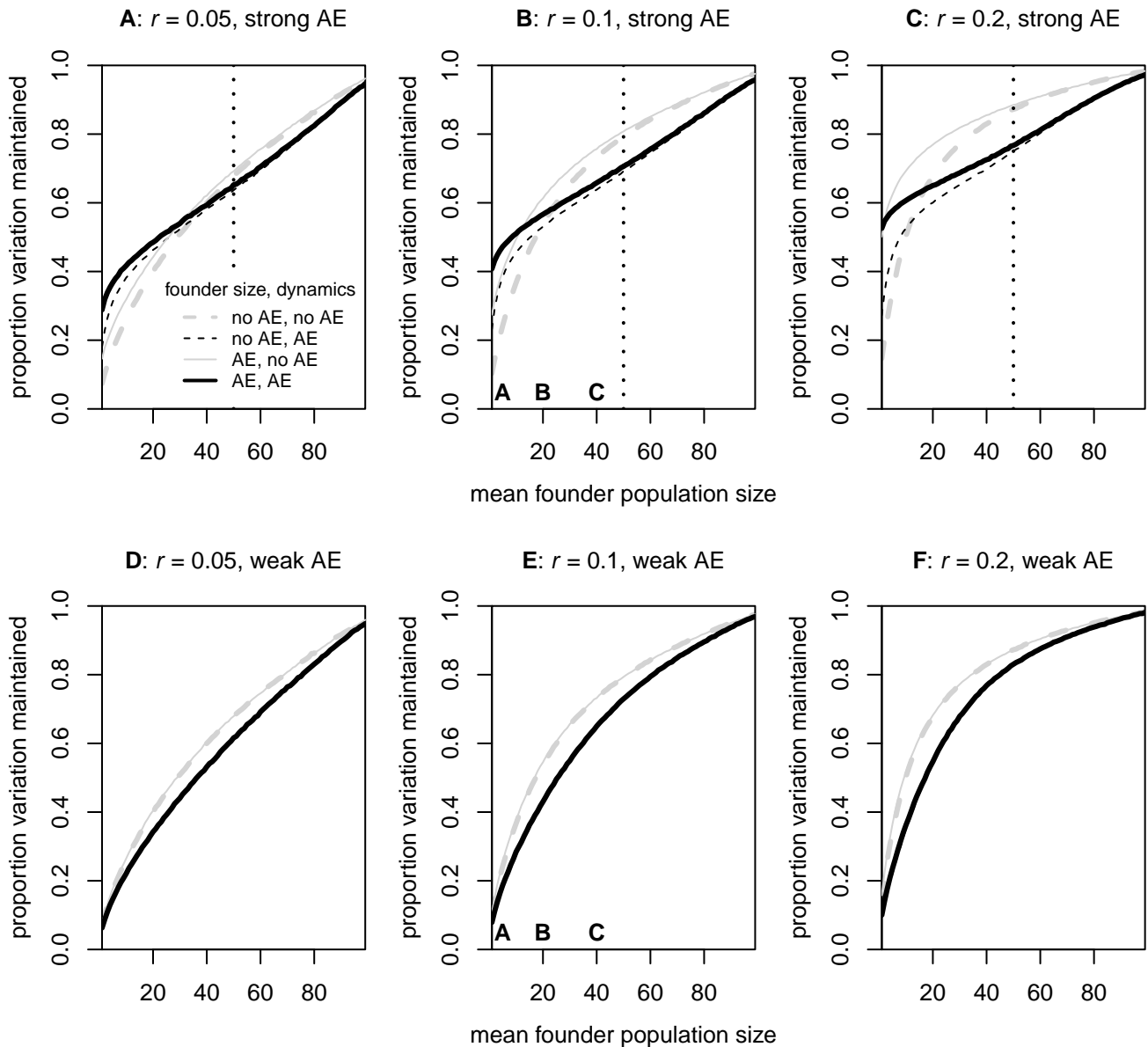


Figure S3 Average proportion of genetic variation from the source population (based on the average total length of sample genealogies) that is maintained by an introduced population upon reaching size z . The subplots differ in the value of the growth rate parameter r and in the type of Allee effect. In the upper row, Allee-effect populations have a strong demographic Allee effect with $a = 50$ (indicated by dotted vertical line) and $c = 0$. In the lower row, Allee-effect population have a weak Allee effect with $a = 0$ and $c = 30$. The values on the x -axes correspond to the mean of the original founder-size distribution. The four sets of populations in each subplot serve to disentangle the genetic effects resulting from the shift in founder population sizes and those from the altered post-introduction population dynamics. Dashed lines: founder population size drawn from the success-conditioned distribution without an Allee effect. Solid lines: founder population sizes drawn from the success-conditioned distribution with an Allee effect (strong in the upper row, and weak in the lower row). Black lines: success-conditioned population dynamics with an Allee effect. Gray lines: success-conditioned population dynamics without an Allee effect. The letters A, B, and C in subplots (B) and (E) refer to the subplots in Figures 3 and 4, where we examined for $r = 0.1$ and the respective (mean) founder population sizes how the Allee effect influences the conditioned distribution of founder population sizes and the conditioned population dynamics. Across all points, standard errors were between 0.0004 and 0.0015, and the corresponding standard deviations between 0.689 and 0.203.

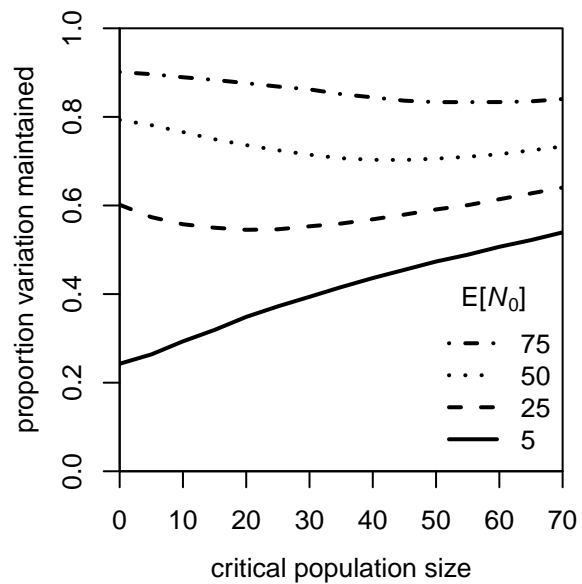


Figure S4 The role of the critical population size a for the average proportion of genetic variation from the source population (based on the average total length of sample genealogies) that is maintained by an introduced population upon reaching size $z = 100$. The average founder population size $E[N_0]$ is held fixed at a different value for each of the four curves. Each point represents the average over 20,000 successful populations. Standard deviations were between 0.085 and 0.158 and standard errors between 0.0006 and 0.0012. $c = 0, r = 0.1$.