Supplementary Information

S1 Description of speciation criterion

We introduce a simple speciation metric, S, that measures the degree to which the population has bifurcated at the genetic loci underlying the ecological trait. We only calculate this metric across the 10 genetic loci in order to control for locus number when making comparisons between "additive" and "redundant" maps. An individual's ecological phenotypic trait value calculated at a subset of 10 genetic loci is

$$x_{\text{gen}} = \sum_{i=1}^{10} x_{i;\text{gen}} \tag{S1}$$

Across the population, we denote the median value of x_{gen} by $\tilde{x}_{\text{gen}}$. In words, our speciation metric is calculated as the fraction of the population whose value of x_{gen} is equal to $\tilde{x}_{\text{gen}}$. Specifically, the speciation criterion, S is defined as

$$S = \frac{\sum_{j=1}^{2*K} i_j}{2 * K} \tag{S2}$$

where the sum is over all $2 * K$ individuals in the population, and i_j is an indicator variable for individual j whose ecological phenotypic trait value is $x_{\text{gen},j}$, for which

$$i_j = \begin{cases} 1, & \text{if } x_{\text{gen},j} = \tilde{x}_{\text{gen}} \\ 0, & \text{otherwise.} \end{cases} \tag{S3}$$

When this speciation metric is high, it means that there is plenty of interbreeding between individuals with high and low ecological trait values (i.e., the population is close to panmixia); however, when it is low, the subsets of the population with high and low

ecological trait values are not frequently interbreeding (i.e., that there is assortative mating). We define speciation to occur when this metric drops below a threshold value of $S = 0.1$.

S2 Description of Assortative Mating Index

We introduce an index, AMI, that measures the degree to which individuals are mating assortatively with respect to ecological genotypes. When this index is small, assortative mating is uncommon and when it is large, assortative mating is common.

We begin with the value $\tilde{x}_{\text{gen}}$ calculated in Section S1. For each mating pair, we then calculate the ecological trait value at the same subset of genetic loci for the father, $x_{\text{gen}}^{\text{father}}$, and for the mother, $x_{\text{gen}}^{\text{mother}}$. AMI then quantifies the fraction of matings in which mothers' and fathers' ecological values are both on the same side of the median, $\tilde{x}_{\text{gen}}$. Specifically:

$$\text{AMI} = \frac{\sum_{p=1}^{M} i_p}{M} \tag{S4}$$

where the sum is over all M mating pairs, and i_p is an indicator variable for mating pair p for which

$$i_p = \begin{cases} 1, & \text{if } (x_{\text{gen},p}^{\text{father}} - \tilde{x}_{\text{gen}}) * (x_{\text{gen},p}^{\text{mother}} - \tilde{x}_{\text{gen}}) > 0 \\ 0, & \text{otherwise.} \end{cases} \tag{S5}$$

S3 Alternative systems for epigenotype & genotype to phenotype mapping

We separately consider two different maps from genetic and epigenetic states to phenotype. The first, which we refer to as the "additive" map is described in the main text. The other, which we term the "redundant" map, is based on the notion that similar phenotypes can be attained through alternative means (i.e., genetics vs phenotypic plasticity). Each genetic locus is assumed to be redundant in its phenotypic effect with exactly one epigenetic locus. In the extreme, it is therefore possible to reach any phenotype through only genetic or only epigenetic change. For our purposes, the important difference between these maps is that in the redundant map (but not the additive map), there is interference between the genetic and epigenetic systems because every genetic allele's effect can be accomplished by an epigenetic marker.

Under the redundant map, we calculate the ecological phenotype of an individual, x, as

$$x = \frac{\sum_i^{n_{\text{ecol}}} \max(x_i^{\text{genetic}}, x_i^{\text{epigenetic}})}{n_{\text{ecol}}}, \tag{S6}$$

where both x_i^{genetic} (which represents the contribution of genetic allele i) and $x_i^{\text{epigenetic}}$ (which represents the contribution of epiallele i), take values of 0 or 1. The number of genetic loci and epigenetic markers are necessarily equal (with $n_{\text{ecol}} = 20$) and we set both equal to the total number of loci used in our additive map.

S4 Soft selection regime

We separately consider "hard" and "soft" selection regimes. Under hard selection an individual's survival probability is given by its fitness $w_{x;k;j}$ whereas, under soft selection, we sample individuals, with replacement to create a new pre-mating population, where

each individual's probability of being sampled is proportional to its fitness $w_{x;k;j}$. The latter case is a Wright-Fisher process with selection. Despite it not being ecologically realistic, we implement the soft selection regime in order to remove the effects of bottlenecks that occur in the more realistic hard selection regime; by comparing the two regimes we can infer the effect of bottlenecking.

S5 Supplementary Tables & Figures

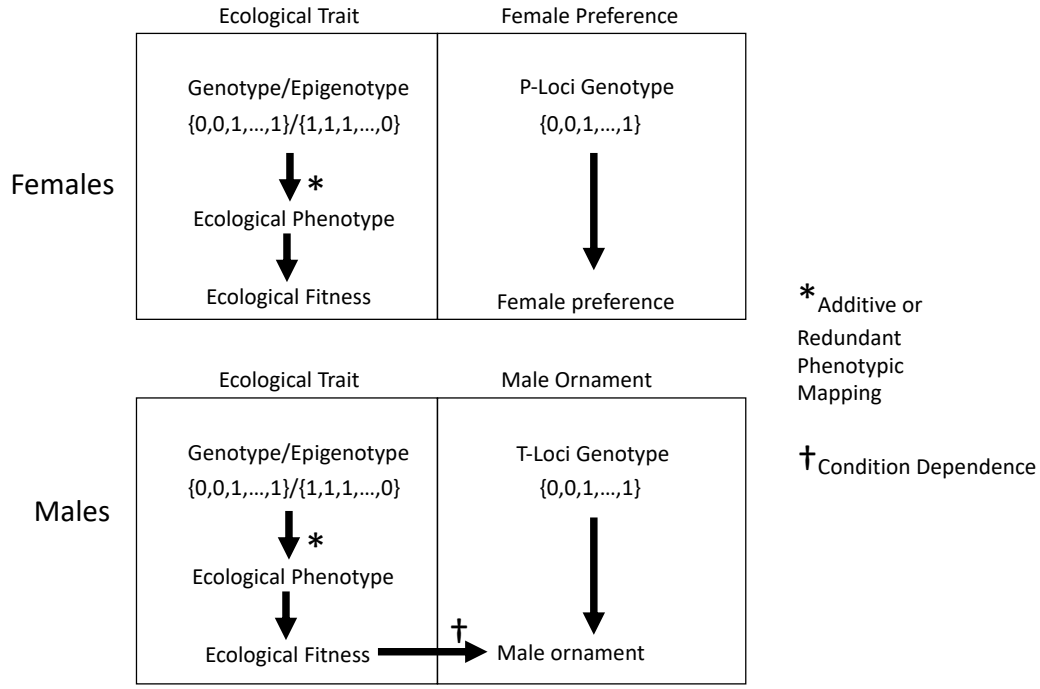

Figure S1: For each individual of the population, genotype and epigenotype is mapped onto phenotype.

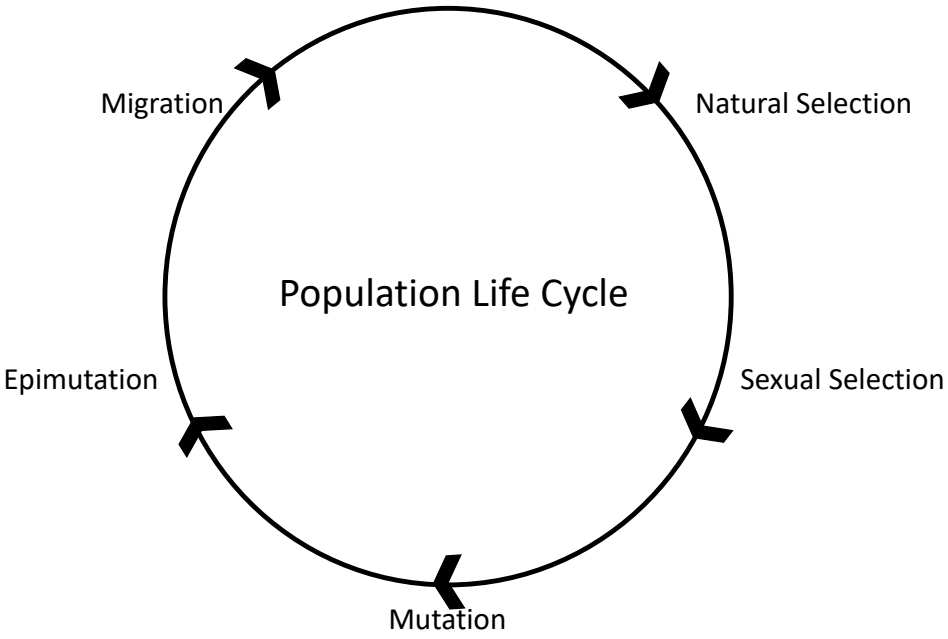

Figure S2: The life cycle of the population. For information about each stage, see the Materials and Methods section.

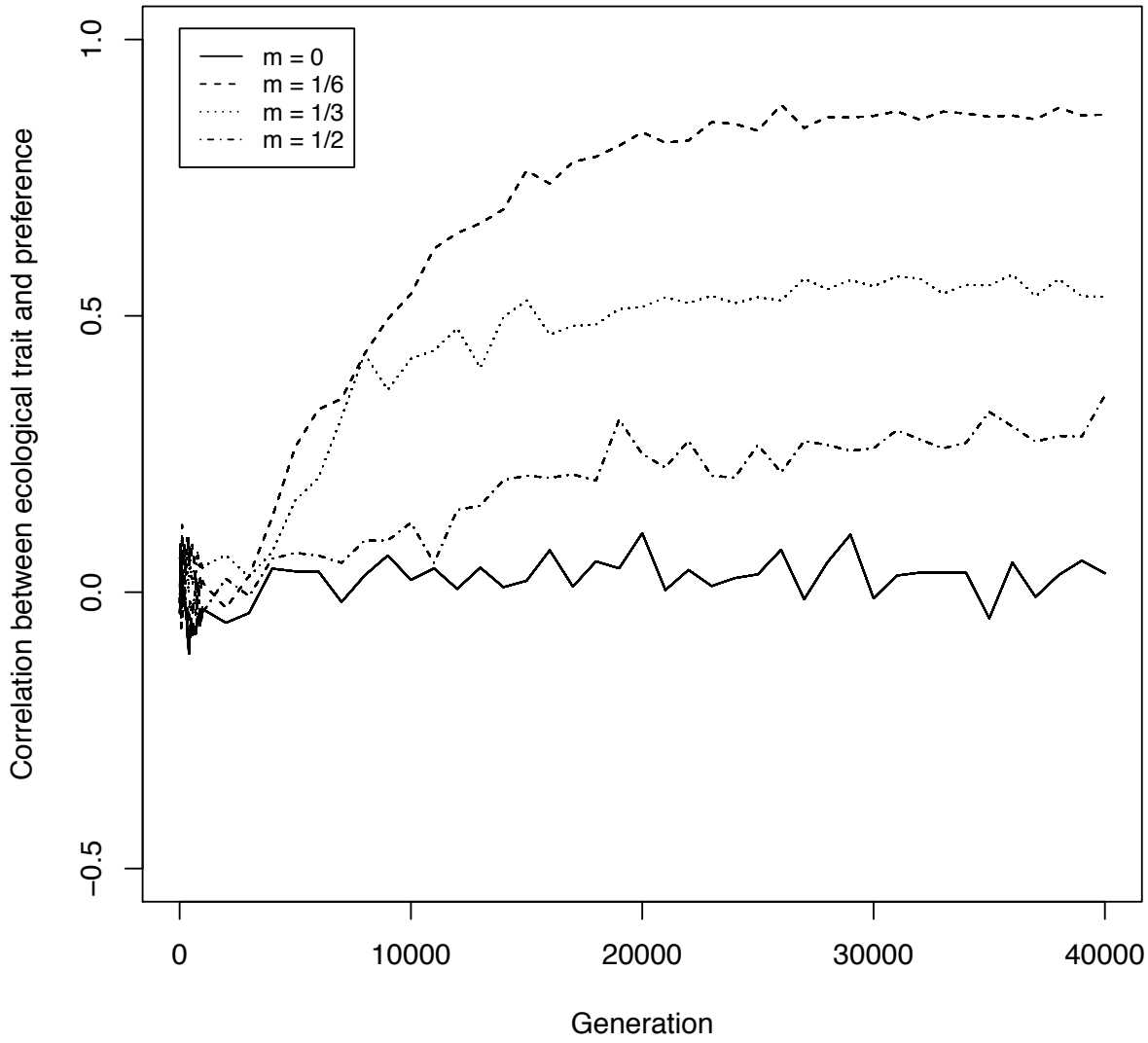

Figure S3: The correlation between the strength of the female preference and the locally adapted genotype over time in patch 1. For each parameter set p, we calculated across replicates, r, the Pearson correlation coefficient, $\rho_{g,a} = \mathrm{cor}_r(g, a)$ between the proportion, g, of locally adapted 1 alleles across all genetic loci of all individuals and the average female preference, a, across all individuals. Shown are the correlations across 35 replicates averaged over values of τ and separated by migration rate, m.

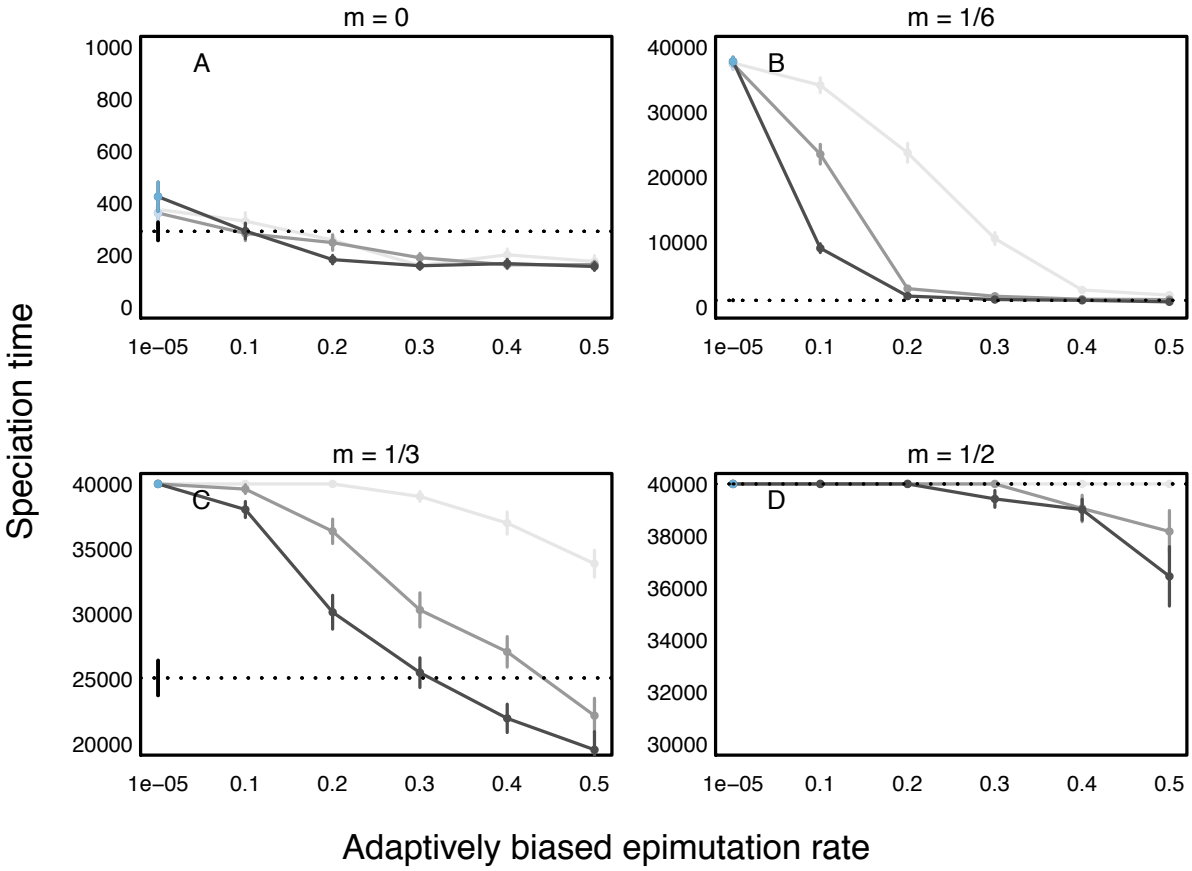

Figure S4: Time to speciation is generally shorter for higher rates of adaptively-biased epimutation ($\mu_{\text{epi;A}}$) when selection is weak. All specifications are as in Fig. 2 except that here $\sigma = 0.4$ (compared to $\sigma = 0.35$, there). Points show mean speciation time when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Parameters values are listed in Table 1, except $\sigma = 0.4$, with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

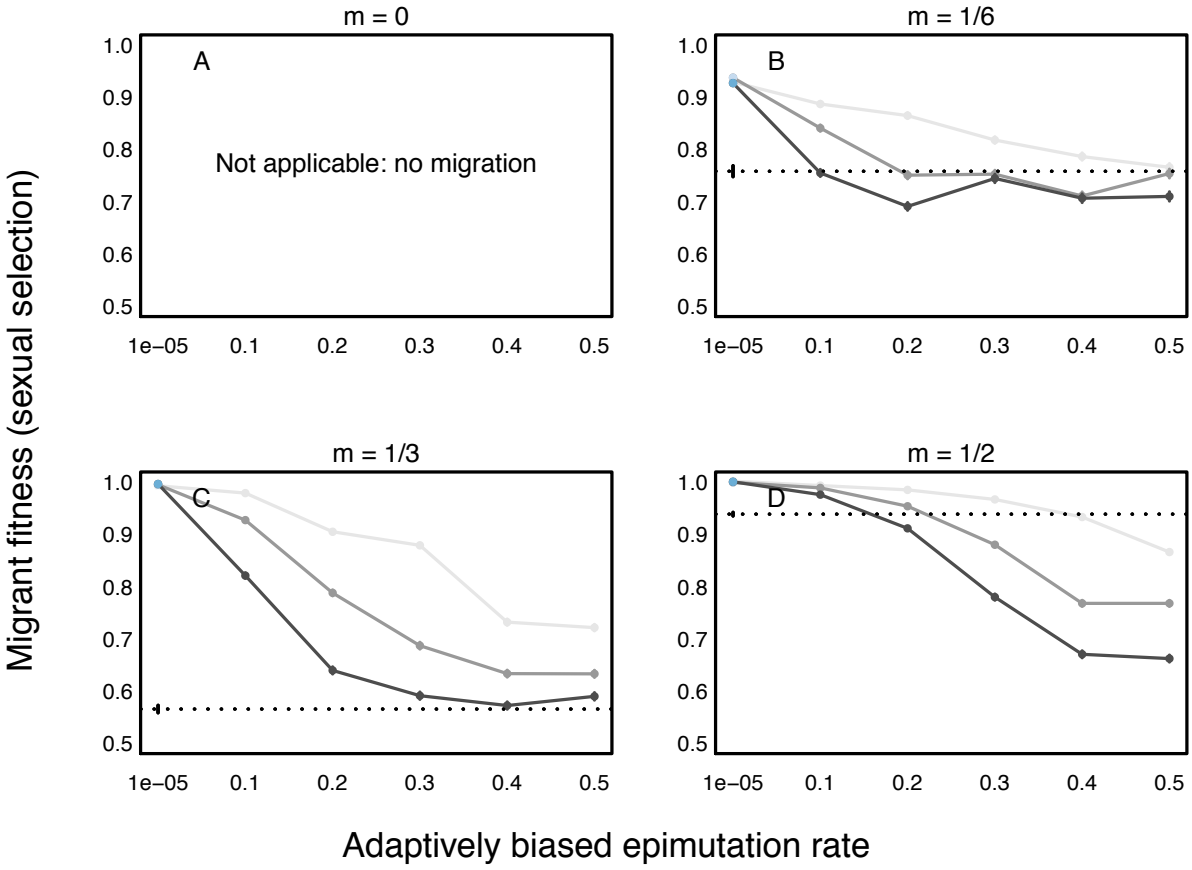

Figure S5: Mean migrant fitness due to sexual selection on males (averaged through time at evenly spaced time points) varies with the rate of adaptively-biased epimutation ($\mu_{\text{epi;A}}$) under our core model. Here, migrant fitness due to sexual selection is simply calculated from simulations as the ratio $\frac{m_{\text{a}}}{m_{\text{b}}}$ where m_b is the frequency of migrants before the mate choice step and m_a is the fraction of migrants succesfully chosen as fathers during mate choice. Points show mean fitness when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows fitness for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black).

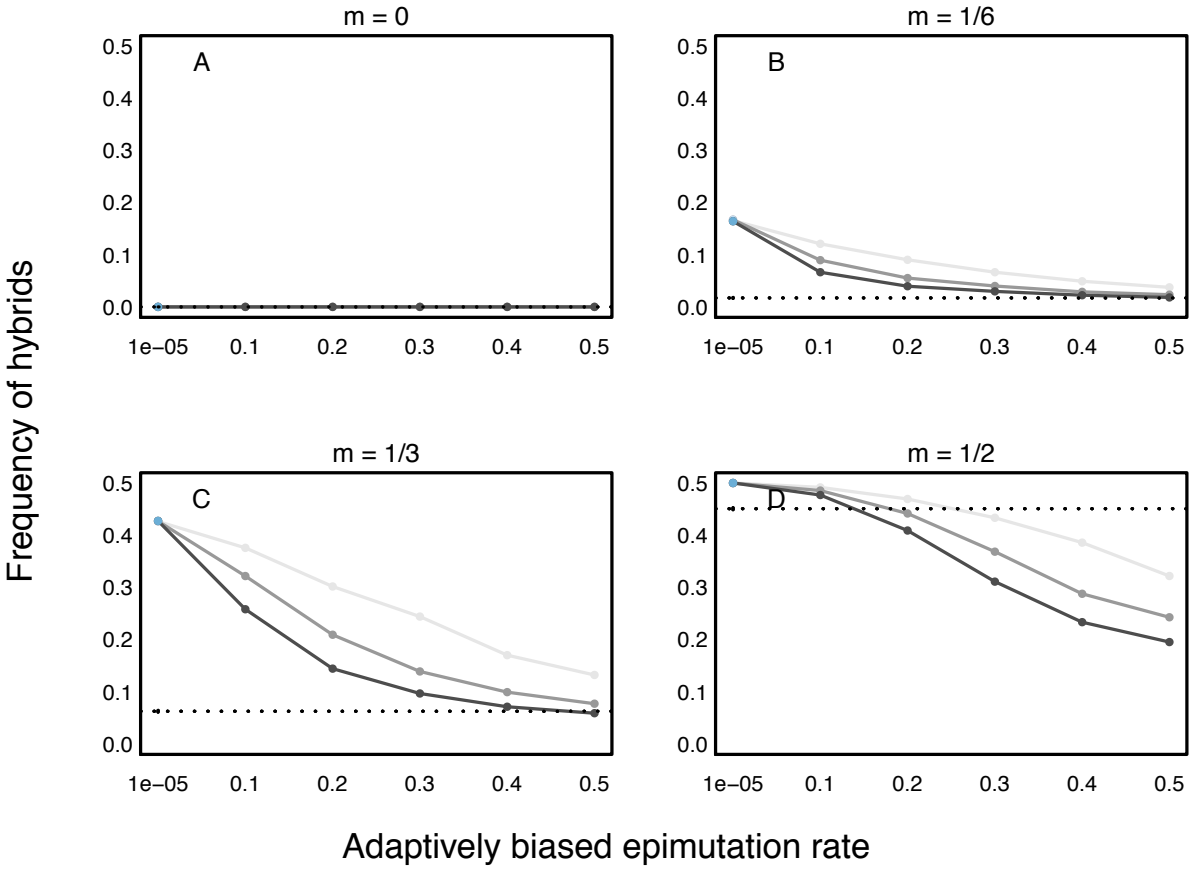

Figure S6: Mean hybrid frequency (averaged through time at evenly spaced time points) is generally lower for higher rates of adaptively-biased epimutation ($\mu_{\text{epi;A}}$) under our core model. Points show mean hybrid frequency when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows hybrid frequency for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black).

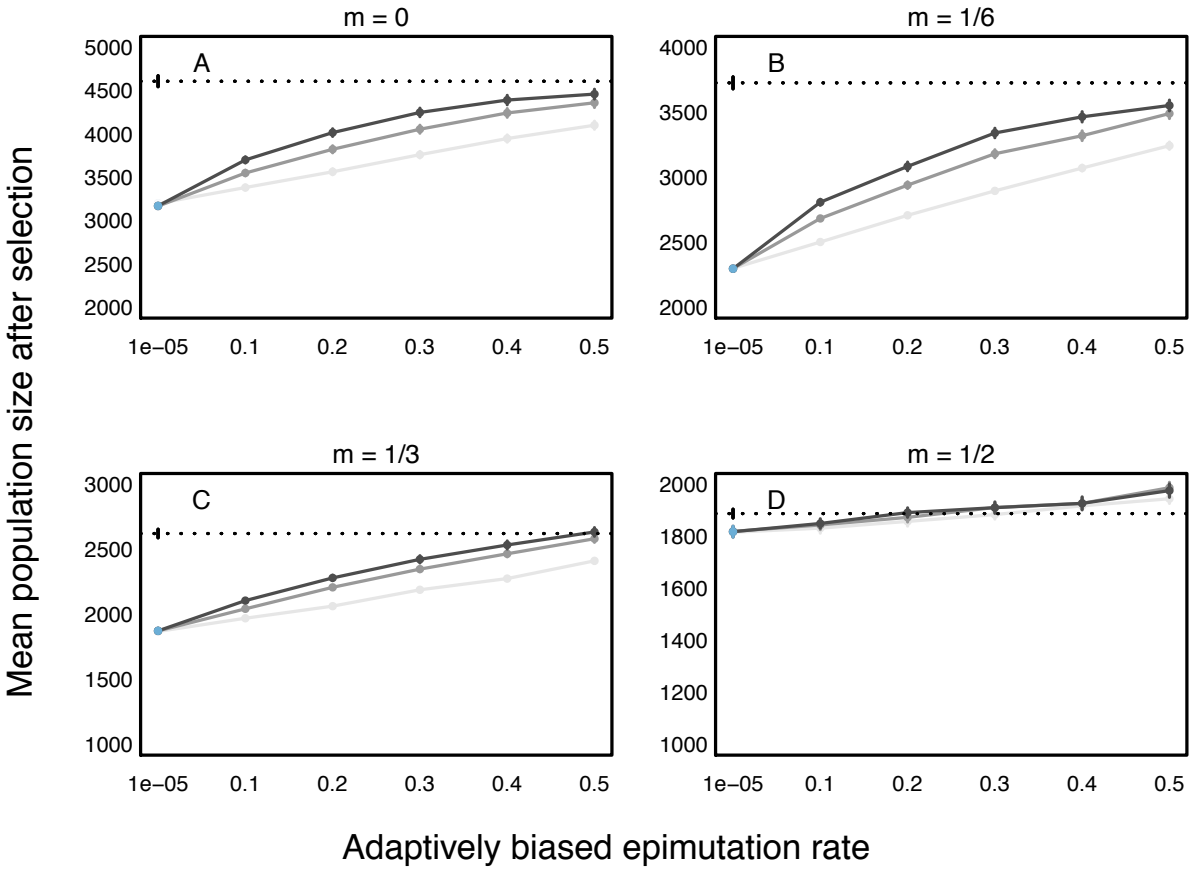

Figure S7: Mean population size after selection (averaged through time at evenly spaced time points) varies with adaptively-biased epimutation rate ($\mu_{\text{epi;A}}$), demonstrating the bottlenecking that recurrently occurs under hard selection. Points show mean population size when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows mean population size for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

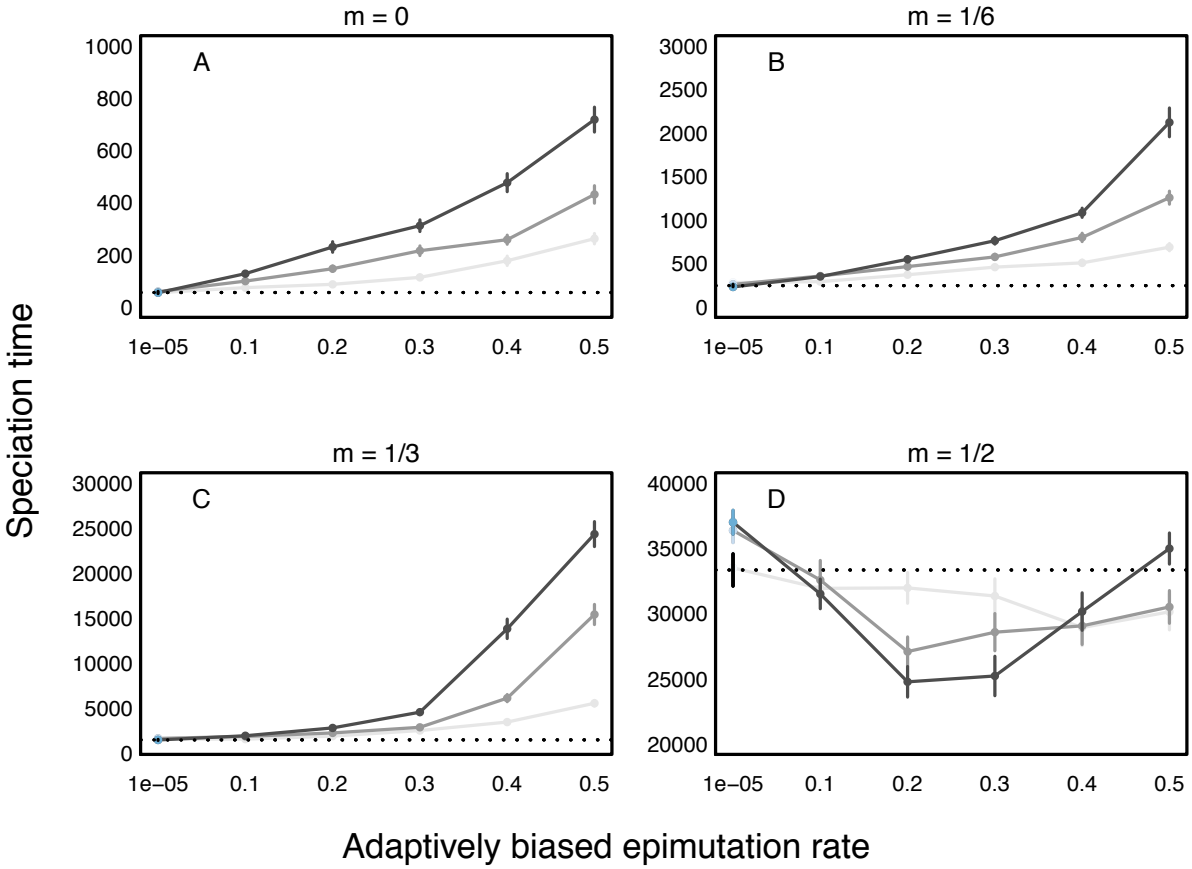

Figure S8: Time to speciation with soft selection under a redundant genotype/epigenotype to phenotype map. Points show mean speciation time when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Other parameters values were as listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

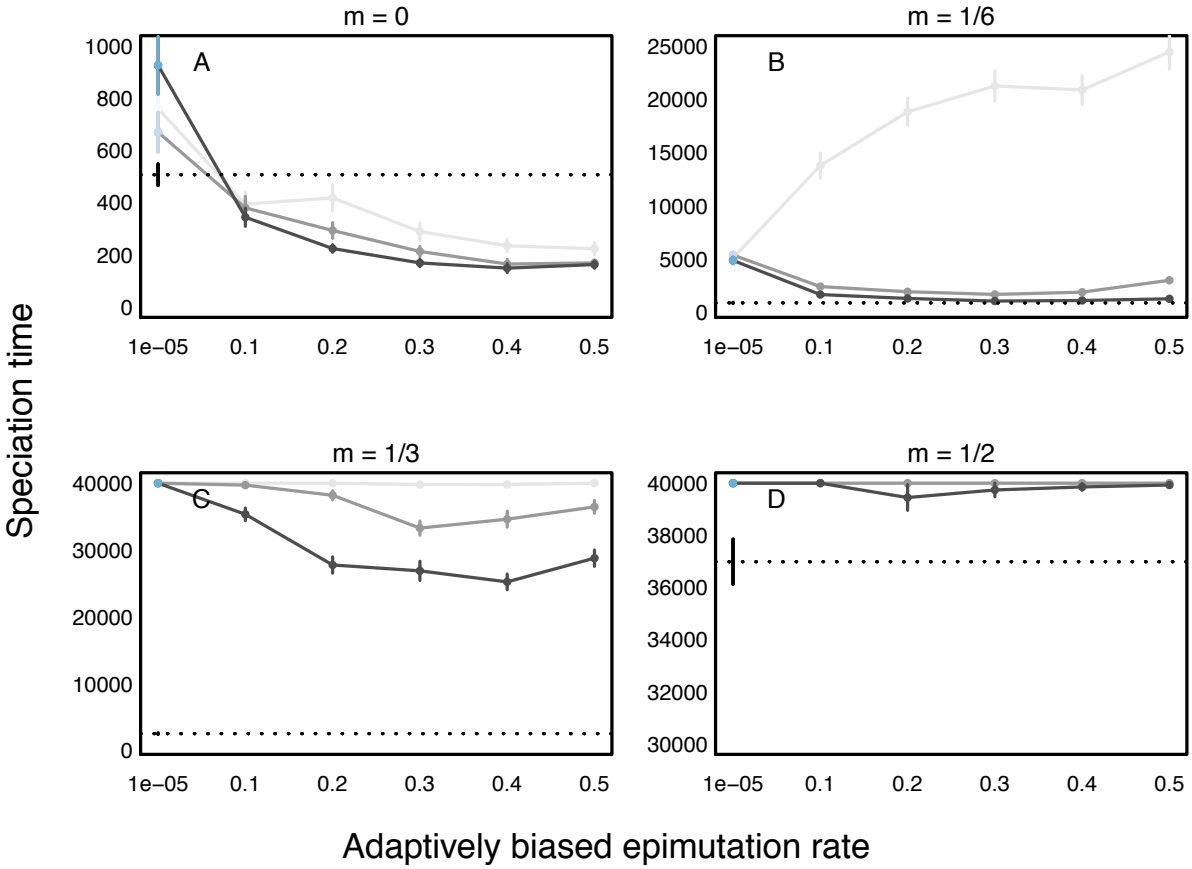

Figure S9: Time to speciation under our core model when genetic and epigenetic mutation happen *after* migration. Points show mean speciation time when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Other parameter values are as listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

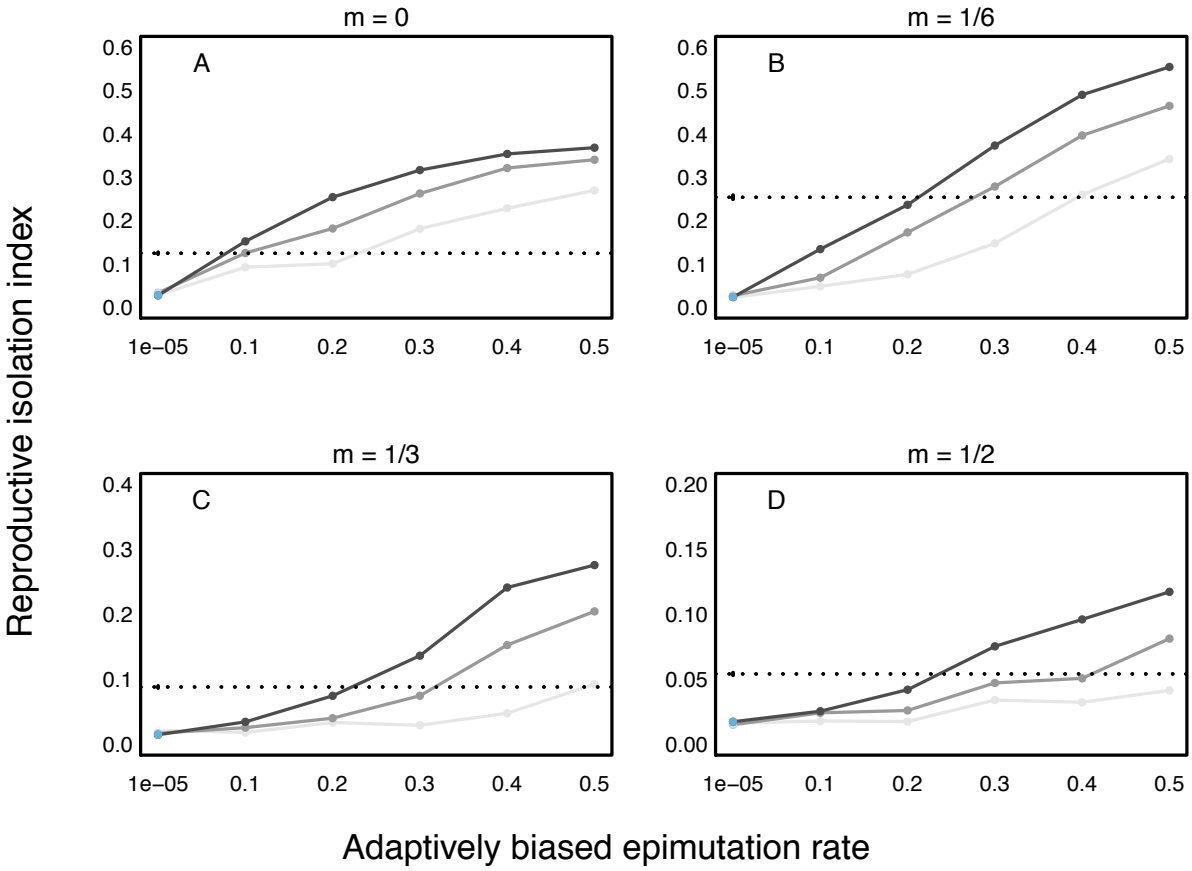

Figure S10: The assortative mating index (averaged through time over the first 1000 time steps at evenly spaced time points) defined in Section S2 under our core model. Points show mean index when epigentic induction is adaptively biased (black) or unbiased (blue; adaptively biased epimutation rate and maladaptive epimutation rate are both equal to 10^{-5} for left-most points); error bars denote standard error. Each point represents the average over 35 replicate model runs. The dotted line shows the index for a model with 20 genetic loci and no epigenetic loci, and its standard error is displayed as a bar on the left side. Other parameters values are as listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

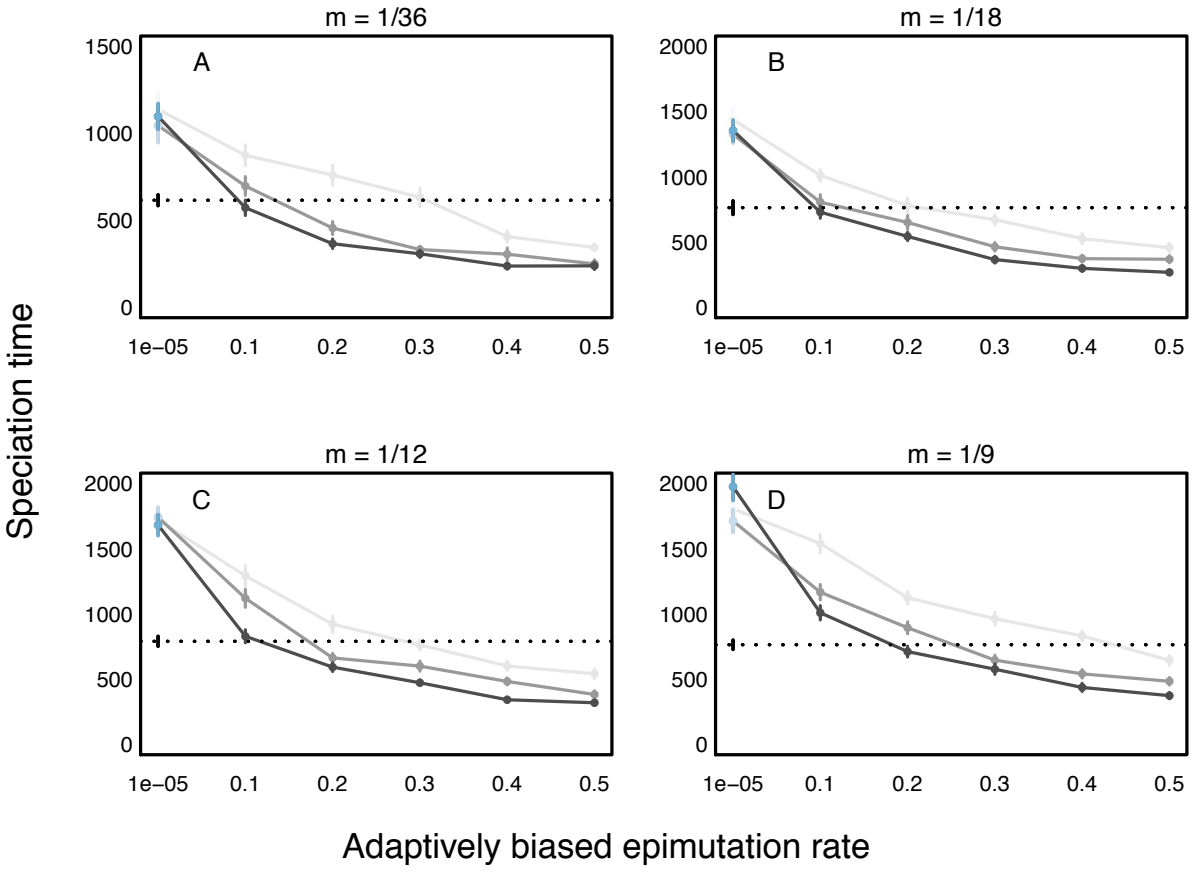

Figure S11: Analog of Fig. 2, but with lower migration rates. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci. Note the differing scales for the y-axes among panels.

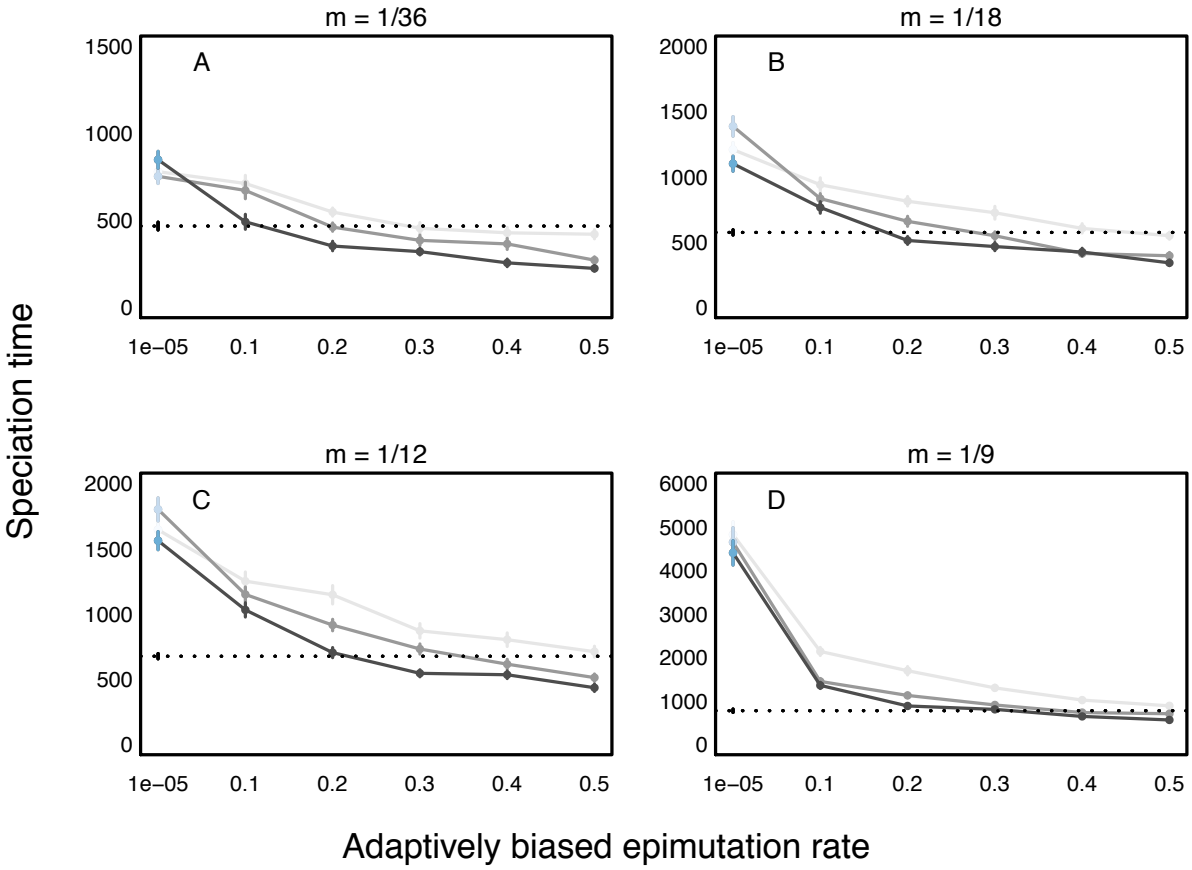

Figure S12: Analog of Fig. S4, but with lower migration rates. Parameters values are listed in Table 1, except $\sigma = 0.4$, with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci. Note the differing scales for the y-axes among panels.

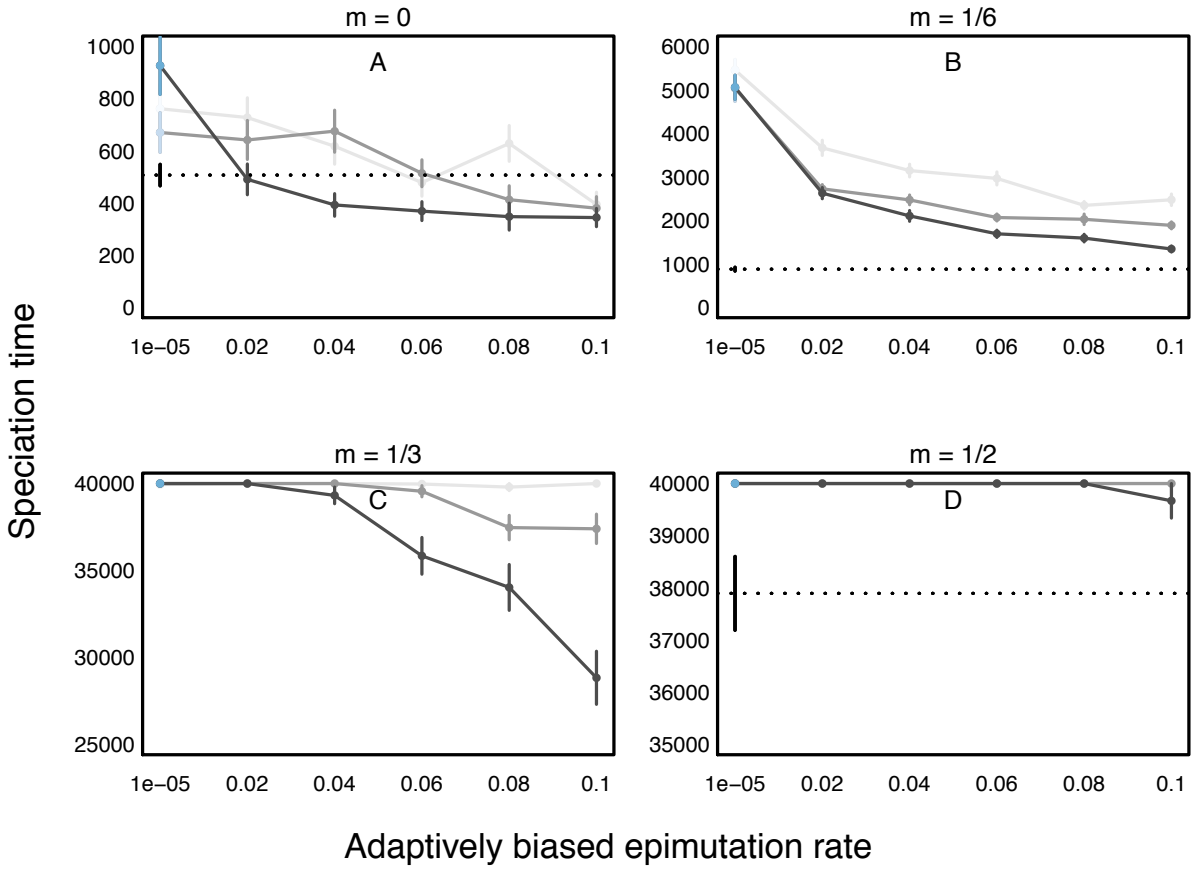

Figure S13: Analog of Fig. 2, but with smaller values of the adaptively biased epimutation rate. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci. Note the differing scales for the y-axes among panels.

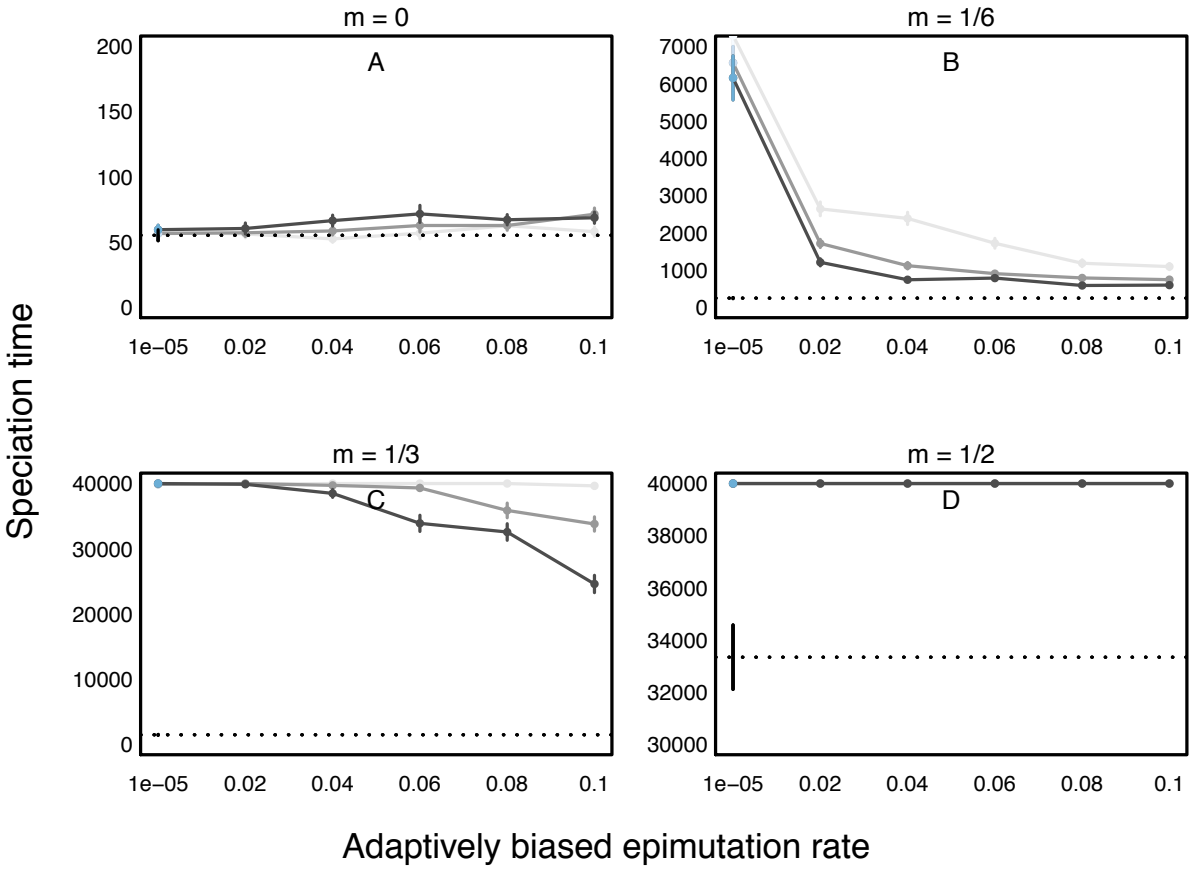

Figure S14: Analog of Fig. 4 (soft selection scenario), but with smaller values of the adaptively biased epimutation rate. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

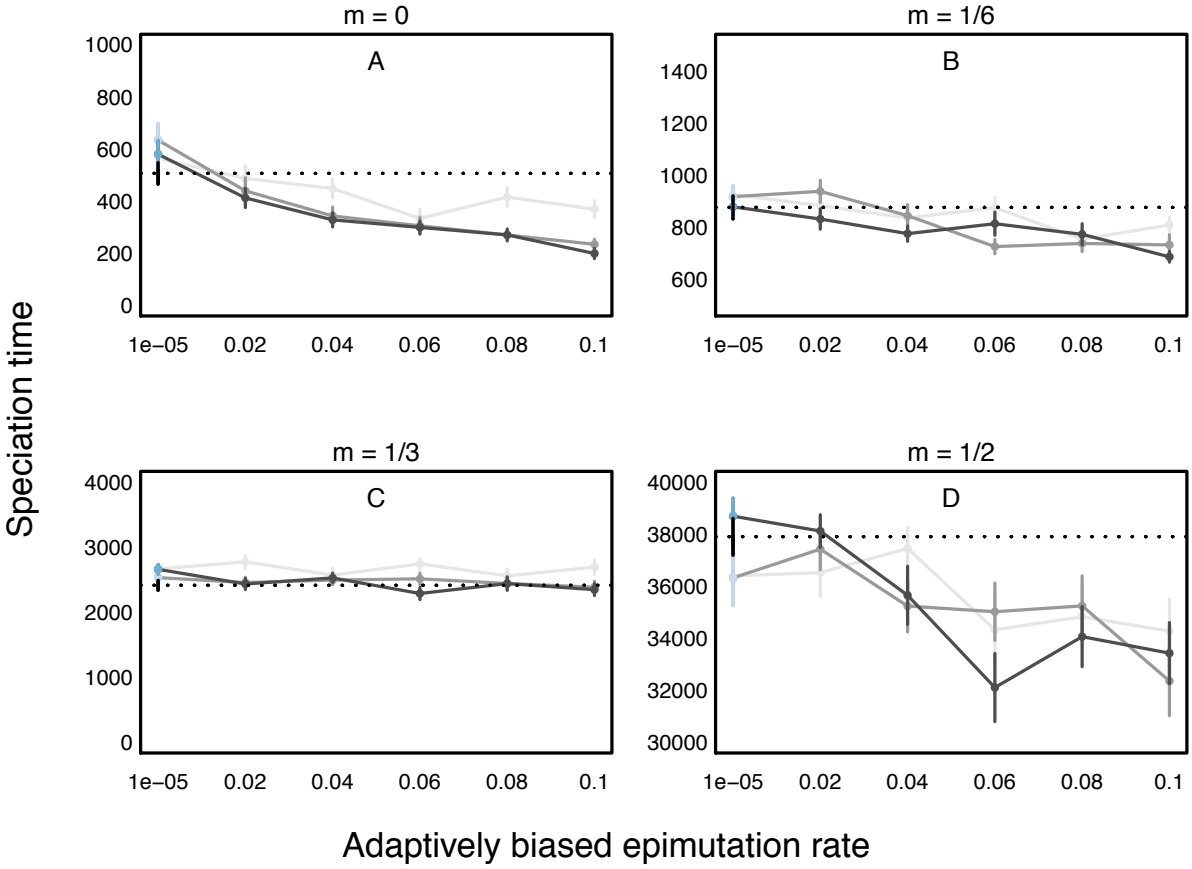

Figure S15: Analog of Fig. 5 (redundant map), but with smaller values of the adaptively biased epimutation rate. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

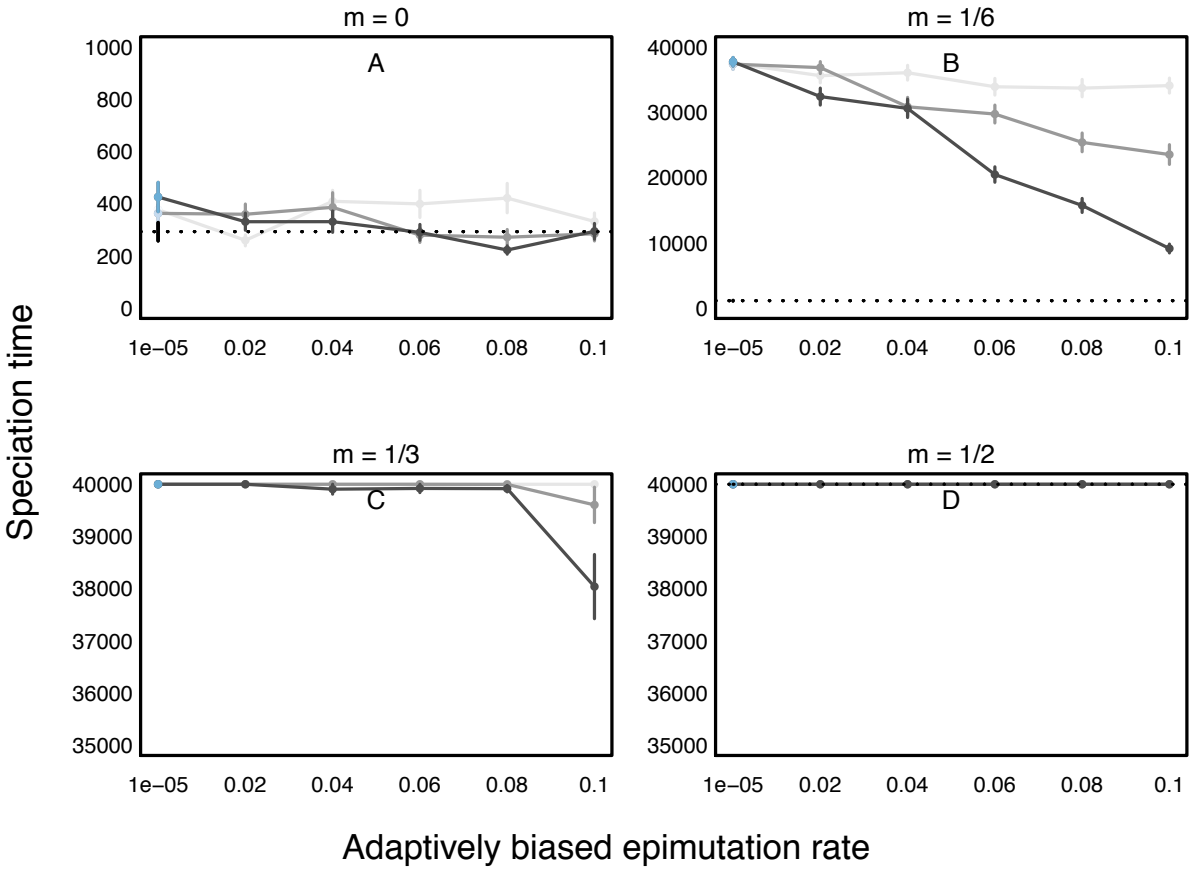

Figure S16: Analog of Fig. S4 (weak selection case), but with smaller values of the adaptively biased epimutation rate. The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci. Parameters values are listed in Table 1, except $\sigma = 0.4$, with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

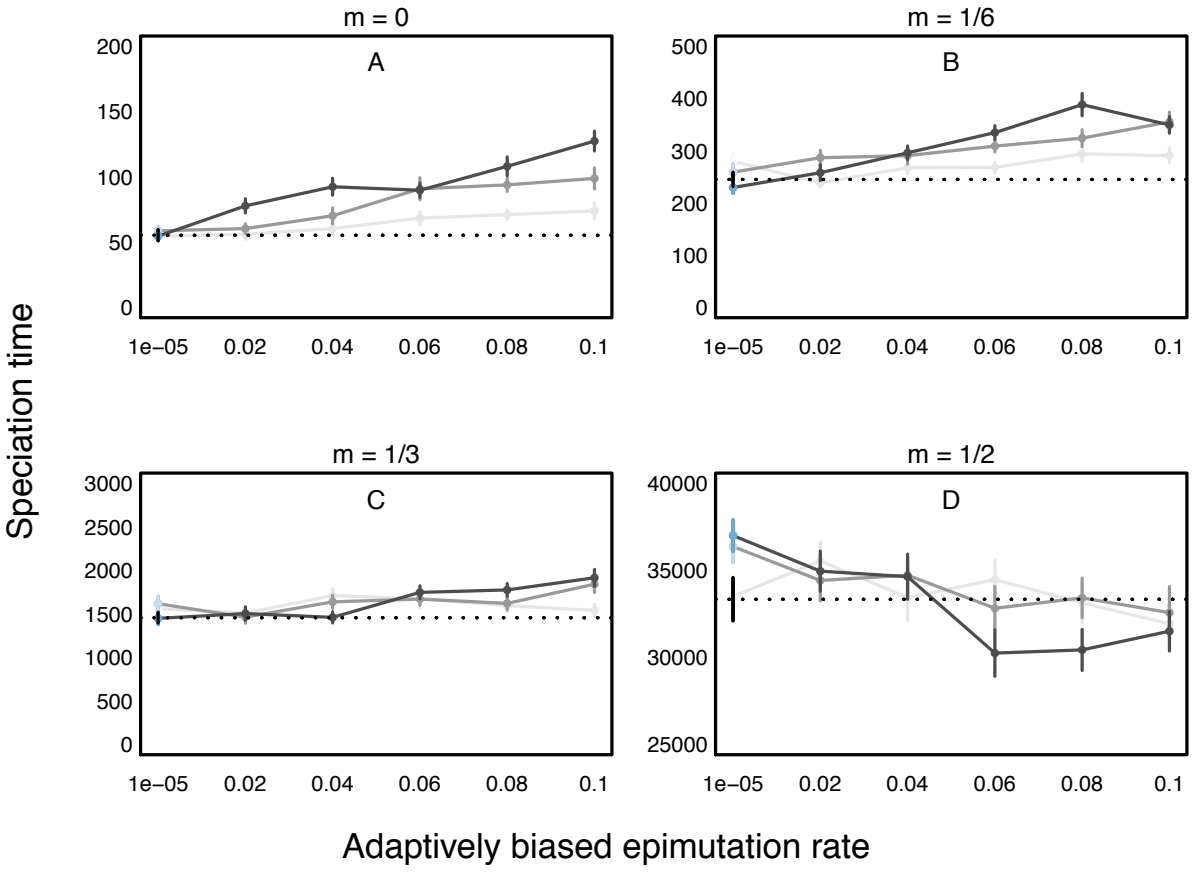

Figure S17: Analog of Fig. S8 (redundant map and soft selection), but with smaller values of the adaptively biased epimutation rate. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.

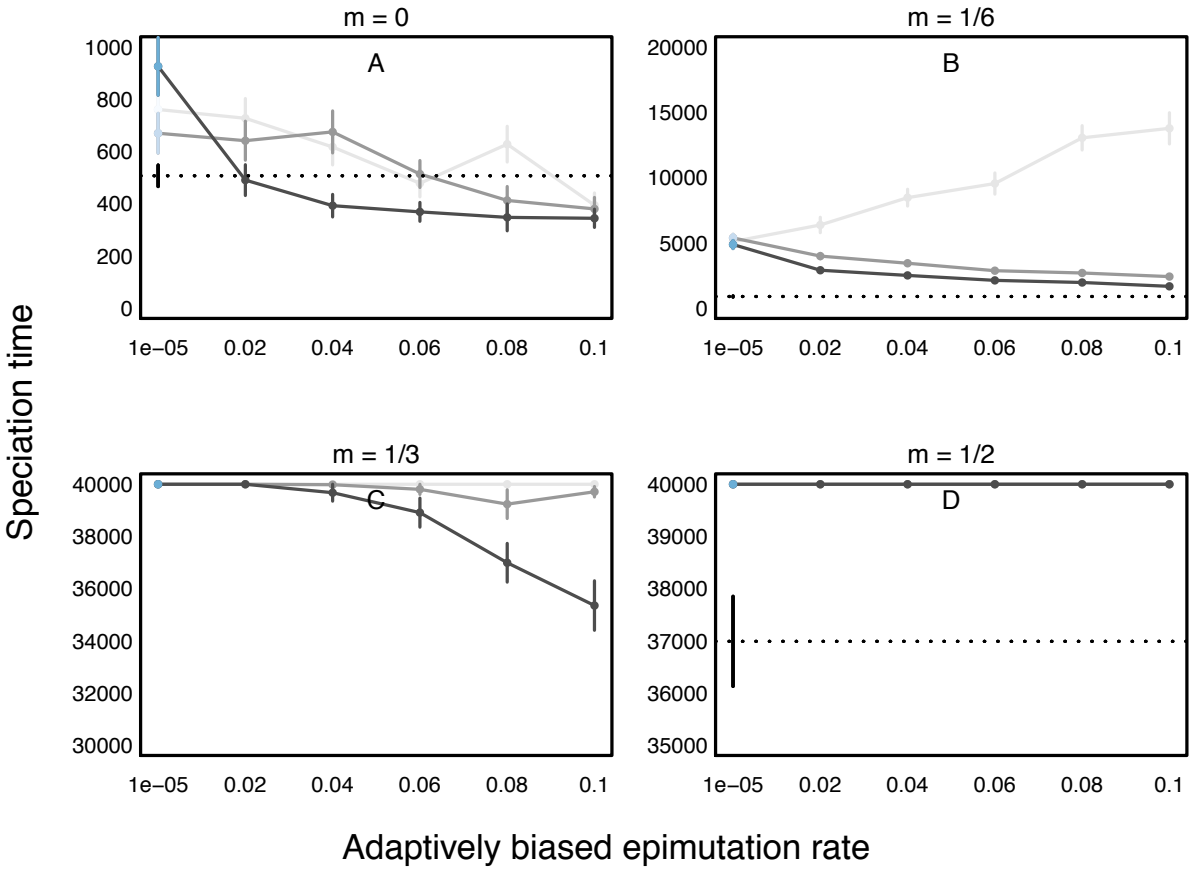

Figure S18: Analog of Fig. S9 (mutation after migration), but with smaller values of the adaptively biased epimutation rate. The dotted line shows the time to speciation for a model with 20 genetic loci and no epigenetic loci. Parameters values are listed in Table 1 with $\tau = 1$ (light grey), $\tau = 2$ (dark grey) and $\tau = 3$ (black). Note the differing scales for the y-axes among panels.