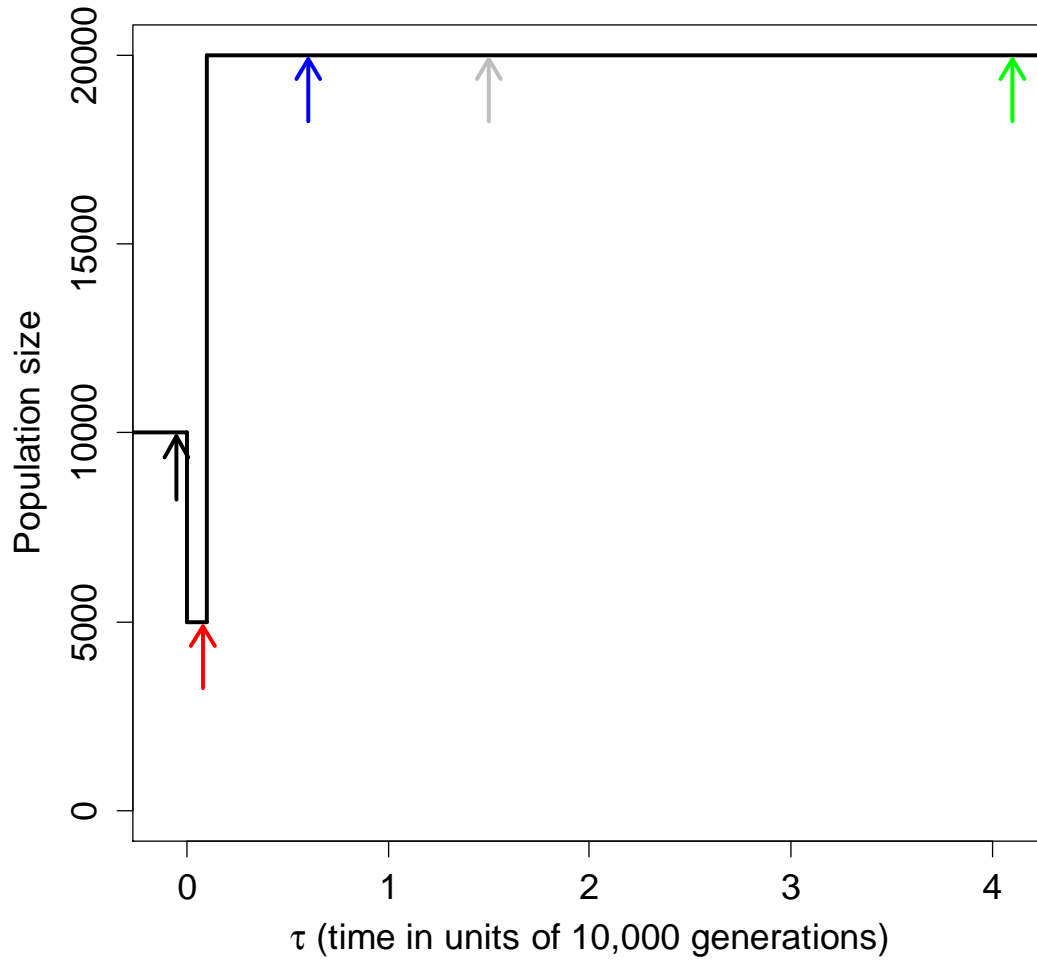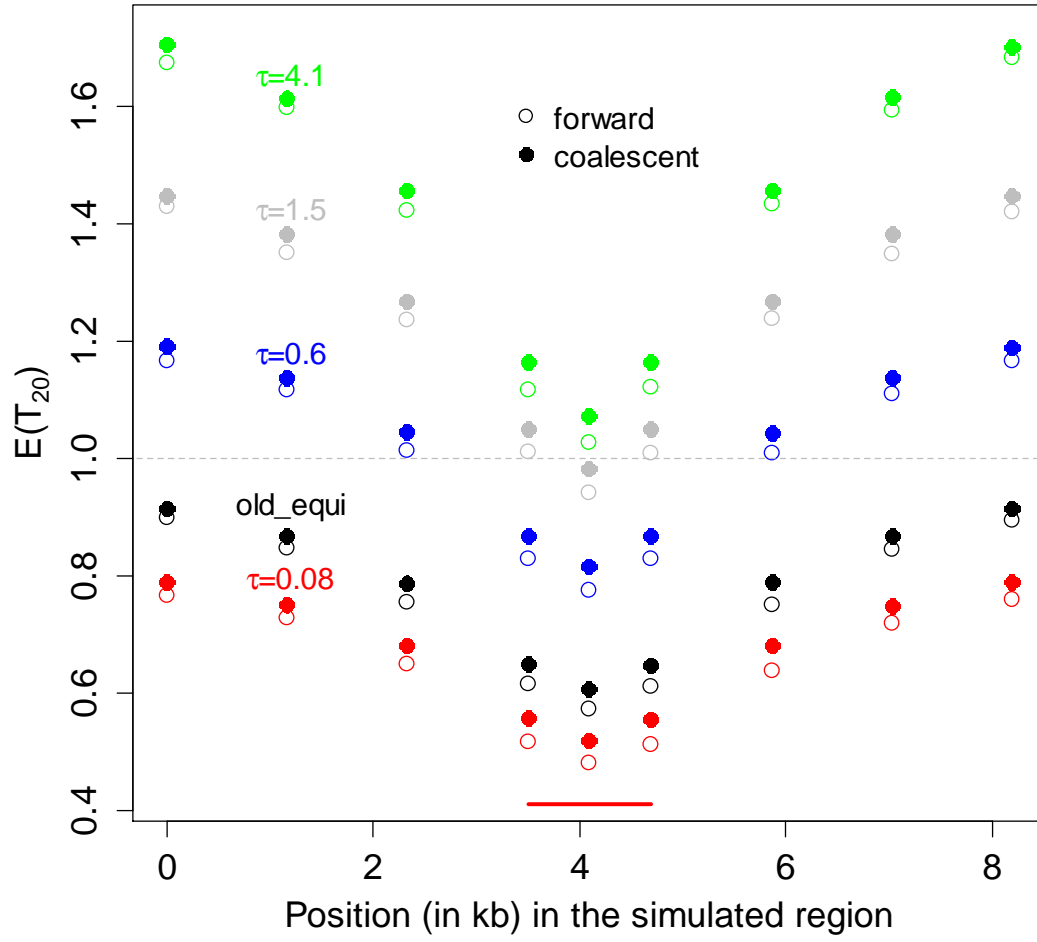**Figure S1 - Patterns of diversity in a region under background selection during the course of a population bottleneck event.** Initially, the population is at equilibrium with $N = 10,000$. Let τ denote time measured in units of 10,000 generations. As shown by (A), the population size decreases instantly to 5,000 at $\tau = 0$ and increases instantly to 20,000 at $\tau = 0.1$. Random samples of size 20 were simulated at the five time points indicated by the coloured arrows in (A). The simulated region is composed of a centrally-located selected region (1,200 sites in length, as indicated by the horizontal red lines in (B) and (C)) and two flanking, neutrally evolving regions (3,500 sites each). All sites in the selected region are subject to selection (i.e., $K = 1$, $L = L_1 = 1,200$). Scaling by $N = 10,000$, we have $\gamma = 12$ and $\theta = 0.01$/site. The per-site recombination rate r is equal to $0.5u$. Estimates of $E(T_{20})$ and $E(\xi_{20})$ are shown in (B) and (C), respectively. In these two plots, open and filled symbols indicate results obtained from forward and coalescent simulations, respectively.

A.

B.

C.

Figure with x-axis "Position (in kb) in the simulated region" and y-axis $E(\xi_{20})$. Labels on plot: τ=0.6, τ=1.5, old_equi, τ=4.1, τ=0.08. Legend: ○ forward, ● coalescent.
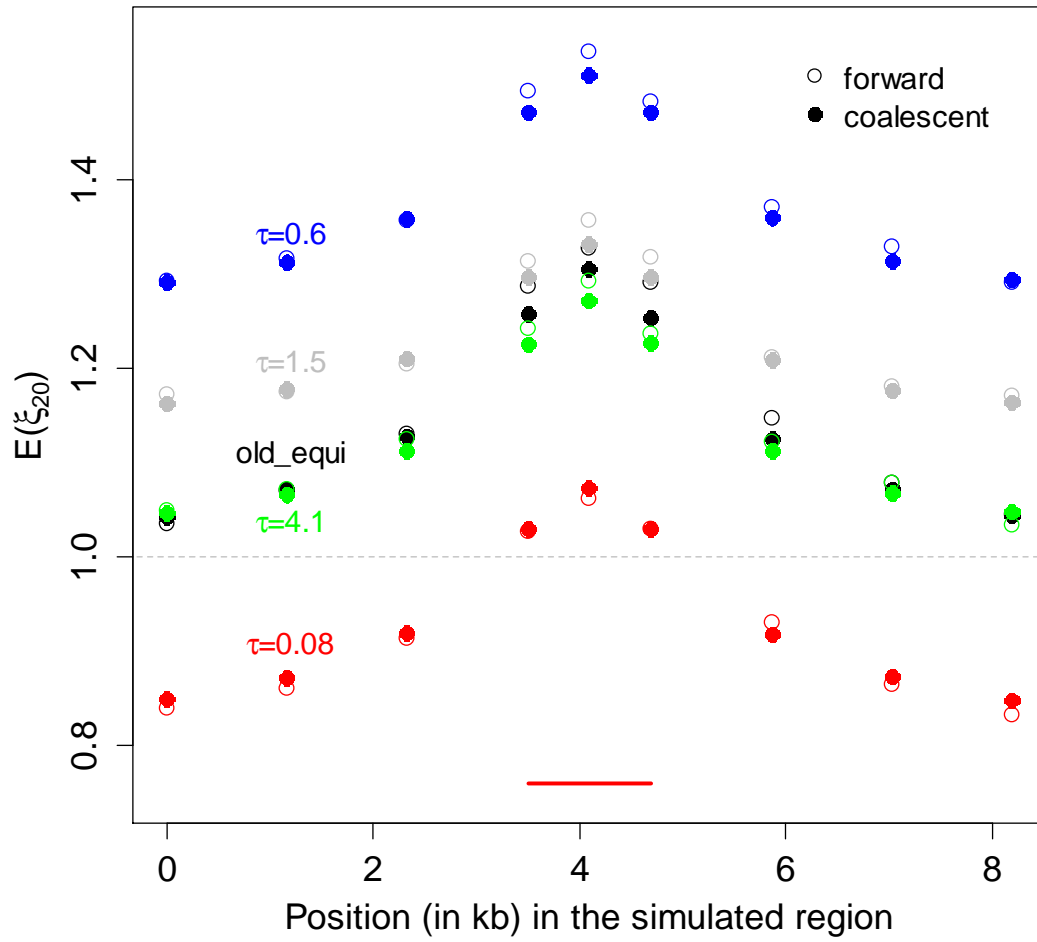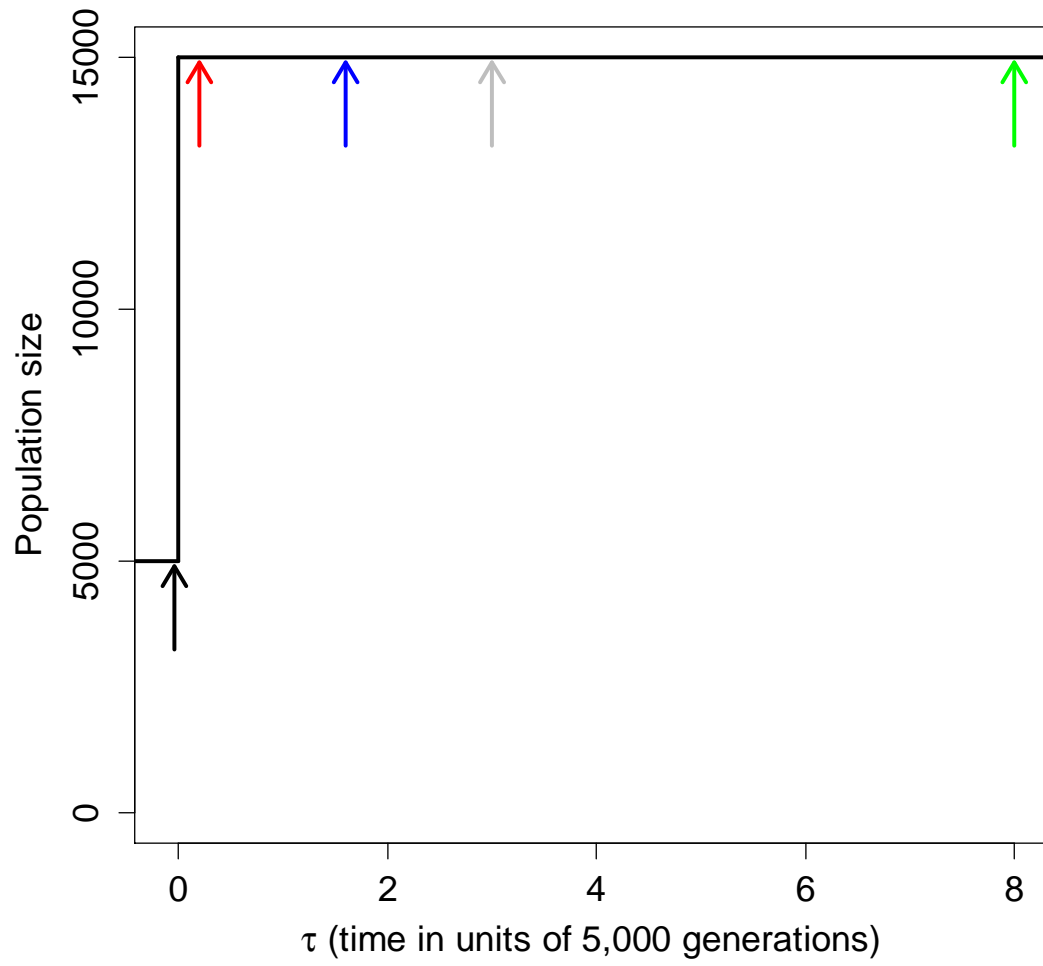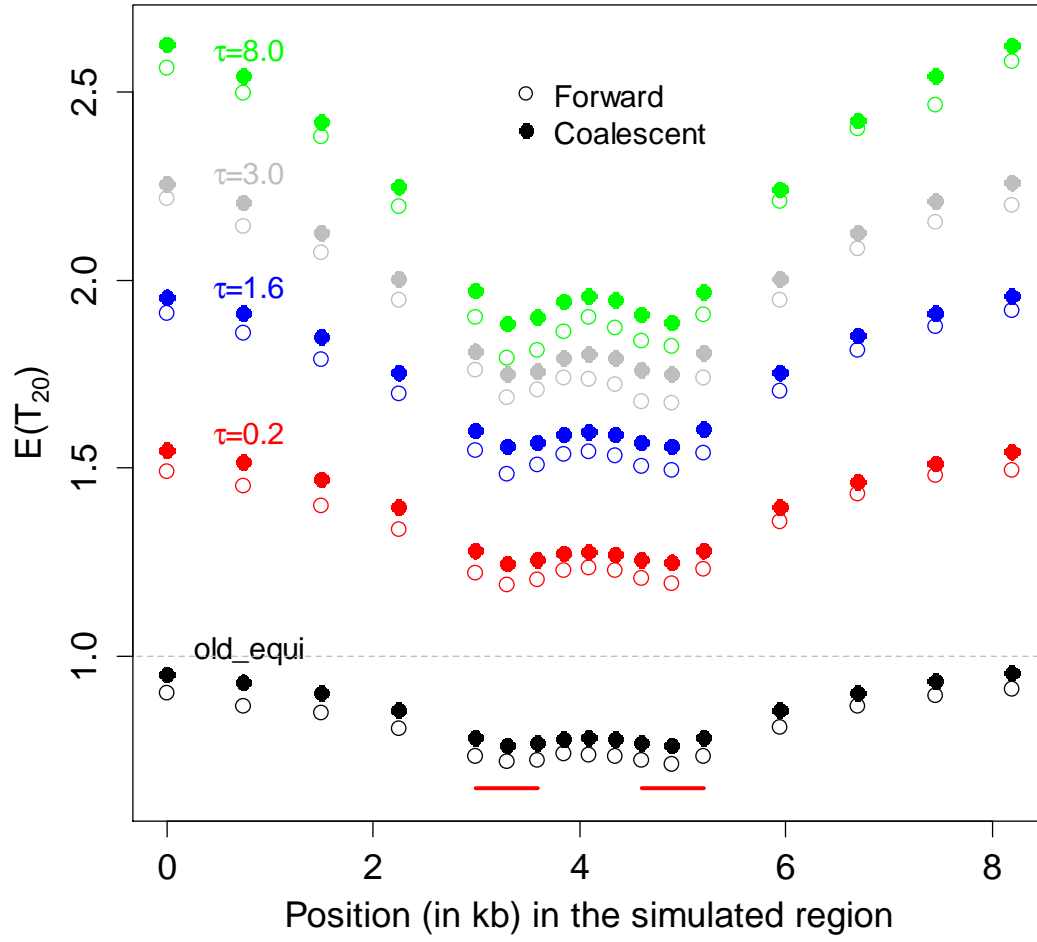
Figure S2 - Patterns of diversity in a region under background selection during the course of a population expansion event. Initially, the population is at equilibrium with N = 5,000. Let τ denote time measured in units of 5,000 generations. As shown by (A), the population size increases instantly to 15,000 at τ = 0. Random samples of size 20 were simulated at the five time points indicated by the coloured arrows in (A). The simulated region is composed of two selected regions (indicated by the horizontal red lines in (B) and (C)), two flanking neutral regions (3,000 sites each) and one centrally-located neutral region (1,000 sites in length). The two selected regions are equal in length, with 600 sites each. All sites in the selected region are subject to selection. Scaling by N = 5,000, we have γ = 6 and θ = 0.005/site. The per-site recombination rate r is equal to $0.5u$. Estimates of $E(T_{20})$ and $E(\xi_{20})$ are shown in (B) and (C), respectively. In these two plots, open and filled symbols indicate results obtained from forward and coalescent simulations, respectively.
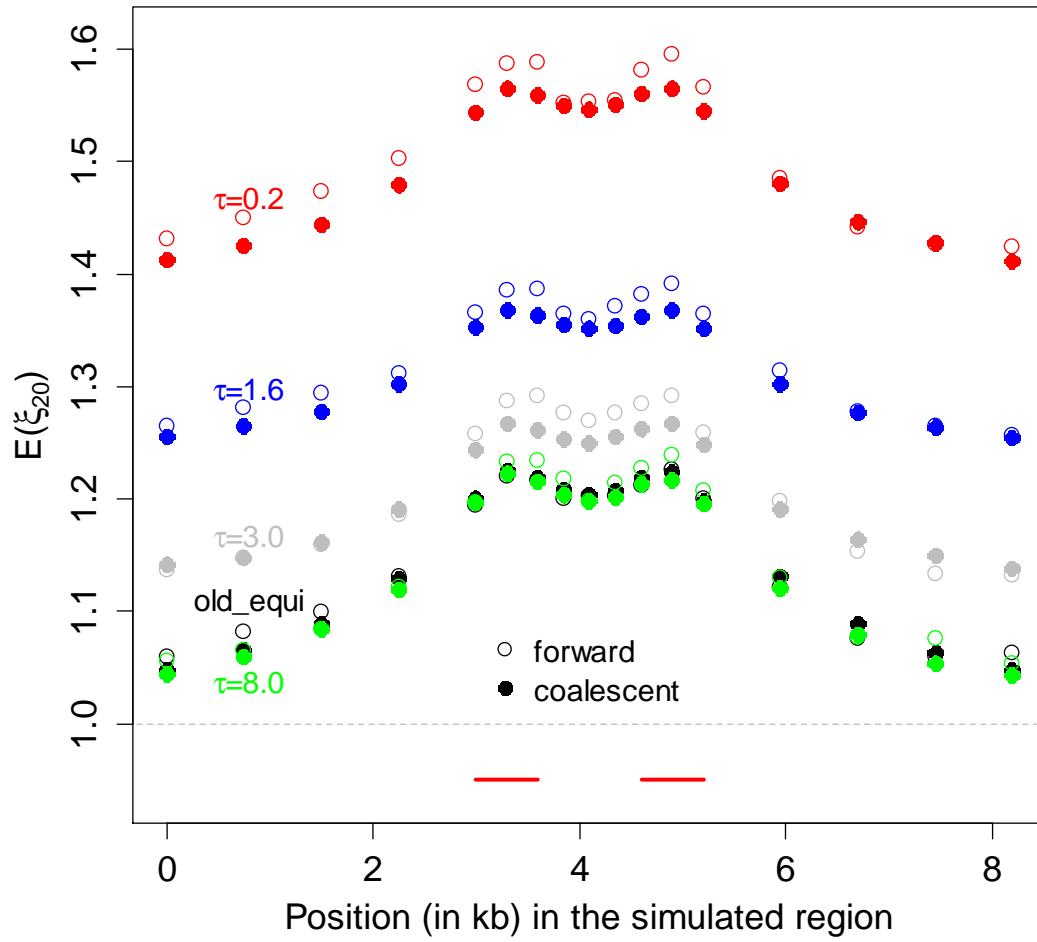
A.

B.

C.

Figure S3 - Patterns of diversity in a region under background selection during the course of a population shrinkage event. Initially, the population is at equilibrium with $N = 10,000$. Let τ denote time measured in units of 10,000 generations. As shown by (A), the population size decreases instantly to 5,000 at $\tau = 0$. Random samples of size 20 were simulated at the three time points indicated by the coloured arrows in (A). The simulated region is composed of one centrally-located selected region (1,200 sites in length, as indicated by the horizontal red lines in (B) and (C)) and two flanking neutral regions (3,500 sites each). All sites in the selected region are subject to selection. Scaling by $N = 10,000$, we have $\gamma = 12$ and $\theta = 0.01$/site. The per-site recombination rate r is equal to $0.5u$. Estimates of $E(T_{20})$ and $E(\xi_{20})$ are shown in (B) and (C), respectively. In these two plots, open and filled symbols indicate results obtained from forward and coalescent simulations, respectively.
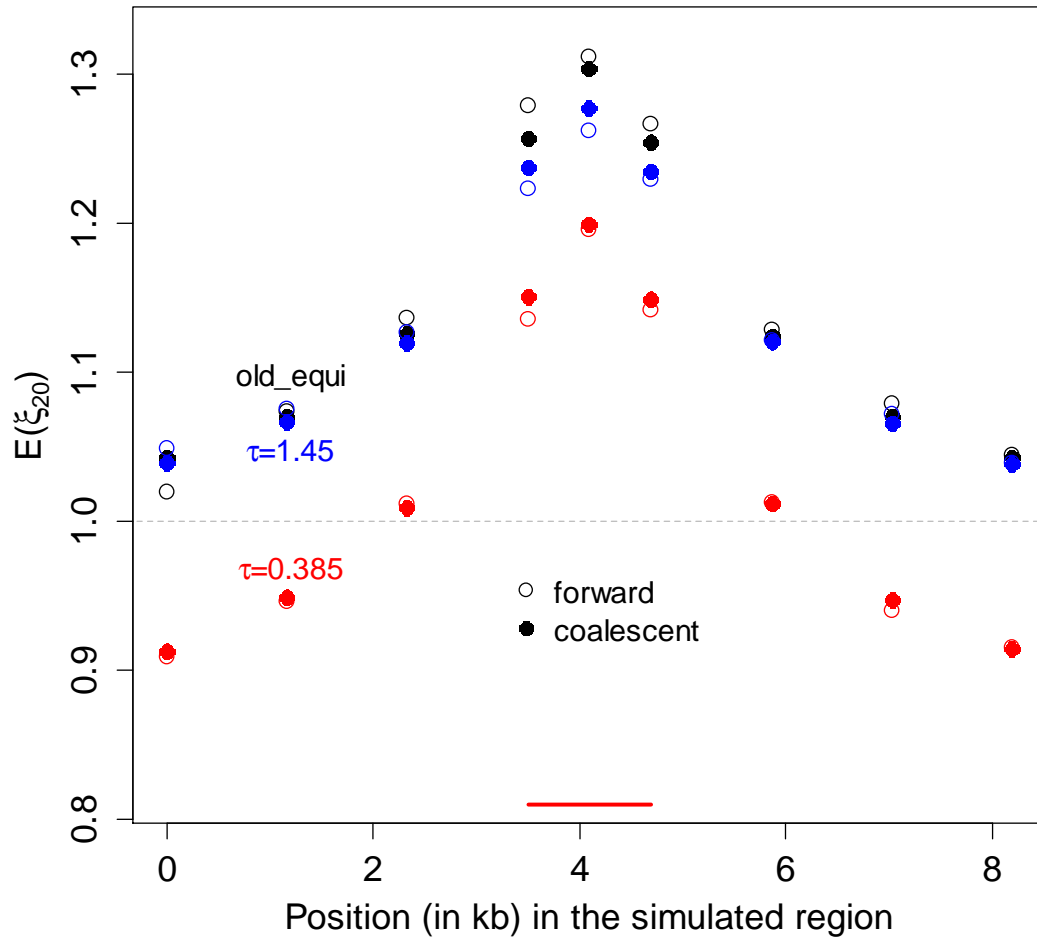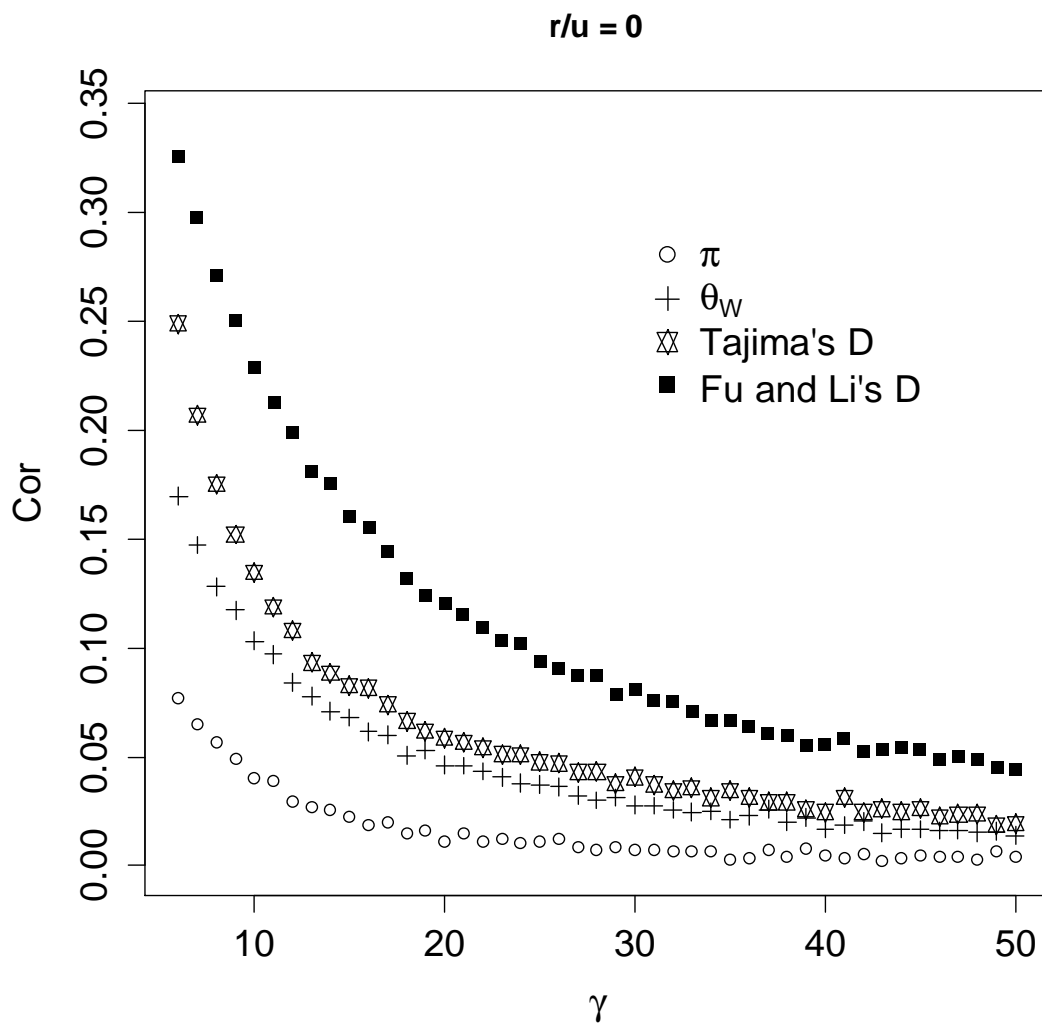
A.
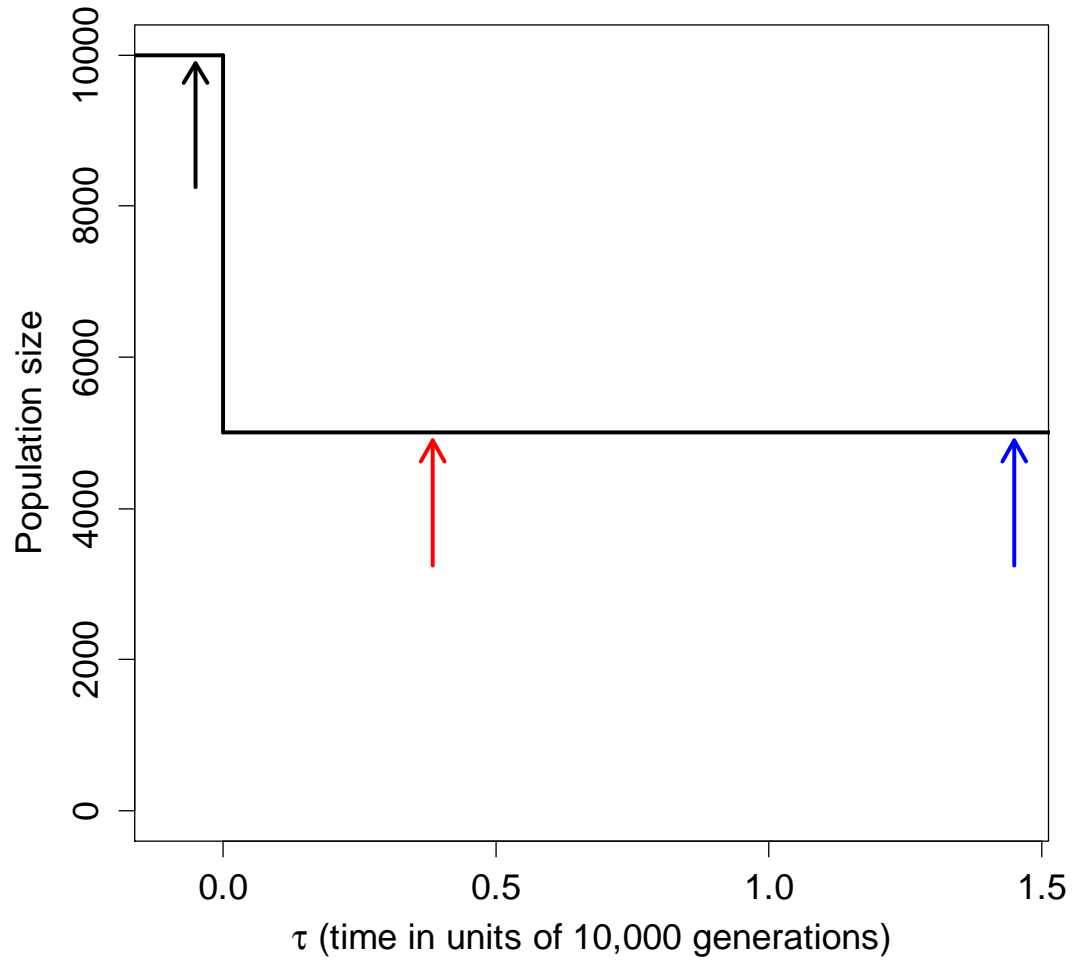
B.
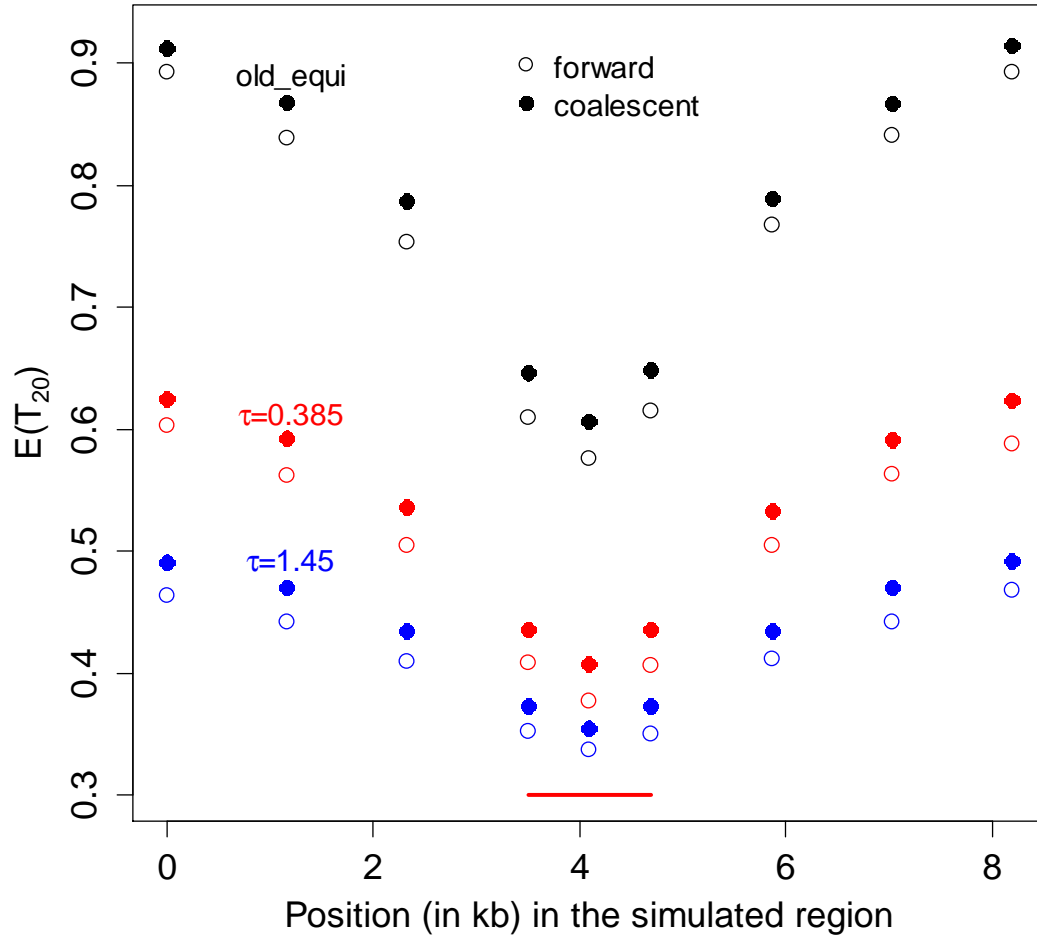
C.

Figure S4 - Correlation coefficients between summary statistics calculated using selected and neutral variants. The model described in Table 3 was simulated using the coalescent model. Two levels of recombination, $r/u = 0$ and 2, were considered. For each parameter combination, 10^5 samples of size 20 were generated and were used to estimate the correlation coefficients. Note that Cor values for π and θ_W for small γ are likely to have been underestimated (see Table 3).

r/u = 2