

Supplementary material

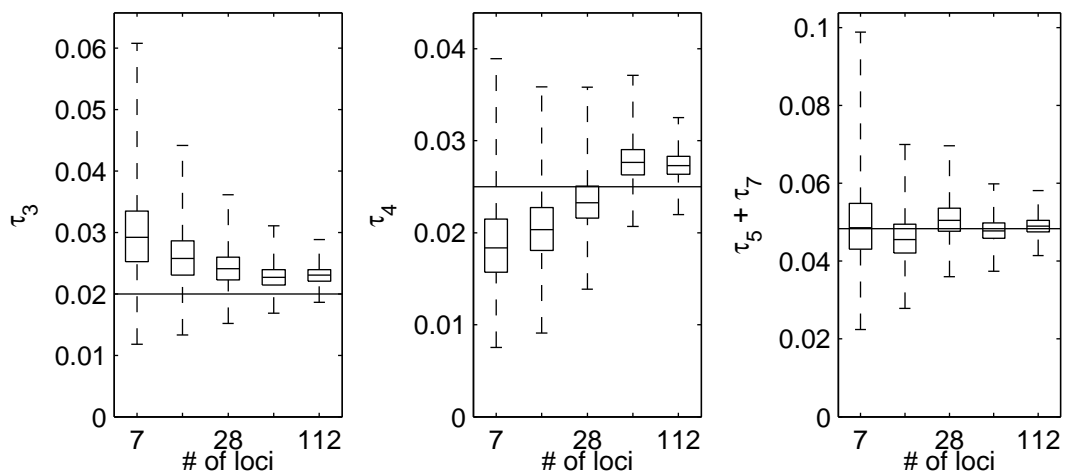


Figure S1. Posterior estimates of the branch lengths for a 3 population subtree with different number of loci. Boxplots of the posterior distributions for the branch lengths τ from the analysis of the simulated data using populations 3, 4 and 5. The number of loci used was 7, 14, 28, 56 and 112. The box depicts the 25 % and 75 % quantiles and the whiskers depict the minimum and maximum among posterior samples. The lengths of the two branches 6 and 8 connected to the root are summed, because the placement of the root is not identifiable under the infinite alleles model. The horizontal line depicts the value used in simulating the data. The subindices for the τ parameters refer to branches in Figure 1A in the main text.

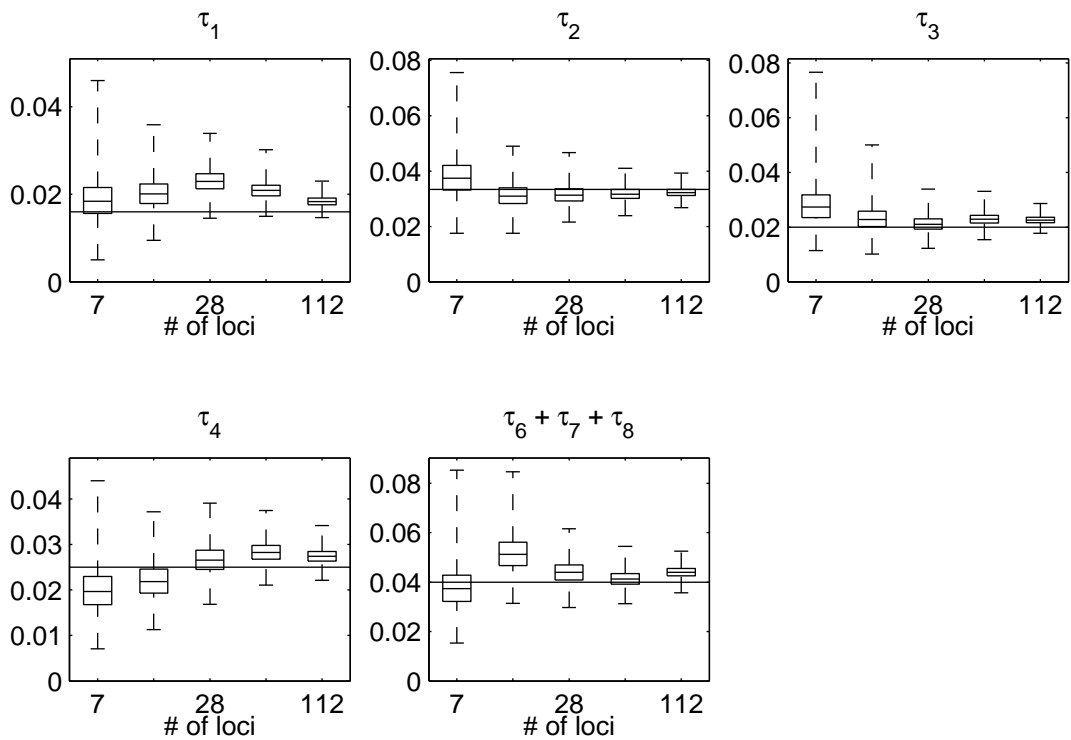


Figure S2. Posterior estimates of the branch lengths for a 4 population subtree with different number of loci. Boxplots of the posterior distributions for the branch lengths τ from the analysis of the simulated data using populations 1, 2,3 and 4. The number of loci used was 7, 14, 28, 56 and 112. The box depicts the 25 % and 75 % quantiles and the whiskers depict the minimum and maximum among posterior samples. The lengths of the two branches 6 and 8 connected to the root are summed, because the placement of the root is not identifiable under the infinite alleles model. The horizontal line depicts the value used in simulating the data. The subindices for the τ parameters refer to branches in Figure 1A in the main text.