

Figure S1: Posterior means and 95% HPD credibility intervals (CI) of parameters under models A and C of Fig. 1 in 10 replicate datasets, each of 10, 100, or 1000 loci, simulated under the parameter combinations: $\varphi = 0.1$, $\theta = 0.001$, and the JC mutation model. The horizontal line represents the true parameter value. Note that there are 13 parameters under model A ($\theta_A, \theta_B, \theta_C, \theta_R, \theta_S, \theta_H, \theta_M, \tau_R, \tau_S, \tau, \tau_H, \tau_M, \tau_S, \varphi$) and 9 under model C ($\theta_A, \theta_B, \theta_C, \theta_R, \theta_S, \theta, \tau_R, \tau_S, \varphi$). Due to the symmetry of the experimental design, the results for some parameters are identical so that only the non-redundant results are shown to save space; for example, θ_A is shown but θ_B is not.

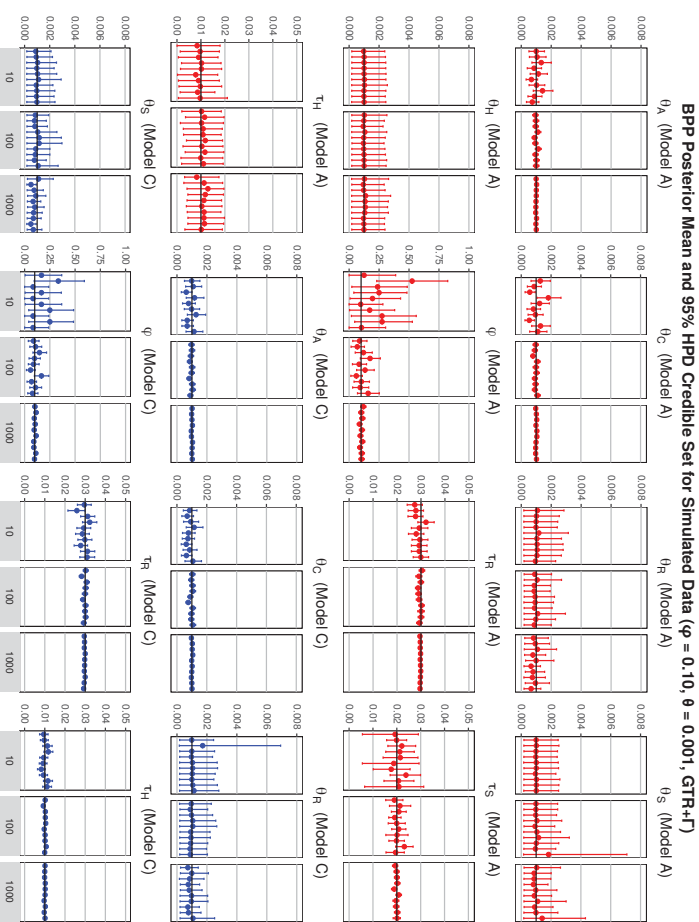


Figure S2: Simulation results for the combination $\varphi = 0.1$, $\theta = 0.001$, and the GTR+I mutation model. See legend to Fig. S1.

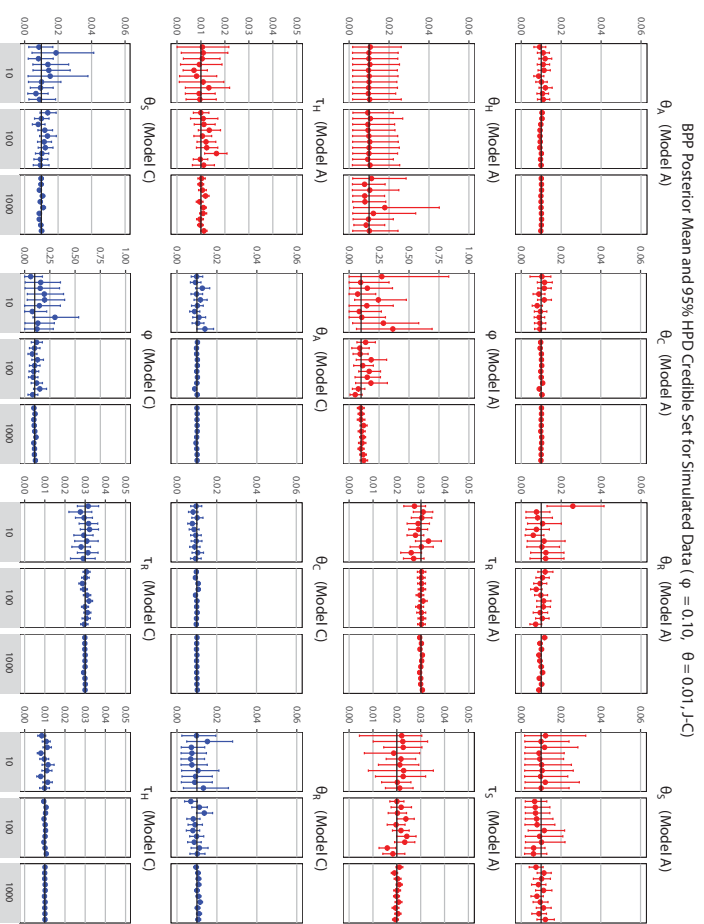


Figure S3: Simulation results for the combination $\varphi = 0.1$, $\theta = 0.01$, and the JC mutation model. See legend to Fig. S1.

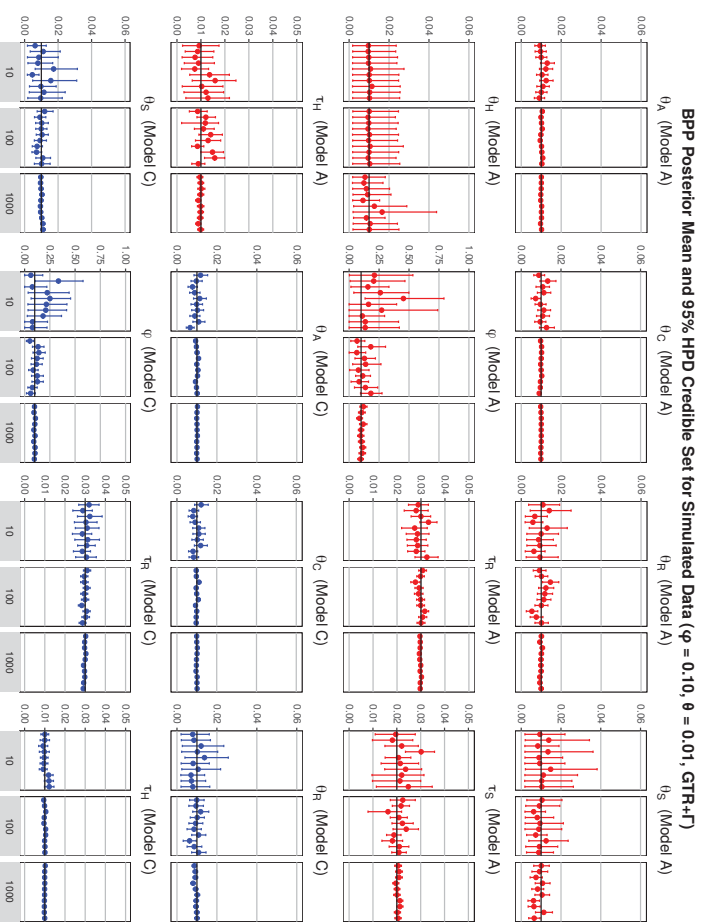


Figure S4: Simulation results for the combination $\varphi = 0.1$, $\theta = 0.01$, and the GTR+I mutation model. See legend to Fig. S1.

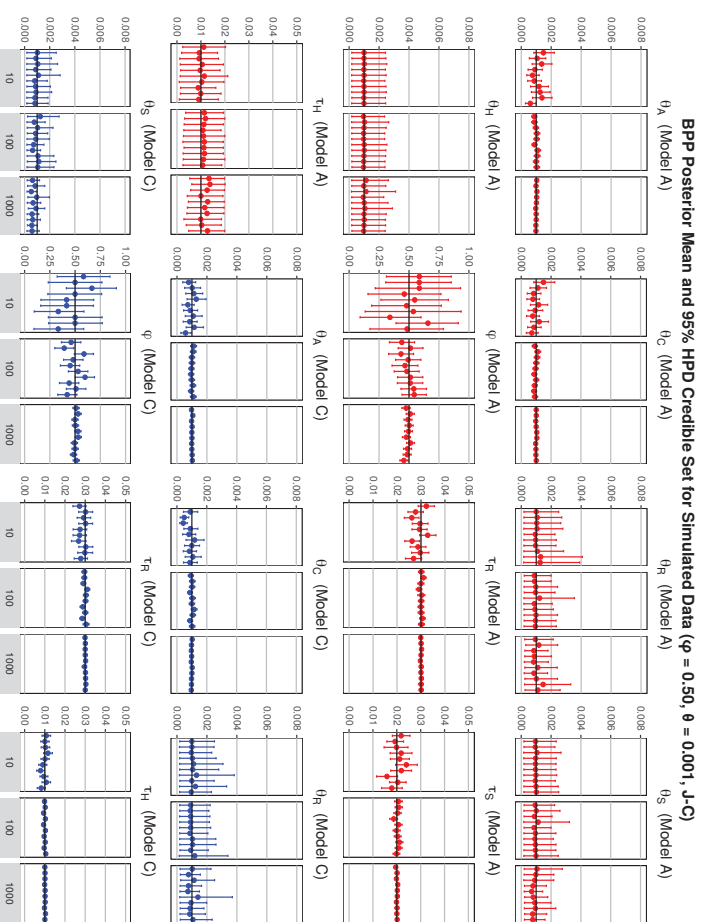


Figure S5: Simulation results for the combination $\varphi = 0.5$, $\theta = 0.001$, and the JC mutation model. See legend to Fig. S1.

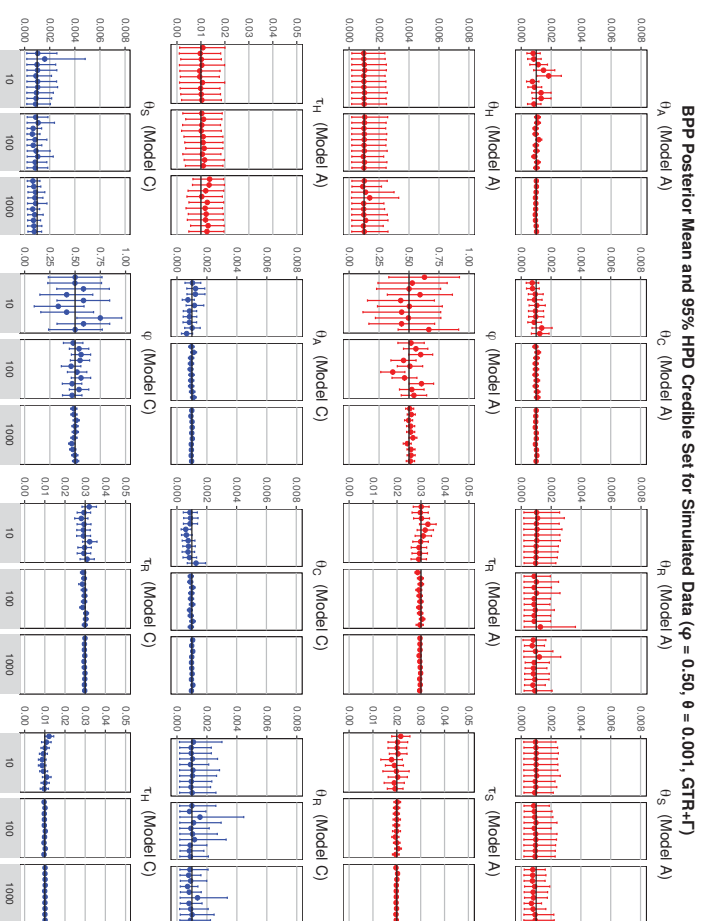


Figure S6: Simulation results for the combination $\varphi = 0.5$, $\theta = 0.001$, and the GTR+I mutation model. See legend to Fig. S1.

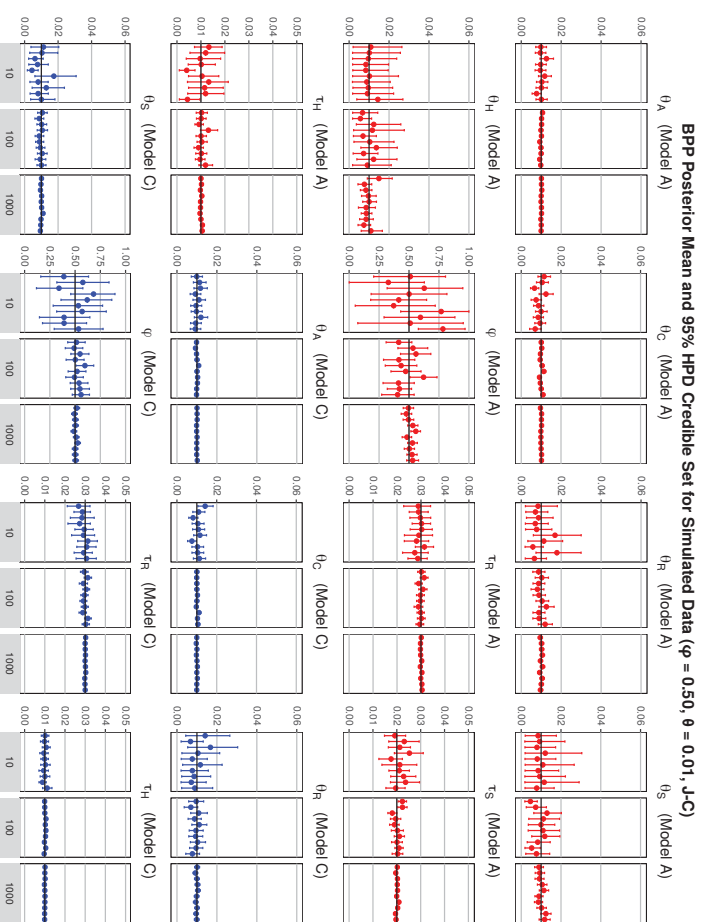


Figure S7: Simulation results for the combination $\varphi = 0.5, \theta = 0.01$, and the JC mutation model. See legend to Fig. S1.

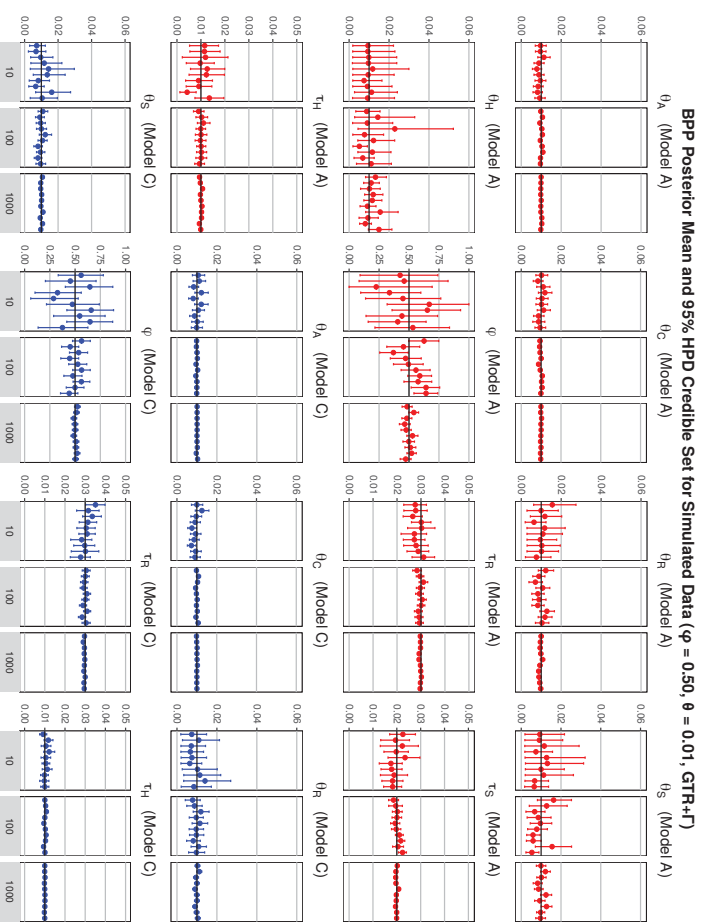


Figure S8: Simulation results for the combination $\varphi = 0.5, \theta = 0.01$, and the GTR+I mutation model. See legend to Fig. S1.

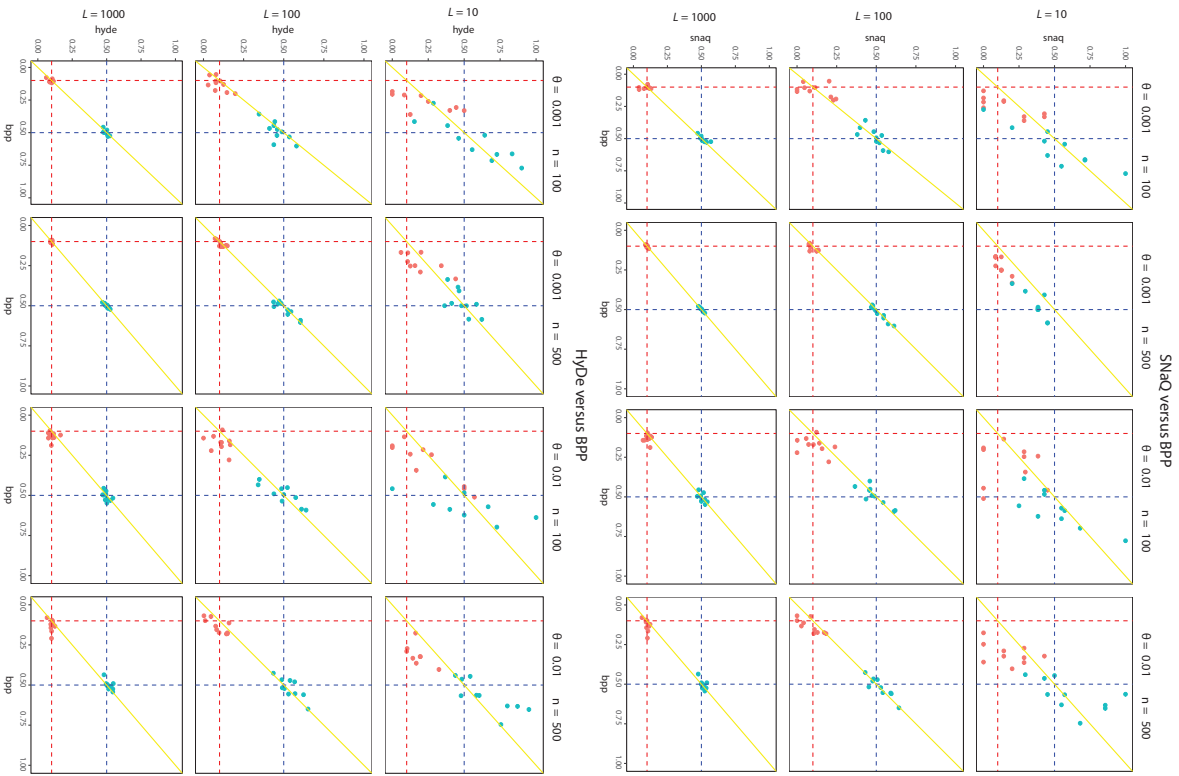


Figure S9: Estimates of φ using SNaQ and HyDe plotted against those from BPP on simulated datasets. Model A for three species (Fig. 1A) was used to simulate 10 replicate datasets, using $\varphi = 0.1$ or 0.5 , $\theta = 0.001$ or 0.01 , the number of loci $L = 10, 100$, or 1000 , and sequence length $n = 100$ or 500 . The dotted lines indicate the true values.

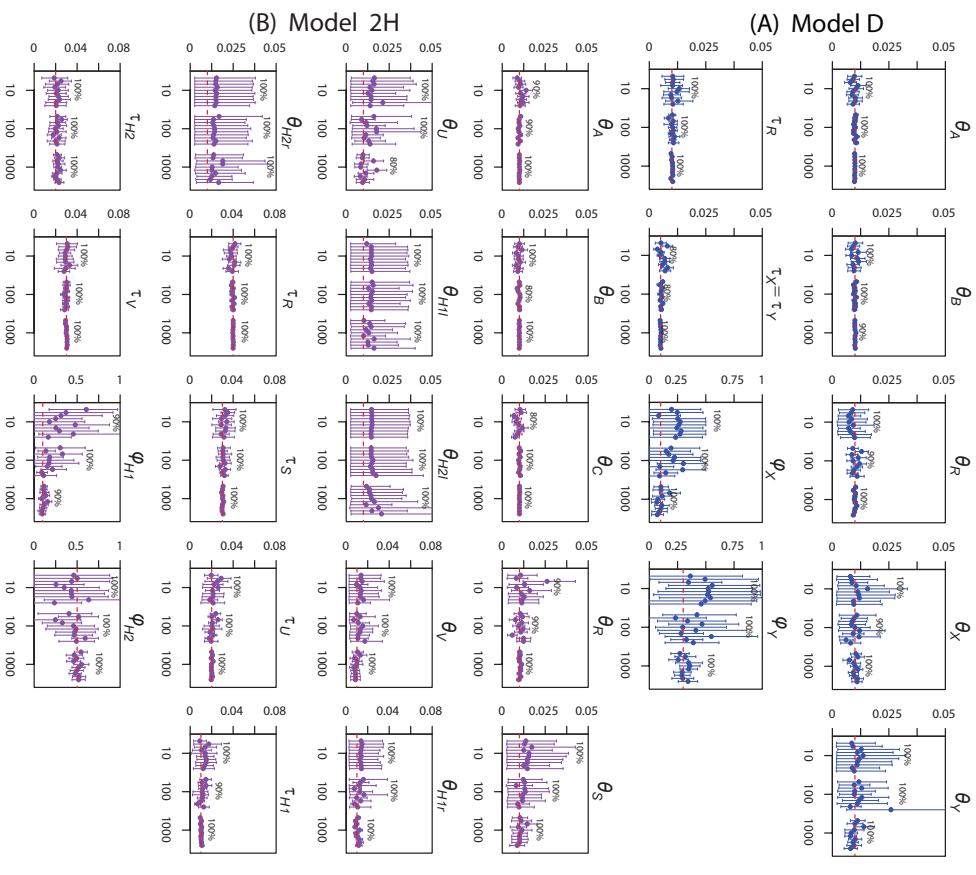


Figure S10: Posterior means and 95% HPD CIs of parameters under model D of Fig. 1 (blue) and model 2H of Fig. 2 (purple) in 10 replicate datasets, each of 10, 100, or 1000 loci. The numbers above the CI bars are the coverage or the proportion of replicate datasets in which the CI bar includes the truth. The horizontal lines represent the true parameter values.