

Supplementary Materials: Can Theory Improve the Scope of Quantitative Metazoan Metabarcoding?

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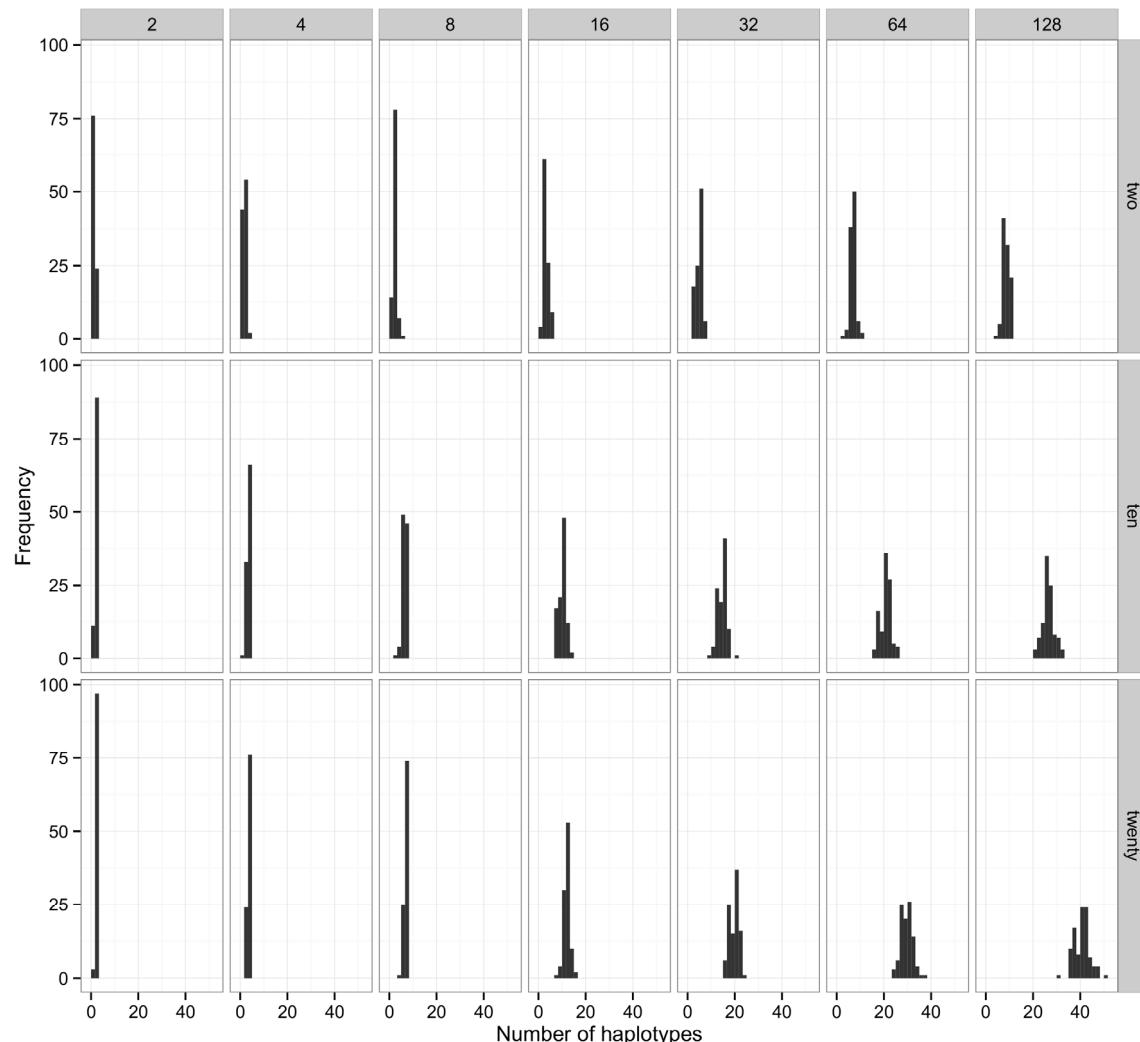


Figure S1. Distribution of the number of haplotypes for each combination of theta (two, ten, twenty) and sampling size (2, 4, 8, 16, 32, 64, 128).

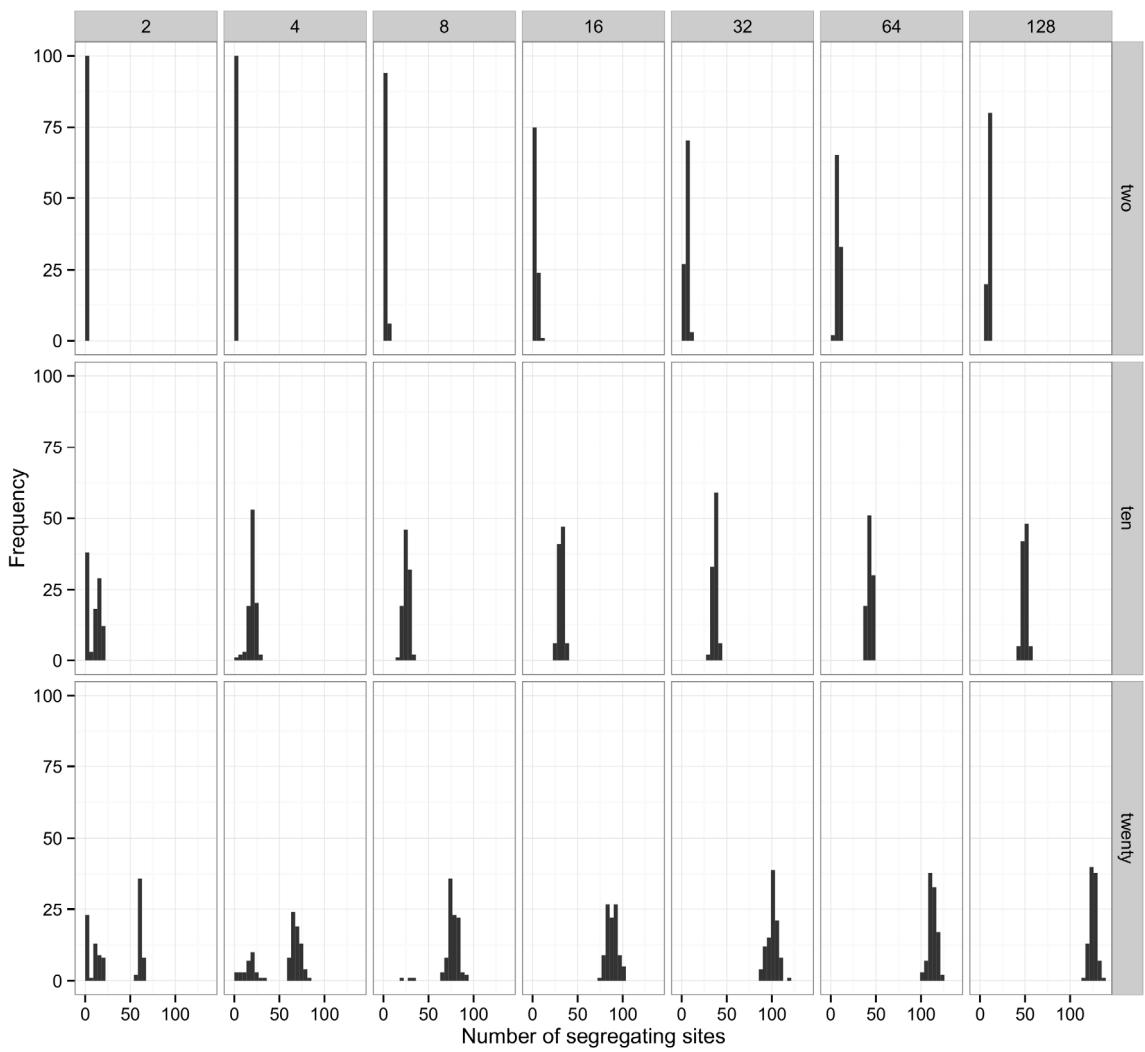


Figure S2. Distribution of the number of segregating sites for each combination of theta (two, ten, twenty) and sampling size (2, 4, 8, 16, 32, 64, 128).

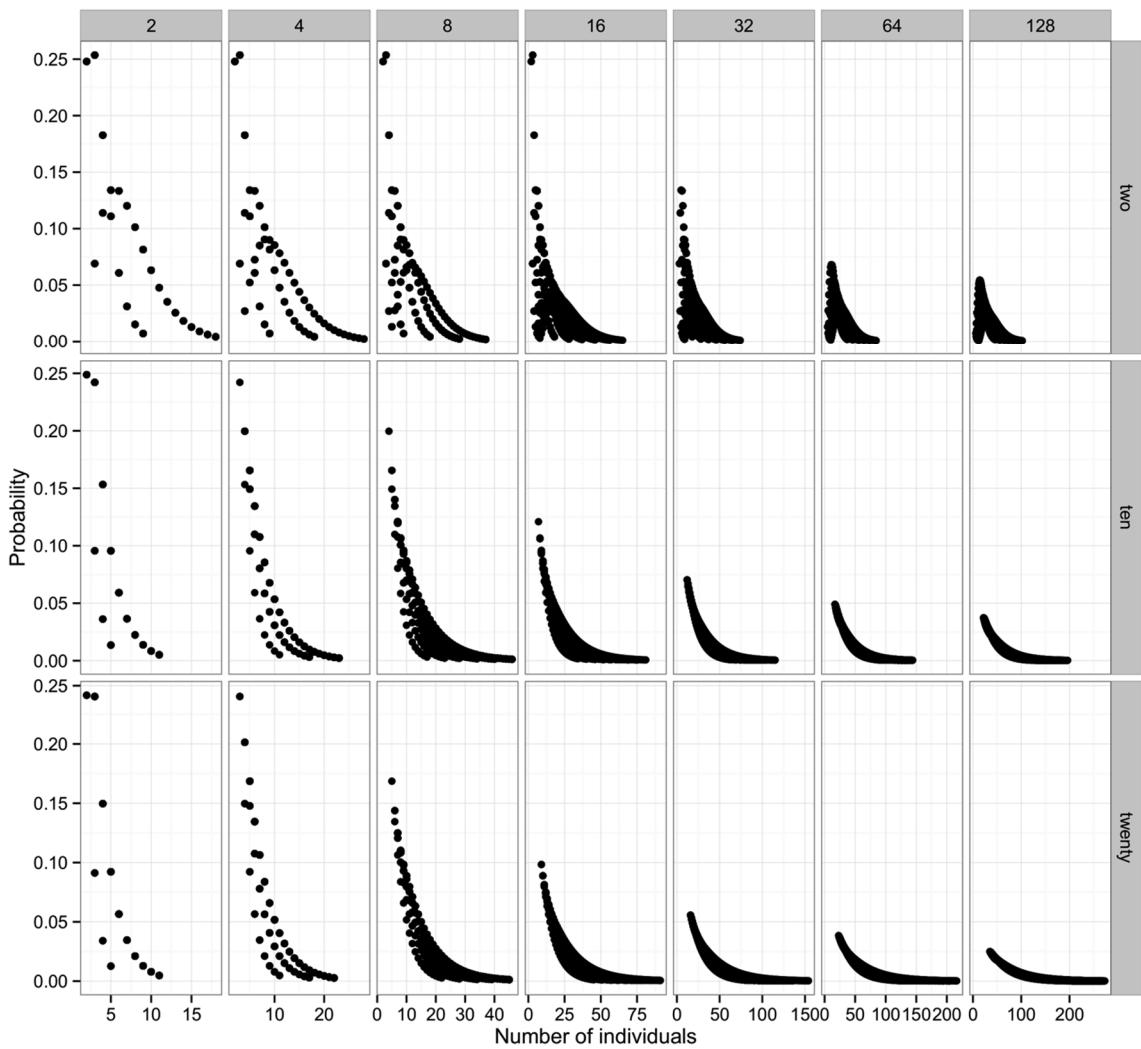


Figure S3. Probability distribution of the number of individuals back calculated using the gamma approach. Each panel shows a combination of simulated sampling size and the mutation rate in the original populations.