Supplementary Information for Haasl & Payseur.

SUPPLEMENTARY FIGURE 1. Using a version of equation (7) that is specific to the actual sample size can lead to large overestimates of θ . In this case, 10 data sets of $n = 25$ were simulated with true $\theta = 10$. This particular set of 10 data sets was chosen for its extremity. The n_a were: 5, 5, 5, 6, 6, 7, 7, 8, 10, 10. These values of n_a are mapped to estimates $\hat{\theta}_{NA}$ using the $n = 25$ regression (left panel) and $n = 1000$ regression (right panel). Despite the fact that the n_a vs θ curve in the left panel accurately corresponds to the average n_a for each θ when n = 25, its flat slope can lead to wild overestimates of θ when an unusually large value of n_a is obtained. Using the $n = 1000$ regression buffers against such overestimates, leading to an MSE that is $1/10$ th of that using the $n = 25$ regression.

SUPPLEMENTARY FIGURE 2. When estimating θ based on the vector of observed allele frequencies, the exponential approximation to the microsatellite frequency spectrum leads to more accurate estimates of θ than the gamma approximation. This is despite the fact that the gamma approximation describes empirical frequencies much better than the gamma approximation. Here, spectra for $\theta = 5, 10, 25, 50,$ and 100 are plotted on the interval $(0, 0.3]$, with the gamma approximation on the left and the exponential approximation on the right. As θ changes, changes to the empirical approximation are most extreme along the very allele frequency intervals that change the most with θ . For example, exponential approximations for $\theta = 5$ and $\theta = 25$ are quite divergent for allele frequencies on the interval $(0, 0.05]$, while the corresponding gamma approximations show much less divergence. To a lesser extent, divergence between the expoential approximations on the allele frequency interval $(0.075, 0.3)$ are greater than those between the corresponding gamma approximations. As θ increases, allele frequencies < 0.05 (especially < 0.01) become much more common and allele frequencies > 0.1 become much more rare. The form of the exponential approximation is better suited to diagnose these differences.

SUPPLEMENTARY TABLE 1. Intercepts and regression coefficients for equations (7) and (8).

SUPPLEMENTARY TABLE 2. Sample size and θ estimation. MSE and bias (in parentheses) are shown. All statistics based on 150 independent data sets. n and θ in the two leftmost columns refer to the simulation parameters. The first row of the header refers to the version of equation (7) used to perform estimation. The results imply a complicated relationship between θ , n, and our methods of estimation. Generally, MSE and bias are reduced by using a version of equation (7) specific to a value of n that is greater than actual sample size.

SUPPLEMENTARY TABLE 3. Effect of subsampling on θ estimation. All subsampling results are based on 10,000 independent estimates of θ . For ease of comparison, the results from non-subsampling estimates are repeated from Table 1. Boldface statistics indicate combinations of θ and n for which subsampling improved estimation in terms of MSE.

