Appendix S14. Effects of sampling design (A: sample size; B: sex ratio; C: timing of sampling) on the estimation of within-population heterozygote deficit ($F_{IS}$) using simulated data under four scenarios (1: drift dominance; 2: dispersal-drift equilibrium; 3: drift dominance; 4: parameter stabilization). Each point represents the raw value calculated for each subsamples (“NoDiff”), the raw difference from reference value (computed – reference; “Normal”), and the absolute difference from reference value (|computed – reference|; “abs(Normal)”) for each subsampled dataset. The reference value is the parameter value calculated for the full dataset. Results are presented for the five simulated populations; the three graphs from the same column (for example a, f and k for sample size and sex ratio, and a, e and i for timing of sampling) pertaining to the same simulated population.

A.1. Sample size, scenario of drift dominance
A.2. Sample size, scenario of dispersal-genetic drift equilibrium
A.3. Sample size, scenario of dispersal dominance
A.4. Sample size, scenario of parameter stabilization
B.1. Sex ratio, scenario of drift dominance
B.2. Sex ratio, scenario of dispersal-genetic drift equilibrium
B.3. Sex ratio, scenario of dispersal dominance
B.4. Sex ratio, scenario of parameter stabilization
C.1. Timing of sampling, scenario of drift dominance
C.2. Timing of sampling, scenario of dispersal-genetic drift equilibrium
C.3. Timing of sampling, scenario of dispersal dominance
C.4. Timing of sampling, scenario of parameter stabilization