



Figure S2 ML estimates of the genotype frequencies. The ML estimates of the A, C, E) major-homozygote frequency and B, D, F) minor-homozygote frequency as functions of the minor-allele frequency are shown when the inbreeding coefficient is A, B) minimized, C, D) equal to zero, or E, F) maximized. The mean and standard deviation of the estimates are shown by the points and bars (gray for mean 3 \times and black for mean 10 \times), respectively. The middle curve represents the ideal situation where the estimate is equal to the true value. The upper and lower curves represent the theoretical asymptotic standard deviation from the mean (calculated as the square root of Equation 17 or 18). Number of sampled individuals $N = 100$, error rate $\epsilon = 0.01$. A total of 10,000 simulation replications were run for each set of parameter values.