

Figure S6. Distributions of the minor allele fractions of the simulated sites with varied expected allele fractions. The expected distributions were generated assuming that the allele fraction followed a binomial sampling process with $P = 0, 0.05, 0.1, 0.2, 0.3, 0.4,$ and 0.5 . The plots demonstrated that our simulation strategy can mimic the real sequencing data at polymorphic sites.

