

TABLE S5 Summary of the realized parameter values in population samples in simulated diploid data at triallelic sites

Mean Coverage	Sample p (Mean \pm SD)	Sample q (Mean \pm SD)	Sample r (Mean \pm SD)	Sample ϵ (Mean \pm SD)
10	0.70 \pm 0.033	0.20 \pm 0.029	0.10 \pm 0.022	0.01 \pm 0.003
15	0.70 \pm 0.033	0.20 \pm 0.028	0.10 \pm 0.021	0.01 \pm 0.003
20	0.70 \pm 0.033	0.20 \pm 0.028	0.10 \pm 0.021	0.01 \pm 0.002
30	0.70 \pm 0.032	0.20 \pm 0.028	0.10 \pm 0.021	0.01 \pm 0.002

p , q , and r are frequencies of the most abundant, second most abundant, and rarest alleles, respectively. SD denotes standard deviation of the mean. Sample size $N = 100$, error rate $\epsilon = 0.01$. Results are based on a total of 10,000 simulation replications for each parameter set.