TABLE S3 Comparison of the allele-frequency estimates and called genotypes by different methods with moderately high depths of coverage.

Method	q	f	$\hat{q}$ (Mean ± 2SE)	Correct-call Rate among Individuals (Mean ± 2SE)	Correct-call Rate among Called Genotypes (Mean ± 2SE)
Proposed	0.1	0 (HWE)	0.10 ± 0.00044	0.99 ± 0.00018	0.99 ± 0.00017
GATK	0.1	0 (HWE)	0.10 ± 0.00042	0.99 ± 0.00019	0.99 ± 0.00019
Samtools	0.1	0 (HWE)	0.11 ± 0.00045	0.97 ± 0.00033	0.97 ± 0.00033
ANGSD	0.1	0 (HWE)	0.10 ± 0.00044	0.99 ± 0.00019	0.99 ± 0.00019
Proposed	0.1	minimized	0.10 ± 0.00041	0.99 ± 0.00018	0.99 ± 0.00017
GATK	0.1	minimized	0.10 ± 0.00041	0.99 ± 0.00020	0.99 ± 0.00020
Samtools	0.1	minimized	0.11 ± 0.00043	0.97 ± 0.00033	0.97 ± 0.00033
ANGSD	0.1	minimized	0.10 ± 0.00041	0.99 ± 0.00019	0.99 ± 0.00019
Proposed	0.1	maximized	0.10 ± 0.00059	1.00 ± 0.00005	1.00 ± 0.00005
GATK	0.1	maximized	0.10 ± 0.00059	1.00 ± 0.00010	1.00 ± 0.00010
Samtools	0.1	maximized	0.11 ± 0.00060	0.97 ± 0.00036	0.97 ± 0.00036
ANGSD	0.1	maximized	0.10 ± 0.00060	0.99 ± 0.00020	0.99 ± 0.00020
Proposed	0.3	0 (HWE)	0.30 ± 0.00066	0.99 ± 0.00024	0.99 ± 0.00023
GATK	0.3	0 (HWE)	0.29 ± 0.00066	0.98 ± 0.00030	0.98 ± 0.00030
Samtools	0.3	0 (HWE)	0.31 ± 0.00065	0.98 ± 0.00031	0.98 ± 0.00031
ANGSD	0.3	0 (HWE)	0.30 ± 0.00066	0.99 ± 0.00024	0.99 ± 0.00024
Proposed	0.3	minimized	0.30 ± 0.00050	0.99 ± 0.00024	0.99 ± 0.00021
GATK	0.3	minimized	0.29 ± 0.00050	0.97 ± 0.00034	0.97 ± 0.00034
Samtools	0.3	minimized	0.31 ± 0.00049	0.98 ± 0.00029	0.98 ± 0.00029
ANGSD	0.3	minimized	0.30 ± 0.00050	0.99 ± 0.00024	0.99 ± 0.00024
Proposed	0.3	maximized	0.30 ± 0.00091	1.00 ± 0.00004	1.00 ± 0.00004
GATK	0.3	maximized	0.30 ± 0.00091	0.99 ± 0.00016	0.99 ± 0.00016
Samtools	0.3	maximized	0.31 ± 0.00090	0.97 ± 0.00036	0.97 ± 0.00036
ANGSD	0.3	maximized	0.30 ± 0.00092	0.98 ± 0.00025	0.98 ± 0.00025

q, $\hat{q}$, and f are the minor-allele frequency, its estimate, and inbreeding coefficient, respectively. $\hat{q}$ by the proposed method and ANGSD are directly estimated from sequence-read data by the genotype-frequency estimator (Maruki and Lynch 2015) and Kim *et al.*'s method (2011), respectively. Called genotypes by the proposed method are by the Bayesian genotype caller. The correct-call rate is a fraction of individuals with correctly called genotypes among N = 100 individuals, where missing genotype calls are considered incorrect. On the other hand, the correct-call rate among called genotypes is calculated only among individuals with called genotypes. SE denotes standard error of the mean. Mean depth of coverage μ = 10, error rate ε = 0.01. Results are based on a total of 10,000 simulation replications for each parameter set.