

**TABLE S4** Summary of the realized parameter values in population samples in simulated diploid data at biallelic sites

Mean Coverage	$\gamma_1$	$\gamma_3$	Sample $\gamma_1$ (Mean $\pm$ SD)	Sample $\gamma_3$ (Mean $\pm$ SD)	Sample $\epsilon$ (Mean $\pm$ SD)
3	0.81	0.01	0.81 $\pm$ 0.039	0.01 $\pm$ 0.010	0.01 $\pm$ 0.006
3	0.8	0	0.80 $\pm$ 0.040	0.00 $\pm$ 0.000	0.01 $\pm$ 0.006
3	0.9	0.1	0.90 $\pm$ 0.030	0.10 $\pm$ 0.030	0.01 $\pm$ 0.006
3	0.49	0.09	0.49 $\pm$ 0.050	0.09 $\pm$ 0.029	0.01 $\pm$ 0.006
3	0.4	0	0.40 $\pm$ 0.049	0.00 $\pm$ 0.000	0.01 $\pm$ 0.006
3	0.7	0.3	0.70 $\pm$ 0.046	0.30 $\pm$ 0.046	0.01 $\pm$ 0.006
10	0.81	0.01	0.81 $\pm$ 0.040	0.01 $\pm$ 0.010	0.01 $\pm$ 0.003
10	0.8	0.0	0.80 $\pm$ 0.040	0.00 $\pm$ 0.000	0.01 $\pm$ 0.003
10	0.9	0.1	0.90 $\pm$ 0.030	0.10 $\pm$ 0.030	0.01 $\pm$ 0.003
10	0.49	0.09	0.49 $\pm$ 0.050	0.09 $\pm$ 0.030	0.01 $\pm$ 0.003
10	0.4	0	0.40 $\pm$ 0.049	0.00 $\pm$ 0.000	0.01 $\pm$ 0.003
10	0.7	0.3	0.70 $\pm$ 0.046	0.30 $\pm$ 0.046	0.01 $\pm$ 0.003

$\gamma_1$  and  $\gamma_3$  are frequencies of major and minor homozygotes, 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.