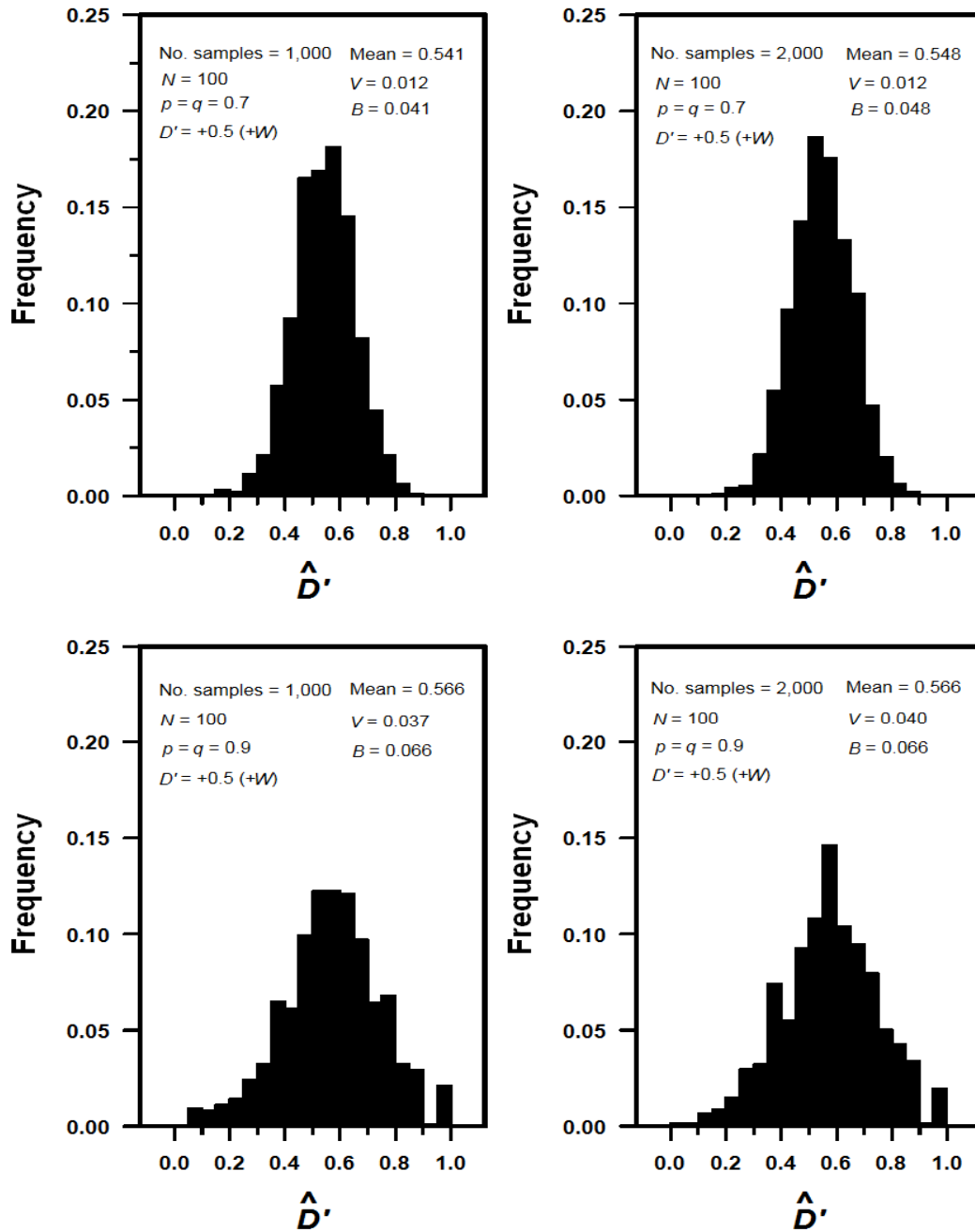


### *Simulation details*

The number of haplotype samples ( $n$ ) used in the simulations was determined after a pilot study, which showed that when  $n$  is higher than 1,000 the sampling distributions of  $\hat{D}'$  and  $\hat{r}$  do not change substantially under the same population conditions and sample size (see, for illustration, suppl. fig. 1). In addition, the  $n$  used in the simulations should not have a significant impact on the downstream statistical analyses by the two following reasons. First, comparisons of the statistical properties of  $\hat{D}'$  and  $\hat{r}$  were performed under the same sampling conditions. Second, comparisons between both coefficients were based on mean values of non-standardised and standardised statistics over replicate sampling distributions from a total number of 50,000 haplotype samples for each case studied (see 'Methods' section). Random numbers were obtained using the standard multiplicative linear congruential generator implemented by Schrage (see [29] and references therein).



**Supplementary Fig. 1.** Comparison of simulated frequency distributions of  $\hat{D}'$  from 1,000 and 2,000 haplotype samples of size  $N=100$  under different population conditions ( $p=q=0.7$  or  $0.9$  and  $D'=0.5$  or  $+W$ ). Note that sampling variances ( $V$ ) and biases ( $B$ ) of  $\hat{D}'$  are similar for 1,000 and 2,000 haplotype samples, otherwise being the same.