

Table S1 Standard error of the estimate of h_G^2 (variance explained by all SNPs) observed from 100 simulations vs. that calculated from our approximation theory.

N	$h_G^2 = 0.2$		$h_G^2 = 0.5$		$h_G^2 = 0.8$		SE (Approx.)
	SE (Obs.)	<i>s.e.m.</i>	SE (Obs.)	<i>s.e.m.</i>	SE (Obs.)	<i>s.e.m.</i>	
500	0.63	2.6E-03	0.63	2.3E-03	0.63	1.3E-03	0.63
1000	0.31	9.8E-04	0.32	8.0E-04	0.32	4.6E-04	0.32
1500	0.21	5.5E-04	0.21	3.8E-04	0.21	2.4E-04	0.21
2000	0.16	3.6E-04	0.16	2.6E-04	0.16	1.9E-04	0.16
2500	0.13	2.6E-04	0.13	1.9E-04	0.13	1.1E-04	0.13
3000	0.11	1.9E-04	0.11	1.4E-04	0.11	9.9E-05	0.11
3500	0.09	1.9E-04	0.09	1.1E-04	0.09	8.8E-05	0.09
4000	0.08	1.4E-04	0.08	8.9E-05	0.08	6.6E-05	0.08
4500	0.07	1.3E-04	0.07	7.1E-05	0.07	5.9E-05	0.07
5000	0.06	9.7E-05	0.07	4.6E-05	0.06	5.7E-05	0.06

N : sample size. h_G^2 : heritability parameter used in simulations. SE(Obs.): mean of the observed standard errors from 100 simulations. *s.e.m.*: standard error of the mean (i.e. SE(Obs.)). SE(Approx.): standard error calculated from our approximation theory.