Supporting Tables

Table S1: **Genotype calling errors**. Genotype calling errors (in %) for different scenarios of sequencing depth and different genotype calling procedures. $GC1$ and $GC2$ assign a heterozygous state if at least 1 or 2 alternate alleles are observed, respectively. $GC3$ and GC assign genotypes according to the maximum genotype likelihood or genotype posterior probability, respectively. We retained only sites with no missing data.

Sequencing depth	Number of valid sites	$GC1$	$GC2$	$GC3$	GC
2X	2,148	2.53	1.72	2.53	1.77
6X	633,751	4.45	0.63	3.27	0.47
20X	700,007	13.36	0.47	0.074	0.0076