Table S2: **SNP calling false positive rates**. SNP calling false positive rates (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 monomorphic sites	$GC1$	$GC2$	$GC3$	GC
2X	2,001	43.28	0.15	43.18	35.78
6X	588,989	83.28	1.75	72.48	11.18
20X	650,838	99.70	17.55	2.93	0.22