

S2 Table. Number of SNPs in each filtering step

From reads to SNPs	Number of SNPs
SNPs in initial genotyping	8443
¹ Removal of loci with > 5% missingness	2400
² Minor allele frequency (MAF) < 0.05	0
Removal of loci with Heterozygosity (Ho) > 0.5	923
Random select one SNP per contig	1978
HWE filter (p-value < 0.001)	0
SNPs used in population genetic analyses	1978

¹ We also removed four samples which had > 10 % of the missingness

² This filtering has been applied in the SNP calling process