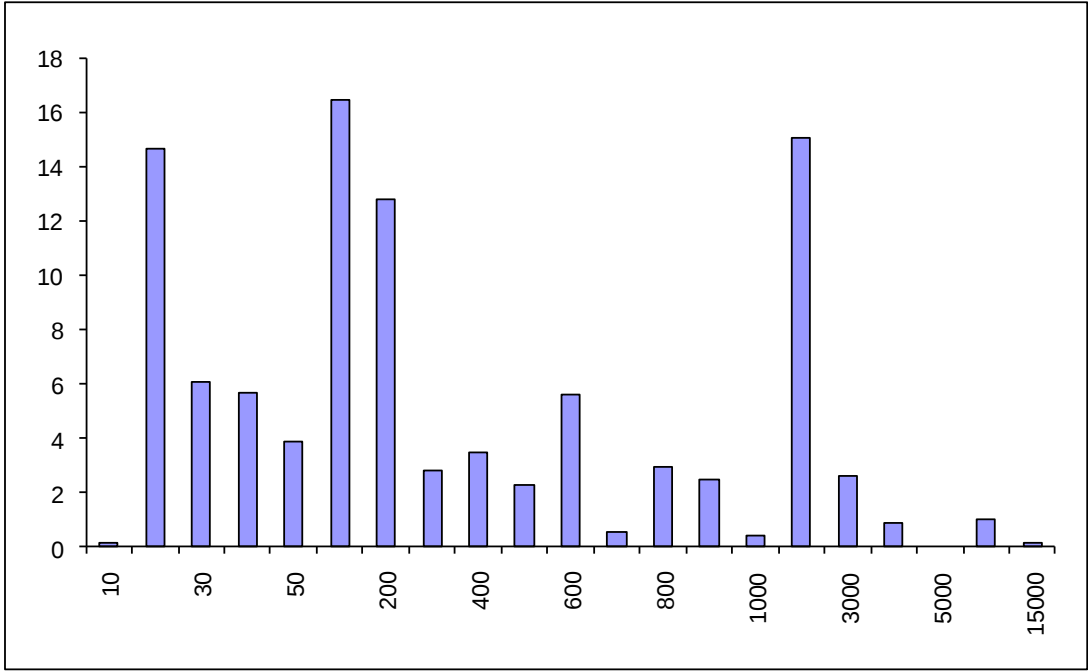


Figure S1. Description of sequencing results. a. Frequency distribution (% on the Y-axis) of the number of reads (the upper limit of the interval is on the X-axis) available for each nucleotide position. For example, around 15% of the nucleotide positions is covered by 1000 to 2000 reads. b. Frequency distribution (% on the Y-axis) of the frequency of the most frequent nucleotide (the upper limit of the % intervals is on the X-axis). For example, at around 85% of the positions the frequency of the most frequent allele among reads is between 99% and 100%.

a)



b)

