

**Table S4.** Values for the parameters  $Nt$ ,  $N_0$ ,  $H_0$ ,  $N$ , and  $H$  in the amplicons obtained for Q $\beta$ -t2 and Q $\beta$ -t25.

Population	Amplicon <sup>1</sup>	$Nt$ <sup>2</sup>	$N_0$ <sup>3</sup>	$H_0$ <sup>4</sup>	$N$ <sup>5</sup>	$H$ <sup>6</sup>
Q $\beta$ -t2	1	324304	309124	13688	266858	30
Q $\beta$ -t2	2	379763	358986	26127	294855	49
Q $\beta$ -t2	3	277476	262456	15078	223334	39
Q $\beta$ -t25 Sample 1	1	286318	274466	14710	235849	84
Q $\beta$ -t25 Sample 2	2	380690	359406	31345	279452	71
Q $\beta$ -t25 Sample 3	3	439189	408717	20728	351353	75

<sup>1</sup>Amplicons corresponding to population Q $\beta$ -t2 were obtained in the same sequencing project as the sample 1 of Q $\beta$ -t25 (see Figure S1). <sup>2</sup>Total number of paired reads obtained per amplicon. <sup>3</sup>Paired reads per amplicon after bioinformatics processing (see section 4.7 in Materials and Methods). <sup>4</sup>Number of different haplotypes contained in  $N_0$ . <sup>5</sup>Number of reads containing haplotypes represented above a frequency of 0.05% in  $N_0$ . <sup>6</sup>Number of different haplotypes in  $N$ .