Additional File 1

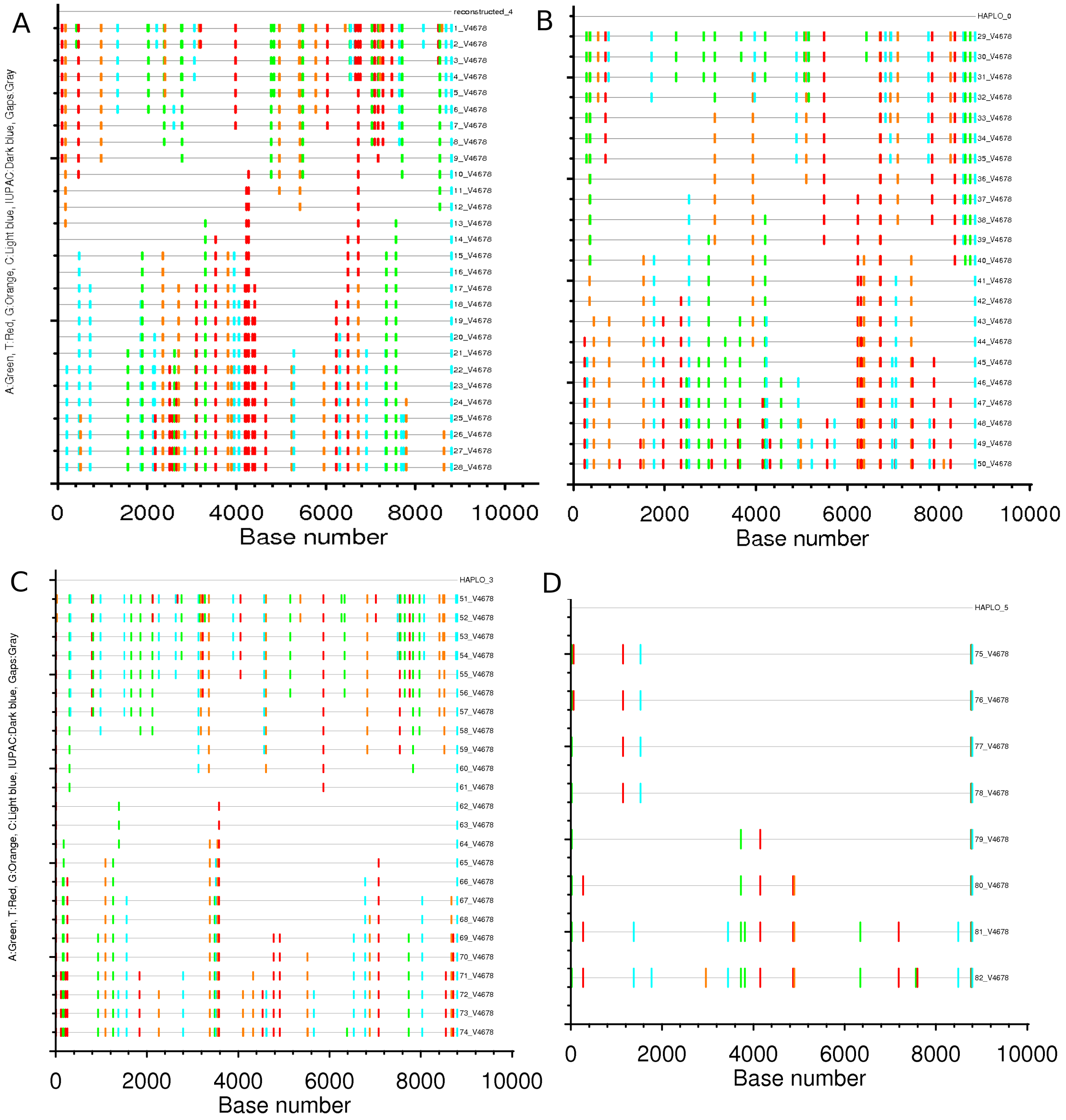

Figure S1: Sequence alignments of the reconstructed haplotype and the corresponding quasispecies. Sequence alignment of four most prevalent haplotypes (A) haplotype_4, (B) haplotype_0, (C) haplotype_3, and (D) haplotype_5 and the corresponding quasispecies. Mismatches between the simulated genomes and the reconstructed haplotype are indicated as vertical lines with different colors corresponding to different nucleotides (A: Green, T: Red, G: Orange, C: Light blue and Gaps: Gray). The variation at each genomic site was present only in a subset of genomes demonstrating that the haplotypes are reconstructed as consensus sequences of the corresponding quasispecies.