

Figure S1 DENV RNA detection from patients. (A) Total DENV RNA-positive samples determined by RT-PCR from total RNA isolated from whole blood or plasma. (B) DENV viremia was estimated by qRT-PCR using RNA isolated from whole blood or plasma. The quantity of DENV RNA is expressed as DENV genome equivalents/ml, as described in the Methods section.

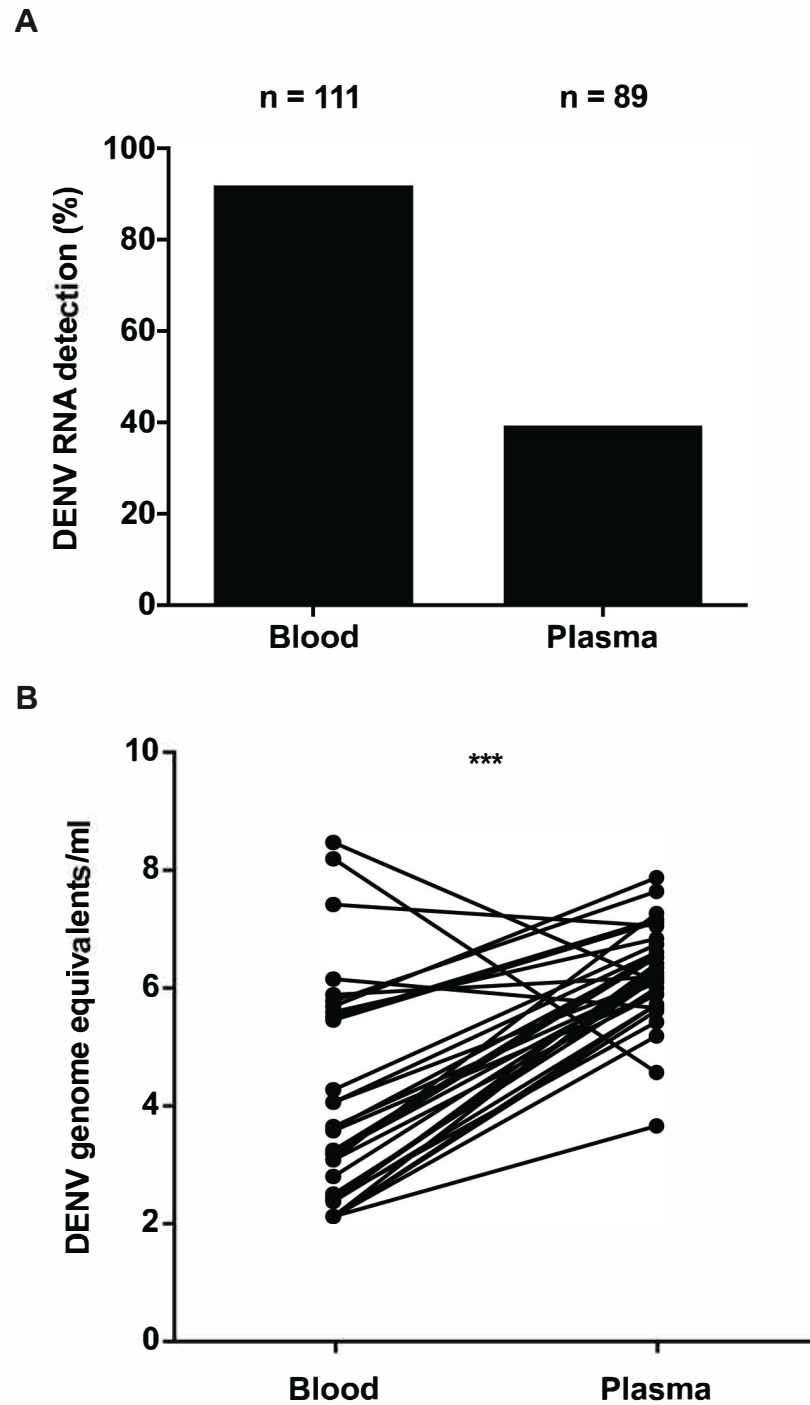


Figure S2 Isolation of DENV from patient samples. The percentage of total samples that yielded viral isolate in C6/36 cells after passage 3 is shown according to (A) day of fever (DOF) and (B) disease severity. (C) The viral titer in P3 supernatant was measured by plaque assay; samples are grouped according to the disease severity at the time of sample collection. DI-mild dengue; DW-Dengue with warning signs; SD-Severe dengue.

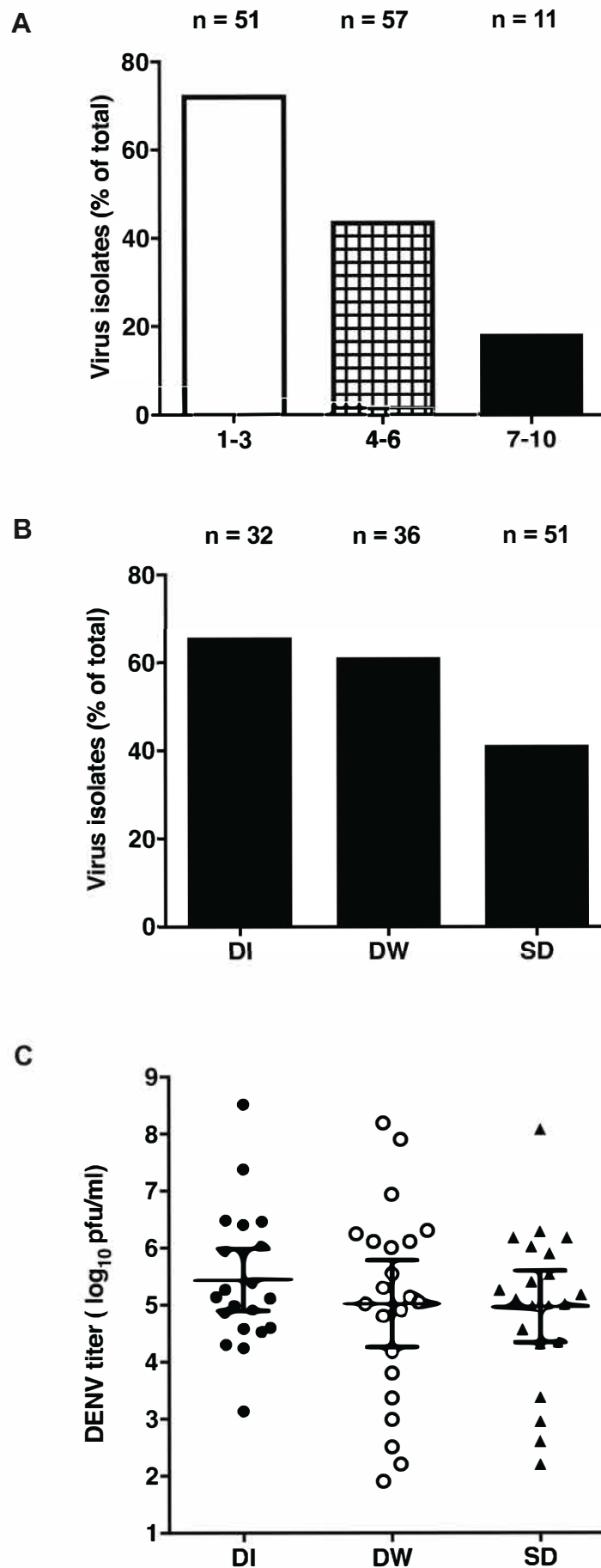


Figure S3 Phylogenetic tree for whole genomes of (A) DENV-1 and (B) DENV-3 using the maximum likelihood method based on the general time reversible model. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Join and BioNJ algorithms to a matrix of pairwise distances estimated using the maximum composite likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. The tree is drawn to scale, with branch lengths measured in the number of substitutions per site.

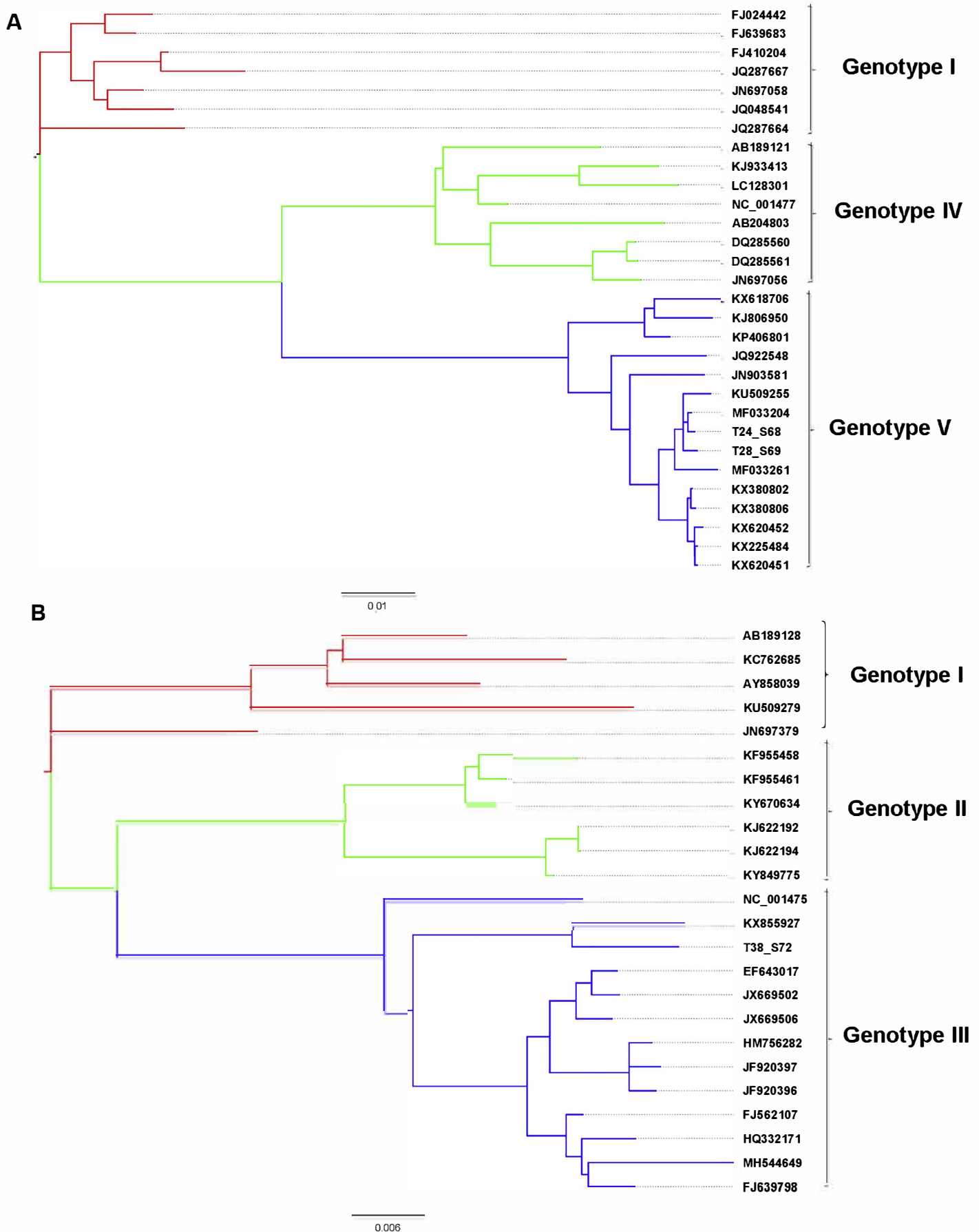


Figure S4 Inter-host variability within 18 samples compared to the consensus generated from the same 18 samples. The dN/dS ratio is plotted at the bottom.

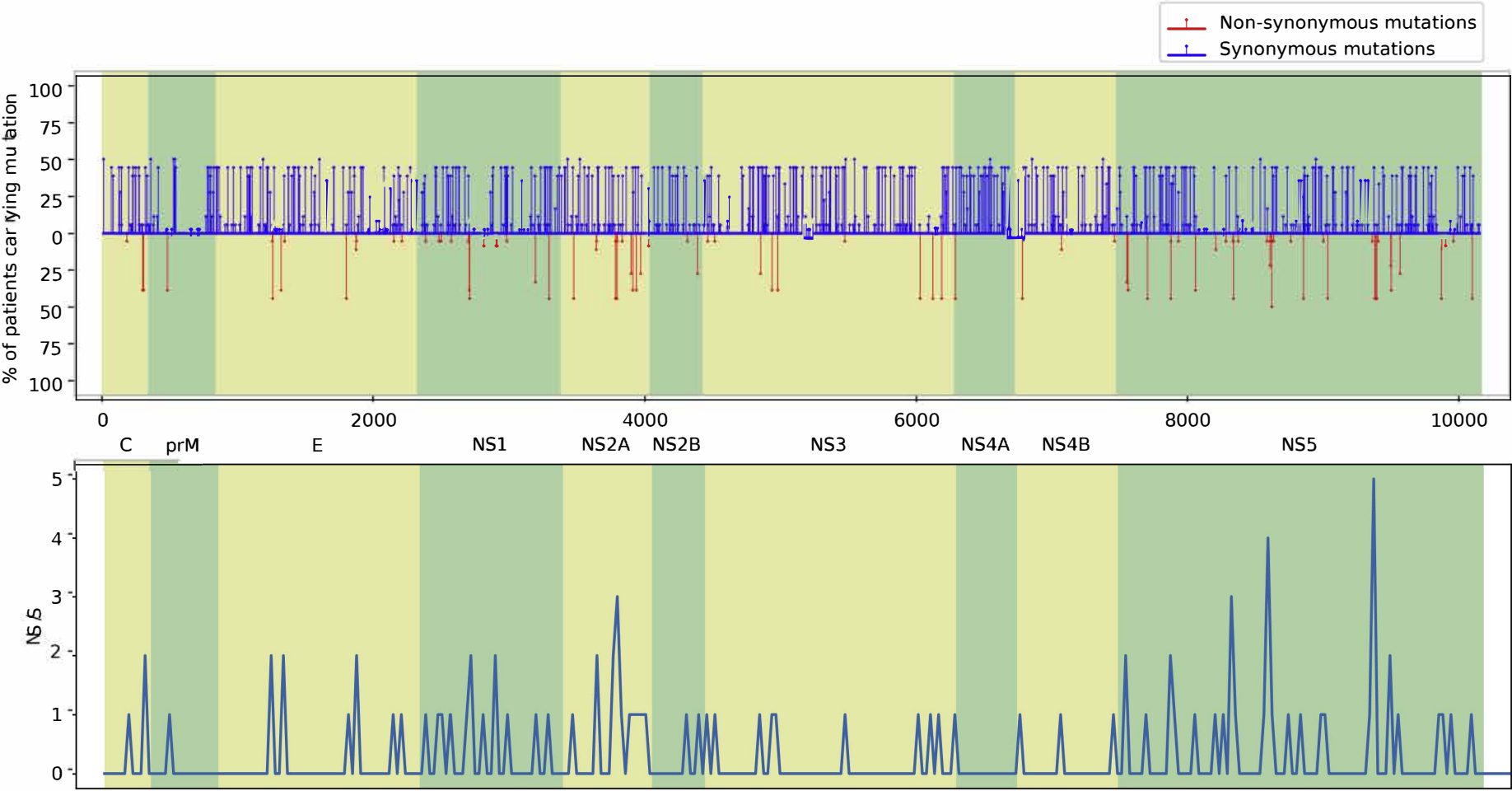


Figure S5 Multiple sequence alignment of the 5'UTR of the 18 DENV-2 strains sequences, the DENV-2 reference strain (NC_001474) and closest BLAST matches (KF479233.1, KY427085.1, KX380828.1, LC121816.1) are shown. Mismatches to the consensus sequence are highlighted. The identity track represents the degree of conservation at the nucleotide, with 100% conservation shown in bright green. C-U mutation in the RNA polymerase binding SLA loop is marked with a red rectangle.

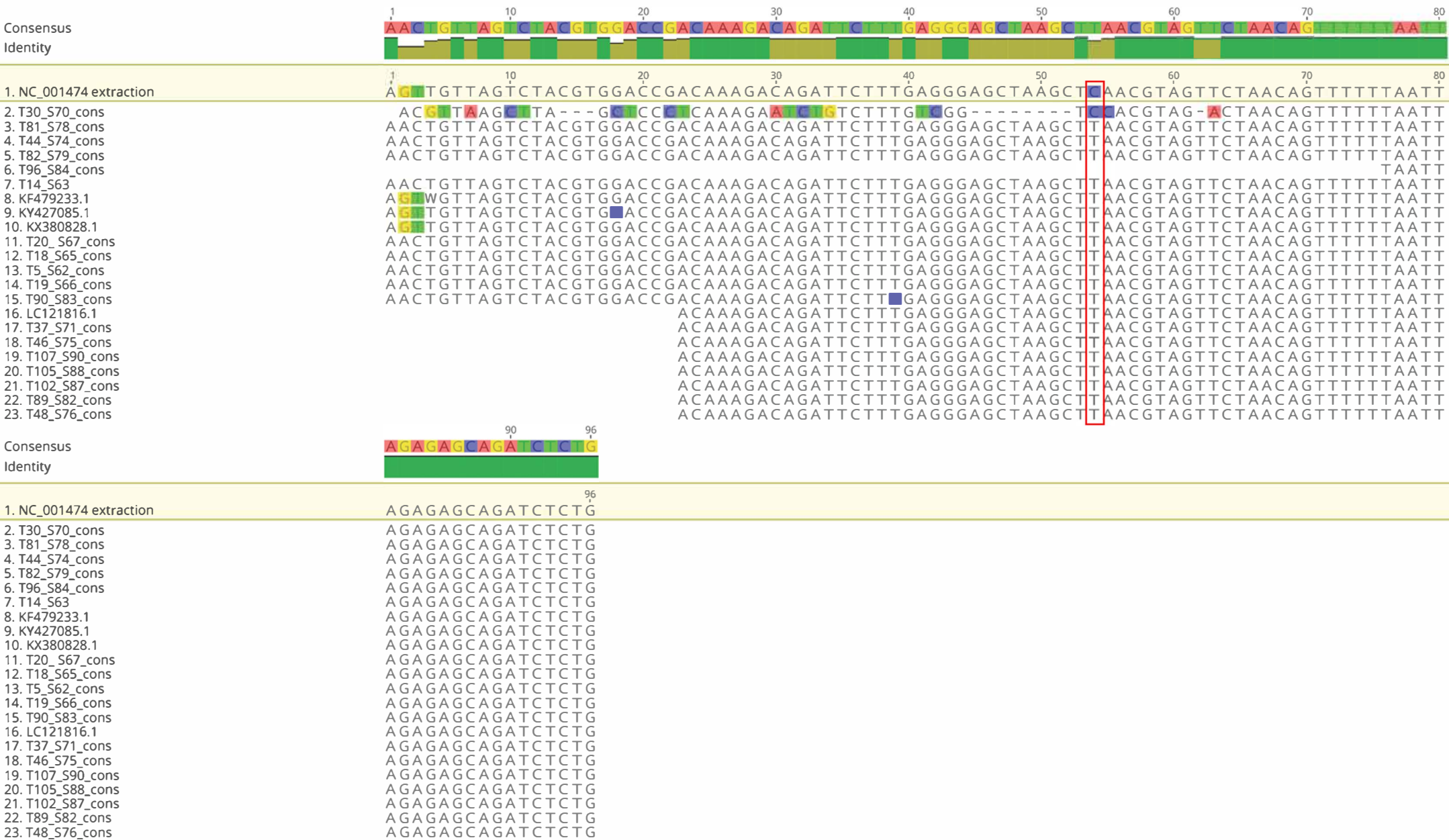


Figure S6 Multiple sequence alignment of the 3' UTR of the 18 DENV-2 strain sequences, the DENV-2 reference strain (NC_001474), and the closest BLAST matches (KF479233.1, KY427085.1, KX380828.1, LC121816.1) is shown. Mismatches to the consensus sequence are highlighted. The identity track represents the degree of conservation at the nucleotide, with 100% conservation shown in bright green.

