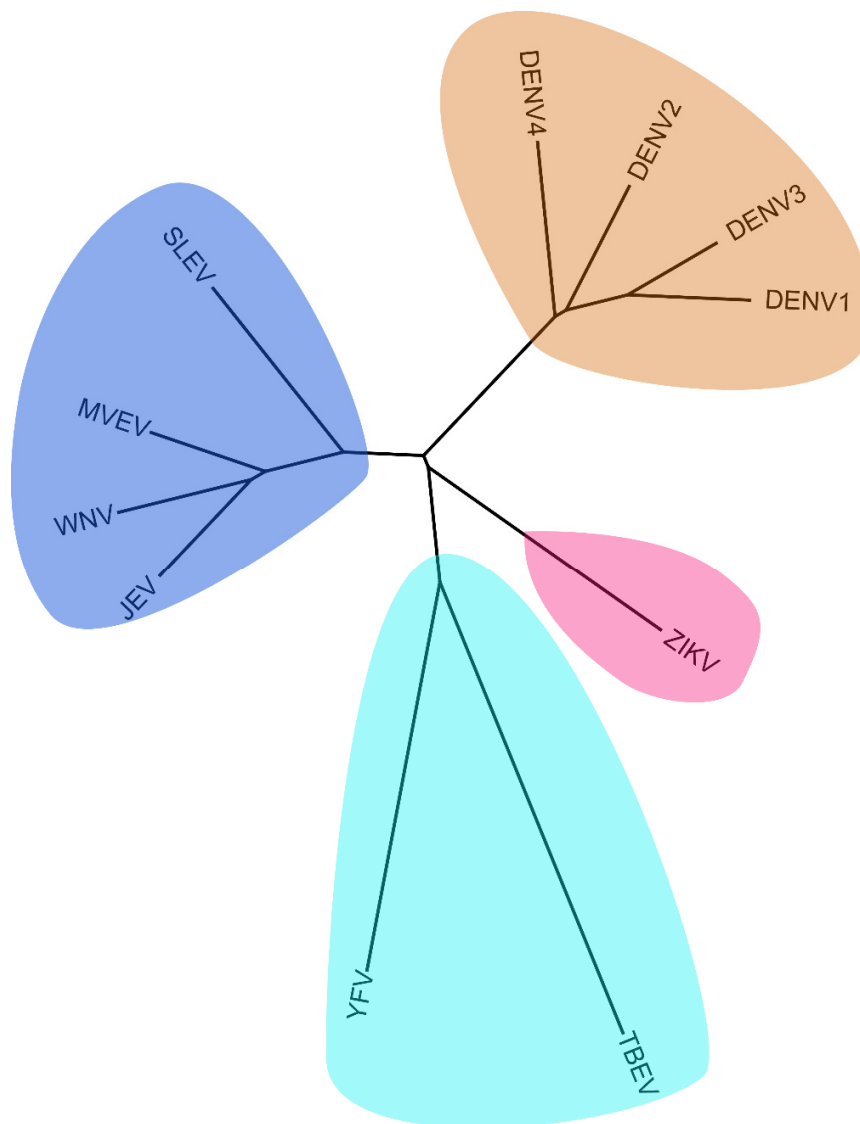


Supplementary Figure 1

Biophysical characterization of the ZIKV NS1₁₇₂₋₃₅₂ protein

(a) Analytical gel filtration of ZIKV NS1₁₇₂₋₃₅₂ protein. The 280-nm absorbance curve and the SDS-PAGE migration profile of the pooled sample are shown. (b) Ultracentrifugation sedimentation profile of ZIKV NS1₁₇₂₋₃₅₂. The calculated molecular weight of the indicated protein species is shown.

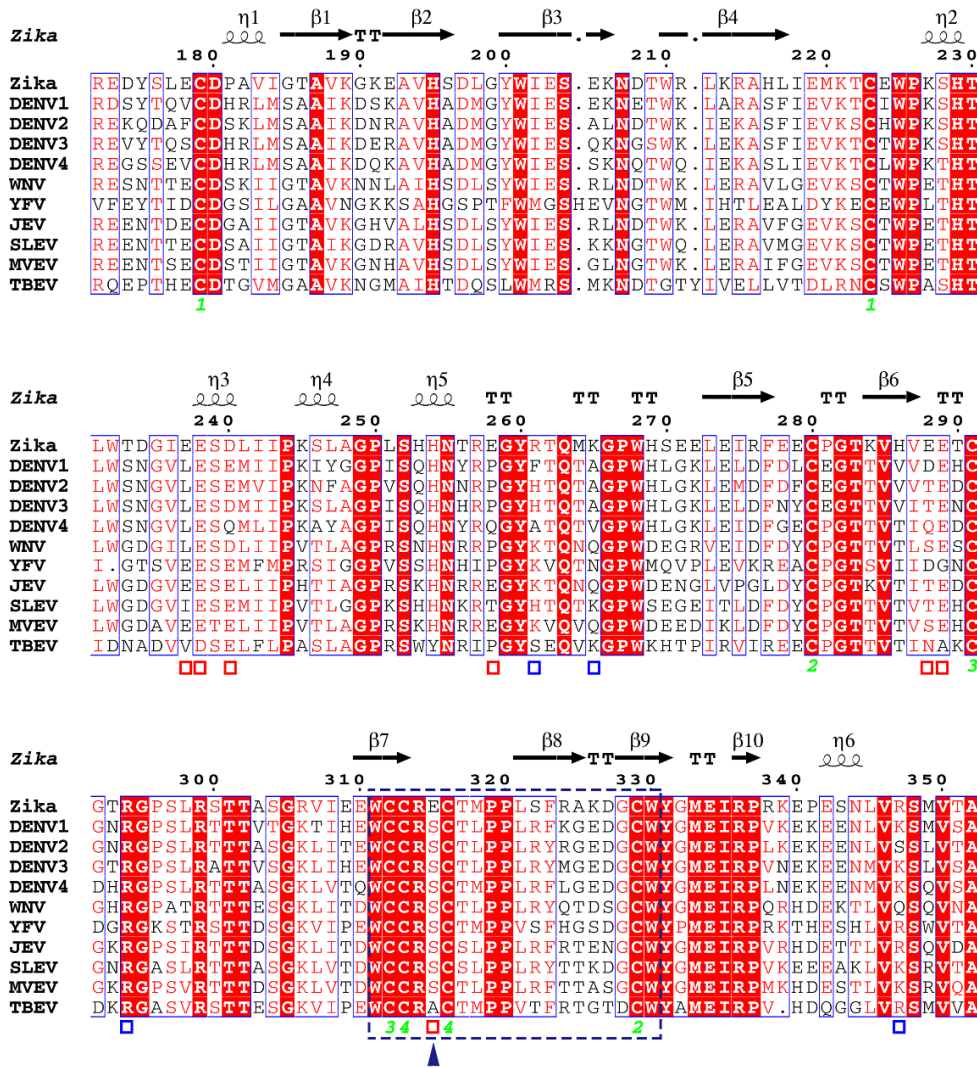


Supplementary Figure 2

Phylogenetic analysis of NS1 proteins from different flaviviruses.

We applied a neighbor-joining method on NS1 protein sequences from ZIKV and ten representative flaviviruses. The eleven flaviviruses can be classified into four groups. ZIKV is an independent group, separated from the ten representative flaviviruses.

Accession codes: Zika virus (ZIKV) strain BeH819015, AMA12085; West Nile virus (WNV), Q9Q6P4; Dengue virus 1 Nauru/West Pac/1974(DENV1), P17763; Dengue virus 2 Puerto Rico/PR159-S1/1969 (DENV2), P12823; Dengue virus 3 Singapore/8120/1995 (DENV3), Q5UB51; Dengue virus 4 Thailand/0348/1991 (DENV4), Q2YHF0; Japanese encephalitis strain K94P05 (JEV), AAC02714; St. Louis encephalitis (SLEV), D8L537; Yellow fever 17D vaccine strain (YFV), CAA27332; Murray Valley encephalitis (MVEV), NP_051124; Tick-borne encephalitis (TBEV), NP_043135.



Supplementary Figure 3

Secondary structure and sequence alignment of flavivirus NS1 proteins.

The charged residues that contribute to the electrostatic characters in the loop surface of ZIKV NS1₁₇₂₋₃₅₂ are indicated by red and blue squares. The region (residues 311 to 330) recognized by autoreactive antibodies is indicated by dot lines. The unique residue of ZIKV in the highly conserved region is indicated by a dark blue arrowhead.

Accession numbers for the NS1 protein sequence are described in the supplementary figure 2 legend.

1 **Supplementary Table 1. Data collection and refinement statistics.**

ZIKV NS1 ₁₇₂₋₃₅₂ (PDB code 5IY3)	
Data collection	
Space group	C2221
Cell dimensions	
<i>a</i> , <i>b</i> , <i>c</i> (Å)	63.868, 103.755, 114.843
α , β , γ (°)	90, 90, 90
Resolution (Å)	50.00-2.20 (2.28-2.20)
<i>R</i> _{merge}	0.081 (0.683)
<i>I</i> / σI	22.7 (2.4)
Completeness (%)	97.6 (92.8)
Redundancy	8.2 (5.9)
Refinement	
Resolution (Å)	39.49-2.17
No. reflections	19693
<i>R</i> _{work} / <i>R</i> _{free}	0.2046/0.2464
No. atoms	
Protein	2820
Ligand/ion	0
Water	79
<i>B</i> -factors	
Protein	54.8
Ligand/ion	
Water	53.0
R.m.s. deviations	
Bond lengths (Å)	0.008
Bond angles (°)	1.046

2 *Values in parentheses are for highest-resolution shell.