Capsid

Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses. Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

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Envelope

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NS1

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NS2A

Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses. Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

NS2B

Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses. Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

NS3

Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses. Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green. Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

NS4A and 2K

Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses. Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

NS4B

Supplementary Figure S2: Alignment of Individual Proteins Across Multiple Flaviviruses. Individual proteins from representative flaviviruses were aligned using the Clustal Omega algorithm in MegAlign Pro v17.2.1 (DNASTAR, Madison, WI). Amino acids are colored by side chain chemistry: aromatic residues (F, W, and Y) are yellow, acidic residues (D and E) are red, basic residues (R, H, and K) are blue, nonpolar residues (A, G, I, L, M, P, and V) are orange, and polar residues (C, N, Q, S, and T) are green). Gaps are represented as dashes. Black rectangles designate cysteine residues predicted to form disulfide bridges.

NS5