

S4 Fig. The alignment of flavivirus amino acid sequences around the NS4B-NS5. (A) The sequence of the natural cleavage sites of the NS3 protease in the NS4B and NS4B/NS5 boundary of the polyprotein precursor. Identical residues are shaded in black and conserved residues are shaded in light grey. (B) Percent identity for flavivirus NS3 protease domain. The amino acid sequences of NS3 protease domain for DENV-1/Hawaii, DENV-3/H-87, DENV-4/H241, Zika virus/PRVABC59, JEV/Beijing-1 are aligned with DENV-2/16681 using the Vector NTI–AlignX software.

A.

	P2	P1	P1'	P2'	P3'
DENV 1_ABG75766.1	GGG	RR	GTG	AA	QG
DENV 2_AAB58782.1	TNT	RR	GTG	NI	IG
DENV 3_M93130.1	GTG	KR	GTG	SQ	QG
DENV 4_AAX48017.1	QTP	RR	GTG	TT	GTG
Zika_AMC13911.1	LVK	RR	GGG	T	G
JEV_AOT86221.1	PSL	KR	GR	P	GGR
HCV_AAK08509.1	ITE	EC	PV	P	CSG

▲
Virus protease cleavage site

B.

	DENV 2	DENV 1	DENV 3	DENV 4	Zika	JEV	HCV
DENV 2	100	74	72	70	58	54	15
DENV 1		100	79	71	58	61	16
DENV 3			100	73	59	56	16
DENV 4				100	60	58	15
Zika					100	62	16
JEV						100	15
HCV							100