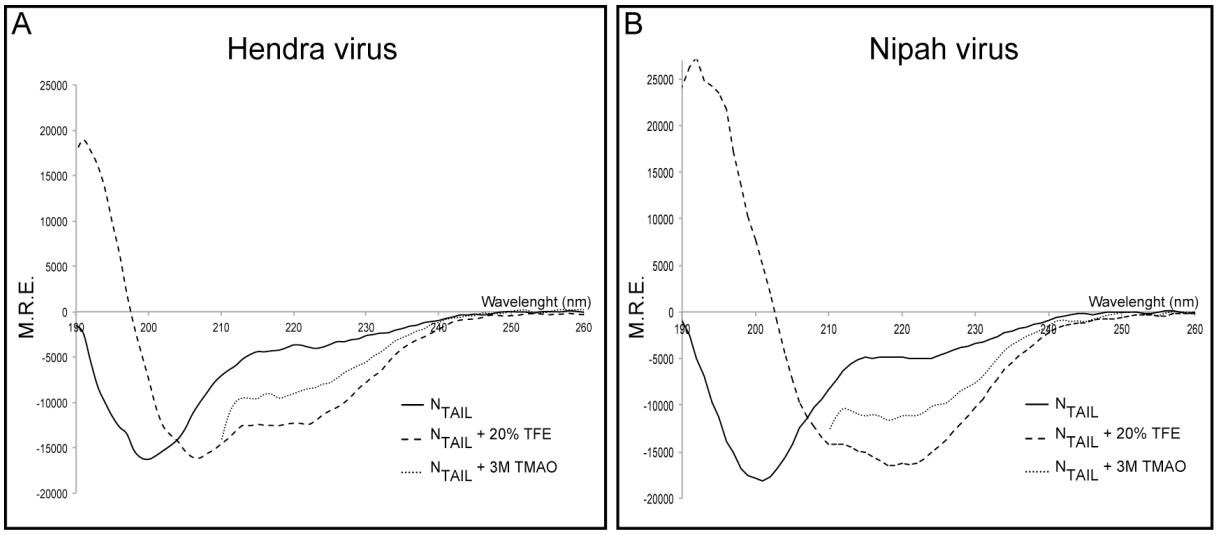

Figure S1. Far-UV CD spectra of HeV **(A)** or NiV **(B)** full-length N_{TAIL} proteins in 10 mM sodium phosphate pH 7 in the absence or in the presence of either 20% TFE or 3 M TMAO. The protein concentration was 0.1 mg/mL. Spectra were recorded at 20°C. Due to high background noise at lower wavelength (beyond 210 nm), the spectra in the presence of TMAO are shown to the point up to which the dyna voltage was in the permissible range. Data are representative of one out of two independent acquisitions.

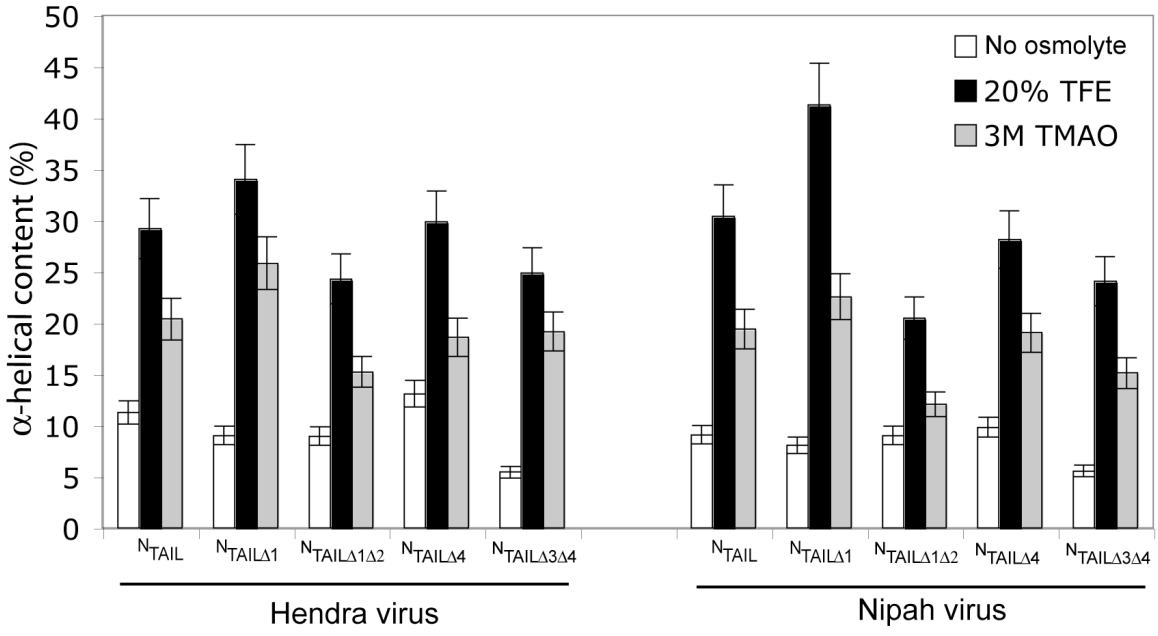

Figure S2. α-helical content (%) of *Henipavirus* N_{TAIL} proteins either in the absence of any osmolytes or in the presence of either 20% TFE or 3M TMAO. The α-helical content was derived from the ellipticity at 222 nm as described in [82]. Values for full-length HeV and NiV N_{TAIL} proteins were derived from the spectra shown in supplementary Fig. S1, whereas the values of truncated proteins were derived from the spectra shown in Fig. 4. The error bar, corresponding to 10% of the value as typically observed in this type of experiments, is shown.

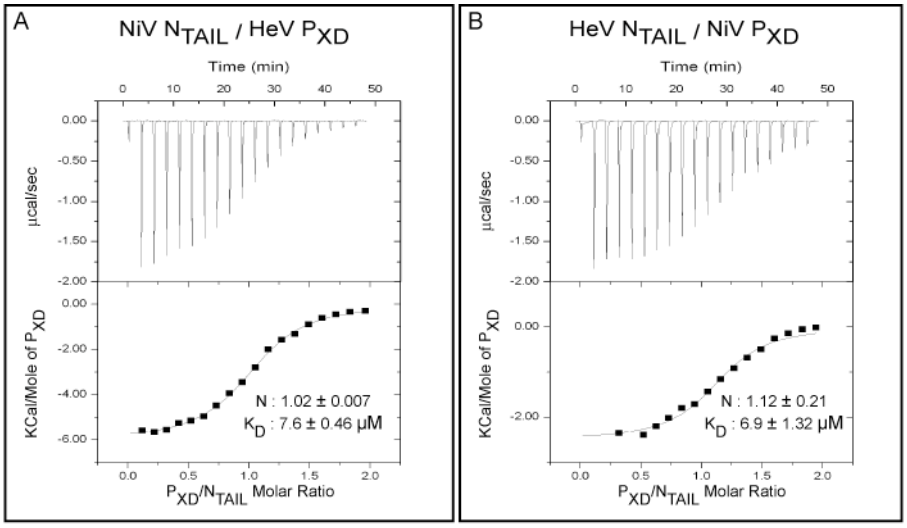

Figure S3. ITC studies of complex formation between HeV N_{TAIL} and NiV P_{XD} **(A)** and NiV N_{TAIL} and HeV P_{XD} **(B)**. Data are representative of at least two independent experiments where the initial concentrations of N_{TAIL} in the microcalorimeter cell and of P_{XD} in the microsyringe were slightly tuned. Panel **(A)** shows the data obtained with the following initial concentrations: 180 μM HeV N_{TAIL} and 1.8 mM NiV P_{XD}. Panel **(B)** shows the data obtained with the following initial concentrations: 150 μM NiV N_{TAIL} and 1.5 mM HeV P_{XD}. Graphs shown in the bottom of each panel correspond to integrated and corrected ITC data fit to a single set of sites model (all sites identical and equivalent). The filled squares represent the experimental data, whereas the solid line corresponds to the model. The derived equilibrium dissociation constant (K_D) as well as the stoichiometric number are shown.

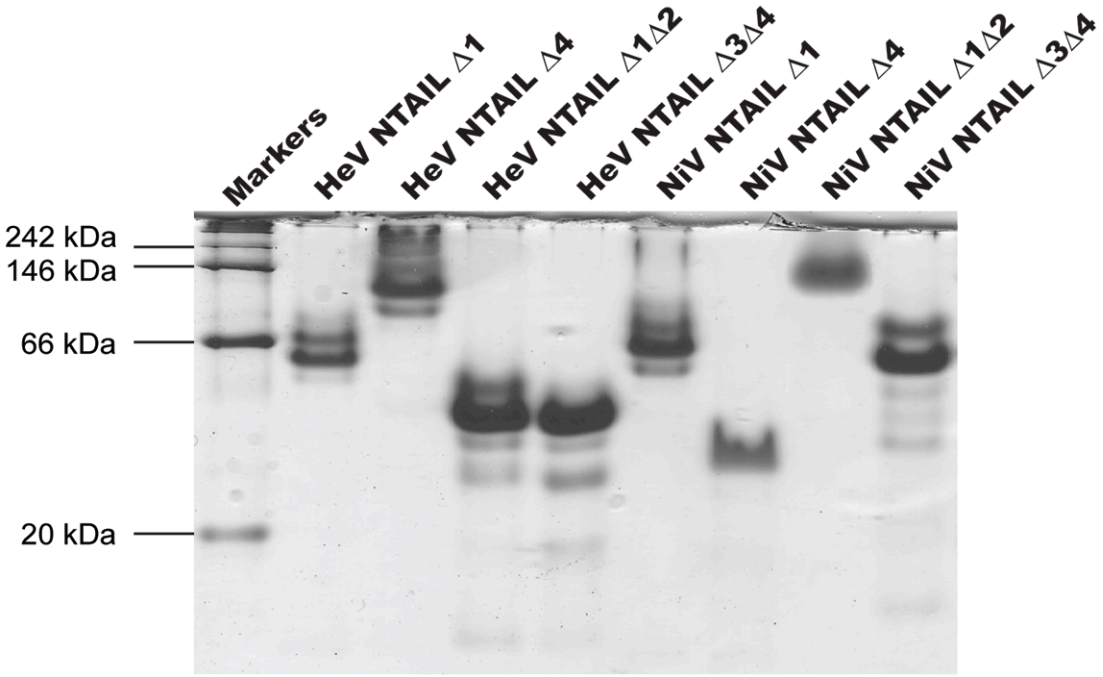

Figure S4. 15% Native PAGE of purified deletion proteins followed by Coomassie blue staining. Markers: NativeMark™ Unstained Protein Standard (Invitrogen).

Table S1. Apparent molecular mass (MM^{app}) of N_{TAIL} proteins as observed by SDS-PAGE, and ratio between the apparent and the theoretical molecular mass (MM^{theo}) as expected from the amino acid sequence.

	MM^{app}	MM^{theo}	MM^{app}/MM^{theo}
HeV			
$N_{TAIL\Delta1}$	18	14.5	1.24
$N_{TAIL\Delta1,2}$	14	10	1.40
$N_{TAIL\Delta4}$	18	15.7	1.15
$N_{TAIL\Delta3,4}$	11.8	10.3	1.15
NiV			
$N_{TAIL\Delta1}$	19.2	14.3	1.34
$N_{TAIL\Delta1,2}$	16.7	9.8	1.70
$N_{TAIL\Delta4}$	19.2	15.5	1.24
$N_{TAIL\Delta3,4}$	11.8	10.1	1.17

Table S2. Sequence properties of N_{TAIL} proteins. N: residue number. f_+: fraction of positively charged residues. f_-: fraction of negatively charged residues. Net charge *per* residue (NCR, $f_+ - f_-$). $|Q|$: absolute value of the difference between the total number of negatively charged and positively charged residues. P_{Pro}: fractional proline content. <H>: mean Kyte-Doolittle hydropathy score. H_{Bound}: value of boundary hydropathy. CH-distance: <H> - H_{Bound}. VL-XT score: average prediction score.

	N	f_+	f_-	NCR	$\|Q\|$	P_{Pro}	<H>	H_{Bound}	CH-distance	VL-XT score
HeV										
N_{TAIL}	140	0.1214	0.1500	-0.0286	4	0.050	0.3860	0.4235	-0.0375	0.75
$N_{TAIL\Delta1}$	132	0.1212	0.1515	-0.0303	4	0.053	0.3770	0.4242	-0.0472	0.73
$N_{TAIL\Delta1,2}$	90	0.1444	0.1111	-0.0333	3	0.055	0.3653	0.4253	-0.0600	0.70
$N_{TAIL\Delta4}$	145	0.1241	0.1310	-0.0069	1	0.048	0.3835	0.4158	-0.0323	0.75
$N_{TAIL\Delta3,4}$	95	0.0947	0.1368	-0.0428	4	0.021	0.4105	0.4284	-0.0179	0.70
NiV										
N_{TAIL}	140	0.1142	0.1357	-0.0215	3	0.028	0.4075	0.4210	-0.0135	0.72
$N_{TAIL\Delta1}$	132	0.1136	0.1363	-0.0227	3	0.030	0.3974	0.4214	-0.0240	0.69
$N_{TAIL\Delta1,2}$	90	0.1333	0.1111	-0.0222	2	0.022	0.3890	0.4213	-0.0323	0.67
$N_{TAIL\Delta4}$	145	0.1172	0.1172	0	0	0.027	0.4043	0.4133	-0.0090	0.72
$N_{TAIL\Delta3,4}$	95	0.0947	0.1157	-0.0217	2	0.021	0.4198	0.4208	-0.0010	0.70