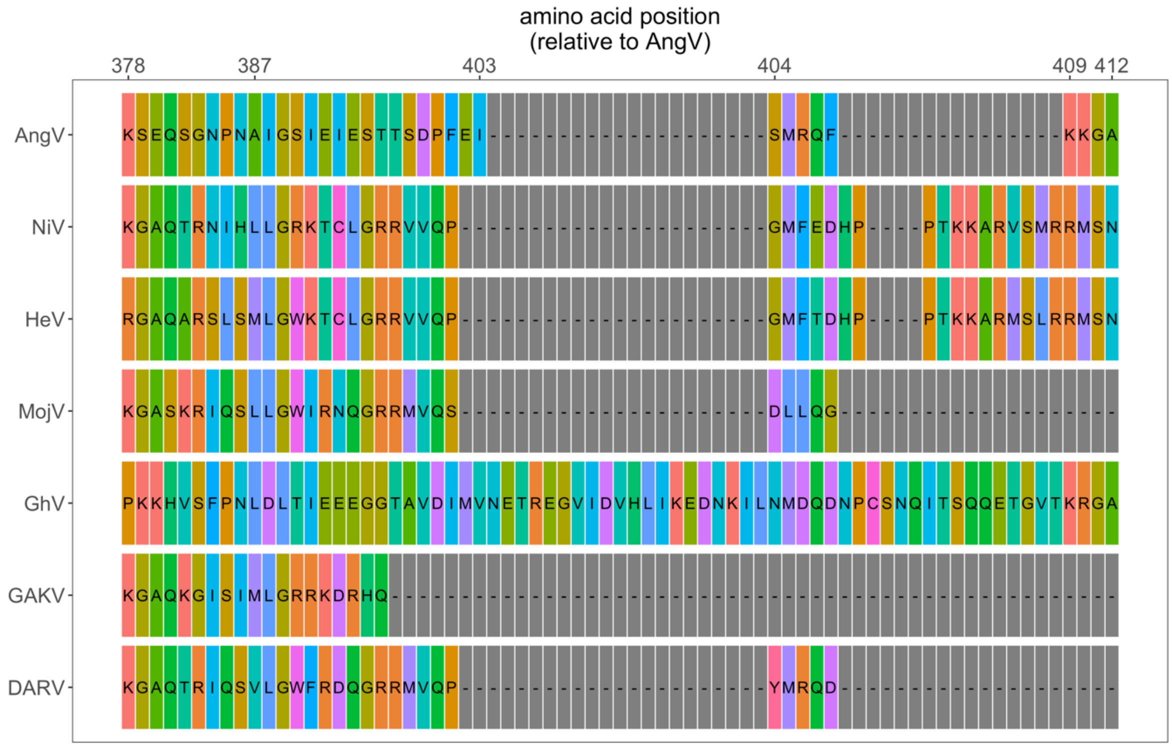
Supplemental Table 1. Comparison of Intergenic Sequences and Transcriptional Start and Stop Signals of AngV and other HNV.

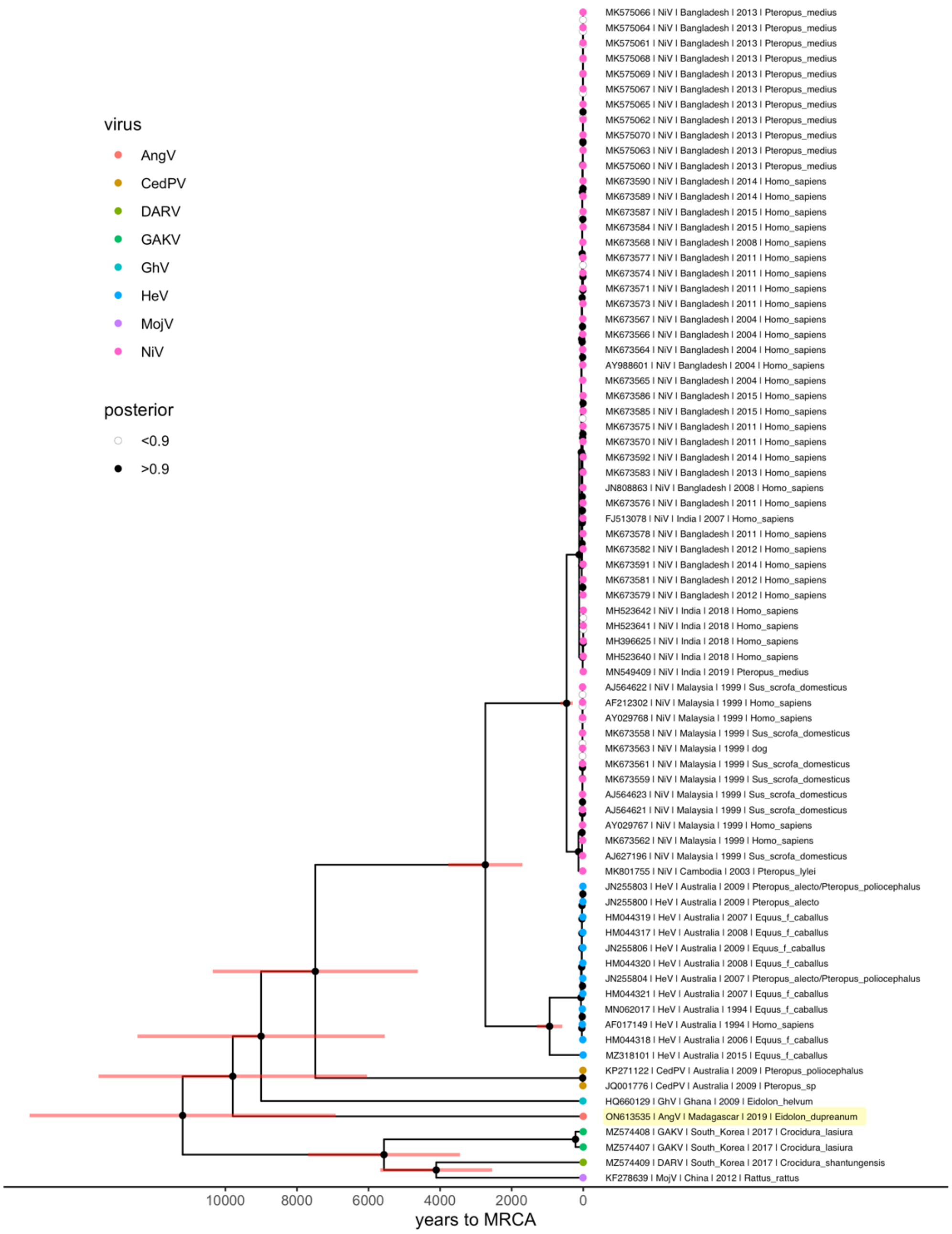
Intergenic Region	Virus	Gene Stop	Junction	Gene Start
N-P	AngV	TTAGAAAAAA	CTT	AGGAGCCAAGT
	NiV	TTAAGAAAAA	CTT	AGGAACCAAGA
	HeV	TTAAGAAAAA	CTT	AGGATCCAAGA
	MojV	TTAAACAAAA	CTT	AGGATCCAAG
	CedV	TTACAAAAAA	CTT	AGGATCCAAG
	GhV	CTATAAAAAA	CTT	AGGATCACAA
	GAKV	TTAAGAAAAA	CTT	AAGAATCAAA
	DARV	TTATAAAAAA	CTT	AGGATGCAAG
P-M	AngV	TTATAAAAAA	CTT	AGGATCAACGA
	NiV	TTAAGAAAAA	CTT	AGGAGACAGGT
	HeV	TTAAGAAAAA	CTT	AGGAGACAGGT
	MojV	TCATAAAAAA	CTT	AGGAGTCAAG
	CedV	TTAGAAAAAA	CTT	AGGATCCCAG
	GhV	AGGATCACAA	CTT	AGGGATCAAG
	GAKV	TTAAGAAAAA	CTT	AAGAGTCAAA
	DARV	TTAAGAAAAA	CTT	AGGGGTAAAG
M-F	AngV	TTAAGGAAAA	CTT	AGGAGTAAAGC
	NiV	TTACAAAAAA	CTT	AGGAGCCAAGC
	HeV	TTAAGAAAAA	CTT	AGGAGCCAAGT
	MojV	ATATAAAAAA	CTT	AGGTGTCAGG
	CedV	TTAAGAAAAA	CTT	AGGATCCCAG
	GhV	CTAAACAAAA	CTT	AGGAAATCAG
	GAKV	TTAGAAAAAA	CTT	AAGAATCAAA
	DARV	TTAAAGAAAA	CTT	AGGACGTCAA
F-G	AngV	TTAGAAAAAA	CTT	AGGATCCAAG
	NiV	TTAATAAAAAA	CTT	AGGACCCAGGT
	HeV	TTACAAAAAA	CTT	AGGACCCAAGT
	MojV	TTAATAAAAA	CTT	AGGAGTCAGG
	CedV	TTAAATAAAA	CTT	AGGATCCCAG
	GhV	AATTAAAGAA	CTT	AATAATCGAG
	GAKV	TTAAGAAAAA	CTT	AAGAATCAAA
	DARV	TTATAAAAAA	CTT	AGGGGTCAAG
G-L	AngV	TTAAGAAAAA	CTT	AGGAGTAATGT
	NiV	TTAAGAAAAA	CTT	AGGACCCAGGT
	HeV	TTAAGAAAAA	CTT	AGGACCCAAGT
	MojV	TTACAAAAAA	CTT	AGGATTCACG
	CedV	TTAAAGAAAA	CTT	AGGATCCCAG
	GhV	CTAAGAAAAA	CTT	AGGAATTCAG
	GAKV	TTAAGAAAAA	CTT	AAGAATCAAA
	DARV	TTAAGAAAAA	CTT	AGGTGCAATG
L	AngV	TTAAGAAAAA	CTT	
	NiV	TTAAGAAAAA	CTT	
	HeV	TTAAGAAAAA	CTT	
	MojV	TTAATAAAAA	CTT	
	CedV	TTAAAGAAAA	CTT	
	GhV	TTAAGAAAAA	CTT	
	GAKV	TTAAGAAAAA	CTT	
	DARV	ATATAAAAAA	CTT	

Supplemental Table 2. Comparison of 5’ and 3’ untranslated regions of AngV and other HNVs.

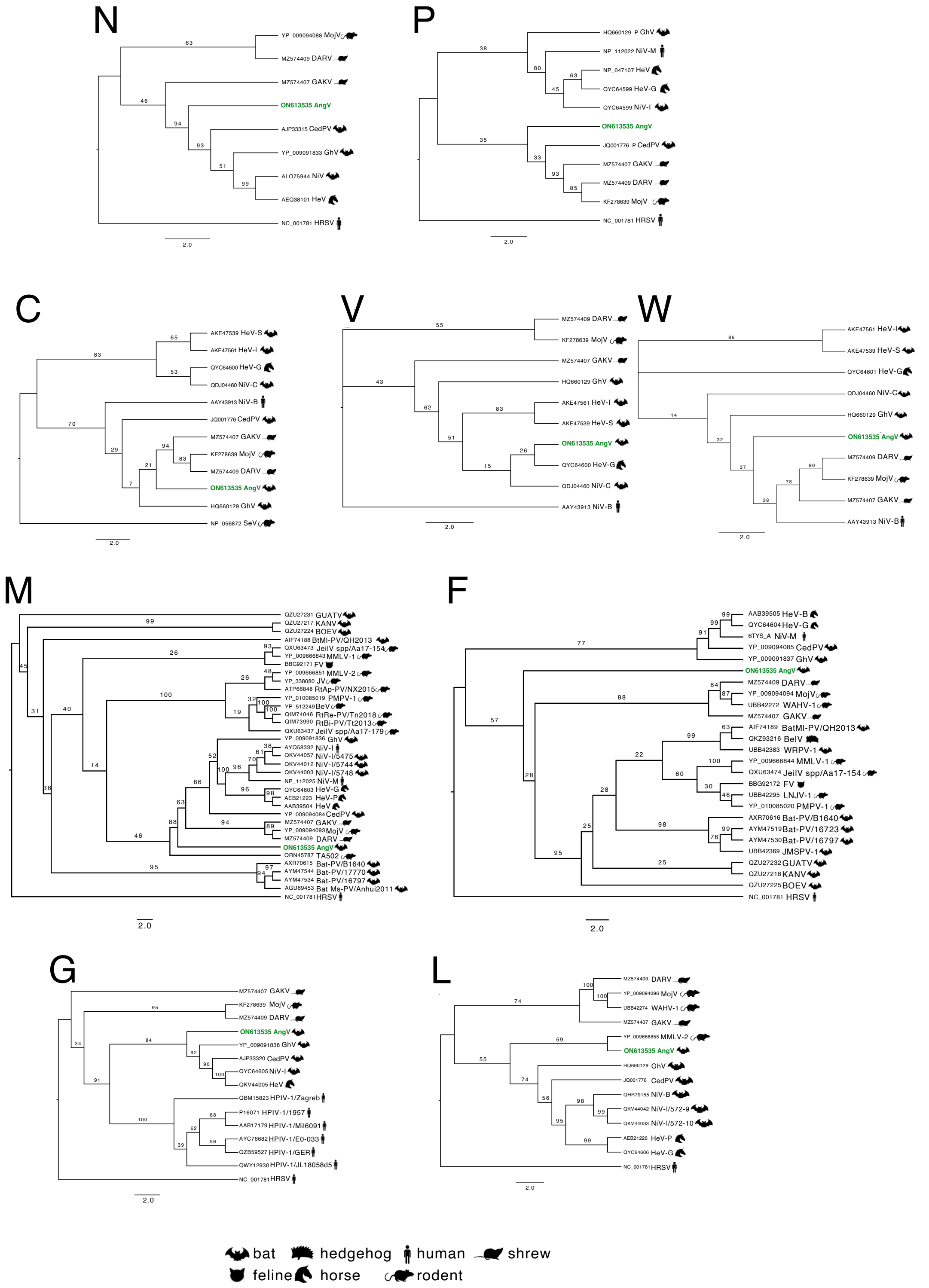
Gene	**Virus**	**5’ untranslated**		**3’ untranslated**	
		Length	**% Homology**	**Length**	**% Homology**
N	AngV			262	
	NiV			576	32.5
	HeV			558	34.8
	MojV			154	36.2
	CedV			334	39.5
	GhV			294	38.7
	GAKV			326	47.0
	DARV			458	39.2
P	AngV	221		56	
	NiV	94	33.3	459	12.8
	HeV	95	34.5	459	17.6
	MojV	254	43.7	134	43.7
	CedV	98	35.5	192	19.0
	GhV	236	42.7	213	20.5
	GAKV	132	35.3	317	13.9
	DARV	324	35.8	199	52.2
M	AngV	33		23	
	NiV	89	26.8	190	64.0
	HeV	89	57.6	190	18.6
	MojV	39	36.4	445	44.2
	CedV	114	24.3	408	7.6
	GhV	243	11.9	314	23.9
	GAKV	49	54.5	326	20.0
	DARV	165	20.0	527	5.1
F	AngV	149		30	
	NiV	273	36.6	401	9.2
	HeV	261	34.6	408	6.7
	MojV	942	12.7	163	28.6
	CedV	276	38.9	88	23.5
	GhV	391	22.7	59	40.9
	GAKV	844	18.2	340	10.6
	DARV	988	17.5	65	42.4
G	AngV	82		223	
	NiV	222	25.7	494	30.8
	HeV	222	27.5	506	29.4
	MojV	111	49.4	533	32.4
	CedV	98	42.0	139	40.8
	GhV	201	26.8	223	20.7
	GAKV	134	39.2	440	30.8
	DARV	289	29.4	529	36.0
L	AngV	245		65	
	NiV	142	38.1	57	45.5
	HeV	142	40.0	57	40.0
	MojV	212	44.6	40	35.8
	CedV	293	42.1	63	50.8
	GhV	576	29.0	67	36.9
	GAKV	355	41.1	14	64.3
	DARV	593	28.6	68	32.6



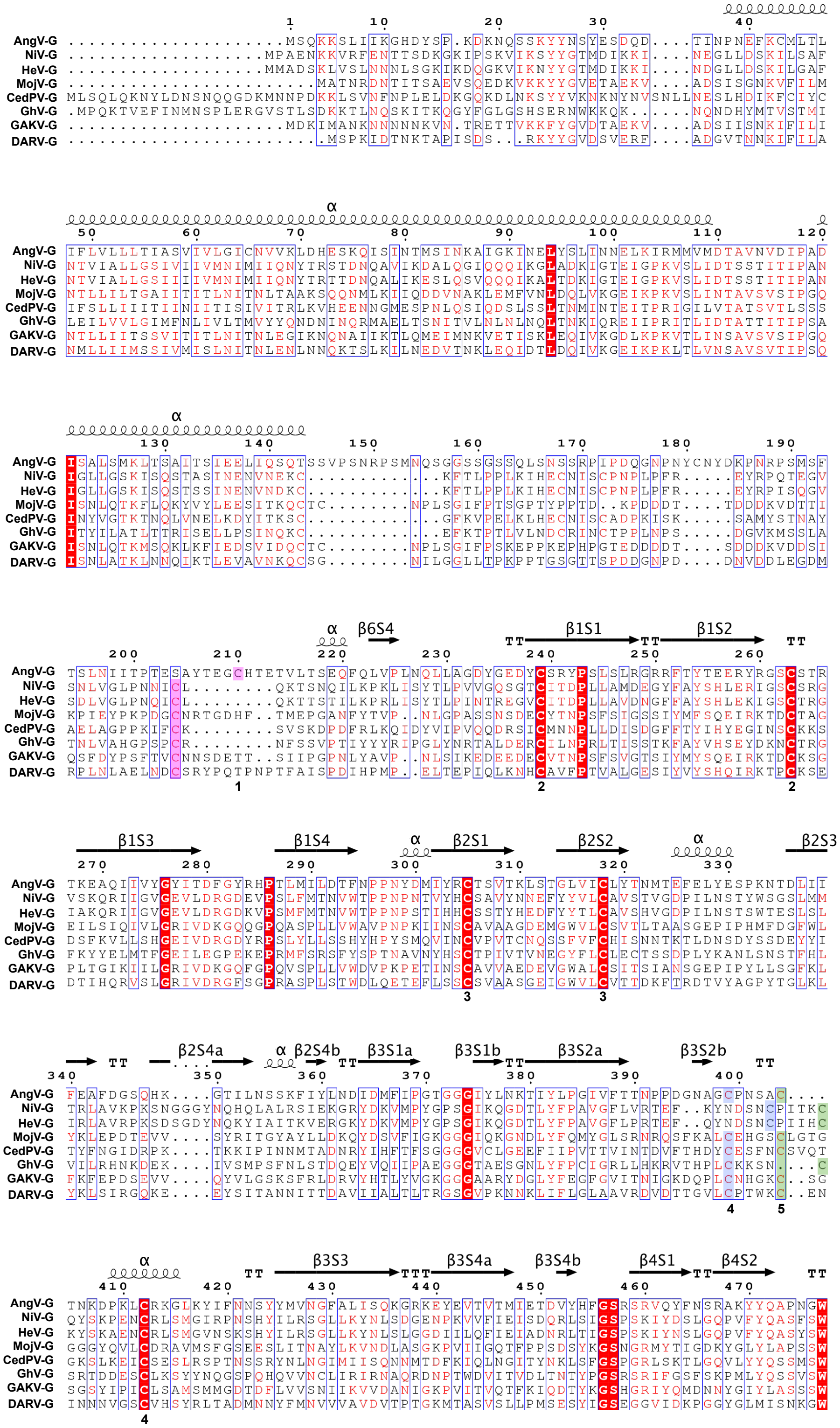
Supplemental Figure 1. Amino acid alignment of the C terminal region of the W protein following the addition of two guanine nucleotides to the putative mRNA editing site. The C-terminal domain of the henipavirus W protein is not conserved to the same extent as the C-terminal domain of the V protein (1). Amino acids are color coded, and position numbers represent amino acid position in the AngV protein. Virus name (abbreviation), followed by GenBank Accession #: Angavokely virus (AngV) ON613535; Nipah virus (NiV) AF212302; Hendra virus (HeV) AF017149; Mojiang virus (MojV) KF278639; Ghanaian bat Henipavirus (GhV) HQ660129; Daeryong virus (DARV) MZ574409; Gamak virus (GAKV) MZ574407. CedV was not included in panel C alignment because it does not encode a W protein.



Supplemental Figure 2. Uncollapsed Bayesian skyline plot of all available *Henipavirus* whole genomes, with the addition of newly discovered GAKV, DARV, and AngV. Nodes with 95% credibility interval are depicted as red lines. *Henipavirus* species are highlighted by colored tip points. The estimated time to MRCA for Angavokely virus and the previously-described bat-borne HNVs is 9,794 (95% HPD: 6,519 – 14,025) years ago.



Supplemental Figure 3. Phylogenetic trees of AngV proteins and top BLASTx hits. Rooted phylogenetic trees, with HRSV or Sendai virus (SeV) as an outgroup. Trees for V and W proteins are unrooted. Novel HNV, AngV depicted in green. Icon represents host from which depicted virus was isolated. GenBank Accessions depicted next to viral abbreviation. Bootstrap support displayed. Scale bars represent substitutions per site. Abbreviations used as follows: Bat Ms-ParaV Bat Miniopterus schreibersii paramyxovirus; Bat-PV Bat paramyxovirus; BelV Belerina virus; BeV Beilong virus; BtMl-ParaV Bat Murina leucogaster paramyxovirus; BOEV Boe virus; CedV Cedar virus; DARV Daeryong virus; FeV Feline paramyxovirus; GAKV Gamak virus; GhV Ghana bat virus; GUATV Guato paramyxovirus; HeV Hendra virus: -B Brisbane, -I Ingham siolate, -G Gympie isolate, -Proserpine isolate, -S Sandgate Isolate; HRSV Human orthopneumovirus; JeilV spp Jeilong virus species; JMSPV-1 Jingmen Miniopterus schreibersii paramyxovirus 1; JV J virus; KANV Kanhgag paramyxovirus; MojV Mojiang virus; MMLV-1 Mount Mabu Lophuromys virus 1; MMLV-2 Mount Mabu Lophuromys virus 2; NiV Nipah virus: -C Cambodia isolate, -B Bangladesh isolate, -I India isolate, -M Mayasia isolate; PMPV-1 Pohorje Myodes paramyxovirus 1; RtAp-ParaV Rat Apodemus peninsulae Paramyxovirus; RtBi-ParaV Rat Bandicota indica paramyxovirus; RtRe-ParaV Rattus exulans paramyxovirus; SeV Sendai virus; TA502 Ruloma virus; WAHV-1 Wenzhou Apodemus agrarius henipavirus 1; WRPV-1 Wufeng Rhinolophus pearsonii paramyxovirus 1.


AngV-G
NiV-G
HeV-G
MojV-G
CedPV-G
GhV-G
GAKV-G
DARV-G
α
β6S4
β1S1
β1S2
β1S3
β1S4
β2S1
β2S2
β2S3
β2S4a
β2S4b
β3S1a
β3S1b
β3S2a
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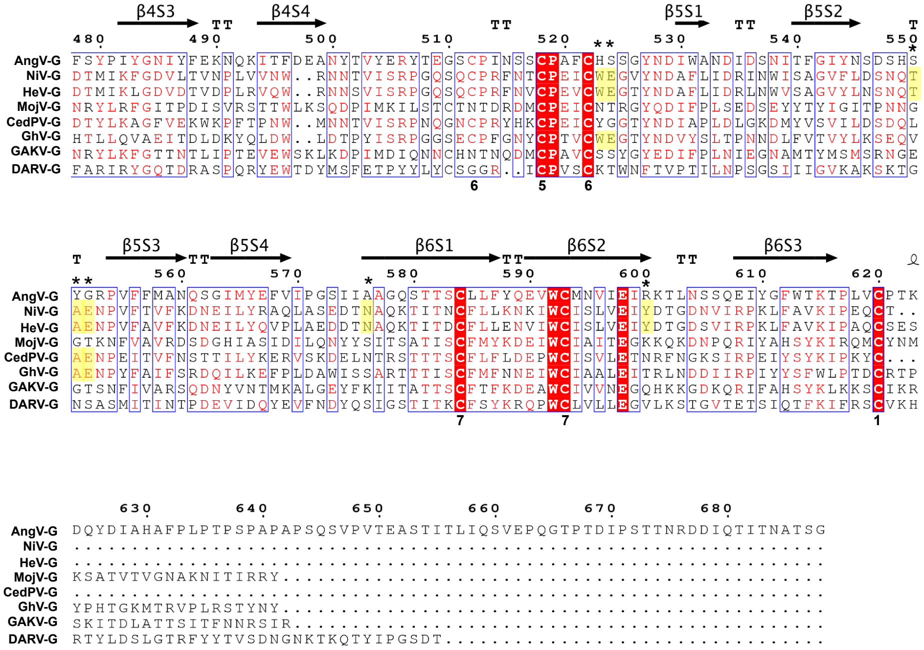
TT
1
2
3
4
5



Supplemental Figure 4. Structure-based alignment of the HNV G protein sequences. The alignment was done with MultAlin (2) and visualized using ESPRIT (3). Residues highlighted red are fully conserved and residues colored red are partially conserved. Disulfide bonds 1 through 6 are indicated numerically underneath the alignment. Notably AngV G protein disulfide bonds 1, 4, and 5 do not align across all HNVs. Homologous residues have been highlighted pink, blue and green for disulfide bonds 1, 4, and 5, respectively. Virus name (abbreviation) GenBank Accession: Angavokely virus (AngV) ON613535, Cedar virus (CedV) JQ001776; Daeryong virus (DARV) MZ574409; Gamak virus (GAKV) MZ574407; Hendra virus (HeV) AF017149; Mojiang virus (MojV) KF278639; Nipah virus (NiV) AF212302; Ghanaian bat Henipavirus (GhV) HQ660129.

Supplemental References

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