Table S1. Viruses used in the present study

Virus	Genetic group	Strain	Isolation year	Location	Source
Severe Fever with Thrombocytopenia Syndrome virus (SFTSV)	SFTS/Heartland group	HB29	2010	China	China CDC[1]
		SD4	2010	China	China CDC
Heartland virus	SFTS/Heartland group	Mo4	2009	Missouli, USA	UTMB[2]
Bhanja virus	Bhanja group	IG690	1954	India	UTMB
		IbAr2709	1968	Nigeria	UTMB
		R-1819	1974	Yugoslavia	CDC[3]
Palma virus	Bhanja group	PoTi4.92	1992	Portugal	UTMB
Forecariah virus	Bhanja group	DakArk4927	1883	Guinea	CDC
Kismayo virus	Bhanja group	LEIV3641A	1974	Somalia	UTMB
Lone Star virus	Bhanja group	TMA 1381	1967	Kentucky, USA	UTMB
Uukuniemi virus	Uukuniemi group	S23	1960	Finaland	UTMB
		SCOT FT 254	1974	Scotland	UTMB
		Potepli 63	1963	Czech	UTMB
EgAN 1825-61 virus	Uukuniemi group	EgAn 1825-61	1961	Egypt	UTMB
Manawa virus	Uukuniemi group	Argas T-461	1964	Pakistan	UTMB
Grand Arbaud virus	Uukuniemi group	Argas 2	1966	France	UTMB
Sunday Canyon virus	Uukuniemi group	RML 52301-11	1969	Texas, USA	UTMB
Zaliv Terpeniya virus	Uukuniemi group	LEIV-271Ka	1970	Kamchatka, Russia	UTMB
Murre virus	Uukuniemi group	Murre H	1973	Alaska, USA	UTMB
FinV707 virus	Uukuniemi group	FinV707	1975	Norway	UTMB
Precarious Point virus	Uukuniemi group	MI 19334	1975	Australia	UTMB
RML-105355 virus	Uukuniemi group	RML-105355	1977	Alaska, USA	UTMB
Chizé virus	Uukuniemi group	Brest Ar/T2913	1993	France	UTMB
Kaisodi virus	Kaisodi group	IG14132	1957	India	UTMB, CDC
Lanjan virus	Kaisodi group	Mal TP94	1960	Malaysia	UTMB
Silverwater virus	Kaisodi group	Can131	1960	Canada	UTMB

1 Key Laboratory of Medical Virology, National Institute for Viral Disease Control and Prevention, China CDC

2 World Reference Center for Emerging Viruses and Arboviruses (WRCEVA), University of Texas Medical Branch (UTMB)

3 Division of Vector-Borne Diseases (DVBD), arbovirus reference collection, Centers for Disease Control and Prevention (CDC)

Table S2. GeneBank sequences used in the full-length phylogeny

Genetic group	Virus	Accession number		
		L segment	M segment	S segment
Bhanja group	Bhanja virus IG690	JX961619	JX961620	JX961621
	Bhanja virus R-1819	JX961622	JX961623	JX961624
	Bhanja virus IbAr2709	JX961616	JX961617	JX961618
	Forecariah virus DakArk4927	JX961625	JX961626	JX961627
	Palma virus PoTi4.92	JX961628	JX961629	JX961630
	Bhanja virus M3811	JQ956376	JQ956377	JQ956378
	Palma virus M3443	JQ956379	JQ956380	JQ956381
	Razdan virus LEIV-Arm2741	KC335496	KC335497	KC335498
	Lone Star virus TMA 1381	KC589005	KC589006	KC589007
SFTS/Heratland group	SFTSV 2010-WSQ	HQ419226	HQ419235	HQ419239
	SFTSV AHZ/China/2011	JQ670929	JQ670931	JQ670933
	SFTSV BX-2010/Henan/CHN	HQ642766	HQ642767	HQ642768
	SFTSV HB29/China/2010	HM745930	HM745931	HM745932
	SFTSV JS4/China/2010	HQ141604	HQ141605	HQ141606
	SFTSV SD4/China/2010	HM802202	HM802203	HM802204
	SFTSV SDLZtick12/2010	JQ684871	JQ684872	JQ684873
	SFTSV XCQ-A112M	JF906056	JF906057	JF906058
	SFTSV YG1	AB817979	AB817987	AB817995
	SFTSV Gangwon/Korea/2012	KF358691	KF358692	KF358693
	Heartland virus Patient 1	JX005846	JX005844	JX005842
	Heartland virus Patient 2	JX005847	JX005845	JX005843
	Malsoor virus NIV1050650	KF186497	KF186498	KF186499
	Malsoor virus NIV1050639	KF186494	KF186495	KF186496
	Hunter Island virus	KF848980	KF848981	KF848982
Uukuniemi group	Uukuniemi virus S23	D10759	M17417	M33551
	Zaliv Terpenia virus	HM566191	HM566193	HM566192
	Precarious point virus	HM566181	HM566179	HM566180
	EgAN 1825-61 virus	HM566159	HM566158	HM566160
	Chize virus strain Brest Ar/T2913	JF838324	JF838325	JF838326
	Grand Arbaud virus Argas 27	JF838327	JF838328	JF838329
	Murre virus strain Murre H	JF838330	JF838331	JF838332
	RML-105355 virus	JF838333	JF838334	JF838335
	FinV707 virus	JQ924562	JQ924563	JQ924564
	Manawa virus PakT 462	JQ924565	JQ924566	JQ924567
	Zaliv Terpenia virus LEIV-279Az	KF767460	KF767461	KF767462
	Zaliv Terpenia virus LEIV-13841Ka	KF767463	KF767464	KF767465
Others	Karimabad virus I-58	KF297912	KF297913	KF297914
	Rift Valley fever virus ZH-548	DQ375403	DQ380206	DQ380151
	Rift Valley fever virus 200803162	JF311368	JF311377	JF311386
	Rift Valley fever virus TAN/Tan-001/07	HM586959	HM586970	HM586981
	Munguba virus	HM566164	HM566165	HM566166
	Alenquer virus	HM119401	HM119402	HM119403
	Ariquemes virus	HM119404	HM119405	HM119406
	Candiru virus	HM119407	HM119408	HM119409
	Aguacate virus VP-175A-Aguacate	NC_015451	NC_015450	NC_015452
	Punta Toro virus W	EU725771	EU725772	EU725773
	Sandfly fever Naples virus Toscana ISS.Phl.3	NC_006319	NC_006320	NC_006318
	Sandfly fever Naples virus AR	EF656363	EF656362	EF656361
	Sandfly fever Sicilian virus Izmir 19	GQ847513	GQ847512	GQ847511
	Khasan virus LEIV-776P	KF892046	KF892047	KF892048
	American dog tick phlebovirus FI6	KM048311	Not available	KM048312
	Blacklegged tick phlebovirus-1 H12	KM048313	Not available	KM048314
	Blacklegged tick phlebovirus-2 H5	KM048315	Not available	KM048316
	Gouleako virus A5/CI/2004	HQ541738	HQ541737	HQ541736

Table S3. Sequence identities among L segment RNAs and L proteins among phleboviruses

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
SFTSV HB29	1		95.3	64.1	61.4	59.4	41.7	42.5	43.7	42.8	42.9	44.1	44.2	44.1	44.6	44.5	44.6	44.2	44.4	44.8	44.3	44.3	42	41.6	42.3	42.2	41.3	35.1
SFTSV YG1	2	99.3		64.1	61	59.3	41.7	42.5	43.8	42.8	42.9	43.9	44	44	44.6	44.6	44.4	44	44.3	44.4	44.2	44.2	41.9	41.5	41.9	42.2	41.1	34.8
Heartland virus	3	73.2	73.4		62	59.8	42.1	41.5	42.5	42.5	42.2	43.5	44	43.8	44	44	43.8	43.9	44.1	44.1	44.7	44.7	42.3	41.6	41.9	41.4	40.8	35.1
Malsoor virus	4	68.6	68.8	70.7		59.4	42.6	42.6	43.5	43.5	43.3	44.2	44.3	44.2	43.7	43.8	44.7	44.3	44.4	43.5	44.4	44.4	41.2	41.6	42	41.6	40.8	34.9
Hunter Island virus	5	65.1	65.3	66.4	66.2		43	43.7	43.9	43.5	43.6	44.5	44.7	44.6	44.8	44.9	44.6	44.3	44.7	44.5	45.3	45.3	43.1	41.3	42	41.6	41.3	35.3
Kisamyo virus	6	33.5	33.6	33.7	34.9	34.9		63.7	65.6	66.5	65.9	42.2	41.5	41.6	41.2	41.2	41.9	41.8	41.7	41.7	42.9	43	39.6	38.8	39.2	40.1	41.2	36.6
Lone Star virus	7	32.8	32.9	32.9	34.6	34.4	70.6		64.1	63.5	63.4	40.7	41	41	41.5	41.6	41.8	41.7	42.2	41.5	42	42	39.2	39	39.8	39.6	40.2	35.8
Bhanja virus IG690	8	34.5	34.5	34.2	35.6	35	72.9	69.5		81.3	79.4	42.6	42.8	43	42.5	42.5	42.9	43.3	43.3	42.8	42.6	42.7	39.8	39.9	40.6	41.6	40.5	36.1
Bhanja virus R-1819	9	34.2	34.3	33.8	35.4	34.7	73.2	69.3	95.2		80.8	42.7	42.8	42.8	42.5	42.4	42.9	42.7	42.7	43	42.8	42.8	39.7	40	41	41.3	40.7	36.4
Bhanja virus IbAr2709	10	33.9	34	33.5	35.1	34.5	72.7	68.7	92.9	94.2		42.4	42.7	42.7	42.6	42.3	43.2	42.7	42.7	42.1	42.5	42.5	39.6	39.8	40.5	41.2	41.4	36.2
Grand Arbaud virus	11	33.2	33.2	33.4	34.6	33.9	30	29.3	29.6	29.5	29.5		70.7	70.7	70.8	70.7	70.5	70.7	70.9	70.2	70.4	70.5	58.5	52	52.5	44.1	45.5	38.6
EgAN 1825-61 virus	12	33.3	33.4	33.2	34.7	34.5	29.3	29.5	29.6	29.9	29.2	78.9		96.9	75.4	75.5	74.8	74.6	75	71.2	72.5	72.5	58.1	52.7	53	45.2	45.9	38.6
Chize virus	13	33.3	33.4	33.2	34.8	34.5	29.4	29.5	29.5	29.9	29.2	78.8	99.8		75.4	75.4	74.6	74.3	74.7	70.9	72.2	72.2	58.2	52.8	53.3	45.3	45.9	38.6
Uukuniemi virus S23	14	32.9	33.1	33.5	34.8	34.2	30.1	30	29.7	29.8	29.8	80.1	85.6	85.6		98.8	77.9	76.8	77	70.9	71.1	71.1	58.5	52.5	52.8	45.7	46.2	39.1
Uukuniemi virus Potepli63	15	33.1	33.3	33.5	34.8	34.2	30.1	30	29.8	29.9	29.9	80.1	85.8	85.7	99.8		78	76.9	77.1	70.9	71.2	71.2	58.6	52.6	52.9	45.7	46.1	39.2
Zaliv Terpenia virus	16	33.1	33.3	33.9	35	34.3	29.9	30.2	30.2	30.3	30.3	80.1	85.6	85.5	91.4	91.6		79.7	80.1	71	71.7	71.7	58.8	52.6	53.6	45.3	45.8	39.1
FinV707 virus	17	32.8	32.9	33.2	34.7	33.9	29.8	30.2	30	30.2	30.2	79.5	84.9	84.9	89.9	90.1	95.2		96	71	71.5	71.6	59.7	52.5	53.5	45.6	46.2	39.3
Uukuniemi virus SCOT FT 254	18	33	33.1	33.4	34.9	34	30	30.2	30.1	30.2	30.2	79.9	85.2	85.2	90	90.2	95.1	99.2		71.3	71.6	71.7	59.1	52.7	53.7	45.9	46.4	39.1
Precarious Point virus	19	33.6	33.7	33.9	35	34.1	30.1	30	30.1	30.3	29.9	77.2	77.6	77.6	78.1	78.1	78.9	78.3	78.5		72.4	72.4	58.4	52.4	53.4	44.4	45.8	38.7
Murre virus	20	33.5	33.6	34.2	35.2	34.6	30.2	29.7	30	30.3	30.3	77.8	80.2	80.2	80.2	80.4	81.1	80	80.2	80.7		100	59.6	52.2	53.3	45.3	46	39.8
RML-105355 virus	21	33.5	33.6	34.2	35.2	34.6	30.2	29.7	30	30.3	30.3	77.8	80.2	80.2	80.3	80.5	81.1	80	80.2	80.8	100		59.6	52.3	53.3	45.3	46	39.8
Manawa virus	22	32.6	32.5	33.4	33.3	33.5	28.7	28.2	29.2	29.2	29	59.3	59.7	59.7	59.3	59.3	59.9	60.7	60.6	60.6	61.1	61.1		49.5	49.5	43.4	43.9	37.2
Silverwater virus	23	32.7	32.8	32.5	33.1	32.5	28.1	28.6	28.8	28.9	28.8	47.6	47.9	47.8	47.3	47.3	48	47.7	47.7	48.1	48.6	48.7	46.7		68.2	41.9	42.4	36.8
Khsan virus	24	32.2	32.2	32	33.1	32.6	28.6	29.3	28.9	29.2	28.9	47.7	47.9	47.8	47.9	47.9	48.2	48.2	48.2	48	48.8	48.8	47.4	79.2		43.2	42.9	36.6
Sandfly fever Naples virus	25	31.2	31.2	31.4	31.7	30.9	29.1	27.7	29.2	29.3	29.4	34.7	36	36	35.6	35.7	36	35.6	35.6	35.1	35.6	35.6	33.8	33.6	34.2		52.2	35.6
Rift Valley fever virus	26	32.5	32.4	31	32.1	32.2	30	28.6	29.4	29.5	29.4	35.7	37.1	37.1	37.4	37.4	37.1	37.2	37.4	36.1	36.8	36.8	35.7	34.3	33.9	51.5		35.9
Gouleako virus	27	23.1	23.1	22.8	22.6	23.1	21.4	21.7	21.2	21.2	21	24.1	24.7	24.6	24.6	24.5	24.7	24.3	24.3	24.4	24.2	24.2	24.1	23.3	23.7	22.5	22.9	

Nucleotide and amino acid sequence identities are shown in percent above and below the diagonal, respectively.

Table S4. Sequence identities among M segment RNAs and glycoproteins among phleboviruses

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27
SFTSV HB29	1		92.2	56.4	53.7	50.1	34.6	34.4	35	35.4	35.9	31.5	33	32.8	32.4	33	32.6	32.3	32.4	32.4	32.1	32.1	29.8	31	31.2	26.8	29.4	28.9
SFTSV YG1	2	97.3		56.1	53.5	50.7	34.4	34	35.3	35.6	36	31.6	33.2	33	32.5	32.9	32.6	32.5	32.4	32	31.7	31.7	29.7	30.7	31	26.7	28.9	28.4
Heartland virus	3	62.2	62.1		52.9	49.3	34.5	33.1	33.7	34.9	34.1	32	32.8	32.5	32.5	32.9	34	33.1	32.8	32.1	32.2	32.2	29.5	31.8	30.6	24.9	28.9	28.5
Malsoor virus	4	56.5	56.6	56.4		50	32.8	33.2	32.1	33.9	32.6	31.3	32.1	32	31.1	31.6	32.4	32	32.3	31.6	31.5	31.4	29.4	30.9	31	24.8	27.6	27.9
Hunter Island virus	5	52.9	53	52.6	49.3		35.4	33.5	35.2	35.5	35	32.4	32.6	32.5	31.5	31.5	33.1	32.8	32.6	31.5	31.9	31.9	30.1	30.3	31.3	25.3	28.3	28.6
Kisamyo virus	6	23.2	23.5	23	23.1	22.1		46.1	48	48.2	47.2	32.5	33.3	33.2	31.9	32.1	32.2	33.4	33.3	30.9	32.7	32.7	29.6	31.4	31.6	26	27.7	28.5
Lone Star virus	7	22.6	22.9	23.7	22.2	23.2	49.8		48.1	49.5	49.4	32.3	32.9	33.3	32.7	33.1	32.9	32.7	33.2	31.7	33.2	33.2	29.7	32.2	31.8	25.7	27.4	28.2
Bhanja virus IG690	8	24.4	24.4	23.6	22.8	23.9	52.5	49.2		76.1	73	31.4	32.7	32.7	32.8	32.7	33.6	34.1	33.9	31.7	32.1	32.1	28.8	30.5	30.8	27	29.3	28.7
Bhanja virus R-1819	9	24.3	24.4	24.4	23.7	24.1	52.7	49.6	88.9		74	31.9	33.7	33.9	33.6	33.7	34.3	34	34.1	32.2	32.7	32.7	29.5	31.4	31.8	27.5	29.9	28.9
Bhanja virus IbAr2709	10	23.6	23.7	23.8	22.9	23.9	51.4	49.9	84.5	83.7		31.5	32.7	32.7	33.4	33.3	33.8	33.8	33.7	32.3	32.2	32.2	29.1	30.9	31.7	26.9	29	28.9
Grand Arbaud virus	11	18.3	18.1	18.4	17.7	19.3	16	17.4	17.6	17.2	16.8		59.8	59.9	60.7	60.3	60.7	60.7	61.5	58.6	60.6	60.6	48.7	44.4	45	28.5	31.6	33.8
EgAN 1825-61 virus	12	18.5	18.5	17.3	18.8	19.3	17.8	18.2	19.2	19	18.8	59		97.2	67.9	68	66.9	67.9	68.4	59.9	63	62.9	47.5	45.1	46.2	28.5	32	33.7
Chize virus	13	18.7	18.6	17.3	18.7	19.5	17.6	18.2	19.1	18.6	18.7	59.4	99.2		68	68.2	67.2	67.9	68.5	60.1	62.9	62.8	47.7	45.1	45.9	28.5	32	33.7
Uukuniemi virus S23	14	19.7	19.7	18	18.9	19.7	17.6	17.6	19	18.3	18.9	60	76.2	76.7		94.5	72.7	71.7	71.7	60.4	61.7	61.6	48.2	46.3	45.6	29.3	31.7	35
Uukuniemi virus Potepli63	15	19.5	19.5	17.8	18.6	19.4	17.8	17.7	19.2	18.4	19	60.3	76.2	76.7	98.5		72.8	71.5	71.7	60.6	61.3	61.2	48	46.4	45.4	29.2	32	34.6
Zaliv Terpenia virus	16	19.5	19.5	17.7	19.1	19.8	17.3	17	18.7	18.2	18.2	57.9	73.5	73.9	81.9	81.9		75.1	75.4	58.9	61.6	61.6	48.8	44.7	45.3	28.8	32.2	33.3
FinV707 virus	17	19.3	19.2	18	18.9	19.4	17.6	17	19	18.3	18.5	58.3	74	74.3	78.9	79	84.9		94.1	60.9	62.1	62	48.2	45.3	45.3	28.9	32.1	33.8
Uukuniemi virus SCOT FT 254	18	19.2	19.1	18	18.8	19.4	17.5	17	19	18.2	18.5	58.1	73.8	74.1	79	78.9	85.3	99		60.9	62	62	48.7	45.9	45.1	29.1	31.9	34
Precarious Point virus	19	18.3	18.5	18.7	18.6	17.7	16.2	17.2	17.8	17.6	18.6	59.1	62.7	62.8	61.9	61.7	59.8	61.4	61.6		61.7	61.7	45.9	44.2	43.2	27.1	31.7	32.8
Murre virus	20	18.3	18.4	18.9	18.2	19	16.2	16.8	18.2	17.8	18.3	58.8	61.3	61	63.1	62.7	61.6	62.5	62.3	64.6		99.8	49	45.4	46.1	28.4	32.1	34
RML-105355 virus	21	18.3	18.4	18.9	18.3	18.8	16.2	16.7	18	17.8	18.3	58.8	61.2	60.9	63	62.6	61.7	62.6	62.4	64.5	98.8		48.9	45.4	46.1	28.3	32.2	34.1
Manawa virus	22	18.3	18.2	18.9	18.6	18.2	15.9	16.1	17.3	16.8	16.6	42.7	44.9	44.8	44.7	44.7	45.5	44.3	44.4	42.8	45.5	45.3		41.8	41.8	24.9	27	29.7
Silverwater virus	23	19.8	19.5	19.6	20.3	19.1	17.7	17.1	18.2	17.9	18.2	35.9	36.2	36	36	36.1	36	36.3	36.1	36	37.3	37.1	36.5		57.9	27.1	29.8	32.1
Khsan virus	24	19.7	19.5	18.6	18.8	19.9	16.7	16.2	17.8	17.9	17.7	34.4	36.1	36.3	35.9	35.8	36.4	36.1	35.9	35	36.8	36.6	34.8	63.2		27.6	29.7	33.1
Sandfly fever Naples virus	25	14.3	14.5	14.4	13.9	15.4	13.3	13.3	13.6	13.6	13.2	15.1	17.6	17.4	17.5	17.2	16.4	17	16.7	15.9	16.1	16	15.3	16.7	17		27.6	22.6
Rift Valley fever virus	26	17.4	17.2	16.4	16.3	16.1	15.5	15.6	17.3	16.6	16.3	18.2	18	18	18	17.9	17.4	17.6	17.6	17.3	17.1	17.2	17.4	17.8	17.8	27.7		25.7
Gouleako virus	27	15.7	15.4	15	13.4	14.3	12.6	14.4	14.3	14.4	14.2	17	16.1	16.1	16.9	16.8	15.9	16.2	16.1	16.1	17	17	14.8	16.5	15.1	11.6	12.5	

Nucleotide and amino acid sequence identities are shown in percent above and below the diagonal, respectively.

Table S5. Sequence identities among S segment RNAs and nucleoproteins among phleboviruses

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	22	23	24	25	26	27	28
SFTSV HB29	1		95.5	64.4	57.6	59.8	50.6	51.9	52.7	51.8	51.1	41.6	39.6	40.6	41.4	41.6	41.5	40.3	40.4	44.5	42.7	42.4	39.9	39.9	40.2	42.1	48.3	33.7
SFTSV YG1	2	99.6		64.6	58.1	59.5	50.2	52.4	52.1	51.8	51.3	41.2	39.5	40.4	41.5	41.5	41.4	40.5	40.6	44.4	42.8	42.6	41	39.7	39.9	42.2	48.4	34
Heartland virus	3	61.6	61.6		58.7	61.5	46.5	48.2	50.1	48.6	49.4	42.1	41.6	42.4	41.3	41.4	41.4	41.8	41.8	45.2	41.6	41.6	40.1	41.7	43.8	42	47.5	32.7
Malsoor virus	4	55.6	55.6	56		56.2	48.8	50.1	48.4	49.4	48	38.8	38.8	39.1	39.2	39.3	41.8	40.6	40.4	42.5	39.7	39.7	41.2	41.3	42	43.7	44.5	35.1
Hunter Island virus	5	60.9	60.9	58.9	54.2		47.3	47.1	49.9	48.8	48.9	42.4	40	40.2	39.7	39.7	39.6	40.7	40.7	42.2	41.2	41.1	42.3	41.8	43.5	46.7	46.1	32.1
Kisamyo virus	6	41.1	41.1	38.7	37.6	37.6		61.3	67.4	68.4	67.4	41	39.1	39.1	40	40	41	41	40.9	42.2	41.8	41.8	41.3	40.3	45.1	42	45.7	35.2
Lone Star virus	7	42.9	42.9	40.5	40.7	38.4	57.7		62.9	64.3	63.3	39.1	40.6	40.5	41.8	41.9	39.3	40.6	40.7	42.6	40.4	40.5	40.7	43.5	43	42.3	44.9	35.1
Bhanja virus IG690	8	41.3	41.3	36.4	37.6	40.8	68.2	57.1		85.6	84.8	41.7	39	39.5	40.7	41.1	40.4	39.6	39.7	42.8	42.8	42.9	41.6	42.7	46.3	42	46.6	36.1
Bhanja virus R-1819	9	41.7	41.7	35.6	36.8	40	67.7	57.1	96.4		85.9	41.7	41.4	41.1	42.2	42.1	40.6	40.4	40.5	44.1	42.8	42.9	42.2	42	45.3	41.5	46.2	36.8
Bhanja virus IbAr2709	10	40.9	40.9	36.8	37.2	40.4	68.2	57.1	95.1	96.4		40.3	40.1	39.6	40	39.8	40.2	39.6	39.6	43.5	41	41.1	43.3	42.1	45.2	42.4	46.1	35.5
Grand Arbaud virus	11	27.5	27.8	27.8	24.9	29.7	25.8	23.8	26.6	25.4	25.8		68.5	69.1	67.7	68	68.4	68	68.1	61.8	59.4	59.4	48.5	45.2	44.6	41.2	43	34.4
EgAN 1825-61 virus	12	27.8	28.2	26.7	26.1	28.5	24.6	23.4	27.3	26.2	26.6	74		98.2	75.4	75.8	76.6	74.8	75.3	63.7	62.8	62.8	51.3	46.4	46.7	42.7	45.7	36.2
Chize virus	13	27.8	28.2	26.7	26.1	28.5	24.6	23.4	27.3	26.2	26.6	74	100		76.6	76.7	76.7	75.6	76.1	63.4	63.4	63.4	51.2	47.1	46.5	43	45.8	35.8
Uukuniemi virus S23	14	27.1	27.5	25.5	22.6	27	24.6	23.8	25.4	25.4	25	72.1	83.5	83.5		97.5	80.5	81.2	81.6	66	66.2	66.2	51.2	47.6	46.5	41.3	45.4	36.1
Uukuniemi virus Potepli63	15	27	27.3	25.8	23	26.9	24.9	24.1	24.9	24.9	24.5	71.4	83.1	83.1	98.8		80.9	81.5	81.9	65.2	65.8	65.8	50.5	47.6	46.9	41.8	44.4	36.7
Zaliv Terpenia virus	16	26.3	26.7	27.5	24.1	26.2	24.6	25	24.6	24.6	25	72.4	81.9	81.9	86.2	85.9		86.7	86.9	65.1	63.4	63.4	51.2	44.2	45.4	40.9	45.7	36
FinV707 virus	17	27.1	27.5	27.5	24.5	27	24.2	25.4	24.6	24.6	24.2	71.3	79.1	79.1	87	87.5	92.9		99.2	63.8	64.2	64.1	51.2	46	46.1	41.4	46.3	36
Uukuniemi virus SCOT FT 254	18	27.1	27.5	27.5	24.5	27	24.2	25.4	24.6	24.6	24.2	71.3	79.1	79.1	87	87.5	92.9	100		64.3	64.2	64.1	51	45.9	46.2	41.6	46.3	36.2
Precarious Point virus	19	28.5	28.1	30	27.6	27.8	28.7	24.8	29.5	29.1	29.9	61.4	65.8	65.8	66.5	66.3	65	65	65		67.8	67.7	51.6	47.5	47.6	41.7	47.3	37.4
Murre virus	20	29.7	29.3	27.3	25.2	29.2	26.1	24.5	28.8	29.2	28.4	58.8	62	62	62.8	61.7	59.6	60.8	60.8	71.8		99.6	48.4	46.5	46.4	42.9	44.8	38.6
RML-105355 virus	22	29.3	28.9	27	25.2	28.8	26.1	24.5	28.8	29.2	28.4	58.4	61.6	61.6	62.8	61.7	59.2	60.4	60.4	71	98.8		48.5	46.5	46.4	42.8	44.5	38.7
Manawa virus	23	27.8	27.5	27.5	26.5	30.5	27.7	26.2	25.4	25.8	26.2	41.3	41.7	41.7	41.3	42	40.6	41.3	41.3	44.1	39.2	38.8		45	47.1	46.1	44.1	34.1
Silverwater virus	24	28.6	28.2	27.4	26.7	29.2	23.9	25	25.4	25.8	25.8	34.1	34.5	34.5	33.3	33.3	32.2	32.2	32.2	36	34.9	35.3	36.8		60.5	47.1	46.5	39
Khsan virus	25	27.7	27.7	30.4	28.2	30.3	27.6	27.6	27.2	27.2	27.6	34.5	35.3	35.3	33.3	33.6	34.1	33.7	33.7	37.3	34.9	35.3	39.2	65.5		44.3	45.8	36.8
Sandfly fever Naples virus	26	31.9	31.5	31.9	31.1	34.1	31.5	29.9	30.3	30.7	30.7	27.2	29.6	29.6	28.8	28.7	26.9	27.2	27.2	29.3	30	29.6	33.9	36.3	34.6		52.7	33.1
Rift Valley fever virus	27	38.2	37.8	35.8	35.5	36.1	34.3	32	33.2	32.8	34.4	35.4	35.8	35.8	35.4	34.9	35.8	36.2	36.2	36.1	35.3	34.9	35	33.7	34.1	48.2		33.9
Gouleako virus	28	17.8	17.5	18.2	21.6	18.6	20.7	19.3	20	20	20.4	19	17.5	17.5	19.7	19.3	18.2	18.6	18.6	20.1	19.3	19.3	19.7	22.7	21.2	15.9	21.2	

Nucleotide and amino acid sequence identities are shown in percent above and below the diagonal, respectively.

Viruses with more than 90% identities in amino acid sequence are indicated by bold boxes.

Table S6. Sequence identities among S segment RNAs and nonstructural proteins among phleboviruses

		1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26
SFTSV HB29	1		95.1	54.5	34.1	33.2	27.4	28.1	25.8	23.9	25.6	30.8	34.6	34.7	35	35	34.7	35	34.5	29.1	31.3	31.3	25.3	29.5	28.5	28.4	25.6
SFTSV YG1	2	97.6		54.7	34.6	34.3	28.2	28.2	26	24	25.1	30.9	34.3	34.5	35	35	34.7	34.8	34.3	30.1	31.5	31.5	25.7	29.6	29.3	28.7	25.8
Heartland virus	3	58.8	58.8		33.6	30.2	26.7	25.9	23.1	26.3	24.2	29.5	31.8	31.8	32.4	32.8	34.1	31.8	31.9	28	28.7	28.7	25.7	26.9	25.9	25.8	22.8
Malsoor virus	4	37.4	37	34.7		24.2	22.3	24.9	21.3	21.4	21.9	26.5	31.7	31.7	30.5	30.8	30.8	30.7	30.8	26.5	26.7	26.7	26.7	22.4	20.8	23.6	21.1
Hunter Island virus	5	29	28.7	26.1	25.2		23.7	21.8	22.3	21.7	20.9	26.7	29.3	29.4	29.6	29.1	28.6	30	30	27.7	28.3	28.3	24.6	27.4	25.7	21.5	23.3
Kisamyo virus	6	12.3	12.3	12.7	15.7	10.9		33.3	34.2	34.3	33.8	27.7	28.4	27.6	29.3	28.9	27	26.1	26.8	23.8	26	26	24.5	23.6	24.6	20.6	23.9
Lone Star virus	7	15.9	15.9	15.1	17.9	12.4	49.2		33.3	34.6	33	27.2	28.9	29.2	29.2	29.7	28.4	29.8	30.1	25.8	27.6	27.6	22.7	22.1	23.2	20.6	20.6
Bhanja virus IG690	8	15.5	15.8	17.4	14	11.2	45.9	39		69.2	68.3	24.7	27.4	27.7	28.5	28.7	28	28.8	28.6	26.3	26	26	23.8	24.5	26.5	22.1	23.4
Bhanja virus R-1819	9	15.3	15.5	16.5	14.9	10.9	44.9	39.9	86.6		71.6	25.3	27.3	27.3	26.9	27.5	27	26.8	27.1	24.7	25.3	25.3	23	24.3	25.9	20.2	20.9
Bhanja virus IbAr2709	10	14.1	14.4	15.9	13.4	10.9	45.2	38.4	84.4	87.5		25.1	28.5	29.2	27.9	27.9	27.9	28.2	28.3	24	26.5	26.5	23	23.5	24.3	22.8	20.7
Grand Arbaud virus	11	14	14	13.1	10.5	10.8	12.2	11.9	11.3	10.4	10.7		49.8	49.4	53.5	53.4	53	53.5	53.5	41.9	43.8	43.8	32.4	29.5	29.8	26	23.8
EgAN 1825-61 virus	12	14.3	14.3	15	10.5	13.8	10.7	9.45	11.6	11.6	9.76	44.7		96.1	60.9	60.6	57.7	57.4	58.5	44.7	42.2	42.2	35.8	32.7	30.5	27.8	27.2
Chize virus	13	14.3	14.3	15	10.5	13.8	11	9.45	11.3	11.9	9.76	44	97.1		61	60.9	57.3	57.9	58.6	44.6	42.2	42.2	35.1	33.3	31.5	28.1	27.8
Uukuniemi virus S23	14	14.9	14.9	15.6	12	10.1	13.1	9.45	14	11.9	11.3	46.9	53.1	52.4		96.7	65.6	64.4	64.7	46.1	46.7	46.7	33.1	32.8	32.3	27.8	27
Uukuniemi virus Potepli63	15	14.9	14.9	15.6	12	10.1	13.1	9.76	13.7	11.6	11	47.6	53.5	52.8	97.8		66.4	65.2	65.6	45.8	46.3	46.3	33.3	32.8	32.2	27.6	26.9
Zaliv Terpenia virus	16	13.3	13.3	15.3	11.7	11.8	11.9	9.76	12.5	11.3	10.7	50.6	51.3	51.3	63	64.5		73.6	73.6	47.3	44.4	44.4	34	31.7	31.4	27.8	26.2
FinV707 virus	17	12.7	12.7	15	11.7	12.8	11.3	9.45	11	10.4	9.45	48.4	50.2	49.5	57.5	58.6	81.7		96.1	46.6	43.8	43.8	35.6	33.3	34	27.8	26.5
Uukuniemi virus SCOT FT 254	18	12.7	12.7	15	12	12.8	11	9.15	11	10.4	9.45	48	50.2	49.5	57.5	58.6	81.3	98.2		47.2	44.6	44.6	35.7	33.4	32.9	28.3	27
Precarious Point virus	19	14.6	14.9	13.1	10.8	11.7	9.15	9.76	10.1	8.84	7.93	36.7	35.6	34.9	36.7	36.4	39.3	38.6	38.2		44.1	44.1	31.7	29.3	27.1	23.9	24.2
Murre virus	20	14	14	13.1	12.3	11.5	8.23	9.45	9.76	9.15	8.84	35.5	33.7	33.7	34.1	34.4	31.9	34.4	34.1	36		100	31.9	30.1	31.6	27.8	25.6
RML-105355 virus	21	14	14	13.1	12.3	11.5	8.23	9.45	9.76	9.15	8.84	35.5	33.7	33.7	34.1	34.4	31.9	34.4	34.1	36	100		31.9	30.1	31.6	27.8	25.6
Manawa virus	22	10.8	10.8	11.6	11.5	11.2	8	9.23	9.85	10.8	10.8	21.3	20.9	20.9	19.9	19.5	20.6	19.9	20.2	21.7	20.2	20.2		25.6	26.1	25.4	20.7
Silverwater virus	23	13.9	13.9	13.5	11.3	12.8	11.8	12.5	16.1	15.2	13.9	17.4	16.7	16.4	17.8	18.2	16.4	18.5	18.9	19.4	17.4	17.4	14.5		33.6	27.3	24.3
Khsan virus	24	13.4	13.4	13.4	12.4	11.3	11.9	10.7	14	13.4	12.5	18.9	18.5	18.5	18.9	19.2	19.9	20.3	20.3	20.2	20.6	20.6	16.3	49.5		23.9	21.5
Sandfly fever Naples virus	25	11.5	11.3	10.5	12	9.24	13.2	10.2	12.6	13.2	13.2	11.6	11.1	11.1	10.8	11.1	12.8	11.3	11.3	10.8	10.8	10.8	10.3	13.6	10.6		21.1
Rift Valley fever virus	26	10.8	11.2	9.73	8.77	6.88	9.38	9.41	11.1	11.1	10.9	9.62	9.94	9.94	9.29	9.62	10.9	9.94	9.62	8.6	7.37	7.37	9.27	9.27	12.1	10.3	

Nucleotide and amino acid sequence identities are shown in percent above and below the diagonal, respectively.