

Supplementary Table 1. Positively selected sites of HPTBVs detected by FEL, FUBAR, and MEME.

Virus	Gene	Codon	FEL				FUBAR			MEME			
			ds	dn	LRT	p-value	ds	dn	Posterior probability	ds	dn	LRT	p-value
CCHFV	Glycoprotein-Gn	28	0.046	1.399	9.348	0.0022	0.576	2.805	0.9865	0.379	11.54	9.832	0.0032
CCHFV	Glycoprotein-Gn	95	0.447	1.502	5.374	0.0204	1.088	2.801	0.9695	3.326	12.43	6.102	0.0214
CCHFV	Glycoprotein-Gn	121	0.291	1.359	5.805	0.016	1.091	2.765	0.9314	2.181	10.7	6.379	0.0186
CCHFV	Glycoprotein-Gn	225	0.463	1.431	5.13	0.0235	1.209	2.757	0.9153	3.316	23.52	6.302	0.0193
SFTSV	Rdrp	2	0	5.398	35.544	0	0.282	29.055	1	0	96.56	37.502	0
SFTSV	Rdrp	719	0	0.407	2.993	0.0836	0.39	1.244	0.9265	0.001	7.83	3.181	0.0971
SFTSV	Glycoprotein-Gn	170	0.191	1.153	4.675	0.0306	0.59	2.815	0.9941	1.613	10.66	5.234	0.0334
SFTSV	Glycoprotein-Gn	298	0.092	1.424	12.286	0.0005	0.502	2.793	0.9979	0.785	300.5	14.991	0.0002
SFTSV	Glycoprotein-Gn	501	0.114	1.033	6.696	0.0097	0.502	2.534	0.9831	0.947	9.46	7.318	0.0115
JMTV	Rdrp	143	0	0.655	4.452	0.0349	0.49	1.804	0.9137	0	32.44	7.603	0.0099
JMTV	Glycoprotein	11	0	0.88	6.393	0.0115	0.278	1.116	0.9313	0	196.11	9.724	0.0034
JMTV	Glycoprotein	24	0	1.253	5.251	0.0219	0.556	1.922	0.9035	0.001	8.3	5.425	0.0303
JMTV	Glycoprotein	46	0	0.794	7.053	0.0079	0.273	0.839	0.9106	0	11.12	7.797	0.009
JMTV	Glycoprotein	91	0	1.699	7.029	0.008	0.488	3.563	0.9832	0.032	185.44	8.969	0.005
JMTV	Glycoprotein	472	0	1.267	6.098	0.0135	0.461	1.514	0.9014	0.001	189.38	10.878	0.0019
JMTV	Membrane protein	4	0	1.277	6.478	0.0109	0.438	5.957	0.9923	0.009	38.99	7.883	0.0086
JMTV	Membrane protein	53	0	1.465	4.435	0.0352	0.636	3.151	0.9315	0	9.86	4.57	0.0471

Supplementary Table 2. Positively selected codon of SFTSV glycoprotein. The proportion of each specific amino acid within the lineage is indicated in parentheses.

Lineage	Codon170	Codon298	Codon501	Sequence number
Genotype_F	D(80.4%); N(19.5%); S(0.1%)	A(97.2%); T(2.7%); S(0.1%)	D(100.0%)	673
Genotype_D	D(95.8%); N(4.2%)	A(95.4%); T(4.2%); S(0.4%)	D(100.0%)	237
Genotype_E	D(100.0%)	A(95.7%); V(4.3%)	D(100.0%)	23
Genotype_A	D(99.2%); N(0.8%)	A(97.9%); T(2.1%)	D(100.0%)	238
Genotype_C	D(100.0%)	A(100.0%)	D(100.0%)	11
Genotype_B2	D(91.2%); N(8.2%); X(0.6%)	A(93.0%); T(7.0%)	D(99.4%); E(0.6%)	171
Genotype_B3	D(78.5%); N(21.5%)	A(98.5%); T(1.5%)	D(100.0%)	130
Genotype_B1	D(100.0%)	A(100.0%)	D(100.0%)	32

Supplementary Table 3. Positively selected codon of CCHFV glycoprotein. The proportion of each specific amino acid in the lineage is indicated in parentheses.

Lineage	Codon28	Codon95	Codon121	Codon225	Sequence number
Europe1	E(96.6%); D(2.3%); G(1.1%)	R(95.5%); H(4.5%)	T(97.7%); I(2.3%)	L(68.6%); V(18.6%); P(11.6%); S(1.2%)	88
Asia1	E(56.2%); G(41.1%); X(1.4%); R(1.4%)	L(72.6%); P(27.4%)	T(97.4%); I(1.3%); K(1.3%)	P(100.0%)	73
Europe & Africa	R(50.0%); G(34.6%); V(7.7%); E(3.8%); X(3.8%)	L(96.2%); P(3.8%)	A(73.1%); T(26.9%)	P(96.2%); X(3.8%)	26
Asia2	E(100.0%)	L(68.0%); P(20.0%); S(8.0%); H(4.0%)	T(100.0%)	S(64.0%); P(32.0%); L(4.0%)	25
Asia & Africa	Q(87.8%); K(9.8%); E(2.4%)	P(50.0%); L(40.5%); X(7.1%); I(2.4%)	T(40.5%); I(38.1%); M(14.3%); V(4.8%); X(2.4%)	S(75.6%); L(12.9%); P(9.7%); V(9.7%)	42
Asia & Africa-Africa1	G(75.0%); E(25.0%)	P(84.6%); S(15.4%)	S(100.0%)	A(69.2%); V(30.8%)	13
Asia & Africa-India	N(100.0%)	Q(100.0%)	L(100.0%)	NA	8
Asia & Africa-Senegal	T(100.0%)	K(100.0%)	S(100.0%)	T(100.0%)	3
Asia & Africa-China1	N(100.0%)	NA	I(66.7%); T(33.3%)	T(83.3%); I(16.7%)	6
Asia & Africa-Uganda	Q(100.0%)	I(80.0%); X(20.0%)	Q(83.3%); X(16.7%)	E(100.0%)	6
Asia & Africa-China2	N(100.0%)	Q(75.0%); R(25.0%)	S(50.0%); P(50.0%)	T(100.0%)	4
Asia & Africa-United Arab Emirates	A(100.0%)	L(100.0%)	I(100.0%)	I(100.0%)	4

Supplementary Table 4. Positively selected codon of JMTV glycoprotein. The proportion of each specific amino acid within the lineage is indicated in parentheses.

Lineage	Codon11	Codon24	Codon46	Codon91	Codon472	Sequence number
China	L(93.7%); P(6.3%)	V(98.8%); A(1.2%)	F(53.8%); S(46.2%)	R(68.3%); Q(26.8%)	V(65.9%); L(34.1%)	82
Japan	L(100.0%)	A(100.0%)	S(100.0%)	R(100.0%)	V(100.0%)	7
Africa	L(100.0%)	A(50.0%); V(50.0%)	S(100.0%)	R(100.0%)	A(50.0%); V(50.0%)	6
Europe	L(100.0%)	G(71.4%); A(21.4%); V(7.1%)	F(64.3%); S(35.7%)	R(71.4%); Q(28.6%)	L(71.4%); V(21.4%); M(7.1%)	14

Supplementary Table 5. Positively selected codon of JMTV membrane protein. The proportion of each specific amino acid within the lineage is indicated in parentheses.

Lineage	Codon4	Codon53	Sequence number
China1	G(72.6%); K(27.4%)	D(100.0%)	62
China2	G(66.7%); R(33.3%)	D(55.6%); N(44.4%)	9
Japan	G(66.7%); R(33.3%)	D(100.0%)	6
Africa	G(100.0%)	N(100.0%)	1
Europe	R(100.0%)	G(83.3%); R(16.7%)	12