

Supplementary materials

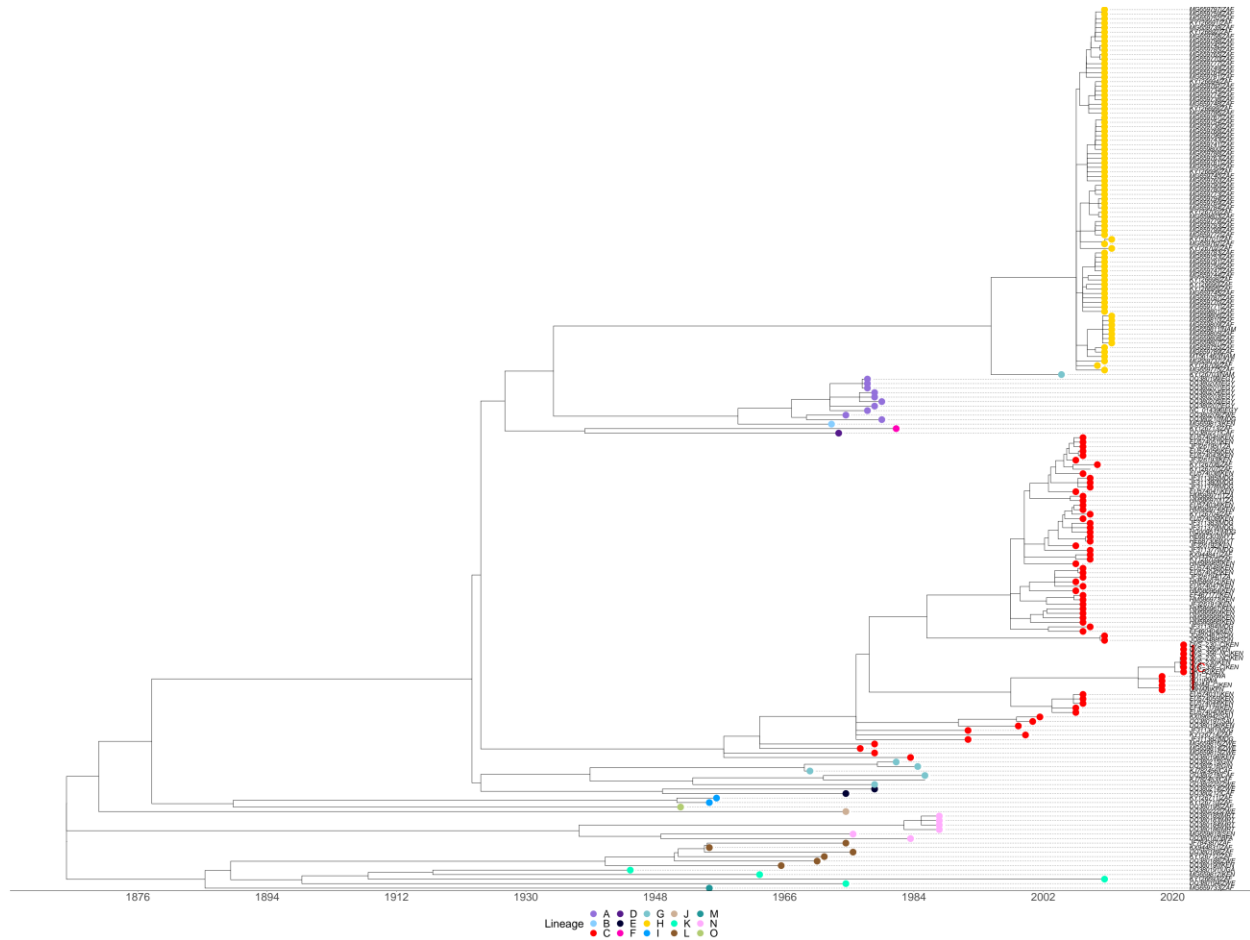
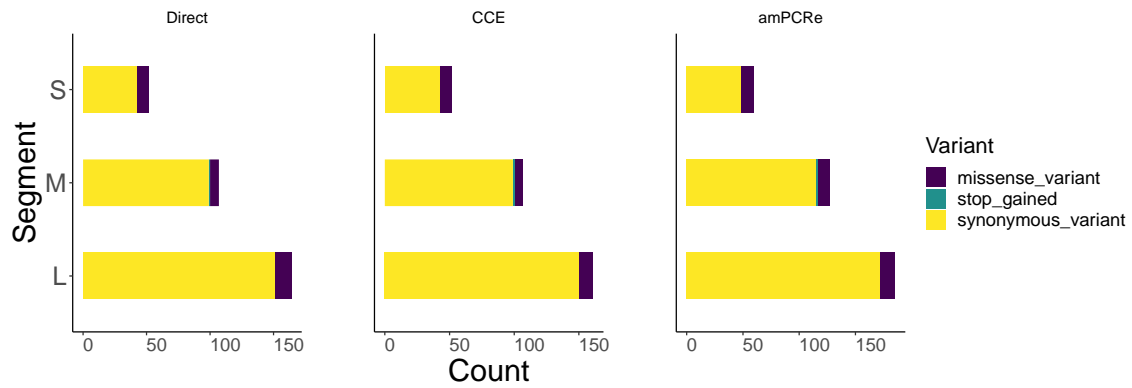


Figure S1. Molecular clock phylogenetic reconstruction. Time scaled phylogenetic tree showing the occurrence of lineages from 1951 to 2021. The tips of the phylogenetic tree are colored according to the lineages and are labeled as accession, country code and year.



	Chrom	Pos	Ref	Alt	Variant	SNP	Gene	AA.change	Segment
1	NC_014397.1	764	G	A	missense_variant	G764A	RdRp	Arg256Lys	L
2	NC_014397.1	851	G	A	missense_variant	G851A	RdRp	Ser285Asn	L
3	NC_014397.1	922	G	A	missense_variant	G922A	RdRp	Val308Ile	L
4	NC_014397.1	1063	G	A	missense_variant	G1063A	RdRp	Val355Met	L
5	NC_014397.1	1250	G	A	missense_variant	G1250A	RdRp	Ser418Asn	L
6	NC_014397.1	1354	G	A	missense_variant	G1354A	RdRp	As452Asn	L
7	NC_014397.1	2005	G	A	missense_variant	G2005A	RdRp	Ala669Thr	L
8	NC_014397.1	5335	A	G	missense_variant	A5335G	RdRp	Ile1779Val	L
9	NC_014397.1	5735	A	G	missense_variant	A5735G	RdRp	Lys1913Arg	L
10	NC_014397.1	5968	G	A	missense_variant	G5968A	RdRp	As1990Asn	L
11	NC_014396.1	715	T	A	missense_variant	T715A	Gn	Leu239Gln	M
12	NC_014396.1	1717	A	G	missense_variant	A1717G	Gn	As573Gly	M
13	NC_014396.1	1911	A	G	missense_variant	A1911G	Gn	Ile638Val	M
14	NC_014396.1	1913	A	G	missense_variant	A1913G	Gn	Ile639Met	M
15	NC_014396.1	3568	C	T	missense_variant	C3568T	Gc	Thr1190Ile	M
16	NC_014395.1	101	T	A	missense_variant	T101A	NSs	Phe35Ile	S
17	NC_014395.1	105	G	A	missense_variant	G105A	NSs	Arg36Lys	S
18	NC_014395.1	432	A	G	missense_variant	A432G	NSs	Asn145Ser	S
19	NC_014395.1	534	C	T	missense_variant	C534T	NSs	Ala179Val	S
20	NC_014395.1	651	C	T	missense_variant	C651T	NSs	Ser218Phe	S
21	NC_014395.1	684	T	C	missense_variant	T684C	NSs	Val229Ala	S
22	NC_014395.1	758	A	G	missense_variant	A758G	NSs	Ile254Val	S
23	NC_014395.1	764	C	T	missense_variant	C764T	NSs	Pro256Ser	S
24	NC_014395.1	792	A	G	missense_variant	A792G	NSs	Glu265Gly	S
25	NC_014395.1	1177	C	T	missense_variant	C1177T	NP	Gly393Glu	S

Figure S2. SNPs annotation and summary. The upper panel shows bar graphs of the SNPs observed in Direct, CCE and amPCRe treated samples. The graphs show the number of SNPs per segment as well as their annotations as synonymous or non-synonymous (stop-gained and missense). The lower panel is a summarized table showing the shared/common SNPs identified in all the three treatments for all the genomic segments.

Table S1. Sample metadata sheet containing sequencing metrics, geographic information, and ELISA results for outbreak samples.

Sample	Ct ¹	Reads	%RVFV ²	Coverage	Depth ³	Treatment	Segment	Host	Country	OD1	OD2
DK-B2	30.6	2940000	5.1	92	2105	amPCRe	L	Cow	Kenya	0.067	0.29
DK-B2	30.6	886000	0.1	24.2	6	Direct	L	Cow	Kenya	0.067	0.29
DVS-230	25.2	3960000	13.9	95.5	6032	amPCRe	L	Cow	Kenya	0.121	1.228
DVS-230	25.2	1668000	29.9	99.9	16019	CCE	L	Cow	Kenya	0.121	1.228
DVS-230	25.2	2848000	14.2	99.9	6811	Direct	L	Cow	Kenya	0.121	1.228
DVS-356	22.7	3640000	48.4	95.4	24230	amPCRe	L	Cow	Kenya	0.079	1.151
DVS-356	22.7	832000	21.4	99.7	5618	CCE	L	Cow	Kenya	0.079	1.151
DVS-356	22.7	1118000	41.9	99.9	8061	Direct	L	Cow	Kenya	0.079	1.151
DK-B2	30.6	2940000	87.1	91.6	61286	amPCRe	M	Cow	Kenya	0.067	0.29
DK-B2	30.6	886000	0	32.2	8	Direct	M	Cow	Kenya	0.067	0.29
DVS-230	25.2	3960000	25.7	95.4	18996	amPCRe	M	Cow	Kenya	0.121	1.228
DVS-230	25.2	1668000	10	99.6	8825	CCE	M	Cow	Kenya	0.121	1.228
DVS-230	25.2	2848000	6	99.8	4738	Direct	M	Cow	Kenya	0.121	1.228
DVS-356	22.7	3640000	34.4	98.8	28541	amPCRe	M	Cow	Kenya	0.079	1.228
DVS-356	22.7	832000	6.2	99.6	2651	CCE	M	Cow	Kenya	0.079	1.151
DVS-356	22.7	1118000	18	99.7	5608	Direct	M	Cow	Kenya	0.079	1.151
DK-B2	30.6	2940000	5.8	93.4	9172	amPCRe	S	Cow	Kenya	0.067	0.29
DK-B2	30.6	886000	0	72.7	18	Direct	S	Cow	Kenya	0.067	0.29
DVS-230	25.2	3960000	8.6	94.6	14117	amPCRe	S	Cow	Kenya	0.121	1.228
DVS-230	25.2	1668000	24	99.8	48512	CCE	S	Cow	Kenya	0.121	1.228
DVS-230	25.2	2848000	42.5	100	78662	Direct	S	Cow	Kenya	0.121	1.228
DVS-356	22.7	3640000	4	97	7306	amPCRe	S	Cow	Kenya	0.079	1.151
DVS-356	22.7	832000	15	99.4	14815	CCE	S	Cow	Kenya	0.079	1.151
DVS-356	22.7	1118000	22.4	99.9	16335	Direct	S	Cow	Kenya	0.079	1.151

¹qRT-PCR cycle threshold values

²Percentage number of reads aligning to the Rift Valley fever reference genome segment

³Mean genome depth of coverage per genomic segment

Table S2. Multiplex PCR amplicon primer scheme for the L-segment. The first column is the reference sequence accession, second column is the start site, third column is the end site, fourth column is the primer name (depicted as either forward, LEFT suffix or reverse depicted with the RIGHT suffix), the fifth column is the pool and the sixth column is the strand.

NC_014397.1	19	47	rvfv-L-400_1_LEFT	1	+
NC_014397.1	394	416	rvfv-L-400_1_RIGHT	1	-
NC_014397.1	332	355	rvfv-L-400_2_LEFT	2	+
NC_014397.1	704	731	rvfv-L-400_2_RIGHT	2	-
NC_014397.1	642	664	rvfv-L-400_3_LEFT	1	+
NC_014397.1	1022	1044	rvfv-L-400_3_RIGHT	1	-
NC_014397.1	948	970	rvfv-L-400_4_LEFT	2	+
NC_014397.1	1339	1361	rvfv-L-400_4_RIGHT	2	-
NC_014397.1	1256	1280	rvfv-L-400_5_LEFT	1	+
NC_014397.1	1636	1660	rvfv-L-400_5_RIGHT	1	-
NC_014397.1	1564	1587	rvfv-L-400_6_LEFT	2	+
NC_014397.1	1932	1954	rvfv-L-400_6_RIGHT	2	-
NC_014397.1	1861	1883	rvfv-L-400_7_LEFT	1	+
NC_014397.1	2239	2259	rvfv-L-400_7_RIGHT	1	-
NC_014397.1	2164	2186	rvfv-L-400_8_LEFT	2	+
NC_014397.1	2545	2568	rvfv-L-400_8_RIGHT	2	-
NC_014397.1	2480	2504	rvfv-L-400_9_LEFT	1	+

NC_014397.1	2853	2876	rvfv-L-400_9_RIGHT	1	-
NC_014397.1	2778	2800	rvfv-L-400_10_LEFT	2	+
NC_014397.1	3168	3193	rvfv-L-400_10_RIGHT	2	-
NC_014397.1	3094	3120	rvfv-L-400_11_LEFT	1	+
NC_014397.1	3474	3495	rvfv-L-400_11_RIGHT	1	-
NC_014397.1	3403	3427	rvfv-L-400_12_LEFT	2	+
NC_014397.1	3790	3812	rvfv-L-400_12_RIGHT	2	-
NC_014397.1	3724	3746	rvfv-L-400_13_LEFT	1	+
NC_014397.1	4110	4133	rvfv-L-400_13_RIGHT	1	-
NC_014397.1	4047	4069	rvfv-L-400_14_LEFT	2	+
NC_014397.1	4423	4452	rvfv-L-400_14_RIGHT	2	-
NC_014397.1	4363	4387	rvfv-L-400_15_LEFT	1	+
NC_014397.1	4731	4758	rvfv-L-400_15_RIGHT	1	-
NC_014397.1	4657	4681	rvfv-L-400_16_LEFT	2	+
NC_014397.1	5041	5067	rvfv-L-400_16_RIGHT	2	-
NC_014397.1	4968	4993	rvfv-L-400_17_LEFT	1	+
NC_014397.1	5355	5377	rvfv-L-400_17_RIGHT	1	-
NC_014397.1	5296	5319	rvfv-L-400_18_LEFT	2	+
NC_014397.1	5674	5697	rvfv-L-400_18_RIGHT	2	-
NC_014397.1	5602	5626	rvfv-L-400_19_LEFT	1	+
NC_014397.1	5984	6008	rvfv-L-400_19_RIGHT	1	-
NC_014397.1	5906	5935	rvfv-L-400_20_LEFT	2	+
NC_014397.1	6279	6302	rvfv-L-400_20_RIGHT	2	-

Table S3. Multiplex PCR amplicon primer scheme for the M-segment. The first column is the reference sequence accession, second column is the start site, third column is the end site, fourth column is the primer name (depicted as either forward, LEFT suffix or reverse depicted with the RIGHT suffix), the fifth column is the pool and the sixth column is the strand.

NC_014396.1	0	24	rvfv-M-400_1_LEFT	1	+
NC_014396.1	396	418	rvfv-M-400_1_RIGHT	1	-
NC_014396.1	329	351	rvfv-M-400_2_LEFT	2	+
NC_014396.1	708	730	rvfv-M-400_2_RIGHT	2	-
NC_014396.1	638	664	rvfv-M-400_3_LEFT	1	+
NC_014396.1	1025	1046	rvfv-M-400_3_RIGHT	1	-
NC_014396.1	965	987	rvfv-M-400_4_LEFT	2	+
NC_014396.1	1345	1368	rvfv-M-400_4_RIGHT	2	-
NC_014396.1	1279	1301	rvfv-M-400_5_LEFT	1	+
NC_014396.1	1667	1690	rvfv-M-400_5_RIGHT	1	-
NC_014396.1	1581	1608	rvfv-M-400_6_LEFT	2	+

NC_014396.1	1969	1991	rvfv-M-400_6_RIGHT	2	-
NC_014396.1	1908	1932	rvfv-M-400_7_LEFT	1	+
NC_014396.1	2292	2312	rvfv-M-400_7_RIGHT	1	-
NC_014396.1	2217	2239	rvfv-M-400_8_LEFT	2	+
NC_014396.1	2612	2636	rvfv-M-400_8_RIGHT	2	-
NC_014396.1	2537	2560	rvfv-M-400_9_LEFT	1	+
NC_014396.1	2934	2957	rvfv-M-400_9_RIGHT	1	-
NC_014396.1	2867	2892	rvfv-M-400_10_LEFT	2	+
NC_014396.1	3242	3268	rvfv-M-400_10_RIGHT	2	-
NC_014396.1	3164	3186	rvfv-M-400_11_LEFT	1	+
NC_014396.1	3551	3576	rvfv-M-400_11_RIGHT	1	-
NC_014396.1	3471	3493	rvfv-M-400_12_LEFT	2	+
NC_014396.1	3864	3885	rvfv-M-400_12_RIGHT	2	-

Table S4. Multiplex PCR amplicon primer scheme for the S-segment. The first column is the reference sequence accession, second column is the start site, third column is the end site, fourth column is the primer name (depicted as either forward, LEFT suffix or reverse depicted with the RIGHT suffix), the fifth column is the pool and the sixth column is the strand.

NC_014395.1	0	22	rvfv-S-400_1_LEFT	1	+
NC_014395.1	386	408	rvfv-S-400_1_RIGHT	1	-
NC_014395.1	328	350	rvfv-S-400_2_LEFT	2	+
NC_014395.1	709	731	rvfv-S-400_2_RIGHT	2	-
NC_014395.1	641	667	rvfv-S-400_3_LEFT	1	+
NC_014395.1	1031	1054	rvfv-S-400_3_RIGHT	1	-
NC_014395.1	957	979	rvfv-S-400_4_LEFT	2	+
NC_014395.1	1339	1361	rvfv-S-400_4_RIGHT	2	-
NC_014395.1	1265	1286	rvfv-S-400_5_LEFT	1	+
NC_014395.1	1658	1684	rvfv-S-400_5_RIGHT	1	-

Table S5. Multiplex PCR amplicon primers for sequencing RVFV. S ($n=10$), M ($n=24$), L ($n=40$). The odd numbered primers belong to pool 1 while even numbered primers belong to pool 2. The primers were designed to amplify a target sequence of approximately 400 bases within the RVFV genome. Reference genomes are used to select primer pairs that maximize the likelihood of successful amplification for known virus diversity. A pairwise local alignment score between each candidate and the reference is calculated to ensure the most 'universal' candidate primers are picked for the scheme.

<i>Primer</i>	<i>name</i>	<i>pool</i>	<i>seq</i>	<i>%gc</i>	<i>Melting temperature (use 65)</i>
<i>rvfv-S-400_1_LEFT</i>	1	ACACAAAGACCCCCTAGTGCTT	22	50.00	61.75
<i>rvfv-S-400_1_RIGHT</i>	1	AGGTCAAAGAAAGCCAGTGAGG	22	50.00	60.67
<i>rvfv-S-400_2_LEFT</i>	2	AGTGATTTCACAAGGTTCCCA	22	45.45	60.01
<i>rvfv-S-400_2_RIGHT</i>	2	TCATGCTAGGAAGTGATGAGCG	22	50.00	60.40
<i>rvfv-S-400_3_LEFT</i>	1	AGGACATTCTAATGCTGTAGTTCCA	26	38.46	60.74
<i>rvfv-S-400_3_RIGHT</i>	1	TGAATGCAGCAGTGAATAGCAAC	23	43.48	60.37
<i>rvfv-S-400_4_LEFT</i>	2	GCTGACGGCTTCCATTAGAAT	22	50.00	60.93
<i>rvfv-S-400_4_RIGHT</i>	2	TCCCGGGATGAGTTGACTCTAT	22	50.00	60.28
<i>rvfv-S-400_5_LEFT</i>	1	AGTGACAGGAAGCCACTCACT	21	52.38	61.14
<i>rvfv-S-400_5_RIGHT</i>	1	AGCTCCCTAGAGATACAAACTATT	26	38.46	59.61
<i>rvfv-M-400_1_LEFT</i>	1	ACACAAAGACGGTGCATTAAATGT	24	37.50	60.28
<i>rvfv-M-400_1_RIGHT</i>	1	CCTGCCATGGTTTCTCTCCCTA	22	54.55	61.68
<i>rvfv-M-400_2_LEFT</i>	2	AAGGGTCCTCCTCACAAAAGC	22	50.00	60.94
<i>rvfv-M-400_2_RIGHT</i>	2	TCCCATGAGCACTCTGAAGGT	22	50.00	61.55
<i>rvfv-M-400_3_LEFT</i>	1	GCTCATCATAGAACTCTACTAGAGGC	26	46.15	60.56
<i>rvfv-M-400_3_RIGHT</i>	1	AACCTCATGTGCAGTGCTGAG	21	52.38	60.98
<i>rvfv-M-400_4_LEFT</i>	2	ACAAAAATGAAAGGGGTCTGCG	22	45.45	60.14
<i>rvfv-M-400_4_RIGHT</i>	2	CCCCTGATACTTGATCTGCACA	23	47.83	60.12
<i>rvfv-M-400_5_LEFT</i>	1	CTCTGCTTATGAGTGCACTGCT	22	50.00	60.86
<i>rvfv-M-400_5_RIGHT</i>	1	GGGCAGTGAGCTACTATTTTGGA	23	47.83	60.63
<i>rvfv-M-400_6_LEFT</i>	2	AGATTACACTCAAGTATCCAGGGATAT	27	37.04	59.55
<i>rvfv-M-400_6_RIGHT</i>	2	CTGACCTCCTTCCATCCATCCT	22	54.55	61.15
<i>rvfv-M-400_7_LEFT</i>	1	GGGTGTATAAGAAGATGGTTGCCA	24	45.83	60.95
<i>rvfv-M-400_7_RIGHT</i>	1	AGTCCAATAGCTCTGGCCCT	20	55.00	60.34
<i>rvfv-M-400_8_LEFT</i>	2	TGTTGAAGGGGGTCAAGGAAGA	22	50.00	61.42
<i>rvfv-M-400_8_RIGHT</i>	2	TGTTGAAACAGAGCCATCAAAGTC	24	41.67	60.28
<i>rvfv-M-400_9_LEFT</i>	1	CAGTCAGTTAGAAAAGAGGCCCT	23	47.83	60.25

<i>rvfv-M-400_9_RIGHT</i>	1	ACCCCTCTCAAAGACAACAAAGG	23	47.83	60.95
<i>rvfv-M-400_10_LEFT</i>	2	GCACCAAACCTTATCTCATACAAGC	25	44.00	60.83
<i>rvfv-M-400_10_RIGHT</i>	2	CACTGATCTTTTGTTCATTCTCTGA	26	38.46	60.01
<i>rvfv-M-400_11_LEFT</i>	1	TGCCTGTCTATCACATCCACAG	22	50.00	60.01
<i>rvfv-M-400_11_RIGHT</i>	1	AGAGGCTGTCTTCCAAGATATAT	25	40.00	59.54
<i>rvfv-M-400_12_LEFT</i>	2	GTTGGTTTGGAGGGCCTCTTAA	22	50.00	60.67
<i>rvfv-M-400_12_RIGHT</i>	2	ACACAAAGACCGGTGCAACTT	21	47.62	61.06
<i>rvfv-L-400_1_LEFT</i>	1	TGGATTCTATATTATCAAACAGCTGGT	28	32.14	59.61
<i>rvfv-L-400_1_RIGHT</i>	1	TCATCTCCCCTAAAGGTGGTGA	22	50.00	60.41
<i>rvfv-L-400_2_LEFT</i>	2	TGATCATTTGAGCCCTGACATGA	23	43.48	60.31
<i>rvfv-L-400_2_RIGHT</i>	2	ACAGATTCTGTGACTGACCAATTTATT	27	33.33	59.83
<i>rvfv-L-400_3_LEFT</i>	1	TCCACAGATGAGGAACTAGGGA	22	50.00	59.87
<i>rvfv-L-400_3_RIGHT</i>	1	GCACAGATCTTTGCCATCGACA	22	50.00	61.69
<i>rvfv-L-400_4_LEFT</i>	2	GCAGAAGACAACCTTAGGGACC	22	54.55	60.80
<i>rvfv-L-400_4_RIGHT</i>	2	TCCACATCATGATCTGGGGAGA	22	50.00	60.55
<i>rvfv-L-400_5_LEFT</i>	1	CATAGCTGCTTTAGGGTTAATGG	24	45.83	59.80
<i>rvfv-L-400_5_RIGHT</i>	1	AAATCCCAGAACCTAGTAGTCGTT	24	41.67	59.55
<i>rvfv-L-400_6_LEFT</i>	2	TGGTCAGTTTGATAGGAGCTGAG	23	47.83	60.06
<i>rvfv-L-400_6_RIGHT</i>	2	CATCCATTGCTGCAGAGTCTGA	22	50.00	60.86
<i>rvfv-L-400_7_LEFT</i>	1	CCTCCTTCTATTCTGGGCAGA	22	54.55	61.67
<i>rvfv-L-400_7_RIGHT</i>	1	AAGCAGTGGAGCGCCCTGAAA	20	55.00	62.35
<i>rvfv-L-400_8_LEFT</i>	2	AGAGAATAGCAGGTGAGCCCTT	22	50.00	61.08
<i>rvfv-L-400_8_RIGHT</i>	2	CCTTCTAGAGTCAACCCACTGA	23	47.83	59.68
<i>rvfv-L-400_9_LEFT</i>	1	AGTCTTAAGGAGCCTCTATGGACA	24	45.83	60.66
<i>rvfv-L-400_9_RIGHT</i>	1	AAGAACTTCCCTATAGACCTGGC	23	47.83	59.55
<i>rvfv-L-400_10_LEFT</i>	2	CAGCATGGAGGTCTGAGAGAGA	22	54.55	61.13
<i>rvfv-L-400_10_RIGHT</i>	2	AGAGATCCATCACAAAGTCATCTCT	25	40.00	59.73
<i>rvfv-L-400_11_LEFT</i>	1	TGTTTACCAGGAAAAGGATGATGATG	26	38.46	60.06
<i>rvfv-L-400_11_RIGHT</i>	1	GCATATAGCTGCGGCCACTTT	21	52.38	61.52
<i>rvfv-L-400_12_LEFT</i>	2	TGCAAGGATCAGATGATAGTAGCA	24	41.67	59.73
<i>rvfv-L-400_12_RIGHT</i>	2	AATAGCTCAGACACTCCCATGC	22	50.00	60.34
<i>rvfv-L-400_13_LEFT</i>	1	GTGGGTCACTTCTCCTTAGCTGC	22	54.55	61.18
<i>rvfv-L-400_13_RIGHT</i>	1	TCTGGTATGTTCAAACGGTCTCT	23	43.48	59.68

<i>rvfv-L-400_14_LEFT</i>	2	GGTGGCGCTCTAATTCTTAGCT	22	50.00	60.66
<i>rvfv-L-400_14_RIGHT</i>	2	CGGGAATAGGAATAATATATCTTCTGGCT	29	37.93	61.03
<i>rvfv-L-400_15_LEFT</i>	1	AGTACAGCTTGCTACAAAAGATGG	24	41.67	59.62
<i>rvfv-L-400_15_RIGHT</i>	1	CCTAACTGAATGTGGTTATTCACTGG	27	40.74	60.85
<i>rvfv-L-400_16_LEFT</i>	2	TGGCTGAATGGGAAAAGCTAAAGA	24	41.67	61.08
<i>rvfv-L-400_16_RIGHT</i>	2	GGTTTTGTCTTACCCTCTGATTCT	26	38.46	60.01
<i>rvfv-L-400_17_LEFT</i>	1	GGCCCATATAGTGAGAGCTATAAGC	25	48.00	60.83
<i>rvfv-L-400_17_RIGHT</i>	1	TGTTTGTGACCCCATGTCTTC	22	50.00	60.93
<i>rvfv-L-400_18_LEFT</i>	2	TCACAACAACTGTCAGAGCAGC	23	47.83	61.05
<i>rvfv-L-400_18_RIGHT</i>	2	TGGCTCCCTCTCAAATAATTGCA	23	43.48	60.57
<i>rvfv-L-400_19_LEFT</i>	1	AACTGCATCAGACAATGATCTCA	24	41.67	60.65
<i>rvfv-L-400_19_RIGHT</i>	1	TCCATCTCGTAAGGACCACTAACA	24	45.83	61.14
<i>rvfv-L-400_20_LEFT</i>	2	TGATGCGTTAATGGATCTAATGATAGAAG	29	34.48	60.32
<i>rvfv-L-400_20_RIGHT</i>	2	TGGTCTTAGCCTAGCATGTCATC	23	47.83	60.18

Table S6. Sequence accessions and metadata (n = 196) used in molecular phylogenetic analyses. The Accession column is separated by '|' with the first string showing the accession from NCBI or strain of sequenced data in this study, the second part is the 3-letter country code and the third is the year of sample collection. The second column additionally provides the year of sample collection.

<i>Accession</i>	<i>Country</i>
<i>DQ380187 BFA 1983</i>	BFA
<i>KJ782453 CAF 1985</i>	CAF
<i>DQ380212 CAF 1974</i>	CAF
<i>KJ782456 CAF 1969</i>	CAF
<i>DQ380219 CAF 1985</i>	CAF
<i>DQ380221 CAF 1973</i>	CAF
<i>DQ380205 EGY 1979</i>	EGY
<i>DQ380203 EGY 1978</i>	EGY
<i>DQ380201 EGY 1977</i>	EGY
<i>DQ380200 EGY 1977</i>	EGY
<i>DQ380199 EGY 1977</i>	EGY
<i>DQ380207 EGY 1978</i>	EGY
<i>DQ380204 EGY 1978</i>	EGY
<i>NC_014396 EGY 1977</i>	EGY
<i>DQ380216 GIN 1984</i>	GIN
<i>DQ380215 GIN 1981</i>	GIN
<i>EU574044 KEN 2007</i>	KEN
<i>EU574043 KEN 2007</i>	KEN
<i>EU574042 KEN 2007</i>	KEN
<i>EU574041 KEN 2006</i>	KEN
<i>EU574040 KEN 2006</i>	KEN
<i>EU574039 KEN 2007</i>	KEN

<i>EU574038 KEN 2007</i>	KEN
<i>EU574045 KEN 2007</i>	KEN
<i>EU574047 KEN 2007</i>	KEN
<i>08HAB KEN 2018</i>	KEN
<i>EU574034 KEN 2007</i>	KEN
<i>HM586974 KEN 2007</i>	KEN
<i>HM586973 KEN 2007</i>	KEN
<i>HM586972 KEN 2006</i>	KEN
<i>JF326191 KEN 2007</i>	KEN
<i>JF326192 KEN 2006</i>	KEN
<i>HM586969 KEN 2007</i>	KEN
<i>EU574048 KEN 2007</i>	KEN
<i>HM586968 KEN 2007</i>	KEN
<i>HM586966 KEN 2007</i>	KEN
<i>HM586965 KEN 2006</i>	KEN
<i>HM586964 KEN 2006</i>	KEN
<i>EU574056 KEN 2007</i>	KEN
<i>EU574055 KEN 2007</i>	KEN
<i>EU574051 KEN 2007</i>	KEN
<i>HM586967 KEN 2007</i>	KEN
<i>EU574031 KEN 2007</i>	KEN
<i>EF460404 KEN 2007</i>	KEN
<i>EF467177 KEN 2007</i>	KEN
<i>08HAB-C KEN 2018</i>	KEN
<i>DK-B2 KEN 2021</i>	KEN
<i>DQ380190 KEN 1965</i>	KEN
<i>EF467178 KEN 2006</i>	KEN
<i>MG659812 KEN 1962</i>	KEN
<i>DQ380196 KEN 1998</i>	KEN
<i>DQ380198 KEN 1983</i>	KEN
<i>MG659813 KEN 1972</i>	KEN
<i>DVS-230-NC KEN 2021</i>	KEN
<i>JF326193 KEN 2006</i>	KEN
<i>DVS-356-C KEN 2021</i>	KEN
<i>DVS-356 KEN 2021</i>	KEN
<i>DVS-356-NC KEN 2021</i>	KEN
<i>DVS-230 KEN 2021</i>	KEN
<i>DVS-230-C KEN 2021</i>	KEN
<i>JF311381 MDG 1991</i>	MDG
<i>JF311380 MDG 2008</i>	MDG
<i>JF311379 MDG 2008</i>	MDG
<i>JF311384 MDG 2008</i>	MDG
<i>JF311382 MDG 1991</i>	MDG
<i>JF311378 MDG 2008</i>	MDG
<i>JF311377 MDG 2008</i>	MDG
<i>JF311383 MDG 2008</i>	MDG
<i>HQ009512 MDG 2008</i>	MDG
<i>DQ380210 MDG 1979</i>	MDG
<i>JF311385 MDG 2008</i>	MDG
<i>DQ380184 MRT 1987</i>	MRT
<i>DQ380186 MRT 1987</i>	MRT
<i>DQ380183 MRT 1987</i>	MRT
<i>DQ380185 MRT 1987</i>	MRT
<i>HE687306 MYT 2008</i>	MYT
<i>HE687303 MYT 2008</i>	MYT
<i>MT561460 NAM 2010</i>	NAM
<i>MG659811 NAM 2011</i>	NAM
<i>KY126703 NAM 2004</i>	NAM
<i>RU1 RWA 2018</i>	RWA

<i>RU1-C/RWA/2018</i>	RWA
<i>DQ380197/SAU/2000</i>	SAU
<i>KX096942/SAU/2001</i>	SAU
<i>JQ820488/SDN/2010</i>	SDN
<i>JQ820487/SDN/2010</i>	SDN
<i>MG659818/SEN/1975</i>	SEN
<i>HM586970/TZA/2007</i>	TZA
<i>HM586971/TZA/2007</i>	TZA
<i>JF326195/TZA/2007</i>	TZA
<i>JF326194/TZA/2007</i>	TZA
<i>DQ380191/UGA/1944</i>	UGA
<i>MG659763/ZAF/2010</i>	ZAF
<i>MG659784/ZAF/2010</i>	ZAF
<i>MG659783/ZAF/2010</i>	ZAF
<i>MG659782/ZAF/2010</i>	ZAF
<i>MG659781/ZAF/2010</i>	ZAF
<i>MG659780/ZAF/2010</i>	ZAF
<i>MG659779/ZAF/2010</i>	ZAF
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<i>MG659775/ZAF/2010</i>	ZAF
<i>MG659774/ZAF/2010</i>	ZAF
<i>MG659785/ZAF/2010</i>	ZAF
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<i>MG659773/ZAF/2010</i>	ZAF
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<i>MG659808/ZAF/2011</i>	ZAF
<i>MG659807/ZAF/2011</i>	ZAF
<i>MG659806/ZAF/2011</i>	ZAF
<i>MG659805/ZAF/2011</i>	ZAF
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<i>MG659801/ZAF/2010</i>	ZAF
<i>MG659800/ZAF/2010</i>	ZAF
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<i>MG659796/ZAF/2010</i>	ZAF
<i>MG659795/ZAF/2010</i>	ZAF
<i>DQ380189/ZAF/1975</i>	ZAF
<i>MG659794/ZAF/2010</i>	ZAF
<i>MG659793/ZAF/2010</i>	ZAF
<i>MG659791/ZAF/2010</i>	ZAF
<i>MG659761/ZAF/2010</i>	ZAF
<i>MG659789/ZAF/2010</i>	ZAF
<i>MG659786/ZAF/2010</i>	ZAF
<i>MG659790/ZAF/2010</i>	ZAF
<i>MG659759/ZAF/2010</i>	ZAF

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KY126709 ZAF 2009	ZAF
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KY126707 ZAF 2008	ZAF
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KY126702 ZAF 2011	ZAF
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KY126699 ZAF 2010	ZAF
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KX944831 ZAF 1955	ZAF
JF784387 ZAF 1974	ZAF
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KY126714 ZAF 1999	ZAF
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MG659755 ZAF 2010	ZAF
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MG659747 ZAF 2010	ZAF
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MG659733 ZAF 1955	ZAF
DQ380188 ZWE 1970	ZWE
DQ380222 ZWE 1974	ZWE
MG659816 ZWE 1978	ZWE
DQ380214 ZWE 1978	ZWE
MG659814 ZWE 1976	ZWE
DQ380220 ZWE 1978	ZWE
DQ380194 ZWE 1974	ZWE
MG659815 ZWE 1978	ZWE
DQ380209 ZWE 1974	ZWE