

## Supplementary Data

**Table S1:** Species names and respective accession numbers of the viral sequences used for phylogenetic analysis in Fig. 3.

Virus name	Accession
<i>Acidomyces richmondensis</i> tobamo-like virus 1	AZT88673
Acute bee paralysis virus	QGL51678
African oil palm ring spot virus	YP_002776347
<i>Agaricus bisporus</i> spherical virus	AQM32769
<i>Agaricus bisporus</i> virus 3	AQM49919
<i>Agaricus bisporus</i> virus 5	AQM49927
<i>Agaricus bisporus</i> virus 6	AQM49948
<i>Agave tequilana</i> leaf virus	YP_009373228
<i>Alternaria alternata</i> virus 1	YP_001976150
Apple chlorotic leaf spot virus	AOF42977
Apple chlorotic leaf spot virus	NP_040551
Apple stem grooving virus	NP_044335
Apple stem pitting virus	NP_604464
Apricot pseudo-chlorotic leaf spot virus	BCA25706
Apricot vein clearing associated virus	YP_008997790
Apricot vein clearing associated virus	BCA25721
<i>Aspergillus foetidus</i> dsRNA mycovirus	YP_007353985
<i>Aspergillus heteromorphus</i> alternavirus 1	AZT88576
<i>Aspergillus</i> mycovirus 341	ABX79997
Atractylodes mottle virus	YP_009508317
Atrato Virga-like virus 7	QHA33778
Atrpec virus 1	AYN75539
<i>Auricularia heimuer</i> myco virgavirus 1	QIM57886
Banana mild mosaic virus	NP_112029
Beihai charybdis crab virus 1	YP_009333242
Beihai picorna-like virus 71	YP_009333456
Betavulgaris mito virus 1	QBN22178
Blackberry vein banding-associated virus	YP_008411010
Blueberry scorch virus	AAY18409
<i>Botrytis</i> virus X	NP_932306
Bundaberg bee virus 2	AWK77852
Camellia ring spot associated virus 1	QEJ80622
<i>Cannabis sativa</i> mitovirus 1	DAB417542
Carrot Ch virus 1	NP_009103999
Cassava common mosaic virus	NP_042695
<i>Chenopodium quinoa</i> mitovirus 1	YP_009551903
Cherry mottle leaf virus	AOY07776
Cherry rusty mottle associated virus	YP_007761581
Cherry symptomless virus	QIA61761
Cherry virus A	ATJ05013
Chrysanthemum virus B	CAO78688
Citrus chlorotic leaf spot virus	QOQ52500
Citrus leaf blotch virus	NP_624333
Citrus virga-like virus	ARO38275
Cnidium virus X	BBI37360
Cole latent virus	QGN03507
Cowpea mild mottle virus	AGS13088

Cucumber vein-clearing virus	YP_009664734
Diuris virus A	YP_006905850
Fig latent virus 1	CAY32622
Fox tail mosaic virus	AWT40556
Fox tail mosaic virus	ABW25054
Frangipani mosaic virus	AEW67306
<i>Fusarium graminearum</i> alternavirus 1	YP_009449446
<i>Fusarium graminearum</i> mycotymo virus 1	YP_009553357
<i>Fusarium incarnatum</i> alternavirus 1	AYJ09266
<i>Fusarium poae</i> alternavirus 1	YP_009272949
Garlic yellow mosaic-associated virus	AZM69107
Grapevine associated jivivirus 1	QIJ25699
Grapevine leafroll-associated virus 1	QBZ78645
Grapevine leafroll-associated virus 3	AXI82159
Grapevine leafroll-associated virus 4	ARP51817
Grapevine Pinotgris virus	QEQ50023
Grapevine virga-like virus	QCF47402
Grapevine virus A	NP_619662
Grapevine virus A	AAO84267
Grapevine virus B	AHZ62715
Grapevine virus B	AWD77984
Grapevine virus B	AOX49252
Grapevine virus E	YP_002117775
Grapevine virus G	ATV81261
Grapevine virus G	YP_009551946
Grapevine virus H	YP_009551905
Grapevine virus L	QBM91193
Grapevine virus M	QCF24338
<i>Haemonchus contortus</i> virus	CDJ82925
Heracleum latent virus	QIQ28218
Hibiscus latent Singapore virus	ARM71140
Hippeastrum latente virus	YP_002308447
Hobart betaflexivirus 1	AWK77906
Hubei virga-like virus 1	YP_009337423
<i>Humulus lupulus</i> mitovirus 1	DAB41749
Hydrangea chlorotic mottle virus	YP_002985636
Hydrangea ring spot virus	BAU45634
Ligustrum virus A	YP_009288956
Little cherry virus 2	ATB18128
Luckshill virus	AWA82251
<i>Macrophomina phaseolina</i> tobamo-like virus 1A	ALD891032
Mexico tricho virus	QDR50348
Mint virus 2	YP_009664761
Odonto glossum rings potvirus	AAZ81884
<i>Oxybasis rubra</i> mitovirus 1	DAB41745
Papaya mottle associated virus	QIJ97108
Peach chlorotic leaf spot virus	AYA62500
Peach mosaic virus	YP_002308565
Pepper virus A	YP_009357230
Perth betaflexivirus 1	AWK77908
<i>Petunia exserta</i> mitovirus 1	DAB41750
Phlox virus B	YP_001552317
Pineapple mealy bug wilt-associated virus 2	QCC20262
Pistachio ampelo virus A	AVN99305
<i>Plasmopara viticola</i> associated tobamo-like virus 1	QIP68002
<i>Podosphaera prunicola</i> tobamo-like virus	ATS94407

Potato vírus H	AYV96574
Potato virus M	QBL75476
Potato virus M	ATG34140
Potato virus M	NP_056767
Potato virus T	AFV39891
Potato virus T	YP_002019748
Potato vírus T	AFV39891
Riboviria sp	QDH89210
<i>Salvia divinorum</i> RNA virus 1	YP_009553026
Shayang virga-like vírus 1	YP_009333208
<i>Solanum chacoense</i> mitovirus 1	DAB41743
<i>Stemphylium lycopersici</i> mycovirus	YP_009551661
Tamus red mosaic virus	YP_004849314
Tobacco mild green mosaic virus	QIM41095
Tulip virus X	NP_702988
Turtle grass vírus X	YP_009552762
Weivirus-like virus	QJI53767
Wenzhou picorna-like vírus 26	YP_009337682
Wenzhou picorna-like vírus 27	YP_009336706
Yam latente virus	YP_009134730

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**Table S2:** General description of deep sequenced libraries and virus detection strategy. Raw counts of RNA and DNA libraries as well as metrics related to transcript assembly and sequence similarity searches are presented in the rows. *Agave* species are indicated in the columns.

	<i>A. fourcroydes</i>	<i>A. sisalana</i>	<i>A. hybrid 11648</i>	Sum
<b>Raw RNAseq reads</b>	200,498,222	208,260,315	150,509,074	559,267,611
<b>Assembled Transcripts</b>	81,190	93,569	77,194	251,953
<b>Mean contig length</b>	599	575	584	1758
<b>Min. contig length</b>	168	171	171	510
<b>Viral Transcripts BLASTN</b>	4	1	5	10
<b>Viral Transcripts BLASTX</b>	49	34	28	79*
<b>Raw DNAseq reads</b>	131,365,537	118,820,218	119,180,610	369,366,365

**Table S3:** Similarity of *Agave*-derived contigs against known CPMMV genomes. Analysis was performed using Blast with the variant BLASTn.

	Plant	AF				AS	HI				
	Contig	DN22786	DN53839	DN59783	DN97584	DN6612	DN10130	DN110105	DN114005	DN42686	DN55516
	Length	270	3600	369	362	867	867	264	387	315	285
KC774019.1	Sim. (%)	97.41	98.31	98.37	98.34	98.62	98.73	98.49	95.87	98.41	98.25
	Length	269	3599	368	361	866	866	263	386	314	284
KC774020.1	Sim. (%)	97.78	98.08	97.29	97.21	98.85	98.96	98.86	95.35	98.73	97.54
	Length	269	3599	368	358	866	866	263	386	314	284
KC884245.1	Sim. (%)	97.05	98.42	98.37	98.62	98.85	98.96	99.24	95.87	97.46	96.49
	Length	270	3599	368	361	866	866	263	386	314	284
MK202583.1	Sim. (%)	98.52	96.25	98.37	96.41	90.31	90.43	99.24	94.32	96.19	
	Length	269	3595	368	361	866	866	263	386	314	
KC884248.1	Sim. (%)	98.15	98.28	98.65	98.34			99.24	95.87	97.46	
	Length	269	3599	368	361			263	386	314	

**Table S4:** Quantitative metrics for the reference genome of CPMMV (CPMMV:BR:MG:09:3) and the genome obtained from the RNA-seq data of *Agave fourcroydes*.

Name	CPMMV:BR:MG:09:3	CPMMV isolate PB:AF
Contigs	1	1
Length	8196	8193
N50	8196	8193
L50	1	1
GC	0.403	0.4
For runs of Ns ( $\geq 10$ Ns):		
Num	0	2
Span	0	47

**Table S5:** BLASTx best hits for each viral contig, and their respective alignment metrics.

qseqid (TRINITY_DN...)	sseqid	pident	length	mismatch	gapopen	qstart	qend	sstart	send	evalue	bitscore	qlen	species
61147	YP_009553503.1	50.9	55	27	0	4	168	1915	1969	8.10E-14	65.9	213	Actinidia seed-borne latent virus
49676	AQM49927.1	39.7	662	384	7	4	1953	1742	2400	5.2E-124	435.3	2163	Agaricus bisporus virus 5
16142	AQM49927.1	32.7	431	252	8	115	1356	1259	1668	1.90E-60	223.4	1359	Agaricus bisporus virus 5
44352	AQM49927.1	30.8	347	226	6	4	1008	1742	2086	2.20E-37	146.4	1011	Agaricus bisporus virus 5
83710	AQM49927.1	46.3	188	100	1	1	564	2214	2400	1.40E-42	163.3	774	Agaricus bisporus virus 5
19804	AQM49927.1	52.9	140	66	0	7	426	2076	2215	4.30E-38	147.5	435	Agaricus bisporus virus 5
24880	AQM32763.1	54.5	411	187	0	37	1269	2132	2542	1.3E-139	486.5	1404	Agaricus bisporus virus 6
27401	AQM49948.1	47.3	281	145	3	1	843	1815	2092	2.10E-68	249.2	846	Agaricus bisporus virus 6
77293	AQM49948.1	59.5	121	47	2	4	366	1700	1818	1.60E-41	158.7	366	Agaricus bisporus virus 6
55189	AQM32763.1	41.1	112	58	3	7	324	642	751	4.70E-21	90.5	327	Agaricus bisporus virus 6
Contig17	YP_459948.1	32.8	186	121	3	271	825	11	193	1.50E-26	110.2	867	Alternanthera mosaic virus
63052	YP_459944.1	43	114	64	1	1	339	1023	1136	1.40E-20	89	342	Alternanthera mosaic virus
81586	YP_001976142.1	85.5	110	16	0	1	330	441	550	3.10E-52	194.1	330	Alternaria alternata virus 1
61614	YP_001976151.1	75	80	20	0	7	246	21	100	1.30E-34	135.2	246	Alternaria alternata virus 1
Contig7	NP_604464.1	49.9	1001	477	6	607	3588	1193	2175	1.80E-286	975.7	3600	Apple stem pitting virus
83885	NP_604464.1	42.8	201	112	3	10	606	1652	1851	8.50E-40	153.7	609	Apple stem pitting virus
Contig14	YP_007353983.1	53.2	538	250	1	1	1614	191	726	2.10E-170	589	1617	Aspergillus foetidus dsRNA mycovirus

73798	YP_007353985.1	76.3	97	23	0	10	300	637	733	3.50E-39	150.6	300	Aspergillus foetidus dsRNA mycovirus
116043	YP_007353985.1	75.9	79	19	0	4	240	307	385	1.20E-34	135.2	240	Aspergillus foetidus dsRNA mycovirus
72309	YP_007353983.1	55.4	56	25	0	64	231	6	61	2.60E-13	64.3	231	Aspergillus foetidus dsRNA mycovirus
Contig19	AZT88576.1	49.6	514	255	3	1	1530	319	832	9.90E-138	480.3	1533	Aspergillus heteromorphus alternavirus 1
83752	AZT88575.1	55.4	112	50	0	1	336	159	270	4.70E-40	153.7	336	Aspergillus heteromorphus alternavirus 1
Contig5	QED22727.1	54.6	1124	502	5	31	3384	13	1134	0.00E+00	1201.8	3387	Botryosphaeria dothidea tobamo- like virus
Contig12	ADD65542.1	41.2	148	82	1	1	444	525	667	6.50E-32	127.1	465	Cassia mild mosaic virus
100760	ARO38275.1	56.7	838	353	3	544	3036	1	835	4.70E-280	954.1	3069	Citrus virga-like virus
26278	ARO38274.1	50.4	125	61	1	4	378	1168	1291	1.00E-31	126.3	432	Citrus virga-like virus
133840	ARO38274.1	62.3	114	42	1	1	339	369	482	9.20E-36	139.4	339	Citrus virga-like virus
88105	YP_006905850.1	32.6	218	120	8	1	612	1107	1311	1.40E-18	83.2	615	Diuris virus A
86319	YP_006908997.1	66.7	105	28	3	1	309	258	357	5.10E-33	130.2	309	Diuris virus A
44239	YP_004732978.2	36.7	256	139	13	7	744	1221	1463	1.10E-25	107.1	765	Grapevine Pinot gris virus
3617	QCF47403.1	38.4	739	391	12	70	2268	25	705	1.80E-138	483.4	2310	Grapevine virga- like virus
65779	QCF47402.1	63.4	134	49	0	1	402	368	501	1.60E-42	162.2	402	Grapevine virga- like virus
52979	YP_009552539.1	26.6	872	538	26	31	2406	16	865	2.30E-73	267.3	2619	Grapevine virus G
46510	YP_009552539.1	25	680	408	23	1	1806	210	865	8.50E-41	158.7	1965	Grapevine virus G
40814	YP_009552542.1	38.3	128	79	0	16	399	74	201	7.60E-21	90.1	402	Grapevine virus G
65618	YP_009552542.1	35.9	128	82	0	10	393	74	201	2.20E-20	88.6	396	Grapevine virus G



42135	YP_009551905.1	54.9	255	115	0	82	846	1368	1622	6.20E-81	290.8	846	Grapevine virus H
52810	YP_009552715.1	38.4	482	281	7	91	1521	1232	1702	3.40E-87	313.9	4224	Halhan virus 3
99951	YP_009552715.1	48.6	72	34	3	1	216	445	513	1.10E-13	65.5	222	Halhan virus 3
Contig9	YP_009109559.1	27.4	1644	930	51	1093	5370	2	1600	3.90E-136	476.9	5397	Macrophomina phaseolina tobamo-like virus
Contig6	YP_009109559.1	32.9	140	77	4	2419	2838	1314	1436	4.50E-10	57.4	3309	Macrophomina phaseolina tobamo-like virus
30831	YP_009109561.1	41.6	370	182	6	1	1110	40	375	1.40E-64	236.9	1110	Macrophomina phaseolina tobamo-like virus
38090	YP_009109562.1	46.1	332	169	2	43	1008	2	333	7.30E-84	300.8	1038	Macrophomina phaseolina tobamo-like virus
Contig8	YP_009109562.1	36.9	293	178	6	31	888	7	299	3.20E-44	169.1	1011	Macrophomina phaseolina tobamo-like virus
105616	YP_009109562.1	36.1	299	180	4	16	891	7	301	2.20E-45	172.9	1005	Macrophomina phaseolina tobamo-like virus
72996	YP_009109559.1	84.3	70	11	0	1	210	1962	2031	1.60E-33	131.3	213	Macrophomina phaseolina tobamo-like virus
26423	YP_009109559.1	48.5	68	35	0	1	204	1766	1833	3.70E-16	73.6	204	Macrophomina phaseolina tobamo-like virus
75281	YP_009109561.1	68.3	63	20	0	13	201	221	283	3.30E-20	87	204	Macrophomina phaseolina tobamo-like virus
85955	YP_009109559.1	84.1	63	10	0	7	195	1351	1413	2.00E-27	110.9	198	Macrophomina phaseolina tobamo-like virus
38752	YP_446996.1	33.8	201	132	1	148	747	16	216	1.20E-33	133.7	774	Nerine virus X
59050	AVN99304.1	41.6	1634	766	18	1	4899	1	1446	0.00E+00	1148.3	4902	Pistachio ampelovirus A
49906	AVN99304.1	42.4	1603	762	17	1	4794	1	1446	0.00E+00	1160.2	4797	Pistachio ampelovirus A
Contig16	AVN99304.1	34.8	1246	655	16	1	3729	1	1091	1.00E-191	661	3732	Pistachio ampelovirus A

59050	AVN99304.1	43.4	670	378	1	1	2010	1	669	8.20E-159	551.6	3561	Pistachio ampelovirus A
2548	AVN99305.1	63.6	453	165	0	1	1359	33	485	3.30E-177	611.3	1362	Pistachio ampelovirus A
Contig15	AVN99306.1	39.1	207	126	0	292	912	150	356	4.10E-38	148.7	924	Pistachio ampelovirus A Plasmopara viticola associated ourmia-like virus 29
75741	QGY72559.1	46.6	131	66	3	7	390	459	588	1.60E-28	115.5	390	Plasmopara viticola associated ourmia-like virus 6
110665	QGY72536.1	61.8	68	26	0	1	204	76	143	2.30E-21	90.9	204	Podosphaera prunicola tobamo-like virus
83949	ATS94408.1	46.4	207	107	3	10	621	614	819	2.90E-43	165.2	621	Podosphaera prunicola tobamo-like virus
77371	ATS94409.1	40.9	171	101	0	61	573	98	268	6.80E-39	150.6	576	Podosphaera prunicola tobamo-like virus
69322	ATS94408.1	49.4	85	42	1	7	261	821	904	3.00E-18	80.9	264	Podosphaera prunicola tobamo-like virus
Contig20	YP_009551663.1	64	339	114	2	4	1011	423	756	2.90E-125	438.3	1014	Stemphylium lycopersici mycovirus
Contig1	YP_009551661.1	68.5	308	87	3	1	924	545	842	8.70E-113	396.7	927	Stemphylium lycopersici mycovirus
17344	YP_009551660.1	64.3	252	90	0	1	756	897	1148	9.70E-102	359.8	759	Stemphylium lycopersici mycovirus
Contig10	YP_009551661.1	56.5	239	98	1	4	702	305	543	1.10E-75	273.1	702	Stemphylium lycopersici mycovirus
Contig11	YP_009551661.1	64.8	128	45	0	1	384	170	297	1.70E-41	158.7	387	Stemphylium lycopersici mycovirus
92324	YP_009551660.1	68	100	32	0	1	300	799	898	3.30E-40	154.1	306	Stemphylium lycopersici mycovirus

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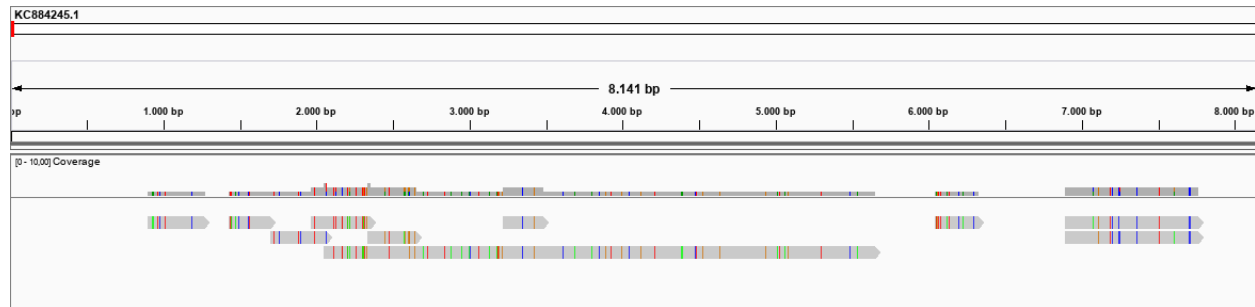
**Table S6:** Overview of the transcripts assigned as false positives (rows) and associated data. Columns indicate transcript name, length (in base pairs), the protein and species hit on BLASTx, their respective accession code, detected protein domains and finally, the reason for discard.

Protein Domain	Discarded by	ORF Pattern
AAA domain	Present in genomic DNA, protein domain not viral	non-fragmented
Cation efflux family, Dimerisation domain of Zinc Transporter	Present in genomic DNA, protein domain not viral	
Thaumatin family	Present in genomic DNA, protein domain not viral	
<i>none identified</i>	<i>no relevant hits</i>	
<i>none identified</i>	<i>no relevant hits</i>	non-fragmented
<i>none identified</i>	<i>no relevant hits</i>	non-fragmented
Cas3	Protein domain not viral	
Viral methyltransferase	CPMMV	
<i>none identified</i>	Present in genomic DNA	non-fragmented
<i>none identified</i>	Present in genomic DNA	non-fragmented
Mitovirus RdRp	Present in genomic DNA	non-fragmented
<i>none identified</i>	Present in genomic DNA	non-fragmented
<i>none identified</i>	Present in genomic DNA	non-fragmented

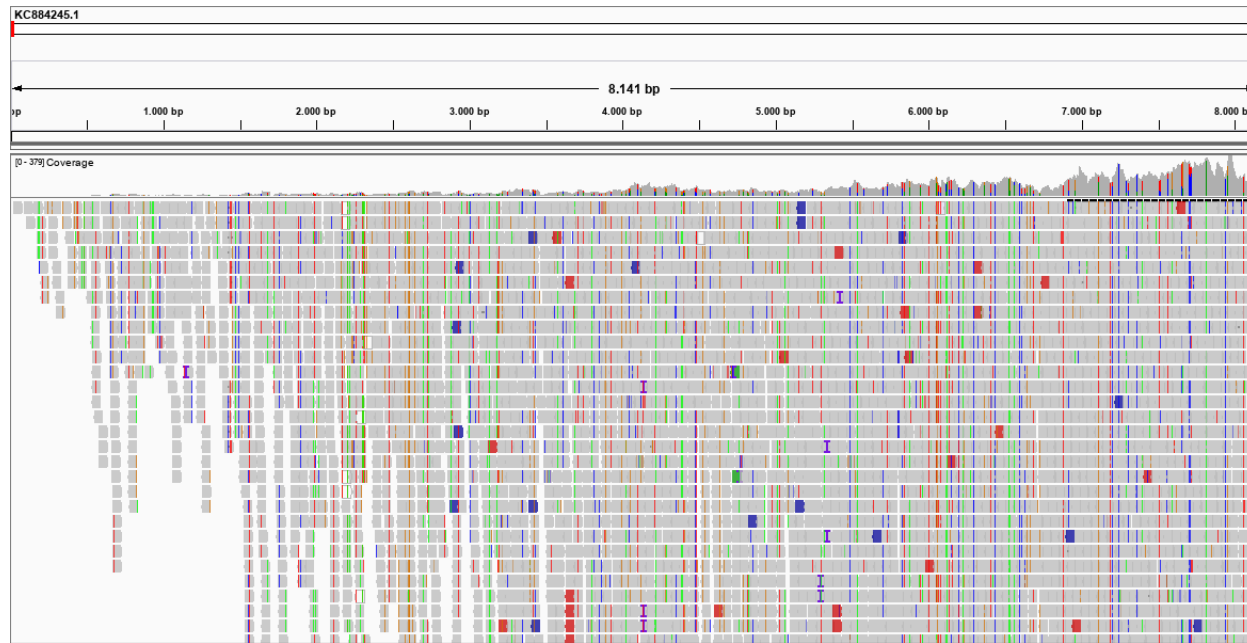
Name	Length	Protein hit	Species	Accession code
<i>disc1</i>	813	RdRp	Macrophomina phaseolina tobamo-like virus	YP_009109559.1
<i>disc2</i>	1197	Putative Protein P31	Pistachio ampelovirus A	AVN99313.1
<i>disc3</i>	762	Putative Protein P33	Pistachio ampelovirus A	AVN99309.1
<i>disc4</i>	201	Hypothetical Protein	Aspergillus foetidus dsRNA mycovirus	YP_007353982.1
<i>disc5</i>	1809	Putative RdRp	Aspergillus mycovirus 341	ABX79997.1
<i>disc6</i>	222	RdRp	Helicobasidium mompa partitivirus V1-2	BAD32678.1
<i>disc7</i>	792	Movement Protein	Podosphaera prunicola tobamo-like virus	ATS94408.1
<i>disc8</i>	369	RdRp	Apple stem pitting virus	NP_604464.1
<i>disc9</i>	693	RdRp	Beta vulgaris mitovirus 1	DAB41759.1
<i>disc10</i>	309	RdRp	Beta vulgaris mitovirus 1	DAB41759.1
<i>disc11</i>	435	RdRp	Beta vulgaris mitovirus 1	DAB41759.1
<i>disc12</i>	207	RdRp	Beta vulgaris mitovirus 1	DAB41759.1
<i>disc13</i>	228	RdRp	Beta vulgaris mitovirus 1	DAB41759.1

**Table S7:** Classification scheme for the phylogenetic analysis. Columns indicate: Class name, the requisites for that given class (characteristics of the viral species, concerning contig length and type), the number of species included in that category, and their correspondent percentage.

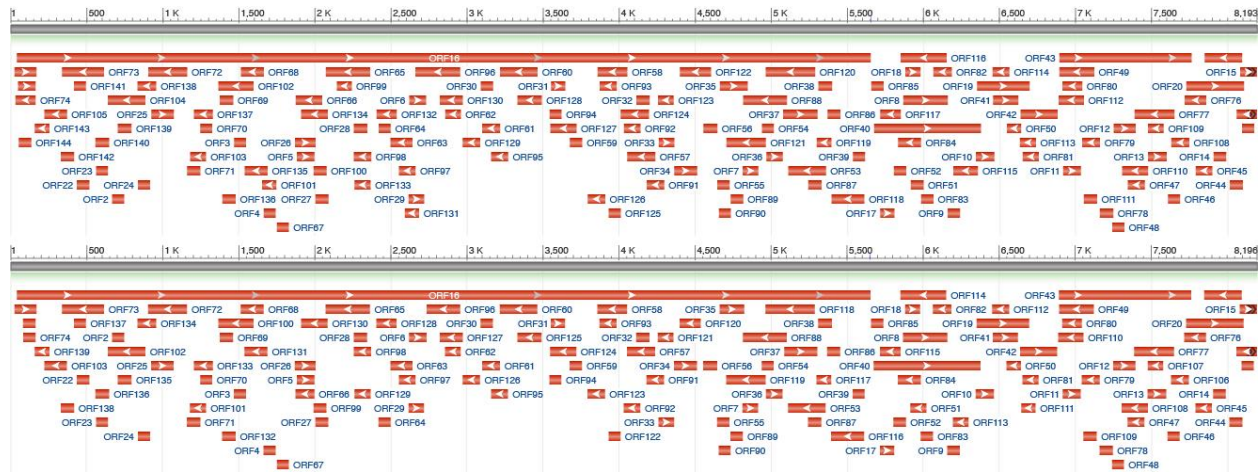
Class	Requisites	Number	(%)
0	No RdRp sequence detected	2	9.52
1	Partial RdRp sequence (<500 bp) accompanied by other transcripts or not	10	40.00
2	Large fragment (>500 bp) of RdRp	8	32.00
3	Large fragment (>500 bp) of RdRp and some other viral protein (except for the coat protein)	1	4.00
4	Large fragment (>500 bp) of RdRp and the coat protein detected, other viral protein facultative	4	16.00



**Figure S1:** Distribution of the assembled transcript on the genome of *Cowpea mild mottle virus* (KC884245.1). Figure as produced using IGV. Colorful lines inside arrows indicate genetic variation in comparison with the reference.

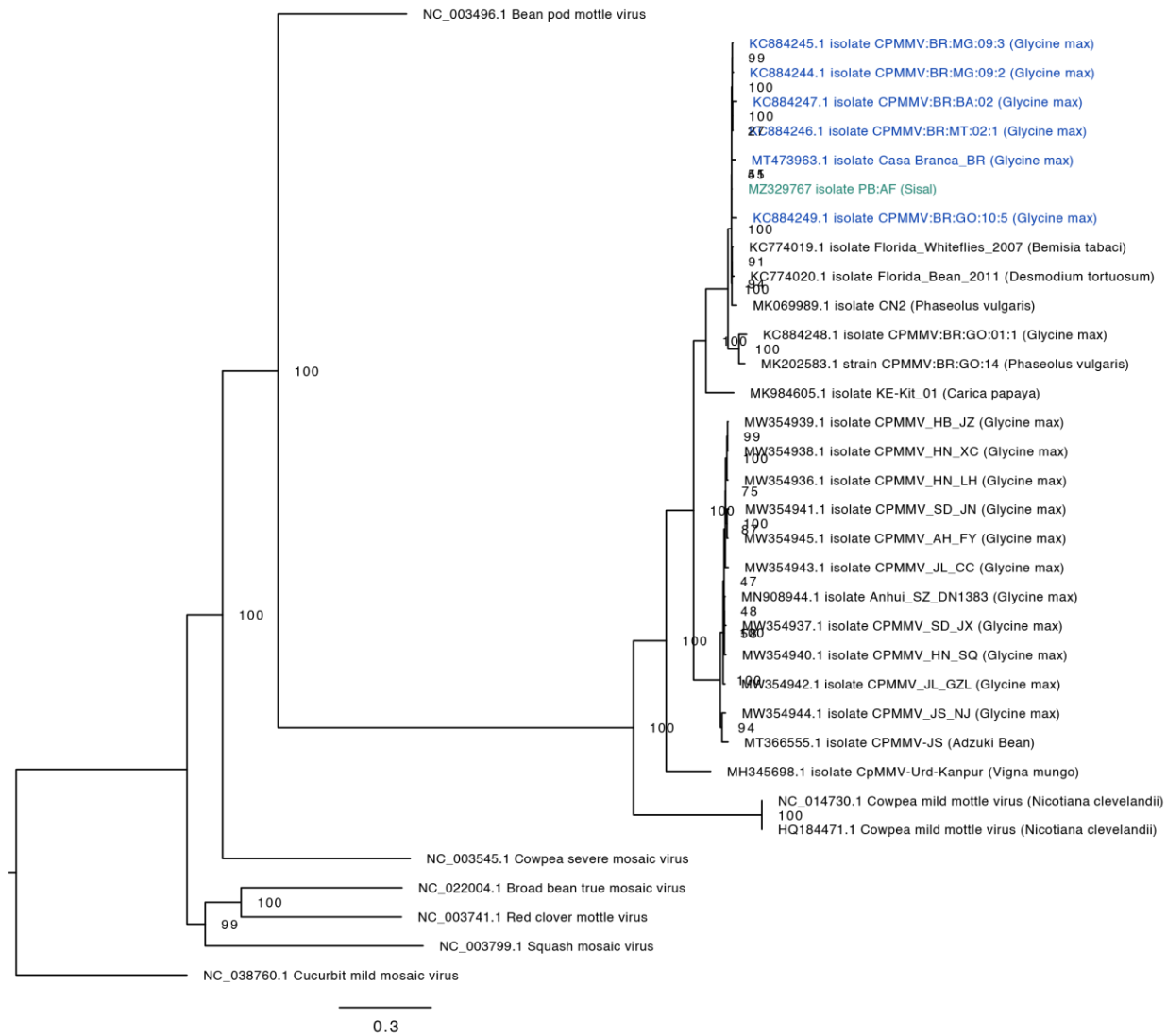


**Figure S2:** Coverage of raw sequencing reads along CPMMV reference genome. Only reads over 50 bp were used in this analysis. The visualization was generated using IGV. Each arrow in the lower part indicates a single sequencing read. In those arrows, colorful regions indicate genetic variation in comparison to the reference. As seen in the middle section, coverage is deeper in the end on the transcript.



**Figure S3:** Structural annotation of CPPMV strains. ORF profile in CPMMV:BR:MG:09:3 (upper) and CPMMV isolate PB:AF (lower). The visualization was produced using orffinder (<https://www.ncbi.nlm.nih.gov/orffinder/>) from NCBI portal. The arrow direction indicates the strand which the ORF was identified.





**Figure S4:** Phylogenetic analysis of Cowpea Mild Mottle virus isolate PB:AF. Accession numbers in blue indicate samples from Brazil, while green indicates the isolate assembled in this work.

**Table S8:** The accession codes and descriptions to each viral contig and their respective viral species. “RdRp” estands for RNA-dependent RNA polymerase, and, in this table, is a synonym to “Replicase”.

Species Name	Contig Name	Acc Code	Protein Type
Cowpea Mild Mottle Virus	Cowpea	MZ329767	Genome
Sisal-associated Alphaflexivirus A	Contig17	MZ599622	Putative coat protein
Sisal-associated Alphaflexivirus A	TRINITY_DN63052_c0_g1_i1	MZ599634	Putative Replicase
Sisal-associated Alphaflexivirus B	Contig12	MZ599625	Putative Replicase
Sisal-associated Alphaflexivirus C	TRINITY_DN38752_c0_g1_i1	MZ599621	Putative coat protein
Sisal-associated Betaflexivirus A	Contig7	MZ329756	RdRp
Sisal-associated Betaflexivirus A	TRINITY_DN83885_c0_g1_i1	MZ599608	Putative Replicase
Sisal-associated Betaflexivirus B	TRINITY_DN88105_c0_g1_i1	MZ329759	RdRp
Sisal-associated Betaflexivirus B	TRINITY_DN86319_c0_g1_i1	MZ599609	Putative Replicase
Sisal-associated Betaflexivirus C	TRINITY_DN44239_c0_g1_i1	MZ329760	RdRp
Sisal-associated Betaflexivirus D	TRINITY_DN52979_c0_g1_i1	MZ329761	RdRp
Sisal-associated Betaflexivirus D	TRINITY_DN46510_c0_g1_i1	MZ599640	Putative Replicase
Sisal-associated Betaflexivirus D	TRINITY_DN40814_c0_g1_i1	MZ599610	Putative coat protein
Sisal-associated Betaflexivirus D	TRINITY_DN65618_c0_g1_i1	MZ599641	Putative coat protein
Sisal-associated Betaflexivirus E	TRINITY_DN42135_c0_g1_i1	MZ329762	RdRp
Sisal-associated Botourmiavirus A	TRINITY_DN75741_c0_g1_i1	MZ599649	Putative Replicase
Sisal-associated Botourmiavirus B	TRINITY_DN110665_c0_g1_i1	MZ599650	Putative Replicase
Sisal-associated Closterovirus A	TRINITY_DN2548_c0_g1_i1	MZ329764	RdRp
Sisal-associated Closterovirus A	TRINITY_DN59050_c1_g1_i1	MZ599642	hypothetical protein
Sisal-associated Closterovirus A	TRINITY_DN49906_c0_g1_i3	MZ599616	hypothetical protein
Sisal-associated Closterovirus A	Contig16	MZ599628	hypothetical protein
Sisal-associated Closterovirus A	TRINITY_DN59050_c1_g1_i2	MZ599643	hypothetical protein
Sisal-associated Closterovirus A	Contig15	MZ599629	Putative coat protein
Sisal-associated Ribovirus A	TRINITY_DN3617_c0_g1_i1	MZ599639	hypothetical protein
Sisal-associated Ribovirus A	TRINITY_DN65779_c0_g1_i1	MZ599646	Putative Replicase
Sisal-associated Unclassified dsRNA virus A	TRINITY_DN81586_c0_g1_i1	MZ599606	Putative Replicase

Sisal-associated Unclassified dsRNA virus A	TRINITY_DN61614_c0_g1_i1	MZ599607	hypothetical protein
Sisal-associated Unclassified dsRNA virus B	Contig14	MZ599623	hypothetical protein
Sisal-associated Unclassified dsRNA virus B	TRINITY_DN73798_c0_g1_i1	MZ599644	Putative Replicase
Sisal-associated Unclassified dsRNA virus B	TRINITY_DN116043_c0_g1_i1	MZ599635	Putative Replicase
Sisal-associated Unclassified dsRNA virus B	TRINITY_DN72309_c0_g1_i1	MZ599636	hypothetical protein
Sisal-associated Unclassified dsRNA virus C	TRINITY_DN17344_c0_g1_i1	MZ329765	RdRp
Sisal-associated Unclassified dsRNA virus C	Contig20	MZ599630	hypothetical protein
Sisal-associated Unclassified dsRNA virus C	Contig1	MZ599631	Putative coat protein
Sisal-associated Unclassified dsRNA virus C	Contig10	MZ599632	Putative coat protein
Sisal-associated Unclassified dsRNA virus C	Contig11	MZ599633	Putative coat protein
Sisal-associated Unclassified dsRNA virus C	TRINITY_DN92324_c0_g1_i1	MZ599619	Putative Replicase
Sisal-associated Unclassified virus A	TRINITY_DN61147_c0_g1_i1	MZ599598	Putative Replicase
Sisal-associated Unclassified virus B	TRINITY_DN49676_c0_g1_i2	MZ329754	RdRp
Sisal-associated Unclassified virus B	TRINITY_DN16142_c0_g1_i1	MZ599599	Putative Replicase
Sisal-associated Unclassified virus B	TRINITY_DN44352_c0_g1_i1	MZ599600	Putative Replicase
Sisal-associated Unclassified virus B	TRINITY_DN83710_c0_g1_i1	MZ599601	Putative Replicase
Sisal-associated Unclassified virus B	TRINITY_DN19804_c0_g1_i1	MZ599602	Putative Replicase
Sisal-associated Unclassified virus C	TRINITY_DN24880_c0_g1_i1	MZ329755	RdRp
Sisal-associated Unclassified virus C	TRINITY_DN27401_c0_g1_i1	MZ599603	Putative Replicase
Sisal-associated Unclassified virus C	TRINITY_DN77293_c0_g1_i1	MZ599604	Putative Replicase
Sisal-associated Unclassified virus C	TRINITY_DN55189_c0_g1_i1	MZ599605	Putative Replicase
Sisal-associated Unclassified virus D	Contig19	MZ599624	hypothetical protein
Sisal-associated Unclassified virus D	TRINITY_DN83752_c0_g1_i1	MZ599637	Putative Replicase
Sisal-associated Unclassified virus E	DN52810	MZ329766	RdRp
Sisal-associated Unclassified virus E	TRINITY_DN99951_c0_g1_i1	MZ599611	Putative Replicase
Sisal-associated Virgavirus A	Contig5	MZ329757	RdRp
Sisal-associated Virgavirus B	TRINITY_DN100760_c0_g1_i1	MZ329758	RdRp
Sisal-associated Virgavirus B	TRINITY_DN26278_c0_g1_i1	MZ599645	hypothetical protein
Sisal-associated Virgavirus B	TRINITY_DN133840_c0_g1_i1	MZ599638	hypothetical protein
Sisal-associated Virgavirus C	Contig9	MZ329763	RdRp

Sisal-associated Virgavirus C	Contig6	MZ599626	Putative Replicase
Sisal-associated Virgavirus C	TRINITY_DN30831_c0_g1_i1	MZ599612	hypothetical protein
Sisal-associated Virgavirus C	TRINITY_DN38090_c0_g1_i1	MZ599620	Putative coat protein
Sisal-associated Virgavirus C	Contig8	MZ599627	Putative coat protein
Sisal-associated Virgavirus C	TRINITY_DN105616_c0_g1_i1	MZ599647	Putative coat protein
Sisal-associated Virgavirus C	TRINITY_DN72996_c0_g1_i1	MZ599613	Putative Replicase
Sisal-associated Virgavirus C	TRINITY_DN26423_c0_g1_i1	MZ599614	Putative Replicase
Sisal-associated Virgavirus C	TRINITY_DN75281_c0_g1_i1	MZ599621	hypothetical protein
Sisal-associated Virgavirus C	TRINITY_DN85955_c0_g1_i1	MZ599615	Putative Replicase
Sisal-associated Virgavirus D	TRINITY_DN83949_c0_g1_i1	MZ599651	hypothetical protein
Sisal-associated Virgavirus D	TRINITY_DN77371_c0_g1_i1	MZ599617	Putative coat protein
Sisal-associated Virgavirus D	TRINITY_DN69322_c0_g1_i1	MZ599618	hypothetical protein

**Table S9:** Diversity indices for the organs and species analyzed.

Index	Leaves AF	Leaves AS	Leaves HI	Stem AF	Stem AS	Stem HI	Roots AF	Roots AS	Roots HI
<b>Number of Taxa (S)</b>	10	8	4	10	10	11	18	13	12
<b>Dominance (D)</b>	0,3837	0,7361	0,8649	0,3072	0,9094	0,3317	0,401	0,2444	0,2648
<b>Simpson Index (1-D)</b>	0,6163	0,2639	0,1351	0,6928	0,09059	0,6683	0,599	0,7556	0,7352
<b>Shannon Index (H)</b>	1,185	0,5205	0,3017	1,414	0,2622	1,323	1,534	1,756	1,747
<b>Evenness (e<sup>H/S</sup>)</b>	0,3271	0,2104	0,338	0,4112	0,13	0,3413	0,2576	0,4452	0,4782
<b>Equitability</b>	0,5147	0,2503	0,2176	0,6141	0,1139	0,5516	0,5307	0,6845	0,7031

**Table S10:** Viral species and their respective detected protein domains (with Pfam/HMMER) and their expression (in tpm, *transcripts per million*) in each analyzed sample, representing the average expression of the three technical replicates.

Viral Species	Proteic Domains Detected	Leaves AF	Leaves AS	Leaves HI	Stem AF	Stem AS	Stem HI	Roots AF	Roots AS	Roots HI
Sisal-associated Unclassified virus A	none	1.79	0.00	0.00	0.00	0.00	0.00	0.00	0.00	0.00
Sisal-associated Unclassified virus B	RdRP, Viral_helicase1	0.00	0.00	0.00	0.01	0.00	0.00	87.08	0.00	0.00
Sisal-associated Unclassified virus C	RdRP, Viral_helicase1, Viral methyltransferase	0.00	0.00	0.00	0.00	0.00	0.00	30.17	0.00	0.00
Sisal-associated Alphaflexivirus A	Viral coat protein	0.00	0.00	0.32	0.00	0.56	0.09	0.00	5.65	21.86
Sisal-associated Unclassified dsRNA virus A	none	0.00	0.00	0.00	0.00	0.00	0.00	6.02	0.00	0.00
Sisal-associated Betaflexivirus A	RdRP	0.01	0.00	0.00	4.94	0.00	0.15	7.33	0.00	23.02
Sisal-associated Unclassified dsRNA virus B	none	0.00	0.01	0.00	0.00	0.01	1.82	7.64	15.29	4.05
Sisal-associated Unclassified virus D	RdRP	0.00	0.25	0.00	0.00	0.00	0.00	0.00	5.30	3.26
Sisal-associated Virgavirus A	none	0.03	0.03	0.02	0.09	0.03	0.04	23.26	30.74	34.15
Sisal-associated Alphaflexivirus B	none	0.00	0.00	0.00	0.00	0.00	0.00	4.09	1.62	0.00
Sisal-associated Virgavirus B	RdRP, Viral_helicase1	0.00	0.02	0.00	0.00	0.01	0.13	0.00	13.10	4.76
Cowpea Mild Mottle Virus	none	0.01	0.00	0.00	21.42	0.56	0.32	18.66	2.66	59.78
Sisal-associated Betaflexivirus B	RdRP	0.00	2.79	0.00	0.00	0.30	0.00	3.85	0.32	0.00
Sisal-associated Betaflexivirus C	Viral_helicase1	4.35	0.00	0.00	0.55	0.00	0.00	0.55	0.00	0.00
Sisal-associated Ribovirus A	RdRP, Viral_helicase1	0.00	0.00	0.00	0.00	0.01	0.20	0.00	13.71	3.94
Sisal-associated Betaflexivirus D	Trichovirus coat protein, Viral_helicase1, Viral methyltransferase	38.15	15.98	0.00	4.97	1.30	0.00	1.14	3.11	0.00

Sisal-associated Betaflexivirus E	RdRP	3.47	0.00	0.00	0.91	0.00	0.00	0.09	0.00	0.00
Sisal-associated Unclassified virus E	RdRP, RNA helicase	0.00	0.00	0.00	0.01	0.00	0.00	14.45	0.00	0.00
Sisal-associated Virgavirus C	DEAD/DEAH box helicase, RdRP, Viral_helicase1, Viral methyltransferase	1.24	0.62	1.06	3.86	0.76	1.75	407.81	106.22	151.75
Sisal-associated Alphaflexivirus C	Viral coat protein	0.00	0.00	0.00	0.00	0.00	0.00	6.59	0.00	0.00
Sisal-associated Closterovirus A	Closterovirus coat protein, RdRP, Viral methyltransferase	26.52	110.78	18.15	26.7 6	72.6 5	18.7 6	15.28	120.90	13.18
Sisal-associated Botourmiavirus A	none	0.00	0.00	0.00	0.00	0.00	6.39	0.00	0.00	0.00
Sisal-associated Botourmiavirus B	none	0.00	0.00	0.00	0.00	0.00	22.1 4	0.00	0.00	0.00
Sisal-associated Virgavirus D	none	0.00	0.00	0.00	0.00	0.00	0.00	14.03	0.00	4.13
Sisal-associated Unclassified dsRNA virus C	none	0.07	0.00	0.00	0.00	0.00	0.00	15.95	19.12	7.53
<b>Mean Sequencing Depth</b>		117.85	131.02	107.70	152. 24	131. 30	107. 42	141.55	124.35	118.69