Supplementary material

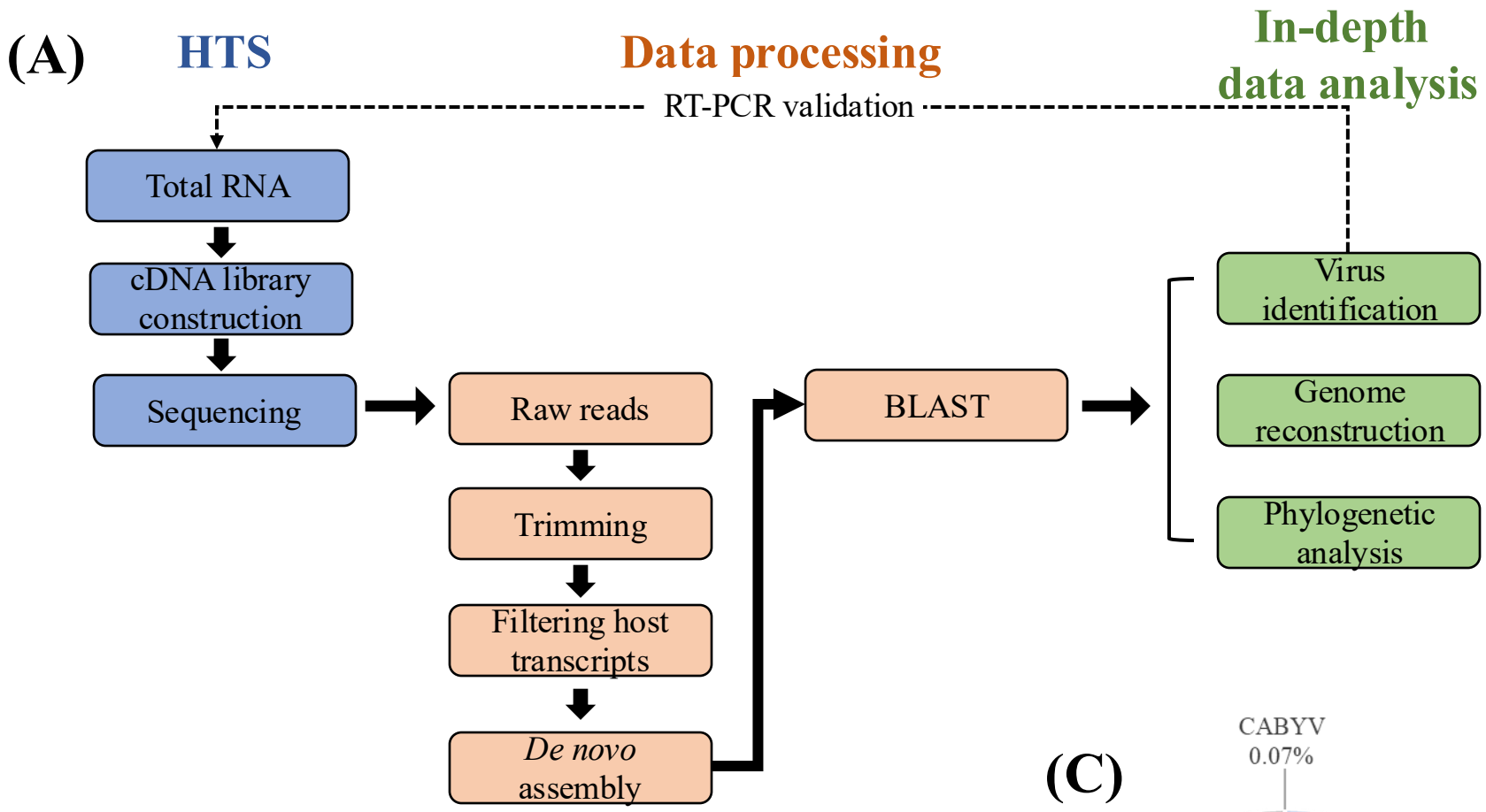
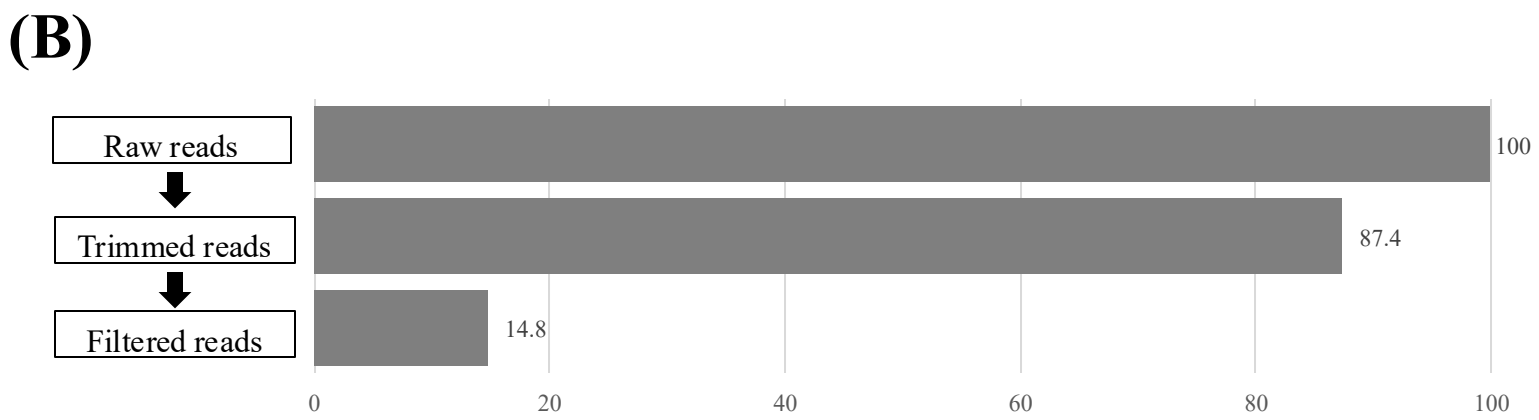


Figure S1 - (A) Workflow of the entire virome analysis. The analysis was performed in three successive main stages: HTS, data processing and in-depth data analysis. (B) The average percentage of reads left after each step. (C) Percentage of viral specific reads



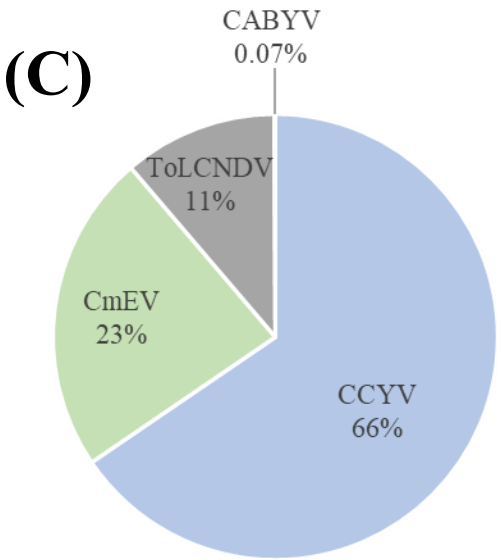


Table S1 – Primers designed and used in the present study for the validation of the HTS results.

Virus name	Primer name	Sequence (5′-3′)	Product size (bp)
Cucurbit chlorotic yellow virus	CCYV_F CCYV_R	CGGGTGCTGGTAAGACAACT AAACACATTCCGGTTGCTGC	509
Cucumis melo alphaendornavirus	CmEV_F CmEV_R	GGCAGTGTTCTGTTGCAGTG CGTAAGAGCGCAATGTGTCG	581
Tomato leaf curl New Delhi virus	ToLCNDV_F ToLCNDV_R	CTTTCCGCAGGTTGTGGTTG GCAAAACAATGTGGGCTCGT	632
Cucurbit aphid-borne yellows virus	CABYV_F CABYV_R	AACAAACGGGAAAACCGCAC AGCTCTGCAGGCGATAAGTC	787

Table S2 - Details of primers used in this study for the detection of cucurbit viruses.

Virus	Primers	Sequence	Size	Reference
ZYMV	ZYMV-CP-5′	GGTTCATGTCCCACCAAGC	605 bp	Yakoubi et al., 2008
	ZYMV-CP-3′	ATGTCGAGTATCACATTTCC		
WMV	W-VVIAM-5′	CTTCTGGTTGTCATTGCTATG	811 bp	Desbiez et al., 2009
	WMV2-3′	CCCAYCAACTGTYGGAAG		
PRSV	PRSV-milCP-5′	TCTAACACTCGTGCCACTCA	560 bp	Lecoq & Desbiez, 2012
	PRSV-finCP-3′	YARTTGCGCATACCCAGGAG		
CMV	CMV-1	GCCGTAAGCTGGATGGACAA	486-488 bp[1]	Parrella & Sorrentino, 2009
	CMV-2	TATGATAAGAAGCTTGTTTCGCG	499-502 bp[2]	
Polerovirus	Pol-G-F	GAYTGCTCYGGYTTYGACTGGAG	1100 bp	Knierim et al., 2010
	Pol-G-R	GATYTTATAYTCATGGTAGGCCTTGAG		
CCYV (+CYSDV)	Crini-s2	CATTCCTACCTGTTTAGCCA	352 bp	Mohammed et al., 2014
	Crini-as2	TGCACTTATAATCTGCTGGTAC		

Table S3 – Sequencing primers designed and used in the present study for the complete genome of CABYV.

Primer name	Sequence (5′-3′)	Product size (bp)
CABYV- seq-F1 CABYV- seq-R1	AGGCTTGGAGAGTTTGCTCC CATCCCTCTCCGTCGTAAGC	648
CABYV- seq-F2 CABYV- seq-R2	GATCTCGTGCTATTGGCGGG CAGGTGTACTGGGCATCGAA	871
CABYV- seq-F3 CABYV- seq-R3	AACAAACGGGAAAACCGCAC AGCTCTGCAGGCGATAAGTC	787
CABYV- seq-F4 CABYV- seq-R4	ACCGCCTGACGCTTGATTTA CGCTGATTTCTTCGCCTTCG	791
CABYV- seq-F5 CABYV- seq-R5	TAGCTCCCTCCAATCCACGA GCCAACTACCGTCCAGTTCA	572

Figure S2 – Genome organization and assembled contigs obtained for each virus detected. Contigs assembled for each viruses are showed as red lines below the genomes.

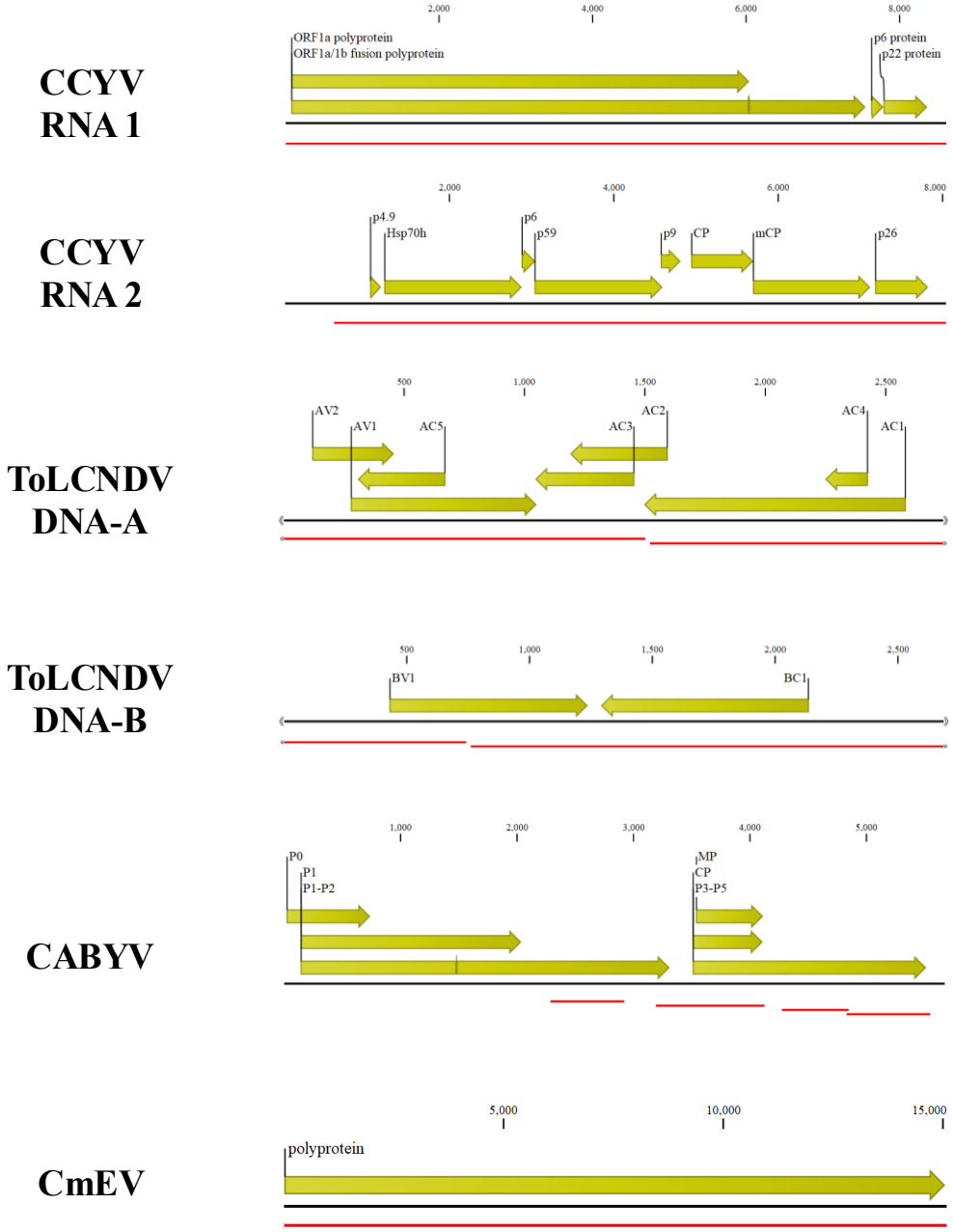
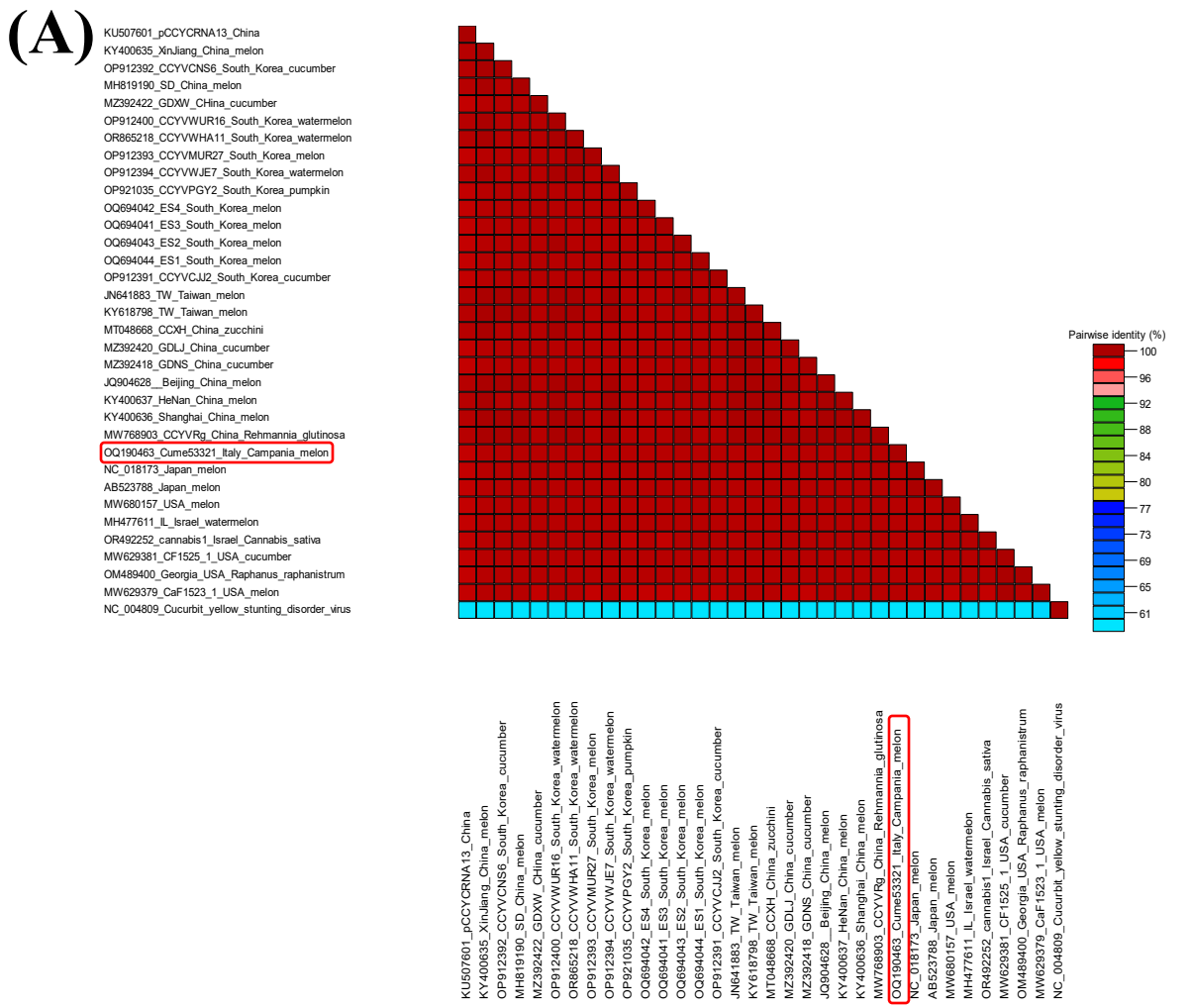
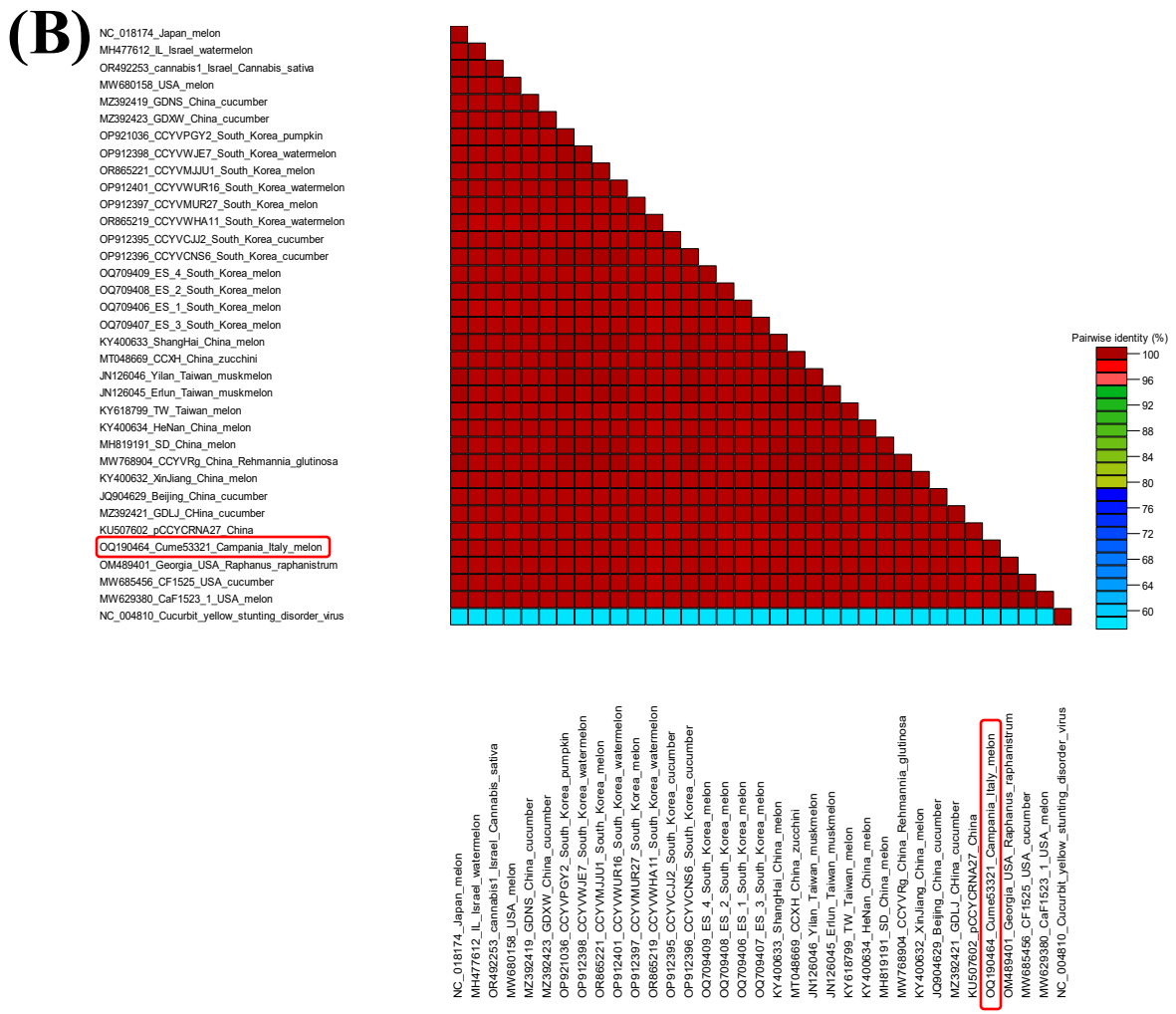


Figure S3 - Pairwise nucleotide comparison of identified viruses along with closely related genomes obtained fro m GenBank NCBI database. Color coded matrix was generated using SDT v1.3 programme. Each color in the mat rix represents percent identity score. (A) Pairwise comparison of CCYV RNA1, (B) pairwise comparison of CCYV RNA2, (C) pairwise comparison of ToLCNDV A, (D) pairwise comparison of ToLCNDV B, (E) pairwise comparis on of CABYV, and (F) pairwise comparison of CmEV.

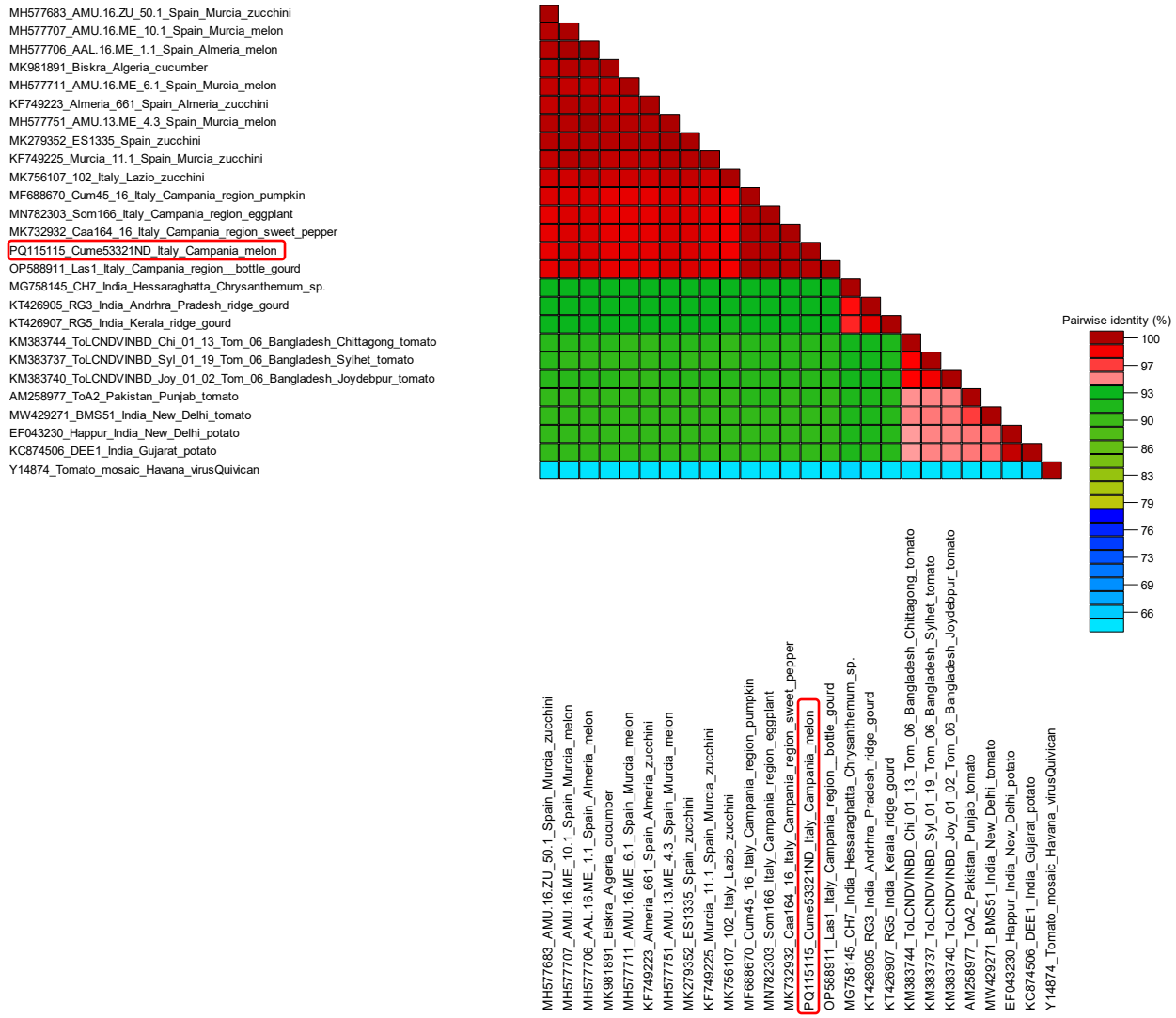




(continue)

Figure S3 (continue)

(C)



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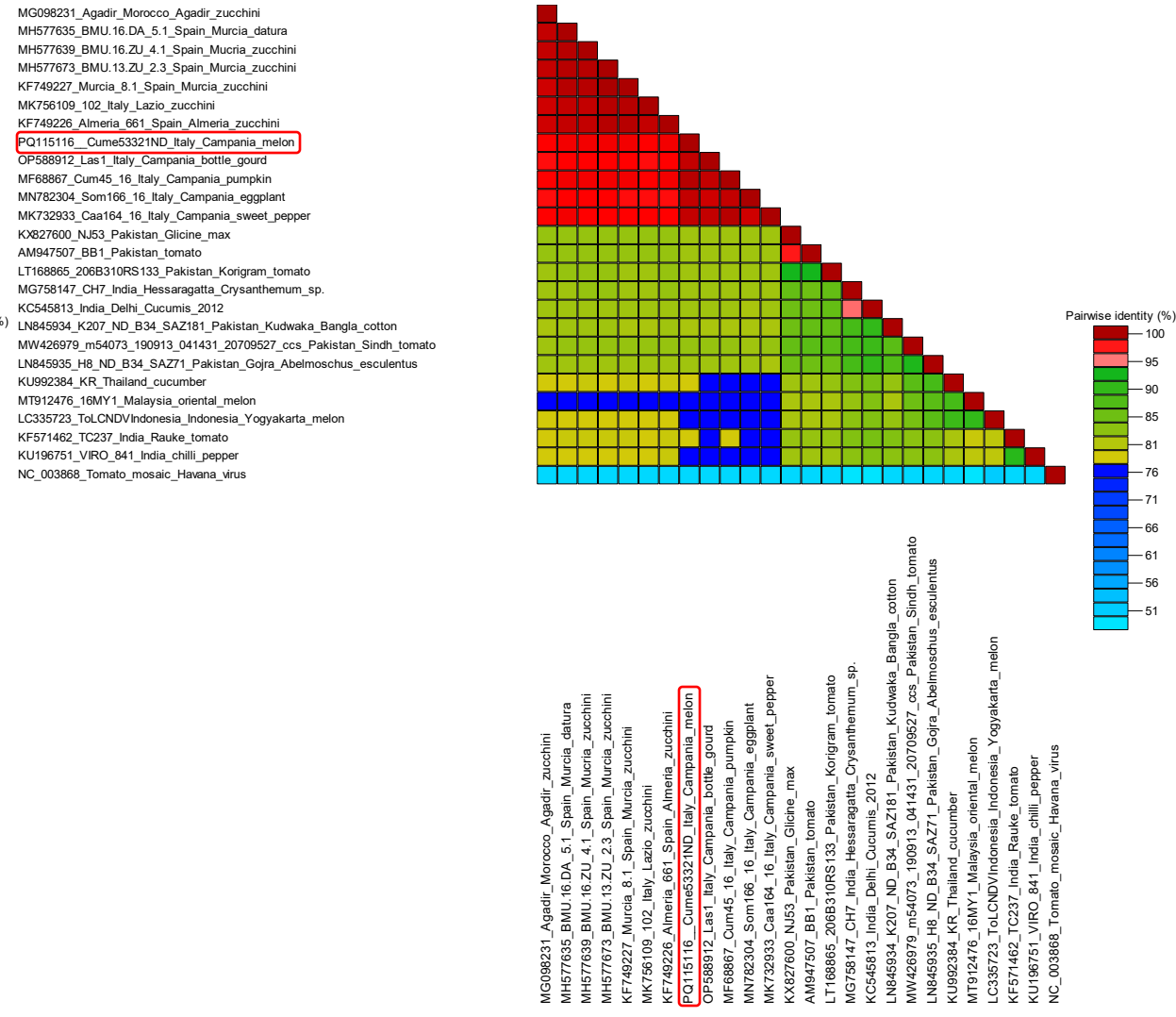
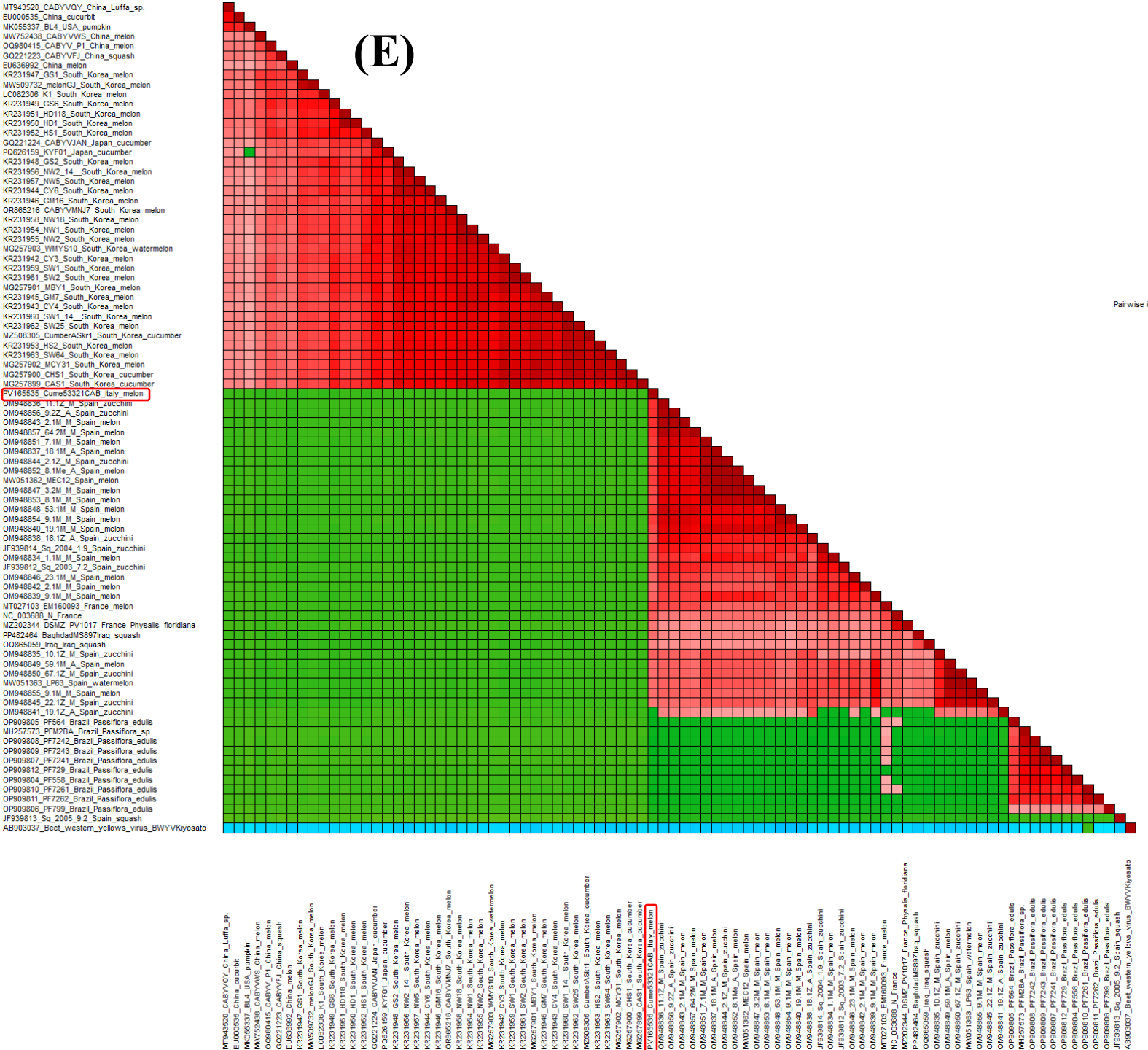


Figure S3 (continue)



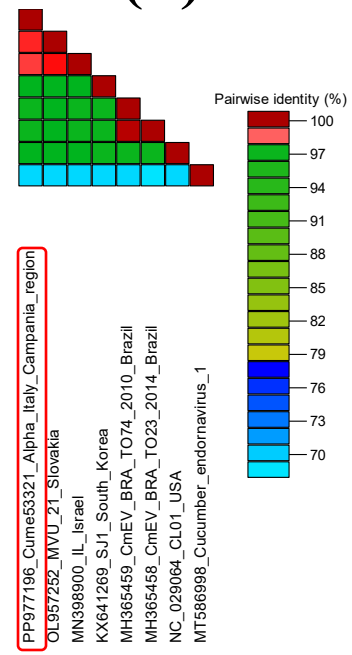


Figure S4 – Acrylamide gel electrophoresis showing the restriction profiles obtained after digestion with *Apo*I end onuclease of the 866 bp COI amplicon of *Bemisia tabaci* individuals rearing on melon with yellowing disease. Mk, 100 bp molecular weight ladder; C1, restriction profile of control *B. tabaci* Q1 mitotype; C2, restriction profile of th e control *B. tabaci* Q2 mitotype; Q2, restriction profiles of the seven *B. tabaci* individuals. Method is described in Pa rrella et al., 2012.

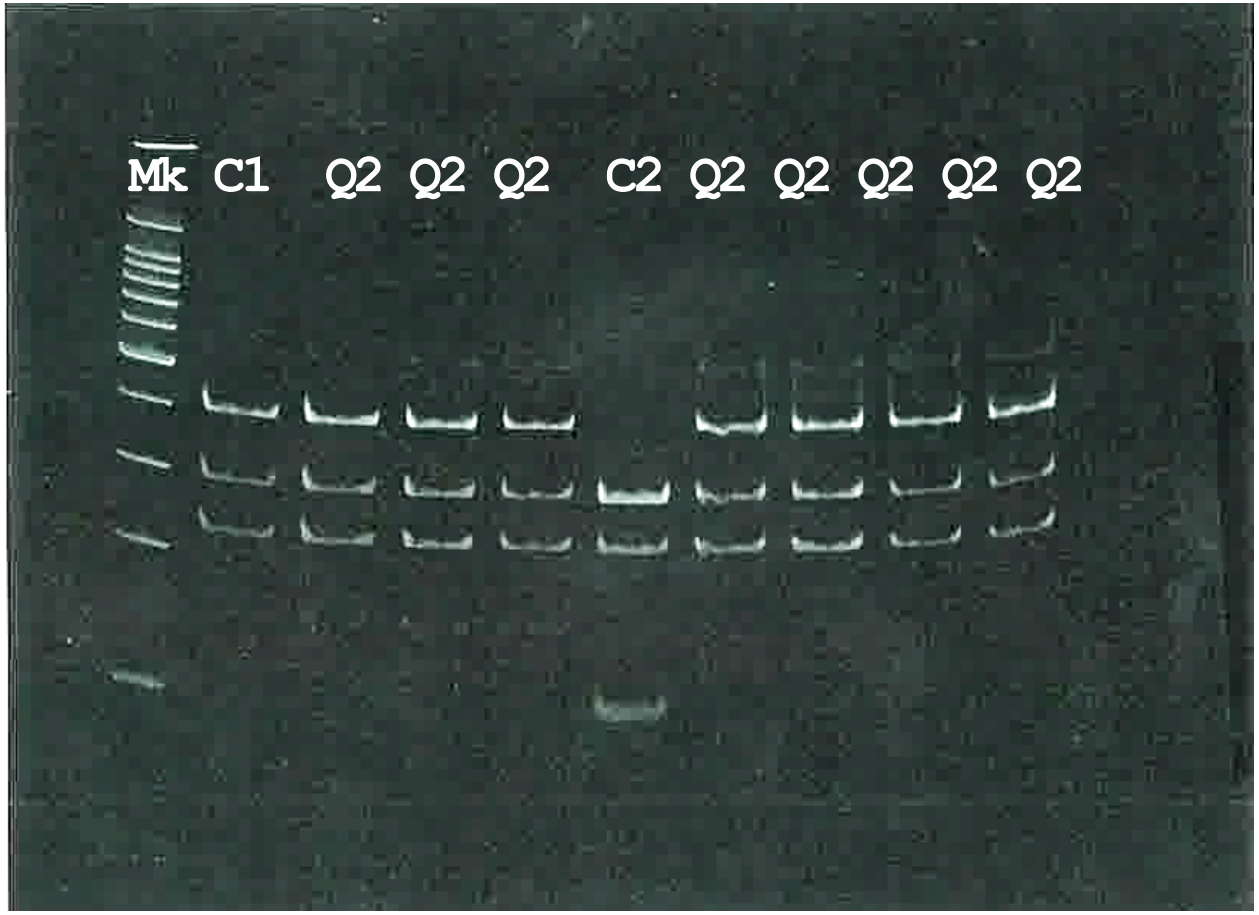
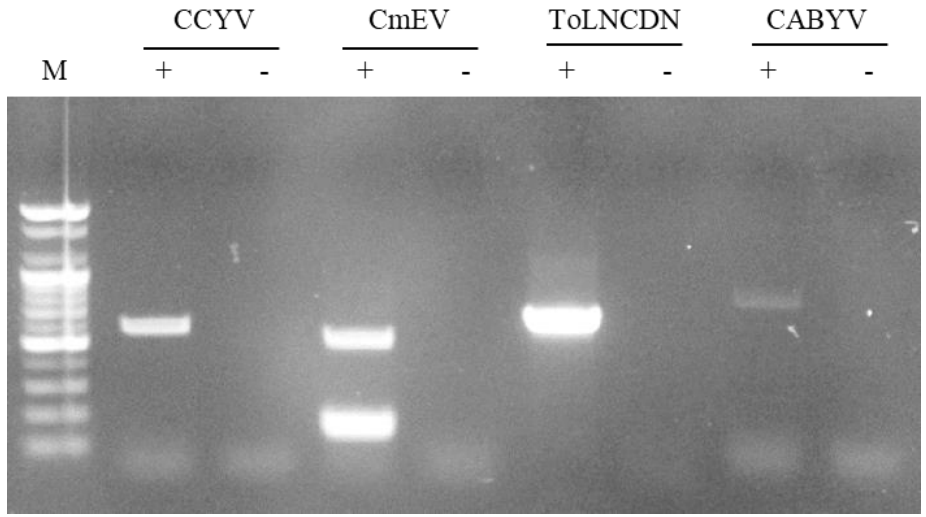


Figure S5 - RT-PCR/PCR confirmation of identified viruses with newly designed virus-specific primers. M = 1 Kb molecular marker; + = RNA from melon plant used for HTS analysis; - = negative control (healthy melon); Viral specific amplicons were: 509 bp for CCYV; 581 bp for CmEV; 632 bp for ToLCNDV and 787 for CABYV.



Original unmodified photo concerning the Figure 2 reported in the paper