

Supplementary table S1. Primers used in this study.

Primer	Sequence (5'-3')	Position ^a (nt)	Use
WMV-F1	GATGAATTAAAGGAACITGC	8,773-8,792	Detection WMV
WMV-R1	TTGCTCATCGTTAAGATCGT	9,281-9,300	Detection WMV
WMV-F2	GCAACTTCGAGTCATACAGAG	4,249-4,269	Detection WMV
WMV-R2	CTCTGTATTCTCTCGCCAT	5,066-5,084	Detection WMV
WMV-F3	TTATGGAGATAGTGGGTTACTGT	1,311-1,333	Detection WMV
WMV-R3	CTTGTAGTTCTGTGTTAACCTCAC	1,816-1,839	Detection WMV
BRV-F1	TACTTGCCCTATCAGTAGGGA	5,451-5,471	Detection BRV
BRV-R1	GAACGATGGCCGCTTAAGAT	5,750-5,770	Detection BRV
SMV-F1	GAGCAAAAGTTGTGTTGATG	7,579-7,599	Detection SMV
SMV-R1	CCATCAAGGTATTGTCCACA	7,931-7,950	Detection SMV
CLRV-F1	GGTAATATCACTAGTGGATT	7,361-7,380	Detection CLRV
CLRV-R1	GATATTCGTTAACGTAAACTT	7,560-7,580	Detection CLRV
GBLV-F1	GAECTCGCCTTGATTATGT	5,231-5,250	Detection GBLV
GBLV-R1	CAGGTTCAATAACATTCAACA	5,580-5,600	Detection GBLV
AMV-F1	CCTGATCATTGATCGGTAATG	1,132-1,152	Detection AMV RNA3
AMV-R1	GGTGCCGGCATGGGACGG	1,496-1,513	Detection AMV RNA3
AMV-R	TCCTATCAGGAGCGAATAG	3,544-3,562 (RNA1) 2,493-2,511 (RNA2) 1,937-1,955 (RNA3)	AMV genome amplification
AMV1-F	GCCTCCATTCAAGGAGATGCTCG	160-182	AMV RNA1 amplification
AMV2-F	TGAAGACGATGCACCGCTTG	333-353	AMV RNA2 amplification
AMV3-F	CTTGTTTAATTGGCCTAACACG	98-121	AMV RNA3 amplification
AMV6	TAACTCGTACCTCAACGAGTC	3276-3296	RNA1 3'RACE
AMV7	CCTTGTGTAAGGAATGCCCT	2315-2335	RNA2 3'RACE
AMV8	CAAGCATTCCATGCCGTAGC	1675-1695	RNA3 3' RACE
AMV9	TATCTTCAAGACTTCACCTT	285-304	RNA1 5'RACE
AMV10	TGTCTGAAGGGAGAGCATCC	265-284	RNA1 5'RACE
AMV11	GAATCTCATTCACGACGTT	364-383	RNA2 5'RACE
AMV12	TGTCTATAAGGCGGTAAAC	304-323	RNA2 5'RACE
AMV13	ATCTTAGGAAGCATAACGATT	466-485	RNA3 5'RACE
AMV14	GCTTTAGCTGATTAGGACCC	366-385	RNA3 5'RACE

^a Binding positions relative to the genome sequences of *Watermelon mosaic virus* (AY437609), *Blackcurrant reversion virus* (NC_003502), *Soybean mosaic virus* (D00507), *Cherry leaf roll virus*(KU215413), and *Grapevine Bulgarian latent virus* (NC_015493) and *Alfalfa mosaic virus* (NC001495, NC002024 and NC002025).