

Table S1. Primer sequences for cloning. The codons containing the mutations are underlined while the restriction enzymes used are in italics.

Primer	Sequence (5'-3')
MP/S28Afor	GGAGATCTTATTT <u>IGCC</u> CCTGAAGCCATTAAGAAAATGGC
MP/S28Arev	GGAGATCTTTTGAAGATCGTCAGACGTATCCGCTGAGG
MP/S28Dfor	GGAGATCTTATTT <u>GACC</u> CCTGAAGCCATTAAGAAAATGGC
MP/S120Afor	GGGAGCTCGCT <u>CCC</u> ATAGATGGGCAATGCGTTTCG
MP/S120Arev	GGGAGCTCCTTGTGCGCTAGATCAGCTAAGTAAATTCTCAA
MP/S120Dfor	GGGAGCTCGAT <u>CCC</u> ATAGATGGGCAATGCGTTTCG
MPrev	GCCGGATCCCTAAAGACCGTTAACCACCTGC
MPSaclfor	GGGAGCTCATGGCTTTCCAAGGTACCAGT
MPeGFPprev	CGCCCTTGCTCACCATAAGACCGTTAACCACCTGC
MPeGFPfor	GTGGTTAACGGTCTTATGGTGAGCAAGGGCGAGG
eGFPBamHlrev	CCGGATCCTCACTTGTACAGCTCGTCCATG
CMVMPpETfor	GGCATATGGCTTTCCAAGGTACCAGTAG
CMVMPpETrev	GCCGGATCCCTAAAGACCGTTAACCACCTGC
Cap. actin for	AGGGATGGGTCAAAGGATGC
Cap. actin rev	GAGACAACACCGCCTGAATAGC

Table S2. Descriptive statistics, Levene's Test of Equality of Error Variances and Tests of Normality of the dataset examined

Descriptive Statistics			
Mutants	Mean	Std. Deviation	N
MP/S28A	0.499	0.015	15
MP/S28D	0.861	0.052	15
MP/S120A	6.363	0.304	15
MP/S120D	8.344	0.552	15
Rs-CMV	8.869	0.571	15
Total	4.987	3.660	75
Levene's Test of Equality of Error Variances			
F	df1	df2	Sig.
1688.542	4	70	0.000
Tests of Normality			Skewness
Kolmogorov-Smirnov			0.550
Statistic	df	Sig.	Kurtosis
0.203	100	0.000	0.926

Figure S1. Sequence comparison of the 1-50 amino acids of plant viruses in the genus Cucumovirus. Ser 28 is indicated with a red rectangle. PSV: Peanut stunt virus, TAV: Tomato aspermy virus.

CMV-Ra (sg I) MAFQGTSRILTIQQSSAATSDDLQKILTSPEAIKKMATECDLGRHHWMRAD
CMV-Tsh (sg II) MAFQGTSRILTIQQSSAASSDDLQKILTSPEAIKKMATECDLGRHHWMRAD
PSV MAFSGSSRILTIQQSSAATSDDLHRILTSPEAIKEMATKCDLGRHHWMRAD
TAV MAFSGTSRILSIQQSSAASTPELHNILTSRRAIQEMATKCDLGRHHWMRAD