

Figure S1: Cellular localization of MP^{AbMV} transiently expressed in HeLa cells (20 hours). Fluorescence microscopy analysis using a primary MP-specific antiserum (a - c) or anti-Myc antibody (d - o) for in situ immunodetection. Red (Alexa Fluor 555-labelled secondary antibody) and green (Alexa Fluor 488-labelled secondary antibody) signals indicate the subcellular distribution of Myc-tagged or unmodified AbMV MP. Nuclei were DAPI-stained and appear as blue. Superposition images of fluorescence emissions are shown on the left (Merge) and individual DAPI and MP-specific signals on the right (Split). A summary of observed localization types (thready, aggregate close to nuclei and homogenous) is given in the table (p). Note that only Myc:MP^{AbMV} exhibited additional cellular localization types. Scale bars represent 10 μ m.

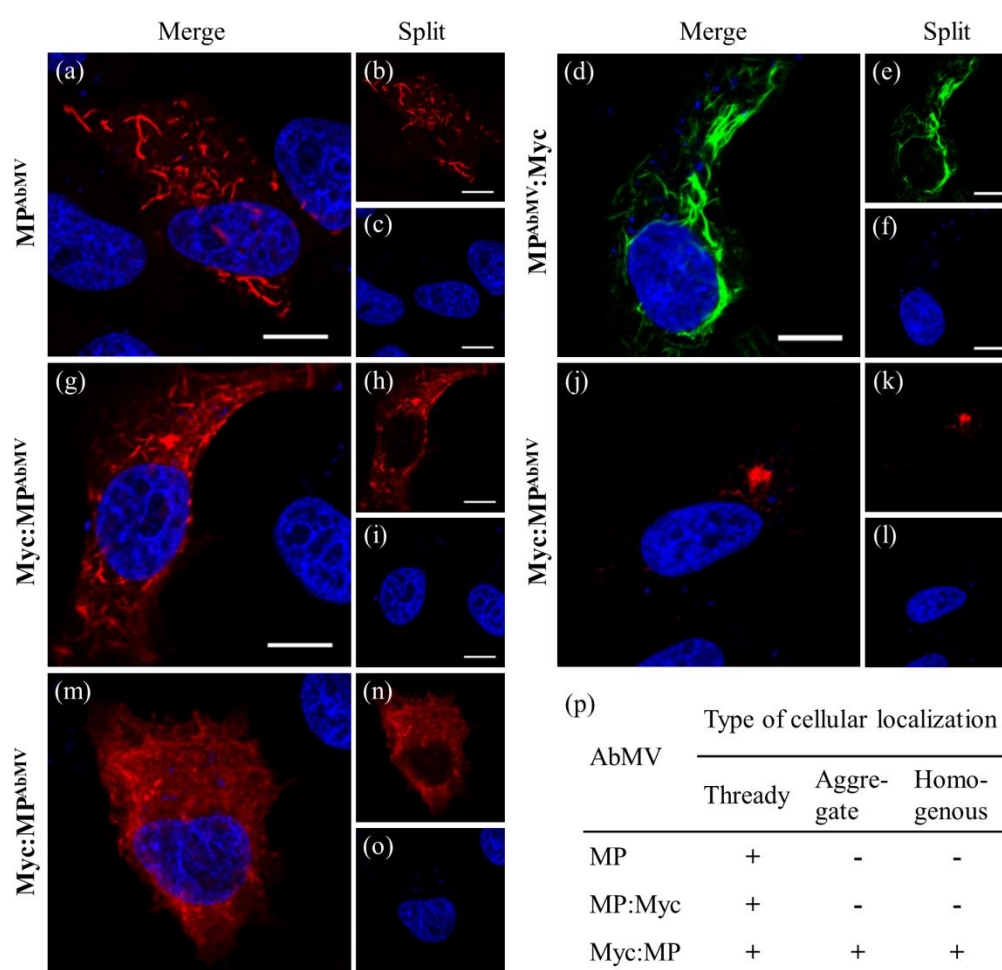


Figure S2: Cellular localization studies of EYFP, MP^{AbMV}, MP^{PNYDV}, P2^{CaMV} (a, b, d, e) in HeLa, and MP^{CILCrV} (c) HeLa and (f) African green monkey kidney cells (COS-7). Blue signal represents DAPI staining. Bar represents 10 μ m.

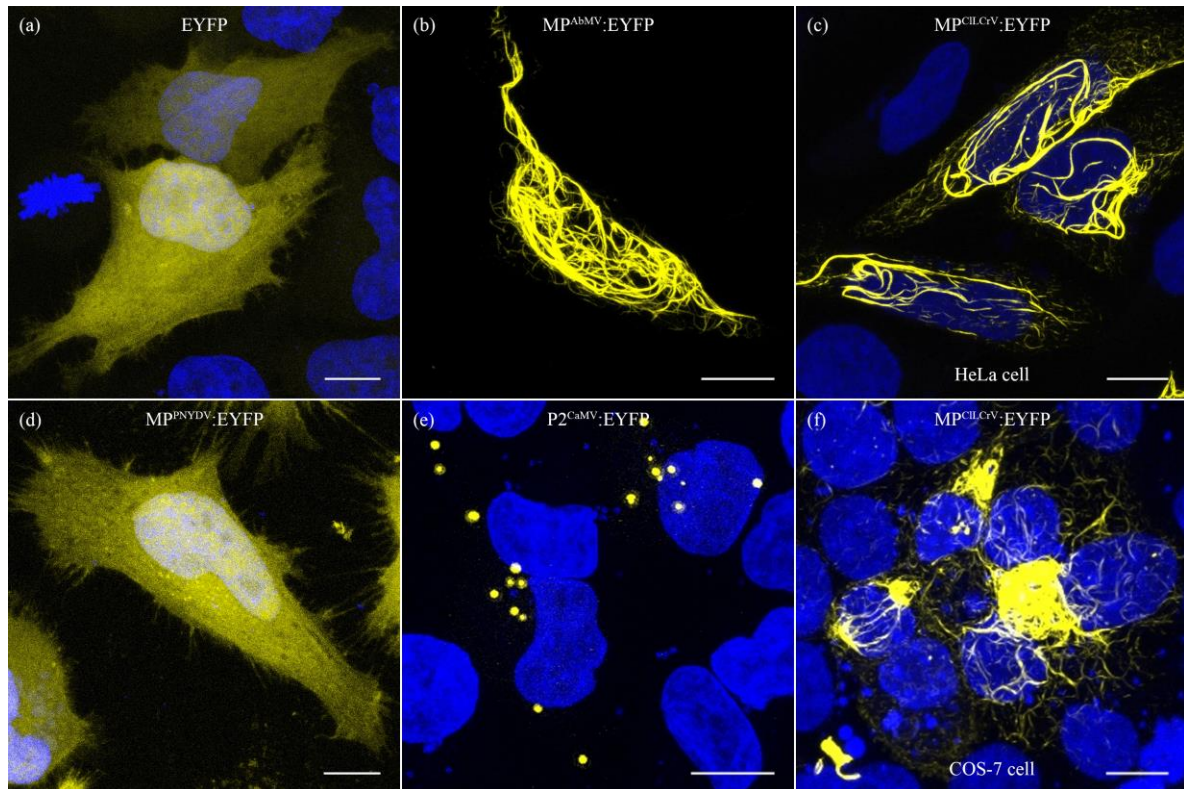


Figure S3: Transient co-expression (a-d) of A.t.Pin4:GFP with MAP4:mcherry, (e-h) co-expression of S.l.SCD2:GFP with MAP4:mcherry in epidermal cells of *N. benthamiana* plants. GFP signals in green, MAP4 in red, co-localization of both signals appears as yellow (b, f; merged pictures). Bar represents 10 μ m.

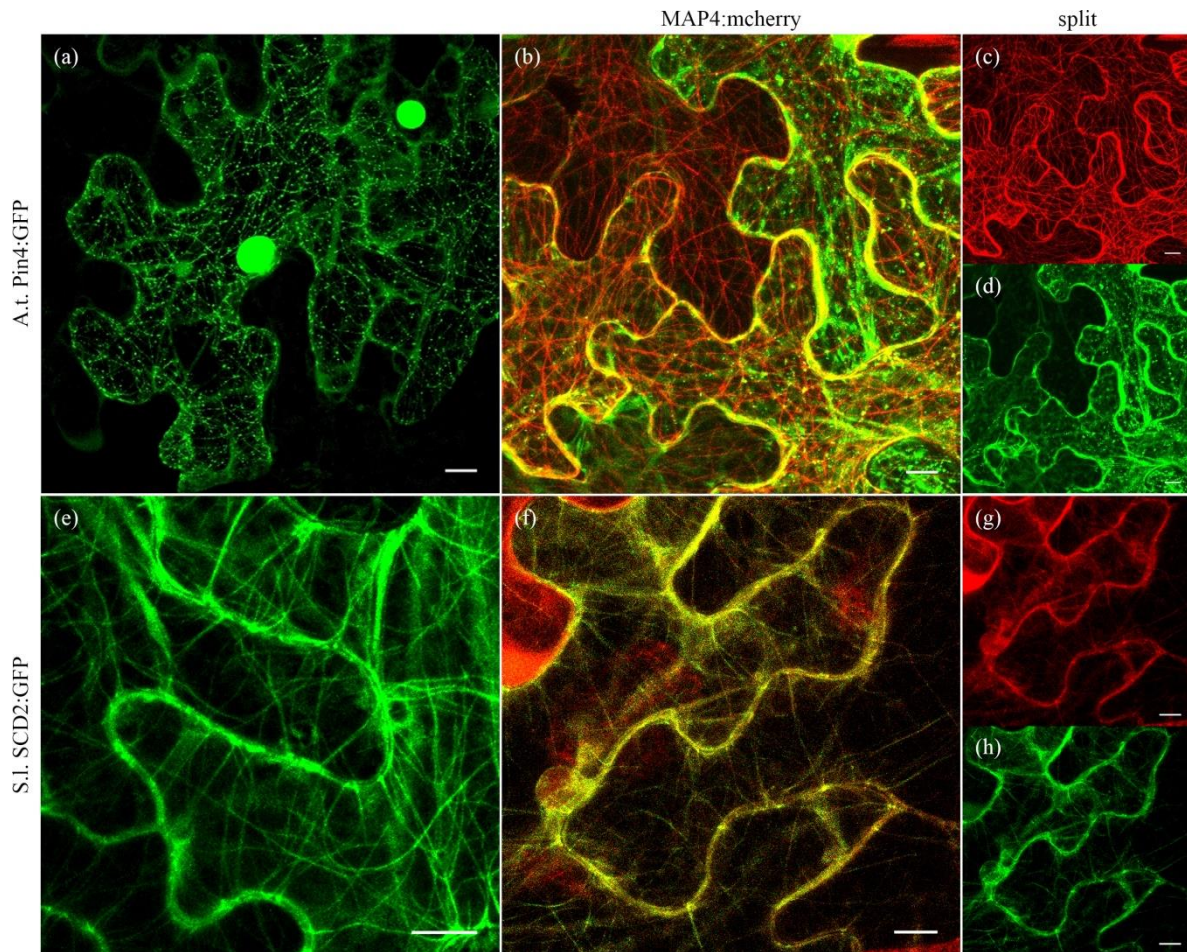


Figure S4: Transient expression (a) of MAP4:mcherry and co-expression with (b) MP^{AbMV} and (c) MP^{AbMV}(1-180aa) in epidermal cells of *N. benthamiana* plants. GFP signals in green, MAP4 in red, co-localization of both signals appear as yellow in merged pictures. Autofluorescence of chloroplasts are shown in white or blue, respectively. Bar represents 10 μ m.

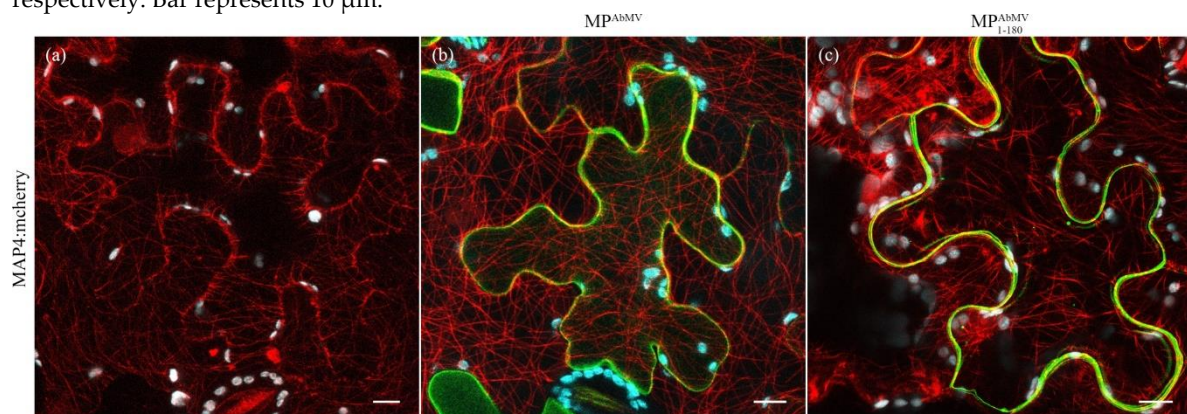


Figure S5: Bimolecular fluorescence complementation experiments of (a) MP^{AbMV}:YFP^N with MP:YFP^C, (b-e) MP^{AbMV}:YFP^N and respective MP deletion mutants (Figure 5a) with A.t.Pin4:YFP^C, or the reciprocal experiments (k-o) A.t.Pin4:YFP^N with MP^{AbMV}:YFP^C and deletion mutants in epidermal cells of *N. benthamiana* plants. BiFC signals in yellow. Pictures (f-j) and (p-t) are merged pictures of (a-e) and (k-o) with brightfield, respectively. Bar represents 10 μ m.

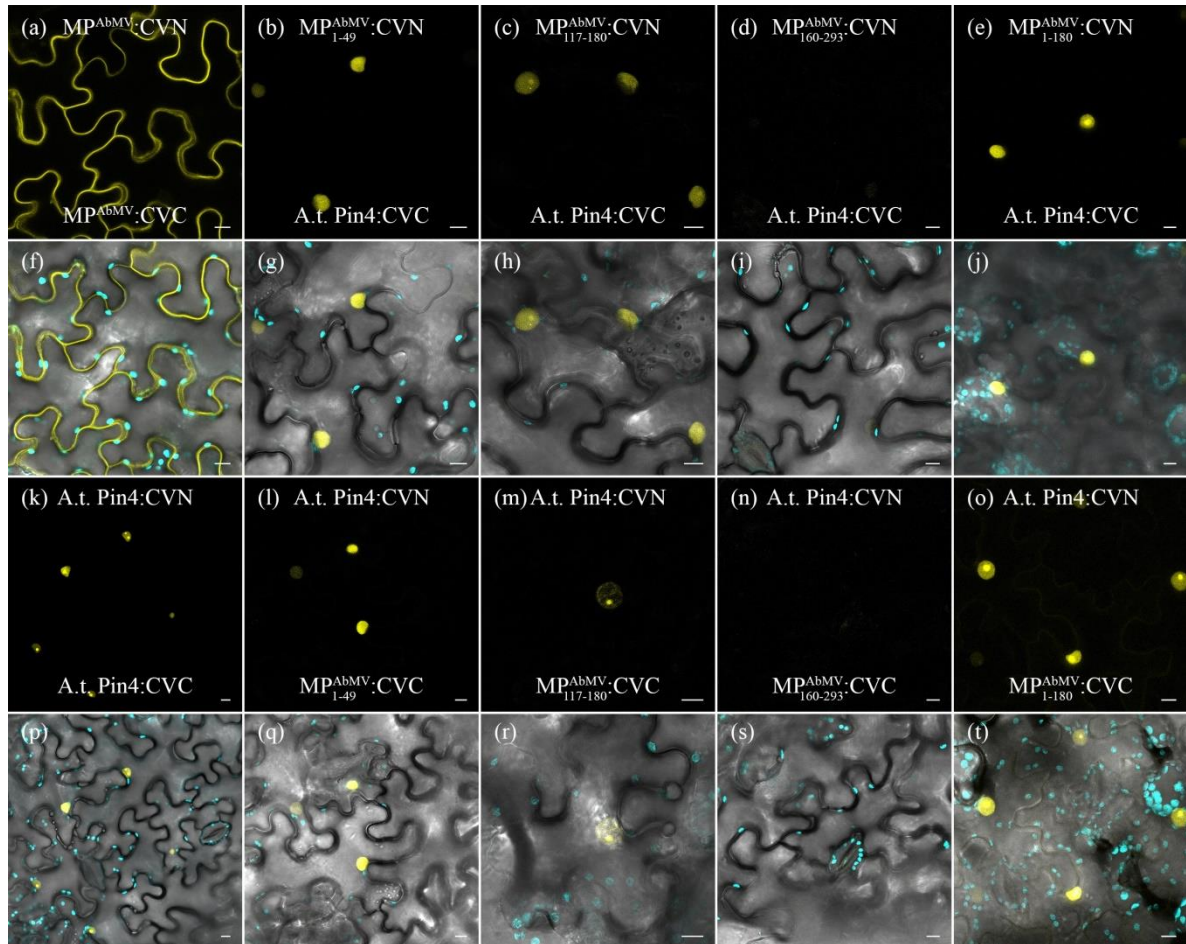


Figure S6: Quantitative PCR (qPCR) analysis of the viral DNA content in AbMV-infected *N. benthamiana*. Plants were either transiently silenced for N.b.Pin4 by a TRV-based system or mock-treated with the empty TRV vectors prior to AbMV application. Relative quantification of AbMV DNA A levels in leaves. Internal reference gene: 25S rRNA gene. Error bars refer to technical replicates.

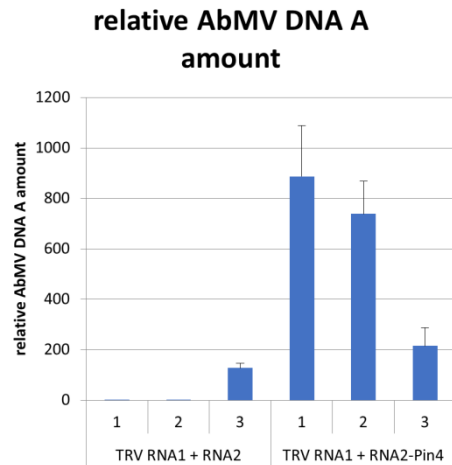


Table S1: List of used oligonucleotides for cloning of mammalian cell culture expression constructs

Oligonucleotide name	Sequence 5' -> 3'
MP ^{CILCrV} FP	AGA ATT CAA TGG AAT CGA AAC TGG TTG TGC C
MP ^{CILCrV} RP	TGG ATC CTT TTG TAA AGC CTT GGA TTG CGA AGG G
MP ^{PNYDV} FP	AGA ATT CAA TGT CGC AAC CTG GAG ATT ATG GAG
MP ^{PNYDV} RP	TGG ATC CTT AAT CAT TCC TCC TGA CGG AGG
P2 ^{CaMV} FP	GAA TTC ATG AGC ATT ACG GGT CAA CC
P2 ^{CaMV} RP	GGA TCC TTG CCA ATA ATA TTC TTT AAT CCT TCT TTG AT
MAP4 FP	AAG CTT ATG TCC CGG CAA GAA GAA GCA AAG
MAP4 RP	GAA TTC TGA TCC CGG GCC CAC
MP ^{AbMV} _HA FP	GAATTC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP ^{AbMV} _HA RP	GCGGCCGC TTA AGC ATA ATC TGG AAC ATC GTA TGG ATA TTT CAA TGA TTT GGC
MP ^{AbMV} _1-49 FP	GAATTC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC

MP^{AbMV}_1-49 RP	GGATCC TT GCT ACG ACT GAG TCT AGC
MP^{AbMV}_117-180 FP	GAATTC ATG TGG AAA TTG TAC TAC AAA GTC TGC GAT ACA A
MP^{AbMV}_117-180 RP	GGATCC TT TTT CCC ATA ATC CAC ATG GGA
MP^{AbMV}_160-293 FP	GAATTC ATG ATA CTG TCC AAA CAG TTC TCC GAA AAA GA
MP^{AbMV}_160-293 RP	GGATCC TT TTT CAA TGA TTT GGC TTG AGA AGC
MP^{AbMV}_1-180 FP	GAATTC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV}_1-180 RP	GGATCC TT TTT CCC ATA ATC CAC ATG GGA
MP^{AbMV}_1-150 FP	GAATTC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV}_1-150 RP	GGATCC TT GAC TGA GTG TTT CGC CG
MP^{AbMV}_25-180 FP	GAATTC ATG CAT GAC CTA ACT GAG ATA ATA CTG CAA TTT C
MP^{AbMV}_25-180 RP	GGATCC TT TTT CCC ATA ATC CAC ATG GGA
MP^{AbMV}_K112A/D113A FP	C TCG CTG GCA GCA CCC ATT C
MP^{AbMV}_K112A/D113A RP	G AAT GGG TGC TGC CAG CGA G
pEYFP-N1/C1 forw	CCC CCG AAT TCC ATG GAT TCT CAG TTA GTA AAT C
pEYFP-N1 rev	CTC TCG GAT CCC CTT TCA ATG ATT TGG CTT GAG

Table S2: List of used oligonucleotides for cloning of plant expression constructs

Oligonucleotide name	Sequence 5' -> 3'
MP^{AbMV} FP	CACC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV} RP	TTT CAA TGA TTT GGC TTG AGA AGC
MP^{AbMV}_1-180 FP	CACC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV}_1-180 RP	TTT CCC ATA ATC CAC ATG GGA
MAP4 FP	GAATTC ATG TCC CGG CAA GAA GAA GC
MAP4 RP	TCTAGA GAT CCC GGG CCC ACC TCC TG

Rep^{AbMV} FP	ACTAGT ATG CCA CCG CCA AAG AAA TTT AG
Rep^{AbMV} RP	GGATCC ATG GCC CTC CTC TTG GCC
MP^{AbMV}:CVN FP	CACC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV}:CVN RP	TTT CAA TGA TTT GGC TTG AGA AGC
MP^{AbMV}:CVC FP	CACC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV}:CVC RP	TTT CAA TGA TTT GGC TTG AGA AGC
A.t. Pin4:CVN FP	CACC ATG GGG AAG GAC GCA AAA GCT GG
A.t. Pin4:CVN RP	GTT CTT CCT TCC CTC TGA TAA AAT AAT G
A.t. Pin4:CVC FP	CACC ATG GGG AAG GAC GCA AAA GCT GG
A.t. Pin4:CVC RP	GTT CTT CCT TCC CTC TGA TAA AAT AAT G
A.t. Pin4:GFP FP	CACC ATG GGG AAG GAC GCA AAA GCT GG
A.t. Pin4:GFP RP	GTT CTT CCT TCC CTC TGA TAA AAT AAT G
S.l. SCD2:GFP FP	CACC ATG GAT CGA CGG AGG AC
S.l. SCD2:GFP RP	TGG AGA TGC CTC CGA ATC ACT ACT CA
S.l. SCD2:CVN FP	CACC ATG GAT CGA CGG AGG AC
S.l. SCD2:CVN RP	TGG AGA TGC CTC CGA ATC ACT ACT CA
S.l. SCD2:CVC FP	CACC ATG GAT CGA CGG AGG AC
S.l. SCD2:CVC RP	TGG AGA TGC CTC CGA ATC ACT ACT CA
MP^{AbMV}_1-49 FP	GAATTC ATG GAT TCT CAG TTA GTA AAT CCT CCG AAC
MP^{AbMV}_1-49 RP	GGATCC GCT ACG ACT GAG TCT AGC
MP^{AbMV}_117-180 FP	GAATTC ATG TGG AAA TTG TAC TAC AAA GTC TGC GAT ACA A
MP^{AbMV}_117-180 RP	GGATCC TTT CCC ATA ATC CAC ATG GGA
MP^{AbMV}_160-293 FP	GAATTC ATG ATA CTG TCC AAA CAG TTC TCC GAA AAA GA
MP^{AbMV}_160-293 RP	GGATCC TTT CAA TGA TTT GGC TTG AGA AGC

TRV RNA2 N.b. Pin4 FP GGATCC ATG GGA AAG GAC TCC AAG GC

TRV RNA2 N.b. Pin4 RP GGATCC TCA ATT TTT CCT CCC TTC AC

Table S3: Proteins interacting with RFP:MP^{AbMV} identified by mass spectrometry.

Accession (<i>N. benthamiana</i>)	Description	Identified peptides
NbS00041310g0002.1 protein AED:0.34 eAED:0.34 QI:0	AT3G48860.2 (e_value=2e-75) Symbols: unknown protein; INVOLVED IN: biological_process unknown; LOCATED IN: plasma membrane; EXPRESSED IN: 22 plant structures; EXPRESSED DURING: 13 growth stages; BEST Arabidopsis thaliana protein match is: unknown protein (TAIR:AT5G23700.1); Has 12429 Blast hits to 9751 proteins in 897 species: Archae - 180; Bacteria - 1190; Metazoa - 6552; Fungi - 1361; Plants - 886; Viruses - 50; Other Eukaryotes - 2210 (source: NCBI BLINK). chr3:18117619-18121853 FORWARD LENGTH=577;; (*ITAG) Solyc03g118390.2.1 (e_value=6e-112) genomic_reference:SL2.40ch03 gene_region:61331348- 61340606 transcript_region:SL2.40ch03:61331348..61340606- functional_description:"Chromosome 14 contig 1 DNA sequence (AHRD V1 *-*- Q00WF1_OSTTA)";	NFMDHTPSVR QWSGGSSTGSSSPAGSPAHPR SGQTPTTHDAVDVER TSAATTTTGAIVPPSR
NbS00018507g0022.1 protein AED:0.42 eAED:0.42 QI:0	gi 217075350 gb ACJ86035.1 (e_value=2e-69) unknown [Medicago truncatula];; (*SWP) sp A6QPY8 PIN4_BOVIN (e_value=5e-24) Peptidyl-prolyl cis-trans isomerase NIMA- interacting 4 OS=Bos taurus GN=PIN4 PE=2 SV=1;; (*TAIR) AT1G26550.1 (e_value=3e-70) Symbols: FKBP-like peptidyl- prolyl cis-trans isomerase family protein chr1:9171800-9172716 FORWARD LENGTH=142;; (*ITAG) Solyc12g036200.1.1 (e_value=1e-70) evidence_code:10F1H1E1IEG genomic_reference:SL2.40ch12 gene_region:29804400- 29807477 transcript_region:SL2.40ch12:29804400..29807477+ go_terms:GO:0016853 functional_description:"Peptidyl-prolyl cis-trans isomerase (AHRD V1 *-*- Q2F670_BOMMO); contains Interpro domain(s) IPR000297 Peptidyl-prolyl cis-trans isomerase, PpiC-type ";	KGGDLGWFP