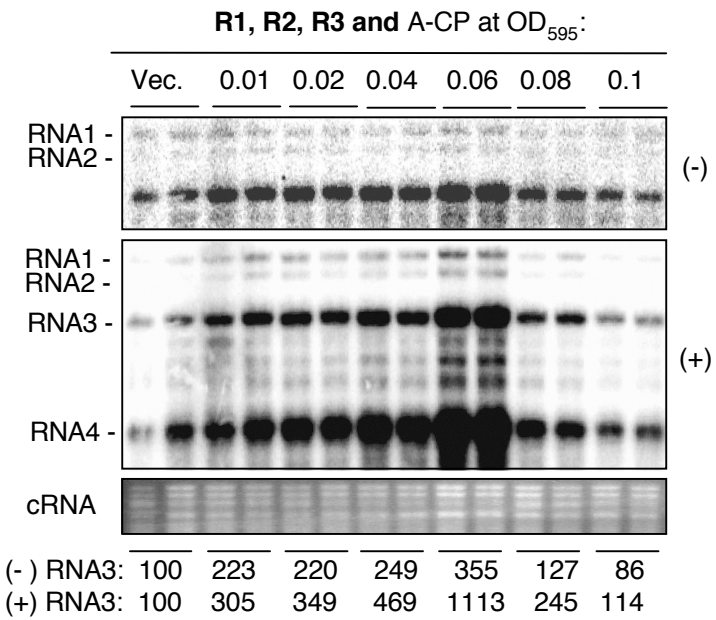
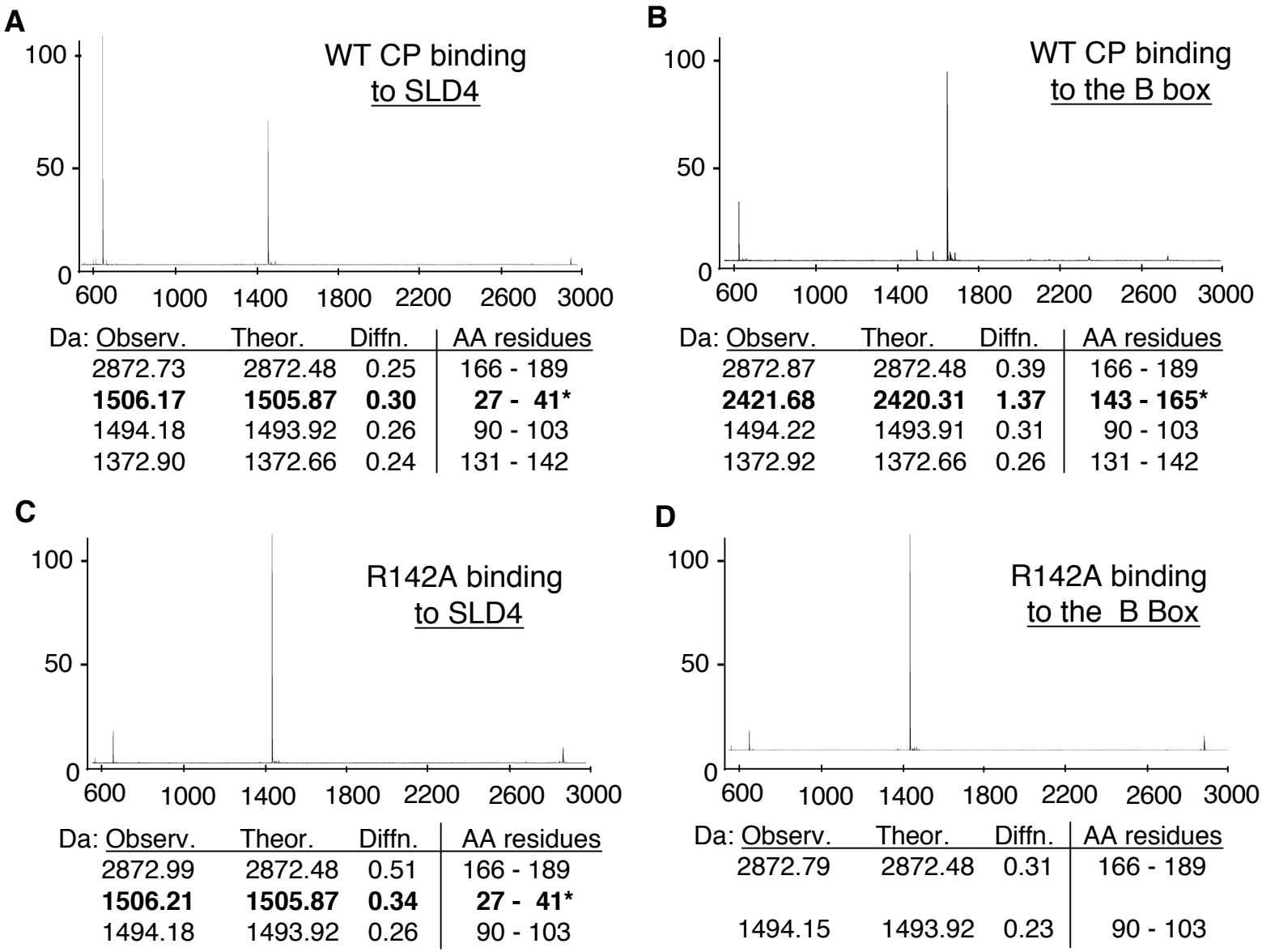


sFig. 1. Effects of transient expression of the BMV capsid protein on RNA accumulation. Densities of *Agrobacterium* expressing BMV CP, named A-pCP, were co-infiltrated with the mixture of *Agrobacterium* cultures that can express the three BMV genomic RNAs, each at OD_{595} of 0.1. Total RNA was isolated at 2 days post-infiltration, and both negative and positive strand RNA was subjected to Northern blot assay with strand-specific probes as described in the Materials and Methods. The image of ethidium bromide-stained cellular RNA (cRNA) served as the loading control for the Northern blot. Quantification of the (-) and (+)-strand BMV RNA3 in the experiment is shown at the bottom of the image as a percentage of the wild-type RNA3. All samples are normalized to the quantity of BMV RNA3 produced in the presence of the empty vector.



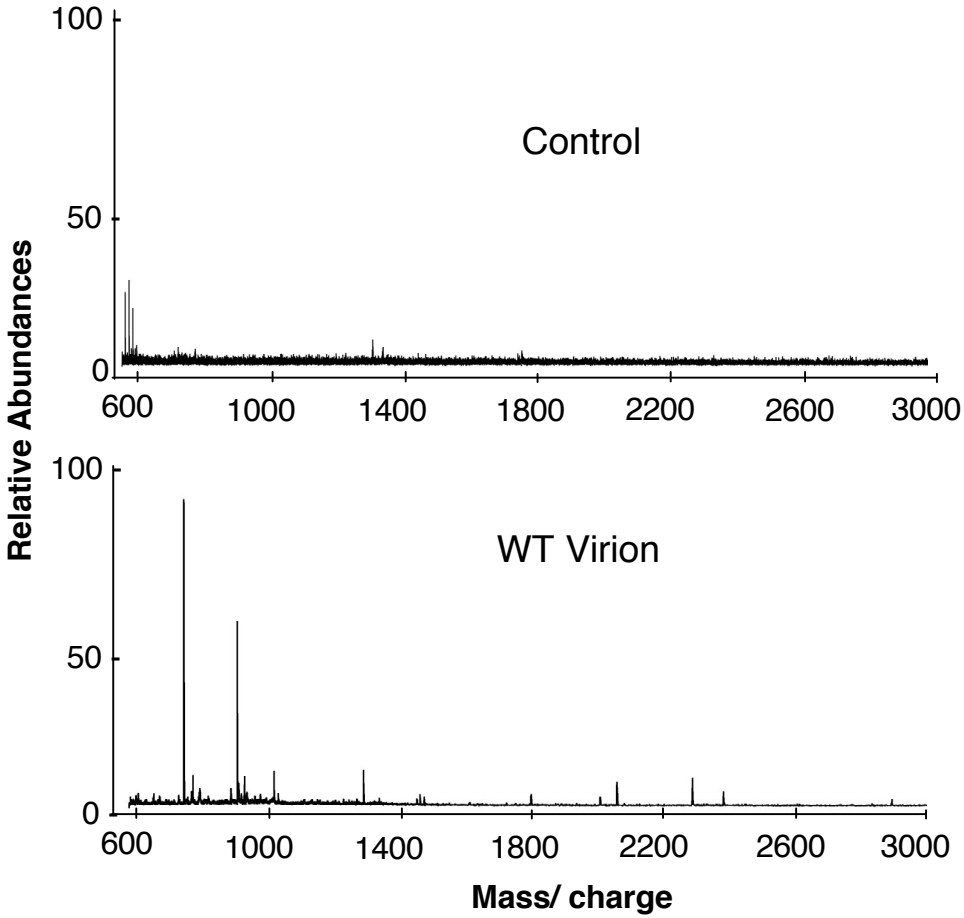
Da: Observ.	Theor.	Diffn.	AA residues
2872.73	2872.48	0.25	166 - 189
1506.17	**1505.87**	**0.30**	**27 - 41***
1494.18	1493.92	0.26	90 - 103
1372.90	1372.66	0.24	131 - 142

Da: Observ.	Theor.	Diffn.	AA residues
2872.87	2872.48	0.39	166 - 189
2421.68	**2420.31**	**1.37**	**143 - 165***
1494.22	1493.91	0.31	90 - 103
1372.92	1372.66	0.26	131 - 142

Da: Observ.	Theor.	Diffn.	AA residues
2872.99	2872.48	0.51	166 - 189
1506.21	**1505.87**	**0.34**	**27 - 41***
1494.18	1493.92	0.26	90 - 103

Da: Observ.	Theor.	Diffn.	AA residues
2872.79	2872.48	0.31	166 - 189
1494.15	1493.92	0.23	90 - 103

sFigure 2. BMV CP peptides crosslinked to RNA motifs. Data was collected on a Bruker Biflex III MALDI-TOF Mass spectrometer. Samples desalted with a Ziptip (Millipore, Bedford, MA)were eluted directly onto the sample plate in α-cyano-4-hydroxycinnamic acid matrix (mass: 189.17 Da). Positive ions from mass 400-4,000 Da were analyzed in reflectron mode. Peaks that were 3 times above the background signal were considered significant. The peptides that differed between WT CP and the R142A CP are in bold and dented with an asterisk. A) Peptides from WT CP crosslinked to SLD4. B) Peptides from the WT CP crosslinked to the B Box. C) Peptides from R142A crosslinked to SLD4. D) Peptides from R142A crosslinked to the B Box.



Da: Observ.	Theor.	Diffn.	AA residues
2872.03	2872.48	0.55	166 - 189
2382.75	2381.27	1.48	42 - 64
2290.73	2290.28	0.45	21 - 41
2069.46	2069.06	0.40	45 - 64
1818.45	1818.09	0.37	27 - 44
959.77	959.53	0.24	20 - 26
803.66	803.43	0.24	21 - 26

sFigure 3. Representative MALDI-ToF mass spectrometry of peptides from WT virion interacting with viral RNA. The control spectrum was generated concurrently with WT virion without the addition of formaldehyde, but otherwise processed identically. LiCl precipitated RNA-peptide conjugates were resuspended in water and desalted using a Ziptip (Millipore, Bedford, MA) and eluted directly onto the sample plate in a-cyano-4-hydroxycinnamic acid matrix. Peaks that were 3 times above the background signal were considered significant.