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Figure S1 The gRNA sequences in relation to CaMV coat protein coding sequence (strain w260). Targeting sequences of six gRNAs are in bold and PAM sites are underlined. Note the sequence that is also italicized is target on the complementary strand.

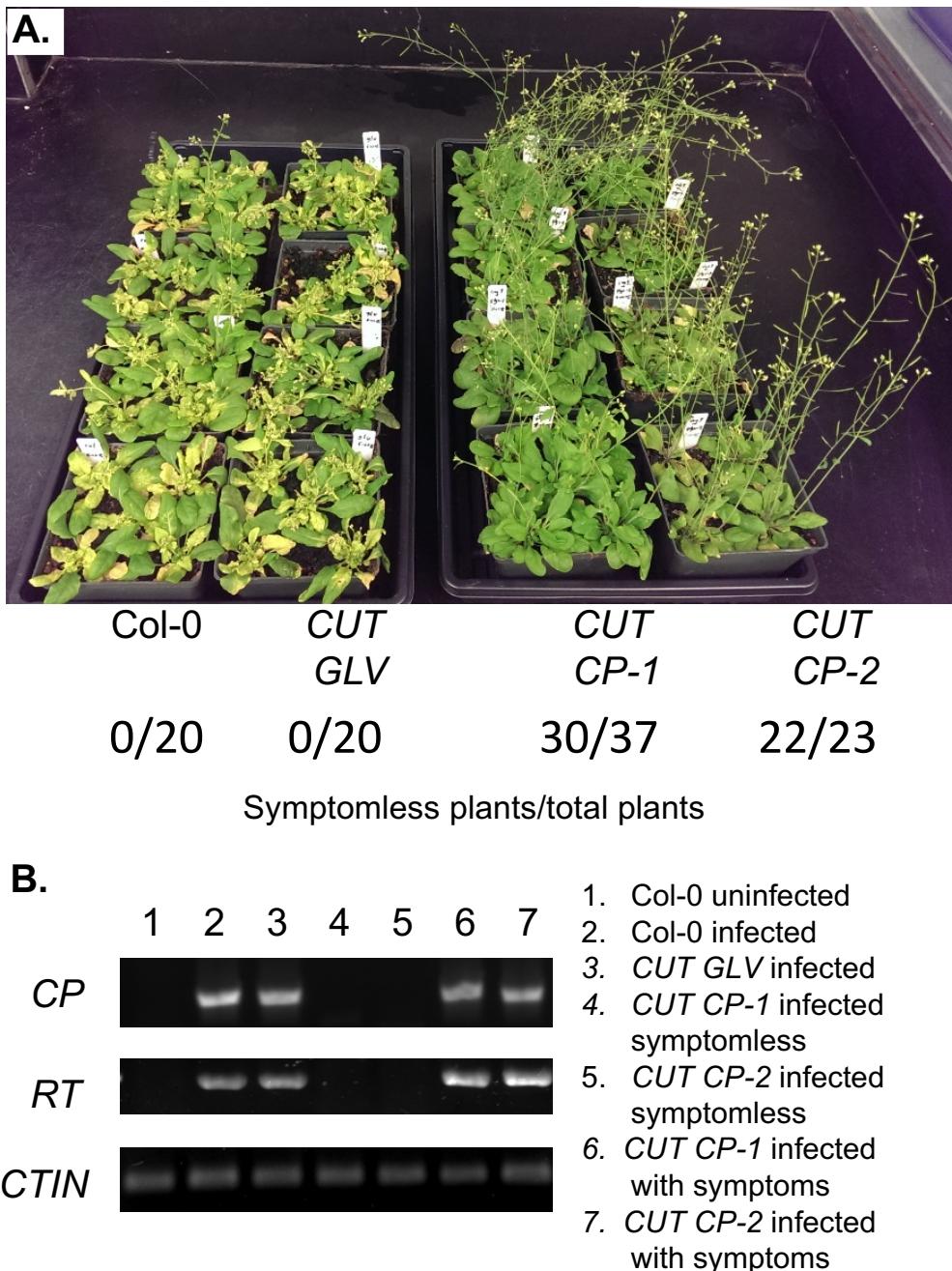


Figure S2. Cas9-mediated viral immunity by targeting the CaMV CP coding sequence.
A. CaMV-infected plants at 26 DPI. Both Col-0 (left) and CUT GLV (middle) transgenic plants display extensive symptoms of chlorosis and stunting, while most CUT CP-1 or CUT CP-2 transgenic plants remain symptomless. Numbers below summarize the number of plants without symptoms/total plants infected. B. The CaMV CP gene is detectable in Col-0, CUT GLV plants and CUT CP plants displaying symptoms, but not in symptomless CUT CP plants. RT, viral reverse transcriptase. Arabidopsis ACTIN was used as a loading control.

**Supplemental Table 1. Cas9-induced mutations
in CaMV *CP* sequences from systemically infected tissue**

Site: All nucleotide (nt) numbers are relative to wt CaMV *CP* sequence. Insertion and deletion are between the given nt numbers.

gRNA: G, gRNA. Numbering as in Supplemental Table 1.

Origin: Origin of inserted gene sequence. *CP* (w260).

Effect on CP protein: wt CP protein: 487 amino acids (aa).

Clone	Mutation in <i>CP</i> gene	Site (nt)	gRNA	Affected sequence	Origin	Effect on CP protein
1A	Single base deletion	330	G5	A		Frame shift after E110, stop codon 35 aa after, total length 145 aa
2A				TTCAGGAGAAGAACCTGAATTCCAGGCAATGGACCGAACAGAG GAACGGAGATTCCTAAAGAAGAAGATGGTGAAGGACCATCAAGATAAA TGAAGAAAGAGAAAGACCCCCGAGGACCGGTACTTCCAAC		
142 bp deletion		257,400	G1, G2			Frame shift after D86, stop codon 12 aa after, total length 98 aa
10B	6 bp deletion	326,333	G5	AGAAGA		In frame deletion of 2 aa (E109-E110)
7B	Single base insertion	330,331	G5	A		Frame shift after E110, stop codon 2 aa after, total length 112 aa
				AGATGGTGAAGGACCATCAAGATACAATGAGAGAAAGAGAAAGACCCG	<i>CP</i>	
	106 bp insertion	330,331	G5	GAGGACCCGTACTTTCAACTCAACCAAAGACCCATTCCAGGACAAAGCA		
9B	Single base insertion	330,331	G5	A		Frame shift after E110, stop codon 2 aa after, total length 112 aa