TMV nanorods with programmed longitudinal domains of differently addressable coat proteins^{\dagger}

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[†]LIST OF SUPPLEMENTARY INFORMATION

This Electronic Supplementary Information (ESI) contains:

1. Two Supplementary Figures [pp. S1-2]

<u>Supplementary Figure S1</u>: Phenotype of different *Nicotiana* plant species systemically infected with TMV_{wt} , TMV_{Cys} , or TMV_{Lys} at 9 and 15 days post inoculation. [p. S1]

<u>Supplementary Figure S2</u>: Length distributions of partially and completely *in vitro* assembled VLP rods using TMV_{wt} RNA as a template. [p. S2]

2. SupplementaryTable [p. S2]

Table S1: Sequences of primers used for site-specific mutagenesis of the TMV CP ORF and for sequencing.



Figure S1: *N. benthamiana*, *N. rustica* or *N.tabacum* cv. 'Samsun' nn plants inoculated with wt TMV_{wt}, TMV_{Cys}, TMV_{Lys} particles or buffer (mock), respectively. Pictures were taken at 9 (A) or 15 dpi (B).

n

50

100 150 200 Length (nm)



50 100 150 200 250 300 350

Length (nm)

0

Lys

Cys

Cys

Lys

CP2:

CP1:

Figure S2: Length distributions of in vitro assembled TMV-like rods using TMV_{wt} RNA as a template, with adjacent domains of different CP species after completion as described in Figures 3 and 4 in the main article. The numbers of particles (n) examined of each sample are indicated in the histograms (A). The median values (black squares), upper and lower quartiles (box), and the maximum and minimum values (bars) are summarized in a box plot (B).

on PCR, and for sequencing. Nucleotides inserting mutations are bold and underlined.	
Primer	Sequence (5'-3')
F1	CCAACCTCGAGGATTACAAACGTGAGAGACGGAGG
R1	CCAACCTCGAGCGCGATCCAAGACACAACCCTTCG
RCys	CTGAGATGGAGTAGTGATAC <u>A</u> ATAAG
FCys	TATGTCTTAT <u>T</u> GTATCACTACTCCATC
RLys	TCTTGACTAGCTCA <u>CT</u> TTGCAGGA
FLys	CCTCTAGTCCTGCAA <u>AG</u> TGAGCTAG
CPF	CCGCTTTCTCTGGAGTTTGTGTCG
CPR	CGTGCCTGCGGATGTATATGAACC
INTF	AATCGATGATGATTCGGAGG
INTR	AACACTATGCGTTATCGTACG

Table S1 : Sequences of primers used for site-specific mutagenesis of the TMV CP ORF by overlap
extension PCR, and for sequencing. Nucleotides inserting mutations are bold and underlined.

250 300 350