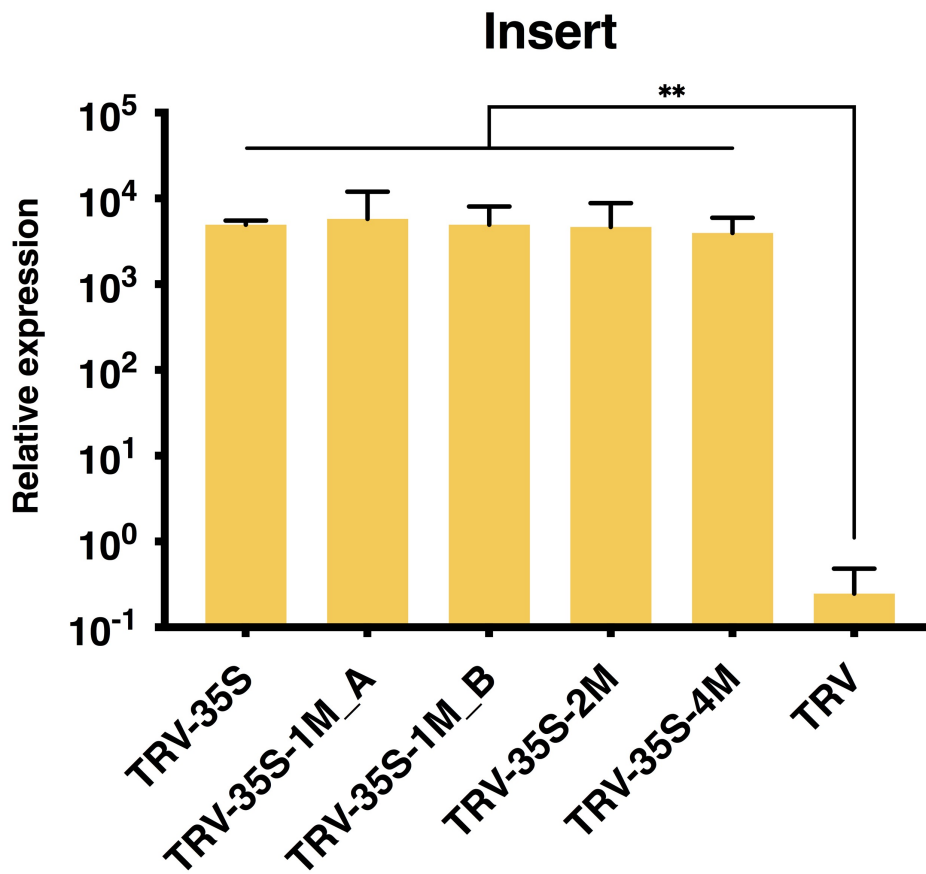
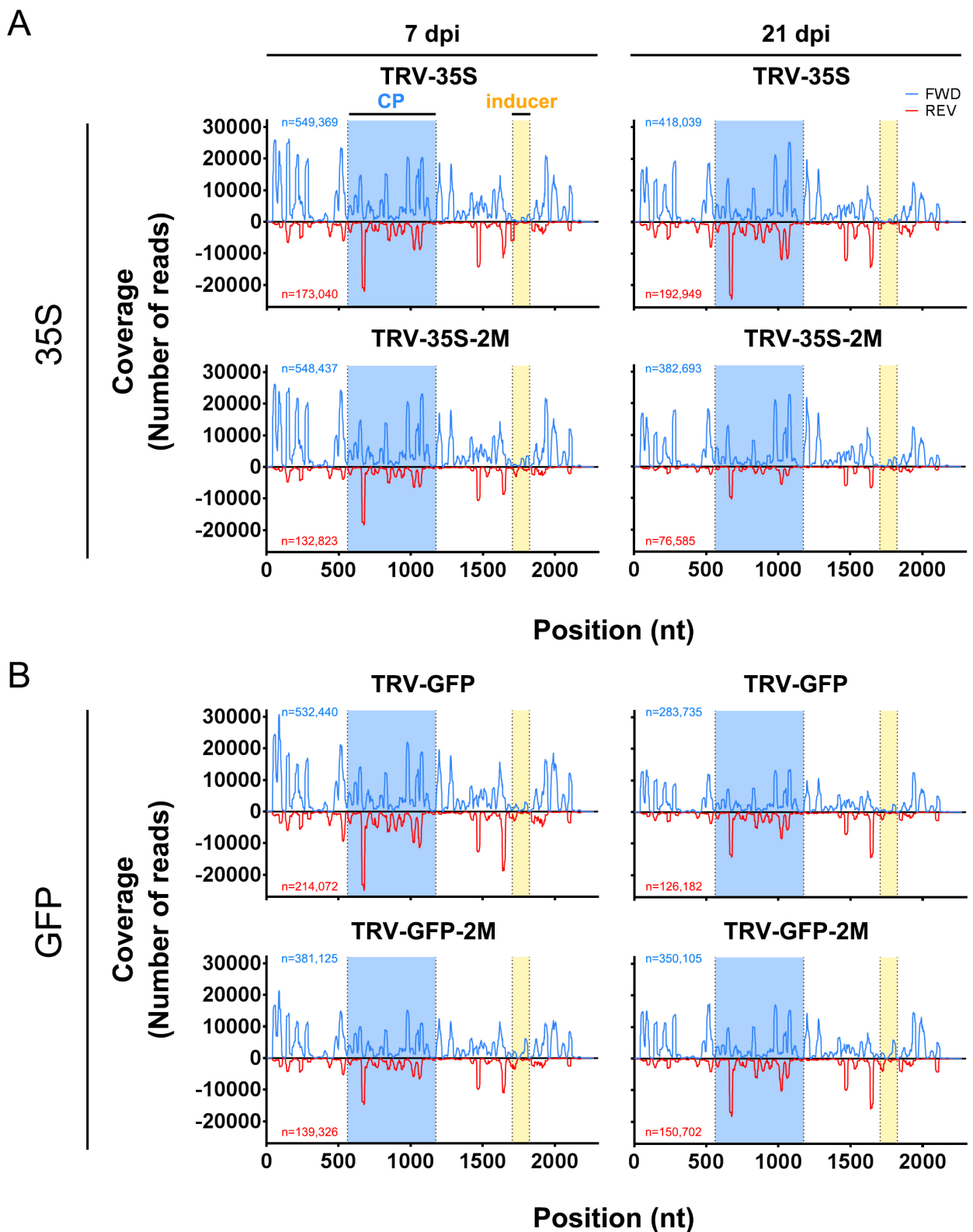


Supplementary Figure S1



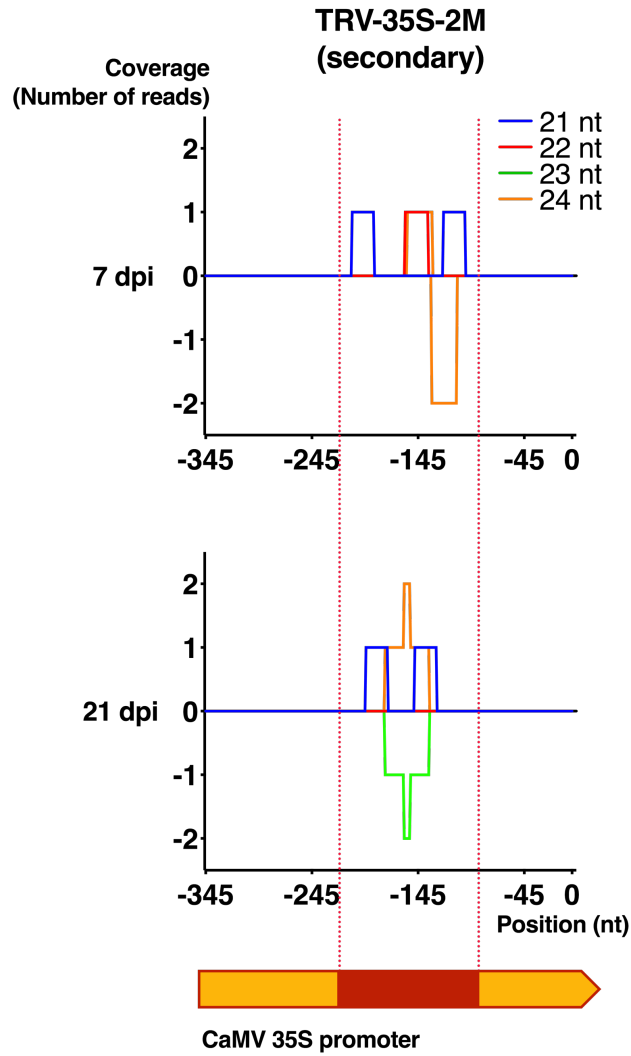
Supplementary Figure S1. Analysis of recombinant TRV in virus-infected *N. benthamiana* plants by qRT-PCR. The same RNA samples were used as in Figure 2. TRV RNA was amplified by insert-specific primers. Error bars show the standard error of the mean (SEM) of three independent biological replicates. Asterisks indicate significant differences (Student's T-test, $p < 0.01$).

Supplementary Figure S2



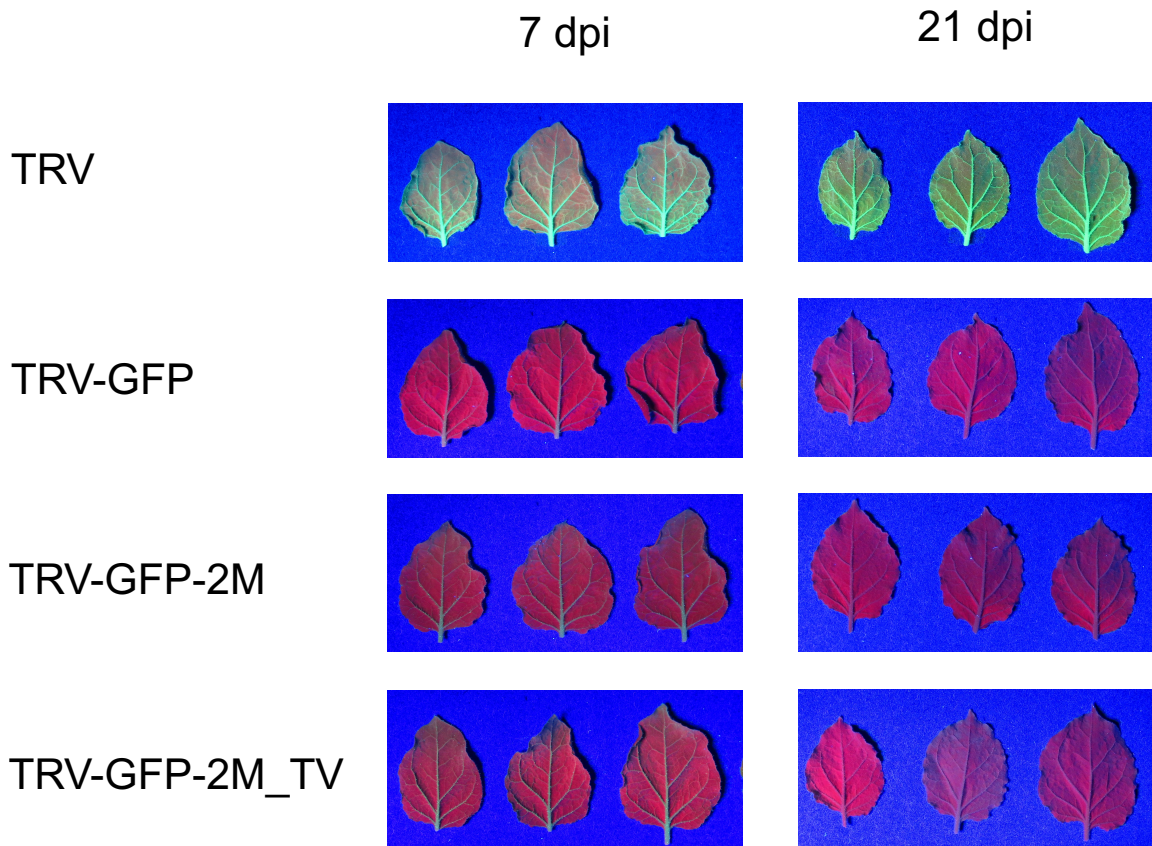
Supplementary Figure S2. Analysis of virus-derived small RNAs in recombinant-TRV-infected plants. Raw small RNA reads were aligned to the corresponding recombinant TRV RNA2 indicated. The positive or negative y-axis values show the number of small RNAs on either plus or minus strand as blue or red lines, respectively. The coat protein and the silencing-inducer sequences are highlighted as blue and yellow boxes, respectively. The total number of small RNAs matching the above selected regions of the viral genome is also indicated in the graph.

Supplementary Figure S3



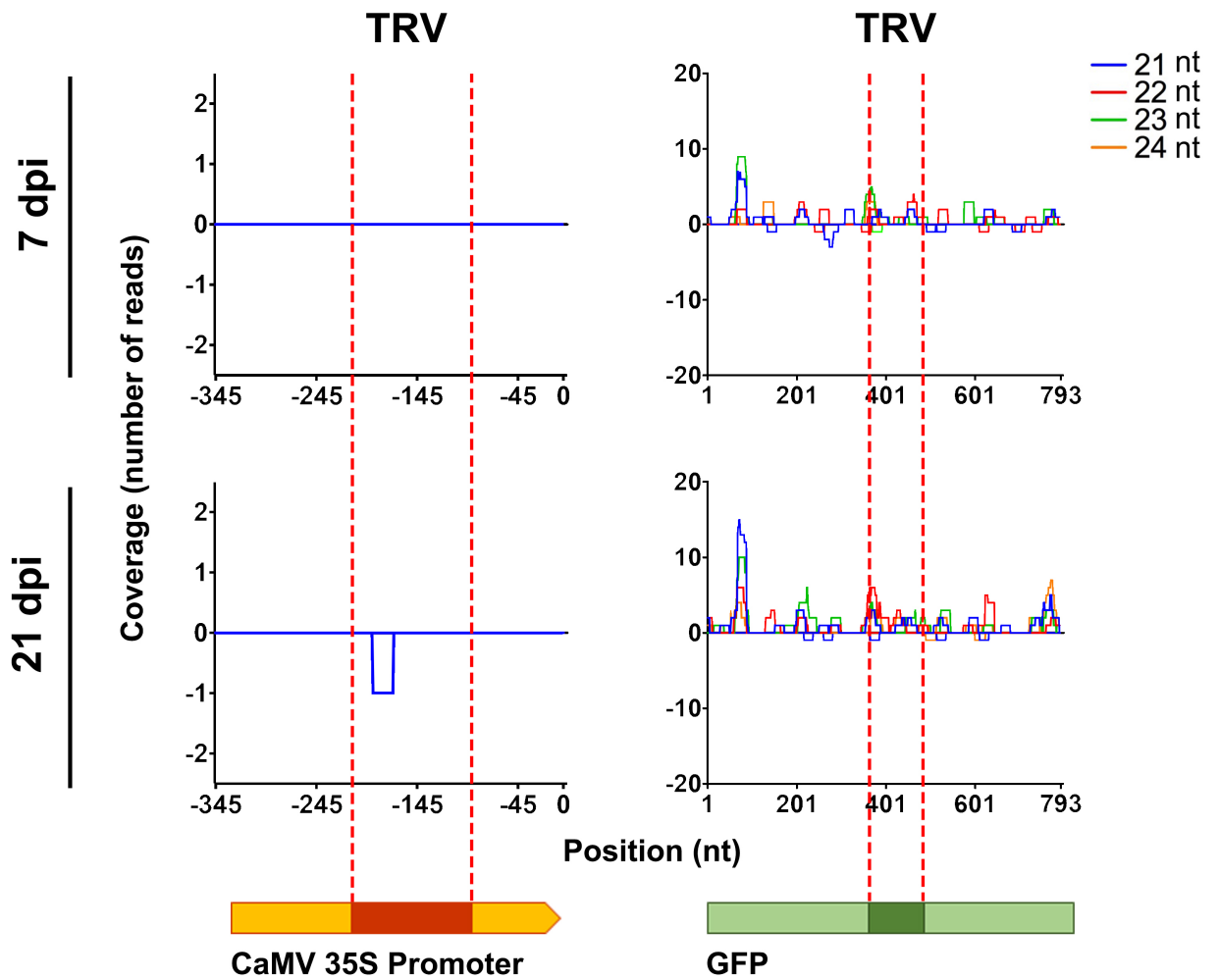
Supplementary Figure S3. Analysis of secondary small RNAs in TRV-35S-2M infected *N. benthamiana* 16c plants at 7 dpi and 21 dpi. High resolution map of small RNAs corresponding to Figure 3 top right panel.

Supplementary Figure S4



Supplementary Figure S4. Non-perfectly matching small RNAs can induce strong post-transcriptional gene silencing in virus-infected plants. 16c plants were infected with wild type TRV, TRV-GFP, TRV-GFP-2M, and TRV-GFP-2M_TV were photographed under UV light at 7 and 21 dpi.

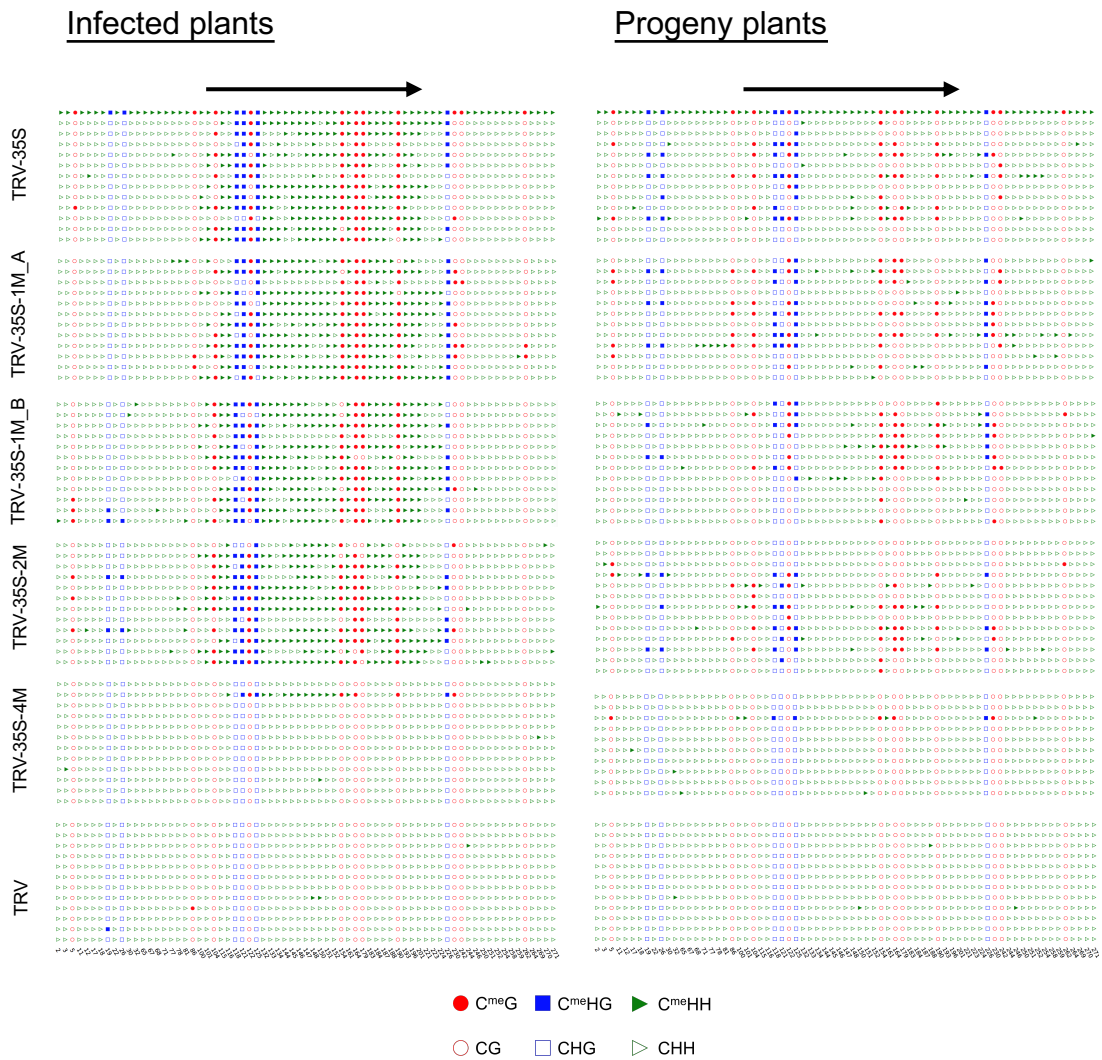
Supplementary Figure S5



Supplementary Figure S5. Analysis of small RNAs in TRV-infected *N. benthamiana* 16c plants at 7dpi and 21 dpi. Small RNA reads were aligned to the 35S promoter and GFP coding sequence. The numbers of sRNAs mapping at each position of the plus strand are shown as positive values, to the minus as negative values, for 21, 22, 23 and 24 nt sRNAs separately. The target sequence is highlighted by dotted lines.

Supplementary Figure S6

A



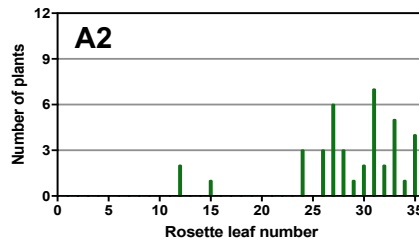
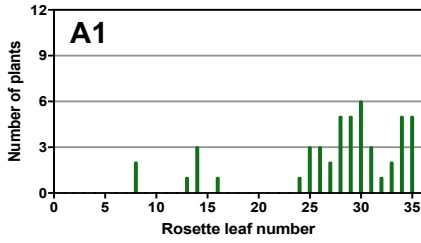
B

| | | Number of clones | Total C sites | Methylated C sites | % C methylation | 95% confidence interval | |
|----------------|--------------|------------------|-----------------|----------------------|-------------------|-------------------------|----------|
| | | | | | | C int- | C int+ |
| Infected plant | TRV-35S | 37 | 1332 | 885 | 66.44 | 63.86 | 68.93 |
| | TRV-35S-1M_A | 25 | 900 | 528 | 58.67 | 55.42 | 61.84 |
| | TRV-35S-1M_B | 30 | 1080 | 654 | 60.56 | 57.61 | 63.43 |
| | TRV-35S-2M | 33 | 1188 | 734 | 61.78 | 58.99 | 64.51 |
| | TRV-35S-4M | 27 | 972 | 89 | 9.16 | 7.50 | 11.13 |
| TRV | 35 | 1260 | 9 | 0.71 | 0.38 | 1.35 | |
| Progeny | TRV-35S | 35 | 1260 | 209 | 16.59 | 14.64 | 18.74 |
| | TRV-35S-1M_A | 30 | 1080 | 195 | 18.06 | 15.88 | 20.46 |
| | TRV-35S-1M_B | 32 | 1152 | 148 | 12.85 | 11.04 | 14.90 |
| | TRV-35S-2M | 33 | 1188 | 198 | 16.67 | 14.66 | 18.89 |
| | TRV-35S-4M | 28 | 1008 | 16 | 1.59 | 0.98 | 2.56 |
| TRV | 30 | 1080 | 7 | 0.65 | 0.31 | 1.33 | |
| | | Number of clones | Total CG sites | Methylated CG sites | % CG methylation | 95% confidence interval | |
| | | | | | | CG int- | CG int+ |
| Infected plant | TRV-35S | 37 | 222 | 175 | 78.83 | 72.99 | 83.69 |
| | TRV-35S-1M_A | 25 | 150 | 125 | 83.33 | 76.55 | 88.45 |
| | TRV-35S-1M_B | 30 | 180 | 145 | 80.56 | 74.16 | 85.67 |
| | TRV-35S-2M | 33 | 198 | 151 | 76.26 | 69.87 | 81.65 |
| | TRV-35S-4M | 27 | 162 | 14 | 8.64 | 5.22 | 13.98 |
| TRV | 35 | 210 | 3 | 1.43 | 0.49 | 4.12 | |
| Progeny | TRV-35S | 35 | 210 | 94 | 44.76 | 38.19 | 51.52 |
| | TRV-35S-1M_A | 30 | 180 | 96 | 53.33 | 46.05 | 60.48 |
| | TRV-35S-1M_B | 32 | 192 | 64 | 33.33 | 27.05 | 40.27 |
| | TRV-35S-2M | 33 | 198 | 94 | 47.47 | 40.63 | 54.41 |
| | TRV-35S-4M | 28 | 168 | 4 | 2.38 | 0.93 | 5.96 |
| TRV | 30 | 180 | 0 | 0.00 | 0.00 | 2.09 | |
| | | Number of clones | Total CHG sites | Methylated CHG sites | % CHG methylation | 95% confidence interval | |
| | | | | | | CHG int- | CHG int+ |
| Infected plant | TRV-35S | 37 | 148 | 110 | 74.32 | 66.73 | 80.68 |
| | TRV-35S-1M_A | 25 | 100 | 78 | 78.00 | 68.93 | 85.00 |
| | TRV-35S-1M_B | 30 | 120 | 101 | 84.17 | 76.59 | 89.62 |
| | TRV-35S-2M | 33 | 132 | 101 | 76.52 | 68.60 | 82.93 |
| | TRV-35S-4M | 27 | 108 | 19 | 17.59 | 11.56 | 25.85 |
| TRV | 35 | 140 | 1 | 0.71 | 0.13 | 3.94 | |
| Progeny | TRV-35S | 35 | 140 | 58 | 41.43 | 33.60 | 49.71 |
| | TRV-35S-1M_A | 30 | 120 | 53 | 44.17 | 35.60 | 53.10 |
| | TRV-35S-1M_B | 32 | 128 | 33 | 25.78 | 18.99 | 33.99 |
| | TRV-35S-2M | 33 | 132 | 53 | 40.15 | 32.18 | 48.68 |
| | TRV-35S-4M | 28 | 112 | 4 | 3.57 | 1.40 | 8.83 |
| TRV | 30 | 120 | 0 | 0.00 | 0.00 | 3.10 | |
| | | Number of clones | Total CHH sites | Methylated CHH sites | % CHH methylation | 95% confidence interval | |
| | | | | | | CHH int- | CHH int+ |
| Infected plant | TRV-35S | 37 | 962 | 600 | 62.37 | 59.27 | 65.38 |
| | TRV-35S-1M_A | 25 | 650 | 325 | 50.00 | 46.17 | 53.83 |
| | TRV-35S-1M_B | 30 | 780 | 408 | 52.31 | 48.80 | 55.79 |
| | TRV-35S-2M | 33 | 858 | 482 | 56.18 | 52.84 | 59.46 |
| | TRV-35S-4M | 27 | 702 | 56 | 7.98 | 6.19 | 10.22 |
| TRV | 35 | 910 | 5 | 0.55 | 0.23 | 1.28 | |
| Progeny | TRV-35S | 35 | 910 | 57 | 6.26 | 4.87 | 8.03 |
| | TRV-35S-1M_A | 30 | 780 | 46 | 5.90 | 4.45 | 7.78 |
| | TRV-35S-1M_B | 32 | 832 | 51 | 6.13 | 4.69 | 7.97 |
| | TRV-35S-2M | 33 | 858 | 51 | 5.94 | 4.55 | 7.73 |
| | TRV-35S-4M | 28 | 728 | 8 | 1.10 | 0.56 | 2.15 |
| TRV | 30 | 780 | 7 | 0.90 | 0.44 | 1.84 | |

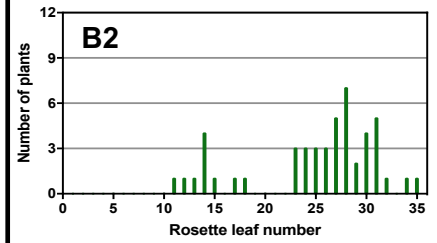
Supplementary Figure S6. Analysis of DNA methylation at the CaMV 35S promoter in recombinant-TRV-infected *N. benthamiana* 16c plants and their progeny. (A) Examination of cytosine methylation by bisulfite sequencing. Raw data is shown from one of the three biological repeats. Up to 12 independent clones of bisulfite-converted DNA were analysed by Cymate from each sample. The position of cytosine residues in the CaMV 35S promoter is indicated at the bottom of the composite figure. CG, CHG and CHH methylation is represented as red circle, blue square and green triangle, respectively. Methylated residues are shown as solid symbols. Black arrow indicates the virus-targeted region of CaMV 35S promoter. **(B)** Raw data from the bisulfite sequencing analysis presented in Figure 4 and Figure 5 including the number of sequenced clones and scored cytosine sites. There are 6 CG sites, 4 CHG sites and 26 CHH sites in the targeted region. The Wilson score was calculated as shown in (1) and (2).

Supplementary Figure S7

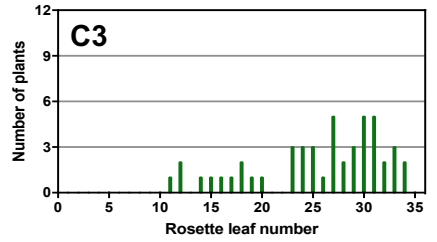
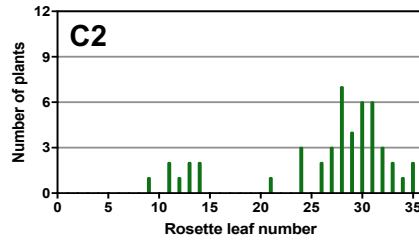
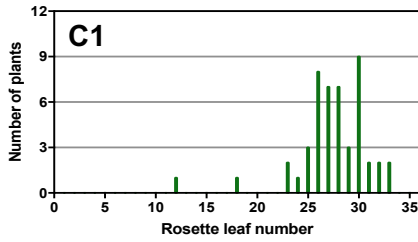
TRV-FWA-B



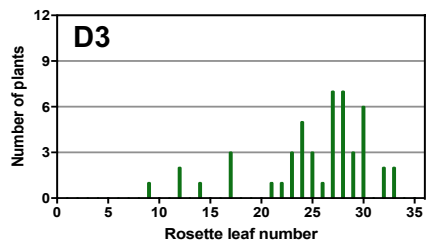
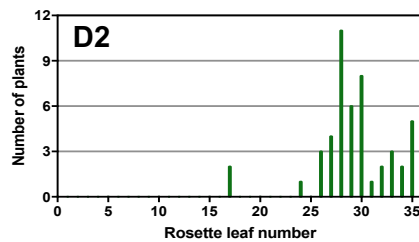
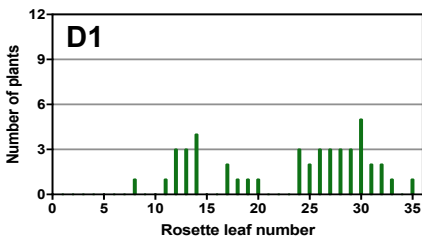
TRV-FWA-Bs



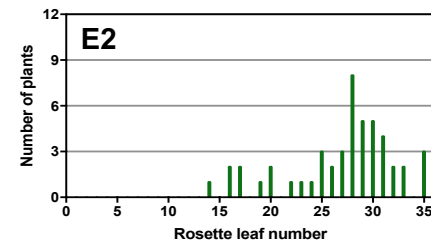
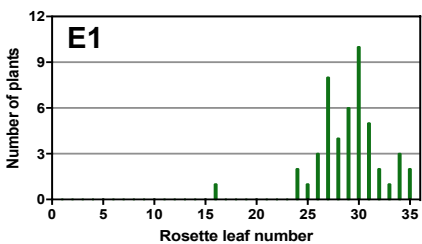
TRV-FWA-Bs-1M_A



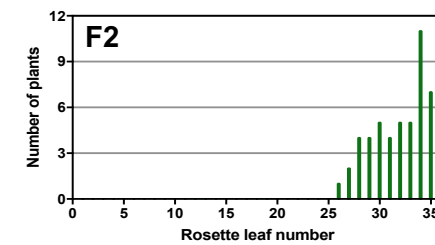
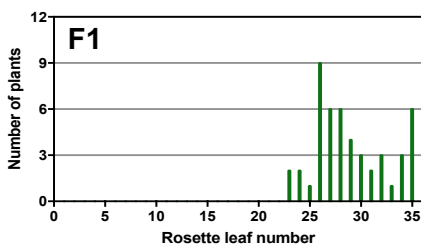
TRV-FWA-Bs-1M_B



TRV-FWA-Bs-2M



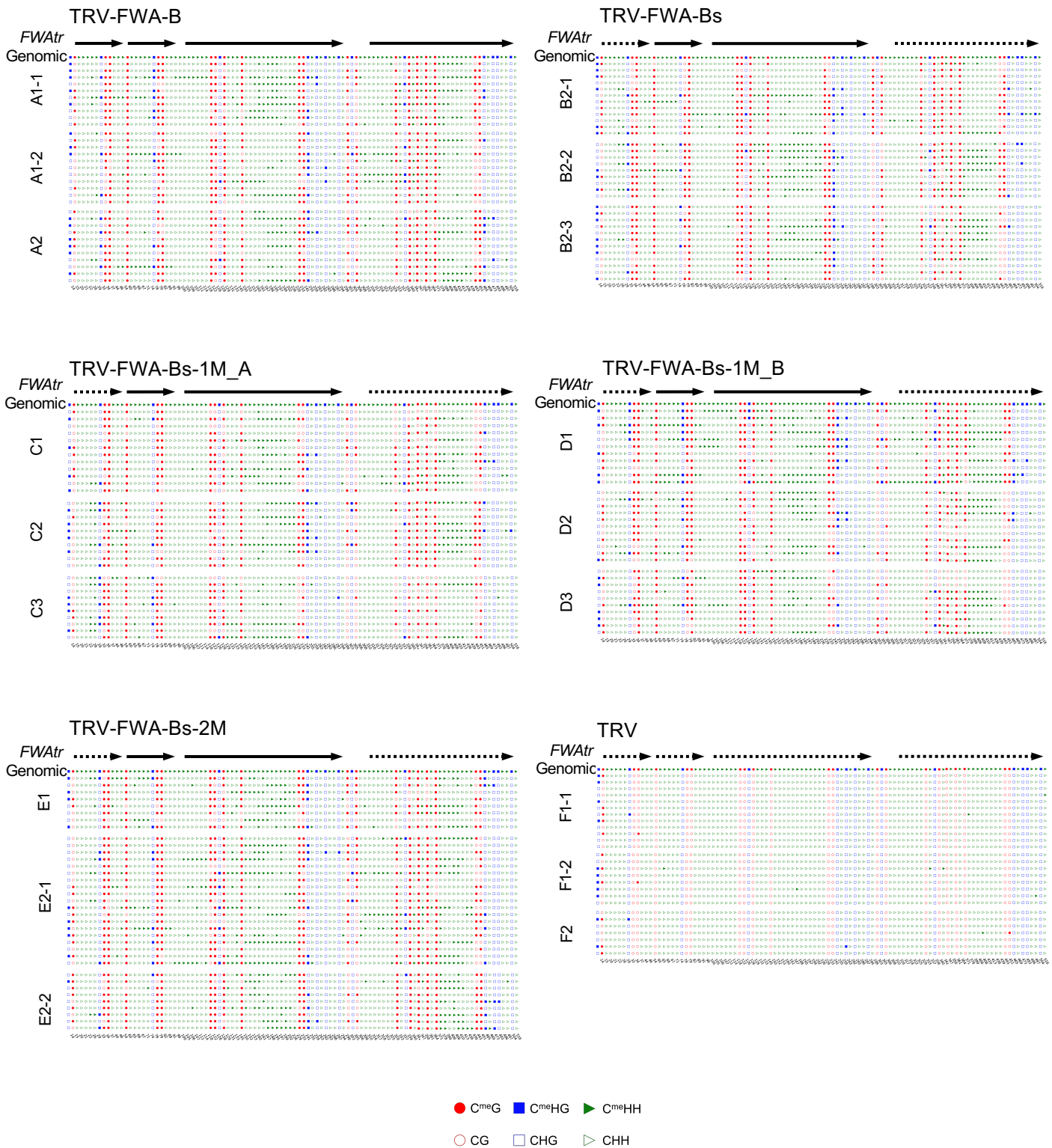
TRV



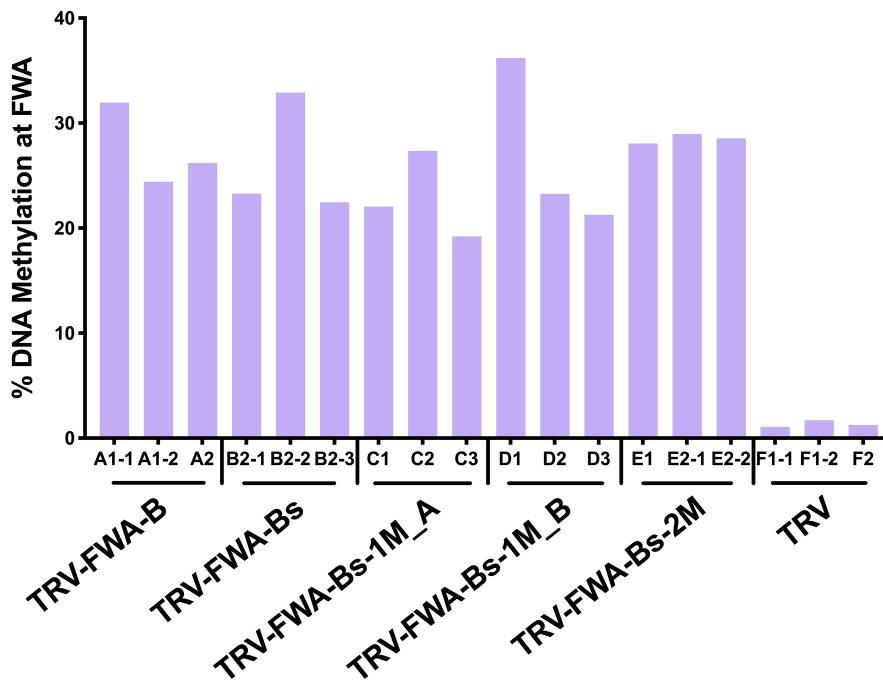
Supplementary Figure S7. Analysis of flowering time (rosette leaf number at the time of bolting) in the progeny of recombinant-TRV-infected *Arabidopsis* plants. Approximately 48 individual plants were analysed from each selected line presented in Figure 7A and B.

Supplementary Figure S8

A



B



C

| | Number of clones | Total C sites | Methylated C sites | % C methylation | 95% confidence interval | |
|-----------------|------------------|---------------|--------------------|-----------------|-------------------------|--------|
| | | | | | C int- | C int+ |
| TRV-FWA-B | 32 | 3264 | 894 | 27.39 | 25.89 | 28.95 |
| TRV-FWA-Bs | 33 | 3366 | 862 | 25.61 | 24.16 | 27.11 |
| TRV-FWA-Bs-1M_A | 32 | 3264 | 745 | 22.82 | 21.42 | 24.30 |
| TRV-FWA-Bs-1M_B | 32 | 3264 | 884 | 27.08 | 25.59 | 28.63 |
| TRV-FWA-Bs-2M | 36 | 3672 | 1052 | 28.65 | 27.21 | 30.13 |
| TRV | 27 | 2754 | 36 | 1.31 | 0.95 | 1.80 |

| | Number of clones | Total CG sites | Methylated CG sites | % CG methylation | 95% confidence interval | |
|-----------------|------------------|----------------|---------------------|------------------|-------------------------|---------|
| | | | | | CG int- | CG int+ |
| TRV-FWA-B | 32 | 672 | 524 | 77.98 | 74.69 | 80.95 |
| TRV-FWA-Bs | 33 | 693 | 514 | 74.17 | 70.78 | 77.29 |
| TRV-FWA-Bs-1M_A | 32 | 672 | 426 | 63.39 | 59.68 | 66.95 |
| TRV-FWA-Bs-1M_B | 32 | 672 | 449 | 66.82 | 63.17 | 70.27 |
| TRV-FWA-Bs-2M | 36 | 756 | 590 | 78.04 | 74.95 | 80.85 |
| TRV | 27 | 567 | 14 | 2.47 | 1.48 | 4.10 |

| | Number of clones | Total CHG sites | Methylated CHG sites | % CHG methylation | 95% confidence interval | |
|-----------------|------------------|-----------------|----------------------|-------------------|-------------------------|----------|
| | | | | | CHG int- | CHG int+ |
| TRV-FWA-B | 32 | 448 | 69 | 15.40 | 12.35 | 19.04 |
| TRV-FWA-Bs | 33 | 462 | 66 | 14.29 | 11.39 | 17.77 |
| TRV-FWA-Bs-1M_A | 32 | 438 | 57 | 13.01 | 10.18 | 16.49 |
| TRV-FWA-Bs-1M_B | 32 | 448 | 67 | 14.96 | 11.95 | 18.56 |
| TRV-FWA-Bs-2M | 36 | 504 | 64 | 12.70 | 10.07 | 15.89 |
| TRV | 27 | 378 | 14 | 3.70 | 2.22 | 6.12 |

| | Number of clones | Total CHH sites | Methylated CHH sites | % CHH methylation | 95% confidence interval | |
|-----------------|------------------|-----------------|----------------------|-------------------|-------------------------|----------|
| | | | | | CHH int- | CHH int+ |
| TRV-FWA-B | 32 | 2144 | 301 | 14.04 | 12.63 | 15.57 |
| TRV-FWA-Bs | 33 | 2211 | 282 | 12.75 | 11.43 | 14.21 |
| TRV-FWA-Bs-1M_A | 32 | 2154 | 262 | 12.16 | 10.85 | 13.61 |
| TRV-FWA-Bs-1M_B | 32 | 2144 | 368 | 17.16 | 15.63 | 18.82 |
| TRV-FWA-Bs-2M | 36 | 2412 | 398 | 16.50 | 15.07 | 18.04 |
| TRV | 27 | 1809 | 8 | 0.44 | 0.22 | 0.87 |

Supplementary Figure S8. Analysis of DNA methylation at the *FWA* promoter in the progeny of recombinant-TRV-infected Col-0 *fwa-d* plants. **(A)** Examination of cytosine methylation by bisulfite sequencing. Raw data is generated from three individual plants of each selected line. Up to 12 independent clones of bisulfite-converted DNA were analysed by Cymate from each sample. Labelling as in Supplementary Figure 6. Black arrows indicate the position of *FWA* tandem repeats. Solid black arrows indicate the virus-targeted region of *FWA* promoter. **(B)** Analysis of the percentage of total methylated cytosine at the *FWA* promoter in each individual plant. **(C)** Raw data from the bisulfite sequencing analysis presented in Figure 7 including the number of sequenced clones and scored cytosine sites. There are 21 CG sites, 14 CHG sites and 67 CHH sites in the amplified region.

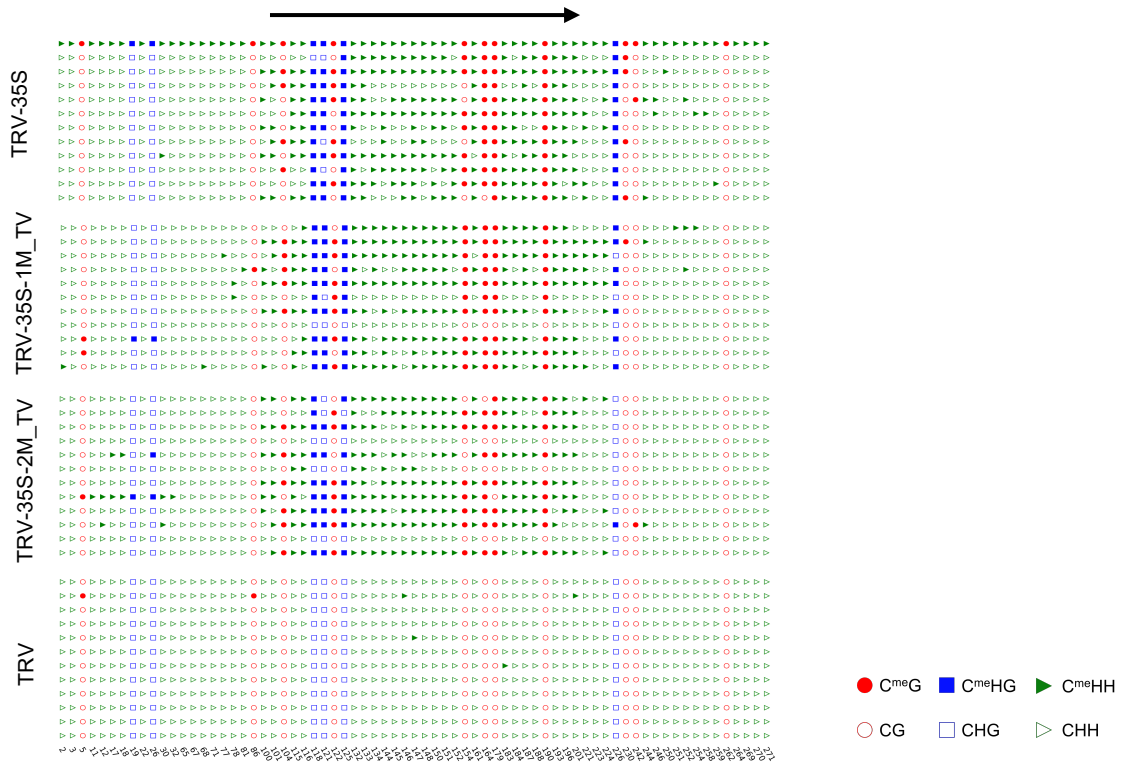
Supplementary Figure S9

| | | |
|------------------------------------|-----|--|
| 2 nd -LR | 1 | TTATCCCATTCAACATTCATACGAGCACCCGCTTTACGGTTTTTGCTTTTC |
| 1 st -LR | 1 | TTATCCCATTCAACATTCATACGAGCGCCGCTCTAGGGTTTTTGCTTTTC |
| 1 st -LR in FWA-Bs-1M_A | 1 | TTATCCCACCTCAACATTCATACGAGCGCTGCTCTAGGGTTTTTGCTTTTCC |
| 1 st -LR in FWA-Bs-1M_B | 1 | TTATCCCATTCAACATTCGTACGAGCGCCGCTCTAGGGCTTTTTGCTTTTC |
| 1 st -LR in FWA-Bs-2M | 1 | TTATCCCACCTCAACATTCGTACGAGCGCTGCTCTAGGGCTTTTTGCTTTCC |
| | | |
| 2 nd -LR | 51 | GACATTGGTCCGAAGTGCTATTTGGTTGTTAAGGTTGCTTTTAGCACACA |
| 1 st -LR | 51 | GCCATTGGTCCAAGTGCTATTTGGTTGTTAAGGTTGCTTTTAGCACACA |
| 1 st -LR in FWA-Bs-1M_A | 51 | GCCATTGGTCCAAGTGCTCTTTGGTTGTTAAGGTTGCCTTTAGCACACA |
| 1 st -LR in FWA-Bs-1M_B | 51 | GCCATTGGCCCAAGTGCTATTTGGTTGCTAAGGTTGCTTTTAGCACATA |
| 1 st -LR in FWA-Bs-2M | 51 | GCCATTGGCCCAAGTGCTCTTTGGTTGCTAAGGTTGCCTTTAGCACATA |
| | | |
| 2 nd -LR | 101 | ACTTTAATATTATTTTTATGTT- TTCTTCTTACGATTTATCGATTGTAG |
| 1 st -LR | 101 | ACTTTAATATTATTTTTATGTTTTCTTCTTACGATTTATCGATTGTGG |
| 1 st -LR in FWA-Bs-1M_A | 101 | ACTTTAATGTTATTTTTATGTTTTCTTTTACGATTTATCGATTGTGTG |
| 1 st -LR in FWA-Bs-1M_B | 101 | ACTTTAATATTATTTTTACGTTTTCTTCTTACGATTTGTCGATTGTGG |
| 1 st -LR in FWA-Bs-2M | 101 | ACTTTAATGTTATTTTTACGTTTTCTTTTACGATTTGTCGATTGTGTG |
| | | |
| 2 nd -LR | 150 | GATACTGACAATCAGATT TTTGTTGTTTTTTT CAGCCAAA AATCAGAT |
| 1 st -LR | 151 | GATACTGACAATCAGATT ATTGTTGTTTTTTCCAGCCAAATATCAGAT |
| 1 st -LR in FWA-Bs-1M_A | 151 | GATACTGACAATCAGATT GTTGTGTTTTTTCCAGCCAGATATCAGAT |
| 1 st -LR in FWA-Bs-1M_B | 151 | GATACTGATAATCAGATT ATTGTTGTTTCTTCCAGCCAAATATCAGAT |
| 1 st -LR in FWA-Bs-2M | 151 | GATACTGATAATCAGATT GTTGTGTTTCTTCCAGCCAGATATCAGAT |

Supplementary Figure S9. Sequence alignment of FWA long repeats and derivatives.

Supplementary Figure S10

A

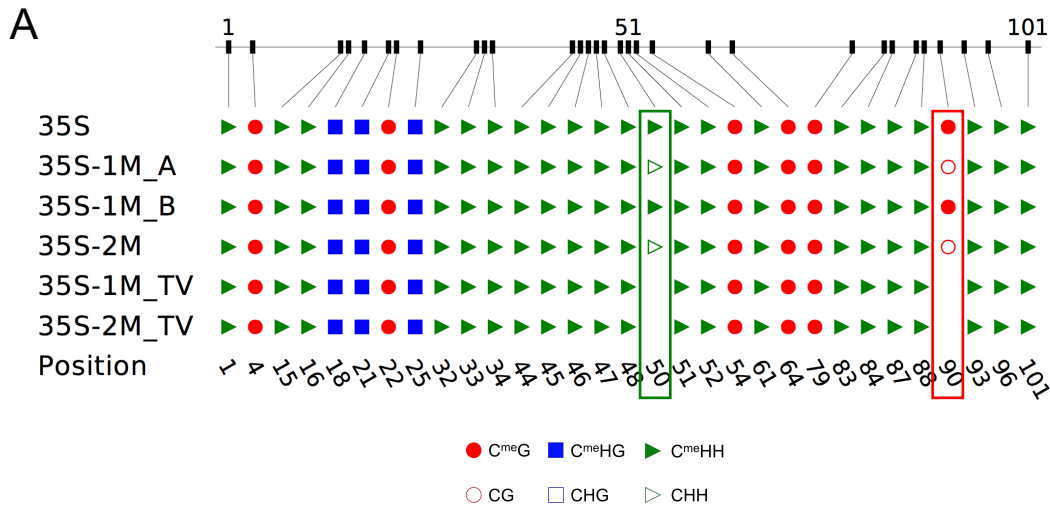


B

| | Number of clones | Total C sites | Methylated C sites | % C methylation | 95% confidence interval | |
|---------------|------------------|-----------------|----------------------|-------------------|-------------------------|----------|
| | | | | | C int- | C int+ |
| TRV-35S | 35 | 1260 | 896 | 71.11 | 68.55 | 73.55 |
| TRV-35S-1M_AT | 34 | 1224 | 826 | 67.48 | 64.81 | 70.05 |
| TRV-35S-2M_AT | 36 | 1296 | 797 | 61.50 | 58.52 | 64.11 |
| TRV | 35 | 1260 | 8 | 0.63 | 0.3221 | 1.248 |
| | | | | | | |
| | Number of clones | Total CG sites | Methylated CG sites | % CG methylation | 95% confidence interval | |
| | | | | | CG int- | CG int+ |
| TRV-35S | 35 | 210 | 178 | 84.76 | 79.28 | 88.99 |
| TRV-35S-1M_AT | 34 | 204 | 162 | 79.41 | 73.34 | 84.39 |
| TRV-35S-2M_AT | 36 | 216 | 126 | 58.33 | 51.67 | 64.71 |
| TRV | 35 | 210 | 0 | 0.00 | 0 | 1.796 |
| | | | | | | |
| | Number of clones | Total CHG sites | Methylated CHG sites | % CHG methylation | 95% confidence interval | |
| | | | | | CHG int- | CHG int+ |
| TRV-35S | 35 | 140 | 123 | 87.86 | 81.41 | 92.28 |
| TRV-35S-1M_AT | 34 | 136 | 106 | 77.94 | 70.26 | 84.09 |
| TRV-35S-2M_AT | 36 | 144 | 80 | 55.56 | 47.4 | 63.42 |
| TRV | 35 | 140 | 0 | 0.00 | 0 | 2.671 |
| | | | | | | |
| | Number of clones | Total CHH sites | Methylated CHH sites | % CHH methylation | 95% confidence interval | |
| | | | | | CHH int- | CHH int+ |
| TRV-35S | 35 | 910 | 595 | 65.38 | 62.23 | 68.41 |
| TRV-35S-1M_AT | 34 | 884 | 558 | 63.12 | 59.89 | 66.24 |
| TRV-35S-2M_AT | 36 | 936 | 591 | 63.14 | 60 | 66.17 |
| TRV | 35 | 910 | 8 | 0.88 | 0.4461 | 1.725 |

Supplementary Figure S10. Analysis of DNA methylation at the CaMV 35S promoter in recombinant-TRV-infected *N. benthamiana* 16c plants. (A) Examination of cytosine methylation by bisulfite sequencing. Raw data is shown from one of the three biological repeats. Up to 12 independent clones of bisulfite-converted DNA were analysed by Cymate from each sample. The position of cytosine residues in the CaMV 35S promoter is indicated at the bottom of the composite figure. CG, CHG and CHH methylation is represented as red circle, blue square and green triangle, respectively. Methylated residues are shown as solid symbols. Black arrow indicates the virus-targeted region of CaMV 35S promoter. (B) Raw data from the bisulfite sequencing analysis presented in Figure 8E and F including the number of sequenced clones and scored cytosine sites. There are 6 CG sites, 4 CHG sites and 26 CHH sites in the targeted region.

Supplementary Figure S11



B

| | Number of clones | Position_50 CHH | | | Position_90 CG | | |
|---------------|------------------|------------------|---------------|------------------------|------------------|---------------|------------------------|
| | | Methylated sites | % methylation | % methylation (global) | Methylated sites | % methylation | % methylation (global) |
| TRV-35S | 37 | 26 | 70 | 62 | 30 | 81 | 79 |
| TRV-35S-1M_A | 25 | 11 | 44 | 50 | 21 | 84 | 83 |
| TRV-35S-1M_B | 30 | 12 | 40 | 52 | 29 | 97 | 81 |
| TRV-35S-2M | 33 | 17 | 52 | 56 | 26 | 79 | 76 |
| TRV-35S-1M_TV | 34 | 24 | 71 | 63 | 30 | 88 | 79 |
| TRV-35S-2M_TV | 36 | 26 | 72 | 63 | 24 | 67 | 58 |

Supplementary Figure S11. Analysis of the effect of direct and indirect pairing of mismatched nucleotides on cytosine methylation at the CaMV 35S promoter in recombinant-TRV-infected *N. benthamiana* 16c plants. (A) Schematic diagram of the position of cytosine residues in the CaMV 35S promoter. CG, CHG and CHH methylation is represented as red circle, blue square and green triangle, respectively. Cytosine residues directly affected by SNS in recombinant TRV/small RNA are shown as empty symbols, and their positions are highlighted in boxes. **(B)** Analysis of bisulfite sequencing data presented in Figure 4 and 8.

Supplementary Table S1. Analysis of sRNA libraries. Related to Figure 3 and Figure S2.

| sRNA library | Total reads | Filtered reads (21-24 nt) | Total reads for | | | % 120 nt/CP |
|------------------|-------------|------------------------------|-----------------|---------|----------------------|-------------|
| | | | TRV-RNA2 | TRV CP | TRV 120 nt insert | |
| TRV-35S 7dpi | 11,647,785 | 5,667,519 | 722,409 | 230,158 | 10,292 | 4.47 |
| TRV-35S 21dpi | 11,506,628 | 6,233,872 | 610,988 | 221,652 | 8,587 | 3.87 |
| TRV-35S-2M 7dpi | 12,521,906 | 6,007,339 | 681,260 | 209,363 | 12,955 | 6.19 |
| TRV-35S-2M 21dpi | 10,670,771 | 3,593,089 | 459,278 | 147,162 | 8,997 | 6.11 |
| TRV-GFP 7dpi | 10,535,377 | 5,922,424 | 746,512 | 237,707 | 20,932 | 8.81 |
| TRV-GFP 21dpi | 10,967,090 | 4,073,630 | 409,917 | 140,555 | 14,244 | 10.13 |
| TRV-GFP-2M 7dpi | 11,557,069 | 6,458,851 | 520,451 | 159,420 | 14,970 | 9.39 |
| TRV-GFP-2M 21dpi | 12,457,417 | 5,635,874 | 500,807 | 166,749 | 14,760 | 8.85 |

Supplementary Table S2. Oligonucleotides used in this study.

| Oligonucleotide name | Sequence | Description |
|----------------------|--|-------------|
| 35S-1M_A forward | CATCGTTGAGGATGCCTCTGCCGACAGTGATCCCAAAGATGGACCCCCATCC ACGAGGAGCATCGTGGAGAAAGAAGACGTTCCAACCATGTCTTCAAAGCAAG TGGATCGATGTGATAT | VIGS |
| 35S-1M_A reverse | ATATCACATCGATCCACTTGGCTTTGAAGACATGGTTGGAACGTCTTCTTTCTC CACGATGCTCCTCGTGGATGGGGTCCATCTTTGGGATCACTGTCCGCAGA GGCATCCTCAACGATG | VIGS |
| 35S-1M_B forward | CATCGTTGAAGATGCCTCTACCGACAGTGGTCCCAAAGACGGACCCCCACC CACGAGGAACATCGTGAAAAAGAAGACATTCCAACCATGTCTTCAAACAA GTGGATTGATGTGATAC | VIGS |
| 35S-1M_B reverse | GTATCACATCAATCCAATTGTTTTGAAGACGTGGTTGGAATGTCTTCTTTTTCC ACGATGTTCTCCTCGTGGTGGGGTCCGTCTTTGGGACCACTGTCCGGTAGAG GCATCTTCAACGATG | VIGS |
| 35S-2M forward | CATCGTTGAGGATGCCTCTACCGACAGTGATCCCAAAGACGGACCCCCATCC ACGAGGAACATCGTGGAGAAAGAAGACATTCCAACCATGTCTTCAAACAAG TGGATCGATGTGATAC | VIGS |
| 35S-2M reverse | GTATCACATCGATCCACTTGTGTTTTGAAGACATGGTTGGAATGTCTTCTTTCTC CACGATGTTCTCCTCGTGGATGGGGTCCGTCTTTGGGATCACTGTCCGGTAGA GGCATCCTCAACGATG | VIGS |
| 35S-4M forward | CATCATTGAGGATGTCTCTACCGATAGTGATCCCGAAGACGGACTCCCATCC ACAAGGAACATCATGGAGAAAGGAGACATTCCGACCATGTCTCAAACAAG CGGATCGATGCGATAC | VIGS |
| 35S-4M reverse | GTATCGCATCGATCCGCTTGTGTTTTGGAGACATGGTCGGAATGTCTCCTTTCTC CATGATGTTCTTGTGGATGGGAGTCCGTCTTCGGGATCACTATCCGGTAGAG ACATCCTCAATGATG | VIGS |
| 35S-1M_TV forward | CATCGTTGATGATGCCTCTGCCGACAGTGCTCCCAAAGATGGACCCCCAGCC ACGAGGAGCATCGTGGATAAAGAAGACGTTCCAACCATGTCTTCAAAGCAAG TGGATAGATGTGATAT | VIGS |
| 35S-1M_TV reverse | ATATCACATCTATCCACTTGTGTTTTGAAGACCTGGTTGGAACGTCTTCTTTATCC ACGATGCTCCTCGTGGCTGGGGTCCATCTTTGGGAGCACTGTCCGCAGAG GCATCATCAACGATG | VIGS |
| 35S-2M_TV forward | CATCGTTGATGATGCCTCTCCCGACAGTGCTCCCAAAGAAGACCCCCAGCC ACGAGGACCATCGTGGATAAAGAAGACCTTCCAACCATGTCTTCAAACAAG TGGATAGATGTGATAA | VIGS |
| 35S-2M_TV reverse | TTATCACATCTATCCACTTGTGTTTTGAAGACCTGGTTGGAAGGTCTTCTTTATC CACGATGGTCTCCTCGTGGCTGGGGTCCCTTCTTTGGGAGCACTGTCCGGAGA GGCATCATCAACGATG | VIGS |
| FWA-Bs-1M_A top | CGAAGCCCACACATCTTTCCGTCGAGAATTTTCATATATACCTTATCCCCTCA ACATTCATACGAGCGCTGCTCTAGGGTTTTTGCTTTCCGCCATTGGT | VIGS |
| FWA-Bs-1M_A middle | AAAGAAAAACATAAAAATAACATTAAGTTGTGTGCTAAAGGCAACCTTAAAC AACCAAACAGCACTTGGACCAATGGCGGAAAGCAAAGCCCTAGAGC | VIGS |
| FWA-Bs-1M_A bottom | CAACTTTAATGTTATTTTTATGTTTTCTTTTTACGATTTATCGATTTGTTGGAT ACTGACAATCAGATTGTTGTTGTTTTTCCAGCCAGATATCAGAT | VIGS |
| FWA-Bs-1M_B top | CGAAGCCCACACATCTTTCTGTCGAGAATCTCATATATATCTTATCCCATTCAA CATTTCGTACGAGCGCCGCTCTAGGGCTTTTGCTTTCCGCCATTGGC | VIGS |
| FWA-Bs-1M_B middle | GAAGAAAAACGTAAAAATAATATTAAGTTATGTGCTAAAAGCAACCTTAGAC AACCAAATAGCACTTGGGCAATGGCGGAAAGCAAAGCCCTAGAGC | VIGS |
| FWA-Bs-1M_B bottom | TAACTTTAATATTATTTTTACGTTTTTCTTCTTACGATTTGTGATTTGTTGGAT ACTGATAATCAGATTATTGTTGTTTTCTTCCAGCCAAATATCAGAT | VIGS |
| FWA-Bs-2M top | CGAAGCCCACACATCTTTCTGTCGAGAATTTTCATATATATCTTATCCCCTCAA CATTTCGTACGAGCGCTGCTCTAGGGCTTTTGCTTTCCGCCATTGGC | VIGS |
| FWA-Bs-2M middle | AAAGAAAAACGTAAAAATAACATTAAGTTATGTGCTAAAGGCAACCTTAGAC AACCAAACAGCACTTGGGCAATGGCGGAAAGCAAAGCCCTAGAGC | VIGS |
| FWA-Bs-2M bottom | TAACTTTAATGTTATTTTTACGTTTTTCTTCTTACGATTTGTGATTTGTTGGAT ACTGATAATCAGATTGTTGTTGTTTTCTTCCAGCCAGATATCAGAT | VIGS |
| FWA-Bs forward | CGAAGCCCACACATCTTTCCG | VIGS |
| FWA-Bs reverse | ATCTGATATTTGGCTGGAAGA | VIGS |
| FWA-Bs-1M_A forward | CGAAGCCCACACATCTTTCCG | VIGS |
| FWA-Bs-1M_A reverse | ATCTGATATCTGGCTGGAAGA | VIGS |
| FWA-Bs-1M_B forward | CGAAGCCCACACATCTTTCTG | VIGS |
| FWA-Bs-1M_B reverse | ATCTGATATTTGGCTGGAAGA | VIGS |
| FWA-Bs-2M forward | CGAAGCCCACACATCTTTCTG | VIGS |
| FWA-Bs-2M reverse | ATCTGATATCTGGCTGGAAGA | VIGS |

| Oligonucleotide name | Sequence | Description |
|-----------------------|--|--------------------------------|
| GFP +364 forward | AAGGACGACGGGAACACTACAAG | VIGS |
| GFP +483 reverse | CTTGTGGCCGAGGATGTTTC | VIGS |
| GFP-2M forward | AAGGACGACAGGAACACTACAGGACACGTGCCGAAGTCAAGCTTGAGGGAGGC ACCCTCGTTAACAGGATCAAGCTTAAGGAAATCGATTTTAAGGAGGACAGAA ACATCCCCGGCCACAAA | VIGS |
| GFP-2M reverse | TTTGTGGCCGGGGATGTTTCTGTCTCCTTAAAATCGATTTTCTTAAGCTTGA TCCTGTTAACGAGGGTGCCTCCCTCAAGCTTGACTTCGGCACGTGTCCTGTA GTTCTGTCTCCTT | VIGS |
| GFP-2M_TV forward | AAGGACGACCGGAACACTACATGACACGTGCAGAAGTCAAGATTGAGGGAGTC ACCCTCGTGAACAGGATCCAGCTTAAGGCAATCGATTTGAAGGAGGACCGAA ACATCCACGGCCACAAC | VIGS |
| GFP-2M_TV reverse | GTTGTGGCCGTGGATGTTTCGGTCTCCTTCAAATCGATTGCCTTAAGCTGG ATCCTGTTCACGAGGGTACTCCCTCAATCTTGACTTCTGCACGTGTCATGTA GTTCCGGTCTCCTT | VIGS |
| 35S_bisulfite forward | TGAGATTTTTTAATAAAGGGTAATTTYGGGAAATT | Bisulfite sequencing PCR |
| 35S_bisulfite reverse | TCCTCTCAAATAAAATAAACTTCTTATATAAAAA | Bisulfite sequencing PCR |
| FWA_bisulfite forward | ATTAAAGAGTTATGGGYGAAGTTTAT | Bisulfite sequencing PCR |
| FWA_bisulfite reverse | CRRRAACCAAATCATTCTCTAAACA | Bisulfite sequencing PCR |
| M13 forward | CGCCAGGGTTTTCCAGTCACGAC | Colony PCR |
| M13 reverse | AGCGGATAACAATTCACACAGGA | Colony PCR |
| Nb-act forward | GAAGATACTCACAGAAAGAGG | qRT-PCR |
| Nb-act reverse | GGAGCTAATGCAGTAATTTCC | qRT-PCR |
| AtEF1a forward | CACCACTGGAGGTTTTGAGG | qRT-PCR |
| AtEF1a reverse | TGGAGTATTTGGGGGTGGT | qRT-PCR |
| TRV-CP-713 forward | TGGGTTACTAGCGGCACTGA | qRT-PCR |
| TRV-CP-856 reverse | GCTCGTCTCTTGAACGCTGA | qRT-PCR |
| mGFP5 +148 forward | ACTGGAAAACCTGTTCC | qRT-PCR |
| mGFP5 +344 reverse | TCAAACCTGACTTCAGCACG | qRT-PCR |
| Insert forward | AATCTCAGACTGTTCCGCTTC | qRT-PCR |
| Insert reverse | GATGGACAACCCGTTCAACCAC | qRT-PCR |

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