a

pV86 promoter

ATTGAATCGGGCTCTCTTCAAATCCCCTATCAATTGGGTGCTTTGGGTGCTCTTAAATACCACCAAGGGGCC
ATCCGCATTAATATTACCGGATGGCCCCCAAAAAATACGTGGCCCAATGAAAATATGCCACGTGGAAAGCTA
AAGATGTTGATGTGATGGATTTGGGCGGGAAACTTCCTGAAGAAGTTTTCATTCCCGCCCCTTTTTTTGACT
TAGTCAAAAAAGTAGCCGACATACTGTTTGAAATAAAGTTAAAAGTAGATCATTGTGGTCCCCACAAGAAA
CTTGCTAAGCAAGTTTCGAATTATTTCTGTTTAAATACGTTATTTTTACATGTATATGTACTTATAAATGATGGT
CTGTCTACCAGACTGGTTATTTTTGCTATTTATCTTCAGTATTCTCCTGCAATCAGGTACGAACTTTTATGGGA
CCTTTCA

b

pC86 promoter

AGGAGCTGTTCTAAGGCGTCTTCTTTGGTTACTGAACATTGAGGGTATGTAAGGAAAAAATTTTTGGCTTT
TTTGTAAAAAGGCATATTGAATCGGGCTCTCTTCAAATCCCCTATCAATTGGGTGCTTTGGGTGCTCTTAAA
TACCACCAAGGGGCCATCCGCATTAATATTACCGGATGGCCCCCAAAAAATACGTGGCCCAATGAAAATAT
GCCACGTGGAAAGCTAAAGATGTTGATGTGATGGATTTGGGCGGGAAACTTCCTGAAGAAGTTTTCATTC
CCGCCCCTTTTTTTGACTTAGTCAAAAAAGTAGCCGACATACTGTTTGAAATAAAGTTAAAAGTAGATCAT
TGTGGTCCCCACAAGAAACTTGCTAAGCAAGTTTCGAATTATTTCTGTTTAAATACGTTATTTTTACATGTA
TATGTACTTATAAATG

**Figure S1.** DNA sequences of the pV86 and pC86 promoters used in this study. The pV86 promoter is colored in black (a) and the pC86 promoter in orange (b).

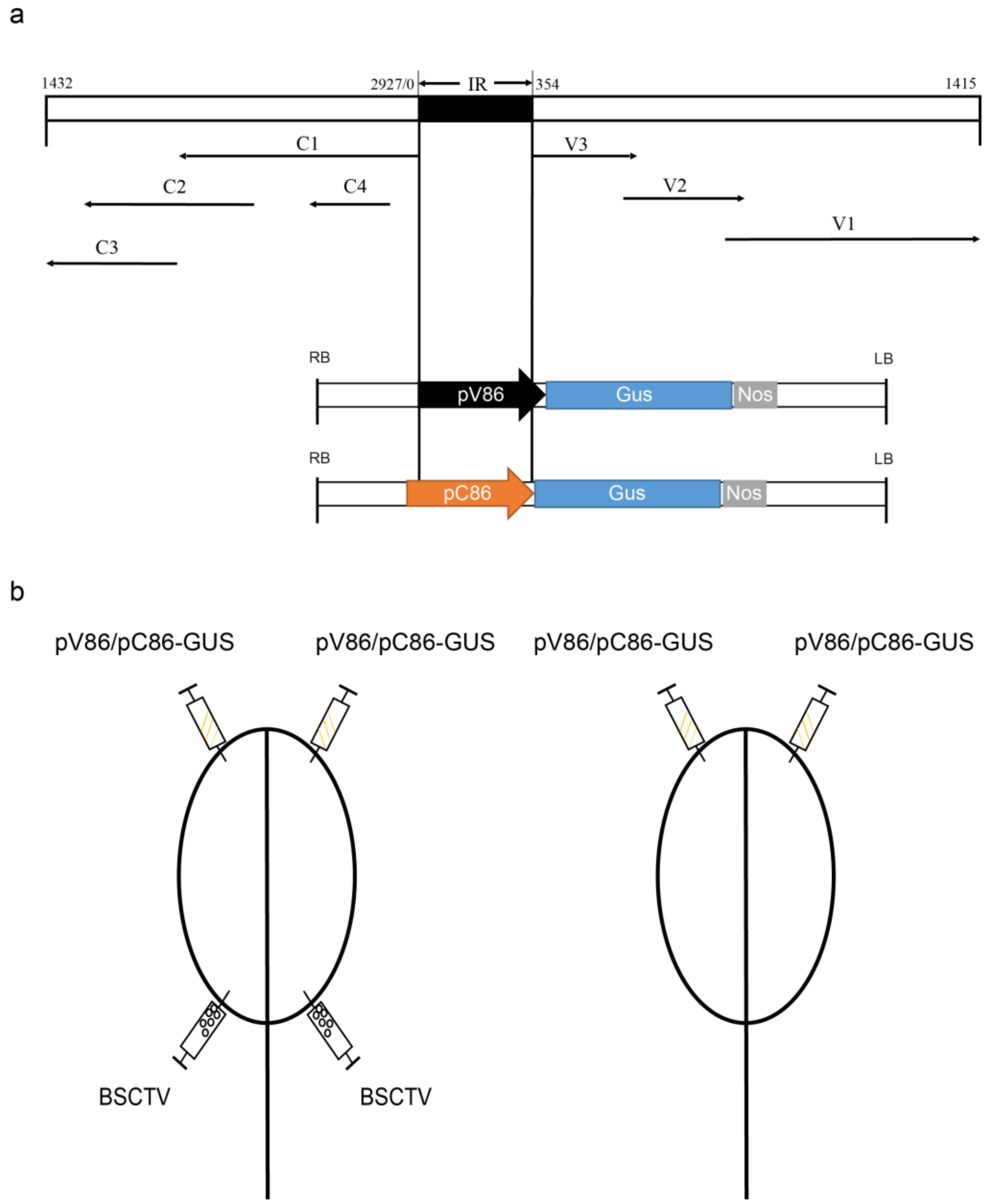


**Figure S2.** Diagram of the transient system used to test the inducible activities of the pV86 and pC86 promoters. (a) GUS reporter constructs based on the pV86 and pC86 promoters. The intergenic region of the BSCTV genome is indicated by a black box, and open boxes are coding regions. Open reading frames are indicated by solid arrows, and numbers indicate nucleotide positions in the BSCTV genomes. The pV86 promoter contains the intergenic region with an additional 86 bp of the V3 coding region while the pC86 promoter contains the intergenic region with an additional 86 bp of the 5' upstream region. (b) Strategy for testing the GUS reporter systems. Thirty-day-old *N. benthamiana* plants with between 6 and 8 true leaves were used.

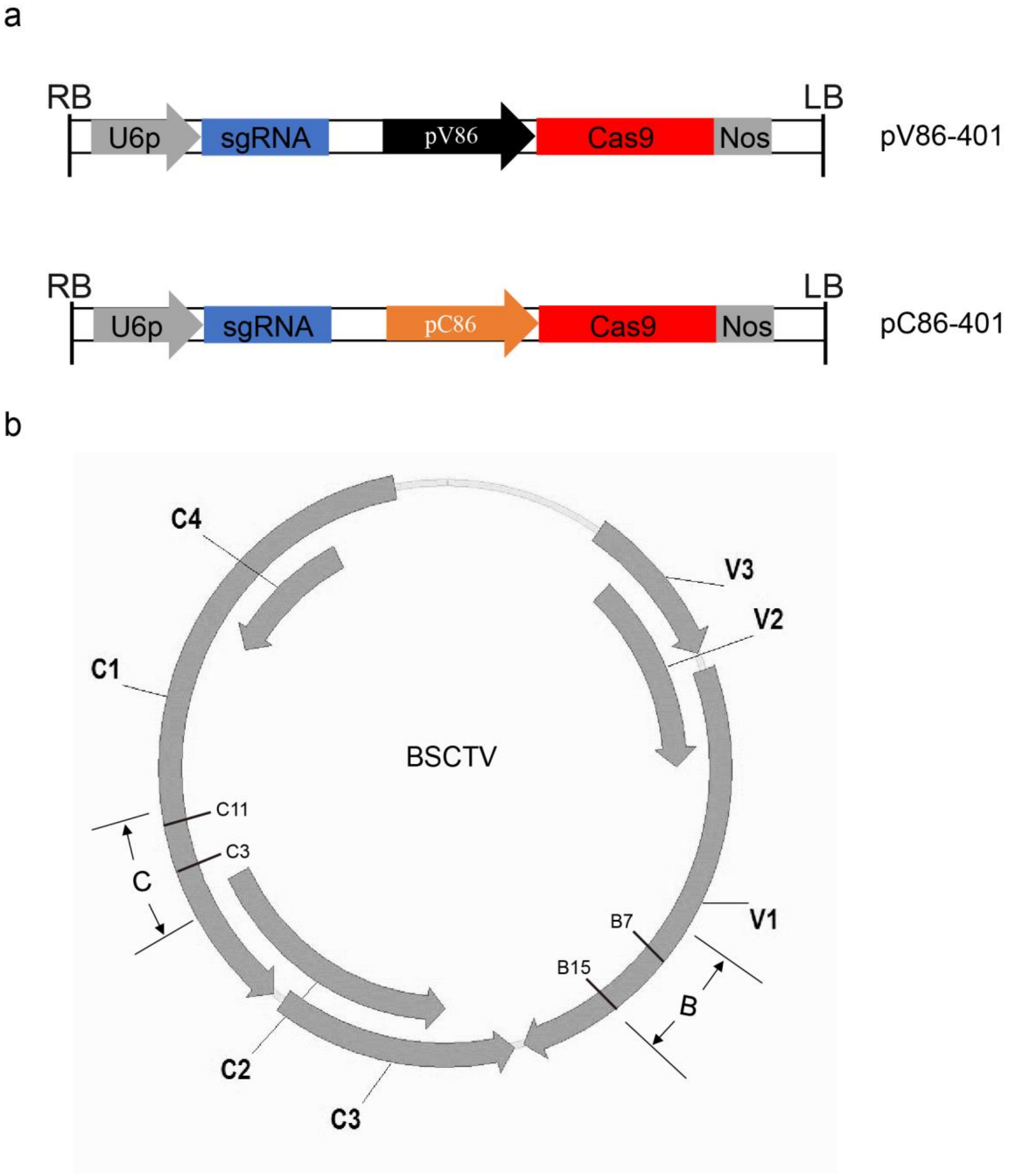
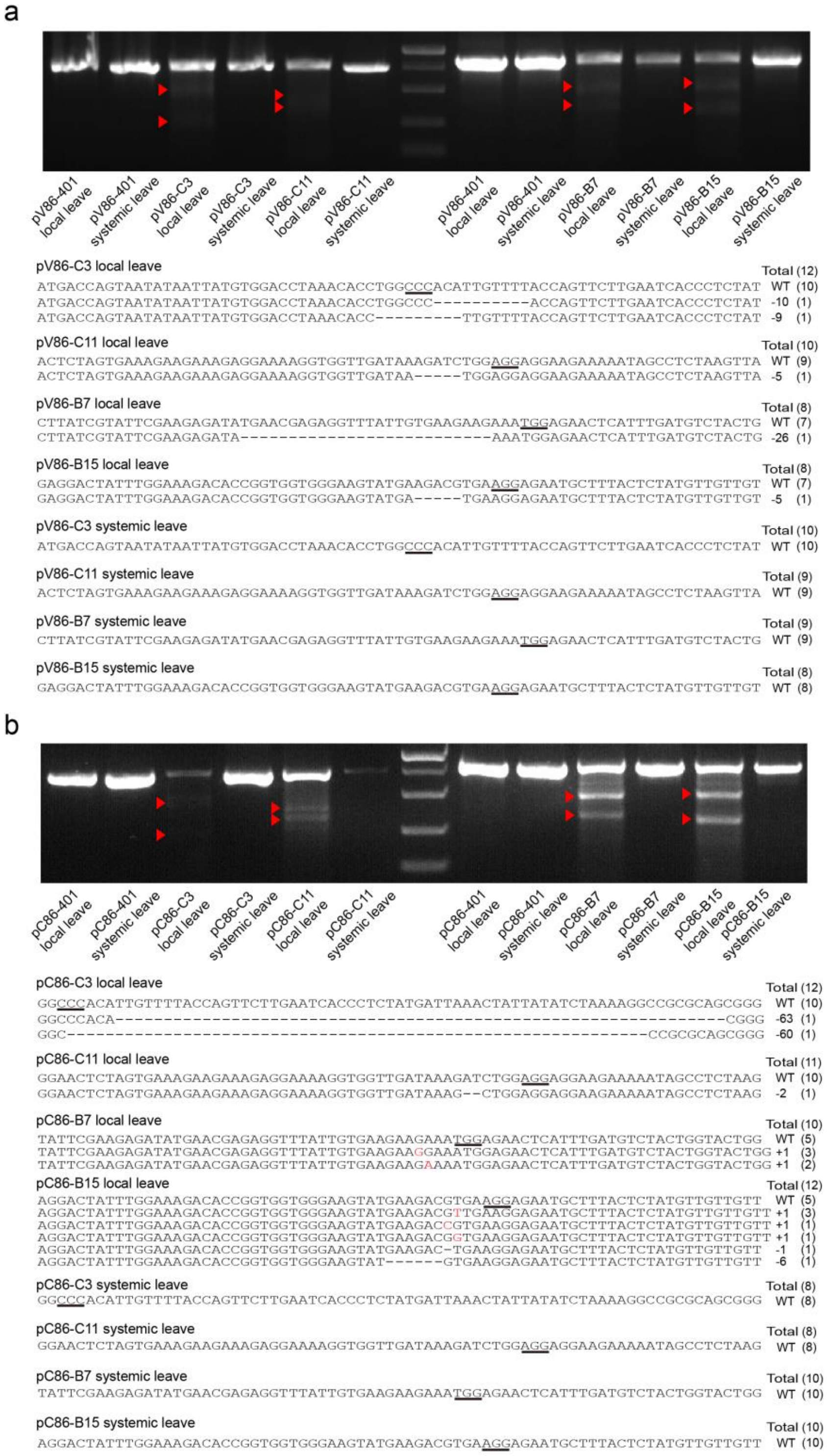


**Figure S3.** Constructs for the two BSCTV-inducible systems. The sgRNA is driven by the AtU6 promoter and Cas9 by the pV86 (black) or pC86 promoter (orange) (a). sgRNAs B7 and B15 are located in the V1 open reading frame and C3 and C11 in the C1 open reading frame (b).



pV86-C3 local leave

```
                                                                                Total (12)
ATGACCAGTAATATAATTATGTGGACCTAAACACCTGGCCCACATTGTTTTACCAGTTCTTGAATCACCCTCTAT  WT  (10)
ATGACCAGTAATATAATTATGTGGACCTAAACACCTGGCCC----------ACCAGTTCTTGAATCACCCTCTAT  -10 (1)
ATGACCAGTAATATAATTATGTGGACCTAAACACC---------TTGTTTTACCAGTTCTTGAATCACCCTCTAT  -9  (1)
```

pV86-C11 local leave

```
                                                                                Total (10)
ACTCTAGTGAAAGAAGAAAGAGGAAAAGGTGGTTGATAAAGATCTGGAGGAGGAAGAAAAATAGCCTCTAAGTTA  WT  (9)
ACTCTAGTGAAAGAAGAAAGAGGAAAAGGTGGTTGATAA-----TGGAGGAGGAAGAAAAATAGCCTCTAAGTTA  -5  (1)
```

pV86-B7 local leave

```
                                                                                Total (8)
CTTATCGTATTCGAAGAGATATGAACGAGAGGTTTATTGTGAAGAAGAAATGGAGAACTCATTTGATGTCTACTG  WT  (7)
CTTATCGTATTCGAAGAGATA--------------------------AAATGGAGAACTCATTTGATGTCTACTG  -26 (1)
```

pV86-B15 local leave

```
                                                                                Total (8)
GAGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACGTGAAGGAGAATGCTTTACTCTATGTTGTTGT  WT  (7)
GAGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGA-----TGAAGGAGAATGCTTTACTCTATGTTGTTGT  -5  (1)
```

pV86-C3 systemic leave

```
                                                                                Total (10)
ATGACCAGTAATATAATTATGTGGACCTAAACACCTGGCCCACATTGTTTTACCAGTTCTTGAATCACCCTCTAT  WT  (10)
```

pV86-C11 systemic leave

```
                                                                                Total (9)
ACTCTAGTGAAAGAAGAAAGAGGAAAAGGTGGTTGATAAAGATCTGGAGGAGGAAGAAAAATAGCCTCTAAGTTA  WT  (9)
```

pV86-B7 systemic leave

```
                                                                                Total (9)
CTTATCGTATTCGAAGAGATATGAACGAGAGGTTTATTGTGAAGAAGAAATGGAGAACTCATTTGATGTCTACTG  WT  (9)
```

pV86-B15 systemic leave

```
                                                                                Total (8)
GAGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACGTGAAGGAGAATGCTTTACTCTATGTTGTTGT  WT  (8)
```

pC86-C3 local leave

```
                                                                                Total (12)
GGCCCACATTGTTTTACCAGTTCTTGAATCACCCTCTATGATTAAACTATTATATCTAAAAGGCCGCGCAGCGGG  WT  (10)
GGCCCACA---------------------------------------------------------------CGGG  -63 (1)
GGC------------------------------------------------------------CCGCGCAGCGGG  -60 (1)
```

pC86-C11 local leave

```
                                                                                Total (11)
GGAACTCTAGTGAAAGAAGAAAGAGGAAAAGGTGGTTGATAAAGATCTGGAGGAGGAAGAAAAATAGCCTCTAAG  WT  (10)
GGAACTCTAGTGAAAGAAGAAAGAGGAAAAGGTGGTTGATAAAG--CTGGAGGAGGAAGAAAAATAGCCTCTAAG  -2  (1)
```

pC86-B7 local leave

```
                                                                                Total (10)
TATTCGAAGAGATATGAACGAGAGGTTTATTGTGAAGAAGAAATGGAGAACTCATTTGATGTCTACTGGTACTGG  WT  (5)
TATTCGAAGAGATATGAACGAGAGGTTTATTGTGAAGAAGGAAATGGAGAACTCATTTGATGTCTACTGGTACTGG +1 (3)
TATTCGAAGAGATATGAACGAGAGGTTTATTGTGAAGAAGAAAATGGAGAACTCATTTGATGTCTACTGGTACTGG +1 (2)
```

pC86-B15 local leave

```
                                                                                Total (12)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACGTGAAGGAGAATGCTTTACTCTATGTTGTTGTT  WT  (5)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACGTTGAAGGAGAATGCTTTACTCTATGTTGTTGTT +1 (3)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACCGTGAAGGAGAATGCTTTACTCTATGTTGTTGTT +1 (1)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACGGTGAAGGAGAATGCTTTACTCTATGTTGTTGTT +1 (1)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGAC-TGAAGGAGAATGCTTTACTCTATGTTGTTGTT  -1  (1)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTAT------GTGAAGGAGAATGCTTTACTCTATGTTGTTGTT  -6  (1)
```

pC86-C3 systemic leave

```
                                                                                Total (8)
GGCCCACATTGTTTTACCAGTTCTTGAATCACCCTCTATGATTAAACTATTATATCTAAAAGGCCGCGCAGCGGG  WT  (8)
```

pC86-C11 systemic leave

```
                                                                                Total (8)
GGAACTCTAGTGAAAGAAGAAAGAGGAAAAGGTGGTTGATAAAGATCTGGAGGAGGAAGAAAAATAGCCTCTAAG  WT  (8)
```

pC86-B7 systemic leave

```
                                                                                Total (10)
TATTCGAAGAGATATGAACGAGAGGTTTATTGTGAAGAAGAAATGGAGAACTCATTTGATGTCTACTGGTACTGG  WT  (10)
```

pC86-B15 systemic leave

```
                                                                                Total (10)
AGGACTATTTGGAAAGACACCGGTGGTGGGAAGTATGAAGACGTGAAGGAGAATGCTTTACTCTATGTTGTTGTT  WT  (10)
```

**Figure S4.** Mutations induced in the BSCTV genome by the inducible pV86-401 (a) and pC86-401 (b) constructs. Red arrowheads indicate fragments generated by T7E1. −/+ indicates deletions/insertions of nucleotides. The number to the right of each row indicate numbers of independent plasmid clones found after cloning and sequencing of PCR amplicons. For systemic leaves, a second round PCR was performed to amplify the rare virus.

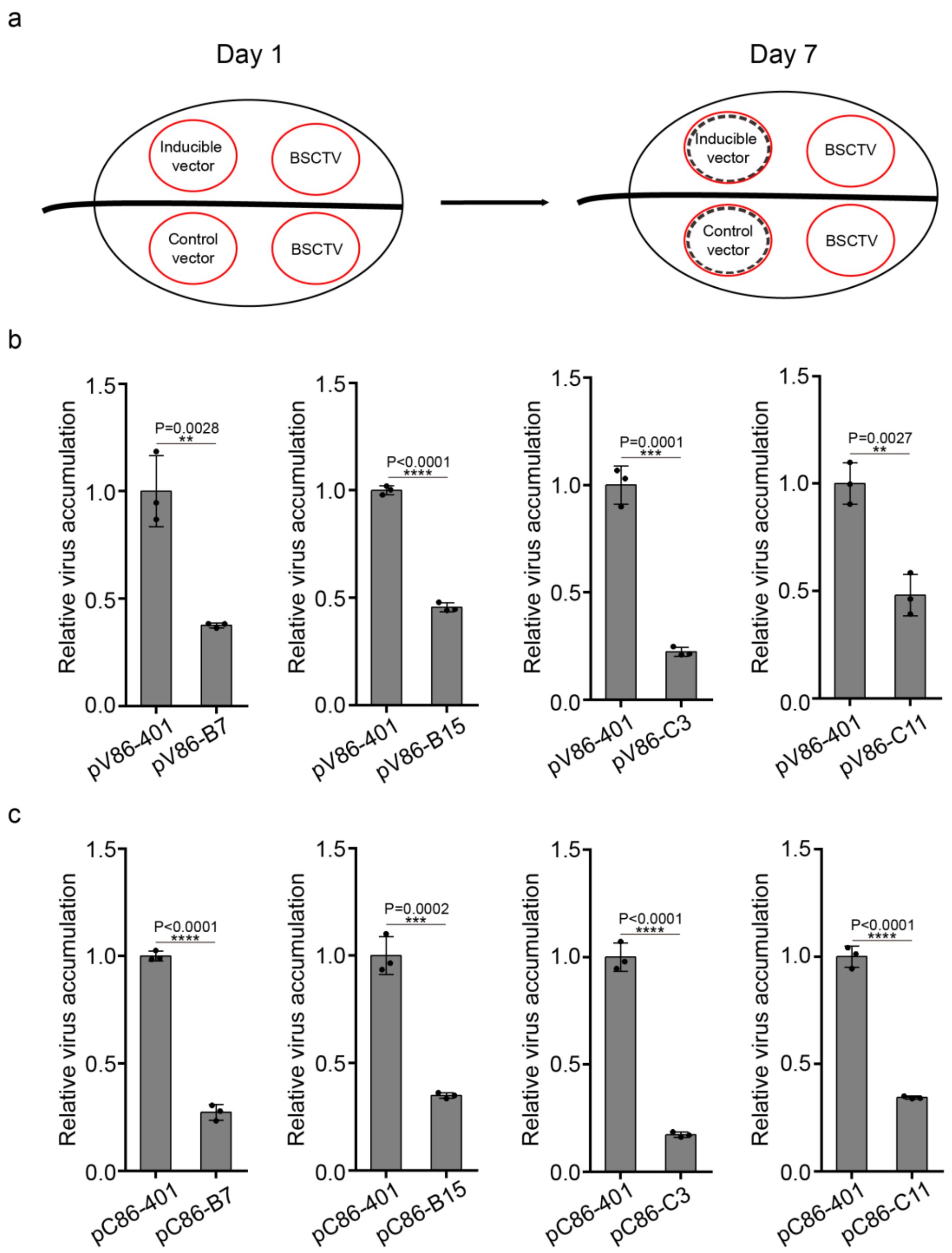


**Figure S5.** qPCR analysis of the sensitivity and efficiency of the inducible pV86-401 (b) and pC86-401 (c) combinations for inhibiting virus replication (n = 3) in *N. benthamiana* plants. (a) Strategy for testing whether the inducible CRISPR/Cas9 system reduced the amount of replicating virus. The DNA in the bottom regions (marked by dashed lines) was extracted and viral accumulation was measured by qPCR. All values represent means ± S.D. $^{**}P < 0.01$, $^{***}P < 0.001$, $^{****}P < 0.0001$; two-tailed Student's t-test.

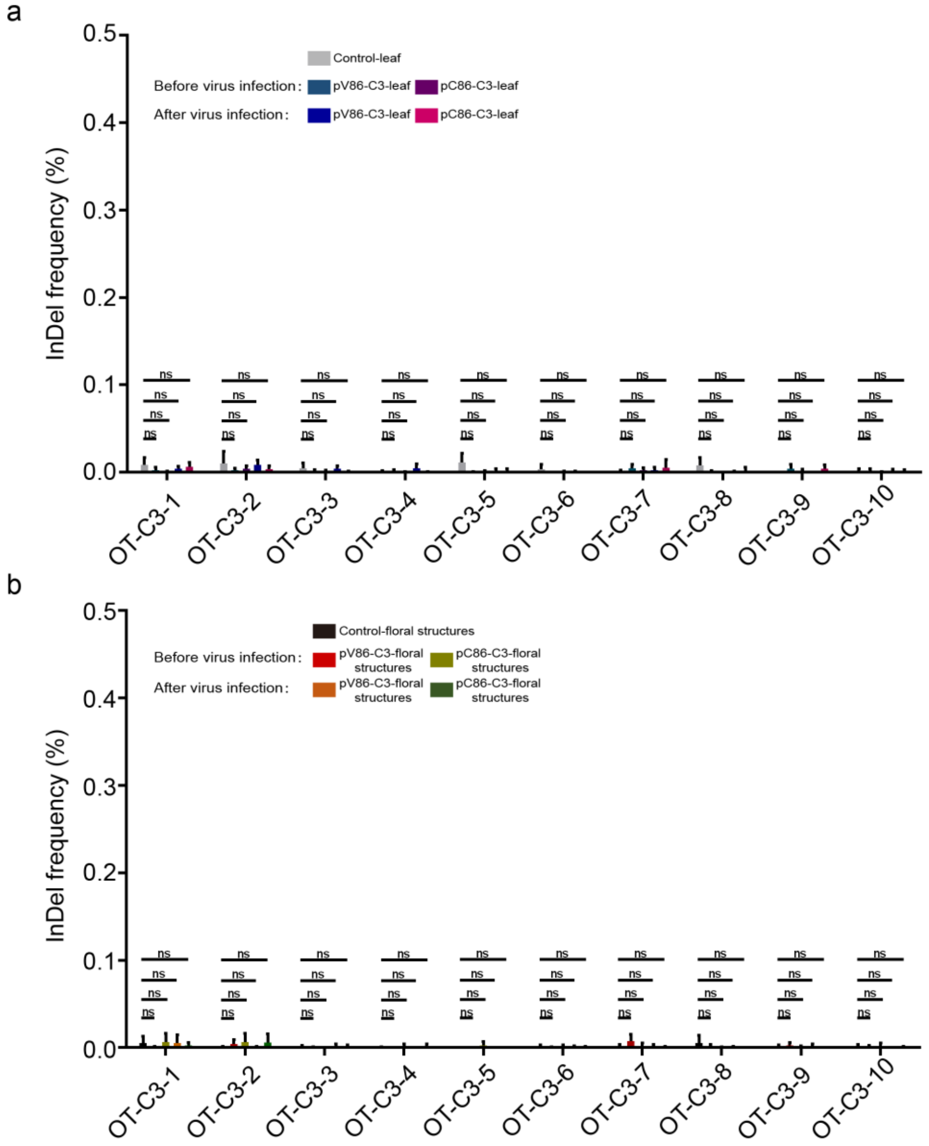


**Figure S6.** Indel frequencies at ten candidate sites in the leaves (a) and floral structures (b) of transgenic pV86-C3 and pC86-C3 *Arabidopsis* plants were similar to the frequencies in non-transgenic control *Arabidopsis* plants (n = 3). All values represent means ± S.D. ns, not significant by two-tailed Student's t-test.

**Table S1.** Potential off-target sites for C3 sgRNA in *Arabidopsis*.

| **sgRNA ID** | **Mismatches** | **Off-target sequence**[a] | **Chromosome** | **Position** | **Direction** |
|---|---|---|---|---|---|
| C3 | 0 | CCCACATTGTTTTACCAGTTCTT | | | |
| OT-C3-1 | 3 | AAGtAaTGGTAAgACAATGTCGG | chr4 | 15495282 | + |
| OT-C3-2 | 3 | AAGAAaTGGTgAAACAgTGTAAG | chr1 | 2064439 | - |
| OT-C3-3 | 3 | AAGAACatGTAAAACAATGaAAG | chr3 | 7075914 | + |
| OT-C3-4 | 4 | AAGgAaaGaTAAAACAATGTCAG | chr5 | 20031389 | + |
| OT-C3-5 | 4 | AAGtAtTcGTcAAACAATGTTGG | chr3 | 17560887 | + |
| OT-C3-6 | 4 | tAGAAaTGGatAAACAATGTAAG | chr3 | 22066699 | + |
| OT-C3-7 | 4 | AAGAgCTcGTAtAAaAATGTAGG | chr4 | 12148731 | + |
| OT-C3-8 | 4 | AAaAACTaGTgAAACcATGTGGG | chr3 | 4078517 | - |
| OT-C3-9 | 4 | AgGAACaGGaAAAACAATGgCGG | chr3 | 694395 | + |
| OT-C3-10 | 4 | AAGAAagGGaAAAACAATGgCGG | chr3 | 4712965 | - |

[a] The mismatch bases in the ten potential off-target sites are shown as lower case letters. The PAM motif is underlined.

**Table S2.** Indel frequencies detected by deep sequencing of transgenic C3 and control *Arabidopsis* plants.

| Material for deep sequencing | Off-target site | Independent experiment repeat | InDel reads | Total reads | InDel frequency (%) | Primers and bar codes[a] |
|---|---|---|---|---|---|---|
| C3 | OT-C3-1 | R1 | 4 | 16105 | 0.0248 | F: GACTAGTATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | R2 | 13 | 71363 | 0.0182 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | R3 | 11 | 67640 | 0.0163 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | OT-C3-2 | R1 | 138 | 199216 | 0.0693 | F: TTAGGCATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | R2 | 91 | 67036 | 0.1357 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | R3 | 78 | 93577 | 0.0834 | F: AAACATCGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | OT-C3-3 | R1 | 157 | 785808 | 0.02 | F: ACAGTGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | R2 | 19 | 53449 | 0.0355 | F: ACTATGCACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | R3 | 10 | 54059 | 0.0185 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | OT-C3-4 | R1 | 32 | 507149 | 0.0063 | F: CAGATCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | R2 | 4 | 67557 | 0.0059 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | R3 | 9 | 83131 | 0.0108 | F: AGAGTCAAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | OT-C3-5 | R1 | 47 | 317358 | 0.0148 | F: GATCAGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | R2 | 8 | 39011 | 0.0205 | F: ACCACTGTTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | R3 | 9 | 49055 | 0.0183 | F: AGATCGCATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | OT-C3-6 | R1 | 136 | 468604 | 0.029 | F: GGCTACGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | R2 | 11 | 52655 | 0.0209 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | R3 | 5 | 44668 | 0.0112 | F: ACATTGGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |

| | | | | | | |
|---|---|---|---|---|---|---|
| | OT-C3-7 | R1 | 861 | 454453 | 0.1895 | F: AGTCAAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | R2 | 136 | 81295 | 0.1673 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | R3 | 125 | 62347 | 0.2005 | F: CAGATCTGGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | OT-C3-8 | R1 | 4089 | 343576 | 1.1901 | F: ATGTCAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | R2 | 426 | 114944 | 0.3706 | F: CCGTGAGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | R3 | 102 | 15547 | 0.6561 | F: GAGCTGAAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | OT-C3-9 | R1 | 3 | 22686 | 0.0132 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | R2 | 14 | 59188 | 0.0237 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | R3 | 5 | 34090 | 0.0147 | F: GATAGACATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | OT-C3-10 | R1 | 3 | 21935 | 0.0137 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | R2 | 9 | 38525 | 0.0234 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | R3 | 7 | 51520 | 0.0136 | F: ACAAGCTATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| WT | OT-C3-1 | R1 | 0 | 49387 | 0 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | R2 | 1 | 189825 | 0.0005 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | R3 | 10 | 252449 | 0.004 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | OT-C3-2 | R1 | 12 | 81718 | 0.0147 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | R2 | 5 | 247317 | 0.002 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | R3 | 5 | 236444 | 0.0021 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | OT-C3-3 | R1 | 0 | 39082 | 0 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | R2 | 0 | 55577 | 0 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | R3 | 0 | 104611 | 0 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | OT-C3-4 | R1 | 3 | 55938 | 0.0054 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |

| | | | | | | |
|---|---|---|---|---|---|---|
| | | R2 | 0 | 81201 | 0 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | R3 | 0 | 194981 | 0 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | OT-C3-5 | R1 | 0 | 36204 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | R2 | 0 | 112484 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | R3 | 0 | 113921 | 0 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | OT-C3-6 | R1 | 0 | 18565 | 0 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | R2 | 9 | 64017 | 0.0141 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | R3 | 0 | 1654 | 0 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | OT-C3-7 | R1 | 0 | 137351 | 0 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | R2 | 18 | 218972 | 0.0082 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | R3 | 24 | 302896 | 0.0079 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | OT-C3-8 | R1 | 0 | 155851 | 0 | F: GAGCTGAAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | R2 | 17 | 204649 | 0.0083 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | R3 | 19 | 143249 | 0.0133 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | OT-C3-9 | R1 | 2 | 24927 | 0.008 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | R2 | 3 | 93319 | 0.0032 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | R3 | 1 | 65265 | 0.0015 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | OT-C3-10 | R1 | 1 | 26248 | 0.0038 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | R2 | 0 | 38128 | 0 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | R3 | 0 | 88703 | 0 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |

[a] The barcodes used for deep sequencing are marked in red.

**Table S3.** Relative levels of virus accumulation for each of the four target sites in the inducible systems.

| Material used in qPCR analysis | ID | Relative virus accumulation in each experimental repeat | | |
|---|---|---|---|---|
| | | 1 | 2 | 3 |
| Local leaves | pV86-401 | 1.1942 | 0.9556 | 0.8503 |
| | pV86-C3 | 0.2635 | 0.0276 | 0.0722 |
| | pV86-C11 | 0.4098 | 0.2551 | 0.5181 |
| | pV86-B7 | 0.0399 | 0.2417 | 0.0533 |
| | pV86-B15 | 0.0439 | 0.1488 | 0.2343 |
| Systemic leaves | pV86-401 | 0.9932 | 0.9125 | 1.0943 |
| | pV86-C3 | 0.0013 | 0.0045 | 0.0017 |
| | pV86-C11 | 0.1476 | 0.2707 | 0.2003 |
| | pV86-B7 | 0.0001 | 0.0002 | 0.0002 |
| | pV86-B15 | 9E-05 | 0.0001 | 0.0007 |
| Local leaves | pC86-401 | 1.1052 | 0.8941 | 1.0007 |
| | pC86-C3 | 0.0149 | 0.0307 | 0.0348 |
| | pC86-C11 | 0.0049 | 0.0012 | 0.0071 |
| | pC86-B7 | 0.1846 | 0.0191 | 0.104 |
| | pC86-B15 | 0.0452 | 0.0997 | 0.1587 |
| Systemic leaves | pC86-401 | 0.9089 | 1.0631 | 1.0281 |
| | pC86-C3 | 0.0356 | 0.0015 | 0.0003 |
| | pC86-C11 | 0.0078 | 0.0182 | 0.0023 |
| | pC86-B7 | 0.0147 | 0.0073 | 0.0005 |
| | pC86-B15 | 0.0048 | 0.0157 | 0.0178 |

**Table S4.** The relative viral load detected from the experiment of inhibiting replicating virus.

| Group | ID | Relative virus accumulation from each experiment repeat | | |
|---|---|---|---|---|
| | | **1** | **2** | **3** |
| 1 | pV86-401 | 0.8996 | 1.0691 | 1.0312 |
| | pV86-C3 | 0.2098 | 0.2142 | 0.2483 |
| 2 | pV86-401 | 0.9043 | 0.9977 | 1.098 |
| | pV86-C11 | 0.4632 | 0.3923 | 0.5839 |
| 3 | pV86-401 | 1.185 | 0.946 | 0.8687 |
| | pV86-B7 | 0.382 | 0.3627 | 0.3836 |
| 4 | pV86-401 | 1.0192 | 1.0026 | 0.9781 |
| | pV86-B15 | 0.4407 | 0.446 | 0.479 |
| 5 | pC86-401 | 0.947 | 0.9793 | 1.0733 |
| | pC86-C3 | 0.162 | 0.1711 | 0.1856 |
| 6 | pC86-401 | 0.9448 | 1.0132 | 1.042 |
| | pC86-C11 | 0.3511 | 0.3389 | 0.342 |
| 7 | pC86-401 | 0.9851 | 0.9896 | 1.0253 |
| | pC86-B7 | 0.3048 | 0.2786 | 0.2329 |
| 8 | pC86-401 | 0.9654 | 0.934 | 1.1006 |
| | pC86-B15 | 0.3352 | 0.3484 | 0.3606 |

**Table S5.** InDel frequencies detected by deep sequencing with their primers in transgenic pV86-C3, pC86-C3 and control *Arabidopsis* plants.

| | Material for deep sequencing | Off-target site | Independent experiment repeat | InDel reads | Total reads | InDel frequency | Primers and barcodes[a] |
|---|---|---|---|---|---|---|---|
| Before virus infection | pV86-C3 leaf | OT-C3-1 | R1 | 5 | 821295 | 6.09E-06 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 0 | 195521 | 0 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 5 | 86218 | 5.8E-05 | F: ACGCTCGATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 43 | 871531 | 4.93E-05 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 1 | 215289 | 4.64E-06 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 1 | 100114 | 9.99E-06 | F: ACGTATCAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 1 | 214992 | 4.65E-06 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 3 | 101658 | 2.95E-05 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 1 | 165140 | 6.06E-06 | F: ACTATGCACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 0 | 627550 | 0 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 4 | 143803 | 2.78E-05 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 0 | 132898 | 0 | F: AGAGTCAAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 1 | 252144 | 3.97E-06 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 90957 | 0 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 0 | 33649 | 0 | F: AGATCGCATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 0 | 175567 | 0 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 0 | 34403 | 0 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 0 | 117065 | 0 | F: AGCAGGAAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3- | R1 | 40 | 936141 | 4.27E-05 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG |

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|---|---|---|---|---|---|---|---|
| | | 7 | | | | | R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 20 | 219013 | 9.13E-05 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 0 | 145886 | 0 | F: AGTCACTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 247472 | 0 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 2 | 112807 | 1.77E-05 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 0 | 33343 | 0 | F: ATCCTGTAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 2 | 134527 | 1.49E-05 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 0 | 30261 | 0 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 4 | 40807 | 9.8E-05 | F: ATTGAGGATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 3 | 75484 | 3.97E-05 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 1 | 118095 | 8.47E-06 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 0 | 107007 | 0 | F: CAACCACATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | pV86-C3 floral structures | OT-C3-1 | R1 | 1 | 88779 | 1.13E-05 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 1 | 153539 | 6.51E-06 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 0 | 111371 | 0 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 45 | 1107572 | 4.06E-05 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 1 | 11077 | 9.03E-05 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 0 | 16914 | 0 | F: AAACATCGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 1 | 119537 | 8.37E-06 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 0 | 13802 | 0 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 10 | 135515 | 7.38E-05 | F: ATGCCTAACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 1 | 374103 | 2.67E-06 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |

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|---|---|---|---|---|---|---|---|
| | | | R2 | 0 | 154429 | 0 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 0 | 160936 | 0 | F: AGTGGTCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 0 | 233549 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 82100 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 0 | 21259 | 0 | F: ACCACTGTTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 2 | 321599 | 6.22E-06 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 0 | 41659 | 0 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 3 | 87336 | 3.44E-05 | F: ACATTGGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 38 | 655325 | 5.8E-05 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 2 | 12494 | 0.00016 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 0 | 129345 | 0 | F: CAGATCTGGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 428306 | 0 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 2 | 48158 | 4.15E-05 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 0 | 53203 | 0 | F: CATCAAGTATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 1 | 130109 | 7.69E-06 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 1 | 16324 | 6.13E-05 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 1 | 281781 | 3.55E-06 | F: CGCTGATCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 1 | 32969 | 3.03E-05 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 0 | 90191 | 0 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 5 | 269732 | 1.85E-05 | F: ACAAGCTATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | pC86-C3 leaf | OT-C3-1 | R1 | 0 | 12571 | 0 | F: GACTAGTATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 1 | 104907 | 9.53E-06 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |

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|---|---|---|---|---|---|---|---|
|  |  |  | R3 | 0 | 26463 | 0 | F: ACGCTCGATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
|  |  | OT-C3-2 | R1 | 20 | 1470627 | 1.36E-05 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
|  |  |  | R2 | 10 | 136743 | 7.31E-05 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
|  |  |  | R3 | 1 | 26565 | 3.76E-05 | F: ACGTATCAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
|  |  | OT-C3-3 | R1 | 1 | 132928 | 7.52E-06 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
|  |  |  | R2 | 2 | 75945 | 2.63E-05 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
|  |  |  | R3 | 0 | 71067 | 0 | F: ACTATGCACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
|  |  | OT-C3-4 | R1 | 2 | 438760 | 4.56E-06 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
|  |  |  | R2 | 0 | 155860 | 0 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
|  |  |  | R3 | 0 | 65204 | 0 | F: AGAGTCAAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
|  |  | OT-C3-5 | R1 | 0 | 165144 | 0 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
|  |  |  | R2 | 2 | 121345 | 1.65E-05 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
|  |  |  | R3 | 0 | 82031 | 0 | F: AGATCGCATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
|  |  | OT-C3-6 | R1 | 2 | 869497 | 2.3E-06 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
|  |  |  | R2 | 1 | 97175 | 1.03E-05 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
|  |  |  | R3 | 1 | 101866 | 9.82E-06 | F: AGCAGGAAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
|  |  | OT-C3-7 | R1 | 56 | 1021602 | 5.48E-05 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
|  |  |  | R2 | 0 | 86113 | 0 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
|  |  |  | R3 | 1 | 52823 | 1.89E-05 | F: AGTCACTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
|  |  | OT-C3-8 | R1 | 0 | 173719 | 0 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
|  |  |  | R2 | 0 | 5858 | 0 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
|  |  |  | R3 | 0 | 19138 | 0 | F: ATCCTGTAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |

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|---|---|---|---|---|---|---|---|
| | | OT-C3-9 | R1 | 2 | 54886 | 3.64E-05 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 0 | 20697 | 0 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 3 | 228724 | 1.31E-05 | F: AACTCACCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 0 | 34189 | 0 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 0 | 35319 | 0 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 2 | 296920 | 6.74E-06 | F: CAACCACATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | pC86-C3 floral structures | OT-C3-1 | R1 | 3 | 16966 | 0.00017 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 2 | 125692 | 1.59E-05 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 0 | 80020 | 0 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 259474 | 1.16E-05 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 22 | 122748 | 0.00018 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 0 | 76531 | 0 | F: AAACATCGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 0 | 93771 | 0 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 0 | 39079 | 0 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 1 | 103622 | 9.65E-06 | F: ATGCCTAACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 1 | 361689 | 2.76E-06 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 5 | 112351 | 4.45E-05 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 1 | 102784 | 9.73E-06 | F: AGTGGTCA GAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 0 | 55107 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 2 | 25991 | 7.69E-05 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 0 | 11946 | 0 | F: ACCACTGTTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 0 | 62128 | 0 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |

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|---|---|---|---|---|---|---|---|
| | | | R2 | 1 | 27875 | 3.59E-05 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 2 | 111170 | 1.8E-05 | F: ACATTGGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 31 | 562000 | 5.52E-05 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 1 | 176916 | 5.65E-06 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 1 | 76410 | 1.31E-05 | F: CAGATCTGGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 1 | 342936 | 2.92E-06 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 1 | 92118 | 1.09E-05 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 0 | 14696 | 0 | F: CATCAAGTATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 2 | 103172 | 1.94E-05 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 0 | 50235 | 0 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 1 | 65866 | 1.52E-05 | F: CGCTGATCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 1 | 16993 | 5.88E-05 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 0 | 52218 | 0 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 0 | 52840 | 0 | F: ACAAGCTATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| After virus infection | pV86-C3 leaf | OT-C3-1 | R1 | 1 | 264290 | 3.78E-06 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 4 | 67680 | 5.91E-05 | F: CGACTGGATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 3 | 66400 | 4.52E-05 | F: TATCAGCATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 91649 | 3.27E-05 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 3 | 40189 | 7.46E-05 | F: CGCATACAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 4 | 28637 | 0.00014 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 0 | 100687 | 0 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 3 | 71760 | 4.18E-05 | F: CTCAATGACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |

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|---|---|---|---|---|---|---|---|
| | | | R3 | 6 | 85626 | 7.01E-05 | F: TCTTCACACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 1 | 128030 | 7.81E-06 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 7 | 71201 | 9.83E-05 | F: CTGAGCCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 2 | 59546 | 3.36E-05 | F: TGAAGAGAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 0 | 6697 | 0 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 67905 | 0 | F: CTGGCATATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 2 | 46306 | 4.32E-05 | F: TGGAACAATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 1 | 103394 | 9.67E-06 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 0 | 63669 | 0 | F: GAATCTGAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 0 | 69604 | 0 | F: TGGCTTCAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 8 | 135723 | 5.89E-05 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 0 | 136431 | 0 | F: CAAGACTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 0 | 44781 | 0 | F: TGGTGGTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 32144 | 0 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 1 | 94892 | 1.05E-05 | F: GAGCTGAAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 0 | 85475 | 0 | F: TTCACGCAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 0 | 22422 | 0 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 0 | 51825 | 0 | F: GATAGACATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 0 | 54777 | 0 | F: AACTCACCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 0 | 17407 | 0 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 2 | 63133 | 3.17E-05 | F: GCCACATATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 1 | 74383 | 1.34E-05 | F: AAGAGATCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |

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|---|---|---|---|---|---|---|---|
| | pV86-C3 floral structures | OT-C3-1 | R1 | 1 | 238214 | 4.2E-06 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 10 | 61964 | 0.00016 | F: GACTAGTATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 4 | 65989 | 6.06E-05 | F: GCGAGTAATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 246290 | 1.22E-05 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 0 | 36317 | 0 | F: CAATGGAAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 2 | 74311 | 2.69E-05 | F: GCTAACGAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 0 | 65255 | 0 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 4 | 90566 | 4.42E-05 | F: CACTTCGACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 5 | 117086 | 4.27E-05 | F: GCTCGGTACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 0 | 130602 | 0 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 0 | 69962 | 0 | F: CAGCGTTAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 1 | 119863 | 8.34E-06 | F: GGAGAACAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 0 | 108358 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 56972 | 0 | F: CATACCAATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 0 | 62863 | 0 | F: GGTGCGAATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 0 | 115349 | 0 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 2 | 103209 | 1.94E-05 | F: CCAGTTCAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 1 | 130208 | 7.68E-06 | F: GTACGCAAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 8 | 198508 | 4.03E-05 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 0 | 62510 | 0 | F: CCGAAGTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 4 | 25455 | 0.00016 | F: GTCGTAGAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 2 | 123402 | 1.62E-05 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |

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|---|---|---|---|---|---|---|---|
| | | | R2 | 0 | 6768 | 0 | F: CCGTGAGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 0 | 26279 | 0 | F: GTCTGTCAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 2 | 48476 | 4.13E-05 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 4 | 254278 | 1.57E-05 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 3 | 81444 | 3.68E-05 | F: GTGTTCTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 0 | 14703 | 0 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 1 | 271767 | 3.68E-06 | F: CGAACTTATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 9 | 73245 | 0.00012 | F: TAGGATGATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | pC86-C3 leaf | OT-C3-1 | R1 | 1 | 166305 | 6.01E-06 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 10 | 105609 | 9.47E-05 | F: CGACTGGATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 4 | 46162 | 8.67E-05 | F: TATCAGCATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 91946 | 3.26E-05 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 8 | 106344 | 7.52E-05 | F: CGCATACAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 0 | 13321 | 0 | F: GCTAACGAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 1 | 106603 | 9.38E-06 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 1 | 162675 | 6.15E-06 | F: CTCAATGACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 0 | 53057 | 0 | F: TCTTCACACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 1 | 147228 | 6.79E-06 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 0 | 94656 | 0 | F: CTGAGCCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 0 | 57359 | 0 | F: TGAAGAGAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 0 | 37232 | 0 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 53098 | 0 | F: CTGGCATATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |

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|---|---|---|---|---|---|---|---|
| | | | R3 | 2 | 46306 | 4.32E-05 | F: TGGAACAATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 0 | 104079 | 0 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 0 | 384679 | 0 | F: ACATTGGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 0 | 69604 | 0 | F: TGGCTTCAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 35 | 224709 | 0.00016 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 0 | 95776 | 0 | F: CAAGACTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 0 | 6201 | 0 | F: TGGTGGTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 68204 | 0 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 0 | 30943 | 0 | F: GAGCTGAAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 1 | 17235 | 5.8E-05 | F: TTCACGCAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 0 | 22642 | 0 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 5 | 60134 | 8.31E-05 | F: GATAGACATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 2 | 61165 | 3.27E-05 | F: AACTCACCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 0 | 11997 | 0 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 0 | 46252 | 0 | F: GCCACATATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 1 | 31127 | 3.21E-05 | F: AAGAGATCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | pC86-C3 floral structures | OT-C3-1 | R1 | 1 | 193662 | 5.16E-06 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 6 | 97054 | 6.18E-05 | F: GACTAGTATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 0 | 41752 | 0 | F: GCGAGTAATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 246290 | 1.22E-05 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 18 | 106051 | 0.00017 | F: CAATGGAAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 20 | 74467 | 0.00027 | F: GCTAACGAATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |

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|---|---|---|---|---|---|---|---|
| | | OT-C3-3 | R1 | 1 | 50958 | 1.96E-05 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 4 | 127493 | 3.14E-05 | F: CACTTCGACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 13 | 78476 | 0.00017 | F: GCTCGGTACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 5 | 107216 | 4.66E-05 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 0 | 101778 | 0 | F: CAGCGTTAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 0 | 80273 | 0 | F: GGAGAACAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 0 | 86842 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 13552 | 0 | F: CATACCAATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 0 | 83766 | 0 | F: GGTGCGAATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 0 | 79098 | 0 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 1 | 68376 | 1.46E-05 | F: CCAGTTCAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 0 | 39787 | 0 | F: GTACGCAAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 1 | 76908 | 1.3E-05 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 2 | 476678 | 4.2E-06 | F: AGTCACTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 0 | 106829 | 0 | F: GTCGTAGAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 117542 | 0 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 0 | 48835 | 0 | F: CCGTGAGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 0 | 38560 | 0 | F: GTCTGTCAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 0 | 41127 | 0 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 1 | 250275 | 4E-06 | F: CCTCCTGATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 1 | 57396 | 1.74E-05 | F: GTGTTCTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 0 | 10139 | 0 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |

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|---|---|---|---|---|---|---|---|
| | | | R2 | 3 | 171847 | 1.75E-05 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 0 | 23296 | 0 | F: TAGGATGATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | WT leaf | OT-C3-1 | R1 | 1 | 79026 | 1.27E-05 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 18 | 101590 | 0.00018 | F: GTTTCGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 6 | 101912 | 5.89E-05 | F: ACGCTCGATTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 91946 | 3.26E-05 | F: AAACATCGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 0 | 46115 | 0 | F: CGTACGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 6 | 23916 | 0.00026 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 2 | 142901 | 1.4E-05 | F: ATGCCTAACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 1 | 98368 | 1.02E-05 | F: GAGTGGCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 14 | 121284 | 0.00011 | F: ACTATGCACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 0 | 68768 | 0 | F: AGTGGTCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 2 | 134935 | 1.48E-05 | F: GGTAGCGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 1 | 130779 | 7.65E-06 | F: AGAGTCAAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | OT-C3-5 | R1 | 21 | 89767 | 0.00023 | F: ACCACTGTTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 1 | 26249 | 3.81E-05 | F: ACTGATTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 2 | 35376 | 5.65E-05 | F: AGATCGCATTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 0 | 68056 | 0 | F: ATGAGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 5 | 52695 | 9.49E-05 | F: AGCAGGAAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 0 | 138452 | 0 | F: AGCAGGAAGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 0 | 25167 | 0 | F: CAGATCTGGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 0 | 196870 | 0 | F: ATTCCTGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |

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|---|---|---|---|---|---|---|---|
| | | | R3 | 3 | 133414 | 2.25E-05 | F: AGTCACTAGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 62682 | 0 | F: CATCAAGTATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 6 | 35186 | 0.00017 | F: CAAAAGATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 2 | 31151 | 6.42E-05 | F: ATCCTGTAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 0 | 87799 | 0 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 0 | 28564 | 0 | F: CAACTATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 0 | 86646 | 0 | F: ATTGAGGATAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 0 | 13408 | 0 | F: ACAAGCTATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 1 | 109669 | 9.12E-06 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 4 | 96370 | 4.15E-05 | F: CAACCACATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | WT floral structures | OT-C3-1 | R1 | 4 | 422097 | 9.48E-06 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R2 | 24 | 167078 | 0.00014 | F: ATCACGTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | | R3 | 1 | 93120 | 1.07E-05 | F: AACGTGATTTGCTTTATGTGTGTCTTGGTTTT<br>R: CAATCTGAACCGTCCAAACTTC |
| | | OT-C3-2 | R1 | 3 | 246290 | 1.22E-05 | F: AAACATCGATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R2 | 0 | 9062 | 0 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | | R3 | 1 | 11834 | 8.45E-05 | F: CGATGTATAGATACTCATACCGCTTC<br>R: GTTAGTGAATGTGAATTTGCTTTT |
| | | OT-C3-3 | R1 | 2 | 151248 | 1.32E-05 | F: ATGCCTAACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R2 | 2 | 89347 | 2.24E-05 | F: TTAGGCCTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | | R3 | 8 | 175551 | 4.56E-05 | F: ATGCCTAACTCCATATACCCTCATTAGC<br>R: GTTGTTCTGAATAAGGCTGACCAAG |
| | | OT-C3-4 | R1 | 1 | 128113 | 7.81E-06 | F: AGTGGTCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R2 | 0 | 211158 | 0 | F: TGACCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |
| | | | R3 | 0 | 153254 | 0 | F: AGTGGTCAGAGTAGATGGCAGGAGAAAA<br>R: CTCATAAGTCCAATGCCCAG |

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|---|---|---|---|---|---|---|---|
| | | OT-C3-5 | R1 | 0 | 72929 | 0 | F: ACCACTGTTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R2 | 0 | 24856 | 0 | F: ACAGTGTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | | R3 | 3 | 36167 | 8.29E-05 | F: ACCACTGTTTCTTCTGATAGTGTCACTG<br>R: CACTTAAAAAAACGTAATGTTAC |
| | | OT-C3-6 | R1 | 1 | 72557 | 1.38E-05 | F: ACATTGGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R2 | 2 | 60363 | 3.31E-05 | F: TAATCGGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | | R3 | 1 | 50995 | 1.96E-05 | F: ACATTGGCGCTTCTCTTATCTTTTCTAC<br>R: CTTTTTTTTTTCTGTAGACC |
| | | OT-C3-7 | R1 | 5 | 133637 | 3.74E-05 | F: CAGATCTGGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R2 | 3 | 254421 | 1.18E-05 | F: CAGATCGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | | R3 | 3 | 116387 | 2.58E-05 | F: CAGATCTGGTGTAGTGGAAGAGAGCTGG<br>R: ATGTATGTGTAAATTGTGAG |
| | | OT-C3-8 | R1 | 0 | 224555 | 0 | F: CATCAAGTATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R2 | 12 | 79087 | 0.00015 | F: ACTTGAATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | | R3 | 8 | 58364 | 0.00014 | F: CATCAAGTATATAATACTGTATTGGGCTTGG<br>R: GTTACCTTTAGCTTCTCTAG |
| | | OT-C3-9 | R1 | 0 | 31493 | 0 | F: CGCTGATCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R2 | 1 | 29276 | 3.42E-05 | F: GATCAGTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | | R3 | 0 | 66318 | 0 | F: CGCTGATCTAGCTACCTCAACCGCCAAC<br>R: TCCATGGTCTATTTGGGTGTC |
| | | OT-C3-10 | R1 | 1 | 27058 | 3.7E-05 | F: ACAAGCTATGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R2 | 0 | 41680 | 0 | F: TACAGCTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |
| | | | R3 | 5 | 189043 | 2.64E-05 | F: CACCGGTGAAACCACTTCAAACTCTTCC<br>R: TTGTTTGACGACGACGTTTC |

[a] The barcodes used for deep sequencing are marked in red.

**Table S6.** Other primers used in this study.

| Primer name | Primer sequence | Application |
|---|---|---|
| pV86-GUS-R1-F | GTACCCGGGGATCCTATTGAATCGGGCTCTCTTC | Construction of pV86-GUS reporter vector |
| pV86-GUS-R1-R | ACGTAACATTGAAAGGTCCCATAAAAGTTC | |
| pV86-GUS-R2-F | GACCTTTCAATGTTACGTCCTGTAGAAACC | |
| pV86-GUS-R2-R | GCCTGCAGGTCGACTCGATCTAGTAACATAGATGACACC | |
| pC86-GUS-R1-F | GTACCCGGGGATCCTAGGAGCTGTTCTAAGGCG | Construction of pC86-GUS reporter vector |
| pC86-GUS-R1-R | ACGTAACATCATTTATAAGTACATATACATGTAAAAATAAC | |
| pC86-GUS-R2-F | CTTATAAATGATGTTACGTCCTGTAGAAACC | |
| pC86-GUS-R2-R | CGACGGCCAGTGCCACGATCTAGTAACATAGATGACACC | |
| pV86-401-F | GCATGCATTGAATCGGGCTCTCTTC | Construction of pV86-401 vector |
| pV86-401-R | TCTAGATGAA AGGTCCCATA AAAG | |
| pC86-401-F | GCATGCAGGAGCTGTTCTAAGGCG | Construction of pC86-401 vector |
| pC86-401-R | TCTAGACATTTATAAGTACATATACATG | |
| B7-F | ATTGGGTTTATTGTGAAGAAGAAA | B7 sgRNA oligos |
| B7-R | AAACTTTCTTCTTCACAATAAACC | |
| B15-F | ATTGTGGGAAGTATGAAGACGTGA | B15 sgRNA oligos |
| B15-R | AAACTCACGTCTTCATACTTCCCA | |
| C3-F | ATTGAAGAACTGGTAAAACAATGT | C3 sgRNA oligos |
| C3-R | AAACACATTGTTTTACCAGTTCTT | |
| C11-F | ATTGGGTGGTTGATAAAGATCTGG | C11 sgRNA oligos |
| C11-R | AAACCCAGATCTTTATCAACCACC | |
| BSCTV-B-F | ATATGTTGGGTGCTGGTGGTATAG | Mutation analysis in B7/B15 target site |
| BSCTV-B-R | CTGGATCGCACAGGACATTAACTGG | |
| BSCTV-C-F | GCCTTCGCCTGGATTGCATAATAT | Mutation analysis in C3/C11 target site |
| BSCTV-C-R | GTCCAGATCCGTAATGCCCGTTA | |
| qPCR-BSCTV-F | CAGGGATTTTCGCACAGAGGAAC | qPCR and ddPCR for BSCTV accumulation |
| qPCR-BSCTV-R | GATTCGGTACCAAGTCCACGGG | |
| qPCR-PPR-F | CTCGGCCAAGAAGATCAACCATAC | qPCR for *PPR* DNA and RNA level |
| qPCR-PPR-R | GGTGCTTTATGTGGTTGTAGTTATGC | |
| qPCR-Cas9-F | CACGTTGCGCAGATTCTCGACTC | qPCR for *Cas9* RNA level |
| qPCR-Cas9-R | CTCCCGAACCTTGTAGAACTGGA | |