# Supplementary Materials

**Supplementary Text 1:**

Double-repeat units (underlines from 5’ to 3’ are restriction sites of Spe I, Nhe I, and Hind III, sequences with grey background encode RVDs):

dTpT

ACTAGTAATGGCGGCGGCAAGCAGGCGCTGGAGACGGTGCAGCGCCTGTTGCCGGGTCTGTGCCAGGACCATGGCTTGTCGCCCGCCCAAGTAGTCGCGATTGCAAACAACGGGGGGGGAAAACAAGCTCTCGAAATGGTTCAAAGATTGCTGCCCATGCTTTGTCAAGCGCACGGGCTGACCCCGGACCAGGTGGTGGCCATCGCTAGCGGGAAGCTT

dTpC

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dTpA

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dTpG

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dCpT

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dCpA

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dApT

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Flank_seq1 (underlines are *Nde* I, *Nhe* I, *Hind* III, and *Xho* I restriction sites):
CCATATGGTGGATCTACGCACGCTCGGCTACAGCCAGCAGCAACAGGAGAAGATCAAAC
CGAAGGTTCGTTCGACAGTGGCGCAGCACCACGAGGCACTGGTCGGCCATGGGTTTACAC
ACGCGCACATCGTTGCGCTCAGCCAACACCCGGCAGCGTTAGGGACCGTCGCTGTCAAGT
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AGGTCCACCGTTACAGTTGGACACAGGCCAACTTCTCAAGATTGCAAAACGTGGCGGCGT
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GACCCCGGACCAGGTGGTGGCCATCGCTAGCAATGGCGGCGGCAAGCAGGCGCTGGAGA
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CGTCGCCTTGGCCTGCATCGGCGGACGCTCTGCGCTGAATGCAGTGAAAGACGGATTGCC
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GCTCGAGG

TALE1 (underlines are *Nde* I, *Hind* III, and *Xho* I restriction sites):
CCATATGGTGGATCTACGCACGCTCGGCTACAGCCAGCAGCAACAGGAGAAGATCAAAC
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CGGTGCAGCGCCTGTTGCCGGGTCTGTGCCAGGACCATGGCTTGTCGCCCGCCCAAGTAG
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AGCAATGGCGGCGGCAAGCAGGCGCTGGAGAGCATTTTTGCACAGTTATCTCGCCCTGAT
CCGGCGTTGGCCGCGTTGACCAACGACCGCCTCGTCGCCTTGGCCTGCATCGGCGGACGC
TCTGCGCTGAATGCAGTGAAAGACGGATTGCCGAATGCGCTGACATTGATCAGAAGAGCC
AATAGCCGTATTCCCGAACGCACAAAGCTTGGGCTCGAGG

TALE2(underlines are Nde I, Hind III, and Xho I restriction sites):
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CGGTGCAGCGCCTGTTGCCGGGTCTGTGCCAGGACCATGGCTTGTCGCCCGCCCAAGTAG
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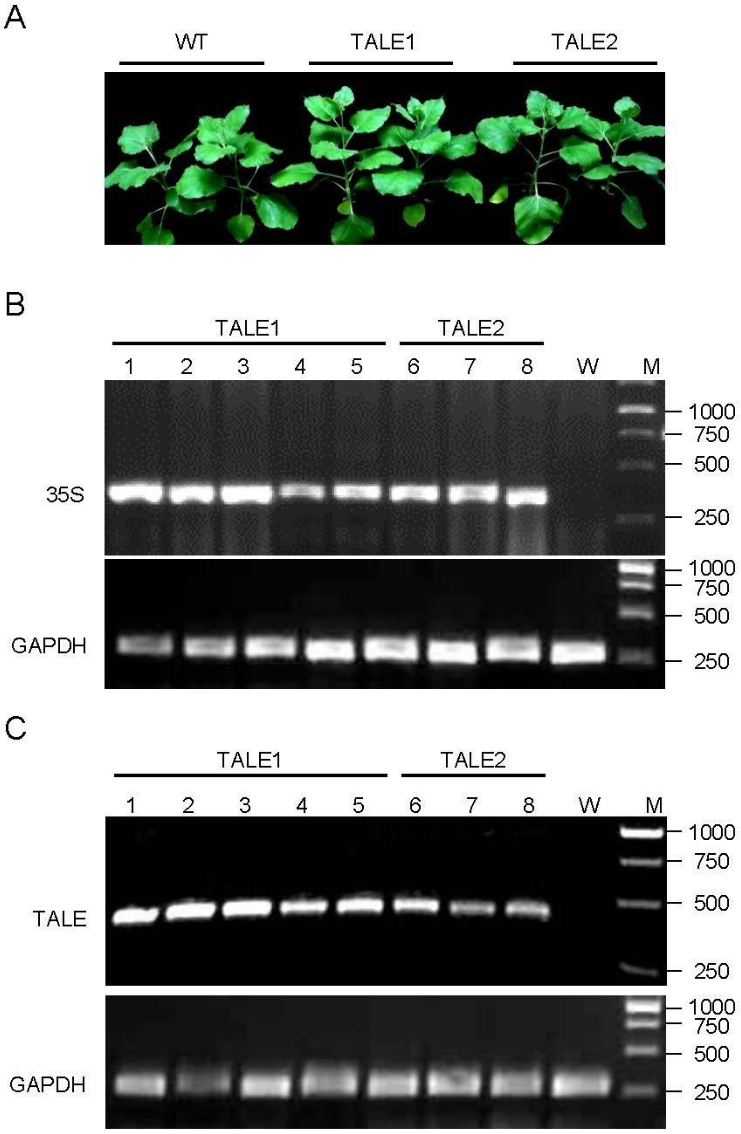

**Figure S1.** Production and analysis transgenic *N. benthamiana* plants. (**A**) Phenotypes of TALE1 and TALE2 transgenic *N. benthamiana* plants. Pictures were taken at 4 weeks post germination; (**B**) Detection of T-DNA insertion in transgenic *N. benthamiana* plants. The presence of T-DNA insertion in *N. benthamiana* genome was determined by amplified 350 bp fragments from 35S promoter. A 250 bp fragment of GAPDH gene was amplified as loading controls; (**C**) Detection of expression of TALE1 and TALE2 in transgenic *N. benthamiana* plants. A 420 bp fragment of artificial *TALE1* and *TALE2* was amplified from cDNA transcribed from total RNA extracted from transgenic *N. benthamiana* leaves with oligodT$_{15}$. A 250 bp fragment of GAPDH gene was amplified as loading controls. DNA ladders from top to bottoms represent 1000, 750, 500, and 250 bp binds, respectively.

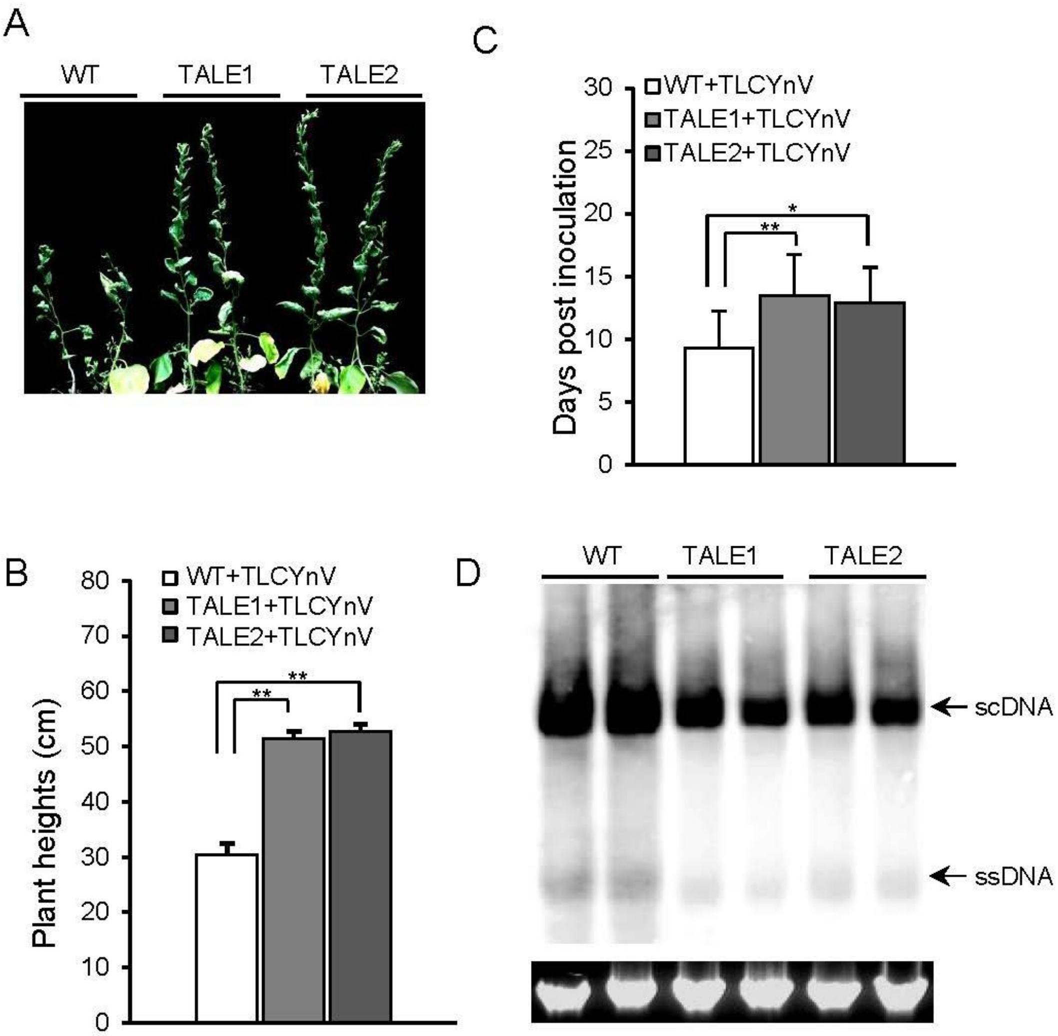

**Figure S2.** Transgenic plants show resistance to TLCYnV. (**A**) Symptoms induced by TLCYnV on wild-type and transgenic TALE1 and TALE2 *N. benthamiana* plants. Picture was taken at 20 dpi; (**B**) Average plant height of wild-type and transgenic TALE1, and TALE2 plants infected by TLCYnV. Numbers were calculated from two independent trials with each trial of 10 plants. ** indicates $P < 0.01$; (**C**) Average time for TLCYnV inducing viral symptom on systemic leaves of wild-type and transgenic plants. Numbers were calculated from two independent trials with each trial of 10 plants. * indicates $P < 0.05$, whereas ** indicates $P < 0.01$; (**D**) Southern blot detection of TLCYnV genomic DNA in wild-type, TALE1, and TALE2 transgenic plants. An ethidium bromide stained gel was shown at the bottom for indicating DNA loadings.

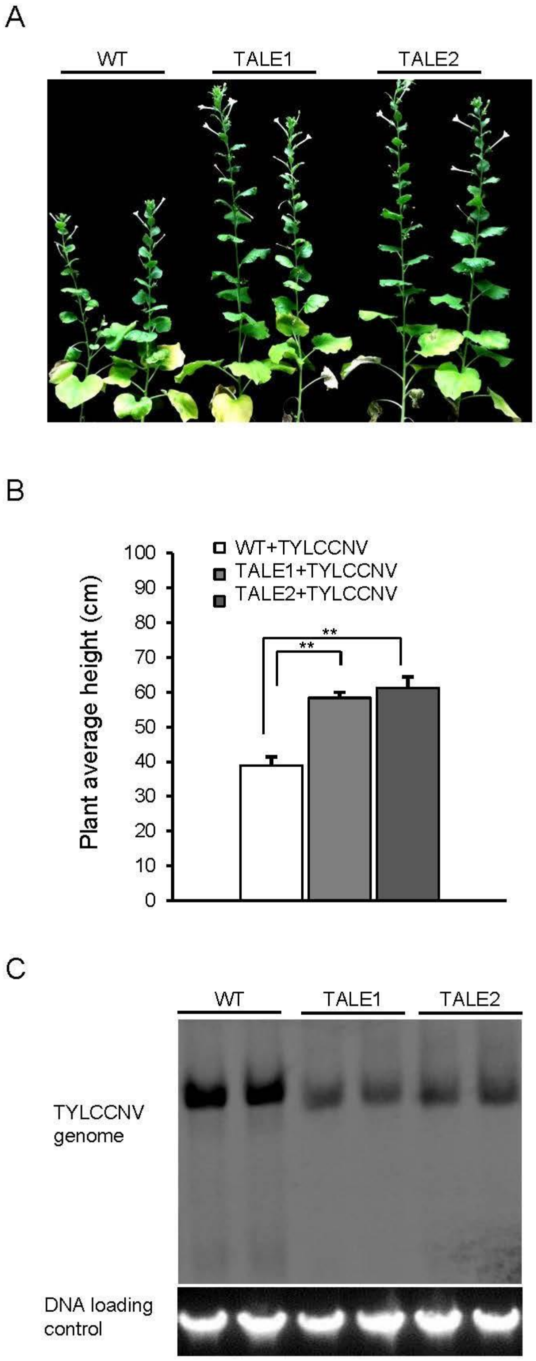

**Figure S3.** Transgenic plants show resistance to TYCCNV. (**A**) Phenotypes of wild-type and transgenic TALE1 and TALE2 *N. benthamiana* plants infected by TYCCNV at 20 dpi; (**B**) Average plant height of wild-type and transgenic TALE1 and TALE2 plants after infecting by TYCCNV. Numbers were calculated from two independent trials with each trial of 10 plants. ** indicates *P< 0.01*; (**C**) Southern blot detection of TYCCNV genomic DNA in wild-type, TALE1, and TALE2 transgenic plants. An ethidium bromide stained gel showed at the bottom for indicating DNA loadings.