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Supplementary Materials for

Viruses mobilize plant immunity to deter nonvector insect herbivores

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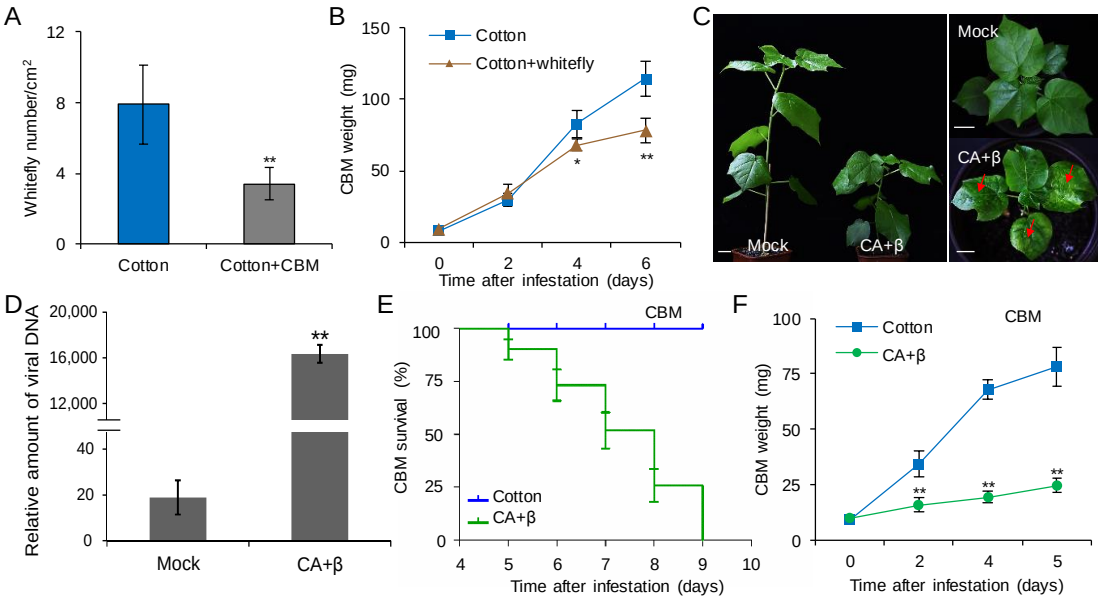

Fig. S1. Whitefly vector competes with nonvector CBM on cotton. (A) Survival numbers of adult whiteflies after four days of infestation on healthy cotton, or cotton bollworm (CBM)-infestated cotton. **(B)** Larval weight of CBM reared on healthy cotton, or whiteflies-infestated cotton. **(C)** Phenotypes of healthy Xinhai 21 cotton and CLCuMuV complex (CA+β)-infected Xinhai 21 cotton. Scale bars, 1 cm. Red arrows indicate viral symptoms on CA+β-infected cotton leaves. **(D)** Quantification of viral DNA accumulation by qPCR in healthy cotton and CA+β-infected cotton. Bars represent means ± SD (n=3) (**, P< 0.01, Student's *t*-test). **(E)** Survival rates of CBM larvae infested on healthy cotton and CA+β-infected cotton together with whitefly infestation. **(F)** Larval weight of CBM infested on healthy and CA+β-infected cotton together with whitefly infestation. **(A**, **B**, **E**, and **F)** Bars represent means ± SD (n=10) (*, P< 0.05; **, P< 0.01, Student's *t*-test). (Photo credit: Pingzhi Zhao, Chinese Academy of Sciences).

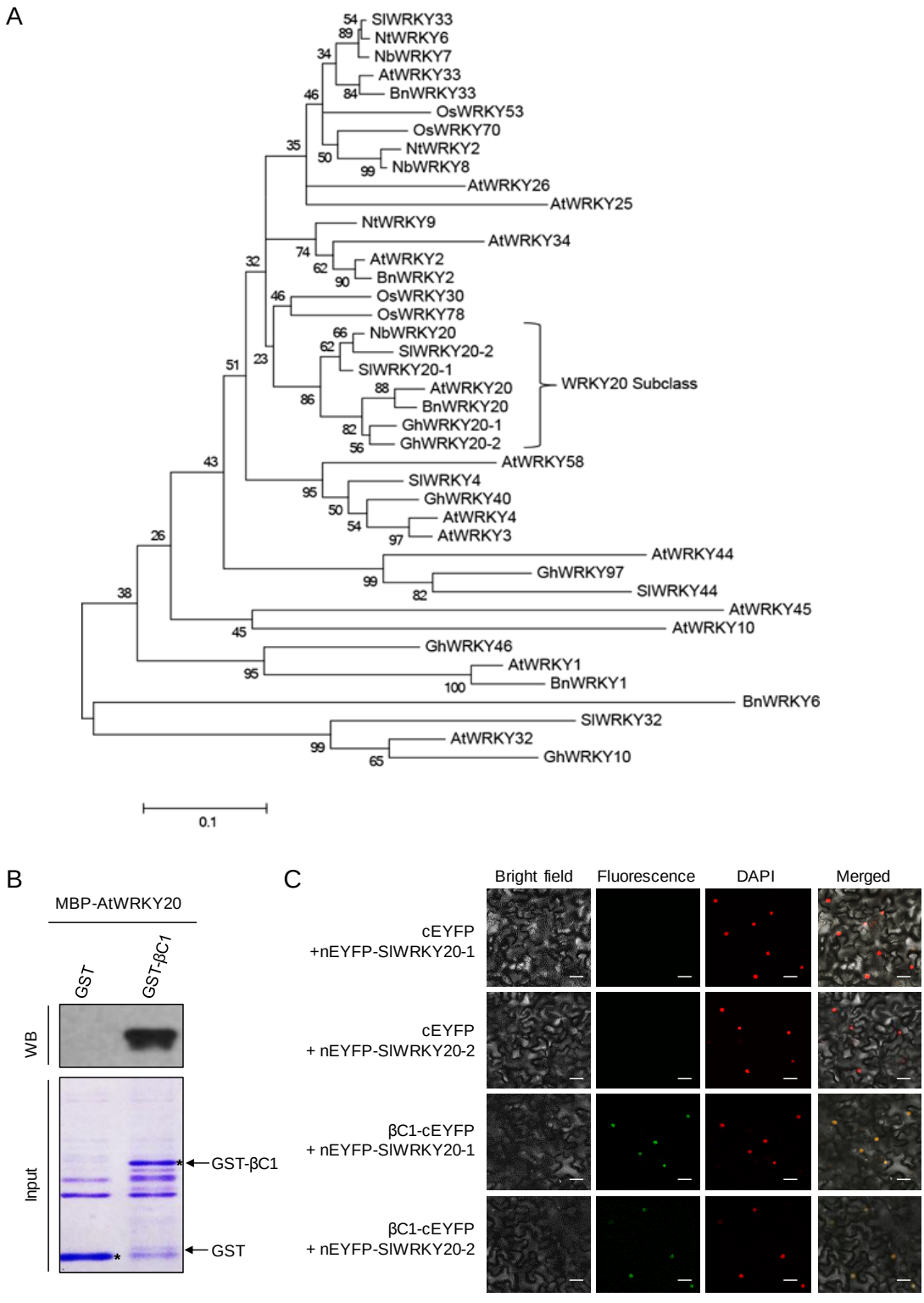

Fig. S2. TYLCCNV βC1 protein interacts with WRKY20 proteins. (A) Phylogenetic analysis of plant group I WRKY family proteins. Neighbor-joining phylogenetic trees were constructed using MEGA6 based on entire lengths of plant group I WRKY proteins sequence alignments made with ClustalX2. Species acronyms are included before the protein name: At, *Arabidopsis thaliana*; Os, *Oryza*

sativa; Sl, *Solanum lycopersicum*; Bn, *Brassica napus*; Gh, *Gossypium hirsutum*; Nb, *Nicotiana benthamiana*; Nt, *Nicotiana tabacum*. The scale bar represents 0.1 amino acid substitutions per site in the primary structure. Accession numbers of the amino acid sequences included in the phylogenic tree as following as: AtWRKY1, NP_178565.1; AtWRKY2, NP_200438.1; AtWRKY3, NP_178433.1; AtWRKY4, NP_172849.1; AtWRKY10, NP_175956.1; AtWRKY20, NP_849450.1; AtWRKY25, NP_180584.1; AtWRKY26, NP_196327.1; AtWRKY32, NP_567862.3; AtWRKY33, NP_181381.2; AtWRKY34, NP_194374.1; AtWRKY44, NP_181263.2; AtWRKY45, NP_186846.1; AtWRKY58, NP_186757.2; GhWRKY10, AIE43817.1; GhWRKY20-1, AIE43819.1; GhWRKY20-2, AIE43818.1; GhWRKY40, AIE43824.1; GhWRKY46, AIE43823.1; GhWRKY97, AIE43909.1; NbWRKY7, BAI63295.1; NbWRKY8, BAI63296.1; NbWRKY20, BAS69353.1; NtWRKY2, BAA77383.1; NtWRKY6, BAB61053.1; NtWRKY9, BAB61056.1; OsWRKY30, NP_001062148.1; OsWRKY53, NP_001055252.1; OsWRKY70, NP_001055828.1; OsWRKY78, NP_001060116.1; SlWRKY4, XP_004239088.1; SlWRKY20-2, XP_004244048.1; SlWRKY20-1, XP_004251909.1; SlWRKY32, XP_004242596.1; SlWRKY33, XP_004246308.1; SlWRKY44, XP_004249802.1; BnWRKY1, ACI14383.1; BnWRKY2, XP_013714348.1; BnWRKY6, ACI14403.1; BnWRKY20, ACI14387.1; BnWRKY33, ACI14397.1. **(B)** GST-pull down assay. Two micrograms of MBP-AtWRKY20 fusion protein was used to pull down 2 μg of GST or GST-βC1 fusion. Membrane was stained with coomassie brilliant blue to monitor input protein amounts. **(C)** BiFC analysis of TYLCCNV βC1 protein interaction with tomato (*Solanum lycopersicum*) SlWRKY20 homologs (SlWRKY20-1 or SlWRKY20-2). Fluorescence was observed owing to complementation of βC1 fused with the C-terminal part of EYFP and SlWRKY20 proteins fused with the N-terminal part of EYFP. Scale bars, 50 μm.

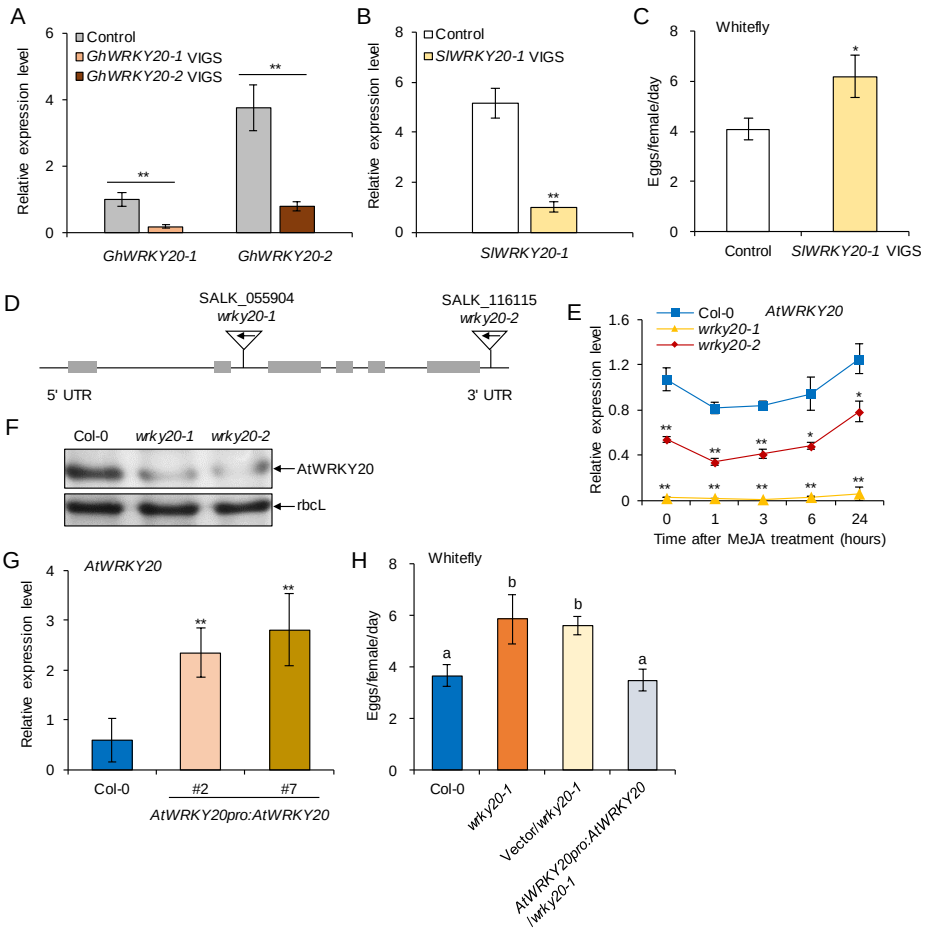

Fig. S3. WRKY20 mediates plant immunity against whitefly. (A) Relative expression level of *GhWRKY20* in vector control- and *GhWRKY20* VIGS Xinhai 21 cotton plants. **(B)** Relative expression level of *SlWRKY20-1* in vector control- and *SlWRKY20-1* VIGS Zhongza No.9 tomato plants. **(C)** Daily number of eggs laid per female whitefly on vector control- and *SlWRKY20-1* VIGS tomato plants. Bars represent means ± SD (n=8) (*, P< 0.05, Student's *t*-test). **(D)** Schematic diagram of *Arabidopsis wrky20-1* (SALK_055904) and *wrky20-2* (SALK_116115) mutants with the T-DNA insertion shown as an inverted triangle. **(E)** Relative expression level of *AtWRKY20* in *Arabidopsis* Col-0 and *wrky20* mutant plants under MeJA treatment. **(F)** Detection of AtWRKY20 protein in *Arabidopsis* Col-0 and *wrky20* mutant plants by immunoblot using anti-AtWRKY20$^{1\text{-}300}$ monoclonal antibody. Stained membrane bands of the large subunit of Rubisco (rbcL) were used as a loading control. **(G)** Relative expression level of *AtWRKY20* in overexpressing *AtWRKY20* plants. **(H)** Daily number of eggs laid per female whitefly on *Arabidopsis* plants. *AtWRKY20pro: AtWRKY20/wrky20-1* is the complementary line of *wrky20-1* mutant. *Vector/wrky20-1* line is transferred empty vector into *wrky20-1* mutant as the negative control. Bars represent means ± SD (n=8). Means with different letters are significantly different (P < 0.05, one-way ANOVA along with Duncan's multiple range test). **(A**, **B**, **E**, and **G)** Bars represent means ± SD (n=3) (*, P< 0.05; **, P< 0.01, Student's *t*-test).

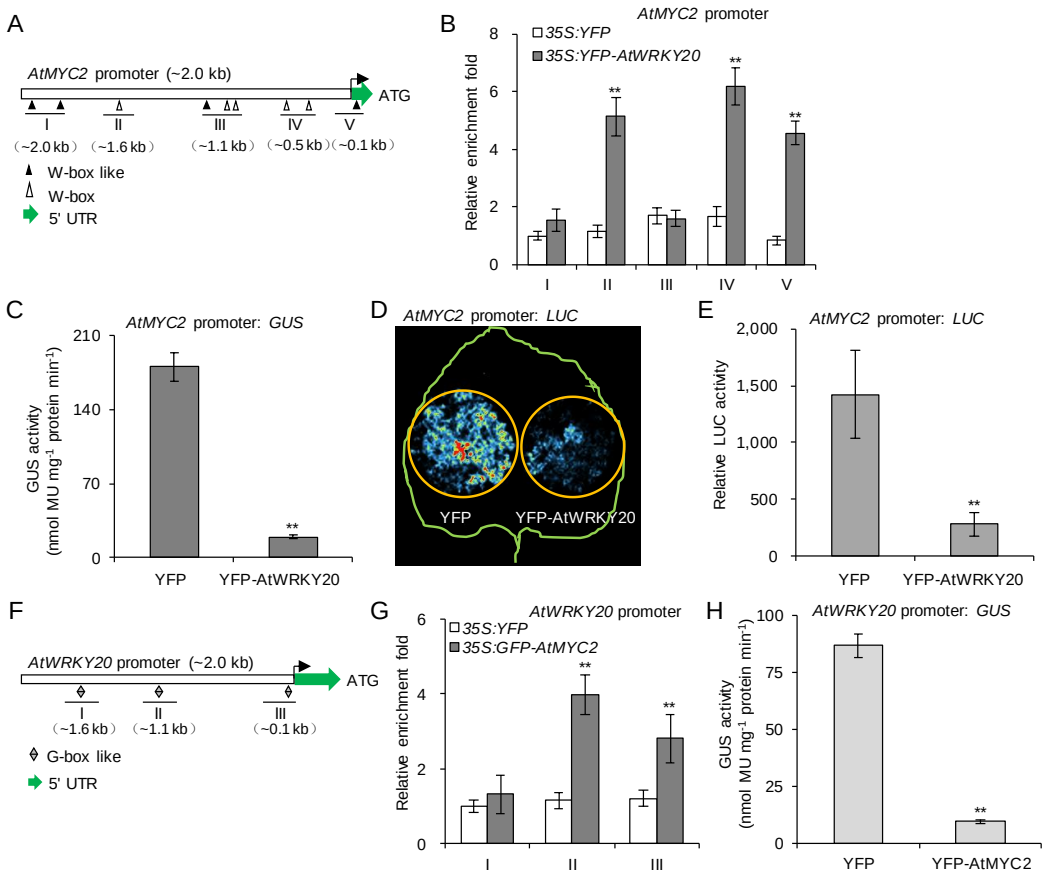

Fig. S4. WRKY20 and MYC2 form a negative feedback loop. (A) Schematic diagram of *AtMYC2* promoter. The black triangles represent W-box like motifs and small hollow triangles represent W-box motifs. **(B)** Fold enrichment of YFP-AtWRKY20 associated with each of five DNA fragments of *AtMYC2* promoter in ChIP assay. **(C)** Promoter activity of *AtMYC2* in YFP expressing leaves and YFP-AtWRKY20 expressing leaves was measured by GUS quantification. **(D)** Luciferase imaging of AtWRKY20 suppressing *AtMYC2* promoter activity in *N. benthamiana*. *N. benthamiana* leaves infiltrated with *AtMYC2* promoter*: LUC* and *35S:YFP*, or *AtMYC2* promoter*: LUC* and *35S:YFP-AtWRKY20* were subjected to luciferase complementation imaging assay. **(E)** Quantitative luminescence of AtWRKY20 suppressing *AtMYC2* promoter activity in *N. benthamiana*. *N. benthamiana* leaves infiltrated with indicated constructs were sliced into strips, and relative luminescence was determined by a microplate luminometer. **(F)** Schematic diagram of *AtWRKY20* promoter. The diamonds represent G-box like motifs. **(G)** Fold enrichment of GFP-AtMYC2 associated with each of three DNA fragments of *AtWRKY20* promoter in ChIP assay. **(H)** Promoter activity of *AtWRKY20* in YFP expressing leaves and YFP-AtMYC2 expressing leaves was measured by GUS quantification. **(B** and **G)** Bars represent means ± SD (n=4) (**, P< 0.01, Student's *t*-test). **(C**, **E** and **H)** Bars represent means ± SD (n=8) (**, P< 0.01, Student's *t*-test).

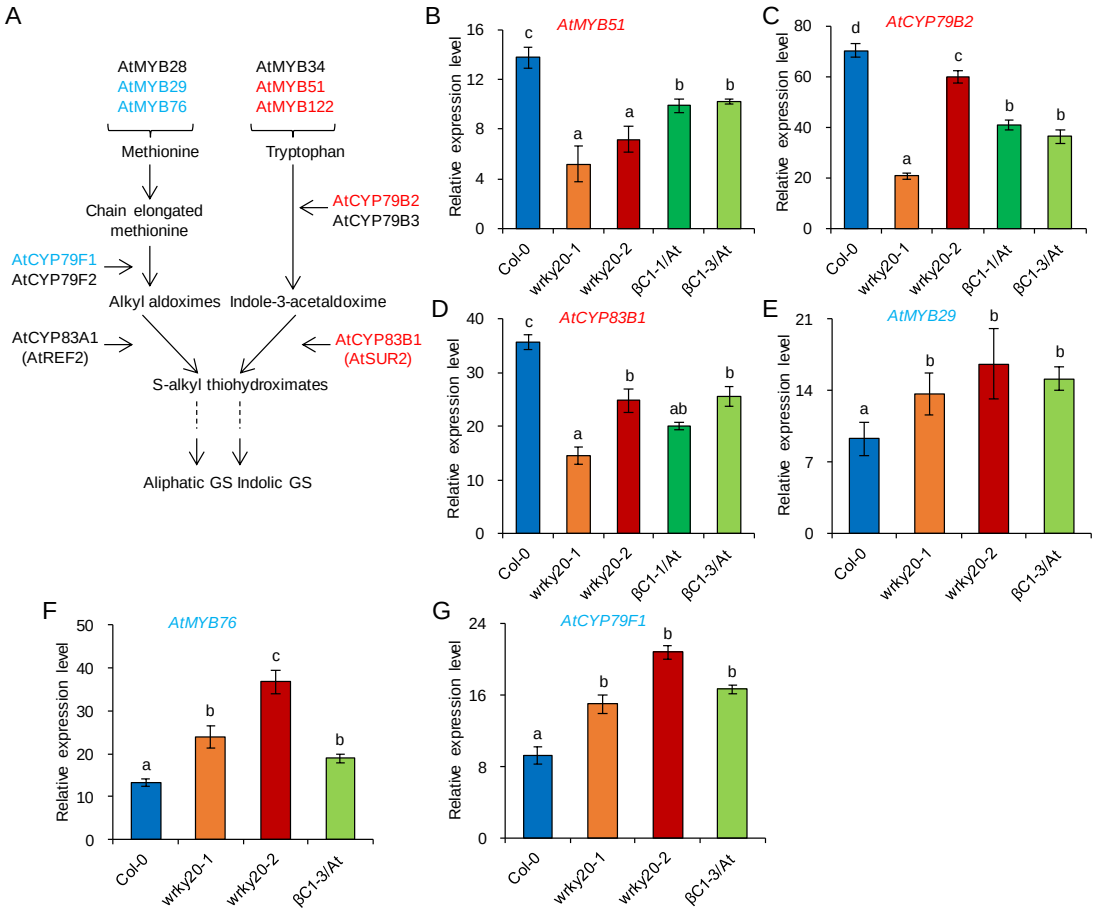

Fig. S5. Plant WRKY20 is a dual-function transcription factor controlling GS biosynthesis. (A) The biosynthetic pathway of aliphatic- and indole-glucosinolates in *Arabidopsis*. **(B** to **G)** Relative expression levels of glucosinolate biosynthesis related-genes, *AtMYB51* **(B)**, *AtCYP79B2* **(C)**, *AtCYP83B1* **(D)**, *AtMYB29* **(E)**, *AtMYB76* **(F)** and *AtCYP79F1* **(G)** in six-week-old *Arabidopsis* Col-0, *wrky20* mutants and βC1-3/At plants after MeJA treatment for 6h. Bars represent means ± SD (n=3). Means with different letters are significantly different ($P < 0.05$, one-way ANOVA along with Duncan's multiple range test).

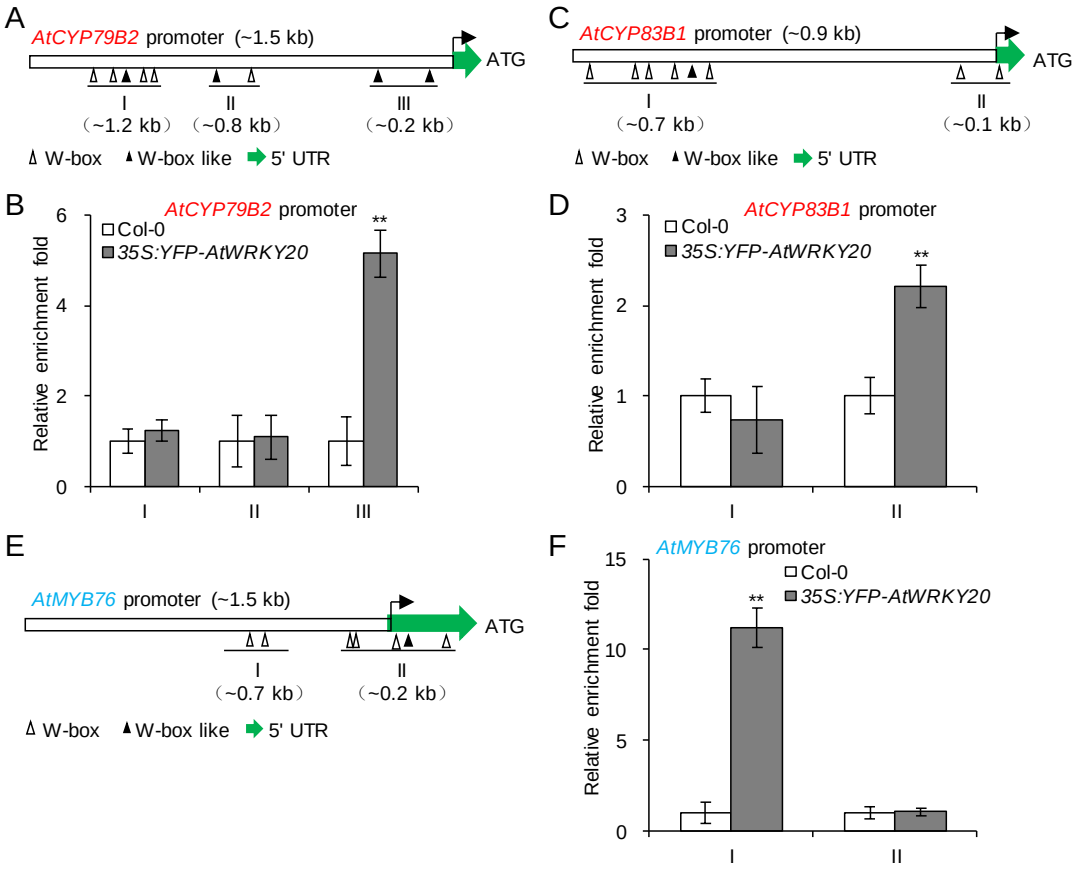

Fig. S6. WRKY20 directly targets GS biosynthetic-related genes by binding to their promoters. (A), **(C)**, and **(E)** Schematic diagram of *AtCYP79B2* promoter **(A)**, *AtCYP83B1* promoter **(C)** or *AtMYB76* promoter **(E)**. The black triangles represent W-box like motifs and small hollow triangles represent W-box motifs. Lines under triangles various DNA fragments were amplified in ChIP assay. **(B)**, **(D)**, and **(F)**, Fold enrichment of YFP-AtWRKY20 associated with each DNA fragments of *AtCYP79B2* promoter **(B)**, *AtCYP83B1* promoter **(D)** or *AtMYB76* promoter **(F)** in ChIP assay. Bars represent means ± SD (n=4) (**, P< 0.01, Student's *t*-test).

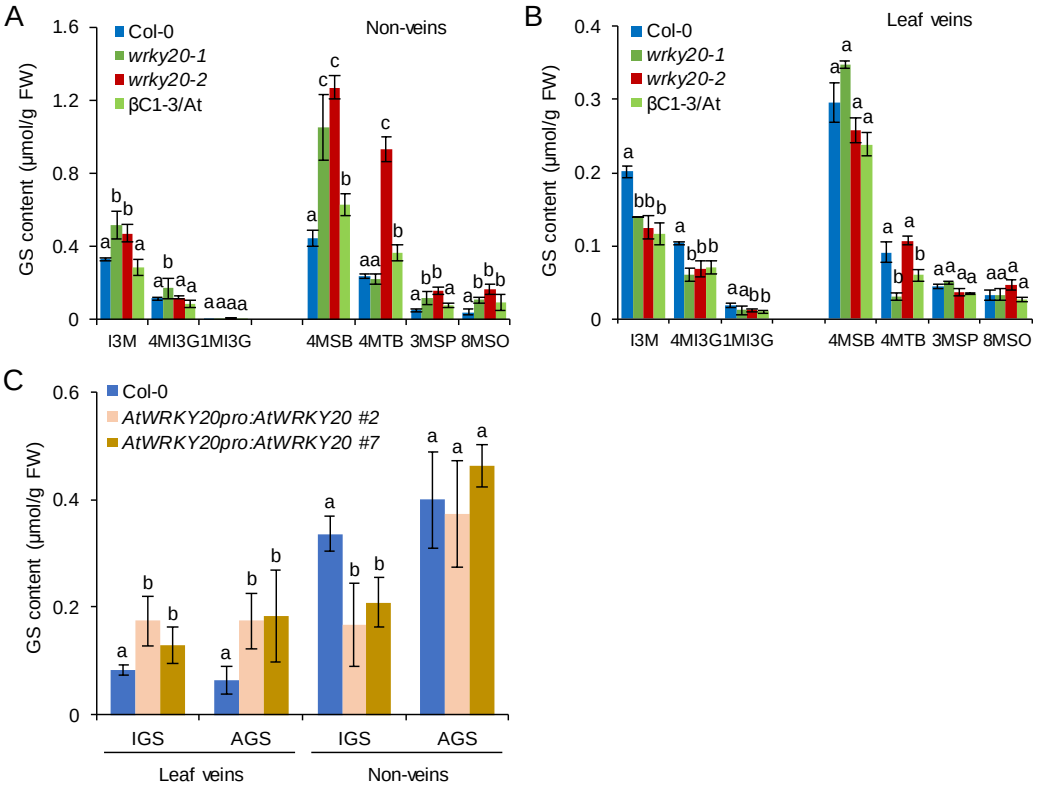

Fig. S7. WRKY20 regulates a JA-mediated GS accumulation in a vascular-specific pattern. (A) and **(B)** Contents of three IGSs (I3M, 4MI3G and 1MI3G) and four AGSs (4MSB, 4MTB, 3MSP and 8MSO) in non-veins tissues **(A)** or leaf veins **(B)** of six-week-old *Arabidopsis* plants after 6 h MeJA treatment. **(C)** Contents of AGS and IGS in leaf-veins and non-veins, respectively of six-week-old overexpressing *AtWRKY20* plants after 6 h MeJA treatment. Bars represent means ± SD (n=4). Means with different letters are significantly different ($P < 0.05$, one-way ANOVA along with Duncan's multiple range test).

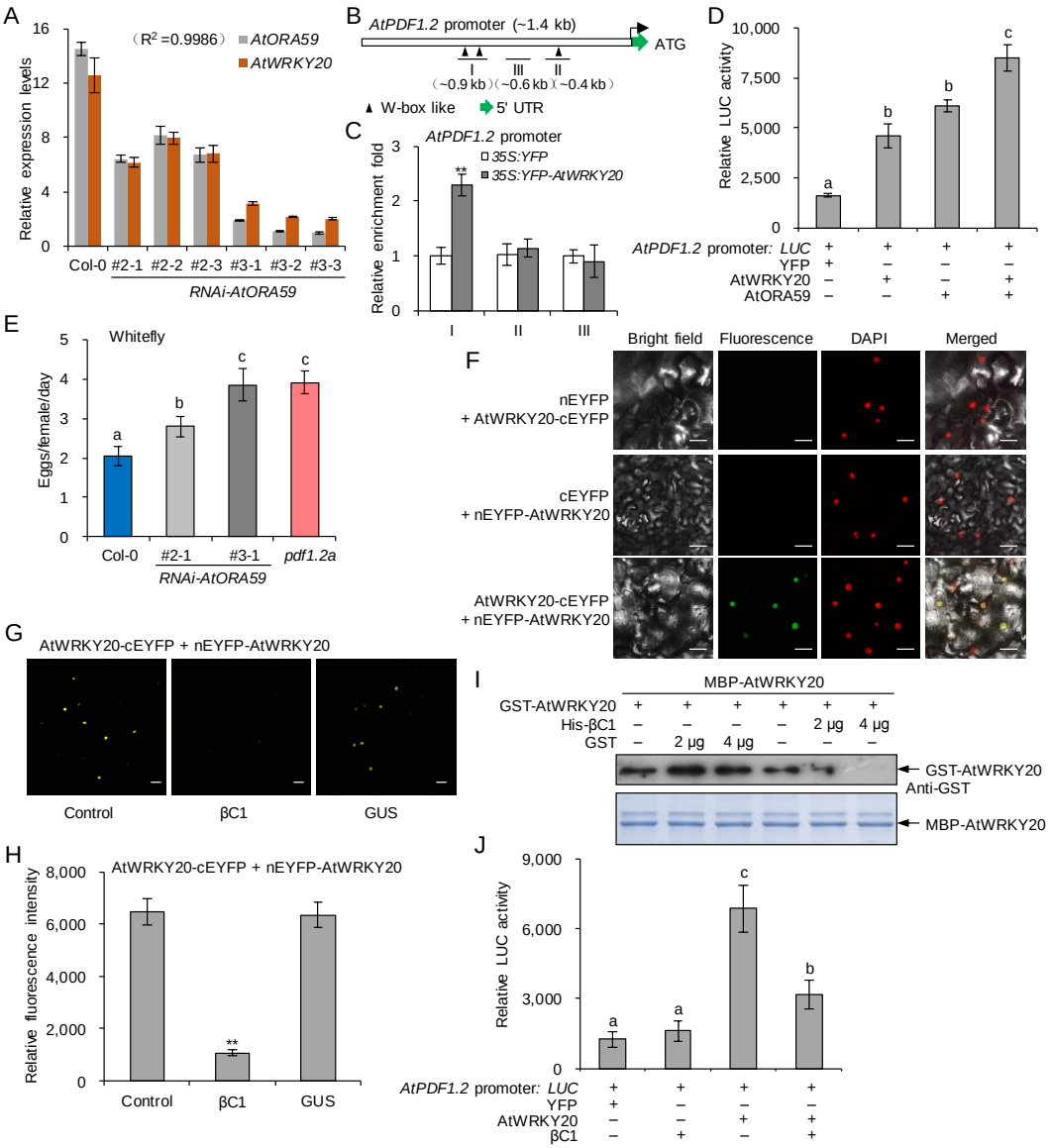

Fig. S8. βC1 suppresses the WRKY20 activity by interfering with its homodimerization. (A) Relative expression levels of *AtORA59* and *AtWRKY20* genes in Col-0, *RNAi-AtORA59* #2 and #3 lines. R2 indicated squared correlation coefficient. Bars represent means ± SD (n=3). **(B)** Schematic diagram of *AtPDF1.2* promoter. The black triangles represent W-box like motifs in the schematic diagram of the promoters. Three lines under triangles various DNA fragments were amplified in ChIP assay. **(C)** Fold enrichment of YFP-AtWRKY20 associated with DNA fragments of the *AtPDF1.2* promoter in a ChIP assay. Bars represent means ± SD (n=4) (**, P< 0.01, Student's *t*-test). **(D)** Effects of WRKY20 and ORA59 on the trans-activation of *AtPDF1.2* promoter. Bars represent means ± SD (n=8). **(E)** Daily number of eggs laid per female whitefly on wild-type Col-0, *RNAi-AtORA59* #2 and #3 lines, and *pdf1.2a* mutant. Bars represent means ± SD (n=8). **(F)** Self-interaction of WRKY20 was confirmed by BiFC assay. Scale bars, 50 μm. **(G)** Modified BiFC competition assays.

The EYFP fluorescence was detected after coexpession of AtWRKY20-cEYFP + nEYFP-AtWRKY20 (Control), βC1 + AtWRKY20-cEYFP + nEYFP-AtWRKY20 (βC1), or GUS + AtWRKY20-cEYFP + nEYFP-AtWRKY20 (GUS). Scale bars, 50 μm. **(H)** Quantitative data of EYFP fluorescence intensity shows effects of βC1 on the formation of WRKY20 homodimers. Bars represent means ± SD (n=20) (**, P< 0.01, Student's *t*-test). **(I)** Pull-down protein competition assays. The indicated protein amount of His-βC1 or GST was mixed with 2 μg of GST-AtWRKY20 and pulled down by 2 μg of MBP-AtWRKY20. Immunoblots were performed using anti-GST antibody to detect the associated proteins. Membranes were stained with Coomassie Brilliant Blue to monitor input protein amount. **(J)** Effects of βC1 on the trans-activation activity of AtWRKY20 on the *AtPDF1.2* promoter. Bars represent means ± SD (n=8). **(D**, **E**, and **J)** Means with different letters are significantly different (P < 0.05, one-way ANOVA along with Duncan's multiple range test).

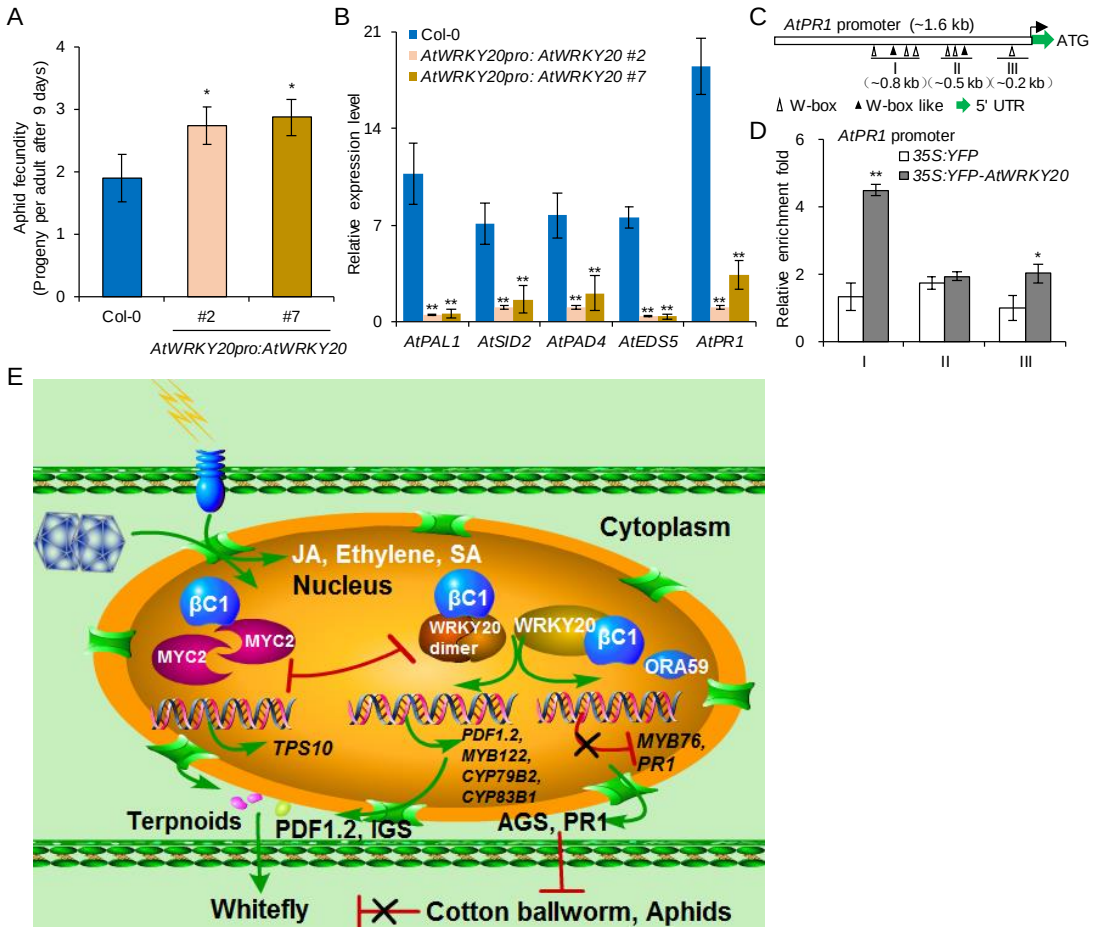

Fig. S9. WRKY20 negatively regulates SA-mediated defense against the green peach aphid. (A) Number of progeny produced by each aphid nine days after infestation of six-week-old overexpressing *AtWRKY20* plants. Bars represent means ± SD (n=6) (*, P< 0.05, Student's *t*-test). **(B)** Relative expression levels of SA related-genes (*AtPAL1*, *AtSID2*, *AtPAD4*, *AtEDS5*, and *AtPR1*) in six-week-old overexpressing *AtWRKY20* plants. Bars represent means ± SD (n=3) (**, P< 0.01, Student's *t*-test). **(C)** Schematic diagram of *AtPR1* promoter. The black triangles represent W-box like motifs and small hollow triangles represent W-box motifs in the schematic diagram of the promoters. Three lines under triangles various DNA fragments were amplified in ChIP assay. **(D)** Fold enrichment of YFP-AtWRKY20 associated with DNA fragments of the *AtPR1* promoter in a ChIP assay. Bars represent means ± SD (n=4) (*, P< 0.05; **, P< 0.01, Student's *t*-test). **(E)** A working model of begomoviruses manipulating plant immunity to promote performance of vector whitefly but deter non-vector herbivores. Host plants have evolved many immune mechanisms to circumvent against infections of arboviruses. Whitefly-transmitted begomovirus triggers several immune responses, including the emissions of terpenoids, the synthesis of glucosinolates, phytohormones (e.g., JA, ethylene, SA), and toxic polypeptides (e.g., defensin and

PATHOGENESIS-RELATED 1). The betasatellite of begomoviruses encoded βC1 interferes with multiple host defensive responses regulated by WRKY20 and MYC2 transcription factors. βC1 disrupts the dimerization of WRKY20-WRKY20 and WRKY20-ORA59, thereby mobilizing the biosynthesis and accumulation of aliphatic glucosinolates and several defensive compounds (e.g. PDF1.2 and PR1). This viral hijacking of WRK20 and other host targets confers benefits to whitefly but deters non-vector cotton bollworm and aphids.

Table S1. DNA primers used in this study.

Gene	Primer Sequence (5'-3')	Purpose
βC1-F (KpnI)	GGTACCATGACTATCAAATACAAC	Cloning
βC1-R (XhoI)	CTCGAGACATCTGAATTTGTAAAT	Cloning
βC1-C-F(BamHI)	GGATCCATGACGAGGAGCAGAACAAACA	Cloning
βC1-C-R(XhoI)	CTCGAGACGGTGAACTTCTTATTGAA	Cloning
GhWRKY20-1-F(BamHI)	GGATCCATGGAGGAACAAATACTAGC	Coning
GhWRKY20-1-R(XhoI)	CTCGAGGGACCTGTTAGTATTCTTCC	Cloning
GhWRKY20-2-F(BamHI)	GGATCCATGGAGGAGCAAATATTAGC	Cloning
GhWRKY20-2-R(XhoI)	CTCGAGGGACCGGTTAGTATTCTTCC	Cloning
SlWRKY20-1-F(Kpn1)	GGTACCATGGAAGACTCTCACTCT	Cloning
SlWRKY20-1-R(Xho1)	CTCGAGGGGCCAAGAAGTATCTT	Cloning
SlWRKY20-2-F(Kpn1)	GGTACCATGCAAGGCTCTAGTGGG	Cloning
SlWRKY20-2-R(Xho1)	CTCGAGGGGCCCAAAAGTATCCT	Cloning
AtWRKY20-F(KpnI)	GGTACCATGAACCCTCAAGCTAATGACCG	Cloning
AtWRKY20-R(NotI)	GCGGCCGCGGACCCGATTGTACTCTC	Cloning
AtWRKY20$^{1\text{-}300}$-F	CGCGGCAGCCATATG ATGAACCCTCAAGCTA	Cloning
AtWRKY20$^{1\text{-}300}$-R	GTGGTGGTGCTCGAGAGAACTTGAGCTAGCAG	Cloning
AtORA59-F(Kpn1)	GGTACCATGGAATATCAAACTAAC	Cloning
AtOR59-R(Xho1)	CTCGAGGAACATGATCTCATAAGC	Cloning
AtERF1-F(Kpn1)	GGTACCATGGATCCATTTTTAATTCAGTCC	Cloning
AtERF1-R(Xho1)	CTCGAGCAAGTCCCACTATTTTCA	Cloning
AtMYC2-F(Kpn1)	GGTACCATGACTGATTACCGGCTACA	Cloning
AtMYC2-R(NotI)	GCGGCCGCCCGATTTTTGAAATCAAACT	Cloning
GhWRKY20-1-F(XbaI)	TCTAGACCAACATGTATGGCCAGATG	VIGS
GhWRKY20-1-R(BamHI)	GGATCCAGTGCATTTACAGTTACTGG	VIGS
GhWRKY20-2-F(XbaI)	TCTAGAATTGCGGTTATGGCCAGATGG	VIGS
GhWRKY20-2-R(BamHI)	GGATCCGGCCCACACATTGCTACTGG	VIGS
SlWRKY20-1-F(BglII)	CAAGAGATCTCCTAATCCTAGGAGCTATT	VIGS
SlWRKY20-1-R(XbaI)	CAAGTCTAGAGAAGGTTGTAAAGGCAAAG	VIGS
AtWRKY20-qF	TATACAGGCAGGGGGTTCCA	RT-qPCR
AtWRKY20-qR	GCCTTTCTTCTTGTGCAGCC	RT-qPCR
GhWRKY20-1-qF	TTATAACCACGTATGAGGGA	RT-qPCR
GhWRKY20-1-qR	GATCCATACTGGTTCATGCC	RT-qPCR
GhWRKY20-2-qF	CCACATACGAGGGAAAACAC	RT-qPCR
GhWRKY20-2-qR	CATACTGATTCATGCTGCCA	RT-qPCR
GhUB7-qF	AGGCATTCCACCTGACCAAC	RT-qPCR
GhUB7-qR	CTTGACCTTCTTCTTCTTGTGCTTG	RT-qPCR

SlWRKY20-1-qF	CCTAATCCTAGGAGCTATT	RT-qPCR
SlWRKY20-1-qR	GAAGGTTGTAAAGGCAAAG	RT-qPCR
SlACTIN2-qF	TTGCTGACCGTATGAGCAAG	RT-qPCR
SlACTIN2-qR	GGACAATGGATGGACCAGAC	RT-qPCR
AtMYC2-qF	AACCACGTCGAAGCAGAGAG	RT-qPCR
AtMYC2-qR	TGCGTCACCGAGTAACGAAG	RT-qPCR
AtMYC3-qF	TGTTGAAGCAGAGAGGCAGA	RT-qPCR
AtMYC3-qR	CTCCGAGAAGCGAAGCTTTA	RT-qPCR
AtMYC4-qF	AGGAGCAAACGAGAACTGGA	RT-qPCR
AtMYC4-qR	CCATCTCCCCAACCTAACAA	RT-qPCR
AtMYB51-qF	AGCTCGTGGACTACCAGGAA	RT-qPCR
AtMYB51-qR	GGAGGTTATGCCCTTGTGTG	RT-qPCR
AtMYB122-qF	CAGGATCATCATCAGCTCGGT	RT-qPCR
AtMYB122-qR	CGTTGACCTCTCACCTTCTGA	RT-qPCR
AtCYP79B2-qF	AACAAAAAGAAACCGTATCTGCCAC	RT-qPCR
AtCYP79B2-qR	TCCTAACTTCACGCATGCTATCTC	RT-qPCR
AtCYP83B1-qF	GGCAACAAACCATGTCGTATCAAG	RT-qPCR
AtCYP83B1-qR	CGTTGACACTCTTCTTCTCTAACCG	RT-qPCR
AtMYB29-qF	CGAAGGGGAAGAAGCTGACA	RT-qPCR
AtMYB29-qR	TCGTCGTAATCTTGGCTCGT	RT-qPCR
AtMYB76-qF	TTGAGCCCATGAAGTTCGA	RT-qPCR
AtMYB76-qR	CGATCATGTACTCATATGATTG	RT-qPCR
AtCYP79F1-qF	GCATCGGTGTTAAAGTCGGG	RT-qPCR
AtCYP79F1-qR	TGGCTCAACGGACAAGTGAA	RT-qPCR
AtPDF1.2-qF	TTTGCTGCTTTCGACGCAC	RT-qPCR
AtPDF1.2-qR	GATTCTTGCATGCATTACTG	RT-qPCR
AtORA59-qF	GCTTATGATCAGGCGGCTTT	RT-qPCR
AtORA59-qR	GCGTCATAACAACACTCTGT	RT-qPCR
AtPR1-qF	TTCATTAGTATGGCTTCTCGTTCA	RT-qPCR
AtPR1-qR	GAAAACTTAGCCTGGGGTAGC	RT-qPCR
AtPAL1-qF	ATCTCCAGCCTAAGGAAGGTCT	RT-qPCR
AtPAL1-qR	AAAACCGCCGACAAAATCTCAG	RT-qPCR
AtSID2-qF	GAATTTGCAGTCGGGATCAG	RT-qPCR
AtSID2-qR	AATTAATCGCCTGTAGAGATGTTG	RT-qPCR
AtEDS5-qF	ATCATATCCGAGATGCATAGACTG	RT-qPCR
AtEDS5-qR	CGAACATTAGTGTGAGACAACCA	RT-qPCR
AtPAD4-qF	GGTTCTGTTCGTCTGATGTTT	RT-qPCR
AtPAD4-qR	GTTCCTCGGTGTTTTGAGTT	RT-qPCR

AtACTIN2-qF	AGTGGTCGTACAACCGGTATTGT	RT-qPCR
AtACTIN2-qR	GATGGCATGAGGAAGAGAGAAAC	RT-qPCR
CLCuMuV-V1-qF	ACAACAGGCATGGACAAACA	RT-qPCR
CLCuMuV-V1-qR	CCAATACGATGGGTCAAACC	RT-qPCR
AtWRKY20 promoter-F(KpnI)	GGTACCATGATGGTGTGGTTATGTG	promoter
AtWRKY20 promoter-R(XhoI)	CTCGAG TTCAGAGATTCGCAAGGGT	promoter
AtMYC2 promoter-F(KpnI)	GGTACCTGTACACCAATTGATGAT	promoter
AtMYC2 promoter-R(XhoI)	CTCGAGTCCATAAACCGGTGACCG	promoter
AtMYB122 promoter-F(KpnI)	GGTACCCCACAACTCGTGAGA	promoter
AtMYB122 promoter-R(XhoI)	CTCGAG GTATGTTCAGCCAAG	promoter
AtMYC2-Region I-F	CTCTAAATCTAAGAATAACTCG	ChIP-RT-qPCR
AtMYC2-Region I-R	GCTTAGAATGGGGATGAT	ChIP-RT-qPCR
AtMYC2-Region II-F	TTGTTGTTTTCTAGTGGCG	ChIP-RT-qPCR
AtMYC2-Region II-R	CTGAGACATCTGTATTGGG	ChIP-RT-qPCR
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AtMYC2-Region V-F	ACAACCATCCACGTTTCC	ChIP-RT-qPCR
AtMYC2-Region V-R	TCCATAAACCGGTGACCG	ChIP-RT-qPCR
AtMYB122-Region I-F	ACGAATGTATCCTTTATC	ChIP-RT-qPCR
AtMYB122-Region I-R	CTATGCACTATTTATTAG	ChIP-RT-qPCR
AtMYB122-Region II-F	GTGCATAGAAAACTTACA	ChIP-RT-qPCR
AtMYB122-Region II-R	TTTTAAACCAATGATATT	ChIP-RT-qPCR
AtMYB122-Region III-F	CAATATATGGCTAGGTAAG	ChIP-RT-qPCR
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AtMYB51-Region III-F	ATCATATCAGATGTGGCGGT	ChIP-RT-qPCR
AtMYB51-Region III-R	AGCCCATCTCTATTTATGCT	ChIP-RT-qPCR
AtCYP79B2-Region I-F	GCTCATCATCAACAGACAAG	ChIP-RT-qPCR
AtCYP79B2-Region I-R	GAGAGTTCACCTGCCAAATA	ChIP-RT-qPCR
AtCYP79B2-Region II-F	CCAATTTCTATAGTTGGGAA	ChIP-RT-qPCR
AtCYP79B2-Region II-R	GCTAGTATTGTCGCAGTGGT	ChIP-RT-qPCR
AtCYP79B2-Region III-F	CTGTTTTTCGGCTGGACCGG	ChIP-RT-qPCR
AtCYP79B2-Region III-R	GTTAGTTTATGTGAAATGAC	ChIP-RT-qPCR

AtCYP83B1-Region I-F	GTCACACTTCTTGTCAACCTTAA	ChIP-RT-qPCR
AtCYP83B1-Region I-R	CTAAACTCTCAGTTTTTAAG	ChIP-RT-qPCR
AtCYP83B1-Region II-F	GTAACCCAAGTTACATTTTT	ChIP-RT-qPCR
AtCYP83B1-Region II-R	TTTTTTCTGTTTGACTTACT	ChIP-RT-qPCR
AtMYB76-Region I-F	TGTGTGACATATATGGGCAG	ChIP-RT-qPCR
AtMYB76-Region I-R	TGATAATATGCAATTGCTAA	ChIP-RT-qPCR
AtMYB76-Region II-F	TCATTGTAAAACTTACCTTATAA	ChIP-RT-qPCR
AtMYB76-Region II-R	TCAGAGATTACGAATACGGT	ChIP-RT-qPCR
AtPDF1.2-Region I-F	GTTGAATGTCGTTGTTTACG	ChIP-RT-qPCR
AtPDF1.2-Region I-R	CCTTAAACGTAATGGACTATCG	ChIP-RT-qPCR
AtPDF1.2-Region II-F	GGTGATCCTCTAATCGAA	ChIP-RT-qPCR
AtPDF1.2-Region II-R	CCTAAGCGGCTGCTTCGG	ChIP-RT-qPCR
AtPDF1.2-Region III-F	CCCAGGGATATATAAATGG	ChIP-RT-qPCR
AtPDF1.2-Region III-R	TCGATTAGAGGATCACCC	ChIP-RT-qPCR
AtPR1-Region I-F	TTAAAGCCAGTGCATATCAG	ChIP-RT-qPCR
AtPR1-Region I-R	ATGCCGCCACATCTATGACG	ChIP-RT-qPCR
AtPR1-Region II-F	GGACTTTTCAGCCATAGGCA	ChIP-RT-qPCR
AtPR1-Region II-R	GAAGATATCTTCCTGTAAAT	ChIP-RT-qPCR
AtPR1-Region III-F	CTTCATTTAGGGTATACTTACA	ChIP-RT-qPCR
AtPR1-Region III-R	CTATAGATCTCACGTTTTTG	ChIP-RT-qPCR
AtWRKY20-Region I-F	CTGTTGCTTTATCATTTTACCG	ChIP-RT-qPCR
AtWRKY20-Region I-R	CCACCTCAAATCTTGTTAGA	ChIP-RT-qPCR
AtWRKY20-Region II-F	AACTGAGAACGGCCCAAAGA	ChIP-RT-qPCR
AtWRKY20-Region II-R	AAGTACCGAGTGGACAAGCG	ChIP-RT-qPCR
AtWRKY20-Region III-F	GACTGTTGATACCTGATCC	ChIP-RT-qPCR
AtWRKY20-Region III-R	GCAACAACAACAAACGTT	ChIP-RT-qPCR
Actin2-F	CGTTTCGCTTTCCTTAGTGTTAGCT	ChIP-RT-qPCR
Actin2-R	AGCGAACGGATCTAGAGACTCACCTTG	ChIP-RT-qPCR