Supplementary material

The cotton MYB108 forms a positive feedback regulation loop with CML11 and participates in defense response against *Verticillium dahliae* infection

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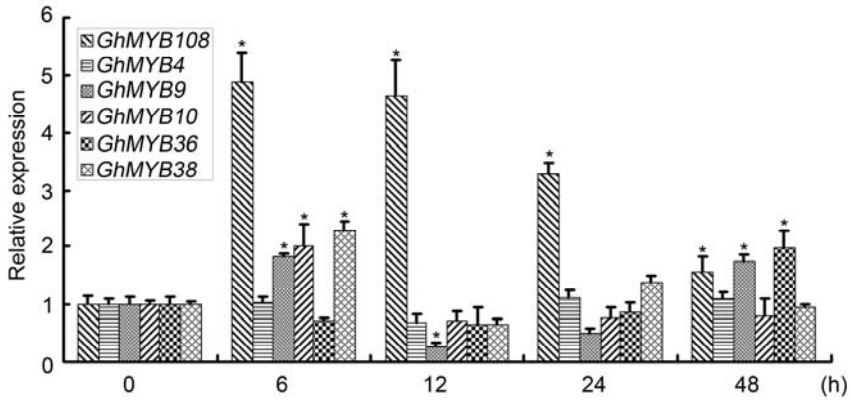
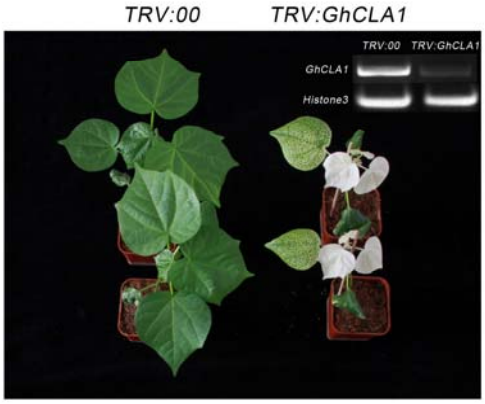
Supplementary Fig. S1. Multiple sequence alignments of *GhMYB108* and potential off-target *MYB* genes.

Sequence used for *GhMYB108* VIGS construct was marked with single line. CotAD_39363, CotAD_06007, CotAD_23926, CotAD_43649, CotAD_64321, CotAD_20091: potential off-target *MYB* genes.



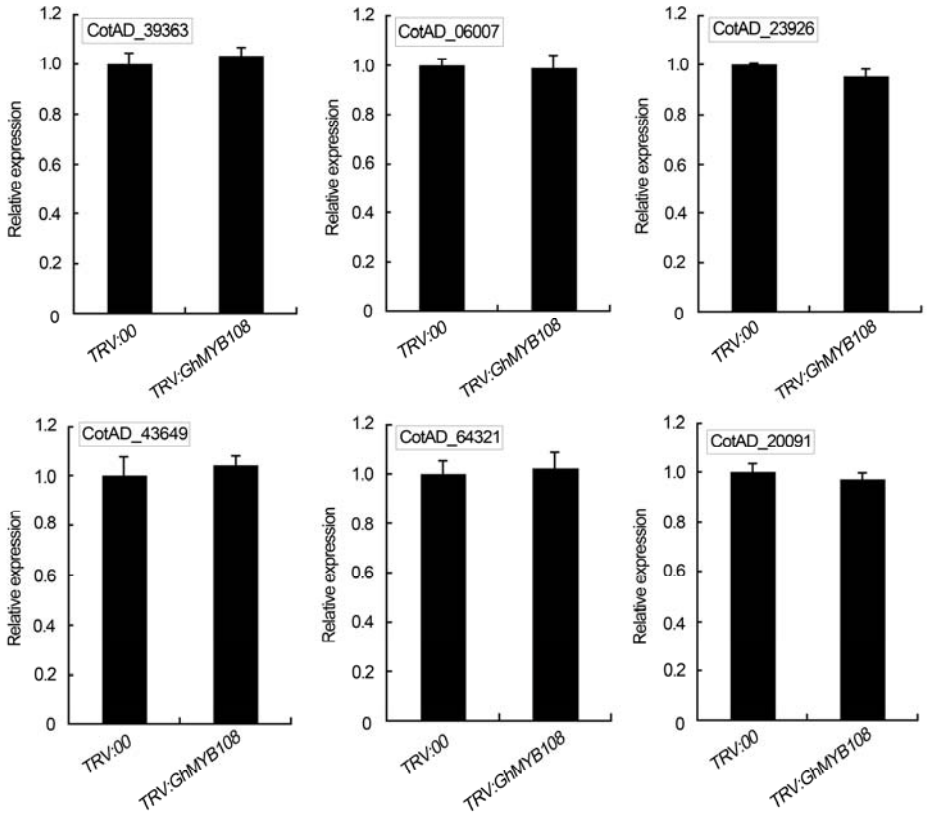
Supplementary Fig. S2. Expression pattern of *GhMYB* genes upon *V. dahliae* infection in cotton plant.

Expression of *GhMYB108*, *GhMYB4*, *GhMYB9*, *GhMYB10*, *GhMYB36*, and *GhMYB38* genes in cotton roots in response to *V. dahliae* infection. Error bars represent the SD of three biological replicates. Asterisks indicate statistically significant differences, as determined by Student's *t*-test (*$P < 0.05$).



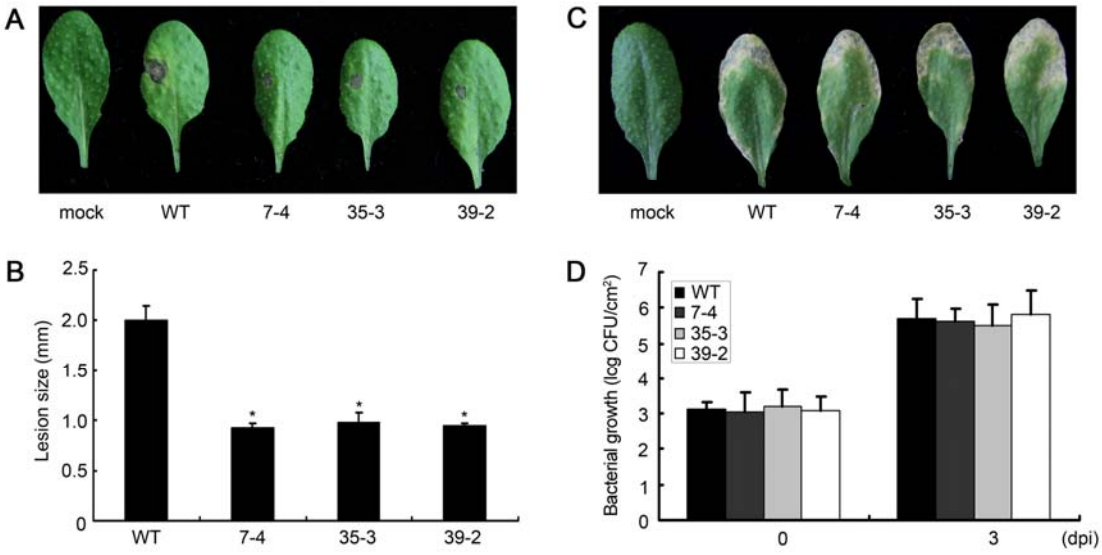
Supplementary Fig. S3. Photobleaching phenotype in *GhCLA1*-silenced cotton plants.

The *GhCLA1* gene was used as a positive control with a photobleaching phenotype after VIGS in cotton. Plants infiltrated with *Agrobacterium* containing empty vector (*TRV:00*) or pTRV2-GhCLA1 (*TRV2:GhCLA1*) showed different phenotypes in leaves. Photo was taken 14 days after VIGS. The inset indicated the expression levels of *GhCLA1* in control and *GhCLA1*-silenced cotton plants analyzed by RT-PCR. *Histone3* was used as an internal control.



Supplementary Fig. S4. qRT-PCR analysis of expression levels of six potential off-target *MYB* genes in control and *GhMYB108*-silenced plants.

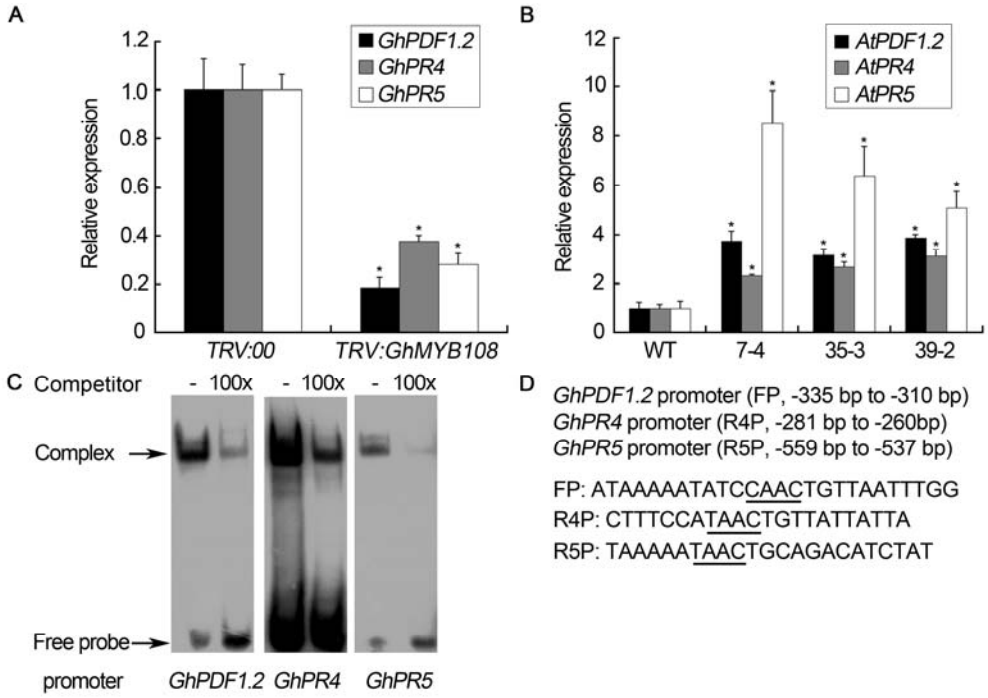
TRV:00: control plants; *TRV:GhMYB108*: *GhMYB108*-silenced plants. Error bars represent the SD of three biological replicates.



Supplementary Fig. S5. Disease symptoms of *GhMYB108*-overexpressing Arabidopsis plants inoculated with *B. cinerea* or *Pst* DC3000.

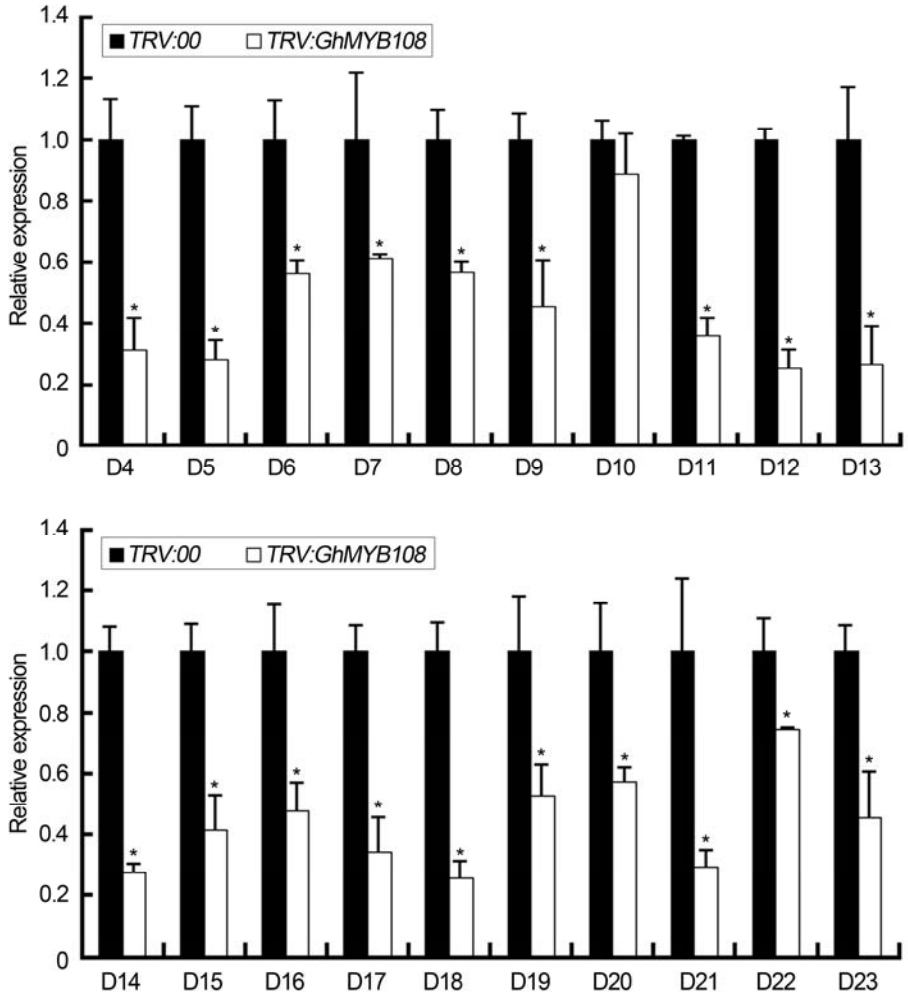
(A) Photographs of leaves 3 days post inoculation with *B. cinerea* between WT (wild type) and *GhMYB108* transgenic Arabidopsis lines (7-4, 35-3 and 39-2). (B) Lesion size measured at 3 days after *B. cinerea* inoculation. Error bars represent the SD (n = 25) of three biological replicates. Asterisks indicate statistically significant differences, as determined by Student's *t*-test (*$P < 0.05$). (C) Symptoms of WT and *GhMYB108* transgenic Arabidopsis lines infected with *Pst* DC3000. Photos were taken 3 days post inoculation. (D) Growth of *Pst* DC3000 in infected leaves of WT and *GhMYB108* transgenic plants. Error bars represent the SD (n = 20) of three biological replicates**.**

Supplementary Fig. S6. The Ca^{2+}-dependent mobility shift assay of GhCML11. GhCML11 proteins were separated on a 15% SDS-PAGE gel in the presence of Ca^{2+} or EGTA in sample buffers. Protein bands were visualized with Coomassie brilliant blue staining. M: molecular weight marker (kDa).



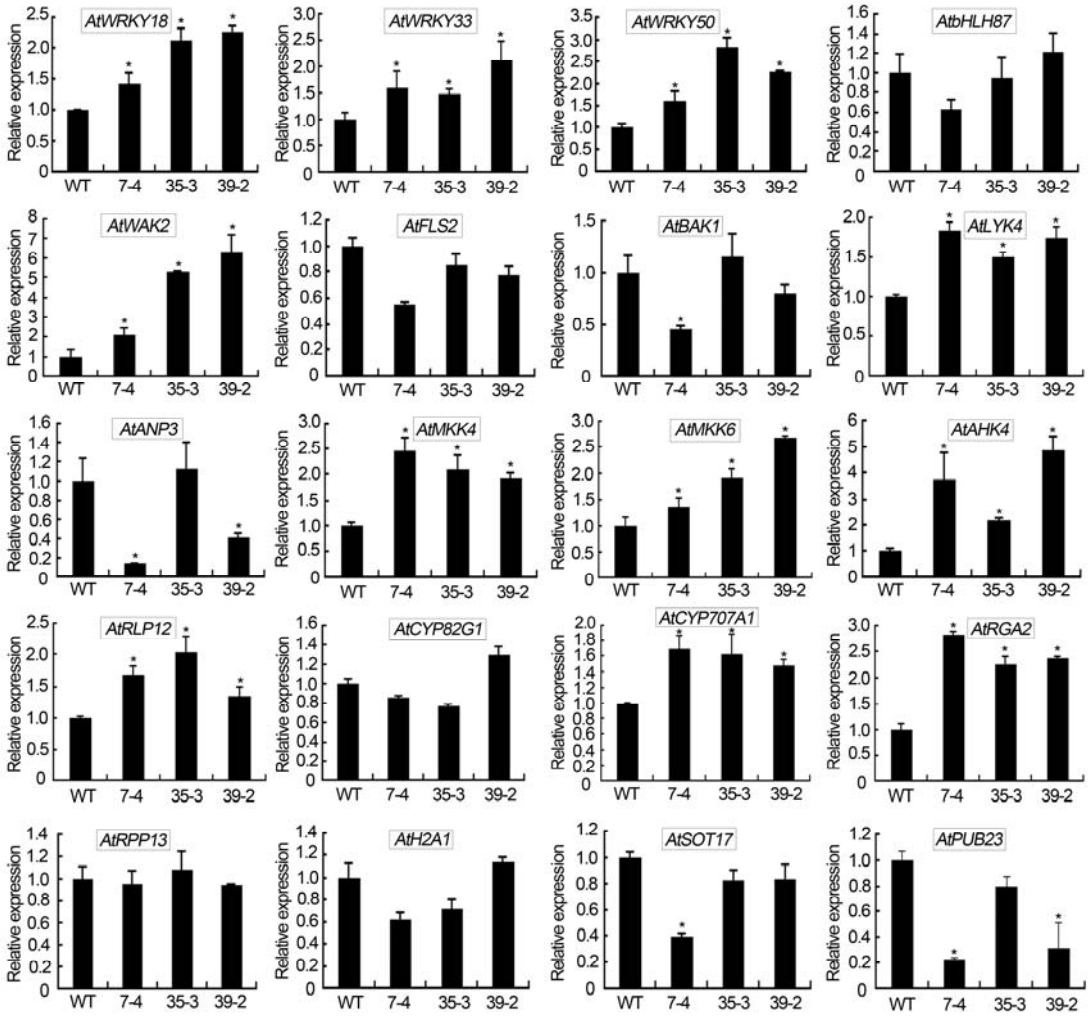
Supplementary Fig. S7. Expression of *PDF1.2*, *PR4*, and *PR5* genes in *GhMYB108*-silenced and *GhMYB108*-overexpressing plants and binding of GhMYB108 to their promoter sequences.

(A) Expression levels of *GhPDF1.2*, *GhPR4*, and *GhPR5* in control (*TRV:00*) and GhMYB108-silenced (*TRV:GhMYB108*) cotton plants. (B) Expression levels of *AtPDF1.2*, *AtPR4*, and *AtPR5* in WT (wild-type) and *GhMYB108* transgenic Arabidopsis plants (7-4, 35-3, and 39-2). Asterisks indicate statistically significant differences, as determined by Student's *t*-test (**P* < 0.05). (C) Binding of GhMYB108 to the promoter sequences of *GhPDF1.2*, *GhPR4*, and *GhPR5*. EMSA analysis was performed with the purified recombinant GhMYB108 proteins and DNA sequences containing the promoter region of *GhPDF1.2*, *GhPR4*, and *GhPR5* genes, respectively. Purified proteins were incubated with labeled DNA probes from corresponding genes in the absence or presence of 100-fold molar excess of unlabelled probes. (D) The promoter sequences used in EMSA. Numbers indicate positions relative to the translation start site of the corresponding gene. The underlined sequence indicates the core motif of MYB binding site.



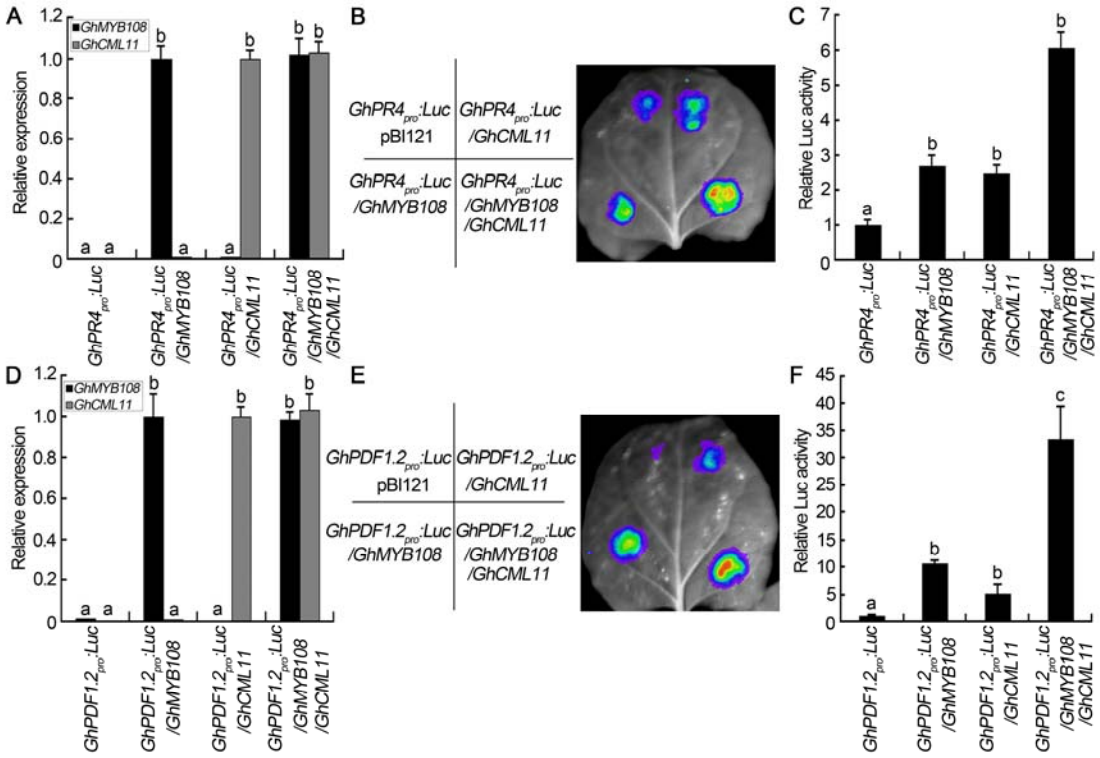
Supplementary Fig. S8. Verification of transcriptomic data in *GhMYB108*-silenced cotton plants.

The down-regulated defense-related genes from the transcriptomic data were verified by qRT-PCR. *TRV:00*: control plants; *TRV:GhMYB108*: *GhMYB108*-silenced plants. Error bars represent the SD of three biological replicates. Asterisks indicate significant differences, as determined by Student's *t*-test (*$P < 0.05$).



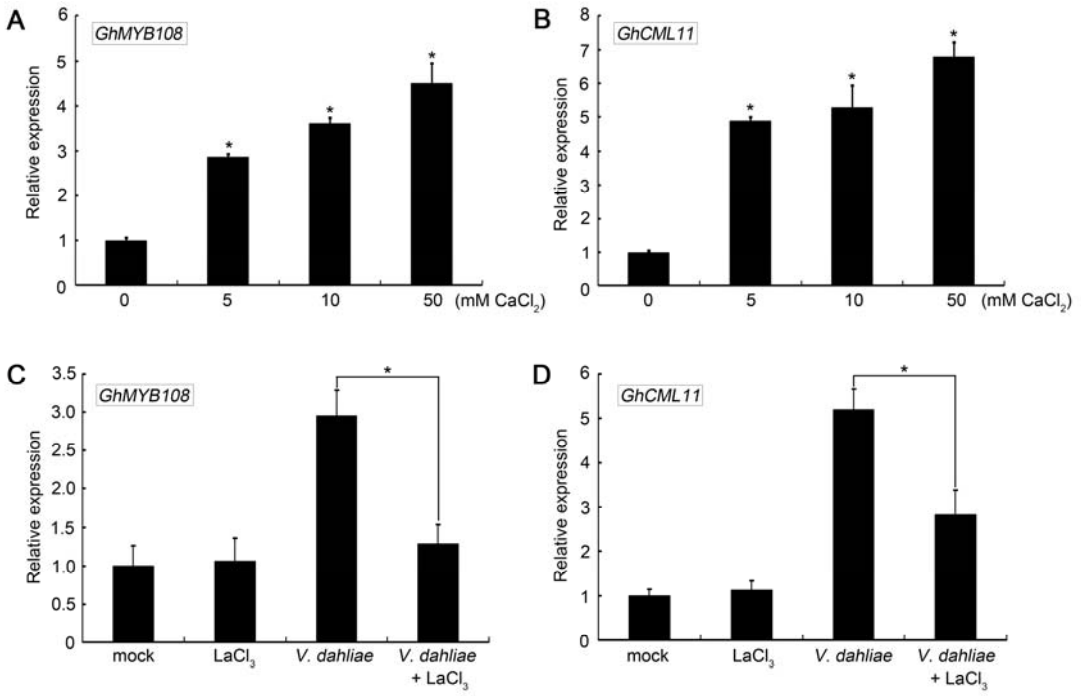
Supplementary Fig. S9. Expression levels of defense-related genes in *GhMYB108* transgenic Arabidopsis plants.

qRT-PCR analysis of expression levels of defense-related genes in *GhMYB108* transgenic Arabidopsis plants. WT: wild-type plants; 7-4, 35-3, 39-2: *GhMYB108* transgenic lines. Error bars represent the SD of three biological replicates. Asterisks indicate statistically significant differences, as determined by Student's *t*-test (*$P < 0.05$).



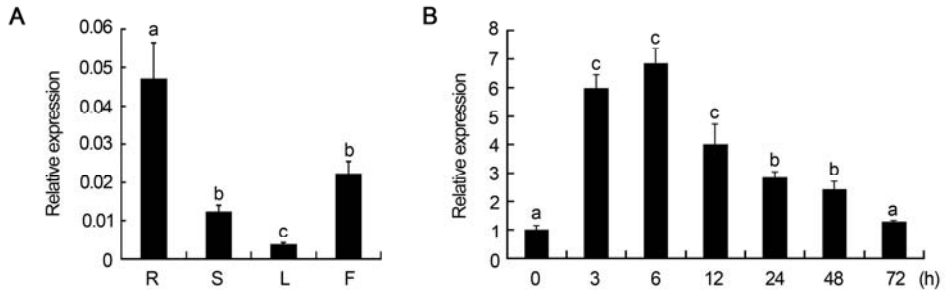
Supplementary Fig. S10. Transient expression analysis of GhCML11-enhanced transcriptional activation activity of GhMYB108.

(A and D) Expression levels of *GhMYB108* and *GhCML11* in tobacco leaves transformed with indicated constructs in (B) and (E). Different letters indicate significant differences at $P < 0.01$ (Student's *t*-test, $n \geq 15$, 3 biological repeats). (B and E) Luminescence signal on *N. benthamiana* leaves. Luminescence imaging was performed 48 h after co-infiltrated with *Agrobacterium* strains containing indicated constructs on the left panel. (C and F) Quantitative analysis of luminescence intensity in (B) and (E). Different letters indicate significant differences at $P < 0.05$ (Student's *t*-test, $n = 30$, 3 biological repeats).



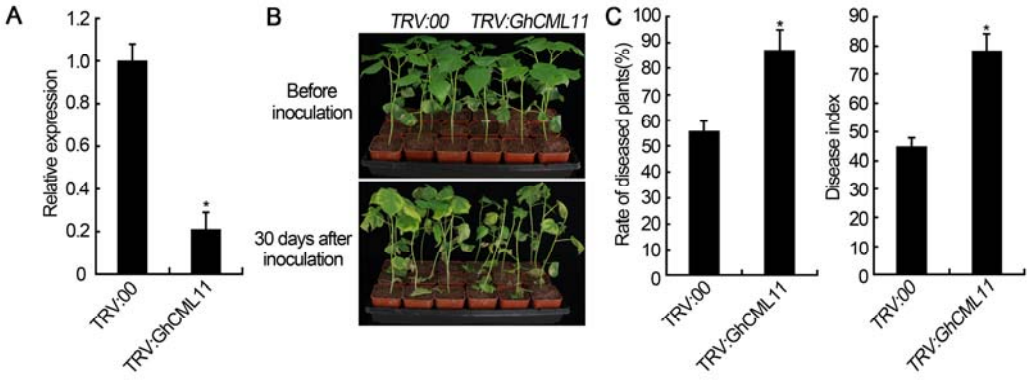
Supplementary Fig. S11. Effects of Ca^{2+} on the expression of *GhMYB108* and *GhCML11*.

(A and B) qRT-PCR analysis of expression levels of *GhMYB108* and *GhCML11* after treatment of cotton roots with different concentrations of $CaCl_2$. (C and D) qRT-PCR analysis of expression levels of *GhMYB108* and *GhCML11* after treatment with $LaCl_3$ before and after *V. dahliae* inoculation. $LaCl_3$, Ca^{2+} influx blocker. Error bars represent the SD of three biological replicates. Asterisks indicate statistically significant differences, as determined by Student's *t*-test (*$P < 0.05$).



Supplementary Fig. S12. Expression pattern of *GhCML11* in cotton plants.

(A) qRT-PCR analysis of *GhCML11* gene expression in root (R), stem (S), leaf (L), and flower (F) of cotton plants. Error bars represent the SD of three biological replicates. (B) Accumulation of *GhCML11* transcripts in cotton roots in response to *V. dahliae* infection. Error bars represent the SD of three biological replicates. Different letters indicate significant differences, as determined by Student's *t*-test ($P < 0.05$).



Supplementary Fig. S13. Increased susceptibility of *GhCML11*-silenced cotton plants to *V. dahliae*.

(A) Analysis of *GhCML11* expression levels. Total RNAs were extracted from leaves of cotton plants at 14 days post agroinfiltration and the expression level of *GhCML11* in VIGS plants was compared with that of control plants (*TRV:00*). Error bars represent the SD of three biological replicates. Asterisks indicate statistically significant differences, as determined by Student's *t*-test (*$P < 0.05$). (B) Disease symptom of control (*TRV:00*) and *GhCML11*-silenced (*TRV:GhCML11*) plants infected by *V. dahliae*. (C) Rate of diseased plants and disease index of the control and *GhCML11*-silenced plants. Error bars represent the SD of three biological replicates ($n \geq 30$). Asterisks indicate statistically significant differences, as determined by Student's *t*-test (*$P < 0.05$).

Supplementary Table S1. Primers used in this study.

Primer name	Sequence (5' to 3')
GhMYB4-qRT-F	AAGCGAGGAGAGAGAGAGCCTGGTG
GhMYB4-qRT-R	TTCGGTGAAAATGTTTTCTTCAATC
GhMYB9-qRT-F	ATTACCAGCAAACCCAACCAGAGTC
GhMYB9-qRT-R	ATTCCAAGATACCAGATTTCAAGCC
GhMYB10-qRT-F	TGATTCGTCACCCTCACCGGATCAG
GhMYB10-qRT-R	AGAAGAAGAGCAGAATTATTGATGG
GhMYB36-qRT-F	TCCTATGCAGCAGCACTTTCCGTTG
GhMYB36-qRT-R	CAGTACTGATATTCGTATCATGGCC
GhMYB38-qRT-F	ACGGGGAGTACAGTCATGGTACCGA
GhMYB38-qRT-R	TAATACAACAAAGTGCGAACTTTGG
GhMYB108-qRT-F	ACGTCATCAGACTCCCTTGACACCC
GhMYB108-qRT-R	ACCAACAAACCATTGCCATGCTCCT
GhMYB108-pBI121-F	CGGCTCTAGAATGGATGTTTACAAG
GhMYB108-pBI121-R	CCAGAGCTCGATCCCATCACGAAGC
GhMYB108-5-race-R	TCAACTAAACGGGGGATCCAAACGTAACGC
GhMYB108-3-race-F	TCAACCTTCTACCACCACCAAAACCACCTA
GhMYB108-mbp-F	CTAGTCGACATGGATGTTTACAAGAGAGG
GhMYB108-mbp-R	GACAAGCTTTTAGATCCCATCACGAAGC
GhMYB108-gfp-F	CTAGTCGACATGGATGTTTACAAGAGAGG
GhMYB108-gfp-R	CTTGGTACCGATCCCATCACGAAGCTGC
GhMYB108ΔC-gfp-F	ACTCGTCGACATGGATGTTTACAAGAGAG
GhMYB108ΔC-gfp-R	CTACAAGCTTTTAAACTAAACGGGGGATC
GhMYB108ΔN-gfp-F	ACTCGTCGACATGAACGGATCCGTGCTTC
GhMYB108ΔN-gfp-R	CATCAAGCTTTTAGATCCCATCACGAAGC
GhMYB108-vigs-F	CGACGAATTCTTGATTCAGCAAC
GhMYB108-vigs -R	ACTAGGTACCTTCATCTCTGCCC
GhMYB108-dlr-F	CGGCTCTAGAATGGATGTTTACAAGAGAGG
GhMYB108-dlr-R	CGATGTCGACGATCCCATCACGAAGCTGC
GhMYB108-BD-F	CGACCATATGATGGATGTTTACAAGAGAG
GhMYB108-BD-R	CTCAGTCGACTTAGATCCCATCACGAAGC
GhMYB108-AD-F	CGACCATATGATGGATGTTTACAAGAGAG
GhMYB108-AD-R	CTTCGGATCCTTAGATCCCATCACGAAGC
GhCML11-AD-F	CGACCATATGATGGGTGATATACTAACTC
GhCML11-AD-R	CATAGGATCCTCATCCAACGGTCGTCATC
GhCML11-BD-F	CGACCATATGATGGGTGATATACTAACTC
GhCML11-BD-R	CTACGTCGACTCATCCAACGGTCGTCATC
GhMYB108-NLuc-F	CCGAGGTACCATGGATGTTTACAAGAGAG
GhMYB108-NLuc-R	CATGGTCGACGATCCCATCACGAAGCTGC
GhMYB108-pro-R1	GTGGATATTGACATGCGCCTTAAGC
GhMYB108-pro-R2	CATCCATTTCTCAACTTAAAACAGG
ITS1-F	AAAGTTTTAATGGTTCGCTAAGA
ST-VE1-R	CTTGGTCATTTAGAGGAAGTAA

GhCML11-CLuc-R	CATGGTCGACTCATCCAACGGTCGTCATC
GhCML11-mCherry-F	CGACGGATCCATGGGTGATATACTAACTC
GhCML11-mCherry-R	CATCGTCGACTCCAACGGTCGTCATCATT
GhCML11-gst-F	CATAGGATCCATGGCGGACCAGCTTACCG
GhCML11-gst-R	CGCCGTCGACTTAAAGAAAAATGCATTTACG
GhCML11-vigs-F	CTACGGATCCCCAAGGTACCAAATTGA
GhCML11-vigs-R	CATAGGTACCACTTTGGGAAGTTTAAG
GhCML11-qRT-F	ATTTCCTTGCATTGAAACTCC
GhCML11-qRT-R	GTTTTGTTTGTTTTGGTGAGC
$GhCML11_{pro}$-pGWB435-F	TCCAGCTCACCAAAACAAACAAAAC
$GhCML11_{pro}$-pGWB435-R	CGAGGGTCTCAAGAAGGTACAGCCT
$GhPDF1.2_{pro}$-pGWB435-F	ATTCCTCGAAAAATAATAATCTAGAAAGA
$GhPDF1.2_{pro}$-pGWB435-R	TAAATATTATTATAACCGAGCGAATGATTGAAA
$GhPR4_{pro}$-pGWB435-F	TTTGGGGGTCCAAAATGAAGCCACC
$GhPR4_{pro}$-pGWB435-R	TTCAGTTTTGTGTAATTTTCATGCT
$GhPR5_{pro}$-pGWB435-F	ATCAAATATAATCCTTATTAATAATTCAAT
$GhPR5_{pro}$-pGWB435-R	GGTTGGTTTTTACTTGGTGATTTGTTCATA
GhPR4-qRT-F	GCTACCTACCATTACTACAACCCTG
GhPR4-qRT-R	TTGCTGCACTGATCCACAATTCTTA
GhPR5-qRT-F	AGCCGCCTCAGCGTTTATTTTTAAA
GhPR5-qRT-R	TACGAGCCATGGCTGTGCCAGCAG
GhPDF1.2-qRT-F	CTGTGGTAGCGGATGGTGATAAG
GhPDF1.2-qRT-R	GTGCAGACGCATTTGCGAAGGAA
Histone3-F	GCCAAGCGTGTCACAATTATGC
Histone3-R	ACATCACATTGAACCTACCACTACC
AtPR4-qRT-F	GAAGAACACAAGAACAAATGCTGCA
AtPR4-qRT-R	GTAGACCGATCGATATTGACCTCAA
AtPR5-qRT-F	GCTACGCTTATGACGACGAAACGAG
AtPR5-qRT-R	AAATCAGCTGAGTGTAACAACTGAC
AtPDF1.2-qRT-F	GGAGCCAAACATGGATCATGCAACT
AtPDF1.2-qRT-R	TGTAACAACAACGGGAAAATAAACA
AtEF-1α-F	TTGGCGGCACCCTTAGCTGGATCA
AtEF-1α -R	ATGCCCCAGGACATCGTGATTTCAT
GhEHD2-qRT-F	GGCAAAGCTAAAGCTCAAC
GhEHD2-qRT-R	CTGGGATTTCATATCCTAAC
GhPBP1-qRT-F	TTGGAAACCTCAACTCACC
GhPBP1-qRT-R	TGATGGAGGAATCGCAGAC
GhNRT1.2-qRT-F	ACCTTACCCGTGACTTTCC
GhNRT1.2-qRT-R	GTGCATCGCCTTCCTCGTA
GhRBOHF-qRT-F	AGCAGCAATGAATCAACCA
GhRBOHF-qRT-R	GTGCATCGCCTTCCTCGTA
GhIQD1-qRT-F	ATACAATGCCGACTTCAGA
GhIQD1-qRT-R	GTGGATACAGTGGCCGAGA
GhIQD14-qRT-F	AAGGCATGGAGAAACCAAT

GhIQD14-qRT-R	AAGCATCTTTATGAGGCAC
GhIQD31-qRT-F	TGATTTGGCTGTGGCTCCTC
GhIQD31-qRT-R	CGCCGATTGTTCTTGCTTTAT
GhCLA1-vigs-F	GCTCGAATTCCACAACATCGATGAT
GhCLA1-vigs-R	CCGAGAGCTCATGATGAGTAGATTGCACAA
GhCIPK6-qRT-F	AAAACCCATCTTTACTCCAT
GhCIPK6-qRT-R	TGATCTGCTCCATCATCCC
CotAD_39363-qRT-F	CGGGACTCAAGTTTCACCAAT
CotAD_39363- qRT -R	CATCACCATCACCTACCCAAT
CotAD_06007- qRT -F	CAATAATGGGTTCCAGGTTAC
CotAD_06007- qRT -R	ACATGGGATAATTGTTGGTCT
CotAD_23926- qRT -F	TACCCGAATAGCTTACAGAAC
CotAD_23926- qRT -R	CATATCATCCTTGTCATCATAAA
CotAD_43649- qRT -F	CTTCGTCGGAAACCCAAGTCA
CotAD_43649- qRT -R	AAGCTGCTGTTGTAAGAACCAA
CotAD_64321- qRT -F	CTTCGTCGGAAATCCAAGTCA
CotAD_64321- qRT -R	AAGCTGCTGTTGTAAGAACCA
CotAD_20091- qRT -F	TCATAACCCTAATCCAAACTG
CotAD_20091- qRT -R	TTGCTGCTGTAAGAAGTAAA
D4-qRT-F	CACAACCATCTTCCTCCTT
D4-qRT-R	GTAGCCATCTGTTCCACCA
D5-qRT-F	AGTCAGCCTAACAATACAATG
D5-qRT-R	AGACAGTAATCCGTCCAAA
D6-qRT-F	TATGGGAAGAAATGGGTGAA
D6-qRT-R	GCGAGATAGTAACGGTAAAA
D7-qRT-F	CCAGAGGCCATTGCACAAA
D7-qRT-R	TGCTCCCACCAGGAACCAG
D8-qRT-F	TTGACCCTGAGTATTTCCA
D8-qRT-R	GCCATTGCCGTTACCATTT
D9-qRT-F	GTGGCTAATCATCACTGCA
D9-qRT-R	GTGGGAATAGACCCGACAG
D10-qRT-F	GCTAATCCAGGTGGCTCTG
D10-qRT-R	TGGGCTTGGTTGAACTCTT
D11-qRT-F	AGCACTTGATTGAACCCTC
D11-qRT-R	ATCCCATGTCGATGAACTA
D12-qRT-F	CCGAGACGACGACACCCAT
D12-qRT-R	CGAACCGATCCAACAAGCT
D13-qRT-F	GTAGGCTGGCGGAACTAAC
D13-qRT-R	CATAAAGGCGAGACGAAGG
D14-qRT-F	ATGTGCTATTGGACGTTTC
D14-qRT-R	ATGCTCTTTCTTTAGGGTT
D15-qRT-F	CAGGCAAATGAACAGATGA
D15-qRT-R	TGCTACAGCCAGGTAAAGA
D16-qRT-F	GTTTATGTTTGGGCTGCTA

D16-qRT-R	GAAATGGTGCCTGTGAGAT
D17-qRT-F	AATACCTCCCATAATCACCA
D17-qRT-R	ATTGGCTCTTTCCCACCTA
D18-qRT-F	TTTGATCCCTCAAGATTTG
D18-qRT-R	GCTGTTACTACCCACCATT
D19-qRT-F	CACTTCACTTATTTCGTCTACC
D19-qRT-R	ATTCTACTCTTGCCCACCA
D20-qRT-F	CTGGAAAGACTACCAAACC
D20-qRT-R	CGATGTATCACCAAATGCT
D21-qRT-F	CCCTCACATTCACAAGTCT
D21-qRT-R	ATCCCTACCCTAAACAAAG
D22-qRT-F	TCATCGGTTATCCTTTCTC
D22-qRT-R	AGCAGCCATTTCAGGTGTC
D23-qRT-F	TGCGAGATGATACTAACGG
AtWRKY18-qRT-F	TAGCGACATACGAAGGGAC
AtWRKY18-qRT-R	ATAGCAGCAGCAAGAGCAG
AtWRKY33-qRT-F	TGCTATTGCTGGTCACTCC
AtWRKY33-qRT-R	AGGTCTCCTCGTTTGGTTC
AtWRKY50-qRT-F	GTATGGGAAGAAGATGGTG
AtWRKY50-qRT-R	CTTGAGTGATTGTGGGAAC
AtbHLH87-qRT-F	ACTTCTGTGACAAGGGTGG
AtbHLH87-qRT-R	GCAATTATCTTACGCTATCT
AtWAK2-qRT-F	CCGACAATGACCGAAGTAG
AtWAK2-qRT-R	GTTTCTGAGGGATAACGAC
AtFLS2-qRT-F	AACGACCCTTTAGGAGTATTA
AtFLS2-qRT-R	TATGGCTGGAGACAGAACA
AtBAK1-qRT-F	CTGGGTGAAAGGGTTGTTA
AtBAK1-qRT-R	GTTGGGTAGTTGAAATCTTGTCT
AtLYK4-qRT-F	GAGTTGCGGTTCTTGAGCT
AtLYK4-qRT-R	ACAGATGGACGCGAGTTAA
AtANP3-qRT-F	AGATTAACTCTAGTATCCGTAGC
AtANP3-qRT-R	GACCCTGAGTCTTCTCCTT
AtMKK4-qRT-F	GTCGCCGTCCTGATCTTAC
AtMKK4-qRT-R	ATACCGTTCCACCTGCTCC
AtMKK6-qRT-F	CTTGGCAGCAATAGTAGAG
AtMKK6-qRT-R	AACAGGTGGTTCCAGAGTG
AtAHK4-qRT-F	GATGGACGGATTTGAAGCA
AtAHK4-qRT-R	TACGACGAAGGTGAGATAGGA
AtRLP12-qRT-F	CTCCCTCCTTGTTCACTCT
AtRLP12-qRT-R	TGACTCCATTCCAAAGACA
AtCYP82G1-qRT-F	GCCTCTATTCGGACACCTC
AtCYP82G1-qRT-R	TGCTGTAGCCAAGTCGTTG
AtCYP707A1-qRT-F	TTCATCATCTCACCACCAA
AtCYP707A1-qRT-R	AAGGCAATTCTGTCATTCTAC

AtRGA2-qRT-F	TGCTATTGCTGGTCACTCC
AtRGA2-qRT-R	GAGGAGCATTCAGCTACGA
AtRPP13-qRT-F	GGATAGTAGAAGAAGGGTCG
AtRPP13-qRT-R	AAATTGAACATCGGGAATG
AtH2A1-qRT-F	AGTTGGCGATTAGAGGAGA
AtH2A1-qRT-R	GGATAAAGGAAAATGAGTC
AtSOT17-qRT-F	ACTGGCTTTCTTTCTTCAA
AtSOT17-qRT-R	GTTCACCACATATTCCTCC
AtPUB23-qRT-F	AAGCGATAGAGCGGTTAGG
AtPUB23-qRT-R	TCAGCAGGGATATGCAAGA

Supplementary Table S3. Defense-related genes down-regulated in *GhMYB108*-silenced cotton plants.

Custom ID	Gene ID	Ratio	Annotation
D1	Unigene24024	-3.219552634	Defensin-like protein 16 (PDF1.2)
D2	Unigene39636	-2.144169535	Pathogenesis-related protein PR-4A
D3	Unigene24561	-1.109232546	Pathogenesis-related protein 5
D4	CL11789	-1.392639921	WRKY transcription factor 18
D5	CL5469	-1.103135385	Probable WRKY transcription factor 33
D6	Unigene14461	-1.22437439	Probable WRKY transcription factor 50
D7	CL4272	-1.496137059	Transcription factor bHLH87
D8	CL3156	-2.951792885	Wall-associated receptor kinase 2
D9	CL5714	-1.660371486	LRR receptor-like serine/threonine-protein kinase FLS2
D10	Unigene13686	-1.236825379	BRASSINOSTEROID INSENSITIVE 1-associated receptor kinase 1(BAK1)
D11	Unigene11352	-1.017808689	LysM domain receptor-like kinase 4
D12	CL10768	-1.206741829	Mitogen-activated protein kinase kinase kinase 3
D13	CL6810	-1.25759391	Mitogen-activated protein kinase kinase 4
D14	Unigene3343	-1.257265737	Mitogen-activated protein kinase kinase 6
D15	Unigene42675	-1.363014048	Histidine kinase 4
D16	CL2475	-6.764145213	Receptor-like protein 12
D17	CL9316	-2.240225367	Cytochrome P450 82G1
D18	CL4312	-2.189863033	Abscisic acid 8'-hydroxylase1 (CYP707A1)
D19	Unigene27837	-2.533284106	Disease resistance protein RGA2
D20	Unigene11468	-1.469416175	Disease resistance protein RPP13
D21	Unigene14161	-1.807599783	Histone H2A variant 1
D22	Unigene15182	-1.668735646	Cytosolic sulfotransferase 17
D23	CL1628	-1.009230557	E3 ubiquitin-protein ligase PUB23