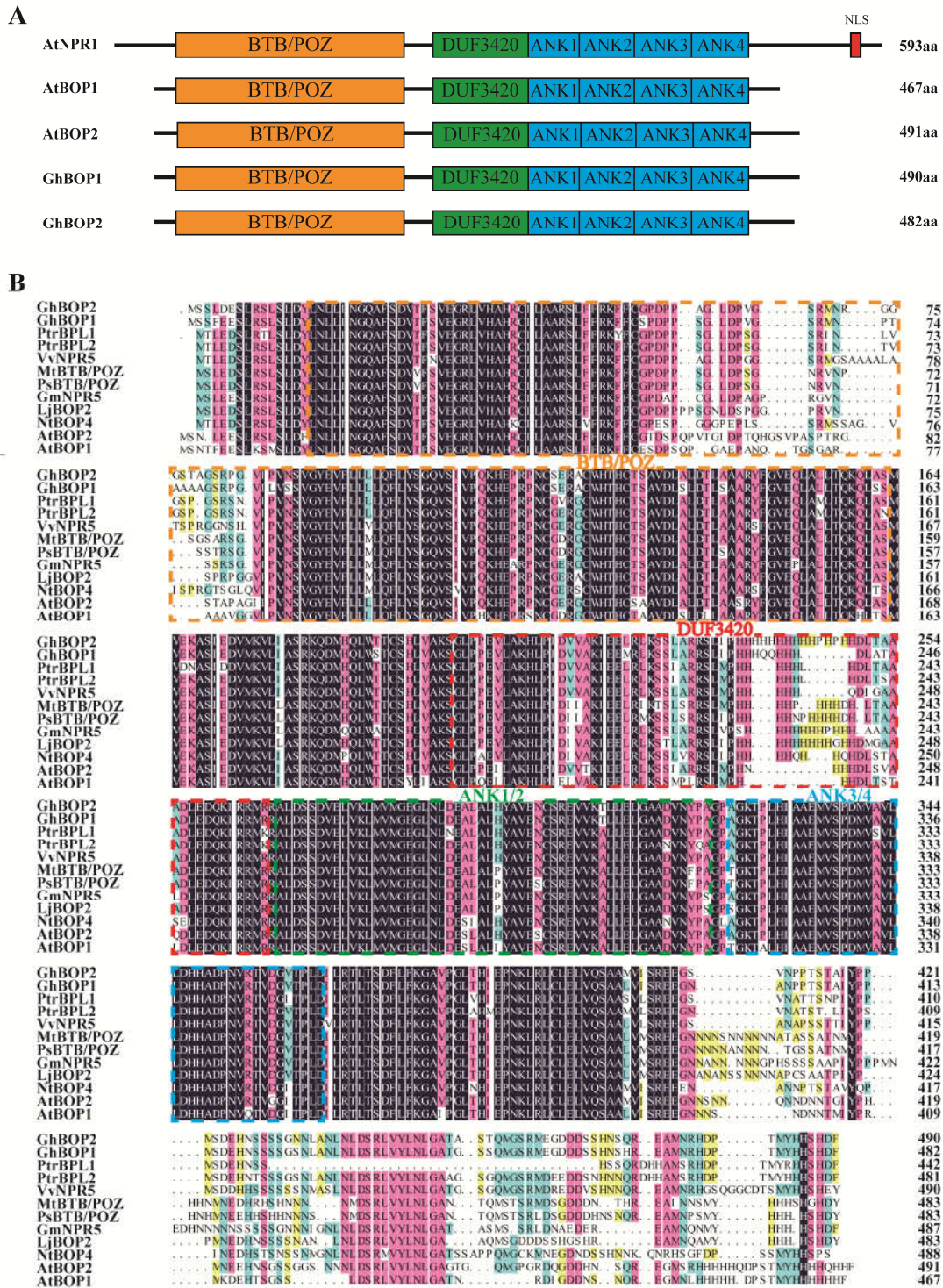


1 Supplementary Information

2

Supplementary Figure 1



3

4 Supplementary Figure 1. Domain structures of BOPs and NPR1 and amino acid
5 sequence analysis of BOPs from different plant species.

6 (A) Structural drawing of BOPs from *G. hirsutum* and *A. thalaisana* compared with AtNPR1.

7 BTB/POZ domain (Pfam: 00651), DUF3420 domain (Pfam: 11900), Blue, ANK domain

8 (Pfam: 00023) and NLS (Nuclear localization signal) were indicated in orange, green, blue
9 and red, respectively.

10 (B) Amino acid alignment of BOP proteins from *G. hirsutum* and other species. The complete
11 amino acid sequences of BOPs were acquired from NCBI database and performed on
12 DNAMAN 7.0. The conserved domain of BTB/POZ, DUF3420, ANK1/2 and ANK3/4 was
13 noted in dotted line frame with orange, red, green and blue, respectively.

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Supplementary Figure 2

GhBOP1_At	ATGAGTAGCTTTGAGGAGTCTTAAGATCTCTCCCTGGACTACCTCAATCTCCTCATCAATGGCCAAGCTTTC	75
GhBOP1_Dt	ATGAGTAGCTTTGAGGAGTCTTAAGATCTCTCCCTGGACTACCTCAATCTCCTCATCAATGGCCAAGCTTTC	75
GhBOP1_At	TCCGATGTAACCTTCAGTGTAGAGGGTCGGTTAGTTCATGCCACAGGTGATTTTAGCAGCCAGGAGCCTTTTC	150
GhBOP1_Dt	TCCGATGTAACCTTCAGTGTAGAGGGTCGGTTAGTTCATGCCACAGGTGATTTTAGCAGCCAGGAGCCTTTTC	150
GhBOP1_At	TTTAGGAAATCTTTTGCTCACCTGATCCTCCGCTCGGGTTAGACCCGGTTGGTTCAAGGATGAACCCAACAGCA	225
GhBOP1_Dt	TTTAGGAAATCTTTTGCTCACCTGATCCTCCGCTCGGGTTAGACCCGGTTGGTTCAAGGATGAACCCAACAGCA	225
GhBOP1_At	GCAGCAGCAGGATCAAGGCCGGTGTATTCTAGTGAGCTCAGTGGGATATGAGGTGTTCTTGCTGCTGTTACAG	300
GhBOP1_Dt	GCAGCAGCAGGATCAAGGCCGGTGTATTCTAGTGAGCTCAGTGGGATATGAGGTGTTCTTGCTGCTGTTACAG	300
GhBOP1_At	TTCTTGATAGTGGCCAAGTCTCTATTGTGCCTAAAAGCAGCAGCCGAGGCCAATTGTAGTGAAGAGCGTGT	375
GhBOP1_Dt	TTCTTGATAGTGGCCAAGTCTCTATTGTGCCTAAAAGCAGCAGCCGAGGCCAATTGTAGTGAAGAGCGTGT	375
GhBOP1_At	TGGCATAACACATTGCACCTCTGCCGTTGATCTTCTCTTGATACTCTTCTGCCGCTAGATACTTTGGTGTGAA	450
GhBOP1_Dt	TGGCATAACACATTGCACCTCTGCCGTTGATCTTCTCTTGATACTCTTCTGCCGCTAGATACTTTGGTGTGAA	450
GhBOP1_At	CAGCTTGCATTGCTTACTCAGAAACAATTATCCAGCATGGTCGAGAAGGCCCAATTGAAGATGTTATGAAAGTA	525
GhBOP1_Dt	CAGCTTGCATTGCTTACTCAGAAACAATTATCCAGCATGGTCGAGAAGGCCCAATTGAAGATGTTATGAAAGTA	525
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GhBOP1_Dt	CTAATAGCTTCAAGAAAGCAAGACATGCACCAACTTTGGTCTACTTGTCCACCTAGTGGCCAATCAGGCCTA	600
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GhBOP1_Dt	CCACCAGAAGTTCGCGCAAGCATCTTCCCATCGATGTGGTTGCCAAAATGAGGAGATGCGTCTCAAGTCATCC	675
GhBOP1_At	CTTGCTCGAGCTCCCTCATCCCTCATCATCATCAGCAGCATCACCATGATCTTGCTACGGCCGCTCATCTTGAG	750
GhBOP1_Dt	CTTGCTCGAGCTCCCTCATCCCTCATCATCATCAGCAGCATCACCATGATCTTGCTACGGCCGCTCATCTTGAG	750
GhBOP1_At	GACCAAAAGATTTCGTAGGATGAGAAGGGCATTAGACTCATCGGATGTTGAACCTGTTAAGCTCATGGTCATGGGA	825
GhBOP1_Dt	GACCAAAAGATTTCGTAGGATGAGAAGGGCATTAGACTCATCGGATGTTGAACCTGTTAAGCTCATGGTCATGGGA	825
GhBOP1_At	GAGGGTCTTAATCTTGATGAAGCATTGGCTTTACACTATGCTGTGAGAACTGCAGCCGGGAAGTGGTTAAGACG	900
GhBOP1_Dt	GAGGGTCTTAATCTTGATGAAGCATTGGCTTTACACTATGCTGTGAGAACTGCAGCCGGGAAGTGGTTAAGACG	900
GhBOP1_At	TTGTTAGAGCTTTGGGCAGCCGATGTTAACTACCCGGCCGGCCCTGCAGGTAAMACCCCACTTCATATGCGGGC	975
GhBOP1_Dt	TTGTTAGAGCTTTGGGCAGCCGATGTTAACTACCCGGCCGGCCCTGCAGGTAAMACCCCACTTCATATGCGGGC	975
GhBOP1_At	GAAATGGTATCACCAGATATGGTTGCAGTGTCTTAGATCACCACGGGACCCTAATGTAAGAACCGTTGATGGG	1050
GhBOP1_Dt	GAAATGGTATCACCAGATATGGTTGCAGTGTCTTAGATCACCACGGGACCCTAATGTAAGAACCGTTGATGGG	1050
GhBOP1_At	GTGACTCCTTTGGACATCTTCGAACACTAACCTCTGATTTCTTGTTCAAAGGTGCGGTGCCGGGGCTTACTCAC	1125
GhBOP1_Dt	GTGACTCCTTTGGACATCTTCGAACACTAACCTCTGATTTCTTGTTCAAAGGTGCGGTGCCGGGGCTTACTCAC	1125
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GhBOP1_Dt	ATTGAACCGAATAAGCTTAGGCTATGTCTTGAGCTTGTTCAATCCGCAGCTTTGGTTATCTCGCGTGAAGAAGGA	1200
GhBOP1_At	AACGCAAAACCACCAACTTCAACTGCCATTTACCCACCAATGAGTGTGAACATAACAGCAGTAGCAGTGGAAAGC	1275
GhBOP1_Dt	AACGCAAAACCACCAACTTCAACTGCCATTTACCCACCAATGAGTGTGAACATAACAGCAGTAGCAGTGGAAAGC	1275
GhBOP1_At	AATCTTGCTAACCTTAATCTGGATTCAAGGTTGGTTTATCTCAATCTAGGTGCTACAGGTTCAAATCAAATGGGT	1350
GhBOP1_Dt	AATCTTGCTAACCTTAATCTGGATTCAAGGTTGGTTTATCTCAATCTAGGTGCTACAGGTTCAAATCAAATGGGT	1350
GhBOP1_At	TCGAGAATGGAGGGTATGATGATAGCAGCCACAACAGCCACAGAGAAGCCATGAACCGACATGACCCAAACATG	1425
GhBOP1_Dt	TCGAGAATGGAGGGTATGATGATAGCAGCCACAACAGCCACAGAGAAGCCATGAACCGACATGACCCAAACATG	1425
GhBOP1_At	TACCATCACTCTCATGATTTCTAG	1449
GhBOP1_Dt	TACCATCACTCTCATGATTTCTAG	1449

17 **Supplementary Figure 2. Alignment of CDS sequences between *GhBOP1* at At and Dt**
 18 **subgenome.** The red asterisks indicate the mismatched nucleotides.

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Supplementary Figure 3

GhBOP1_At	MSSFEESLRSLSDYLNLLINGQAFSDVTFVSEGRVLAHRCILAARSLFFRKFCCSPDPPSGLDPVGSRMNPTA	75
GhBOP1_Dt	MSSFEESLRSLSDYLNLLINGQAFSDVTFVSEGRVLAHRCILAARSLFFRKFCCSPDPPSGLDPVGSRMNPTA	75
GhBOP1_At	AAAGSRPGVILVSSVGYEVFLLLLQFLYSGQVSIVPQKHEPRPNCSEACWHTHCTSAVDLSLDTLSAARYFGVE	150
GhBOP1_Dt	AAAGSRPGVILVSSVGYEVFLLLLQFLYSGQVSIVPQKHEPRPNCSEACWHTHCTSAVDLSLDTLSAARYFGVE	150
GhBOP1_At	QLALLTQKQLSSMVEKASIEDVMKVLIASRKQDMHQLWSTCSHLVAKSGLPPEVLAKHLPIDVVAKTEEMRLKSS	225
GhBOP1_Dt	QLALLTQKQLSSMVEKASIEDVMKVLIASRKQDMHQLWSTCSHLVAKSGLPPEVLAKHLPIDVVAKTEEMRLKSS	225
GhBOP1_At	LARRSLIPHHHQHHHDLATAADLE [*] EDQKIRRMRRALDSSDVELVKLMVMGEGLNDEALALHYAVENC [*] SREVVK [*] T	300
GhBOP1_Dt	LARRSLIPHHHQHHHDLATAADLE [*] EDQKIRRMRRALDSSDVELVKLMVMGEGLNDEALALHYAVENC [*] SREVVK [*] T	300
GhBOP1_At	LLELGAADVNYAPAGPAGKTPLHTAAEMVSPDMVAVLLDHHADPNVRTVDGVTPLDLRLTSDFLFKGAVPGLTH	375
GhBOP1_Dt	LLELGAADVNYAPAGPAGKTPLHTAAEMVSPDMVAVLLDHHADPNVRTVDGVTPLDLRLTSDFLFKGAVPGLTH	375
GhBOP1_At	TEPNKLRCLCELVQSAALVISREEGNANPPTSTAI [*] YPPMSDEHNSSSSGSNLANLNLDSRLVYLNLGATGSS [*] QMG	450
GhBOP1_Dt	TEPNKLRCLCELVQSAALVISREEGNANPPTSTAV [*] YPPMSDEHNSSSSGSNLANLNLDSRLVYLNLGATGSS [*] QMG	450
GhBOP1_At	SRMEGDDSSSHNSHREAMNRHDP [*] TMYHHSHDF	482
GhBOP1_Dt	SRMEGDDSSSHNSHREAMNRHDP [*] TMYHHSHDF	482

22 **Supplementary Figure 3. Alignment of amino acid sequences between *GhBOP1* at At**
 23 **and Dt subgenome. The red asterisks indicate the mismatched amino acids.**

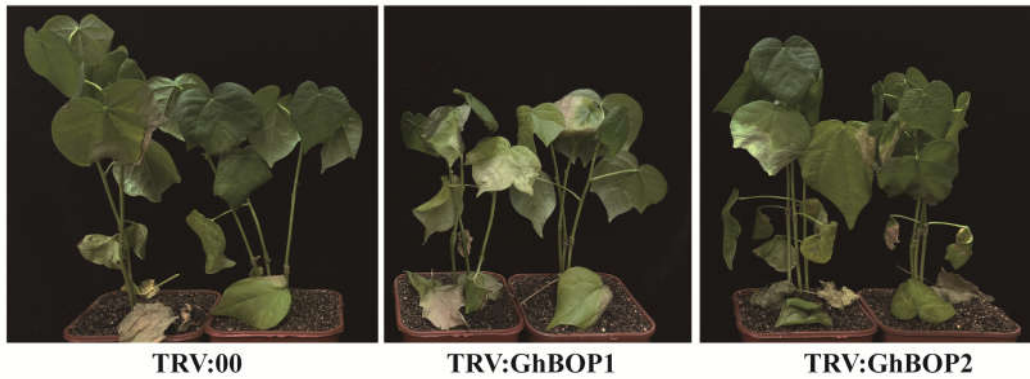
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25

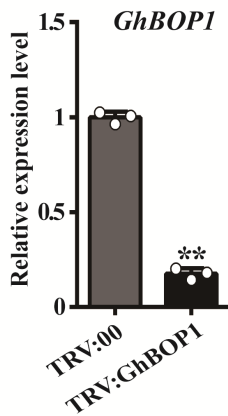
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Supplementary Figure 4

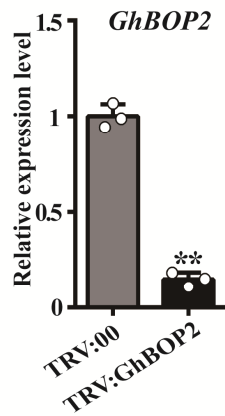
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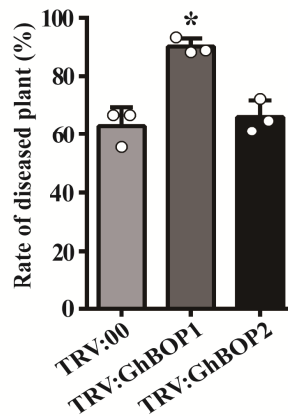
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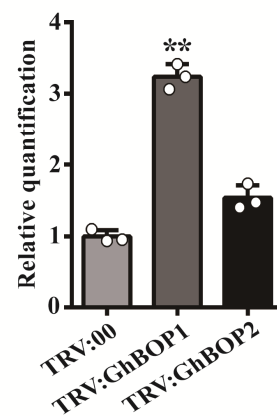
C



D



E



27

28 **Supplementary Figure 4. *GhBOP1*-silenced plants decreased the resistance to *V. dahliae*.**

29 (A) Disease symptoms of TRV:00, TRV:GhBOP1 and TRV:GhBOP2 plants inoculated with *V.*

30 *dahliae*.

31 (B) Relative expression levels of *GhBOP1* in roots of TRV:00 and TRV:GhBOP1 plants. Error

32 bars represent the SD of three biological replicates. Asterisks indicate statistically significant

33 differences, as determined by Student's *t*-test (***P* < 0.01).

34 (C) The relative expression levels of *GhBOP2* in roots of TRV:00 and TRV:GhBOP2 plants.

35 Error bars represent the SD of three biological replicates. Asterisks indicate statistically

36 significant differences, as determined by Student's *t*-test (***P* < 0.01).

37 (D) Diseased rate analysis of TRV:00, TRV:GBOP1 and TRV:GhBOP2 plants. Error bars

38 represent the SD of three biological replicates. Asterisks indicate statistically significant

39 differences compared to TRV:00 as determined by Student's *t*-test (***P* < 0.01).

40 (E) Relative quantification of the fungal biomass in the infected stems of TRV:00,

41 TRV:GBOP1 and TRV:GhBOP2 plants. Error bars represent the SD of three biological

42 replicates. Asterisks indicate statistically significant differences compared to TRV:00, as

43 determined by Student's *t*-test (***P* < 0.01).

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Supplementary Figure 5



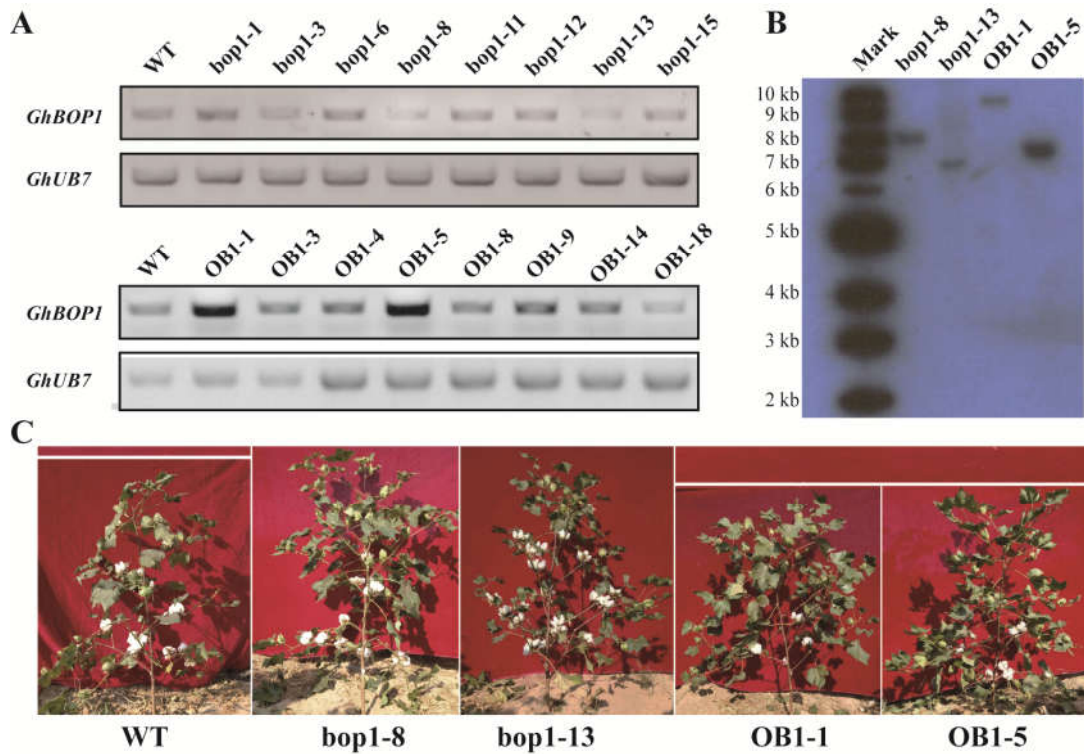
Mock *V.d*

47 **Supplementary Figure 5. GUS staining analysis the expression level of GhBOP1.** The
48 expression level of GhBOP1 in the roots of GhBOP1pro:GUS transgenic plants were analyzed
49 by GUS staining at 3 d after inoculated with *V. dahliae*. The scale bars indicate 1 mm.
50

51

52

Supplementary Figure 6



53

54 **Supplementary Figure 6. Molecular identification and adult phenotypes of GhBOP1**
55 **transgenic plants.**

56 (A) PCR was performed to detect the *GhBOP1* and the *GhUB7* expression levels in roots. The
57 *GhUB7* gene was used as internal control.

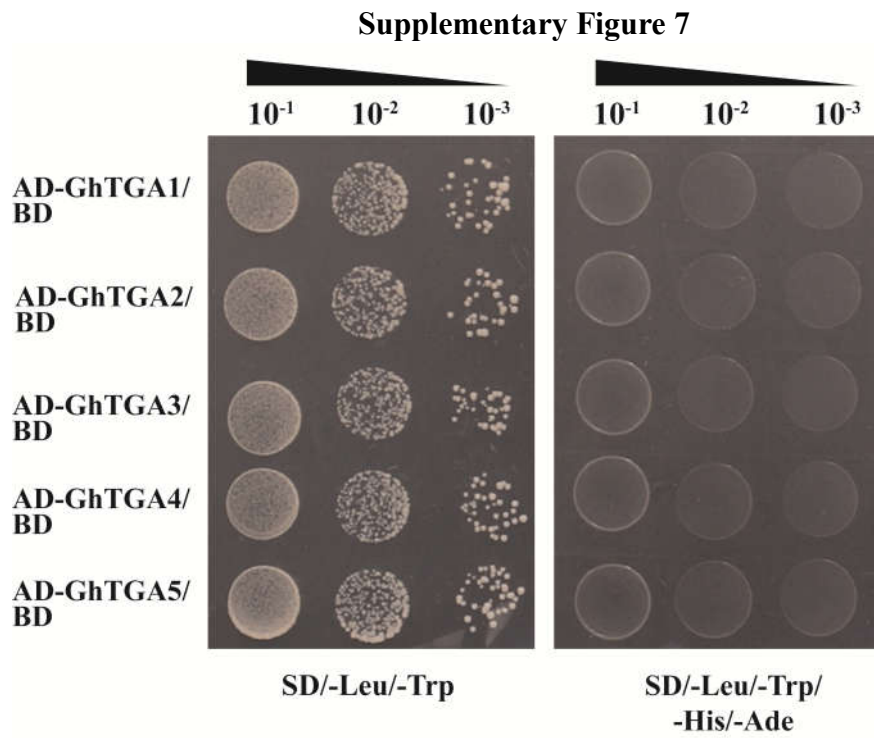
58 (B) Southern blotting analysis in the four transgenic lines.

59 (C) Adult phenotypes of WT and transgenic cotton plants.

60

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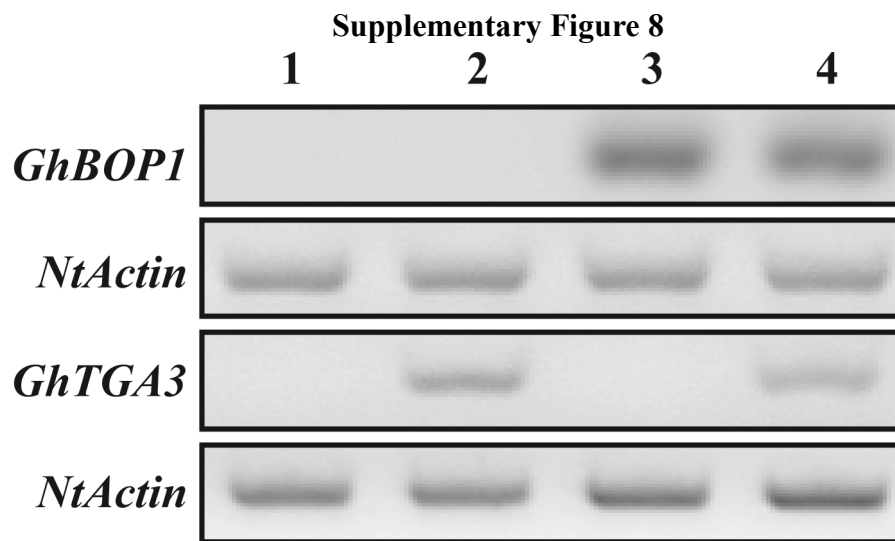
Supplementary Figure 7. Self-activation assay of AD-GhTGAs in yeast.

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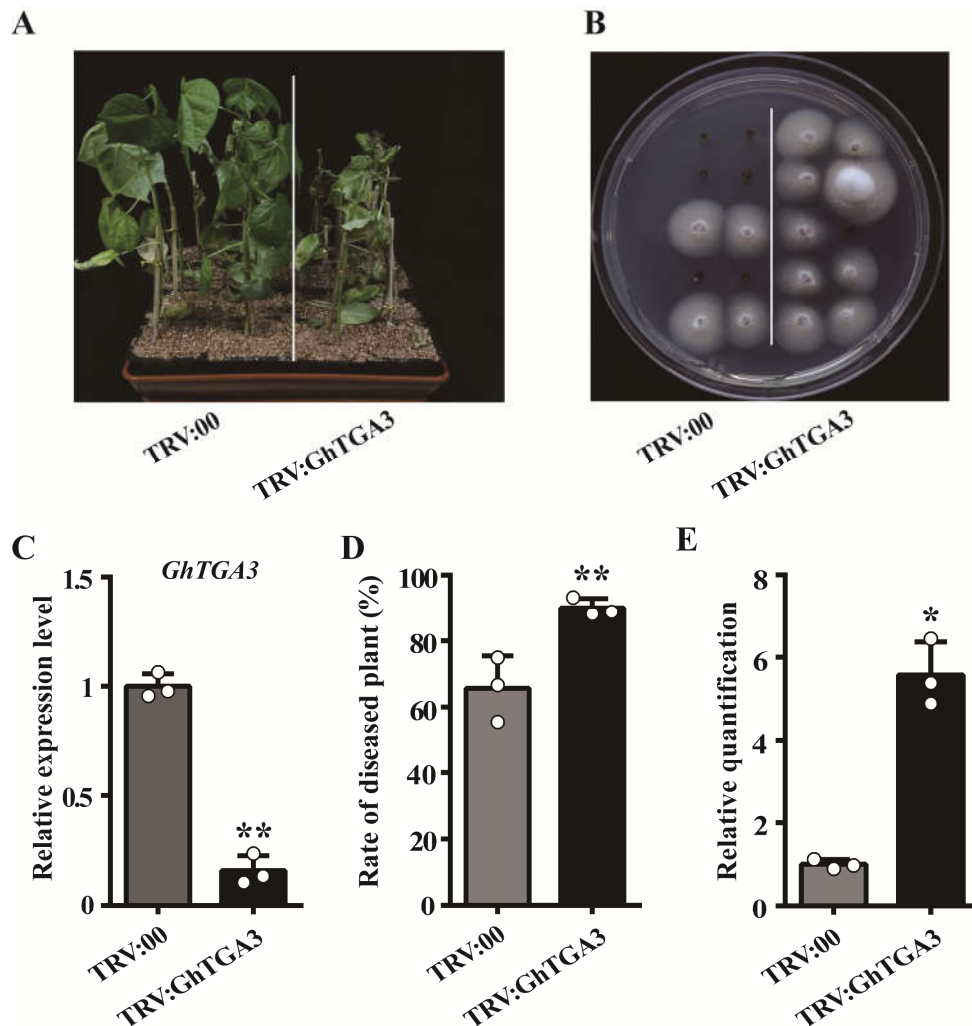
69 **Supplementary Figure 8. RT-PCR detected the *GhBOP1* and *GhTGA3* expression levels**

70 **in tobacco leaf at 48h after infiltrated by the vectors shown in Figure 6A.**

71

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73

Supplementary Figure 9

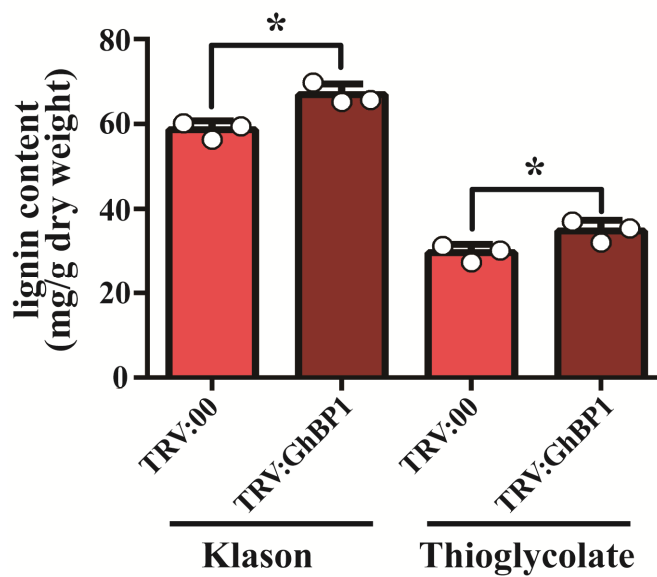


74 **Supplementary Figure 9. GhTGA3 positively regulating plant defence against *V. dahliae***
75 (A) Disease symptoms of TRV:00 and TRV:GhTGA3 inoculated with *V. dahliae*. Photographs
76 were taken at 18 d after pathogen inoculation.
77 (B) Fungal recovery assay to detect the morbidity of TRV:00 and TRV:GhTGA3 plants. The
78 stem section of the inoculated plants was placed on PDA medium and taken photographs at 4
79 d after culture.
80 (C) Relative expression levels of *GhTGA3* in roots of TRV:00 and TRV:GhTGA3 plants.
81 Error bars represent the SD of three biological replicates. Asterisks indicate statistically
82 significant differences, as determined by Student's *t*-test (** $P < 0.01$).
83 (D) Diseased rate analysis of TRV:00 and TRV:GhTGA3 plants. Error bars represent the SD
84 of three biological replicates. Asterisks indicate statistically significant differences compared
85 to TRV:00 as determined by Student's *t*-test (** $P < 0.01$).
86 (E) Relative quantification of the fungal biomass in the infected stems of TRV:00 and
87 TRV:GhTGA3 plants. Error bars represent the SD of three biological replicates. Asterisks
88 indicate statistically significant differences, as determined by Student's *t*-test ($P < 0.05$).

89

90

Supplementary Figure 10



91 **Supplementary Figure 10. GhBP1 negatively regulating lignin deposition.** Analysis of
92 lignin content in *GhBP1*-silenced plant stems through Klason and thioglycolate methods.
93 Error bars represent the SD (n=18) of three biological replicates. Asterisks indicate
94 statistically significant differences, as determined by Student's *t*-test (** $P < 0.01$).
95

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Supplementary Figure 11

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GhBOP1                               AGGGCCGCTATTTA 14
GhBOP2 CACTCCCTCTCCCTCTCCCTCTCCCTCTTCTAAAGTTTTCTCTTTTCTCTGTCTATCAAAA  

                                         AAAAAATATAATATATC 75
GhBOP1 AATACAGAAACAAACCACAGCACTCATCGGGATGGAAAGAATCTCTC...TACAAAAACCA  

                                         GTAACAGTAACCTC 86
GhBOP2 CCTATCGACAAAAACCCACACCACTTTCATCGAGAGGAAAGAATCTCTCAA  

                                         TACAAAAACCAATTACAGTAACCTC 105
GhBOP1 CATTCTTCTTCCCTTGGAAATGA.....AAACCATCGTCTCCGTCTCCATCTTCTCTTTT  

                                         GTCTATCTCCT 155
GhBOP2 CTCCGTTTCTTTCAAAATGAAACCATCATCTAAATCCCTACTTATTCTCTAACTACTACTT  

                                         CTCTCTCTTCT 255
GhBOP1 TCATCTTTTCTTAAT...CGAGACCCCTGGTTTTCAGAAGCAACAGAATTTCTTTTTCTT  

                                         TACTCGTGAA 224
GhBOP2 TCTTCGTGTACTTGATTCAACAACATACTTGTATCCAAAAAGAGAAGATTTTCTTTTTGTA  

                                         TTCCTCTGGGA 300
GhBOP1 AGACAACCCATAAATGAGTAGC..... 246
GhBOP2 AAACAACCTAAATGAGTAGC..... 322

```

98 **Supplementary Figure 11. Alignment of 5'UTR sequences between *GhBOP1* and**
 99 ***GhBOP2*.** The opposite blue and green arrows indicate the specific primer sequences used for
 100 VIGS analysis of *GhBOP1* and *GhBOP2*, respectively. The red hollow frame indicates
 101 initiation codon.
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Supplementary Figure 12

Figure 4B

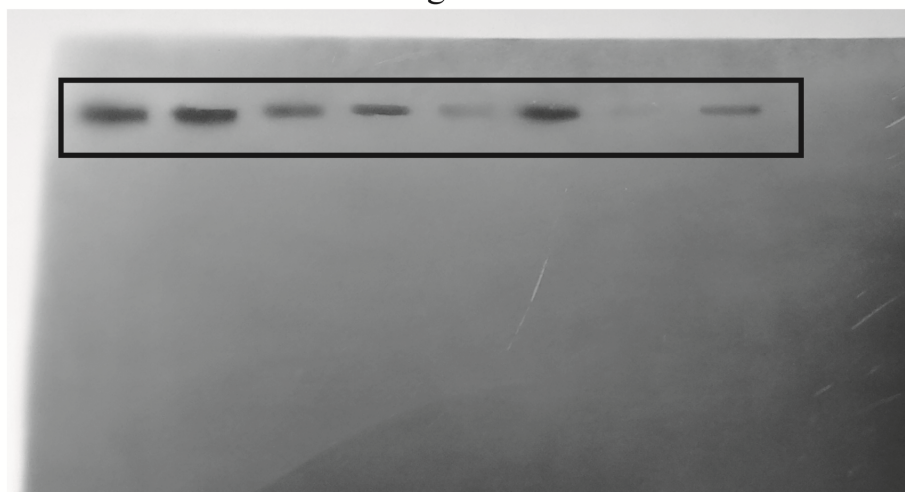


Figure 5A

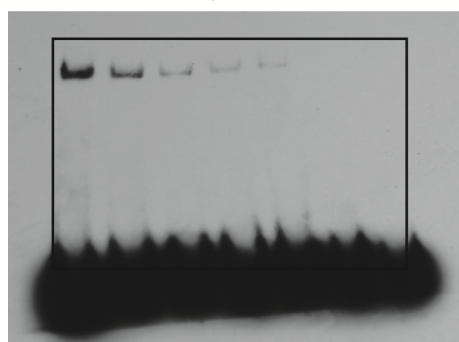
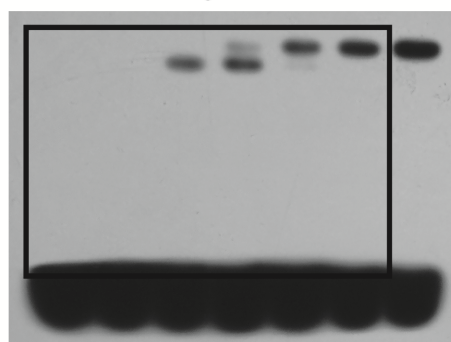


Figure 5B



106

107 **Supplementary Figure 12. Uncropped blot and gel images.** The black rectangles shown the
108 final cropped part of the image from main figures (figure 4 to 5).

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Supplementary Table 1. Cis-element analysis of GhPR1 promoter

	motif name	motif sequence	motif site upstream of ATG	direction
PlantCARE_13222	ERE	ATTTTAAA	1228	+
PlantCARE_13222	MYB-like sequence	TAACCA	383	-
PlantCARE_13222	CGTCA-motif	CGTCA	846	+
PlantCARE_13222	AAGAA-motif	GGTAAAGAAA	1447	-
PlantCARE_13222	AAGAA-motif	GAAAGAA	347	+
PlantCARE_13222	P-box	CCTTTTG	1049	-
PlantCARE_13222	Unnamed__1	CGTGG	1068	+
PlantCARE_13222	GARE-motif	TCTGTTG	1004	-
PlantCARE_13222	I-box	TGATAATGT	1282	+
PlantCARE_13222	Box 4	ATTAAT	1382	+
PlantCARE_13222	Box 4	ATTAAT	1158	+
PlantCARE_13222	Box 4	ATTAAT	316	-
PlantCARE_13222	TGACG-motif	TGACG	846	-
PlantCARE_13222	AuxRR-core	GGTCCAT	403	+
PlantCARE_13222	TATC-box	TATCCCA	622	+
PlantCARE_13222	W box	TTGACC	786	+
PlantCARE_13222	F-box	CTATTCTCATT	1458	+
PlantCARE_13222	Unnamed__6	taTAAATATct	87	+
PlantCARE_13222	chs-CMA1a	TTACTTAA	1038	+
PlantCARE_13222	Sp1	GGGCGG	1175	+
PlantCARE_13222	WUN-motif	AAATTACT	728	-
PlantCARE_13222	WUN-motif	AAATTTCTT	589	-
PlantCARE_13222	AT~TATA-box	TATATA	1377	+
PlantCARE_13222	AT~TATA-box	TATATA	1375	+
PlantCARE_13222	AT~TATA-box	TATATA	1019	+
PlantCARE_13222	AT~TATA-box	TATATA	1017	+
PlantCARE_13222	AT~TATA-box	TATATAAA	771	-
PlantCARE_13222	AT~TATA-box	TATATA	769	-
PlantCARE_13222	AT~TATA-box	TATATA	767	-
PlantCARE_13222	AT~TATA-box	TATATA	765	-
PlantCARE_13222	AT~TATA-box	TATATA	376	-
PlantCARE_13222	AT~TATA-box	TATATAAA	191	-
PlantCARE_13222	AT~TATA-box	TATATA	189	-
PlantCARE_13222	CAAT-box	CAAT	1489	+
PlantCARE_13222	CAAT-box	CAAT	1484	+
PlantCARE_13222	CAAT-box	CCAAT	1406	-
PlantCARE_13222	CAAT-box	CAAAT	1394	+
PlantCARE_13222	CAAT-box	CAAAT	1331	-

PlantCARE_13222	CAAT-box	CAAT	1287	+
PlantCARE_13222	CAAT-box	CAAAT	1285	-
PlantCARE_13222	CAAT-box	CAAT	1057	-
PlantCARE_13222	CAAT-box	CAAT	1009	-
PlantCARE_13222	CAAT-box	CAAT	982	-
PlantCARE_13222	CAAT-box	CAAAT	880	+
PlantCARE_13222	CAAT-box	CAAAT	816	+
PlantCARE_13222	CAAT-box	CAAT	787	-
PlantCARE_13222	CAAT-box	CAAAT	753	+
PlantCARE_13222	CAAT-box	CAAAT	724	-
PlantCARE_13222	CAAT-box	CAAAT	699	-
PlantCARE_13222	CAAT-box	CAAT	692	+
PlantCARE_13222	CAAT-box	CAAT	558	+
PlantCARE_13222	CAAT-box	CAAT	540	-
PlantCARE_13222	CAAT-box	CAAAT	427	-
PlantCARE_13222	CAAT-box	CAAAT	422	-
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PlantCARE_13222	GATA-motif	GATAGGA	1064	+
PlantCARE_13222	O2-site	GATGATGTGG	913	+
PlantCARE_13222	GT1-motif	GGTAAAT	382	+
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PlantCARE_13222	TATA-box	TATAAA	1088	-
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PlantCARE_13222	TATA-box	TATATAA	1020	-
PlantCARE_13222	TATA-box	TATATA	1019	+
PlantCARE_13222	TATA-box	ATATAT	1018	+
PlantCARE_13222	TATA-box	TATATA	1017	+
PlantCARE_13222	TATA-box	ATATAA	1016	+
PlantCARE_13222	TATA-box	TATA	1015	+
PlantCARE_13222	TATA-box	ATTATA	877	+
PlantCARE_13222	TATA-box	TATAA	876	-
PlantCARE_13222	TATA-box	TATA	875	-
PlantCARE_13222	TATA-box	TATAA	865	-
PlantCARE_13222	TATA-box	TATA	864	-
PlantCARE_13222	TATA-box	taTATAAAtc	773	-
PlantCARE_13222	TATA-box	TATAAAT	772	-
PlantCARE_13222	TATA-box	TATAAA	771	-
PlantCARE_13222	TATA-box	TATATAA	770	-
PlantCARE_13222	TATA-box	TATATA	769	-
PlantCARE_13222	TATA-box	ATATAT	768	-
PlantCARE_13222	TATA-box	TATATA	767	-
PlantCARE_13222	TATA-box	ATATAT	766	-
PlantCARE_13222	TATA-box	TATATA	765	-
PlantCARE_13222	TATA-box	ATATAA	764	+
PlantCARE_13222	TATA-box	TATA	763	-
PlantCARE_13222	TATA-box	TATAAATA	555	-
PlantCARE_13222	TATA-box	TATAAAT	554	-
PlantCARE_13222	TATA-box	TATAAA	553	-
PlantCARE_13222	TATA-box	TATAA	552	-
PlantCARE_13222	TATA-box	TATA	551	-
PlantCARE_13222	TATA-box	ATATAT	377	-
PlantCARE_13222	TATA-box	TATATA	376	-
PlantCARE_13222	TATA-box	ATATAT	375	-
PlantCARE_13222	TATA-box	TATA	374	-
PlantCARE_13222	TATA-box	ATTATA	302	+
PlantCARE_13222	TATA-box	TATAA	301	-
PlantCARE_13222	TATA-box	TATA	300	-
PlantCARE_13222	TATA-box	TATA	249	-

PlantCARE_13222	TATA-box	TATAAAA	192	-
PlantCARE_13222	TATA-box	TATAAA	191	-
PlantCARE_13222	TATA-box	TATATAA	190	-
PlantCARE_13222	TATA-box	TATATA	189	-
PlantCARE_13222	TATA-box	ATATAT	188	-
PlantCARE_13222	TATA-box	TATA	187	-
PlantCARE_13222	TATA-box	TATA	87	-
PlantCARE_13222	TATA-box	TATAAGAA	23	-
PlantCARE_13222	TATA-box	TATAA	20	-
PlantCARE_13222	TATA-box	TATA	19	-
PlantCARE_13222	ARE	AAACCA	224	+
PlantCARE_13222	MYB	CAACAG	1004	+
PlantCARE_13222	MYB	CAACAG	688	+
PlantCARE_13222	MYB	TAACCA	383	-
PlantCARE_13222	chs-CMA2a	TCACTTGA	1306	-
PlantCARE_13222	TCT-motif	TCTTAC	1098	-
PlantCARE_13222	Myb-binding site	CAACAG	1004	+
PlantCARE_13222	Myb-binding site	CAACAG	688	+
PlantCARE_13222	ABRE	ACGTG	1069	+
PlantCARE_13222	ABRE	TACGGTC	406	+

115 TGACG-element is highlight in red

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