FIG S1 Identification of the cell death-inducing activities of 67 candidate effectors in *Nicotiana benthamiana*. The cell death inducing activity of 67 candidate effectors in 4-week-old *N. benthamiana* leaves was detected at 7 days after infiltration with *Agrobacterium tumefaciens* carrying the indicated genes. The green fluorescent protein (GFP) and BAX (Bcl-2-associated X) were used as the negative and positive controls, respectively.

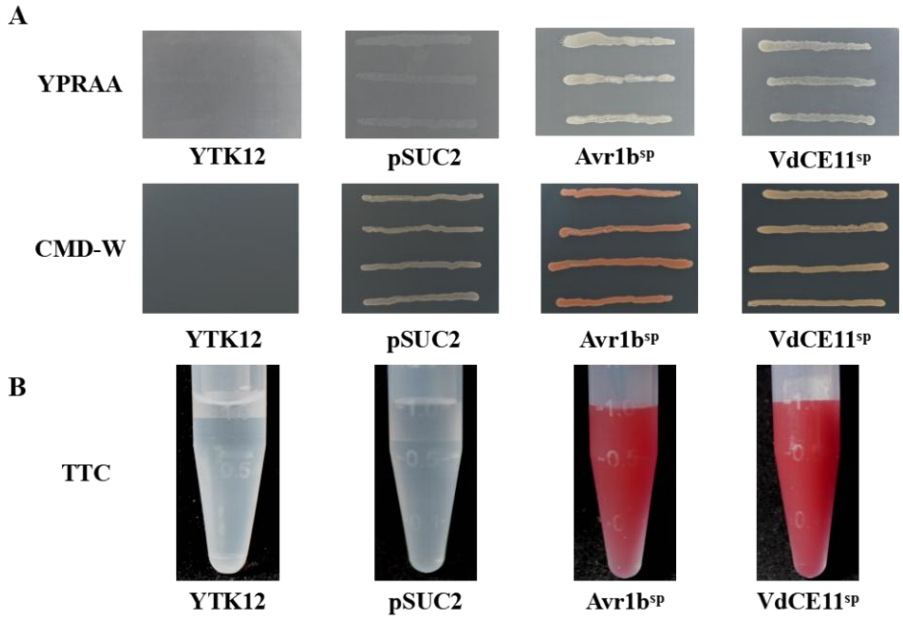

FIG S2 Validation of secretory function of the putative N-terminal signal peptides in VdCE11 using the yeast invertase secretion assay. (A) Yeast strains YTK12 transformed with indicated constructs were cultured on YPRAA and CMD-W media. (B) Confirmation of the secretory function of VdCE11 signal peptide by TTC chromogenic reaction. The secreted effector Avr1b from oomycetes was regarded as positive controls.

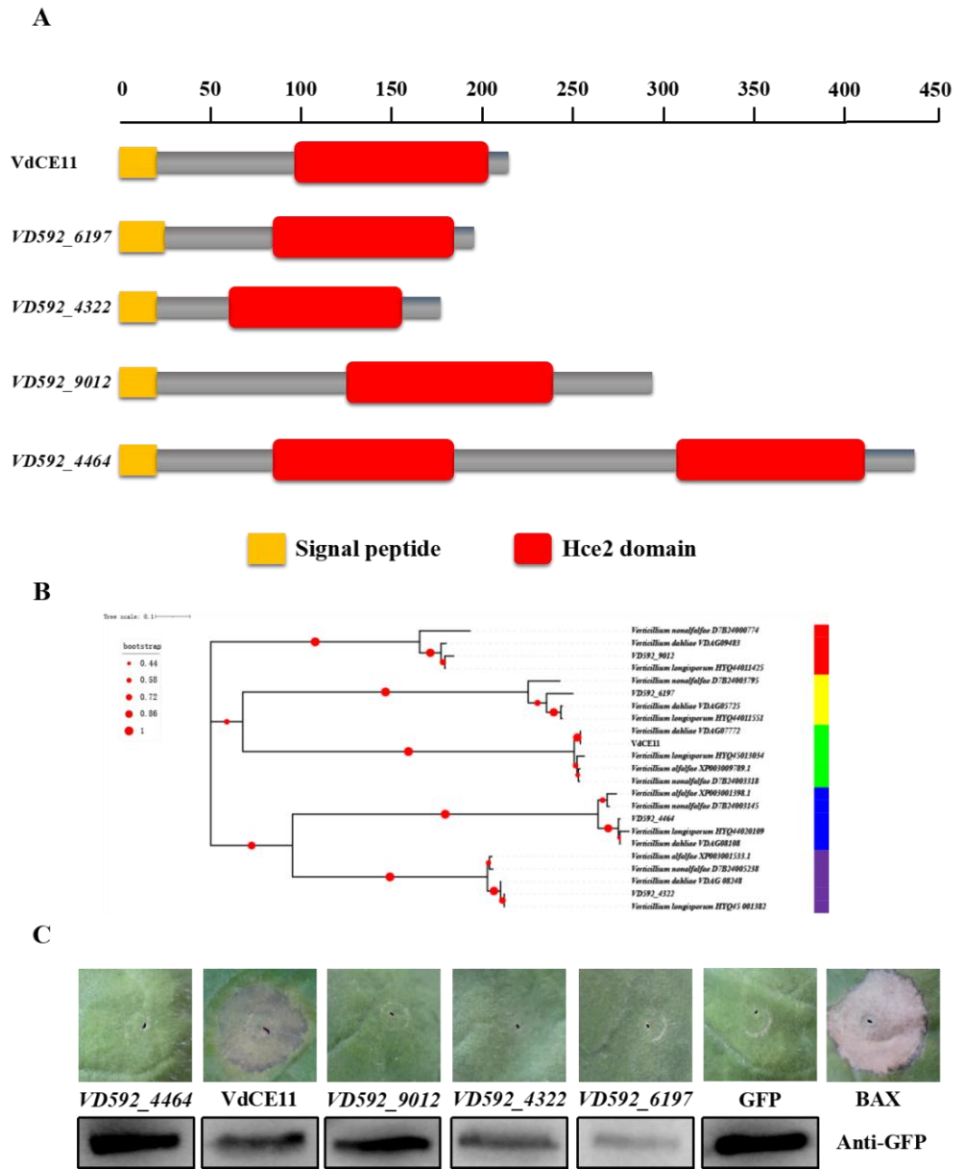

FIG S3 Identification of Hce2 domain in *Verticillium dahliae* XJ592 genome. (A) Schematic diagrams of five Hce2 domain-containing proteins identified from *V. dahliae*. The yellow colour shows the position of the predicted signal peptides, and red colour indicates the Hce2 domain. (B) Phylogenetic analysis of Hce2 domain-containing proteins in *Verticillium* spp. (C) Transient expression of five Hce2 domain-containing proteins on the leaves of *Nicotiana benthamiana*. The green fluorescent protein (GFP) and BAX (Bcl-2-associated X) were used as the negative and positive controls, respectively. Western blot showed the expression of five Hce2 domain-containing proteins.

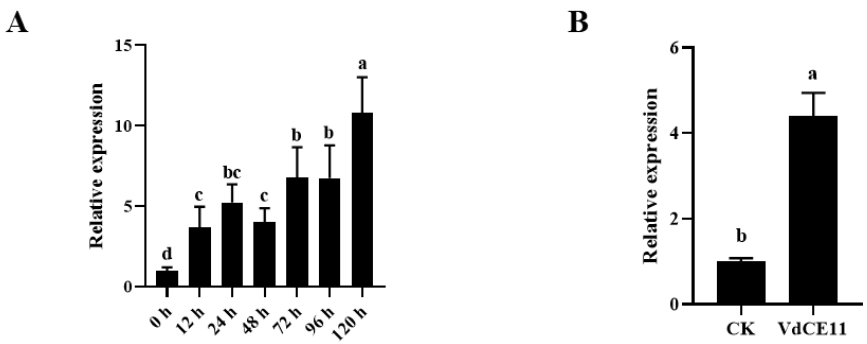

FIG S4 Expression of VdCE11 was induced by cotton or its root extract. (A) Relative expression of *VdCE11* in cotton plants (susceptible cultivar *Gossypium hirsutum* cv. Junmian 1) inoculated by *Verticillium dahliae* wild type strain XJ592 at 0, 12, 24, 48, 72, 96 and 120 hours post inoculation. (B) Relative expression of *VdCE11* in XJ592 at 48 h after being induced by cotton's root extract. The data shown represents the mean across three independent experiments. Different letters represent significant differences ($p < 0.05$), according to Student's *t*-test. Bars indicate SE.

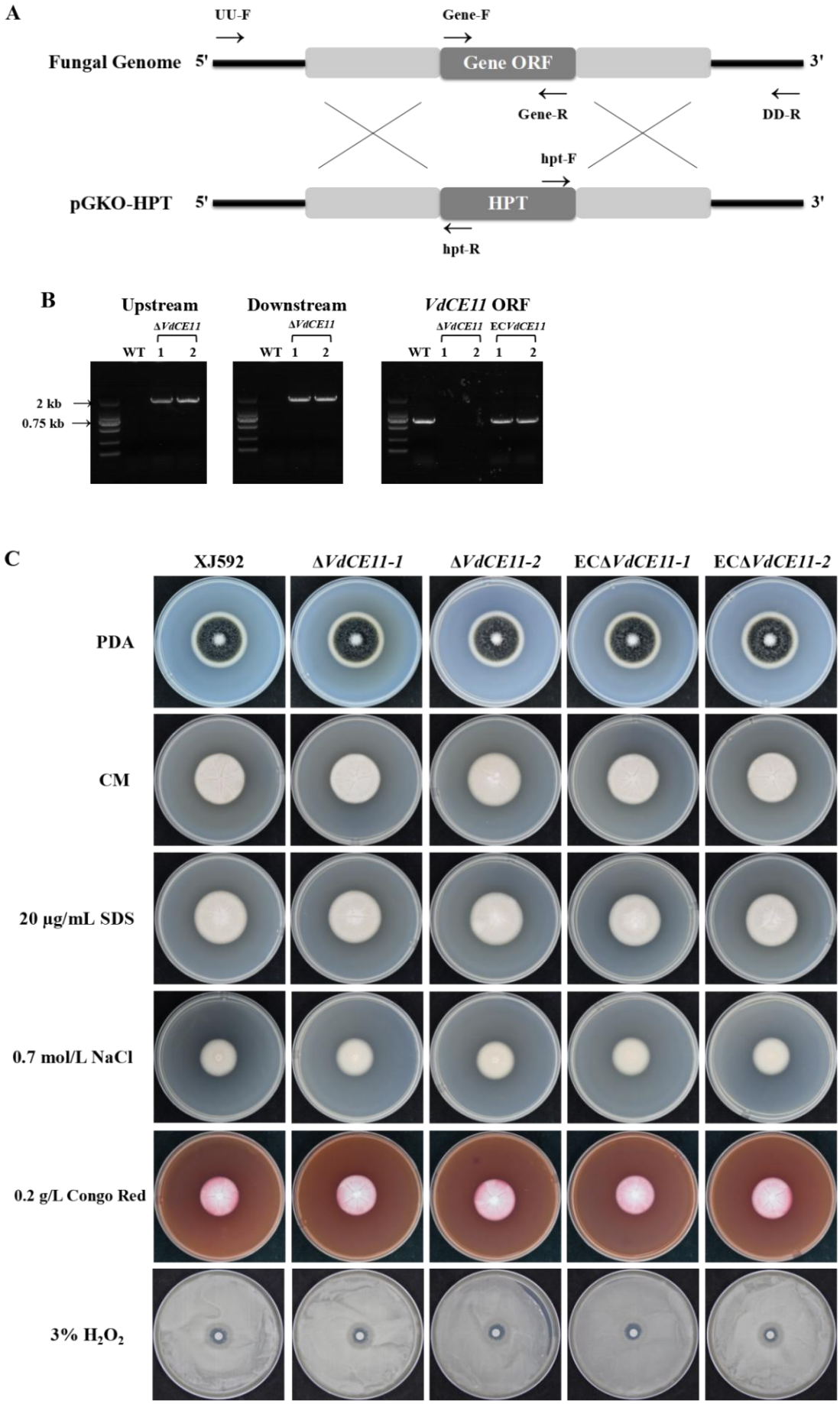
A
UU-F
Gene-F
Fungal Genome
5'
Gene ORF
3'
Gene-R
DD-R
hpt-F
pGKO-HPT
5'
HPT
3'
hpt-R
B
Upstream
Downstream
VdCE11 ORF
ΔVdCE11
ECVdCE11
WT
1
2
2 kb
0.75 kb
C
XJ592
ΔVdCE11-1
ΔVdCE11-2
ECΔVdCE11-1
ECΔVdCE11-2
PDA
CM
20 μg/mL SDS
0.7 mol/L NaCl
0.2 g/L Congo Red
3% H2O2

FIG S5 Knockout of *VdCE11* by targeted gene replacement and gene complementation. (A) Schematic description of *VdCE11* locus before and after homologous recombination in wild type strain XJ592. Orientation of the target gene and HPT are indicated by black arrows, respectively. Upstream (5') and downstream (3') flanks of target gene are shown with light grey frames. (B) PCR confirmation of Δ*VdCE11* knockout mutants and complementary mutants. (C) Radial growth of XJ592, Δ*VdCE11* knockout mutants and complementary mutants on different agar plates. Representative cultures at 10 days post incubation were shown.

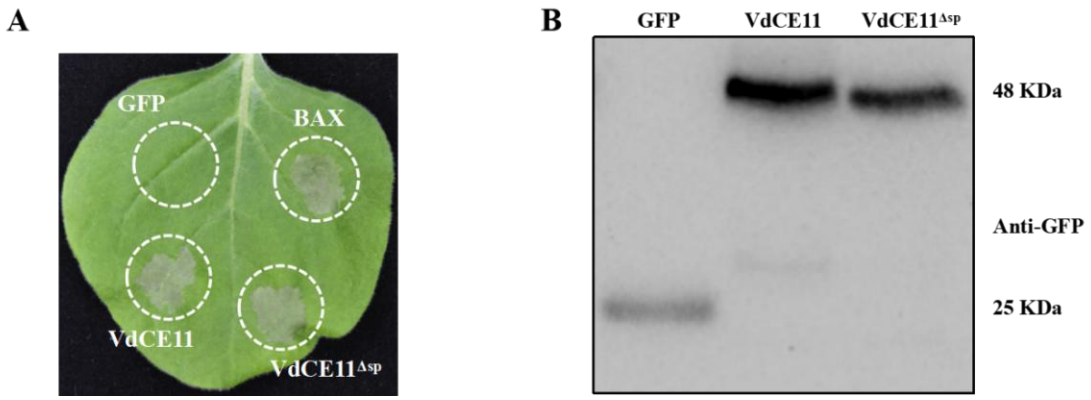

FIG S6 Signal peptide is not required for VdCE11-induced cell death. (A) *Nicotiana benthamiana* leaves were infiltrated with *Agrobacterium tumefaciens* carrying VdCE11, VdCE11$^{\Delta sp}$, the positive control BAX, and the green fluorescent protein (GFP) control. Photographs of *N. benthamiana* leaves were taken at 7 days post infiltration. (B) Western blotting (WB) analysis of transient expression of VdCE11 and VdCE11$^{\Delta sp}$ fused to the GFP-tag in *N. benthamiana* leaves 48 hours after infiltration.

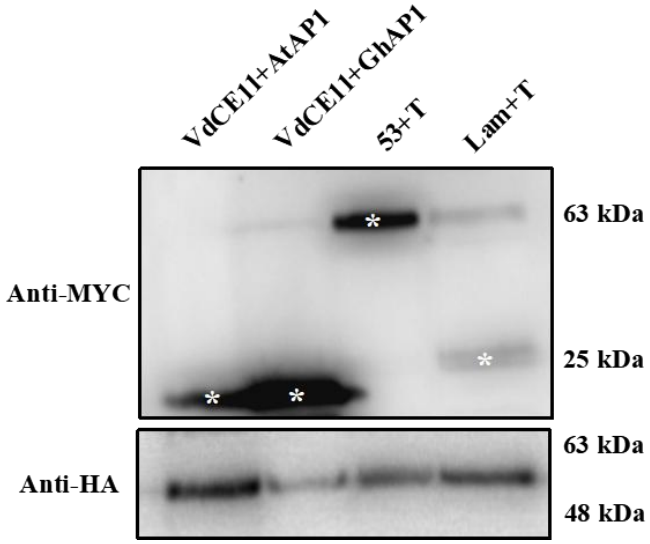

FIG S7 Detection of protein expression in yeast strain Y2HGold by western blot. pGBKT7-VdCE11 and pGADT7-T-GhAP1/AtAP1 were detected by the anti-MYC and anti-HA antibodies, respectively. Yeast transformed with pGBKT7-53 and pGADT7-T was used as the positive control, while Yeast transformed with pGBKT7-Lam and pGADT7-T as the negative control.

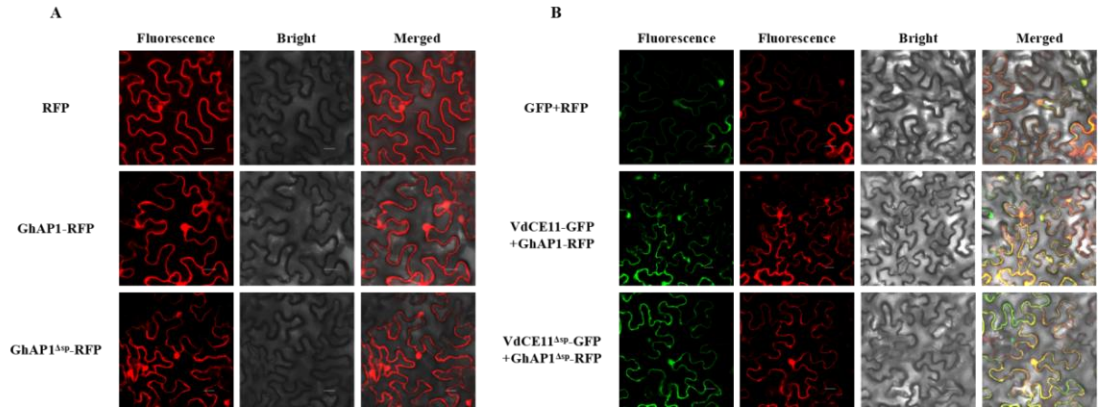

FIG S8 Subcellular localization of GhAP1 and GhAP1$^{\Delta sp}$ in *Nicotiana benthamiana* epidermal cells. (A) Confocal microscopy imaging of *N. benthamiana* leaves with transiently expressing red fluorescent protein (RFP)-tagged GhAP1, GhAP1 without signal peptide (GhAP1$^{\Delta sp}$), and RFP control. Pictures were taken 72 hours post agroinfiltration. Bars = 20 μm. (B) Confocal microscopy imaging of *N. benthamiana* leaves with transiently co-expressing VdCE11 and GhAP1, VdCE11$^{\Delta sp}$ and GhAP1$^{\Delta sp}$, or GFP and RFP control. Pictures were taken 72 hours post agroinfiltration. Bars = 20 μm.

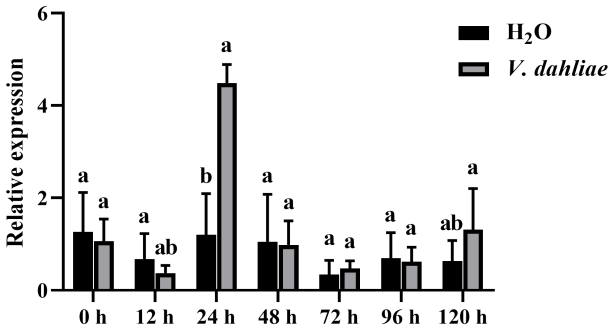

FIG S9 Expression pattern of *GhAP1* in response to *Verticillium dahliae* infection was analysed by qRT-PCR in the susceptible cultivar *Gossypium hirsutum* cv. Junmian 1. The data shown represents the mean across three independent experiments. Different letters represent significant differences ($p < 0.05$), according to Duncan's multiple comparison. Bars indicate SE.

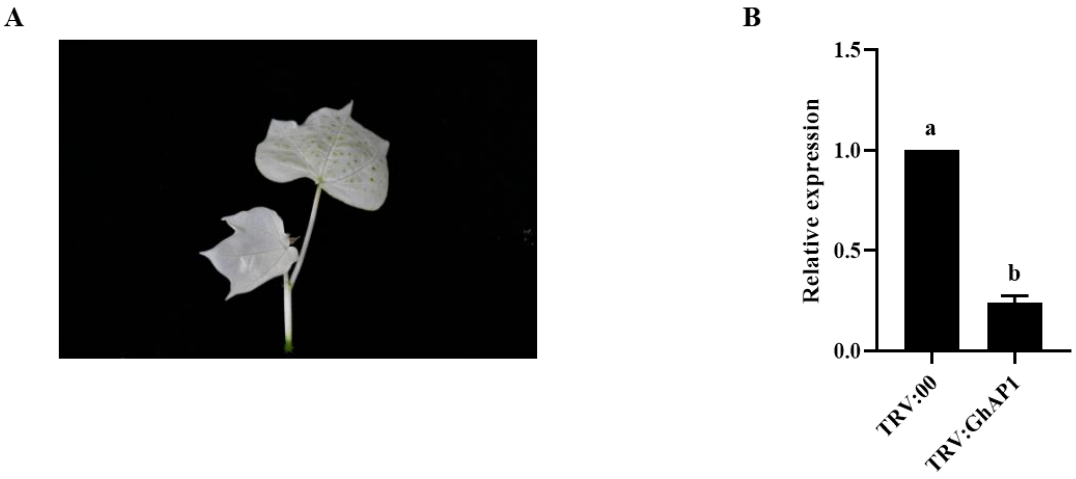

FIG S10 Verification of VIGS silencing system and detection of silencing efficiency of *GhAP1*. (A) Photobleaching phenotype of cotton at 2 weeks post silence of *GhCLA1*. (B) Gene expression of *GhAP1* in TRV:00 and TRV:*GhAP1* plants at 2 weeks post agroinfiltration. The data shown represents the mean across three independent experiments. Different letters represent significant differences ($p < 0.05$), according to Student's *t*-test. Bars indicate SE.

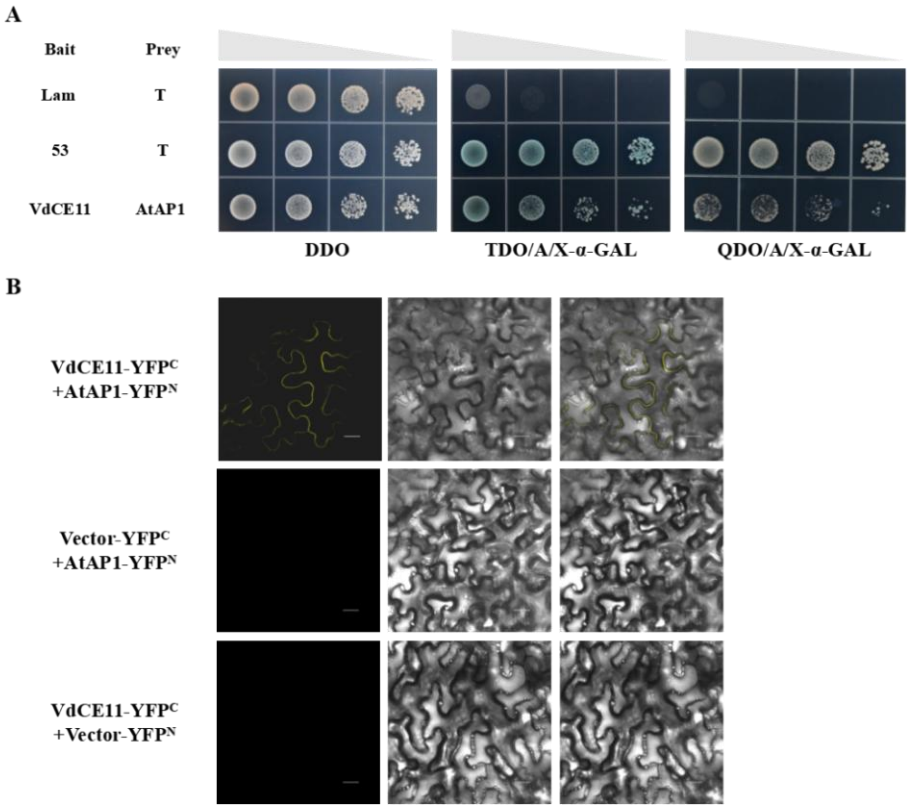

FIG S11 VdCE11 interacts with AtAP1 in *Arabidopsis*. (A) Yeast two-hybrid (Y2H) analysis of the interaction between VdCE11 and AtAP1. Double dropout (DDO, SD/-Trp/-Leu,) triple dropout (TDO, SD/-Trp/-Leu/-Ade) and quadruple dropout (QDO, SD/-Trp/-Leu/-Ade/-His) were used as non-selective and selective media, respectively. pGBKT7-53 and pGADT7-T was used as the positive control, while pGBKT7-Lam and pGADT7-T the negative control. (B) Bimolecular fluorescence complementation (BiFC) analysis of the interaction between VdCE11 and AtAP1. VdCE11-YFP^{C} and AtAP1-YFP^{N} were transiently co-expressed in *Nicotiana benthamiana*. Bars = 20 μm.

Table S1 Candidate effectors predicted by bioinformatics analysis.

Gene ID	Gene name	Probability	Gene ID	Gene name	Probability
VD592_112	*VdCE1*	0.819	*VD592_5128*	*VdCE35*	0.767
VD592_435	*VdCE2*	0.620	*VD592_5180*	*VdCE36*	0.704
VD592_617	*VdCE3*	0.656	*VD592_5852*	*VdCE37*	0.920
VD592_793	*VdCE4*	0.681	*VD592_5853*	*VdCE38*	0.810
VD592_832	*VdCE5*	0.829	*VD592_5991*	*VdCE39*	0.702
VD592_850	*VdCE6*	0.774	*VD592_6001*	*VdCE40*	0.767
VD592_871	*VdCE7*	0.808	*VD592_6181*	*VdCE41*	0.715
VD592_905	*VdCE8*	0.705	*VD592_6574*	*VdCE42*	0.618
VD592_951	*VdCE9*	0.632	*VD592_6770*	*VdCE43*	0.808
VD592_1144	*VdCE10*	0.907	*VD592_6789*	*VdCE44*	0.615
VD592_1125	*VdCE11*	0.631	*VD592_7012*	*VdCE45*	0.683
VD592_1205	*VdCE12*	0.644	*VD592_7091*	*VdCE46*	0.701
VD592_1321	*VdCE13*	0.720	*VD592_7413*	*VdCE47*	0.659
VD592_1489	*VdCE14*	0.874	*VD592_7797*	*VdCE48*	0.948
VD592_1945	*VdCE15*	0.629	*VD592_7812*	*VdCE49*	0.948
VD592_2054	*VdCE16*	0.759	*VD592_7905*	*VdCE50*	0.839
VD592_2243	*VdCE17*	0.652	*VD592_7786*	*VdCE51*	0.660
VD592_2249	*VdCE18*	0.729	*VD592_7913*	*VdCE52*	0.888
VD592_2881	*VdCE19*	0.795	*VD592_7927*	*VdCE53*	0.704
VD592_3198	*VdCE20*	0.736	*VD592_7964*	*VdCE54*	0.852
VD592_3247	*VdCE21*	0.686	*VD592_8212*	*VdCE55*	0.678
VD592_3354	*VdCE22*	0.922	*VD592_8250*	*VdCE56*	0.766
VD592_3368	*VdCE23*	0.911	*VD592_8342*	*VdCE57*	0.858
VD592_3587	*VdCE24*	0.697	*VD592_8389*	*VdCE58*	0.916
VD592_3650	*VdCE25*	0.614	*VD592_8400*	*VdCE59*	0.693
VD592_3690	*VdCE26*	0.615	*VD592_8403*	*VdCE60*	0.835
VD592_4001	*VdCE27*	0.773	*VD592_8663*	*VdCE61*	0.905
VD592_4010	*VdCE28*	0.652	*VD592_9068*	*VdCE62*	0.715
VD592_4254	*VdCE29*	0.708	*VD592_9472*	*VdCE63*	0.782
VD592_4328	*VdCE30*	0.799	*VD592_9829*	*VdCE64*	0.714
VD592_4427	*VdCE31*	0.766	*VD592_9935*	*VdCE65*	0.874
VD592_4923	*VdCE32*	0.914	*VD592_10247*	*VdCE66*	0.860
VD592_5095	*VdCE33*	0.710	*VD592_4968*	*VdCE67*	0.854
VD592_5106	*VdCE34*	0.728			

Note: Software Python 3.7 was used to screen for proteins less than or equal to 300 aa.

Table S2 The sequences of Hce2 domain-containing proteins in *Verticillium dahliae* XJ592.

Gene ID	Protein sequence
VdCE11 **(*VD592_1125*)**	**MFAHALLALTLGASSFATASALPPQVPDGDVVPLPASVDVNSVDLHN FTASDGNTYTVWVAKMQSPEDVQPTGANDDSNLVRRWQWEHWPN GVDACGAASFRDETSNGPPLTDHCICVRDYARDQLRGRWAFGRDDK PNNGWFNLVGCGECGFRVYTDNFFGAFVGDTDVRDLSTDSINRYNR GGRVVRVGTWVAATGQSSPRFIGVSSAK**
VD592_4464	**MLKKLLVGLLVVHTWAFSVQHPALSPGHAKDTVENSDSTKINRSVD DPTTLSFRISNGSSIIITVPALATTEDGDHFTVEKANEAITHCGGSVYD SVHTSTDSPLVSDCKALLEYFDAEDRRWFLDPAEDYPKLFTLASTGT CAVKALVYDKTYIGNGDGAAILRRAFDLGSSVVDGRIEARGNKYCD ECFQDCDGFRTQTPAQWQVEDPQKPDPNAEEESEVEDWGIKGKNG NDTAPDNSARSIVSDKAKLLGTREDHTNWMEHVLKTDDGKEVTFQ VNAAVMRSEMVPGDGGAESNDRVTYVTTEKSSIRCHPITAQKQTKD LLALTDDCRELVSVLAHSAWHGYWLFSHDDVQWCHKGFGTAIIQLG TCVFSACPVARIGMGNEDVKRFIQSGIDKVAGGENMRVTGEGGCEL ENKRDWKFETEWMVFAKASPVQV**
VD592_6197	**MARRTFNVLALIALLLTACSPVLSAALPACNPPIPNTTCEALKMSSGD PKPLYLSTTFEKTIDASPAGQHAPNRTTTTPCPSLLCDAASAIFSGKST DPSAPETADCALLKTWAAGRAATGCSPRQGGWGWTPLVATGTCAVV ARAEGAFAIGTEDVADLLGTSIRDYGMGDRVEVLGVMPCAEARGFA AGGGEKGRTIGMEWWVVRPDMMESLGGGKYR**
VD592_4322	**MRSAVHLLLGVVSALALLASASPINTSLNPSTLARRALDYQHPVYTA GGRFEYCGEVAVTPTPDTSSAAPLAADCSLIADDVGARQGAYTFAAA DFKHDGWAWVAAKGTCTFAARFDTAAARTKLLVGTNDVRFYISSSS WLAKNGRLGVKAGVTCFNGEGQKGITWGLIRTPKPV**
VD592_9012	**MSPLMTLVAILALLPQGQGLVIPGFLNLTSLAPVLTQVFTILPYPKHT PATPMQPRDFTILPYPLHRTTSKTTTFMTQTTPTSQGATATATATATK TPTPPFTAAPRQAVDVDPTTPISWHEASHRNNISDCLALAAALRAKK GYFVARGFTDTTTLVGLATEGSCIFGVRPATPSHFHEVIGALDAAAFL DDAVRDLSSPAGGATAGDGS**

Table S3 The sequences of aspartic protease 1 (AP1) protein in *Gossypium hirsutum* and *Arabidopsis thaliana.*

Protein name	Protein sequences
GhAP1	**MGTTVKGVVLSLFISSLLCSVVLASNDGLVRIGLKKMKLDPNNRLA AQLDSKDREALRASIAKKYRFRNDLGDSEETDIVALKNYMDAQYYG EIGIGTPPQKFTVIFDTGSSNLWVPSTKCYFSVACFFHSKYKSSESSTY KKNGKSASIQYGTGAISGFFSNDSVKVGNLVAKDQEFIEATKEPGVT FIAAKFDGILGLGFKEISVGDAVPVWYNMVEQGLIKDQVFSFWLNR NVGEEMGGEIVFGGIDPNHYKGKHTYVPITQKGYWQFDMGDVLIG DKPTGYCAGGCAAIADSGTSLLAGPTTVITMINQAIGASGVASQECK AVVQQYGQTIIDLLVSQAEPMKICSRIGLCAFDGSHGVSMGIENVVD ESNGKSSGILHSAMCPACEMAVVWMQNQLIENQTQDRILDYANQL CDRVPNPMGESTVDCGSLSSMPTISFTIGGKAFDLTPEEYILKVGEG AEAQCISGFTALDVPPPRGPLWILGDAFMGRYHTVFDFGKLRVGFA EAA**
AtAP1	**MKIYSRTVAVSLIVSFLLCFSAFAERNDGTFRVGLKKLKLDSKNRLA ARVESKQEKPLRAYRLGDSGDADVVVLKNYLDAQYYGEIAIGTPPQ KFTVVFDTGSSNLWVPSSKCYFSLACLLHPKYKSSRSSTYEKNGKAA AIHYGTGAIAGFFSNDAVTVGDLVVKDQEFIEATKEPGITFVVAKFD GILGLGFQEISVGKAAPVWYNMLKQGLIKEPVFSFWLNRNADEEEG GELVFGGVDPNHFKGKHTYVPVTQKGYWQFDMGDVLIGGAPTGF CESGCSAIADSGTSLLAGPTTIITMINHAIGAAGVVSQQCKTVVDQY GQTILDLLLSETQPKKICSQIGLCTFDGTRGVSMGIESVVDKENAKL SNGVGDAACSACEMAVVWIQSQLRQNMTQERILNYVNELCERLPSP MGESAVDCAQLSTMPTVSLTIGGKVFDLAPEEYVLKVGEGPVAQCI SGFIALDVAPPRGPLWILGDVFMGKYHTVFDFGNEQVGFAEAA**

Table S4 Primers used in this study.

Primer name	Sequences (5'-3')
pBin-VdCE11-F	CATTTGGAGAGGACCTCGAGATGTTTGCCCATGCACTCTTG
pBin-VdCE11$^{\Delta SP}$-F	CATTTGGAGAGGACCTCGAGATGCTACCACCCCAGGTGCCG
pBin-VdCE11-R	CTTTTGCTTTAAAAGAAATGATTTTTTGGCGGAAGACACTCCAA
pBin-4464-F	CATTTGGAGAGGACCTCGAGATGCTCAAGAAGCTTCTTGTCG
pBin-4464-R	CTTTTGCTTTAAAAGAAATGATTTGACCTGGACAGGAGAAGCCT
pBin-9012-F	CATTTGGAGAGGACCTCGAGATGTCTCCCCTCATGACGCT
pBin-9012-R	CTTTTGCTTTAAAAGAAATGATTTCGACCCATCCCCGGCCGTC
pBin-4322-F	CATTTGGAGAGGACCTCGAGATGCGCTCCGCCGTCCAC
pBin-4322-R	CTTTTGCTTTAAAAGAAATGATTTAACGGGTTTAGGCGTCCTG
pBin-6197-F	CATTTGGAGAGGACCTCGAGATGGCCCGCCGCACCTTCAA
pBin-6197-R	CTTTTGCTTTAAAAGAAATGATTTTCGATACTTCCCCCCTCCC
pCambia1302-VdCE11-GFP-F	CGACGGTACCGCGGGCCCATGTTTGCCCATGCACTCTTG
pCambia1302-VdCE11-GFP-R	TTCCAGGATCCCGGGCCCTTTGGCGGAAGACACTCCAA
pCambia1302-VdCE11$^{\Delta SP}$-GFP-F	CGACGGTACCGCGGGCCCCTACCACCCCAGGTGCCG
pSUC2-SP^{VdCE11}-F	CGGAATTTTAATTAAGAATTCATGTTTGCCCATGCACTCTT
pSUC2-SP^{VdCE11}-R	CACTATAGGGAGAACCTCGAGTGCCGAAGCTGTCGCAAAAG
VdCE11up-F	GAGCTCGCTGAGGGTTTAATTAACCGACAACATCAACTTCGGC
VdCE11up-R	ATGGGCCCGCTGAGGACTTAATTAATTGAAGGGGTGCGTATGGTC
VdCE11down-F	ACTAGTGCTGAGGCATTAATTAAATGGTTTCTCGGACTGCGTT
VdCE11down-R	AAGCTTGCTGAGGTCTTAATTAATGTTCTTCGGTGCCCTCTTC
VdCE11uu-F	TCGTGCCTGTGCCATTTGC
VdCE11uu-R	CCGAGATCCTGATCCTGATGA
VdCE11uu-F	GTCCATCCCAAGCCCATGAT
VdCE11dd-R	GGTACGCCATACTGACGGAG
BK-VdCE11-F	ATGGCCATGGAGGCCGAATTCACCCTACCACCCCAGGTGCCG
BK-VdCE11-R	CCGCTGCAGGTCGACGGATCCCTATTTGGCGGAAGACACTCC
Psul-VdCE11-F	CGGCCAGTGCCAAGCTTACGTTGAGGTTAGAGCTCGA
Psul-VdCE11-R	GCAGCTTCTGCGAATTCAACGCAGTCCGAGAAACCAT
Psul-F	ACGTCAGAAGCCGACTGC
Psul-R	TGAACTTGTGGCCGTTTACG
VdCE11-Nluc-F	GAGCTCGGTACCTCCGGATCCATGCTACCACCCCAGGTGCCG
VdCE11-Nluc-R	CAGTCGACGCGTTGTGGATCCTTTGGCGGAAGACACTCCAA
GhAP1-Cluc-F	CGGGGCGGTACCTCCGGATCCATGTCCAATGATGGGCTGGTTAGA
GhAP1-Cluc-R	CAGTCGACGCGTTGTGGATCCTCATGCTGCTTCTGCAAACCCAA
GhAP1-qPCRF	TTCATAGTGCTATGTGCCCTGC
GhAP1-qPCRR	TGGGTTTGGCACCCGATC
GhAP1-NYFP-F	TCTGAGGAGGATCTTCCTAGGATGTCCAATGATGGGCTGGTTAGA

GhAP1-NYFP-R	GGGAGGCCTGGATCGACTAGTTGCTGCTTCTGCAAACCCAA
VdCE11-CYFP-F	CTAGTCGACTCTAGCCTCGAGATGCTACCACCCCAGGTGCCG
VdCE11-CYFP-R	ATCGTATGGGTACATCCTAGGTTTGGCGGAAGACACTCCAA
AD-GhAP1-F	GCCATGGAGGCCAGTGAATTCACCATGGGAACCACGGTCAAAGG
AD-GhAP1-R	ATGCCCACCCGGGTGGAATTCTTATGCTGCTTCTGCAAACCC
VdCE11-qPCR-F	ACTCTTGGCGTTGACTCTCG
VdCE11-qPCR-R	GGACAAGGTTGCTGTCGTCA
VdEF1-α-F	TGAGTTCGAGGCTGGTATCT
VdEF1-α-R	CACTTGGTGGTGTCCATCTT
NbEF1α-F	TGAGTTCGAGGCTGGTATCT
NbEF1α-R	CACTTGGTGGTGTCCATCTT
qPCR-HSR203-F	GGCAGTGGAGGAGCTTAAAT
qPCR-HSR203-R	GCTATGTCCCACTCCATTGTTA
qPCR-HIN1-F	ATCCTCGGAGTGATTGCATTAG
qPCR-HIN1-R	TGTTGTTTGTGGTGGACAAATC
qPCR-PR1-F	GTGGGTCGATGAGAAACAGTAT
qPCR-PR1-R	GAACCCTAGCACATCCAACA
qPCR-PR4-F	GGCCAAGATTCCTGTGGTAGAT
qPCR-PR4-R	CACTGTTGTTTGAGTTCCTGTTCCT
qPCR-GLNb-F	GGCATCTGTAGGGATTGTTGT
qPCR-GLNb-R	GTCTCAATAGGTCCAGGCTTTC
qPCR-GRAS2-F	GCAAGGAGTACTGTGTCCATTA
qPCR-GRAS2-R	CCTTGCACCTCAAACTCCTAT
pCambia1302-RFP-GhAP1-F	CGACGGTACCGCGGGCCCATGGGAACCACGGTCAAAGG
pCambia1302-RFP-GhAP1$^{\Delta SP}$-F	CGACGGTACCGCGGGCCCATGTCCAATGATGGGCTGGTTAGA
pCambia1302-RFP-GhAP1-R	ATCCAGGATCCCGGGCCCTGCTGCTTCTGCAAACCCAA
pgex-VdCE11-F	CCGCGTGGATCCCCGGAATTCATGCTACCACCCCAGGTGCCG
pgex-VdCE11-R	GATGCGGCCGCTCGAGTCGACCTATTTGGCGGAAGACACTCC
TRV-AP1-F	TGAGTAAGGTTACCGAATTCACTTGTTTGACGGGTAGTTTTGAC
TRV-AP1-R	GGAGGCCTTCTAGAGAATTCCCCATCATTGGATGCAAGTACT
TRV-GhCLA1-F	TGAGTAAGGTTACCGAATTCCCACAACATCGATGATTTAG
TRV-GhCLA1-R	GGAGGCCTTCTAGAGAATTCATGATGAGTAGATTGCAC
GhSSU-F	AACTTAAAGGAATTGACGGAAG
GhSSU-R	GCATCACAGACCTGTTATTGCC
HPT-3F	TCTCCTTGCATGCACCATTCCTTG
HPT-5R	AAATTTTGTGCTCACCGCCTGGAC
AD-AtAP1-F	GCCATGGAGGCCAGTGAATTCACCATGAAGATATACTCTAGAACGGTTGCT
AD-AtAP1-R	ATGCCCACCCGGGTGGAATTCTTAGGCTGCCTCTGCAAACC
GhPR-1-F	GGCACAGAACTACGCTAATCAACG

GhPR-1-R	GCTTTACCCTCTCACTAACCCACAT
GhPR2-F	CCACCAGCAGCAGAAGTTATCG
GhPR2-R	TTCAAGGTTTGCACTCGGAAGA
GhPR3-F	ACTCCACAATCACCGAAGCCAT
GhPR3-R	GCATTCCAACCCTTACCACATTC
GhPR-4-F	TAGCCGTGTTCCAGCAGATTG
GhPR-4-R	TTTTGGCTTTTTCTCTTTATC
GhPR-5-F	GCCGTGATTCATACAGTTATCCTCA
GhPR-5-R	TTGGCTCTTACTTCCGACCATCT
GhPR-6-F	CTGGGTGTCCTGGGAAGAAC
GhPR-6-R	TTGTAGGGGGACGAACAACG
GhPR10-F	TTTTACACTGTTGGCGACTATGTGA
GhPR10-R	TTAGTTGCAGGCATCAGGGTTAG
AtAP1-NYFP-F	TCTGAGGAGGATCTTCCTAGGCGCAATGACGGGACCTTCAG
AtAP1-NYFP-R	GGGAGGCCTGGATCGACTAGTGGCTGCCTCTGCAAACCC
his-GhAP1-F	ATGGGTCGCGGATCCGAATTCATGTCCAATGATGGGCTGGTTAGA
his-GhAP1-R	TTGTCGACGGAGCTCGAATTCTTATGCTGCTTCTGCAAACCC
qNbCYP71D20-F	AAGGTCCACCGCACCATGTCCTTAGAG
qNbCYP71D20-R	AAGAATTCCTTGCCCCTTGAGTACTTGC
qNbPti5-F	CCTCCAAGTTTGAGCTCGGATAGT
qNbPti5-R	CCAAGAAATTCTCCATGCACTCTGTC
qNbWRKY7-F	CACAAGGGTACAAACAACACAG
qNbWRKY7-R	GGTTGCATTTGGTTCATGTAAG
qNbWRKY8-F	AACAATGGTGCCAATAATGC
qNbWRKY8-R	TGCATATCCTGAGAAACCATT
qNbPR1a-F	CCGCCTTCCCTCAACTCAAC
qNbPR1a-R	GCACAACCAAGACGTACTGAG
AtUBC21-F	TCAAATGGACCGCTCTTATC
AtUBC21-R	CACAGACTGAAGCGTCCAAG
AtPR1-F	GGAGCTACGCAGAACAACTAAGA
AtPR1-R	CCCACGAGGATCATAGTTGCAACTGA
AtPR2-F	CGGTACATCAACGTTGGAA
AtPR2-R	GCGTAGTCTAGATGGATGTT
AtPR5-F	TCTCTTCCTCGTGTTCATC
AtPR5-R	AAGCACCTGGAGTCAATT