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Supplementary Materials for

Jasmonate promotes artemisinin biosynthesis by activating the TCP14-ORA complex in *Artemisia annua*

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SUPPLEMENTARY MATERIALS



Fig. S1. A schematic diagram of the artemisinin biosynthetic pathway and its regulation in A. annua, and AaORA activates the ADS, CYP71AV1, DBR2, and ALDH1 promoters. (A) Biosynthetic pathways and regulation of artemisinin in Artemisia annua. MVA, mevalonate; MEP, 2-C-methyl-D-erythritol 4-phosphate; IPP, isopentenyl diphosphate; DMAPP, dimethylallyl diphosphate; FPS, farnesyl diphosphatesynthase; ADS, amorpha-4,11-diene synthase; CYP71AV1, cytochrome P450 monooxygenase; CPR, cytochrome P450 reductase; ADH1, alcohol dehydrogenase 1; DBR2, artemisinic aldehyde∆11(13) reductase; ALDH1, aldehyde dehydrogenase 1; WRKY1, WRKY transcription factor; GSW1, Glandular Trichome-Specific WRKY1; MYC2, basic helix-loop-helix (bHLH) transcription factor; bZIP1, basic leucine zipper transcription factor; ERF1 and ERF2, ETHYLENE-RESPONSIVE FACTOR 1 and 2; TAR1, TRICHOME AND ARTEMISININ REGULATOR1. (B) Top, Schematic diagrams of the effector (AaORA-GFP) and reporter (35S: REN-UBQ/ADS/CYP/DBR2/ALDH1 pro:LUC) plasmids used for the Dual-LUC assays. CYP, CYP71AV1. REN, Renilla luciferase. LUC, firefly luciferase. Bottom, Dual-LUC experiments showing the activation of the UBQ, ADS, CYP71AV1, DBR2 and ALDH1 promoters by ORA in N. benthamiana leaves. GFP was used as a negative control, and the LUC/REN ratios of GFP were set as 1. Three independent transfection

experiments were performed. The data represent the means \pm SD of three replicates from three independent experiments. ***P* < 0.01, Student's *t*-test. (C) Yeast one-hybrid assay showing that AaORA dose not bind to the *ADS*, *CYP71AV1*, *DBR2* and *ALDH1* promoters. The combination of pB42AD-AabZIP1 and *ADSpro(3×E1):LacZ* was used as a positive control. Yeast cells co-expressing pB42AD, pB42AD-AaORA or pB42AD-AabZIP1 and the full-length *ADS*, *CYP71AV1*, *DBR2* or *ALDH1* promoters or the DNA motif from the *ADS* promoter were grown on selective medium, SD/-Trp/-Ura, containing 20 mg/L X-gal, and pictures were taken after 4 days of incubation at 30°C. Blue plaques indicate protein-DNA interactions. The Y1H assays were repeated three times, and representative results are shown.



Fig. S2. Y2H assay showing the regions of AaORA with autoactivation activity. Left, schematic representations of the full-length and truncated AaORA proteins used in this experiment. Numbers indicate the amino acid positions of the truncated AaORA variants. The AP2 domain is indicated by a blue box. Right, Y2H assays of the interactions between AD and truncated versions of BD-AaORA. Transformed yeast cells were grown on selective medium, SD/-Trp/-Leu/-His/-Ade (QDO), and control medium, SD/-Trp/-Leu (DDO), and pictures were taken after 4 days of incubation at 30°C. The Y2H assays were repeated three times, and representative results are shown.



Fig. S3. Alignment of the protein sequences of AaTCP14 and 29 related proteins.

Alignment of the amino acid sequences of AaTCP14 and other TCP14 proteins. Identical amino acids are shaded in black, conserved residues are shaded in dark grey and similar residues are shaded in light grey. The conserved TCP domains are outlined with a blue box. The accession numbers of the sequences shown are as follows: CAE45599.1 from *Antirrhinum majus*; XP_012853009.1 from *Erythranthe guttata*; XP_016578353 from *Capsicum annuum*; NP120033815.1 from *Solanum lycopersicum*; XP_016472329.1 from *Nicotiana tabacum*; XP_019198053.1 from *Ipomoea nil*; AT3G47620_AtTCP14 from *Arabidopsis thaliana*; MF770262_AaTCP14 from *Artemisia annua*; KVI06398 from *Cynara cardunculus*; OTG1568.1 from *Helianthus annuus*; KYP55528.1 from *Cajanus cajan*;

XP_003549670.1 from *Glycine max*; XP_014510533.1 from *Vigna radiate*; XP_019464078.1 from *Lupinus angustifolius*; XP_003609053.1 from *Medicago truncatula*; XP_010258392.1 from *Nelumbo nucifera*; XP_015883510.1 from *Ziziphus jujube*; OMP06507.1 from *Corchorus capsularis*; XP_007037311.2 from *Theobroma cacao*; XP_012488907.1_GrTCP14a, XP_012469542.1_GrTCP14b and XP_012438750.1_GrTCP14c from *Gossypium raimondii*; XP_012080249.1 from *Jatropha curcas*; XP_002511563.1 from *Ricinus communis*; XP_011027800.1 from *Populus euphratica*; XP_004138164.2 from *Cucumis sativus*; XP_004299376.1 from *Fragaria vesca*; NP001280900.1 from *Malus domestica*; XP_018826533.1 from *Juglans regia*.



Fig. S4. Phylogenetic analysis of TCP14 proteins from *A. annua* and other plants. TCP14 sequences from different plant species were aligned with Clustal W, and a neighbor-joining phylogenetic tree was constructed using MEGA. Bootstrap values indicate the percentage of 1000 replicates. AaTCP14 is marked with a red star. The amino acid sequences are named based on the NCBI accession number and species name.



Fig. S5. Relative expression levels of transcription factors positively regulating artemisinin biosynthesis and JA biosynthetic genes in *AaTCP14* **transgenic plants.** (A-P) The expression levels of *AaWRKY1* (A, I), *AaMYC2* (B, J), *AaGSW1* (C, K), *AaORA* (D, L), *AaAOS* (E, M), *AaAOC* (F, N), *AaOPR3* (G, O) and *AaOPCL1* (H, P) in 3-month-old *A. annua AaTCP14*-overexpression and antisense (ANTCP14) plants, plants transformed with the empty vector (Vector) and wild-type (WT) were determined by quantitative real-time PCR (qRT-PCR). *Actin* was used as an internal control. The data represent the means ± SD of three replicates from three cutting propagations.



Fig. S6. Characterization of *A. annua* **transgenic plants.** (**A**, **B**, **D**, **E**, **G**, **H**) HPLC analysis of dihydroartemisinic acid (DHAA) and artemisinic acid (AA) in the leaves of different *A. annua AaTCP14*-overexpression lines (A and B), *AaTCP14*-antisense lines (D and E), *AaTCP14-AaORA* co-overexpression lines (G and H), plants transformed with the empty vector (Vector) and WT plants. The data represent the means \pm SD of three replicates from three cutting propagations. (**C** and **F**) The phenotypes of 3-month-old *A. annua* plants transformed with the empty vector (control plants, labled as Vector), three independent *AaTCP14*-overexpression lines (C) and *AaTCP14*-antisense lines (F). (**I**) The phenotypes of 2-month-old *A. annua* plants transformed with the empty vector (control plants, labled as Vector) and three independent *AaTCP14-AaORA* co-overexpression (*AaTCP14-AaORA*) lines. Scale bar = 10 cm.



Fig. S7. Neither AaORA nor AaJAZ8 affects the ability of AaTCP14 to bind DNA. (A-C) EMSA assay of AaTCP14 binding to the D2 motif from the DBR2 promoter (A, C), and the A1 motif from the ALDH1 promoter (B). Binding reactions contained 0.5 µg of His-AaTCP14 protein and an increasing amount (0.5 µg, 1 µg, 2 µg, 4 µg) of His-AaORA or His-AaJAZ8 protein. The labeled D2q and A1q probes are the same as in Fig. 4.



Fig. S8. The expression patterns of *AaJAZ8*, MeJA-induced AaJAZ8 degradation, and analysis of artemisinin biosynthesis in *A. annua* plants overexpressing *AaJAZ8* or *AaJAZ8* Δ *jas*. (A) Relative expression levels of *AaJAZ8* in different tissues, including roots, stems, flowers, shoots, buds, leaves and trichomes, were measured by quantitative real-time PCR. The expression level of *AaJAZ8* in roots was set as 1. *Actin* was used as an internal control. The data represent the means \pm SD from three replicates from three independent *A. annua* plants. (B) The expression levels of *AaJAZ8* in plants treated with 100 μ M MeJA or 0.1% ethanol (Mock) over 24 hours. *Actin* was used as an internal control. The data represent the means \pm SD of three replicates from three independent *A. annua* plants. (C) MeJA stimulates AaJAZ8 turnover in a 26S proteasome-dependent manner. *N. benthamiana* leaves expressing JAZ8-Flag were pretreated with or without the 26S proteasome inhibitor MG132 (100 μ M) for 1 hour, and then the leaves were treated with MeJA (50 μ M) for 0, 0.5, 1, 2, and 4 hours.

Western blot analysis with anti-Flag antibody was done to measure the levels of JAZ8-Flag. A Coomassie-stained SDS-PAGE gel (Coomassie) was used to confirm equal sample loading. (**D**) Expression levels of *JAZ8*, *ADS*, *CYP71AV1*, *DBR2* and *ALDH1* in different *A. annua AaJAZ8*-overexpression lines, plants transformed with the empty vector (Vector) and WT. *Actin* was used as the internal control. The data represent the means \pm SD from three replicates from three cutting propagations. (**E**) HPLC analysis of artemisinin (AN) in the leaves of *AaJAZ8*-overexpression lines, plants transformed with the empty vector (Vector) and WT plants. The data represent the means \pm SD of three replicates from three cutting propagations. (**F**) Expression levels of *JAZ8Ajas*, *ADS*, *CYP71AV1*, *DBR2* and *ALDH1* in different *A. annua AaJAZ8Ajas*-overexpression lines, plants transformed with the empty vector and WT. *Actin* was used as the internal control. The data represent the means \pm SD from three cutting propagations. (**F**) Expression levels of *JAZ8Ajas*, *ADS*, *CYP71AV1*, *DBR2* and *ALDH1* in different *A. annua AaJAZ8Ajas*-overexpression lines, plants transformed with the empty vector and WT. *Actin* was used as the internal control. The data represent the means \pm SD from three technical replicates.



Fig. S9. AaTCP14 and AaORA interact with AaJAZ proteins and mapping of the domains involved in the interaction between AaJAZ8, AaORA, and AaTCP14 using Y2H assays. (A) Interactions between AaJAZ proteins and AaTCP14, AaORA or AaMYC2 in Yeast two hybrid (Y2H) assays. (B) Y2H assays showing the interactions between AaTCP14, AaORA and truncated versions of AaJAZ8. Left, schematic representations of the truncated AaJAZ8 protein used in this experiment. Numbers indicate the amino acid positions of the

truncated AaJAZ8 variants. The ZIM and jas domains are indicated by the red box and green box, respectively. Right, Y2H assays of protein interactions between AD-TCP14, AD-ORA and truncated versions of BD-JAZ8. (C) Y2H assays showing the interactions between AaTCP14, AaJAZ8 and truncated versions of AaORA. Left, schematic representations of the truncated AaORA protein used in this experiment. Numbers indicate the amino acid positions of the truncated AaORA variants. The AP2 domain is indicated by a blue box. Right, Y2H assays of protein interactions between AD-TCP14, AD-JAZ8 and truncated versions of BD-ORA. Transformed yeast cells were grown on the selective medium QDO and control medium DDO, and pictures were taken after 4 days of incubation at 30°C. The Y2H assays were repeated three times, and representative results are shown.



Fig. S10. Artemisinin content in *AaTCP14* transgenic plants under MeJA treatment. (A and B) Artemisinin content in *A. annua AaTCP14*-overexpression lines (A), *AaTCP14*-antisense lines (B) and plants transformed with the empty vector (control plants, labeled as Vector) was measured by HPLC after 48 h of treatment with 100 μ M MeJA or 0.1% ethanol (Mock). The data represent the means \pm SD of three replicates from three cutting propagations.

Name	Primer sequence (5'-3')	
Primers for the Dual-LUC assay		
1300-AaORA-GFP-F	GGGGCCCGGGGTCGACATGTTTGCTACTTGCATTCG	
1300-AaORA-GFP-R	TACCGGATCCACTAGTAAAAAAAAAAAAAGTCATCAT	
1300-AaTCP14-GFP-F	GGGGCCCGGGGTCGACATGGATGGTGGTGATGATCA	
1300-AaTCP14-GFP-R	TACCGGATCCACTAGTCGACTGATGGCTAGTTGTAT	
1300-AaJAZ8-GFP-F	GGGGCCCGGGGTCGACATGGAGAGGGATTTTATGGG	
1300-AaJAZ8-GFP-R	TACCGGATCCACTAGTCTTGCTTGCAACAGCGATAG	
pGreen0800-UBQ-F	CGGTATCGATAAGCTTGCGGATACAATTTCAATATA	
pGreen0800-UBQ-R	ATCCCCCGGGCTGCAGGGTCTTACCAGTGAGGGTCT	
pGreen0800-ADS-F	CGGTATCGATAAGCTTCTCGAGTATGGTGTTTCAAC	
pGreen0800-ADS-R	ATCCCCCGGGCTGCAGGATTTTCAAAACTTTGAATA	
pGreen0800-CYP-F	CGGTATCGATAAGCTTAATGGGTCAATTTCGGGTTG	
pGreen0800-CYP-R	ATCCCCCGGGCTGCAGCATGCTTTTAGTATACTC	
pGreen0800-DBR2-F	CGGTATCGATAAGCTTAAGAACTTCGAGATAGAAAA	
pGreen0800-DBR2-R	ATCCCCCGGGCTGCAGTCAGTGATGGAGTTGGTAAA	
pGreen0800-ALDH1-F	CGGTATCGATAAGCTTATGAACCATTAGAAGGGAAG	
pGreen0800-ALDH1-R	ATCCCCCGGGCTGCAGCTTTGTTTTTATGAAATTT	
Primers for constructs used in t	he Y1H assay	
pB42AD-AaORA-F	TGCCTCTCCCGAATTCATGTTTGCTACTTGCATTCG	
pB42AD-AaORA-R	TCCAAAGCTTCTCGAGTCAAAAAAAAAAAAAAGTCAT	
pB42AD-AabZIP1-F	TGCCTCTCCCGAATTCATGAACTACAAGAATTTTGG	
pB42AD-AabZIP1-R	TCCAAAGCTTCTCGAGTCACCATGGACCGGAAAGTG	
pB42AD-AaTCP14-F	TGCCTCTCCCGAATTCATGGATGGTGGTGATGATCA	
pB42AD-AaTCP14-R	TCCAAAGCTTCTCGAGTCACGACTGATGGCTAGTTG	
ADSpro:LacZ-F	TATTGGATCGGAATTCCTCGAGTATGGTGTTTCAAC	
ADSpro:LacZ-R	GAGCACATGCCTCGAGGATTTTCAAAACTTTGAATA	
CYP71AV1pro:LacZ-F	TATTGGATCGGAATTCAATGGGTCAATTTCGGGTTG	
CYP71AV1pro:LacZ-R	GAGCACATGCCTCGAGCATGCTTTTAGTATACTC	
DBR2pro:LacZ-F	TATTGGATCGGAATTCAAGAACTTCGAGATAGAAAA	
DBR2pro:LacZ-R	GAGCACATGCCTCGAGTCAGTGATGGAGTTGGTAAA	
ALDH1pro:LacZ-F	TATTGGATCGGAATTCATGAACCATTAGAAGGGAAG	
ALDH1pro:LacZ-R	GAGCACATGCCTCGAGCTTTGTTTTTTATGAAATTT	
DBR2pro(3×D1):LacZ-F	AATTCCACGGTCCCACTTTCACGGTCCCACTTTCACGGTCCCACTTTC	
DBR2pro(3×D1):LacZ-R	TCGAGAAAGTGGGACCGTGAAAGTGGGACCGTGAAAGTGGGACCGTGG	
DBR2pro(3×D2):LacZ-F	AATTCTAAGCCCAAATTAAGCCCAAATTAAGCCCAAATC	
DBR2pro(3×D2):LacZ-R	TCGAGATTTGGGCTTAATTTGGGCTTAATTTGGGCTTAG	
ALDH1pro(3×A1):LacZ-F	AATTCTCTGGCCCCACCGTTCTGGCCCCACCGTTCTGGCCCCACCGTC	
ALDH1pro(3×A1):LacZ-R	TCGAGACGGTGGGGCCAGAACGGTGGGGCCAGAACGGTGGGGCCAGAG	
ALDH1pro(3×A2):LacZ-F	AATTCCCAGCCCAATACCAGCCCAATACCAGCCCAATAC	
ALDH1pro(3×A2):LacZ-R	TCGAGTATTGGGCTGGTATTGGGCTGGG	
ALDH1pro(3×A3):LacZ-F	AATTCTTAGCCCAATATTAGCCCAATATTAGCCCAATAC	

Table S1. List of primers used in this study.

ALDH1pro(3×A3):LacZ-R	TCGAGTATTGGGCTAATATTGGGCTAATATTGGGCTAAG	
ABI5pro(3×B1):LacZ-F	AATTCCATGGGTCCCACACACCATGGGTCCCACACACCATGGGTCCCACACACC	
ABI5pro(3×B1):LacZ-R	TCGAGGTGTGTGGGACCCATGGTGTGTGGGACCCATGGTGTGGGACCCATGG	
Primers used to generate DNA constructs for the Y2H assay		
BD-AaORA-F	GGAGGACCTGCATATGATGTTTGCTACTTGCATTCG	
BD-AaORA-R	GGATCCCCGGGAATTCTCAAAAAAAAAAAAAAGTCAT	
BD-AaORA-∆C1-F	GGAGGACCTGCATATGATGTTTGCTACTTGCATTCG	
BD-AaORA-∆C1-R	GGATCCCCGGGAATTCTCAACGTCTCCTGACTCCTC	
BD-AaORA-∆C2-F	GGAGGACCTGCATATGATGTTTGCTACTTGCATTCG	
BD-AaORA-∆C2-R	GGATCCCCGGGAATTCTCAACAGCCTATTAAGAGAG	
BD-AaORA-∆N1-F	GGAGGACCTGCATATGTTAATAGGCTGTGATGATCG	
BD-AaORA-∆N1-R	GGATCCCCGGGAATTCTCAAAAAAAAAAAAAAGTCAT	
BD-AaORA-∆N2-F	GGAGGACCTGCATATGGTCAGGAGACGTCCGTGGGG	
BD-AaORA-∆N2-R	GGATCCCCGGGAATTCTCAAAAAAAAAAAAAAGTCAT	
BD-AaORA-MC-F	GGAGGACCTGCATATGGTCAGGAGACGTCCGTGGGG	
BD-AaORA-MC-R	GGATCCCCGGGAATTCTCAACAGCCTATTAAGAGAG	
BD-AaTCP14-F	GGAGGACCTGCATATGATGGATGGTGGTGATGATCA	
BD-AaTCP14-R	GGATCCCCGGGAATTCTCACGACTGATGGCTAGTTG	
BD-AaTCP14-∆C1-F	GGAGGACCTGCATATGATGGATGGTGGTGGTGATGATCA	
BD-AaTCP14-∆C1-R	GGATCCCCGGGAATTCTCATTTTTTCGAGGGTTCTGTTG	
BD-AaTCP14-∆C2-F	GGAGGACCTGCATATGATGGATGGTGGTGGTGATGATCA	
BD-AaTCP14-∆C2-R	GGATCCCCGGGAATTCTCAATTTAAGGAAGTGAAGTTAG	
BD-AaTCP14-∆N1-F	GGAGGACCTGCATATGACTTCCTTAAATATTTCACT	
BD-AaTCP14-∆N1-R	GGATCCCCGGGAATTCTCACGACTGATGGCTAGTTG	
BD-AaTCP14-∆N2-F	GGAGGACCTGCATATGCCCTCGAAAAAACTAGCTCC	
BD-AaTCP14-∆N2-R	GGATCCCCGGGAATTCTCACGACTGATGGCTAGTTG	
BD-AaTCP14-MC-F	GGAGGACCTGCATATGCCCTCGAAAAAACTAGCTCC	
BD-AaTCP14-MC-R	GGATCCCCGGGAATTCTCAATTTAAGGAAGTGAAGTTAG	
BD-AaJAZ8-F	GGAGGACCTGCATATGATGGAGAGGGATTTTATGGG	
BD-AaJAZ8-R	GGATCCCCGGGAATTCTCACTTGCTTGCAACAGCGA	
BD-AaJAZ8-∆ZIM-F	GGAGGACCTGCATATGGGACAAGCGATGCAATCAGC	
BD-AaJAZ8-∆ZIM-R	GGATCCCCGGGAATTCTCACTTGCTTGCAACAGCGA	
BD-AaJAZ8-∆jas-F	GGAGGACCTGCATATGATGGAGAGGGATTTTATGGG	
BD-AaJAZ8-∆jas-R	GGATCCCCGGGAATTCTCATTGCATCGCTTGTCCGA	
BD-AaJAZ1-F	GGAGGACCTGCATATGATGTCGATGGCTAGAAACTT	
BD-AaJAZ1-R	GGATCCCCGGGAATTCCTATACGTTGAGATCAAATT	
BD-AaJAZ2-F	GGAGGACCTGCATATGATGTCATCGGCTAAACAATT	
BD-AaJAZ2-R	GGATCCCCGGGAATTCCTATAAATTTAGATCGAACT	
BD-AaJAZ3-F	GGAGGACCTGCATATGATGGAAAGGGATTTCATGGG	
BD-AaJAZ3-R	GGATCCCCGGGAATTCTCACTTTGTATCATCTTTGC	
BD-AaJAZ4-F	GGAGGACCTGCATATGATGGGTTCATCAGAAATTGT	
BD-AaJAZ4-R	GGATCCCCGGGAATTCTTATTGGACATGAGATTGTG	
BD-AaJAZ5-F	GGAGGACCTGCATATGATGTCTGAGACTGTGGATTC	

BD-AaJAZ5-R	GGATCCCCGGGAATTCTTATTGGGCACCAGAAGATT	
BD-AaJAZ6-F	GGAGGACCTGCATATGATGTCGGCTGCCCAACGTTT	
BD-AaJAZ6-R	GGATCCCCGGGAATTCTTACATATTAAGGTCGAAAC	
BD-AaJAZ7-F	GGAGGACCTGCATATGATGGAACGAGATTTTATGGG	
BD-AaJAZ7-R	GGATCCCCGGGAATTCCTAATGCTCGCCTGCTGCTA	
BD-AaJAZ9-F	GGAGGACCTGCATATGATGTTGAGATCACCCTCGGT	
BD-AaJAZ9-R	GGATCCCCGGGAATTCTCAATGCAAAGACAAGTCTC	
AD-AaTCP14-F	AGATTACGCTCATATGATGGATGGTGGTGATGATCA	
AD-AaTCP14-R	CACCCGGGTGGAATTCTCACGACTGATGGCTAGTTG	
AD-AaORA-F	TGCCTCTCCCGAATTCATGTTTGCTACTTGCATTCG	
AD-AaORA-R	TCCAAAGCTTCTCGAGTCAAAAAAAAAAAAAAGTCAT	
AD-AaJAZ8-F	AGATTACGCTCATATGATGGAGAGGGATTTTATGGG	
AD-AaJAZ8-R	CACCCGGGTGGAATTCTCACTTGCTTGCAACAGCGA	
AD-AaMYC2-F	AGATTACGCTCATATGATGACGATGAATATATGGAA	
AD-AaMYC2-R	CACCCGGGTGGAATTCTTACCTAGGATCTGACATTC	
Primers for constructs in pull-d	own assay	
pCold-AaTCP14-F	CGAAGGTAGGCATATGATGGATGGTGGTGATGATCA	
pCold-AaTCP14-R	AGATTACCTATCTAGATCACGACTGATGGCTAGTTG	
pGEX4T-1-AaORA-F	GGTTCCGCGTGGATCCATGTTTGCTACTTGCATTCG	
pGEX4T-1-AaORA-R	GTCGACCCGGGAATTCTCAAAAAAAAAAAAAAGTCAT	
Primers for constructs used in t	he BiFC experiment	
Topo-AaTCP14-F	CACCATGGATGGTGGTGATGATCA	
Topo-AaTCP14-R	CGACTGATGGCTAGTTGTAT	
Topo-AaORA-F	CACCATGTTTGCTACTTGCATTCG	
Topo-AaORA-R	AAAAAAAAAAGTCATCAT	
Topo-AaJAZ8-F	CACCATGGAGAGGGATTTTATGGG	
Topo-AaJAZ8-R	CTTGCTTGCAACAGCGATAG	
Primers for constructs used in the Co-IP assays and degradation assay		
1300-AaORA-Flag-F	GGGGCCCGGGGTCGACATGTTTGCTACTTGCATTCG	
1300-AaORA-Flag-R	TACCGGATCCACTAGTAAAAAAAAAAAAAGTCATCAT	
1300-AaJAZ8-Flag-F	GGGGCCCGGGGTCGACATGGAGAGGGATTTTATGGG	
1300-AaJAZ8-Flag-R	TACCGGATCCACTAGTCTTGCTTGCAACAGCGATAG	
Primers for constructs used in the subcellular localization experiment		
pHB-AaTCP14-YFP-F	CGAGCTGCAGGAGCTCATGGATGGTGGTGATGATCA	
pHB-AaTCP14-YFP-R	TGCTCACCATACTAGTCGACTGATGGCTAGTTGTATC	
Primers for analyzing genes expression		
Actin-F	CCAGGCTGTTCAGTCTCTGTAT	
Actin-R	CGCTCGGTAAGGATCTTCATCA	
QPCR-AaTCP14-F	AGGGACGGTATCTACGGGTT	
QPCR-AaTCP14-R	AGCGTGATGCGATTGAGA	
QPCR-antisense-AaTCP14-F	GCTTCTCTCTCTCACAT	
QPCR-antisense-AaTCP14-R	GTGGCAGCACTTGTAGTTA	
QPCR-ADS-F	GGACTAGGTTCAGGCTATG	

QPCR-ADS-R	GGACTAGGTTCAGGCTATG	
QPCR-CYP71AV1-F	TCATTTCAGTCGCTT	
QPCR-CYP71AV1-R	CCAGTTTGCCTCAGTA	
QPCR-DBR2-F	ACTGCTGGTGGCTTTCTTA	
QPCR-DBR2-R	ACCCTCGACTTGTTCCTTA	
QPCR-ALDH1-F	GGACTTGCCTCAGGTGTAT	
QPCR-ALDH1-R	GTGCCTCTAATCCTTGTTC	
QPCR-AaORA-F	TCCTCCTCTTCATCCTCTATCG	
QPCR-AaORA-R	CGTTGTCCTTTCTGTCCTCAGT	
QPCR-AaJAZ8-F	ATGGTCCCTTTATGGCAGC	
QPCR-AaJAZ8-R	AATGATGCTTTGCGAGCC	
QPCR-AaJAZ8∆jas-F	CATTCGGTTCTTCCATCTACC	
QPCR-AaJAZ8∆jas -R	CTGCCATAAAGGGACCATTT	
QPCR-AaMYC2-F	TGAGGAAGTTACTGATACAGAATGG	
QPCR-AaMYC2-R	GTATTCCGAATACCTGACCTTGT	
QPCR-AaGSW1-F	TCTCGTCAAAGACACACACATTC	
QPCR-AaGSW1-R	TTGTTCGTAGTTGCTGTAGTGCT	
QPCR-AaWRKY1-F	TAGCGTTGATGGTGGTTACA	
QPCR-AaWRKY1-R	ACAGGTGGCGAATAGACT	
QPCR-AaAOS-F	CAACTACTACCACAACCACTACTGG	
QPCR-AaAOS-R	TGTCGGGAAAGATTTAGCG	
QPCR-AaAOC-F	GTCCTGCTTACCTACGGTTGGG	
QPCR-AaAOC-R	TTCTGTCGTGATGTATGCGCCT	
QPCR-AaOPR3-F	ATGGTCAAACAGAAGCGGG	
QPCR-AaOPR3-R	TGTCAAGAGAAGGGTAATCCG	
QPCR-AaOPCL1-F	ACAACCTCCACATTCCACAG	
QPCR-AaOPCL1-R	GACGGATTCAACGGCTTT	
Primers for constructs used in the EMSA assays		
pCold-AaORA-F	CGAAGGTAGGCATATGATGTTTGCTACTTGCATTCG	
pCold-AaORA-R	AGATTACCTATCTAGATCAAAAAAAAAAAAAAAGTCAT	
pCold-AaJAZ8-F	CGAAGGTAGGCATATGATGGAGAGGGATTTTATGGG	
pCold-AaJAZ8-R	AGATTACCTATCTAGATCACTTGCTTGCAACAGCGA	
D2q Probe-F	GTCGCTAAACTTGCCACGGTCCCACTTTTTCAACTCTTATTA	
D2q Probe-R	TAATAAGAGTTGAAAAAGTGGGACCGTGGCAAGTTTAGCGAC	
D2q Probe-mutant1-F	GTCGCTAAACTTGCCACGGTAAACATTTTTCAACTCTTATTA	
D2q Probe-mutant1-R	TAATAAGAGTTGAAAAATGTTTACCGTGGCAAGTTTAGCGAC	
D2q Probe-mutant2-F	GTCGCTAAACTTGCCACGTTGAAACATTTTTCAACTCTTATTA	
D2q Probe-mutant2-R	TAATAAGAGTTGAAAAATGTTTCAACGTGGCAAGTTTAGCGAC	
A1q Probe-F	GGTTGGTTGCATTATCTGGCCCCACCGTAAACAATCAAATGC	
A1q Probe-R	GCATTTGATTGTTTACGGTGGGGCCAGATAATGCAACCAAC	
A1q Probe-mutant1-F	GGTTGGTTGCATTATCTGGCAAACACGTAAACAATCAAATGC	
A1q Probe-mutant1-R	GCATTTGATTGTTTACGTGTTTGCCAGATAATGCAACCAAC	
A1q Probe-mutant2-F	GGTTGGTTGCATTATCTTTAAAACACGTAAACAATCAAATGC	

A1q Probe-mutant2-R	GCATTTGATTGTTTACGTGTTTTAAAGATAATGCAACCAAC	
Primers for constructs used to	generate the of AaTCP14, AaTCP14-AaORA, ANTCP14-AaORA, AaJAZ8, AaJAZ8∆jas and	
1391Z-proTCP14 transgenic plants		
pHB- AaTCP14-Flag-F	GGATCCTACCTGCAGATGGATGGTGGTGATGATCA	
pHB- AaTCP14-Flag-R	AACGAAAGCTCTAGACGACTGATGGCTAGTTGTATC	
pHB- ANTCP14-F	CGAGCTGCAGGAGCTCCGACTGATGGCTAGTTGTAT	
pHB-ANTCP14-R	TGCTCACCATACTAGTATGGATGGTGGTGATGATCA	
1305-AaTCP14-Myc-F	GGACTCTTGACCATGGTAATGGATGGTGGTGATGATCA	
1305-AaTCP14-Myc-R	ATTCGAGCTGGTCACCTTATACCGAGTTCAAGTCCT	
1305-AaORA-GFP-F	GACTCTTGACCATGGTAATGTTTGCTACTTGCATTCG	
1305-AaORA-GFP-R	ATTCGAGCTGGTCACCTTACTTGTACAGCTCGTCCA	
1305-ANTCP14-GFP-F	GGACTCTTGACCATGGTACGACTGATGGCTAGTTGTAT	
1305-ANTCP14-GFP-R	ATTCGAGCTGGTCACCTTACTTGTACAGCTCGTCCA	
pHB-AaJAZ8-F	CGAGCTGCAGGAGCTCATGGAGAGGGATTTTATGGG	
pHB-AaJAZ8-R	TGCTCACCATACTAGTCTTGCTTGCAACAGCGATAG	
pHB-AaJAZ8∆jas-YFP-F	CGAGCTGCAGGAGCTCATGGAGAGGGATTTTATGGG	
pHB-AaJAZ8∆jas-YFP-R	TGCTCACCATACTAGTTTGCATCGCTTGTCCGAGTG	
1391Z-proTCP14-F	CCAAGCTTGGCTGCAGGCATTGACCACTGAGATGACAGT	
1391Z-proTCP14-R	GAATTCCCGGGGATCCAGAGAGATAACTAGGCGTGATTG	
Primers for constructs used in (Co-localization experiments	
pHB-AaJAZ8-YFP-F	CGAGCTGCAGGAGCTCATGGAGAGGGATTTTATGGG	
pHB-AaJAZ8-YFP-R	TGCTCACCATACTAGTCTTGCTTGCAACAGCGATAG	
pHB-AaORA-CFP-F	GCAGCCCGGGGGATCCATGTTTGCTACTTGCATTCG	
pHB-AaORA-CFP-R	TGCTCACCATACTAGTAAAAAAAAAAAAAGTCATCAT	
pHB- AaTCP14-CFP-F	GCAGCCCGGGGGATCCATGGATGGTGGTGATGATCA	
pHB- AaTCP14-CFP-R	TGCTCACCATACTAGTCGACTGATGGCTAGTTGTATC	
Primers for constructs used in I	Juciferase complementation assays	
Cluc-JAZ8-F	GTCCCGGGGCGGTACCATGGAGAGGGATTTTATGGG	
Cluc-JAZ8-R	AGCTCTGCAGGTCGACTCACTTGCTTGCAACAGCGA	
TCP14-Nluc-F	GGACGAGCTCGGTACCATGGATGGTGGTGATGATCA	
TCP14-Nluc-R	ACGAGATCTGGTCGACCGACTGATGGCTAGTTGTATC	
ORA-Nluc-F	GGACGAGCTCGGTACCATGTTTGCTACTTGCATTCG	
ORA-Nluc-R	ACGAGATCTGGTCGACAAAAAAAAAAAAAGTCATCAT	
Cluc-AaORA-F	GTCCCGGGGCGGTACCATGTTTGCTACTTGCATTCG	
Cluc-AaORA-R	AGCTCTGCAGGTCGACTCAAAAAAAAAAAAAAAGTCAT	
Primers for constructs used in the Y3H assay		
pBridge(BD)-AaTCP14-F	TGTATCGCCGGAATTCATGGATGGTGGTGATGATCA	
pBridge(BD)-AaTCP14-R	GGCTGCAGGTCGACGTCACGACTGATGGCTAGTTG	
pBridge(Met)-AaJAZ8-F	AAAGGTGGCCGCCAATGGAGAGGGATTTTATGGG	
pBridge(Met)-AaJAZ8-R	ATCAGCCCGAAGATCTTCACTTGCTTGCAACAGCGA	