Appendix for

LncRNA *DANA1* promotes histone deacetylation of drought responsive genes in *Arabidopsis*

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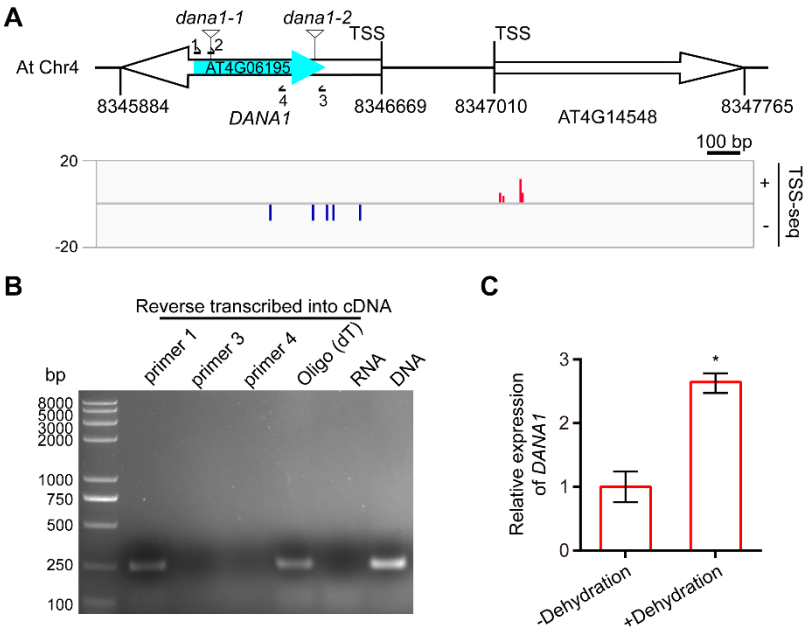
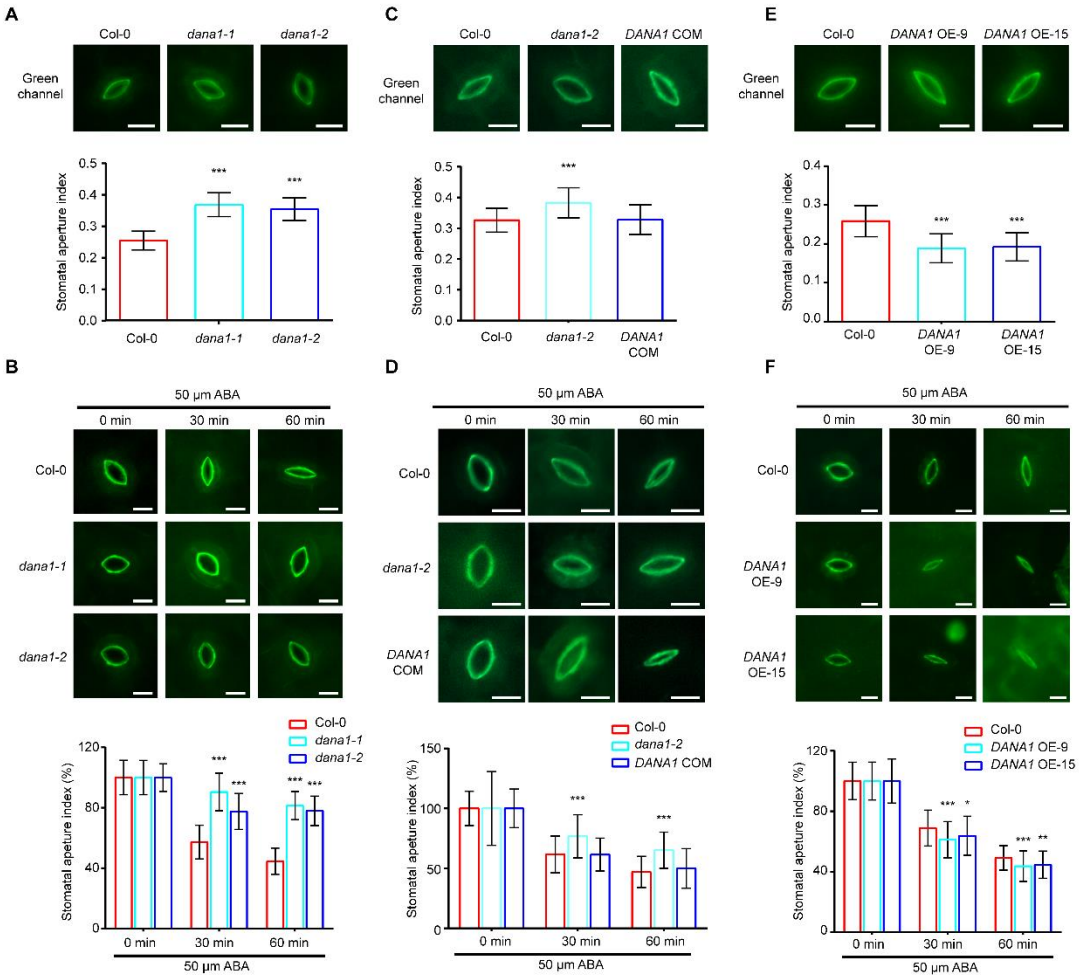


Appendix Figure S1. Detection of transcription direction of *DANA1*.

A Genome browser screenshot of the *DANA1* locus. In TSS-seq (Transcription Start Site sequencing), sense (+) and antisense (-) strands were shown in red and dark blue, respectively. The primer 1, primer 3, primer 4 and oligo (dT) was separately in reverse transcription for producing cDNAs, and primer 2 and primer 4 were used in the PCR reaction presented in (B).

B Strand-specific RT-PCR analysis. RNA and DNA from Col-0 plants were used as negative and positive control, respectively.

C Expression of *DANA1* was induced by dehydration. RNAs were extracted from 10-day-old Col-0 seedlings that were either dehydrated to lose approximately 60% fresh weight or not (-Dehydration), and gene expression level was measured by RT-qPCR normalized against the *UBQ3* gene.



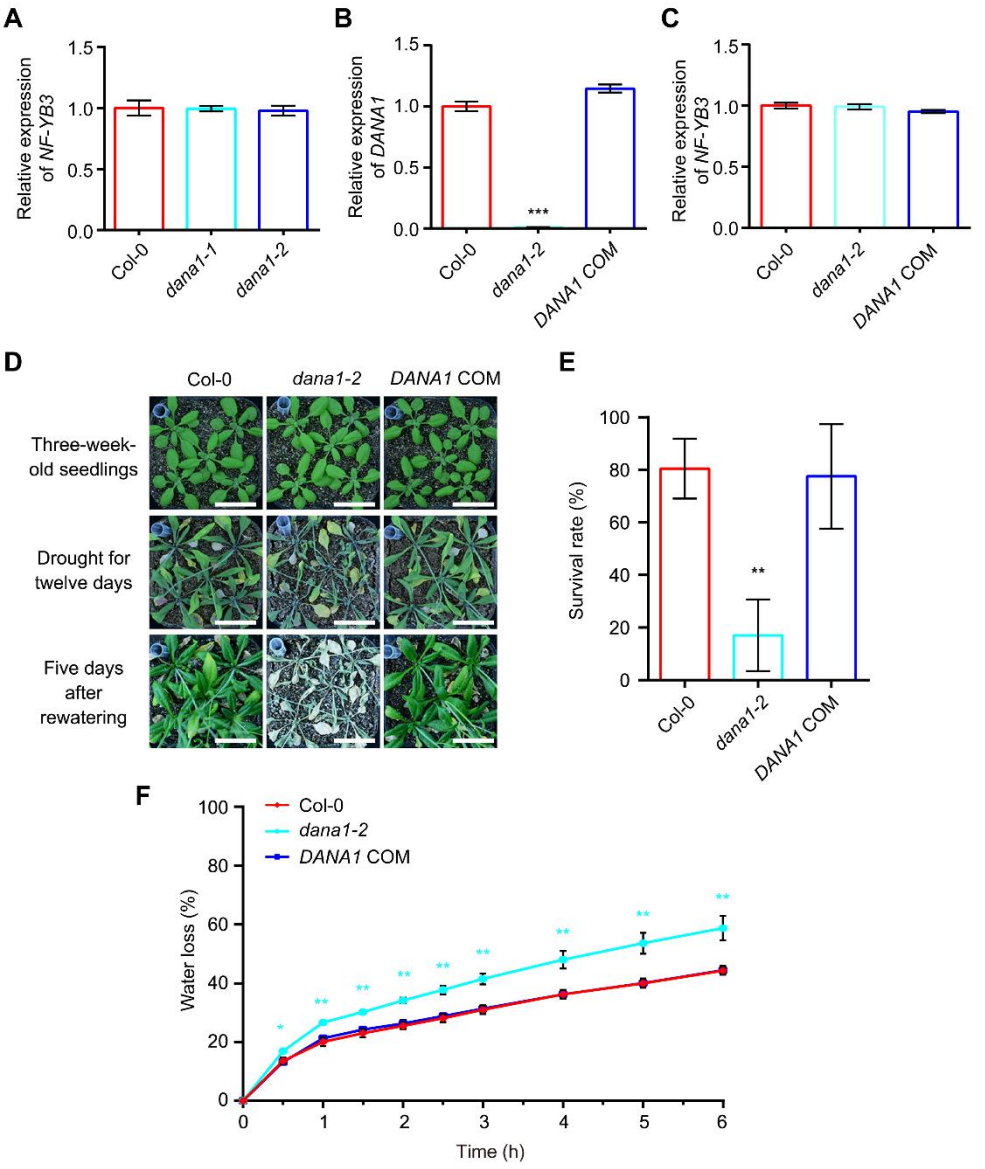
Appendix Figure S2. Stomatal aperture index and ABA-induced stomatal closure in *dana1* mutant, *DANA1* over-expressing and *DANA1* complementation plants.

A, B Mutated *DANA1* increases both stomatal aperture index (A) and ABA-induced stomatal closure (B).

C, D Stomatal aperture index (C) and ABA-induced stomatal closure (D) in *DANA1* COM are similar to Col-0.

E, F Over-expressing *DANA1* decreases both stomatal aperture index (E) and ABA-induced stomatal closure (F).

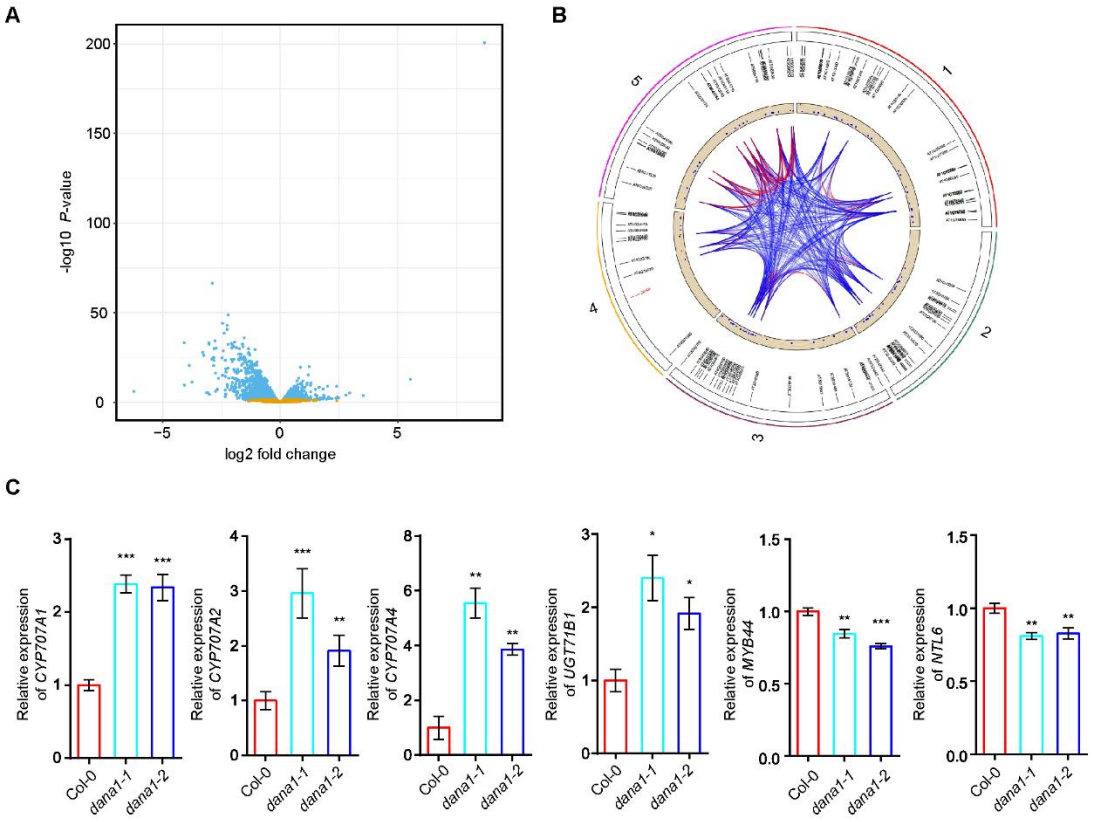
Data information: Data shown as mean ± SD (n = 60). Asterisks represent significant differences determined by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$). Scale bars = 10 μm.



Appendix Figure S3. Drought-tolerant phenotype of *DANA1* complementation plants.

A Quantitative measurement of the transcript levels of *NF-YB3* in Col-0 and the *dana1* mutant plants. *UBQ3* was used as an internal control.
B Quantitative measurement of the transcript levels of *DANA1* in Col-0, *dana1-2* and *DANA1* complementation (*DANA1* COM) plants. *UBQ3* was used as an internal control.
C Quantitative measurement of the transcript levels of *NF-YB3* in Col-0, *dana1-2* and *DANA1* complementation (*DANA1* COM) plants. *UBQ3* was used as an internal control.
D Morphology of seedlings before and after drought stress treatment. Three-week-old Col-0, *dana1-2* and *DANA1* COM plants were subjected to drought stress for twelve days and then rewatered for five days. Scale bars = 3 cm.
E Survival rate after drought treatment (n = 3 biological replates).
F Water loss in detached leaves of three-week-old Col-0, *dana1-2* and *DANA1* COM plants (n = 3 biological replicates, each replicate contains five fully expanded leaves).
Data information: Values shown are means ± SD from three replicates. Asterisks represent significant differences determined by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$;

*** $P < 0.001$).



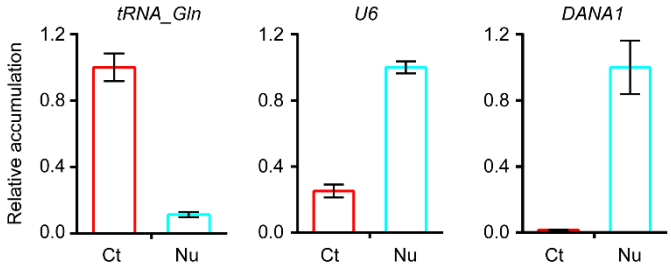
Appendix Figure S4. Gene differential expression analysis of *dana1* mutant using RNA-seq.

A Volcano plot presenting adjusted *p*-value versus gene expression fold change. Blue dots stand for significantly differentially expressed genes (Benjamini-Hochberg method adjusted *P*-value < 0.05).

B Genomic distribution of 100 most significantly differentially expressed genes. Blue and red dots of the scatter plot inside inner track represent down- and up- regulated genes respectively. Links inside the circle plot represent 100 most significantly differentially expressed genes, blue and red lines stand for between- and in-chromosome connections respectively.

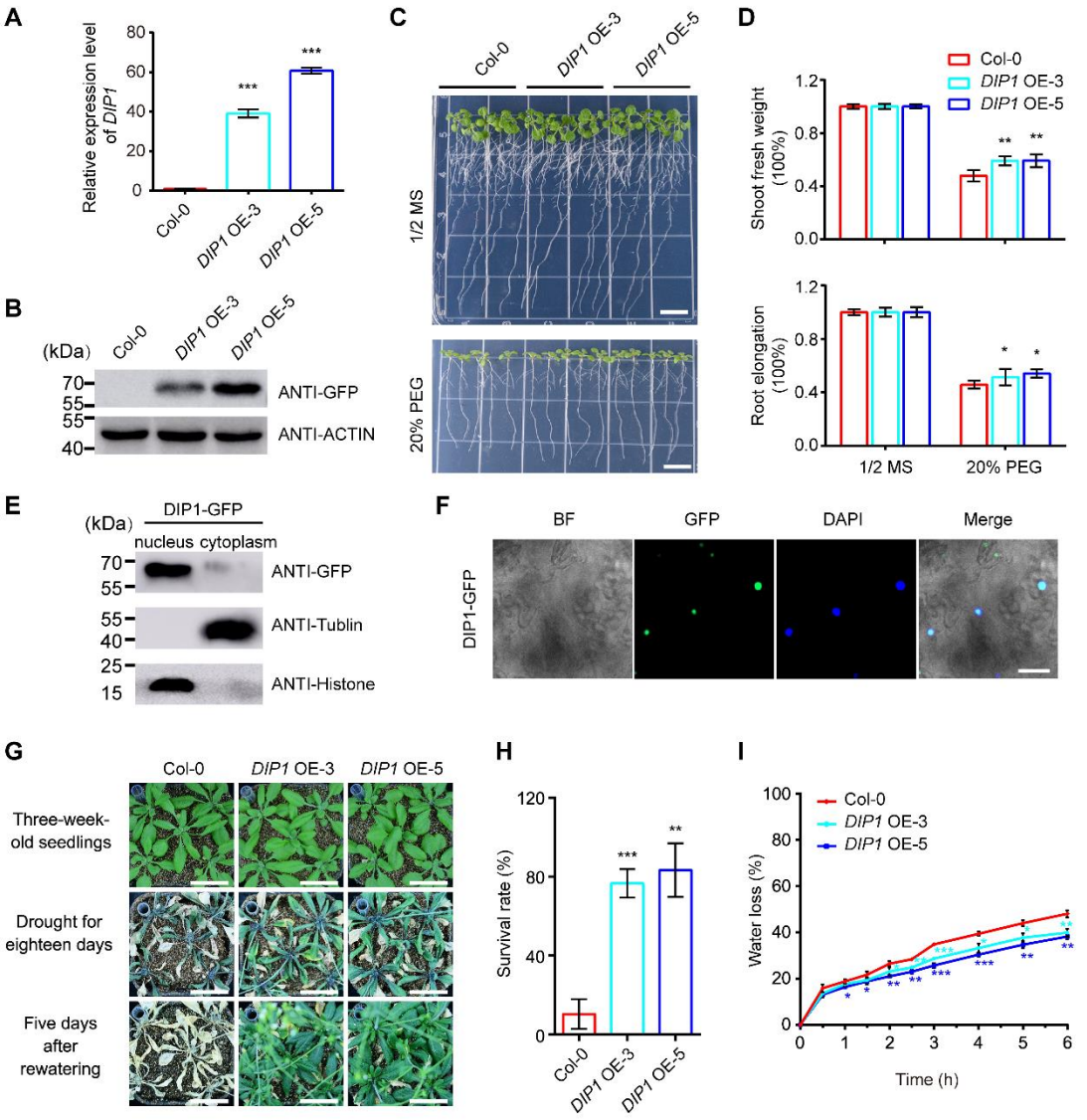
C Expression profiles of drought response related genes in *dana1* mutant. *UBQ3* was used as an internal control.

Data information: Asterisks represent significant differences determined by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).



Appendix Figure S5. *DANA1* is mainly enriched in the nucleus.

Relative subcellular distributions of *DANA1* transcripts. *U6* RNA and Glutamine tRNA (*tRNA_Gln*) were used as nuclear and cytoplasmic RNA controls, respectively. Nu: nucleus; Ct: cytoplasm.



Appendix Figure S6. Drought-tolerant phenotype of *DIP1* over-expressing plants.

A, B Detection on the transcript levels (A) and protein levels (B) of *DIP1* in *DIP1* over-expressing transgenic lines. *DIP1* OE-3 and *DIP1* OE-5 are Col-0 plants transformed with *UBQ10: DIP1-GFP*. *DIP1* OE-5 has been used in RIP assay presented in Fig. 3D. ACTIN is shown as a loading control.

C The *DIP1* over-expressing lines are insensitive to PEG treatment. Scale bars = 1 cm.

D Root length and fresh weight of seedlings shown in (C).

E Immunoblot analyses showing the nucleus and cytoplasmic distributions of DIP1-GFP protein.

F Subcellular localization of DIP1-GFP in rosette leaves of 3-week-old *DIP1* OE-5 plants. Scale bar = 20 μm.

G Drought-tolerance assay. Col-0, *DIP1* OE-3 and *DIP1* OE-5 plants grown under normal growth conditions for three weeks were subjected to drought stress for eighteen days and then rewatered for three days. Scale bars = 3 cm.

H Survival rate after drought treatment (n = 3 biological replates).

I Water loss in detached leaves of three-week-old Col-0, *DIP1* OE-3 and *DIP1* OE-5 plants.

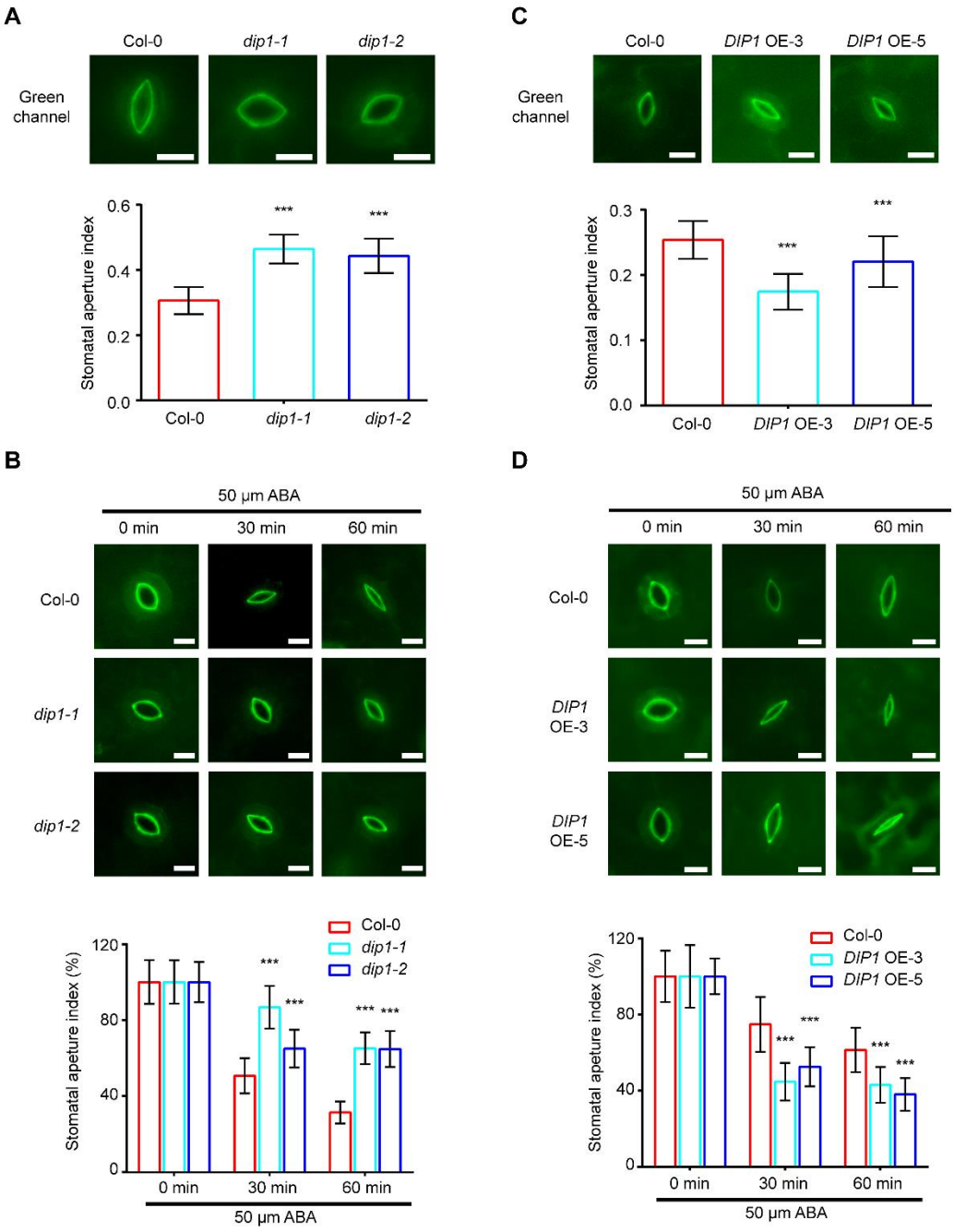
Data information: Values shown are means ± SD from three biological replicates.

Asterisks represent significant differences determined by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).

Appendix Figure S7. Targeted mutagenesis of *DIP1* in *Arabidopsis* using CRISPR/Cas9 system.

A CRISPR/Cas9-induced *DIP1* gene mutations at the target site in the mutants. The protospacer of the sgRNA and protospacer-adjacent motif (PAM) sequences are highlighted in red and bold underlined, respectively. Numbers in parentheses indicate gap length.

B Amino acid sequence alignment of wild type DIP1 protein and the *dip1* mutants. Both nucleotide and amino acid changes in *dip1* mutants are highlighted in blue, and asterisks correspond to stop codons.

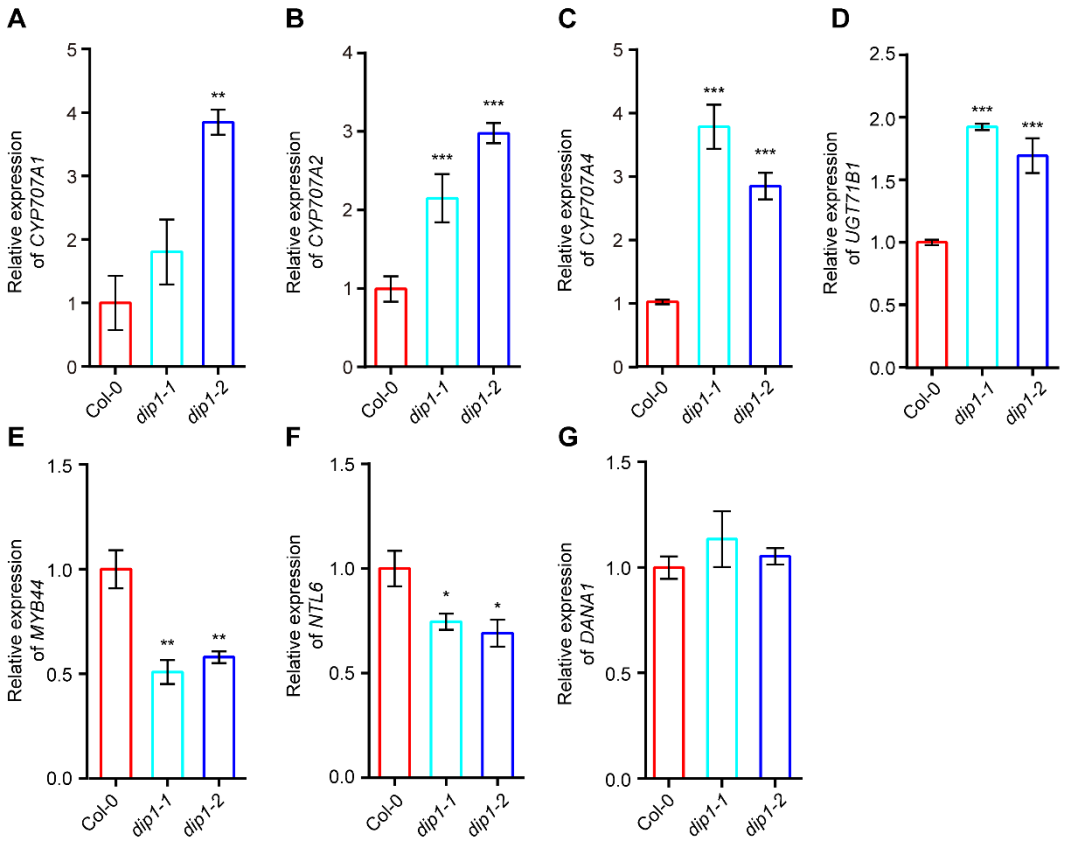


Appendix Figure S8. Stomatal aperture index and ABA-induced stomatal closure in *dip1* mutant and *DIP1* over-expressing plants.

A, B Mutated *DIP1* increases both stomatal aperture index (A) and ABA-induced stomatal closure (B).

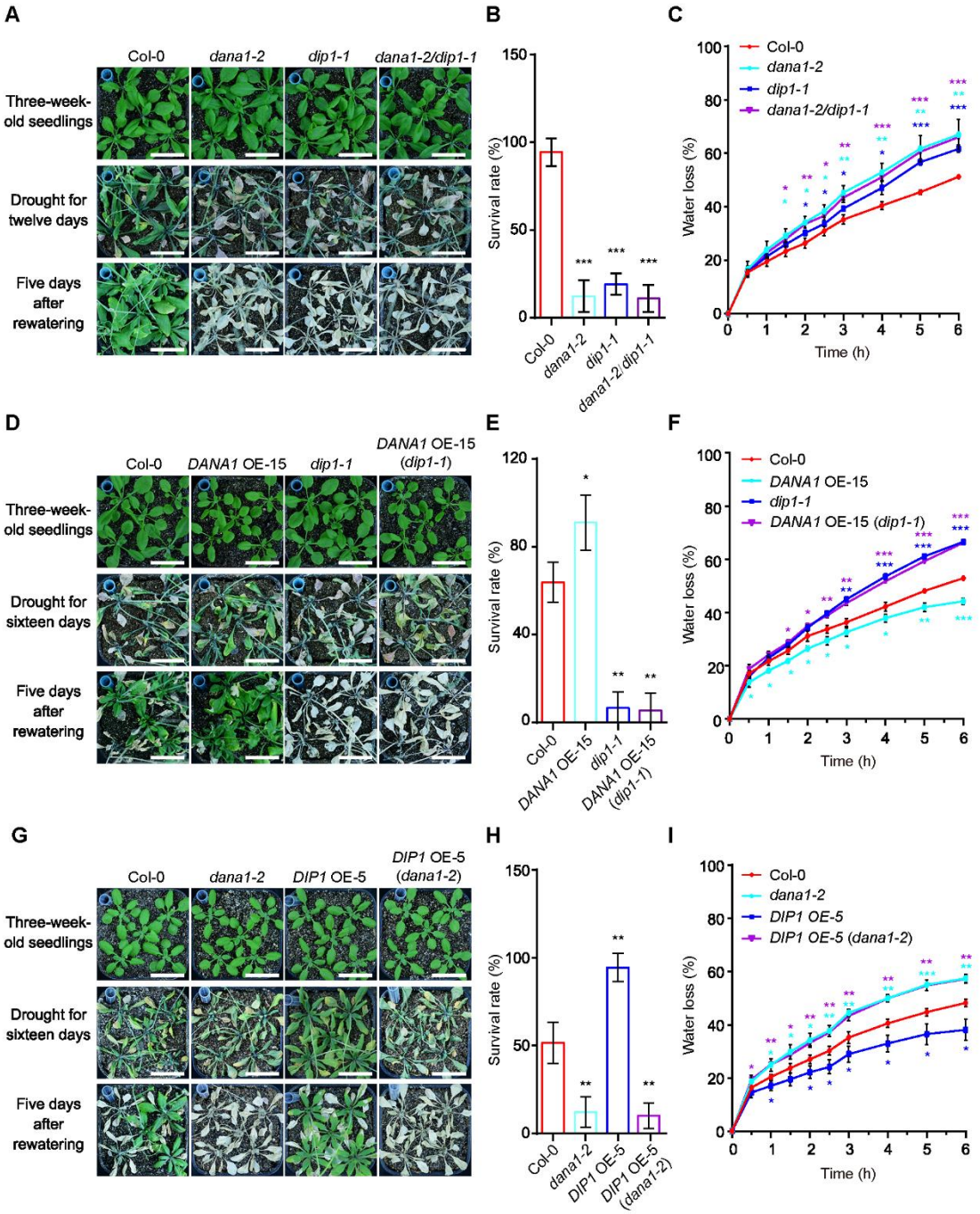
C, D Over-expressing *DIP1* decreases both stomatal aperture index (C) and ABA-induced stomatal closure (D).

Data information: Data shown as mean ± SD (n = 60). Asterisks represent significant differences determined by Student's *t*-test (*** $P < 0.001$). Scale bars = 10 μm.



Appendix Figure S9. Quantitative measurement of the transcript levels of drought response related genes (A-F) and *DANA1* (G) in *dip1* mutant. *UBQ3* was used as an internal control.

Data information: Values shown are means ± SD from three replicates. Asterisks represent significant differences by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).



Appendix Figure S10. Genetic interaction of *DANA1* with *DIP1*.

A Morphology of seedlings before and after drought stress treatment. Three-week-old Col-0, *dana1-2*, *dip1-1* and *dana1-2*/*dip1-1* plants were subjected to drought stress for sixteen days and then rewatered for five days. Scale bars = 3 cm.

B Survival rate after drought treatment (n = 3 biological replates).

C Water loss in detached leaves of three-week-old Col-0, *dana1-2*, *dip1-1* and *dana1-2*/*dip1-1* plants (n = 3 biological replicates, each replicate contains five fully expanded leaves).

D Morphology of seedlings before and after drought stress treatment. Three-week-old Col-0, *DANA1* OE-15, *dip1-1* and *DANA1* OE-15 (*dip1-1*) plants were subjected to drought stress for sixteen days and then rewatered for five days. Scale bars = 3 cm.

E Survival rate after drought treatment (n = 3 biological replates).

F Water loss in detached leaves of three-week-old Col-0, *DANA1* OE-15, *dip1-1* and *DANA1* OE-15 (*dip1-1*) plants (n = 3 biological replicates, each replicate contains five fully expanded leaves).

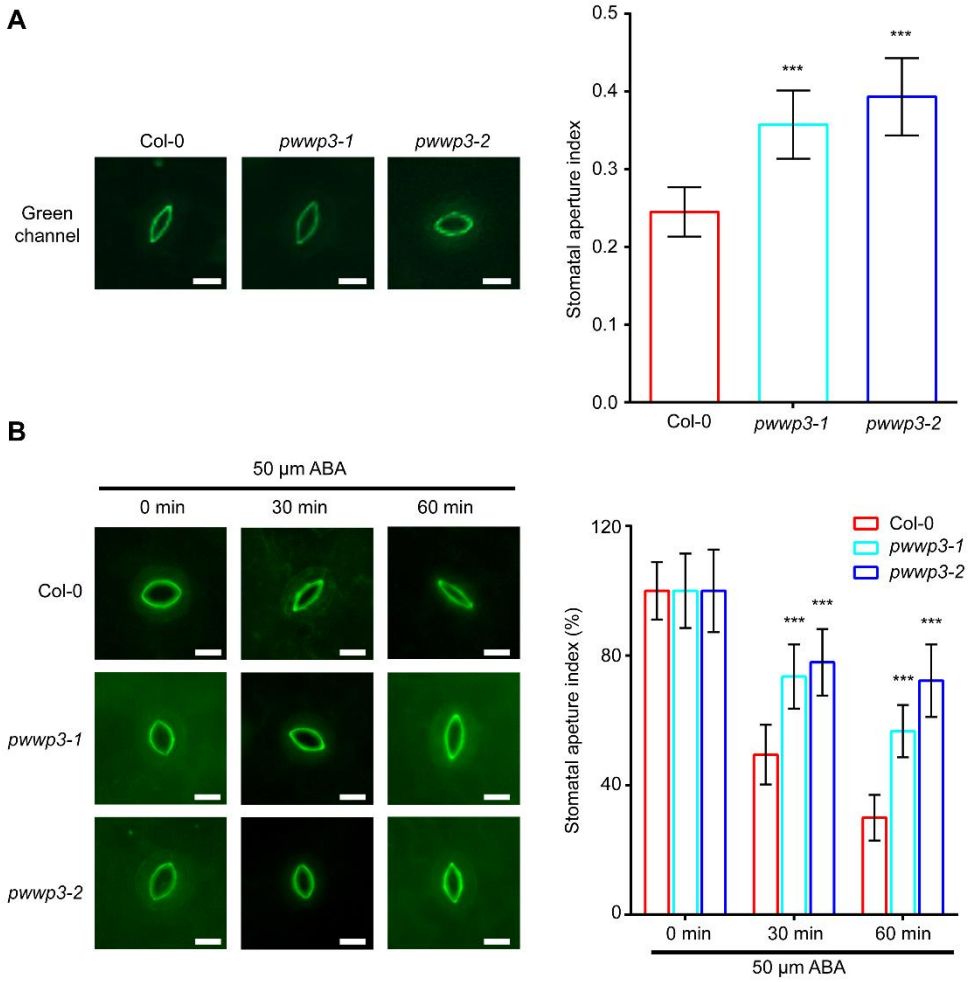
G Morphology of seedlings before and after drought stress treatment. Three-week-old Col-0, *dana1-2*, *DIP1* OE-5 and *DIP1* OE-5 (*dana1-2*) plants were subjected to drought stress for sixteen days and then rewatered for five days. Scale bars = 3 cm.

H Survival rate after drought treatment (n = 3 biological replates).

I Water loss in detached leaves of three-week-old Col-0, *dana1-2*, *DIP1* OE-5 and *DIP1* OE-5 (*dana1-2*) plants (n = 3 biological replicates, each replicate contains five fully expanded leaves).

Data information: Values shown are means ± SD from three biological replicates.

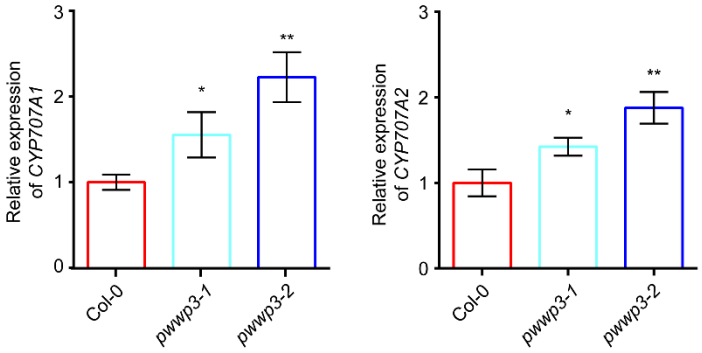
Asterisks represent significant differences by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).



Appendix Figure S11. Mutated *PWWP3* increases both stomatal aperture index (A) and ABA-induced stomatal closure (B).

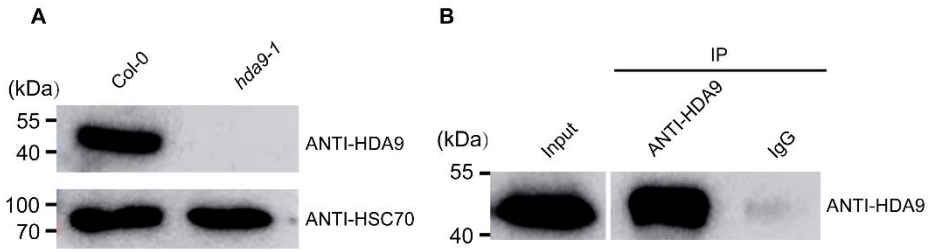
Data shown as mean ± SD (n = 60). The average of stomatal aperture index of Col-0 and *pwwp3* mutant plants in the presence or absence of ABA shown as a percentage relative to the average of stomatal aperture index of Col-0 and *pwwp3* mutant plants not exposed to ABA, which was defined as 100%.

Data information: Asterisks represent significant differences determined by Student's *t*-test (*** $P < 0.001$). Scale bars = 10 μm.



Appendix Figure S12. Quantitative measurement of the transcript levels of *CYP707A1* and *CYP707A2* in Col and the *pwwp3* mutant. *UBQ3* was used as an internal control.

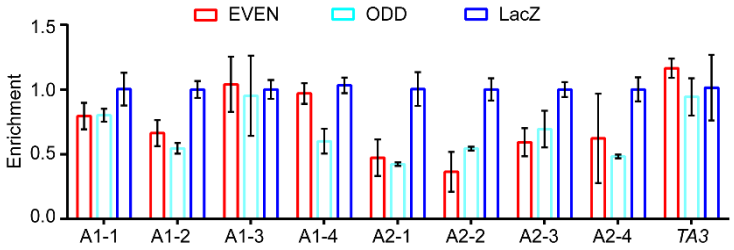
Data information: Asterisks represent significant differences by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$).



Appendix Figure S13. Validation of the anti-HDA9 antibody.

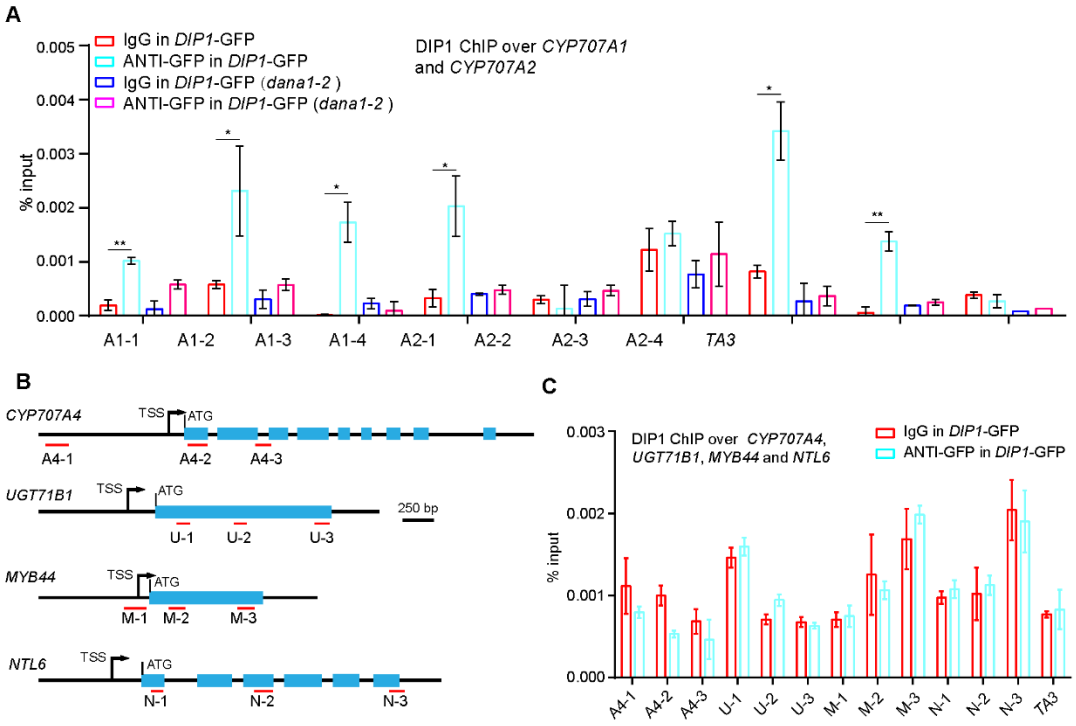
A Validation of anti-HDA9 antibody by immunoblotting of proteins extracted from Col-0 and *hda9-1* mutant plants. HSC70 is shown as a loading control

B Purification of HDA9 was validated by western blot.



Appendix Figure S14. Mutated *DIP1* impairs the association of *DANA1* to DNA at the *CYP707A1* and *CYP707A2* loci.

Data from ChIRP-qPCR are represented relative to the background level of DNA precipitation (*PP2A*), and the *TA3* locus was used as the negative control.



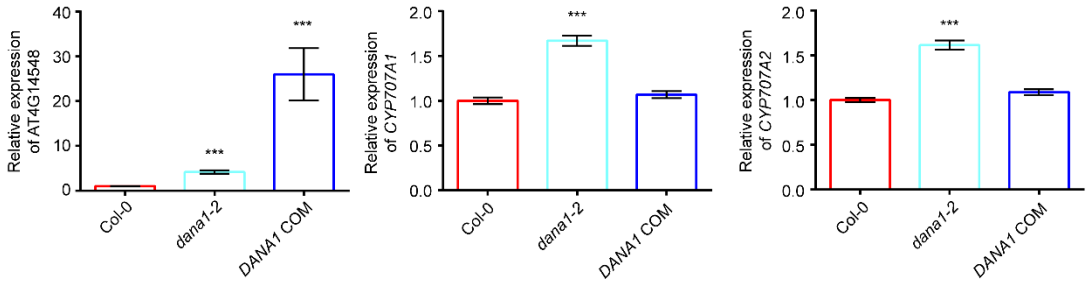
Appendix Figure S15. Mutated *DANA1* impairs the association of *DIP1* to DNA at the *CYP707A1* and *CYP707A2* loci.

A Mutated *DANA1* impairs the association of DIP1 to DNA at the *CYP707A1* and *CYP707A2* loci. The *TA3* locus was used as the negative control.

B Gene structure of *CYP707A4*, *UGT71B1*, *MYB44* and *NTL6*, indicating exons (boxes) and introns (lines). The locations of the gene regions analyzed by ChIP-qPCR are marked.

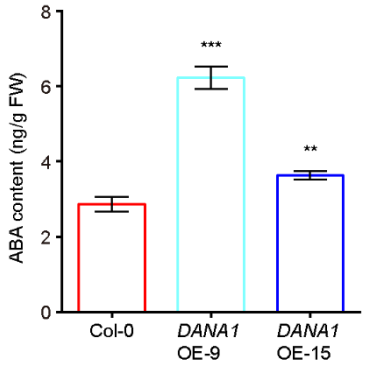
C The association of DIP1 to DNA at the *CYP707A4*, *UGT71B1*, *MYB44* and *NTL6* loci. The *TA3* locus was used as the negative control.

Data information: Asterisks represent significant differences by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).



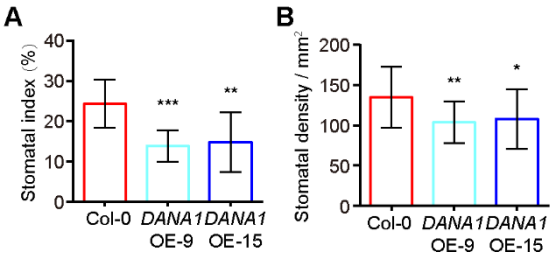
Appendix Figure S16. Quantitative measurement of the transcript levels of AT4G14548, *CYP707A1* and *CYP707A2* in Col-0, *dana1-2* and *DANA1* COM plants. *UBQ3* was used as an internal control.

Data information: Asterisks represent significant differences by Student's *t*-test (*** $P < 0.001$).



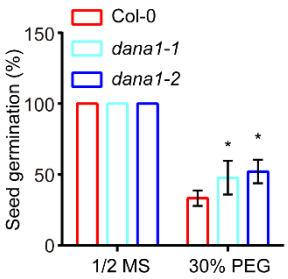
Appendix Figure S17. Measurement of ABA contents in seedlings. The ABA contents were measured in 10-day-old Col-0 and *DANA1*-overexpression seedlings.

Data information: Asterisks represent significant differences by Student's t-test (** $P <$ 0.01; *** $P <$ 0. 001, Student's *t*-test).



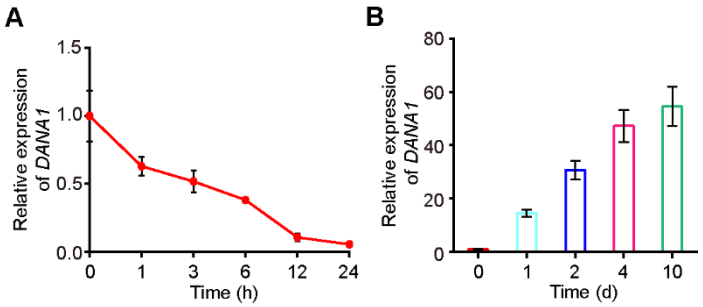
Appendix Figure S18. Both stomatal index (A) and stomatal density (B) are decreased in *DANA1* over-expressing plants.

Data information: Values shown are means ± SD (n = 15). Asterisks represent significant differences determined by Student's t-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).



Appendix Figure S19. Seed germination of Col-0, *dana1-1* and *dana1-2* mutants.

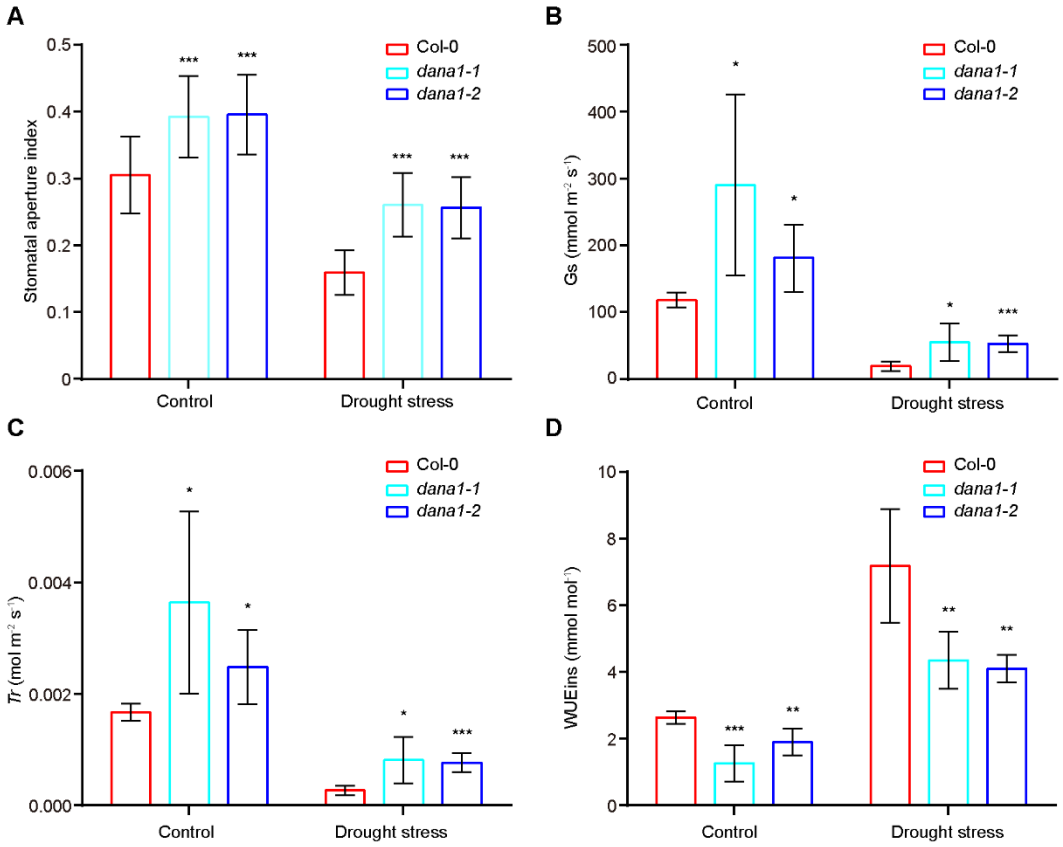
Seeds (30 per genotype) were grown on half MS medium supplemented with 30% (w/v) PEG. Seeds were stratified at 4℃ for 3 days, and germinations of seeds were determined when they had grown for 2 days. Seeds were considered as germinated once radicle penetrated the seed coat. Values shown are means ± SD from three replicates. Asterisks represent significant differences determined by Student's *t*-test (* $P < 0.05$).



Appendix Figure S20. Quantitative measurement of the transcript levels of *DANA1* during pre- (A) and post-germination (B) stages.

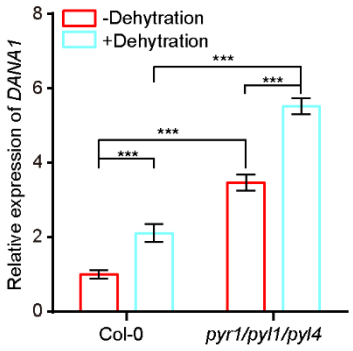
A The RT-qPCR was performed using dry seed and imbibed seed at the designated time points. For seed imbibition, it was carried out as the previous study (Liu *et al*., 2009), and seeds were sown and imbibed on filter paper moistened with water at 22℃ under continuous light.

B The RT-qPCR was performed using dry seed and seed that were sown on 1/2 MS media, stratified for 3 days at 4℃ in the dark and then grown at 22℃ with a 16-h light/8-h dark photoperiod at the designated time points. Expression level of *DANA1* in dry seed was designed as 1, and *UBQ3* was used as an internal control.



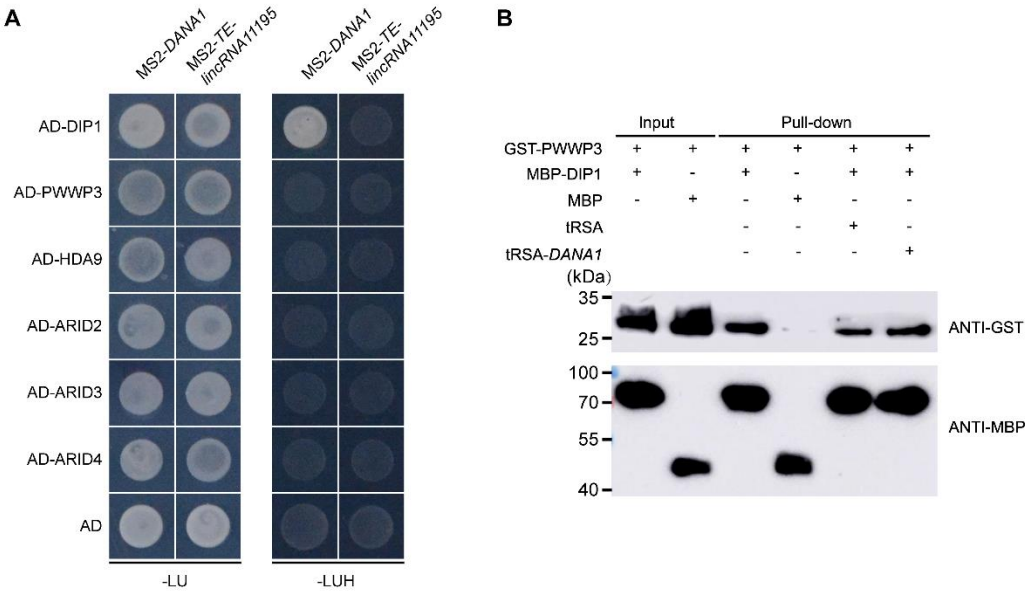
Appendix Figure S21. Stomatal aperture index (A), stomatal conductance (B), transpiration rate (C) and water use efficiency (D) in the rosette leaves of four-week-old Col-0, *dana1-1* and *dana1-2* mutants grown under normal and drought stress conditions.

Data information: Values shown are means ± SD from three replicates. Asterisks represent significant differences determined by Student's *t*-test (* $P < 0.05$; ** $P < 0.01$; *** $P < 0.001$).



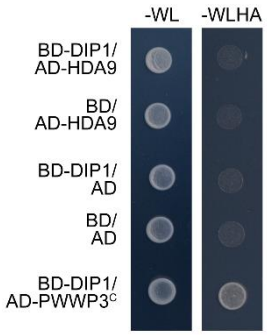
Appendix Figure S22. Expression of *DANA1* in WT and an ABA-insensitive mutant *pyr1*/*pyl1*/*pyl4*. *UBQ3* was used as an internal control.

Data information: Asterisks represent significant differences determined by Student's *t*-test (*** $P < 0.001$).



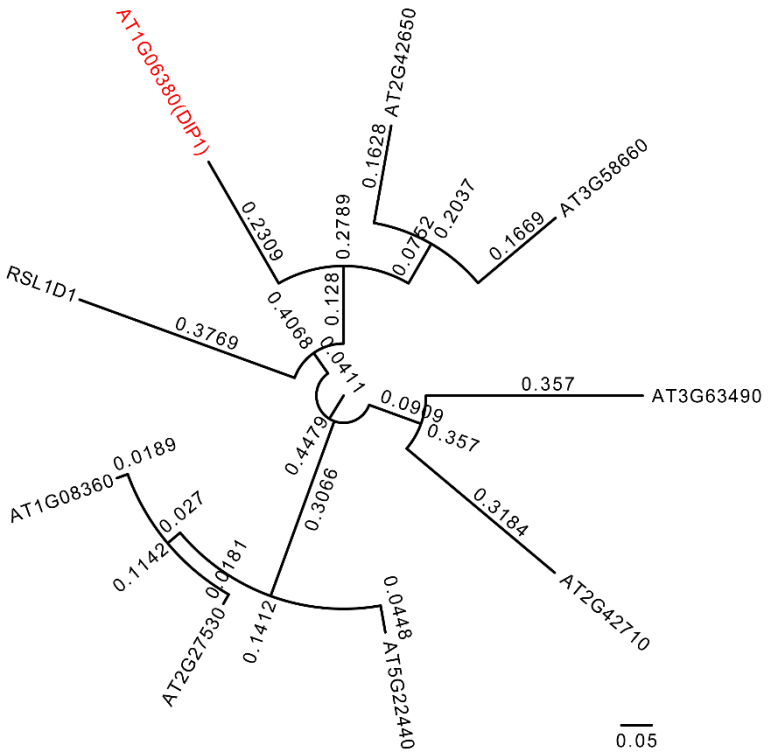
Appendix Figure S23. *DANA1* does not influence the interaction between DIP1 and PWWP3.

A Tests of *DANA1*-PWWP3, *DANA1*-HDA9 and *DANA1*-ARIDs interactions by yeast three-hybrid assays. Full-length PWWP3, HDA9, ARID2, ARID3 and ARID4 proteins were separately fused with the GAL4 activation domain (AD).
B *In vitro* pull-down assay of GST-PWWP3 and maltose binding protein (MBP)-DIP1 with *in vitro* transcribed tRSA-*DANA1* or tRSA (100 pmol).



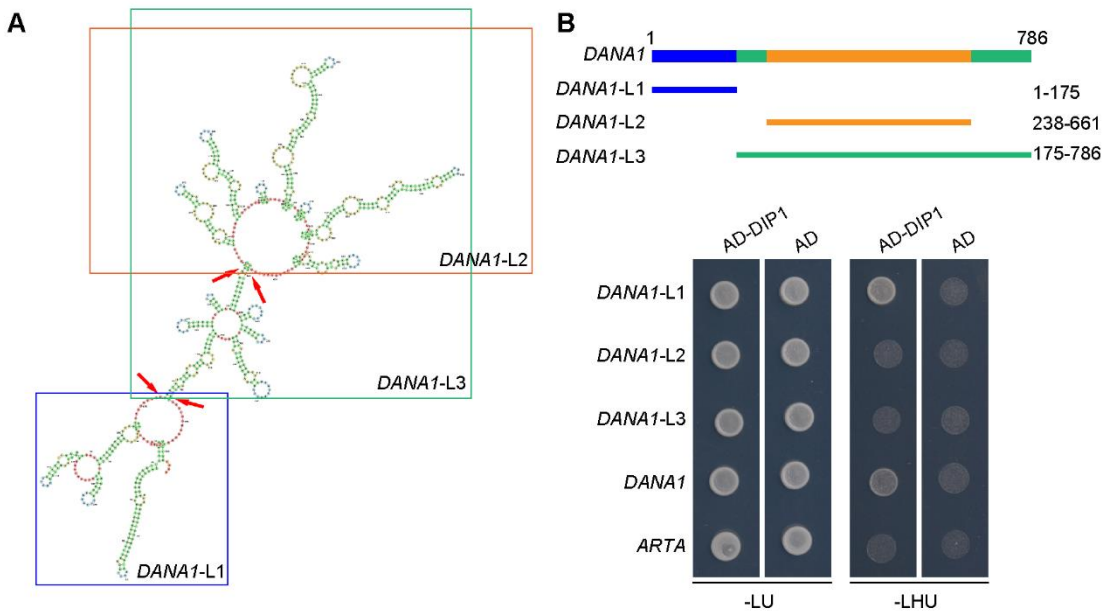
Appendix Figure S24. Tests of DIP1-HDA9 interaction by yeast two-hybrid assays.

Full-length HDA9 protein was fused with the GAL4 activation domain (AD).



Appendix Figure S25. Phylogenetic tree of ribosomal protein L1P/L10e family.

AT5G22440, AT2G27530 and AT1G08360 are components of 80S ribosome (Barakat, Szick-Miranda et al., 2001). RSL1D1 is a human ribosomal L1 domain-containing protein, which directly interacts with c-MYC protein (Cheng, Yuan et al., 2015). The phylogenetic tree was constructed using a neighbour joining clustering method based on the multiple alignment of amino acid sequences of these genes. The scale bar represents the amino acid substitutions per site.



Appendix Figure S26. *DANA1*-L1 interacts with DIP1 in yeast cells.
A Secondary structure of the *DANA1* predicted with *RNAfold*.
B Tests of *DANA1*-DIP1 interactions by yeast three-hybrid assays.

References

Barakat A, Szick-Miranda K, Chang IF, Guyot R, Blanc G, Cooke R, Delseny M, Bailey-Serres J (2001) The organization of cytoplasmic ribosomal protein genes in the Arabidopsis genome. *Plant Physiol* 127: 398-415

Cheng Q, Yuan F, Lu F, Zhang B, Chen T, Chen X, Cheng Y, Li N, Ma L, Tong T (2015) CSIG promotes hepatocellular carcinoma proliferation by activating c-MYC expression. *Oncotarget* 6: 4733-44

Liu Y, Shi L, Ye N, Liu R, Jia W, Zhang J (2009) Nitric oxide-induced rapid decrease of abscisic acid concentration is required in breaking seed dormancy in Arabidopsis. *New Phytol* 183: 1030-1042

Appendix Table S1. Primers and probes used in this study.

Primer name	Sequences	Purpose
DANA1-F	ACTTGCTTTAATGTGGCATTGAGGG	T-DNA detection and RT-PCR
DANA1-R	GTTCCGACGAACCTAAATGAAAGTC	
PWWP3-JC-F	GGCTGTCAAGTATGCCCGTAGAG	
PWWP3-JC-R	AGCCCTTCACTGCTTCGTTTATCCTAC	
DANA1-F2	CCCTACCTATTGAATGATTCCAGC	
DANA1-1	AAAGTCTCCATGACAGACTC	
DANA1-2	AAAGATTAAAGAGAAACTCA	
DANA1-3	ATCCGCCTGTCATCAACAAC	
DANA1-4	ACTCTTTTCCAGCTTCGCTC	
PROKII-LB1	ATGGTTCACGTAGTGGGCCATCG	
pDAP101-LBa1	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC	
DANA1-QF	CCATCCGCCTGTCATCAAC	RT-qPCR
DANA1-QR	GGACCATGCTTTGTGCTCTGTTCTC	
CYP707A1-QF	TGGCTCCAAAACCCAATACGT	
CYP707A1-QR	CGAATGGCCCATACTGAATC	
CYP707A2-QF	GTTCAAGCCAACTTATCC	
CYP707A2-QR	TAAGGGTAGAATGGTATGG	
CYP707A4-QF	ACCTACCAGGAGATGAAG	
CYP707A4-QR	ACATCAAAGGCGAACTGC	
UGT71B1-QF	TAAAGAAGGAGTACCGTAGAGAT	
UGT71B1-QR	GAACAAACTTCTTTAGAGCACAG	
MYB44-QF	TTTAGAGGTGCGATTGAGG	
MYB44-QR	ATCCGCCACCATTGTTCC	
NTL6-QF	ACCTGCTGTCTCGTCTCC	
NTL6-QR	TAGCCTCATCACAAGCATCACT	
NF-YB3-QF	AGGCGATAAGGAAGGTGGAGGAGGA	
NF-YB3-QR	TTGATGTCCCATCGTAGTCACCATG	
AT4G14548-QF	ATCTACGGGATTTGCTGCTTGTTTT	
AT4G14548-QR	CAACACCCGAAGACCCAAAGGAAAA	
UBQ3-QF	ACGGAAGAACTCTTGCTGAC	
UBQ3-QR	AACCTCAAGGGTGATTGTTT	
MS2-QF	GGTCGACTCTAGAAAACATG	
MS2-QR	AGGATCCAATGAACCCGGG	
ACTIN(*N. benthamiana*)-F	CAAGGAAATCACCGCTTTGG	
ACTIN(*N. benthamiana*)-R	AAGGGATGCGAGGATGGA	
U6-QF	TCCCTTCGGGGACATCCGATA	
U6-QR	AAATTTGGACCATTTCTCGATTTGTGC	
tRNA_Gln-QF	CCACCGCTTCTGCCGTTAAA	
tRNA_Gln-QR	GATCCGAGCCAAATCCGAGA	
MS2-DANA1-F	GACTCTAGAGGATCGCCCGGGGATTTTTTTTGAGATGTCATGTTGA	Y3H and Y2H assays
MS2-DANA1-R	AGAACTAGTGGATCCCCCGGGAAATCAGGAAAAAATAAAGAATTA	
MS2-DANA1-L1F	GACTCTAGAGGATCGCCCGGGGATTTTTTTTGAGATGTCAT	
MS2-DANA1-L1R	AGAACTAGTGGATCCCCCGGGGGCGGATGGTGCTGGAATCA	

MS2-DANA1-L2F	GACTCTAGAGGATCGCCCGGGTGTCATCAACAACTTCTACA	
MS2-DANA1-L2R	AGAACTAGTGGATCCCCCGGGAAATCAGGAAAAAATAAAGA	
MS2-DANA1-L3F	GACTCTAGAGGATCGCCCGGGTGTGTTTACGAGGTTTGGCA	
MS2-DANA1-L3R	AGAACTAGTGGATCCCCCGGGGGTGTAGAATTAAAAACAAG	
MS2-TE-lincRNA11195-F	GACTCTAGAGGATCGCCCGGGCTCCTTATCTCTATTATTGT	
MS2-TE-lincRNA11195-R	AGAACTAGTGGATCCCCCGGGCTGACACTTTTCTTTTCTTTTCG	
AD-DIP1-F	GCCATGGAGGCCAGTGAATTCATGAGTACTACTACTACTACGG	
AD-DIP1-R	CAGCTCGAGCTCGATGGATCCAGCAACTGATTGATAAACAGGC	
BD-DIP1-F	ATGGCCATGGAGGCCGAATTCATGAGTACTACTACTACTACGG	
BD-DIP1-R	CCGCTGCAGGTCGACGGATCCAGCAACTGATTGATAAACAGGC	
AD-PWWP3-F	GCCATGGAGGCCAGTGAATTCATGGGTAGTAGTGATGAGCGAAACT	
AD-PWWP3-R	CAGCTCGAGCTCGATGGATCCTCCTGTATTACCTGCAGATGGT	
AD-PWWP3^{c}-F	GCCATGGAGGCCAGTGAATTCGATGTTCCACTAAATGGAGAT	
AD-ARID2-F	CCATGGAGGCCAGTGAATTCATGGAGAATTTGACGGAAAT	
AD-ARID2-R	AGCTCGAGCTCGATGGATCCCTCCAATTGCTCCAGAGGCA	
AD-ARID3-F	CCATGGAGGCCAGTGAATTCATGGTGGATACCGAAATGCA	
AD-ARID3-R	AGCTCGAGCTCGATGGATCCCTGCTCAAACGGAACTCGTA	
AD-ARID4-F	CCATGGAGGCCAGTGAATTCATGATGGCGGATACTGAAATGCAAGA	
AD-ARID4-R	AGCTCGAGCTCGATGGATCCTCACTGCTCAAATGGGACTCGCACAA	
AD-HDA9-F	CCATGGAGGCCAGTGAATTCATGCGTTCCAAGGACAAAAT	
AD-HDA9-R	AGCTCGAGCTCGATGGATCCTGACGCATCGTTATCGTTGT	
GST-DIP1-F	GATCTGGTTCCGCGTGGATCCATGAGTACTACTACTACTACGG	RNA pull-down and protein pull-down assays
GST-DIP1-R	CTCGAGTCGACCCGGGAATTCAGCAACTGATTGATAAACAGGC	
tRSA-F	TAATACGACTCACTATAGGGAAAAAAAA	
tRSA-R	GAATTCTTTTTTTTTTTTCTGCAGTG	
tRSA-DANA1-F	CAGAAAAAAAAAAAAGAATTCGATTTTTTTTGAGATGTCATGTTGA	
tRSA-DANA1-R	AGACTGCAGGTCGACAAGCTTAAATCAGGAAAAAATAAAGAATTA	
DANA1-T-R	AAATCAGGAAAAAATAAAGAATTA	
MBP-DIP1-F	CTGTACTTCCAATCCAATATGAGTACTACTACTACTACGGCTG	
MBP-DIP1-R	CCGTTATCCACTTCCAATAGCAACTGATTGATAAACAGGCAAT	
GST-PWWP3-F	TTCCAGGGGCCCCTGGGATCCATGGGTAGTAGTGATGAGCGAAACT	
GST-PWWP3-R	GACCCGGGAATTCGGGGATCCTCCTGTATTACCTGCAGATGGT	
DANA1-TriFC-F	GGGGACTCTTGACCATGGAGGCCTGATTTTTTTTGAGATGTCATGTTGA	

DANA1-TriFC-R	ACGGCTCGAGCGGCCGCAGGCCTAAATCAGGAAAAAA TAAAGAATTA	TriFC and BiFC assays
DIP1-TriFC-F	ACACGGGGGACTCTTGAAGGCCTATGAGTACTACTACT ACTACGG	
DIP1-TriFC -R	GCCCTTGCTCACCATAGGCCTAGCAACTGATTGATAAA CAGGC	
MSCP-TriFC-F	CAAGGCTAGCGAATTCCACGTGGCTTCTAACTTTACTCA GTTCGT	
MSCP-TriFC-R	GGTCACCTGTAATTCACACGTGTTAGTAGATGCCGGAG TTGGCCG	
DIP1-YC-F	CCTGGCGCGCCACTAGTGGATCCATGAGTACTACTACT ACTAC	
DIP1-YC-R	GGAGCGGTACCCTCGAGGTCGACAGCAACTGATTGATA AACAG	
PWWP3-YN-F	CCTGGCGCGCCACTAGTGGATCCATGGGTAGTAGTGAT GAGCG	
PWWP3-YN-R	GGAGCGGTACCCTCGAGGTCGACTCCTGTATTACCTGC AGATG	
PP2A-QF	TATCGGATGACGATTCTTCGTGCAG	RIP assay
PP2A-QR	GCTTGGTCGACTATCGGAATGAGAG	
DANA1-QF1	ATAATAATAGCTCGTACAGC	
DANA1-QR1	ACAAAGCATGGTCCTTCA	
DIP1-sgRNA1F	TGATTGGAAGTCTCTGCTAAAATGG	CRISPR/Cas9 assay
DIP1-sgRNA1R	AAACCCATTTTAGCAGAGACTTCCA	
DIP1-sgRNA2F	TGATTGGGTTAGTACGATCCAACTG	
DIP1-sgRNA2R	AAACCAGTTGGATCGTACTAACCCA	
DIP1-CX-F	TTGCTCAGAACCCTAAT	
DIP1-CX-R	TCCATCTACCAGGAACT	
CYP707A1-1F	GTAGACTTTACCCCACAT	ChIP and ChIRP qPCR assays
CYP707A1-1R	GGTTAATAATTCGTTCTGTT	
CYP707A1-2F	TCCGCCTTGTTTCTCACT	
CYP707A1-2R	TCCGACGTAAGGCCAACC	
CYP707A1-3F	TTATCACGCTAAACTCAG	
CYP707A1-3R	GAGCGATGGATTCAATAT	
CYP707A1-4F	TGAATCTCCCTGGAACAC	
CYP707A1-4R	GATTACTCCGATTATGTTGT	
CYP707A2-1F	AAGTGTAGTGTGGGGTTAGC	
CYP707A2-1R	CGCAGTACTATTTATGTGGT	
CYP707A2-2F	CAAAGACTACGGCTACCT	
CYP707A2-2R	CGAGTGGCGAAGAAGGAA	
CYP707A2-3F	GTTCAAGCCAACTTATCC	
CYP707A2-3R	TAAGGGTAGAATGGTATGG	
CYP707A2-4F	TTTGGCTTCAATGTCTAAC	
CYP707A2-4R	GGAGAATTGGCTCAGGGT	
CYP707A4-1F	CACCCGTAAATGTTGTCA	
CYP707A4-1R	CAACGGCATGTCGGTATT	
CYP707A4-2F	ATCCTCATCTTATGCTTGC	
CYP707A4-2R	TTTGCTTGGAGGTGAAGA	
CYP707A4-3F	ACCTACCAGGAGATGAAG	
CYP707A4-3R	ACATCAAAGGCGAACTGC	
MYB44-1F	AAAACCGCTTGCGTGGAA	
MYB44-1R	CTTTAGCAATCTTCTCCT	

MYB44-2F	CGCCGCAAGTTGAGCATC	
MYB44-2R	TTCTTCACGGCGTTGTCC	
MYB44-3F	TTTAGAGGTGCGATTGAGG	
MYB44-3R	ATCCGCCACCATTGTTCC	
NTL6-1F	TAATCCGTTACTATCTCCG	
NTL6-1R	AATCCCAAGGTTCCCATT	
NTL6-2F	ACCTGCTGTCTCGTCTCC	
NTL6-2R	CGGTTGTAGCCTCATCAC	
NTL6-3F	TTAGGGCGGCAGTAGTTG	
NTL6-3R	GGGCCGGTTCAAGCACTA	
UGT71B1-1F	ACCGTCTCCGCTACATCC	
UGT71B1-1R	AGCGACCTTGGACACGAC	
UGT71B1-2F	ATGGAACCTCAGGCGTTGA	
UGT71B1-2R	GCCGCTAGATTCTAAGTC	
UGT71B1-3F	GGAGCAGGATAGCAAGAT	
UGT71B1-3R	GACCACGTCTTGAACAAA	
TA3-F	GATTCTTACTGTAAAGAACATGGCATTGAGAGA	
TA3-R	TCCAAATTTCCTGAGGTGCTTGTAACC	
DANA1-OE-F	TATGACCATGATTACGAATTCTCAACATGGTGGAGCACGACACAC	Overexpression and complementation
DANA1-OE-R	CAGGTCGACTCTAGAGGATCCCCGATCTAGTAACATAGATGACACC	
DANA1-COM-F	TATGACCATGATTACGAATTCGCGCATAATGAAAGGATCCGAAGC	
DANA1-COM-R	CAGGTCGACTCTAGAGGATCCCGTAACCTTTGATCTTTGATCTTTG	
DIP1-OE-F	GTTTTTCTGATTAACAGAATTCGATGAGTACTACTACTACTACGG	
DIP1-OE-R	TCTCCATGGTCTAGAGGATCCAGCAACTGATTGATAAACAGGC	
PWWP3-MYC-F	GCTTGGGCGACCTCACCGAATTCATGGGTAGTAGTGATGAGCG	
PWWP3-MYC-R	AGTTATCTAGATCCGGTGGATCCTCCTGTATTACCTGCAGATG	
DANA1_ChIRP_probe_1	CCTCAATGCCACATTAAAGC-3'biotin	ChIRP biotinylated probes
DANA1_ChIRP_probe_2	GCAAGTGGTGAATTCCTAGA-3'biotin	
DANA1_ChIRP_probe_3	TGTAGGCAACAACTTTACCA-3'biotin	
DANA1_ChIRP_probe_4	TGGTGCTGGAATCATTCAAT-3'biotin	
DANA1_ChIRP_probe_5	AGCAGTGCAATGGAGATGTC-3'biotin	
DANA1_ChIRP_probe_6	GTGGTACTCTTATGCCAAAC-3'biotin	
DANA1_ChIRP_probe_7	GCTGGAAAAGAGTTGTGGCG-3'biotin	
DANA1_ChIRP_probe_8	CTCTGTTCTCACAACATTGA-3'biotin	
DANA1_ChIRP_probe_9	ATAGGAGAAGCTTTTACCCT-3'biotin	
DANA1_ChIRP_probe_10	GGATCTCTCCAAAACATTCC-3'biotin	
DANA1_ChIRP_probe_11	TCCATCGAAGTAGAGCTTTC-3'biotin	
DANA1_ChIRP_probe_12	AATAGCTCGTACAGCTAGTG-3'biotin	
DANA1_ChIRP_probe_13	TCCATGACAGACTCCATATT-3'biotin	
DANA1_ChIRP_probe_14	ATAGGAAGTTCCGACGAACC-3'biotin	
DANA1_ChIRP_probe_15	AGAAGATCATACGGTGTAGA-3'biotin	
DANA1_ChIRP_probe_16	ACCAAACTGCTTTCCATTAT-3'biotin	
LacZ_ChIRP_probe_1	CCAGTGAATCCGTAATCATG-3'biotin	
LacZ_ChIRP_probe_2	AATGTGAGCGAGTAACAACC-3'biotin	

LacZ_ChIRP_probe_3	AATAATTCGCGTCTGGCCTT-3'biotin	
LacZ_ChIRP_probe_4	AATTCAGACGGCAAACGACT-3'biotin	
LacZ_ChIRP_probe_5	ATCTTCCAGATAACTGCCGT-3'biotin	
LacZ_ChIRP_probe_6	GCTGATTTGTGTAGTCGGTT-3'biotin	
LacZ_ChIRP_probe_7	AACTGTTACCCGTAGGTAGT-3'biotin	
LacZ_ChIRP_probe_8	TTTCGACGTTCAGACGTAGT-3'biotin	
LacZ_ChIRP_probe_9	ACCATTTTCAATCCGCACCT-3'biotin	
LacZ_ChIRP_probe_10	TTCATCAGCAGGATATCCTG-3'biotin	

Appendix Table S2. The list of *DANA1*-interacting proteins identified by a yeast three-hybrid assay.

Number	Gene ID	Gene description
1	AT1G06380	Ribosomal protein L1p/L10e family (DIP1)
2	AT1G49650	alpha/beta-Hydrolases superfamily protein
3	AT1G58470	Encodes an mRNA-binding protein that contains two RNA recognition motifs (RRMs) and is expressed in proliferating tissues
4	AT3G12470	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
5	AT3G15080	Polynucleotidyl transferase, ribonuclease H-like superfamily protein
6	AT3G07050	Arabidopsis NSN1 encodes a nucleolar GTP- binding protein and is required for maintenance of inflorescence meristem identity and floral organ development
7	AT3G54770	Encodes a putative RNA binding protein that is localized in the nucleus and affects ABA-regulated seed germination of Arabidopsis
8	AT4G04890	Arabidopsis thaliana protodermal factor 2 (PDF2)
9	AT5G14610	DEAD box RNA helicase family protein
10	AT5G46250	AtLARP6a, La related protein 6a
11	AT5G52470	ATFIB1
12	AT5G60980	Nuclear transport factor 2 (NTF2) family protein with RNA binding (RRM-RBD-RNP motifs) domain-containing protein