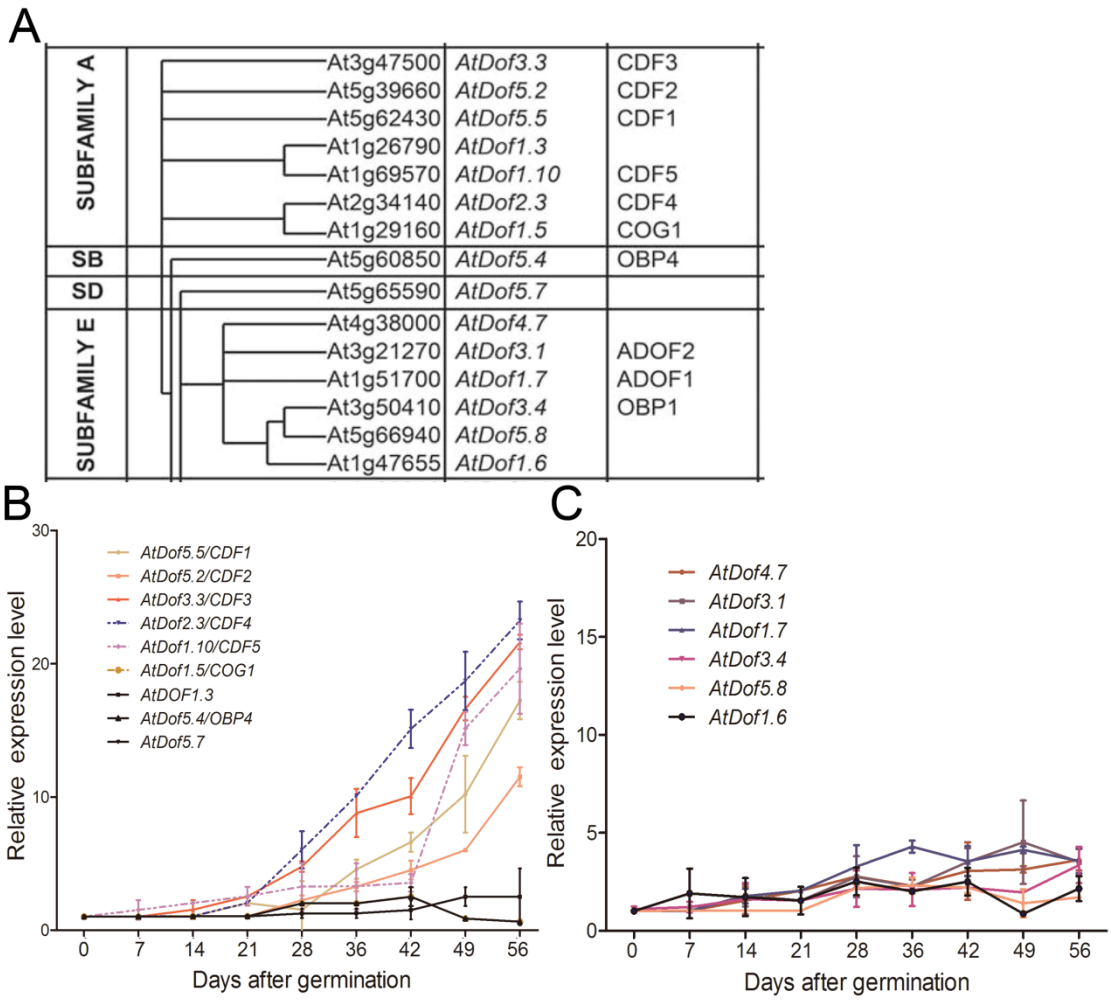
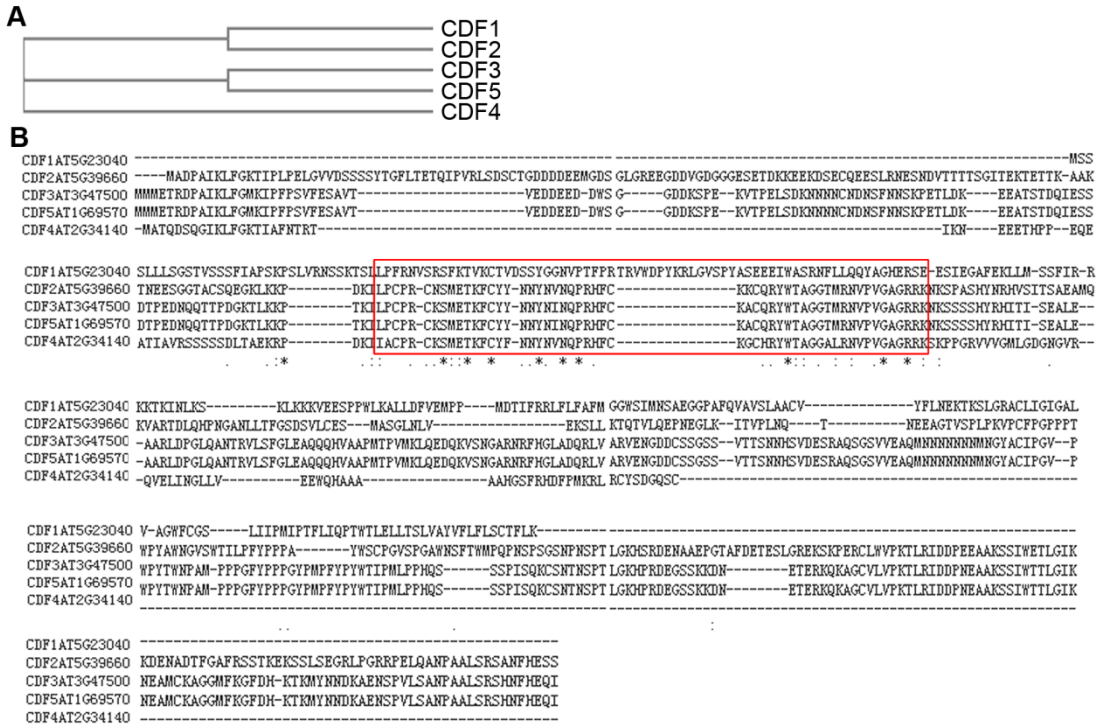
Appendix

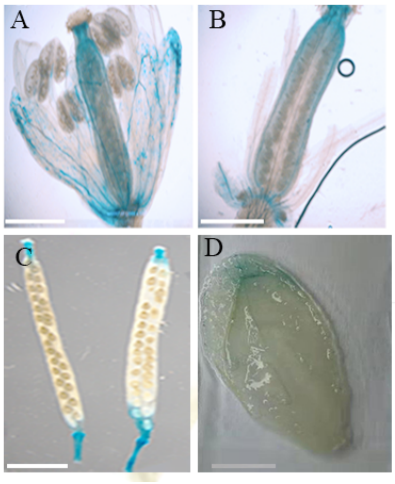


Appendix Figure S1. Relative expression levels of A, B, D and E Subfamily DOF transcription factors at various growth stages in Arabidopsis leaves.

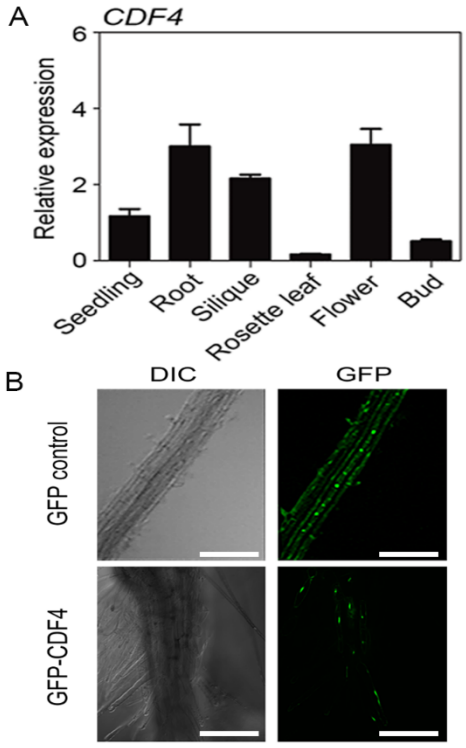
A Phylogenetic tree analysis of A,B,D,E Subfamily DOF TFs. **B** Relative expression levels of A Subfamily DOF TFs *CDF1-5, COG1, AtDOF1.3*； B Subfamily DOF TF *OBP4*； D Subfamily DOF TF *AtDOF5.7* at various growth stages. **C** Relative expression levels of E Subfamily DOF TFs *AtDOF4.7, AtDOF3.1, AtDOF1.7, AtDOF3.4, AtDOF5.8, AtDOF1.6* at various growth stages. RNA was extracted from rosette leaves at the indicated time points. d, days after germination. Values are given as mean ± SD, n=3. Student's *t*-test was applied.



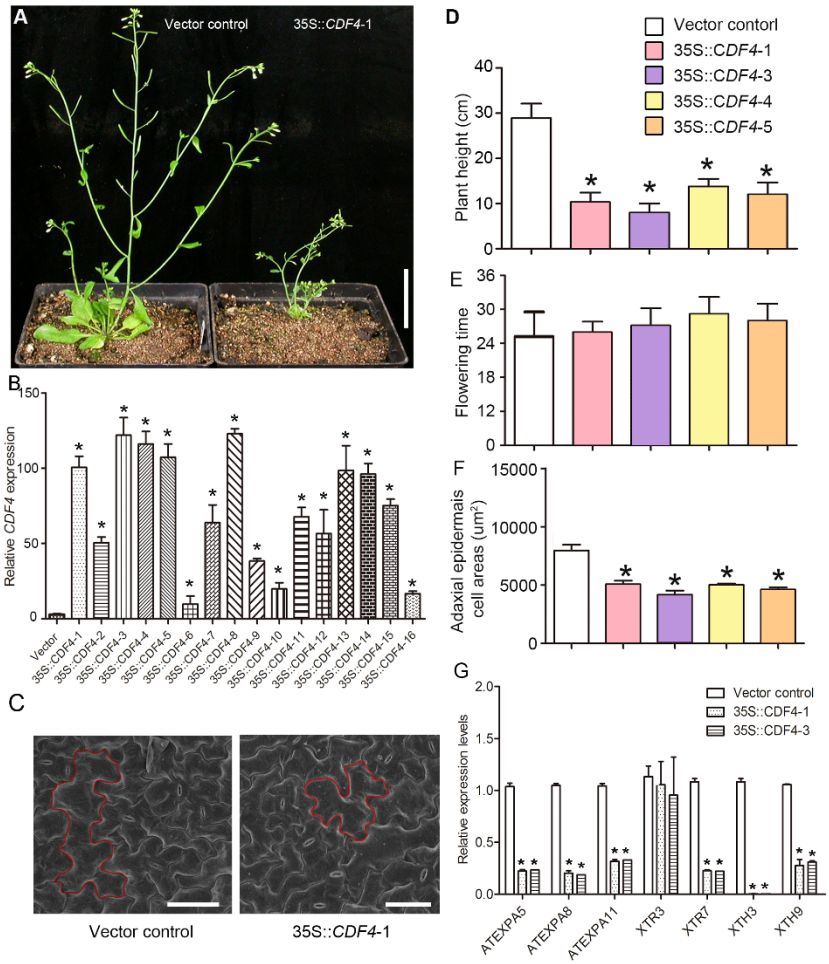
Appendix Figure S2. CDF4 shares similarity with CDF1, CDF2, CDF3 and CDF5 in amino acid sequence. **A** Phylogram and **B** Alignment of Arabidopsis cycling DOF family protein. Multiple sequence alignment of the predicted amino acid sequence and phylogenetic analysis were performed using DNA MAN 6.0 and MEGA 4.1 software.



Appendix Figure S3. Analysis of *CDF4* expression patterns in pro*CDF4*::GUS plants. GUS signals were observed in **A** bract of mature flower; **B,** young siliques; **C** mature siliques floral organ abscission zone； **D** rosette leave at the early senescence stage with GUS signals in the leaf tip. Bars in **A** and **B** indicates 0.2cm, bar in **C** and **D** indicates 0.4cm.



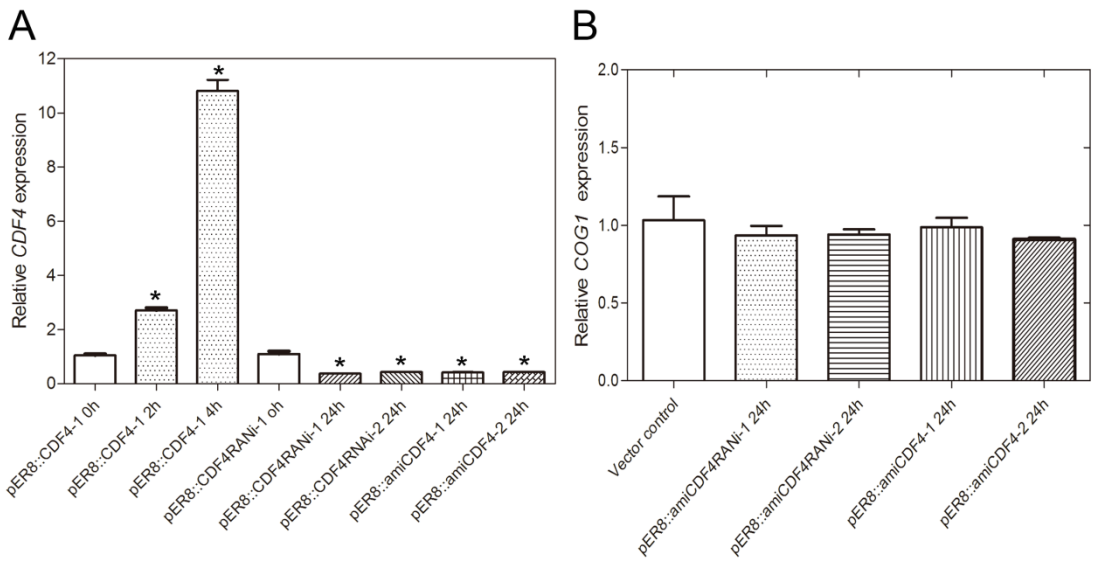
Appendix Figure S4. Relative *CDF4* gene expression in various plant tissues and subcellular localization analysis of CDF4. **A** *CDF4* expression in the seedling, root, silique, rosette leave, flower and bud. Values are given as mean ± SD, n=3. **B** Subcellular localization of the GFP vector control and GFP-CDF4 in transgenic Arabidopsis root cells. DIC, differential interference contrast, referring to bright-field images of the cells. Bar indicates 50μm.



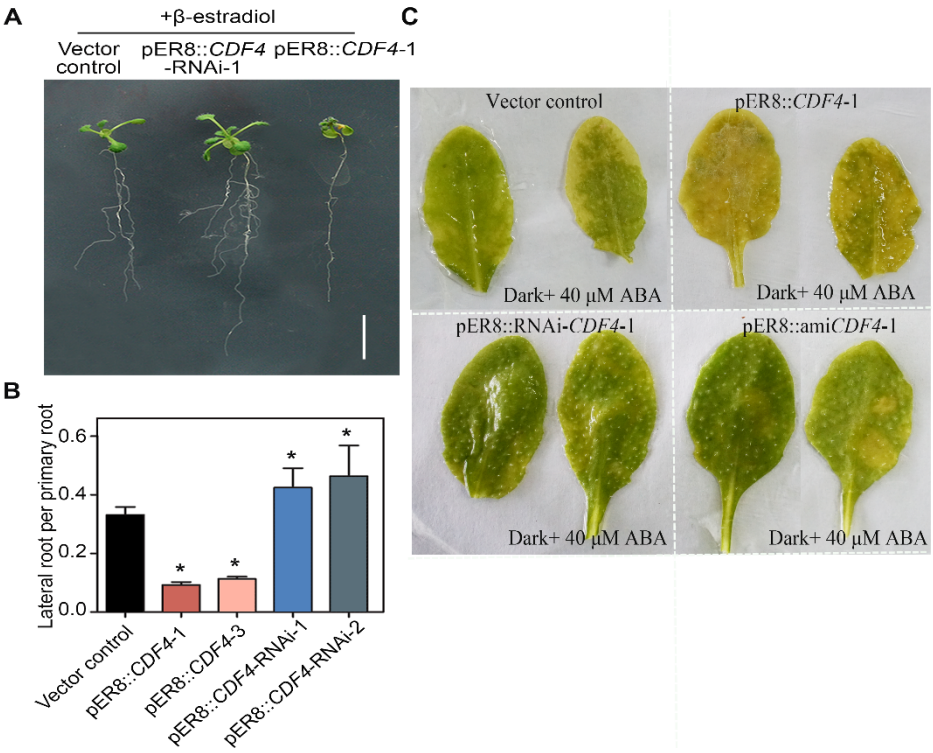
Appendix Figure S5. Phenotypes of adult plants and morphology of epidermal cells in wild-type and 35S::*CDF4* transgenic plants. Five-week-old vector control and 35S::*CDF4*-1 plants grown under long-day conditions. Bar indicates 5cm. **B** *CDF4* expression levels in transgenic 35S::*CDF4* transgenic lines.Values are given as mean ± SD, n=3. *p<0.05 by student's t test. **C** Vector control and 35S::*CDF4*-1 leaves were visualized by scanning electron microscopy. The red outlines indicate the cell boundary of one epidermal cell. Bar indicates 50μm. **D** Plant height and **E** Flowering time of vector control and 35S::*CDF4* plants. Plants were grown in soil under long days until flowering. Values are given as mean ± SD, n=4. *p<0.05 by student's t test. **F** Cell area analysis of epidermal cells in two-week-old vector control and transgenic plants. The indications of columns in histograms **E**, **F** are same as those in **D**. Values are given as mean ± SD, n=4. *p<0.05 by student's t test. **G** qRT-PCR analysis of the transcript levels of cell wall expansion related genes *EXPA5*, *EXPA8*, *EXPA11*, *XTR3*, *XTR7*, *XTH3* and *XTH9*. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.

Appendix Figure S6. Comparison of leaf aging in Col-0 and vector control plants.

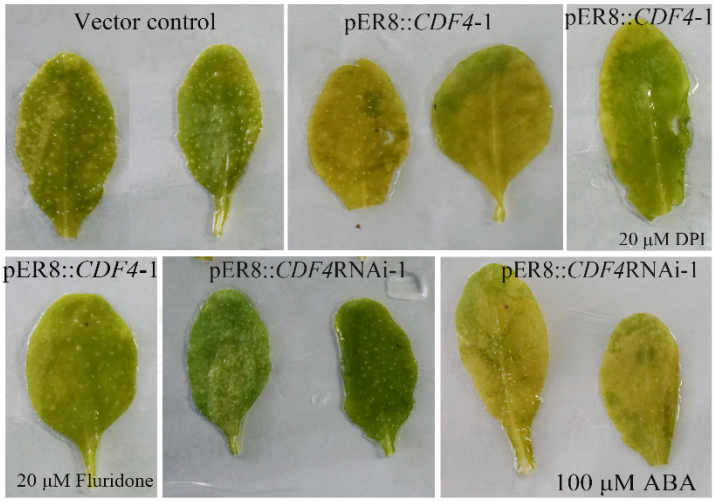
Rosette leaves of 7-week-old plants grown in soil under long day conditions were photographed. Two independent transgenic lines (pHB vector and pER8 vector) were analyzed. Note that leaf aging processes are indistinguishable in Col-0 and vector transgenic plants. Bar indicates 1cm.



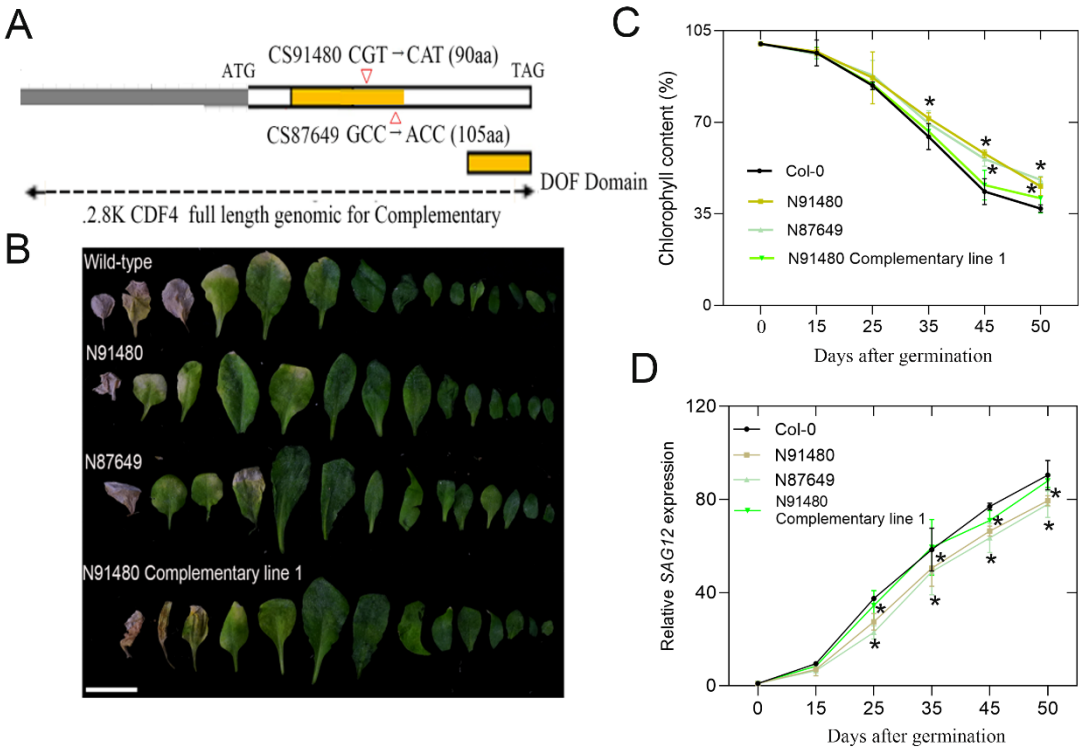
Appendix Figure S7. *CDF4* and *COG1* expression levels in estradiol-induced and inhibited *CDF4* transgenic plants. **A** *CDF4* and **B** *COG1* expression levels in estradiol-induced (pER8::*CDF4*) and inhibited (pER8::*CDF4*-RNAi, pER8::ami*CDF4*) transgenic plants. Three- week-old Arabidopsis plants were sprayed in rosette leaves with 20 μM estradiol for 2, 4 or 24 hours and then used to evaluate the relative *CDF4* and *COG1* expression levels. Values are given as mean ± SD, n=3. **p*<0.05 by student's *t* test.



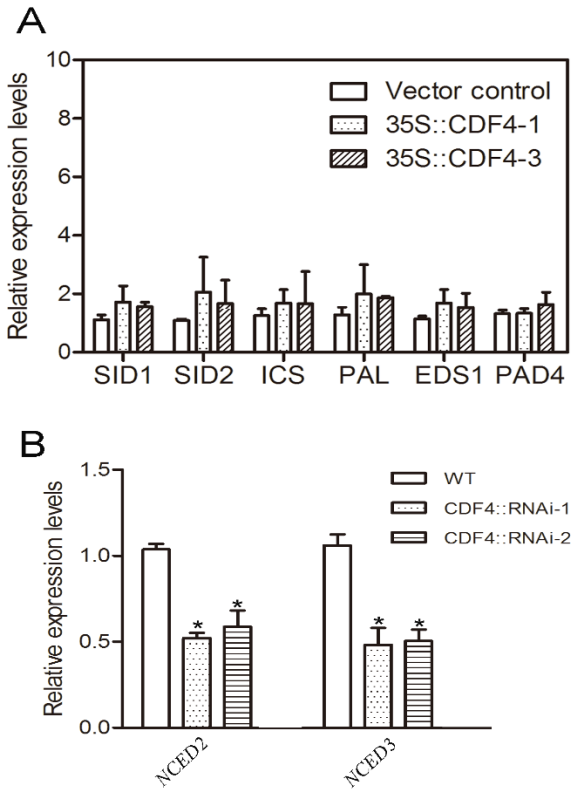
Appendix Figure S8. Inducible overexpression or knockdown of *CDF4* in transgenic plants affects leaf senescence and root growth. **A** Phenotypes of the inducible *CDF4*-overexpressing and RNAi transgenic lines after treatment with 20 μM estradiol for 7 days at one-week-old. Bar indicates 1cm. **B** Lateral root density analysis of the inducible *CDF4*-overexpressing and knockdown plants shown in **A. C** The leaf senescence phenotypes of detached rosette leaves of Vector control, pER8::*CDF4*, pER8:*CDF4*-RNAi and pER8::ami*CDF4* lines after treated with 40 μM ABA in the dark for 2.5 days. Values are given as mean ± SD, n=3. **p*<0.05 by student's *t* test.



Appendix Fig S9. The leaf senescence phenotypes of detached rosette leaves of vector control and pER8::*CDF4* lines after treatment with 20 μM DPI or 20 μM Fluridone and pER8:*CDF4*-RNAi after treatment with 100 μM ABA in the dark for 3.5 days.

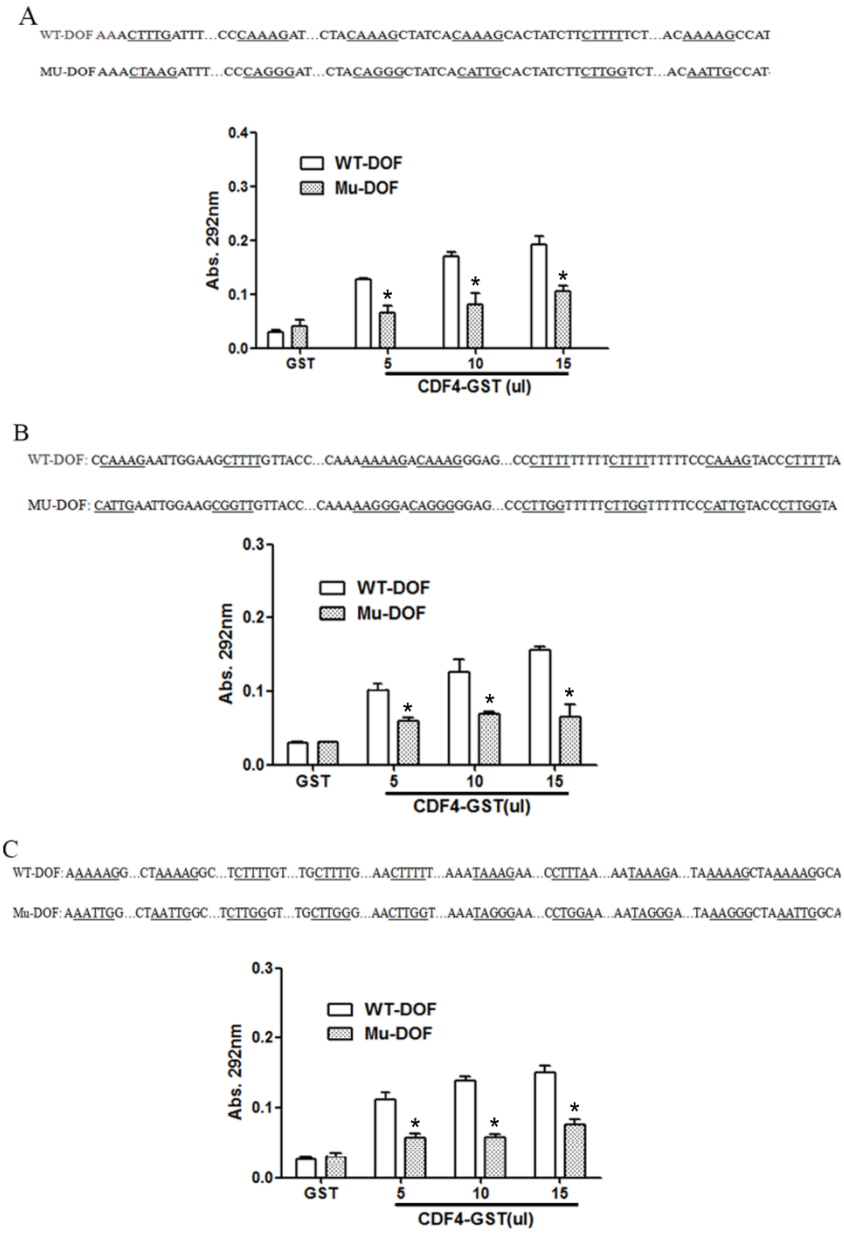


Appendix Figure S10. Comparison of leaf aging in wild-type, CS91480 and CS87649 mutant and complementary transgenic lines. (A, B) Rosette leaves of 5-week-old plants grown in soil under long day conditions were photographed. The wild-type and two independent CS91480 and CS87649 mutants and transgenic line were analyzed. Bar indicates 1.2 cm. Note that leaf aging processes are slowed down in the mutants than wild-type (Col-0). (C) Chlorophyll concentration and (D) *SAG12* expression level in rosette leaves at various development stages. Three independent experiments were conducted. Values are given as mean ± SD, n=3. **p*<0.05 by Student's *t*-test.



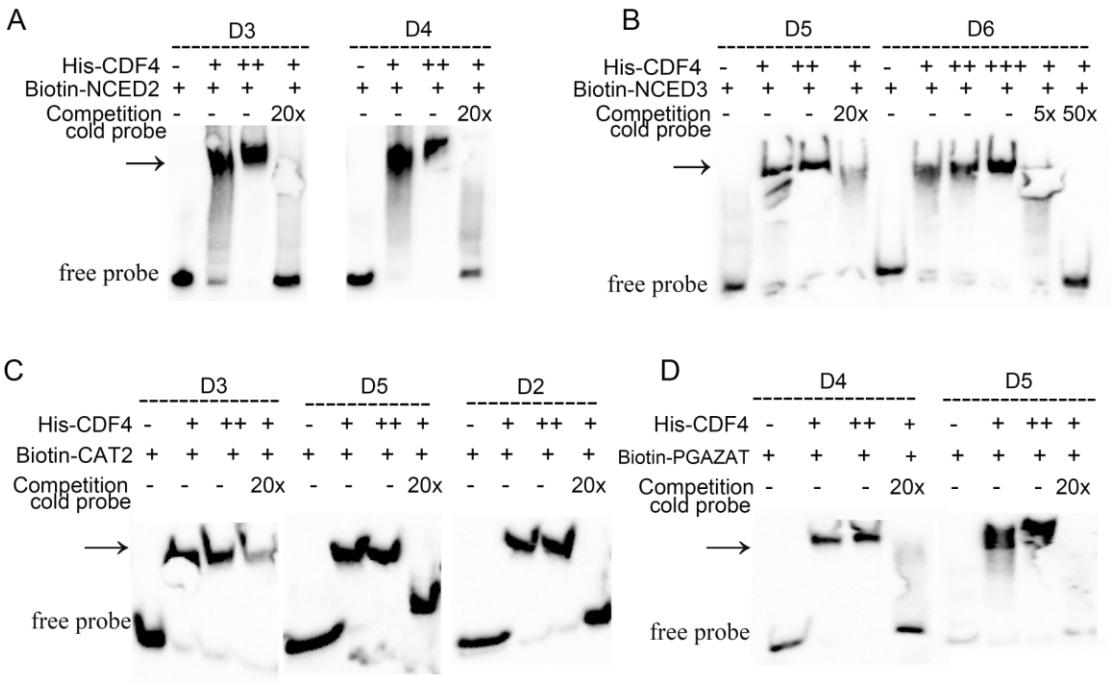
Appendix Figure S11. SA biosynthesis and signaling related genes expression levels in 35S::*CDF4* plants and *NCED2* and *NCED3* genes expression levels in *CDF4*-RNAi plants.

A SA biosynthesis and signaling related genes expression in the 35S::*CDF4* transgenic plants. **B** *NCED2* and *NCED3* expression levels in inducible *CDF4*-RNAi transgenic plants obtained using qRT-PCR analysis of Arabidopsis leaves treatment with 20 μM estradiol for 2 days at two-week-old. The expression of these genes in the vector control is given as 1. The relative expression level represents only the level of expression of the gene relative to the control. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.

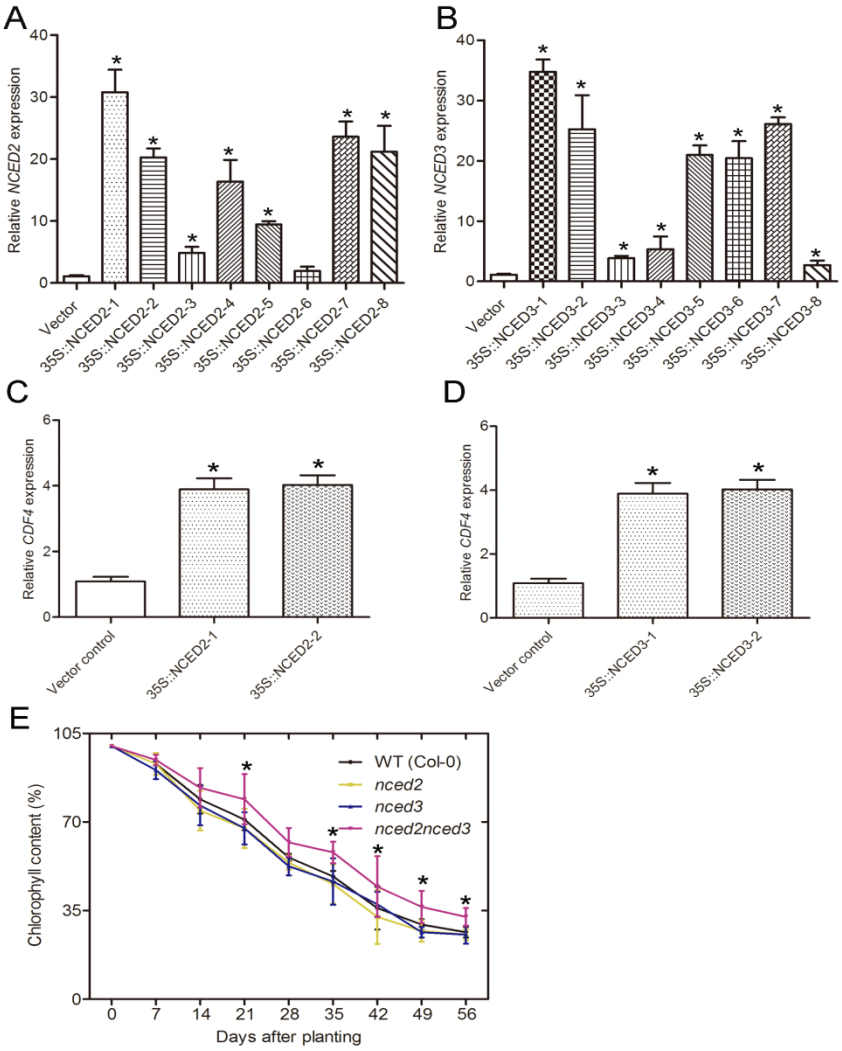


Appendix Figure S12 DPI-ELISA analysis of CDF4 binds to downstream genes promoters.

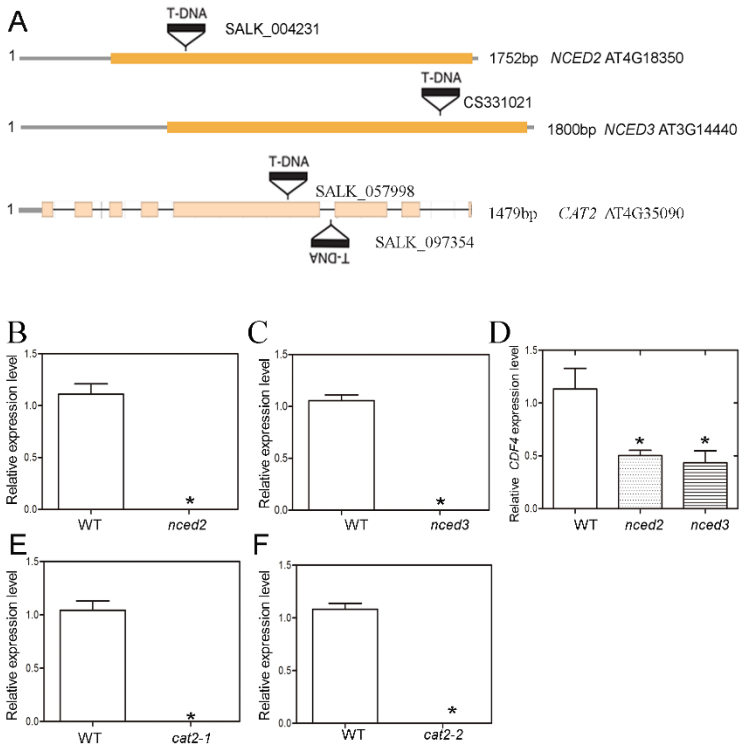
DPI-ELISA analysis of the binding of full-length CDF4 protein to the WT and mutant DOF binding motifs of the downstream target (**A**) *NCED2* (**B**) *NCED3* (**C**) *CAT2* genes promoters. Values are given as mean ± SD, n=3. **p*<0.05 by student's *t* test. Different amounts of CDF4-GST recombinant proteins were used. The numbers indicate the volumes of E. coli extract used in the assay. Binding efficiency was measured by ELISA with an HRP conjugated anti-GST antibody. Control binding reactions were performed with extract from E. coli cells transformed with empty vector pGEX-4T-1.



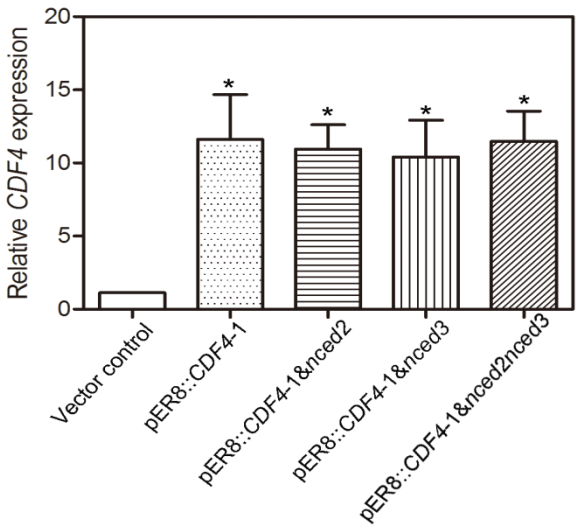
Appendix Figure S13. EMSA analysis was performed to detect the binding of recombinant CDF4 protein to the selected promoter regions of downstream target genes. (A) NCED2 (D3, D4); (B) NCED3 (D5, D6); (C) CAT2 (D2, D3, D5); PGAZAT (D4, D5). The biotin-labeled probes for EMSA assay were described in the Appendix Table S3. Three biological replicates were performed with similar results. 5-, 20- or 50-fold excesses of unlabeled cold probes were used in the competition assay. The arrows indicate the migration protein bands. The bright spots on the gels are likely due to partly incomplete transfer due to air bubbles in the transfer process and/or due to residual balance buffer traces, resulting in local overexposure.



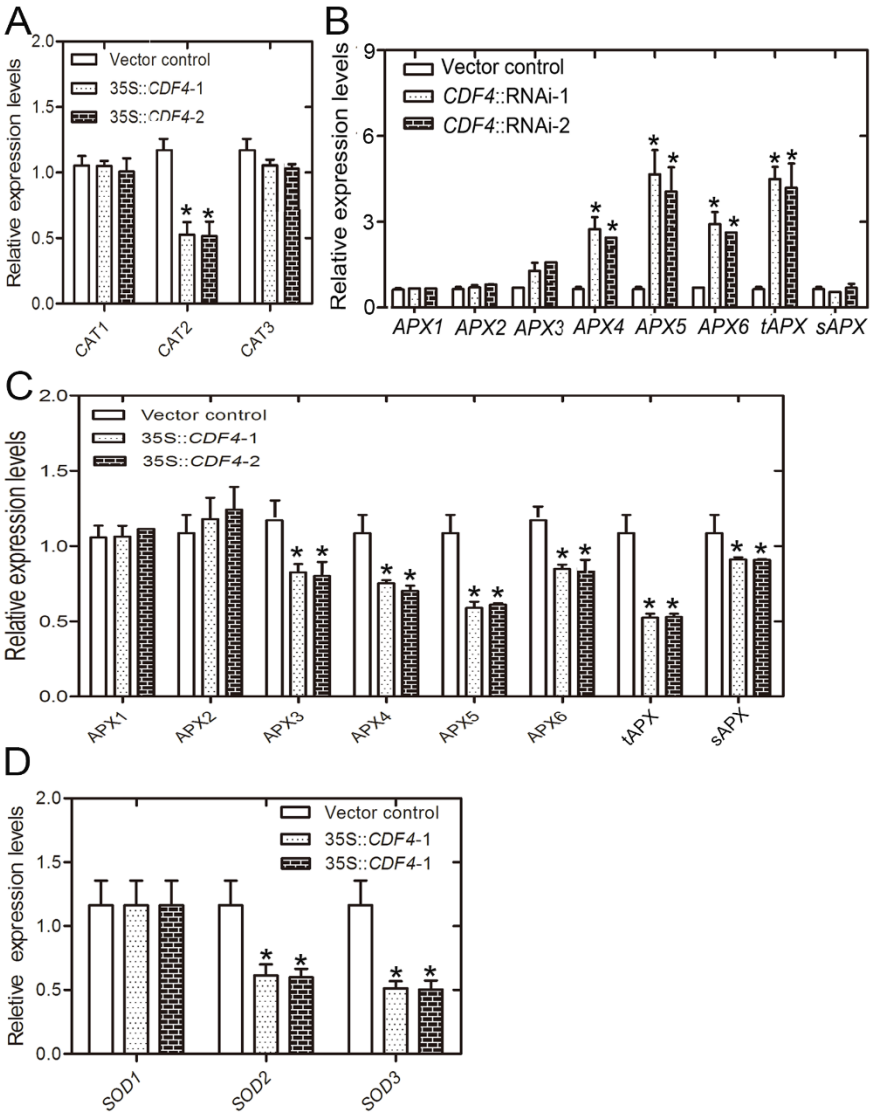
Appendix Figure S14. The expression levels of *NCED2, NCED3* and *CDF4* genes in the *NCED2* and *NCED3* transgenic lines and leaf senescence phenotype in wt, *nced2*, *nced3* and *nced2nced3* mutants. **A** *NCED2* and **B** *NCED3* expression levels in 35S::*NCED2* and 35S::*NCED3* transgenic plants obtained using qRT-PCR analysis. Relative *CDF4* gene expression levels in **C** 35S::*NCED2* and **D** 35S::*NCED3* transgenic plants compared with the vector control. The mRNA abundance of these genes was examined by qRT-PCR in various genotype backgrounds of two-week-old Arabidopsis leaves. **E** Analysis of the chlorophyll content in the third and fourth leaves from the WT, *nced2*, *nced3* and *nced2nced3* plants at various developmental stages. Values are given as mean ± SD, n=3. Values are given as mean ± SD, n=4. *p<0.05 by student's t test.



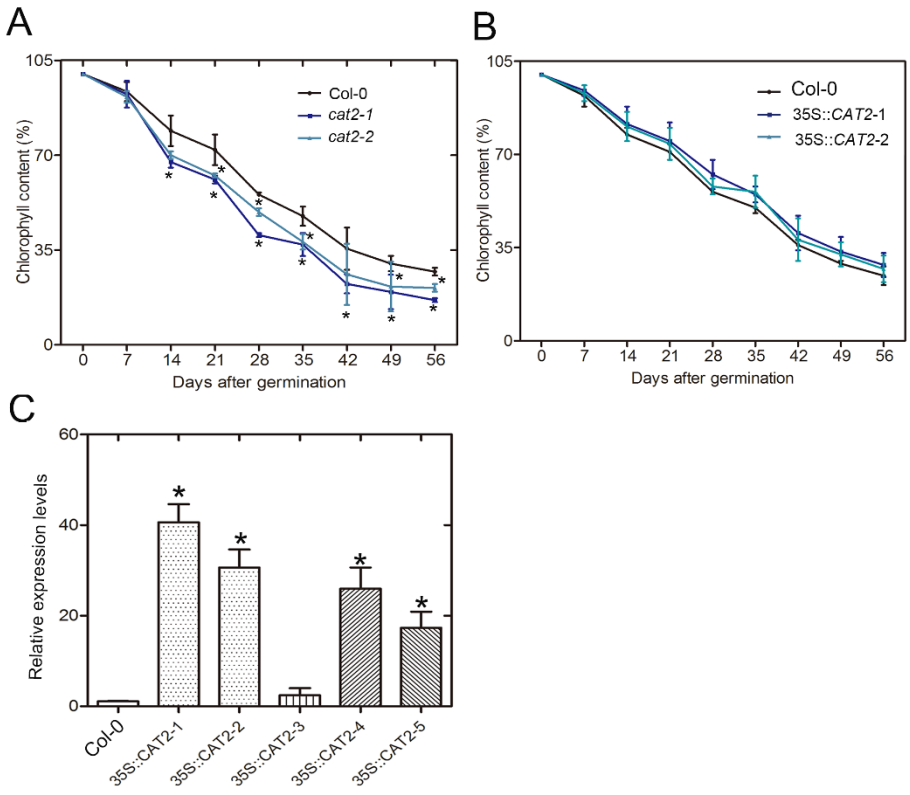
Appendix Figure S15. Identification of *nced2*, *nced3, cat2* mutants and *CDF4* gene expression levels in *nced2* and *nced3* mutants. **A** Genomic organization of the *NCED2, NCED3* and *CAT2* genes. The yellow boxes show the positions and sizes of the exons. The black box indicates the structure of T-DNA, and its site is shown by the triangle. **B** *NCED2,* **C** *NCED3,* **E&F** *CAT2* genes transcript levels in WT (col-0) and mutant plants. **D** Relative *CDF4* gene expression levels in *nced2* and *nced3* mutants compared with WT. The mRNA abundance of these genes was examined by qRT-PCR in various genotype backgrounds of two-week-old Arabidopsis leaves. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.



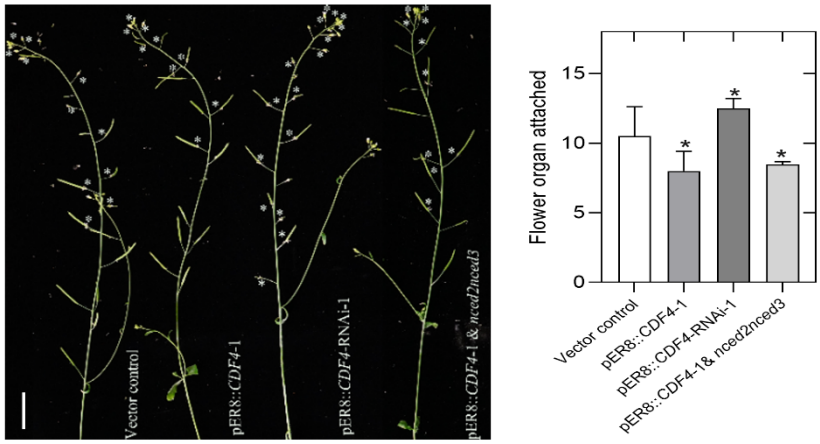
Appendix Figure S16. *CDF4* expression levels in pER8::*CDF4*, pER8::*CDF4*&*nced2*, pER8::*CDF4*&*nced3* and pER8::*CDF4*&*nced2nced3* plants after estradiol induction. Relative *CDF4* expression levels in 14-day-old Arabidopsis transgenic seedlings pER8::*CDF4*-1, pER8::*CDF4*-1&*nced2*, pER8::*CDF4*-1&*nced3* and pER8::*CDF4*-1&*nced2nced3* after estradiol induction for 4 hours. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.



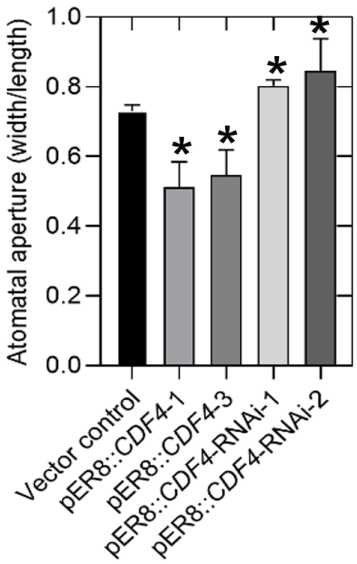
Appendix Figure S17. The *APX*, *CAT* and SOD family genes expression levels in the *CDF4* transgenic plants. qRT-PCR analysis of (A) *CAT* family genes expression in the fourth rosette leaves from 35S::*CDF4* transgenic plants. (B) *APX* family genes expression in the rosette leaves from *CDF4*::RNAi transgenic plants. (C) *APX* and (D) *SOD* family genes expression in the fourth rosette leaves from 35S::*CDF4* transgenic plants. The expression of these genes in the vector control is given as 1. The relative expression level represents only the level of expression of the gene relative to the vector control. Data are represented as means ± SD, n=3. **p*<0.05 by student's *t* test.



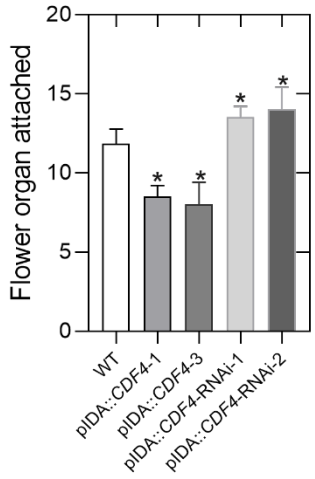
Appendix Figure S18. *CAT2* gene is involved in leaf senescence control. **A** Chlorophyll content in rosette leaves of *cat2* mutants at various development stages. **B** Chlorophyll content in rosette leaves of 35S::*CAT2*-1 and 35S::*CAT2*-2 transgenic plants at various development stages. **C** *CAT2* expression levels in 35S::*CAT2* transgenic plants obtained using qRT-PCR analysis. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.



Appendix Figure S19. Observation of inflorescences and measurement of flower organs attached in 7.5-week-old wild-type Arabidopsis and the *CDF4* transgenic plants after 20 μM estradiol induction for 4 days (once every day). Bar indicates 1.5 cm. The asterisk represents the flower organ attached along the inflorescence. Three independent experiments were conducted. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.



Appendix Figure S20. Measurement of stomatal aperture in the rosette leaves from 18-day-old vector control and transgenic lines with altered *CDF4* expression after estradiol induction for three days (once every day). Three independent experiments were conducted. Values are given as mean ± SD, n=3. **p*<0.05 by student's *t* test.



Appendix Figure S21. Quantification of the flower organ attached showed in Fig 8A. Values are given as mean ± SD, n=3. *p<0.05 by student's t test.

Appendix Table S1. The primers used in vector construction and mutant analysis.

Transgenes	**Primers (Sequence 5'-3')**
Clone *CDF4* cDNA	5'- ATAAGCTATTTTCCATTCTC -3′[a]
	5'- AAAAGAGAGTAAATAATTA-3′[a]
pCAMBIA1300::*CDF4*	5'-CTGCAG AGTTTTAATTAATGTCAAGCC-3′[b]
	5'-GGGCCC AACGTGCAGAGAATGGAAAATA-3′[b]
Double 35S::*CDF4*	5'-GGATCC ATGGCGACTC AAGATTCTCA AGG -3′
	5'-CTAGA**A** TCAGCACGATTGACCGTCGGAGT -3′
pER8::*CDF4*	5'-ACTAGT ATGGCGACTC AAGATTCTCA AGG -3′
	5'-CTCGAG TCAGCACGATTGACCGTCGGAGT -3′
pER8::*CDF4*-HA	5'-ACTAGT ATGGCGACTC AAGATTCTCA AGG -3′
	5'-CTCGAG TCAGCACGATTGACCGTCGGAGT -3′
pER8::*CDF4*RNAi	5'- GGATCC TCTAGA GAGGAGTGGCAGCATGCCGCA-3′
	5'- GAGCTC CTGCAG ATTGACAAATGACAAATTAAC -3′
Double 35S::*NCED2*	5'-GGATCC ATGGTTTCTCTTCTTACAATGC -3′
	5'-CTAGA**A** TTATAATTGATCAACGAGTTCAT -3′
Double 35S::*NCED3*	5'-GGATCC ATGGCTTCTTTCACGGCAAC GG-3′
	5'-CTAGA**A** TCACACGACCTGCTTCGCCAAA -3′
Double 35S::*ORS1*	5'-GGATCC ATGGATTACAAGGTATCAAGAAGT-3′
	5'-CTAGA**A** TCAGAATTTCCAAACGCAATCAA-3′
Double 35S::*CAT2*	5'-GGATCC ATGGATCCTTACAAGTATCGTCCA-3′
	5'-CTAGA**A**TAGATGCTTGGTCTCACGTTCAGA-3′
SALK_057998	LP AGAGGCAAGATATCCTCAGGC
	RP TCTGGTGCTCCTGTATGGAAC
SALK_097354	LP TGCCAAAGAACCTTCATGTTC
	RP TGGGACACTTCTGGCATTTAC
SALK_004231	LP TCTGAGGGAGATTATGGATTGG
	RP CTTCACGCGTTAAGCTACGAC

GABI_129B08	LP ACAGAGGCTCTCCTCCGTAAC
	RP GTCAGCCACGAGAAGCTACAC
pCAMBIA1300::proPGAZAT	AATCACTAAGTCAATTTTCTAT
	GGCAAGGAAATGTGTTTTTT
pCAMBIA1300::proIDA	GGTTCTTACCTAGTTAAAATTT
	GTAGTCAATGTTTTTTTCTTC
CDF4-amiRNA[c]	I miR-s gaTCTTATCCGGACGTTTCGCGGtctctcttttgtattcc
	II miR-a gaCCGCGAAACGTCCGGATAAGAtcaaagagaatcaatga
	III miR*s gaCCACGAAACGTCCCGATAAGTtcacaggtcgtgatatg
	IV miR*a gaACTTATCGGGACGTTTCGTGGtctacatatatattcct

Restriction digestion sites are underlined.

a: Primers designed according to the 5'/3'-UTR for clone *CDF4* gene cDNA.

b: Primers for constitutive overexpression of the *CDF4* gene.

c: Primers for generation of the artificial interference RNA vector for the *CDF4* gene.

Appendix Table S2. Gene-specific primers used in the qRT-PCR experiments.

Genes	Primers (Sequence 5'-3')
ACTIN2	5'-TCAGATGCCCAGAAGTCTTGTT-3'
	5'-CCGTACAGATCCTTCCTGATATC-3'
TUBULIN2	5'-GAGCCTTACAACGCTACTCTGTC-3'
	5'-ACACCAGACATAGTAGCAGAAA-3'
RBOHA	5'-CCGGGGATGATTACCTCAGC-3'
	5'-AGGGAAGTTGACAAACCTTGGA-3'
RBOHB	5'-CCGGGGATGATTACCTCAGC-3'
	5'-AGGGAAGTTGACAAACCTTGGA-3'
RBOHC	5'-CGGCAGGAGTTAGTGGTCTG-3'
	5'-ATTGGTGTGGCTCCAATCCC-3'
RBOHD	5'-ACTCTCCGCTGATTCCAACG -3'
	5'-ATCGCCGGAGACGTTATTCC-3'
RBOHE	5'-AAGACCTCGTCATGTGGTTCA-3'
	5'-AGAACCCAGCTTCTTTGCCA-3'
RBOHF	5'-CTTGGCATTGGTGCAACTCC-3'
	5'-TCTTTCGTCTTGGCGTGTCA-3'
WRKY53	5'-GTAGTAGCCGCAGACTTCTTGT-3′
	5'-GCGAATACGTCTTTGCAGGAAT-3′
PR1	5'-CCTTACGGGGAAAACTTAGCCT-3′
	5'-CCGAGTCTCACTGACTTTCTCC-3′
PR5	5'-AACGGTAGATGTGTAACCGGAG-3′
	5'-CGATCCTCCGGATGGTCTTATC-3′
CAT1	5'-TCAAATGCCTGTCGGATGAG-3'
	5'-GAAGAGATTCCACTGCGGATAG-3'
CAT2	5'-TTTCGACAGGGAACGGATTC-3'
	5'-GTCAGCACAAGTGAGGTTAGAG-3'
CAT3	5'-CTCCAGTCTCCAACAACATCTC-3'
	5'-GGATCCTCTCTCTGGTGAAATTAG-3'

APX1	5'-CCGTCCTTTGGTCGAGAAATA-3'
	5'-GCAAACCCAAGCTCAGAAAG-3'
APX2	5'-GGAAGCTCCGTGGTCTTATT-3'
	5'-CTCCTGTCTTCGTCTTCACATC-3'
APX3	5'-TGATGCGGAGTACTTGAAAGAG-3'
	5'-TGCCAATCGGAGCATGATAG-3'
APX4	5'-GCAACTGTGCAAGAGATGAAAG-3'
	5'-GCTTGATCAGGACCCAAGAA-3'
APX5	5'-CTAAACCGTCCACACAACAAAG-3'
	5'-CAACTCCAGCGAGCTGATAA-3'
APX6	5'-GGTGTGCTTCGTTTAGTGTTTC-3'
	5'-ACCTATGTTCTCAGGTCTCTCA-3'
SOD1	5'-CATGCTGGTGATCTAGGAAACA-3'
	5'-CAACAGCCCTACCAACAATAGA-3'
SOD2	5'-CTCATTCCTCCTTCCTCCAATC-3'
	5'-GCTTTAACGGCGAAGGAAAC-3'
SOD3	5'-CCGCTTAGTGGGCAGTATTC-3'
	5'-CCTGCGTTTCCAGTTGATTTG-3'
NCED1	5'-CCATCCGTGA TGAAACTCCT CC-3'
	5'-ATCTCCATCAAACCAGTGATATC-3'
NCED2	5'-TCCGGTAACGGCGAAGAAAA-3'
	5'-TGCCATGAAACCCATACGGT-3'
NCED3	5'-TCAATGGCCGGTTATTGGCT-3'
	5'- ACTTTCGGGTGGGCAATCAT-3'
NCED4	5'-CTCTTC GACGGCGACG GTATG-3'
	5'-AGGCATAACCGGAGCTCCGGT-3'
NCED5	5'-TTG AAATACTTTA AATTCTCGC-3'
	5'-TCGGAGAGCTTAAACACAACTT-3'
NCED6	5'-AGTGA TAGCGCATCC TAAGGTG-3'
	5'-TGAATCATCGTTGGTTCAGGGAG-3'
NCED9	5'-CCATC CTAAAACGGC GGATCCTG-3'
	5'-ACTGGTTTGTGAAGTGGATTTGCT-3'

SDR1	5'-TGATCTCGG AGGTGAGGTG TGTA-3'
	5'-ATATCAGGGCACGGTGCTCCACA-3'
SDR3	5'- TGGTGGAGGA ATATAGCGCA GCC-3'
	5'-TCAAATGGGCTTAACGACGCTATA-3'
SDR5	5'-GGTG GATTAGGAAA ATATGGTATA-3'
	5'-CACGTGACGAGCTTTCAATACAAT-3'
AAO1	5'-GCGAAAATCG CTACTCATAT GGAG-3'
	5'-GAACTGTTCTTGACTCGAGCTGCTA-3'
AAO2	5'-CTTACGGTT GTGGAAGCAG AGAAG-3'
	5'-ACGCTTCTCACTATCAAACCGAGT-3'
AAO3	5'-TTA TCGGCGAGTA CATTGTATAAG-3'
	5'-CAGGATTAAGACTCTTTCCACAGT-3'
AAO4	5'-TTCAAGGAAT CGGATTTTTC ATGT-3'
	5'-GAGAACGCGGTTCTTGTGATGACC-3'
ZEP	5'-CCATT GAGGATAGTT TTCAACTAG-3'
	5'-AGCCATCCTCGCCATTGCATGGA-3'
CYP707A1	5'-AATAAGGAAA GACAAAGAAGAA-3'
	5'-TCCTTCGTATTCGACATCTTCGAC-3'
CYP707A3	5'-GGC CAGTAAAGAG AGGATGCTTG-3'
	5'-CCCAAGAATTGAGTGATTCTTGAG-3'
ABI1	5'-CGTTCCTGAG AGTTGACTCG GAGA-3'
	5'-GTCAACGGATAATGGAAGTGCAGT-3'
ABI2	5'-CTGTTTGAGTT CAAGTGTGTTCCT-3'
	5'-ATTAGTGACTCGACCATCAAGCAA-3'
ABI3	5'-GGCAT CTCTCTGGCC ATGGAAG-3'
	5'-CGGAGTATATGACTATGAAATCAC-3'
ABI4	5'-GCAACCGCGAAGACGCC GCACGT-3'
	5'-AGGTGGAAGGAGAAGAAGCGGCG-3'
ABI5	5'-ATGTGA GAACGGCAAG AACTTTGG-3'

	5'-ATTAGCCGGAACAGAATGTGAACC-3'
HAESA	5'-AGAACCCGTGATCGATCCCAAA-3'
	5'-ACAAGGAACAGCACCAGAGACT-3'
IDA	5'-TGTGTAGCGGCTGCAAGAATTG-3'
	5'-AGGAGGAATGGGAACGCCTTTA-3'
ARP4	5'-TCCTGACACCACGGAAAGCTA-3'
	5'-TGGACTATGGACGGGTTGAACA-3'
AGL15	5'-GCAAAGCCTTGAGCAGCAACTA-3'
	5'-CGTTGTTCCTTGAGGCGTGATT-3'
PGAZAT	5'-CGGGACATAAGTGGCACTAGCG-3'
	5'-CCTTTATCAACCACATTAGCAT-3'
AtDOF4.7	5'-CTCGTGAGCTTGTAAGAAACCA-3'
	5'-GAGGCAAGGTTGAAGTTAGGAT-3'
HWS	5'-CTATCCTCGATAGGATCACCGT-3'
	5'-GATCATGTTTCCCGATTCCTCC-3'
AtEXP10	5'-TCTATATAGCCAAGGCTACGGG-3'
	5'-CAAGAGGAGGATTACACCAACC-3'

Appendix Table S3. Gene-specific primers used in the Chip-qPCR experiments.

Transgenes	**Primers (Sequence 5'-3')**
NCED2-D1	5'- CCCTTACATCAAATCTTGACT-3'
	5'- GCTTCATATTTTGGGCCTTG-3'
NCED2-D2	5'- AACGTAATATTTGTTTGGAA-3'
	5'- CATCAACAGTGAAATATGGT-3'
NCED2-D3	5'- ATTAATGAATCATTAATATA-3'
	5'- TAATAAACTAATGATAGTG-3'
NCED2-D4	5'- CTATATAAGATTTCTCCTT-3'
	5'- CCATGGTTTCTCTTCTTAC-3'
NCED3-D5	5'-CTTTTACAATTATCATATTCC-3'
	5'- CTTTTTCTATTTGGACAACAC-3'
NCED3-D6	5'- AATTTGATATCCTCAAGTTGC-3'
	5'- GTGGGTTATAGAGGGAATTA-3'
CAT2-D1	5'- AATATCTTAATATTATTTACAC -3'
	5'- TCGATTACTTGTTTTATACATA-3'
CAT2-D2	5'- GGTCGACATGTTTCAATCCGT-3'
	5'- CCTATGGCTATGAGTGCTTGTA-3'
CAT2-D3	5'-CAAGACCATACTAAACCACT-3'
	5'- ATATATATTCTGTACTTAAAA-3'
CAT2-D4	5'- TTGTTAATGTGATGTAAATC-3'
	5'- ACCTACTATTTATTCAAATTC-3'
CAT2-D5	5'-TTTCTTTCCAGTATTTATCA-3'
	5'-ATTTATAAATGGCGTGTGT-3'
PGAZAT-D1	5'- CTAGAAGAAACACGAAATG-3'
	5'- TAAGACATGGGCGACATTTG-3'

PGAZAT-D2	5’- GGAACATTTAATTTGTTAAA-3'
	5’- TAGAAATATAAGAATCTGA-3'
PGAZAT-D3	5’- CAACTTGACAAACAAAC-3'
	5’-TTCAGTTGAAATGGCGATA-3'
PGAZAT-D4	5’- AAAAAAGGGGAAAGTAAA-3'
	5’- AATCCTCTCCTTTAATAAAA-3'
PGAZAT-D5	*5’*- AGAAACCTAAATTTTAAACG-*3′*
	5’-CTTTGTTGCTGGAAAAGGAAT-*3′*