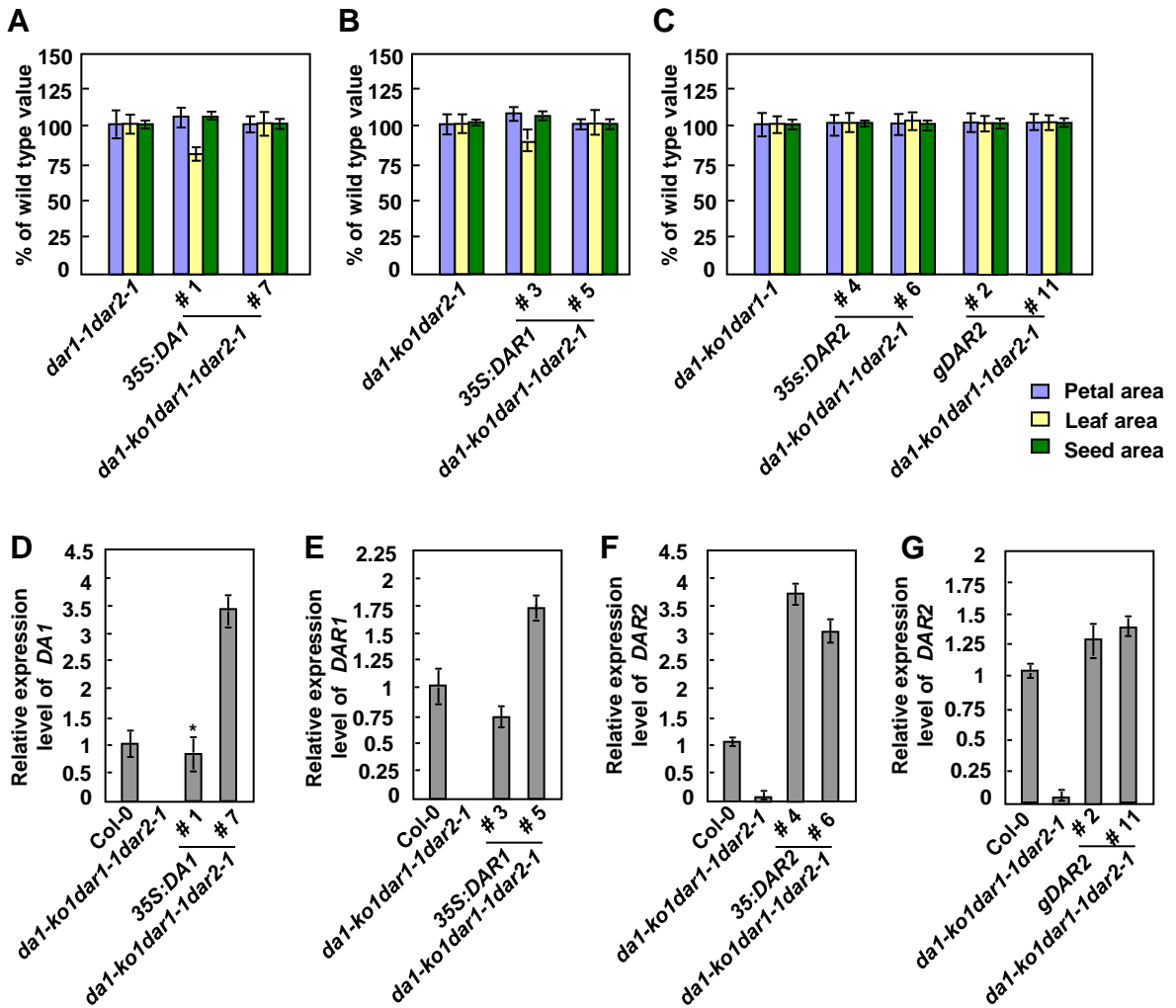


Supplemental Figure 1. *DA1*, *DAR1* and *DAR2* act redundantly to affect organ growth.

Petal area (A), petal cell area (B) and fifth leaf area (C) of Col-0, *da1-ko1*, *dar1-1*, *dar2-1*, *da1-ko1 dar2-1*, *da1-ko1 dar1-1* and *da1-ko1 dar1-1 dar2-1*.

Values (A-C) are given as mean \pm SE relative to the respective wild-type values, set at 100%.



Supplemental Figure 2 . Complementation test of *da1-ko1 dar1-1 dar2-1*.

(A) Petal area, fifth leaf area and seed area of *dar1-1 dar2-1* and *35S:DA1; da1-ko1 dar1-1 dar2-1* plants. Values are given as mean \pm SE relative to *dar1-1 dar2-1* values, set at 100%.

(B) Petal area, fifth leaf area and seed area of *da1-ko1 dar2-1* and *35S:DAR1; da1-ko1 dar1-1 dar2-1* plants. Values are given as mean \pm SE relative to *da1-ko1 dar2-1* values, set at 100%.

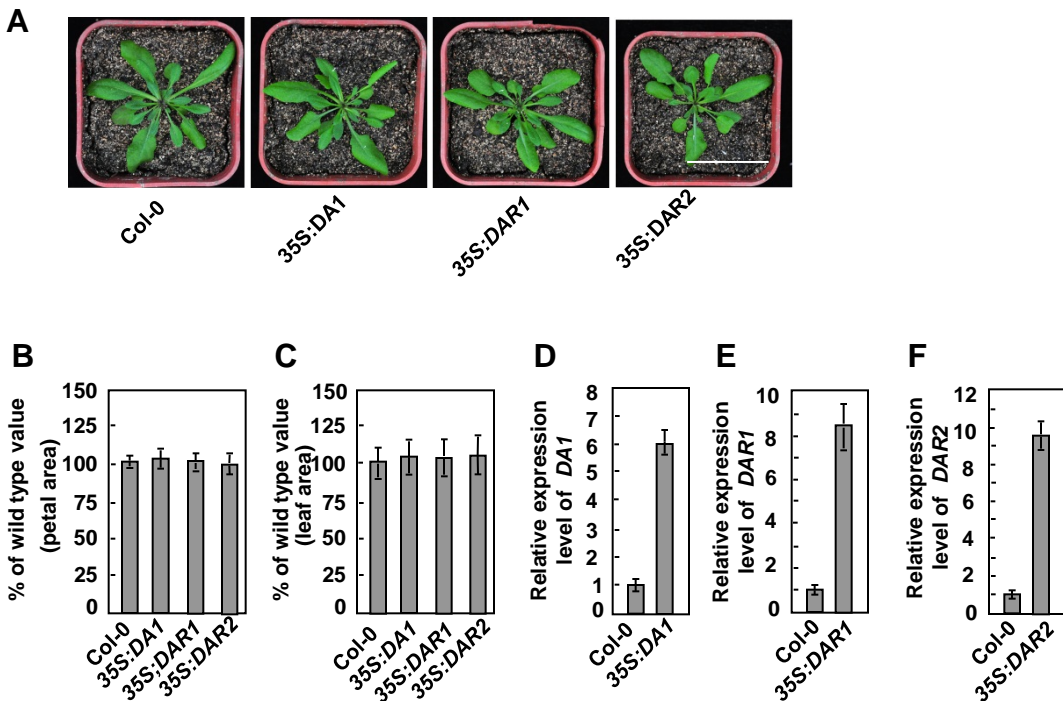
(C) Petal area, fifth leaf area and seed area of *da1-ko1 dar1-1*, *35S:DAR2; da1-ko1 dar1-1 dar2-1* and *gDAR2; da1-ko1 dar1-1 dar2-1* plants. *gDAR2; da1-ko1 dar1-1 dar2-1* is *da1-ko1 dar1-1 dar2-1* transformed with a genomic copy of *DAR2*. Values are given as mean \pm SE relative to *da1-ko1 dar1-1* values, set at 100%.

(D) Relative expression level of *DA1* in Col-0, *da1-ko1 dar1-1 dar2-1* and *35S:DA1; da1-ko1 dar1-1 dar2-1* plants. Data shown are mean \pm SD of three replicates.

(E) Relative expression level of *DAR1* in Col-0, *da1-ko1 dar1-1 dar2-1* and *35S:DAR1; da1-ko1 dar1-1 dar2-1* plants. Data shown are mean \pm SD of three replicates.

(F) Relative expression level of *DAR2* in Col-0, *da1-ko1 dar1-1 dar2-1* and *35S:DAR2; da1-ko1 dar1-1 dar2-1* plants. Data shown are mean \pm SD of three replicates.

(G) Relative expression level of *DAR2* in Col-0, *da1-ko1 dar1-1 dar2-1* and *gDAR2; da1-ko1 dar1-1 dar2-1* plants. *gDAR2; da1-ko1 dar1-1 dar2-1* is *da1-ko1 dar1-1 dar2-1* transformed with a genomic copy of *DAR2*. Data shown are mean \pm SD of three replicates.



Supplemental Figure 3 . Overexpression of *DA1*, *DAR1* or *DAR2* does not affect organ size.

(A) 30-d-old plants of Col-0, 35S:*DA1*, 35S:*DAR1* and 35S:*DAR2*.

(B) Petal area of Col-0, 35S:*DA1*, 35S:*DAR1* and 35S:*DAR2*. Values are given as mean \pm SE relative to wild-type values.

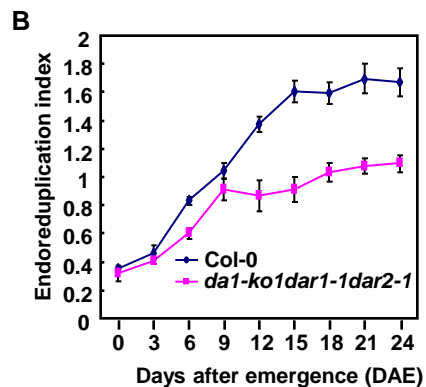
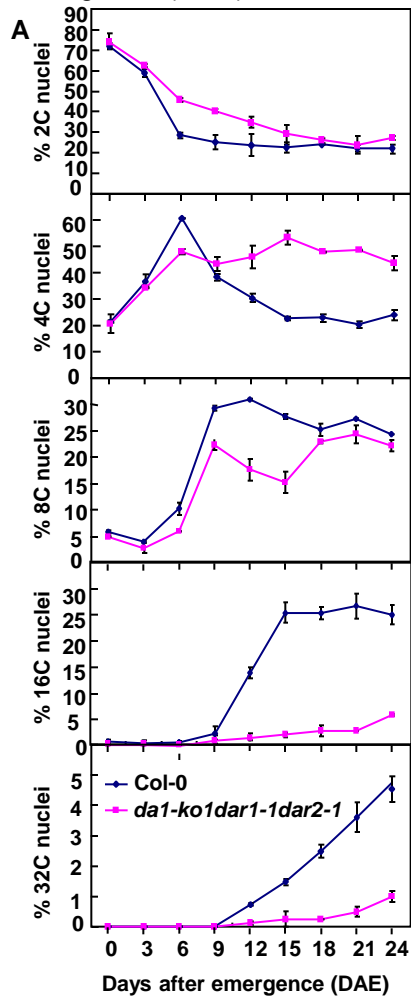
(C) Fifth leaf area of Col-0, 35S:*DA1*, 35S:*DAR1* and 35S:*DAR2*. Values are given as mean \pm SE relative to wild-type values.

(D) Relative expression level of *DA1* in Col-0 and 35S:*DA1* plants. Data shown are mean \pm SD of three replicates.

(E) Relative expression level of *DAR1* in Col-0 and 35S:*DAR1* plants. Data shown are mean \pm SD of three replicates.

(F) Relative expression level of *DAR2* in Col-0 and 35S:*DAR2* plants. Data shown are mean \pm SD of three replicates.

Bar= 5cm in (A)

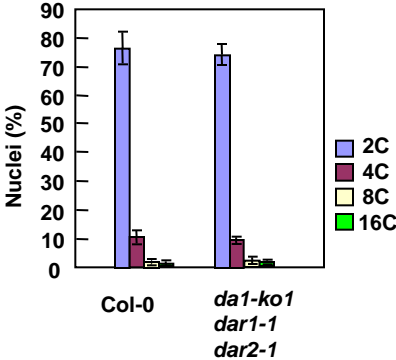


Supplemental Figure 4. *DA1*, *DAR1* and *DAR2* act redundantly to influence endoreduplication during leaf development.

(A) Nuclear DNA ploidy distribution of Col-0 and *da1-ko1 dar1-1 dar2-1* fifth leaves measured over a period of 24 days after emergence (DAE). At 0 DAE, the fifth leaves (~ 0.5 mm²) were visible. The values represent averages of three independent biological replicates.

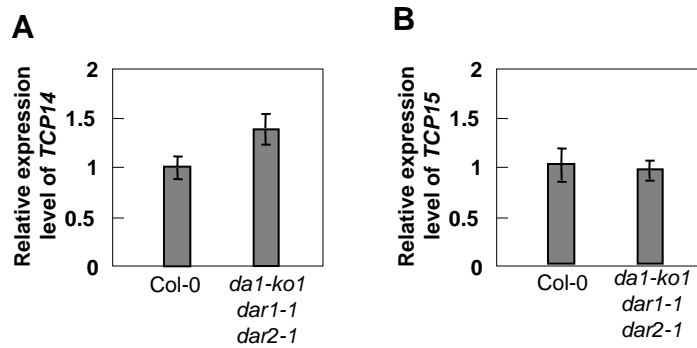
(B) The endoreduplication index (EI) of Col-0 and *da1-ko1dar1-1dar2-1* fifth leaves. The EI represents the average number of endocycles undergone by a given nucleus.

Values (A and B) are given as mean \pm SE.



Supplemental Figure 5. *da1-ko1 dar1-1 dar2-1* is not altered in endoreduplication in petal cells

Nuclear DNA ploidy distribution of Col-0 and *da1-ko1 dar1-1 dar2-1* petals. Values are given as mean \pm SE.



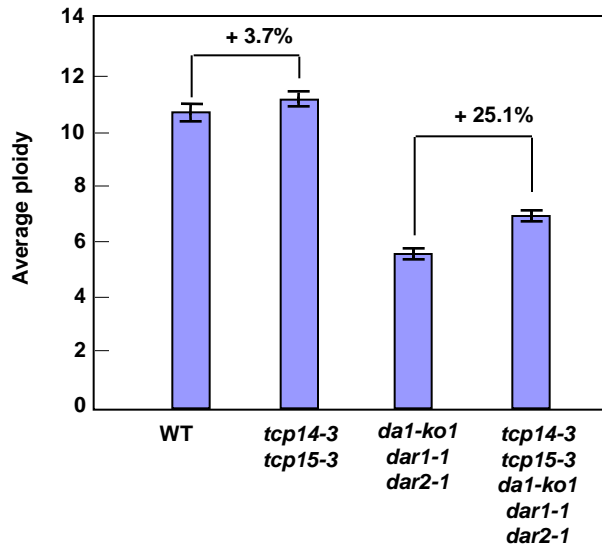
Supplemental Figure 6. Expression of *TCP14* and *TCP15* in Col-0 and *da1-ko1 dar1-1 dar2-1* leaves.

(A) Expression of *TCP14* in Col-0 and *da1-ko1 dar1-1 dar2-1* leaves.

(B) Expression of *TCP15* in Col-0 and *da1-ko1 dar1-1 dar2-1* leaves.

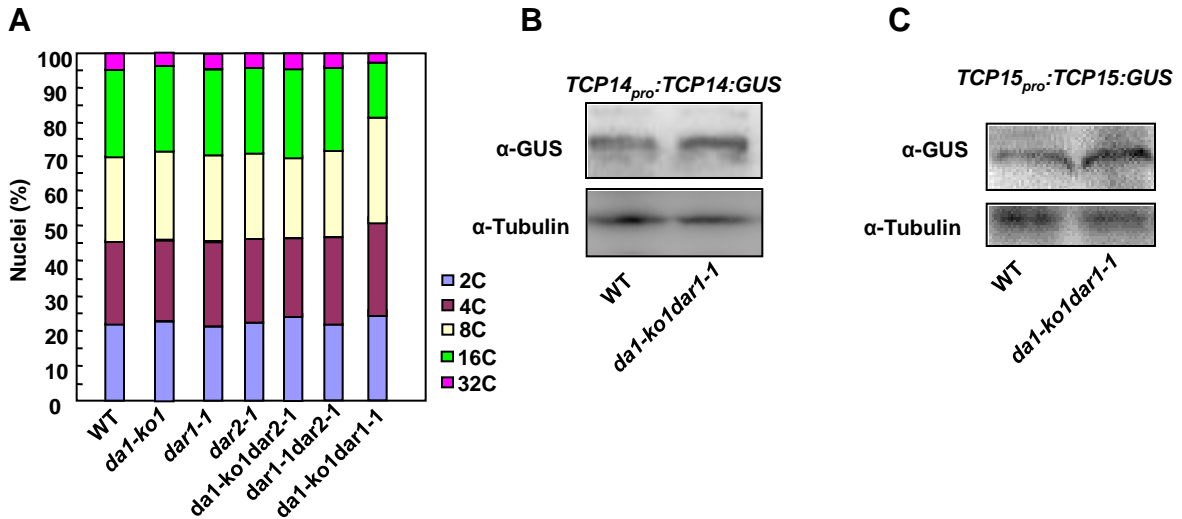
The values represent averages of three independent biological replicates.

Values (A and B) are given as mean \pm SE.



Supplemental Figure 7. *tcp14-3 tcp15-3* partially suppresses the reduced ploidy level phenotype of *da1-ko1 dar1-1 dar2-1*.

The average ploidy level of nuclei in Col-0, *tcp14-3 tcp15-3*, *da1-ko1 dar1-1 dar2-1* and *tcp14-3 tcp15-3 da1-ko1 dar1-1 dar2-1* fifth leaves. Values are given as mean ± SE.

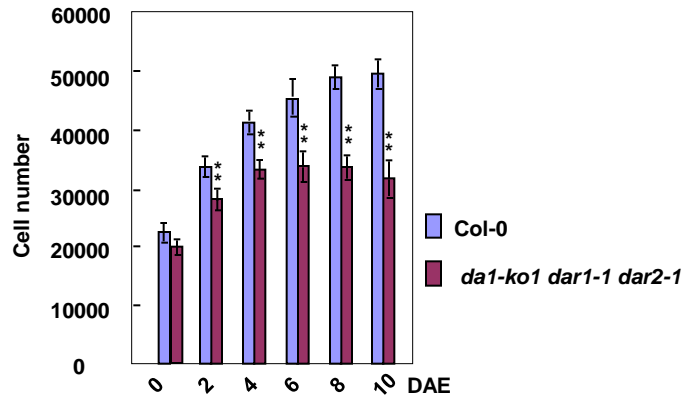


Supplemental Figure 8. DA1, DAR1 and DAR2 redundantly affect endoreduplication.

(A) Nuclear DNA ploidy distribution of Co-0, *da1-ko1*, *dar1-1*, *dar2-1*, *da1-ko1 dar2-1*, *dar1-1 dar2-1* and *da1-ko1 dar1-1* fifth leaves.

(B) The TCP14-GUS protein levels in *TCP14_{pro}:TCP14-GUS* and *TCP14_{pro}:TCP14-GUS;da1-ko1 dar1-1* plants. Total protein extracts were subjected to immunoblot assays using anti-GUS and anti-Tubulin (as loading control) antibodies.

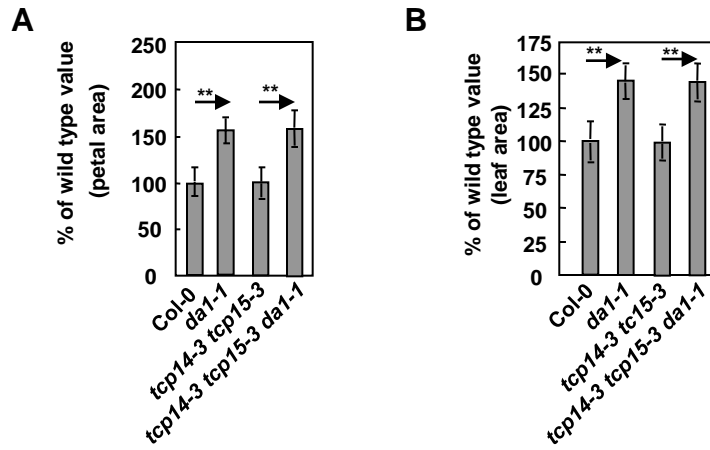
(C) The TCP15-GUS protein levels in *TCP15_{pro}:TCP15-GUS* and *TCP15_{pro}:TCP15-GUS;da1-ko1 dar1-1* plants. Total protein extracts were subjected to immunoblot assays using anti-GUS and anti-Tubulin (as loading control) antibodies.



Supplemental Figure 9. The simultaneous disruption of *DA1*, *DAR1* and *DAR2* affects cell proliferation.

The average number of cells in Col-0 and *da1-ko1 dar1-1 dar2-1* fifth leaves measured over a period of 10 days after emergence (DAE).

Values are given as mean \pm SE. **, $P < 0.01$ compared with the wild type (Student's *t*-test).



Supplemental Figure 10. *tcp14-3 tcp15-3* does not suppress the petal and leaf size phenotypes of *da1-1*.

(A) Petal area of Col-0, *da1-1*, *tcp14-3 tcp15-3* and *tcp14-3 tcp15-3 da1-1*.

(B) Fifth leaf area of Col-0, *da1-1*, *tcp14-3 tcp15-3* and *tcp14-3 tcp15-3 da1-1*.

Values (A and B) are given as mean \pm SE relative to the respective wild-type values, set at 100%. **, $P < 0.01$ compared with the wild type (Student's *t*-test).

Supplemental Table 1. Complementation test of *da1-ko1 dar1-1 dar2-1*.

Constructs	Number of complemented plants	Number of no complemented plants
<i>35S:DAI</i>	21	1
<i>35S:DAR1</i>	30	2
<i>35s:DAR2</i>	28	1
<i>gDAR2</i>	25	0

Supplemental Table 2. List of primers used in this study

Name	Primers
Primers for verifying T-DNA	
SALK_126092-LP	AAGCCAGCTAAATATGATTGG
SALK_126092-RP	AATCCGTTTGGAACCTCGTTTG
SALK_067100-LP	ATTTAGTCGAAGCCATGCATG
SALK_067100-RP	TTACAAGGAGCAGCATCATCC
SALK_016122LP	TTTCATTCCACCTTATGAGCCT
SALK_016122RP	ATCTCCAAGCAACAAATATCCC
SM_3_19812-LP	TTCAGCTAACGCGAGAGCTAG
SM_3_19812-RP	CTTGCTGATCCTCCTCATCAC
SALK_011491-LP	AGAACCACGTAAGCCCATCTC
SALK_011491-RP	TCAAATGAACTCCACTACCGC
SALK_LBa1	TGGTTCACGTAGTGGGCCATCG
SAIL_LB1	GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC
Primers for constructs in yeast two hybrid assays	
DA1-LIM+C- <i>Sall</i> -LP	GTCGACCGGTGGTTTAAACAAGATCTTT
DA1-LIM+C- <i>NotI</i> -RP	GCGGCCGCTTAAACCGGAATCTACCGGTC
DAR1- <i>Sall</i> -LP	GTCGACCGGGTGGCTAACTAAAATCCTTA
DAR1- <i>NotI</i> -RP	GCGGCCGCTTAAAGAAATGTACCGGTCAAGCGA
DAR2- <i>Sall</i> -LP	GTCGACCATGGATTCTTCTCTCTTTC
DAR2- <i>NotI</i> -RP	GCGGCCGCCAAAGGAAAAGTTCCAGTTA
TCP14- <i>EcoRI</i> -LP	GAATTCAAAAGCCAACATCAAGTATCT
TCP14- <i>NotI</i> -RP	GCGGCCGCTAATCTTGCTGATCCTCCTCATCA
TCP15- <i>EcoRI</i> -LP	GAATTCGATCCGGATCCGGATCAT
TCP15- <i>NotI</i> -RP	GCGGCCGCTTAGGAATGATGACTGGTGCTTCC
Primers for constructs in pull-down assays	
GST-DA1-F	GGATCCATGGGTGGTTTAAACAAGAT
GST-DA1-R	GCGGCCGCTTAAACCGGAATCTACCGGTC
GST-DAR1-F	GGATCCATGGGTGGCTAACTAAAATCCT

GST-DAR1-R	CTCGAGTTAAGGAAATGTACCGGTCAAGC
GST-DAR2-F	GGATCCATGGATTCTTCTCCTCTTC
GST-DAR2-R	CTCGAGTCACAAAGGAAAAGTCCAG
TCP14-pMAL-C2- <i>EcoRI</i> -LP	GAATTCACAAAAGCCAACATCAAGTATCTTAAAT
TCP14- pMAL-C2- <i>HindIII</i> -RP	AAGCTTGCCATAATCTTGCTGATCCTCCTCATCACCAC
TCP15- pMAL-C2- <i>EcoRI</i> -LP	GAATTCGATCCGGATCCGGATCATAACCATC
TCP15- pMAL-C2- <i>HindIII</i> -RP	AAGCTTGCCTAGGAATGATGACTGGTGCTTCCATCT

Primers for constructs in ubiquitin binding assays

GST-DAR1-UIMs-F	GGATCCGTAGAAGATAGAACTTGGAAGGTCC
GST-DAR1-UIMs-R	CTCGAGTGGAATGAGGAAGGGATATGGTT
GST-DAR1-delUIMs-F	GGATCTTTGACAAGTATGAATGTGGGATCTCC
GST-DAR1-delUIMs-R	CTCGAGTCATACTTGTCAAAATCAGATCCTTCC
GST-DAR1-F	GGATCCATGGGGTGGCTAACTAAAATCCT
GST-DAR1-R	CTCGAGTTAAGGAAATGTACCGGTCAAGC
GST-DAR2-UIMs-F	GGATCCAAGGTCCTTCTCTACCTCCTT
GST-DAR2-UIMs-R	CTCGAGACCGCCACATATTCTTTGTCT

Primers for constructs in Co-IP assays

DA1-MYC-FP	GGTACCCGGTTGGTTTAAACAAGATCTTT
DA1-MYC-RP	GGATCCTTAAACCGGGAATCTACCGGTC
DAR1-MYC-FP	GGATCCTAGGGTGGCTAACTAAAATCCT
DAR1-MYC-RP	ACTAGTTTTAAGGAAATGTACCGGTCAAG
DAR2-GFP-FP	ATGGATTCTTCTCCTCTTC
DAR2-GFP-RP	CAAAGGAAAAGTCCAGTTA
TCP14-MYC-BamHI-LP	GGATCCTAATGCAAAAGCCAACATCAAG
TCP14-MYC-Sac1-RP	GAGCTCACTAATCTTGCTGATCCTCCTCAT
TCP15-MYC-Kpn1-LP	GGTACCCGATCCGGATCCGGATCAT
TCP15-MYC-Sac1-RP	GAGCTCATTAGGAATGATGACTGGTGCTTCC
TCP14-GFP-FP	ATGCAAAAAGCCAACATCAAGTATCT
TCP14-GFP-RP	CTAATCTTGCTGATCCTCCTCATCA
TCP15-GFP-FP	ATGGATCCGGATCCGGATCAT
TCP15-GFP-RP	TTAGGAATGATGACTGGTGCTTCC

Primers for constructs in complementation test

DA1CDS-F	ATGGGTTGGTTTAAACAAGATCTT
DA1CDS-R	AACCGGGAATCTACCGGTCA
DAR1CDS-F	ATGGGTTGGCTAACTAAAAT
DAR1CDS-R	AGGAAATGTACCGGTCAAGC
DAR2CDS-F	ATGGATTCTTCTCCTCTT
DAR2CDS-R	CAAAGGAAAAGTCCAGTT
gDAR2-F	GGGGACAAGTTTGTACAAAAAGCAGGCTACATTGGTTGATAAAGTCATAAAGTC
gDAR2-R	GGGGACCACTTTGTACAAGAAAGCTGGGTCCAAAGGAAAAGTCCAGTTAAGCGG

Primers for GUS constructs

DAR1 _{pro} -F	GCACCTAAACAATAATTGATTGGC
DAR1 _{pro} -R	TGGCAACAACAATCCCTTACC
DAR2 _{pro} -F	TTATGGACCGGATTAAGTCGG

DAR2pro-R GAGGATGGAAAAATGGCCCC

Primers for qRT-PCR

CYCA2;3-FP AGGCACAGATAACACAGCTG
CYCA2;3-RP TGAGGTAGAGAGTGTGATGC
RBR-FP AGTCGCTGCTGCTAAGACAAA
RBR-RP ATGACAGTCCTGAGCCACTTGG
TCP14-FP AAAGTAGACGGAAGAGGG
TCP14-RP TACCAGGAAACAAAGACG
TCP15-FP CCTCCTCTTCCACTTCCT
TCP15-RP GTAGCCACTCAATAGTTCA
ACTIN2-F GAAATCACAGCACTTGCACC
ACTIN2-R AAGCCTTTGATCTTGAGAGC
