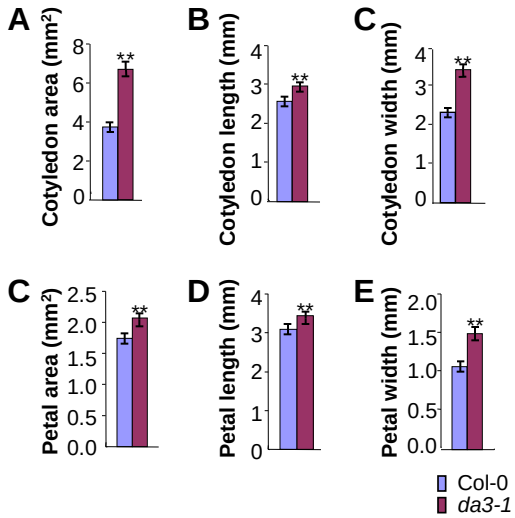
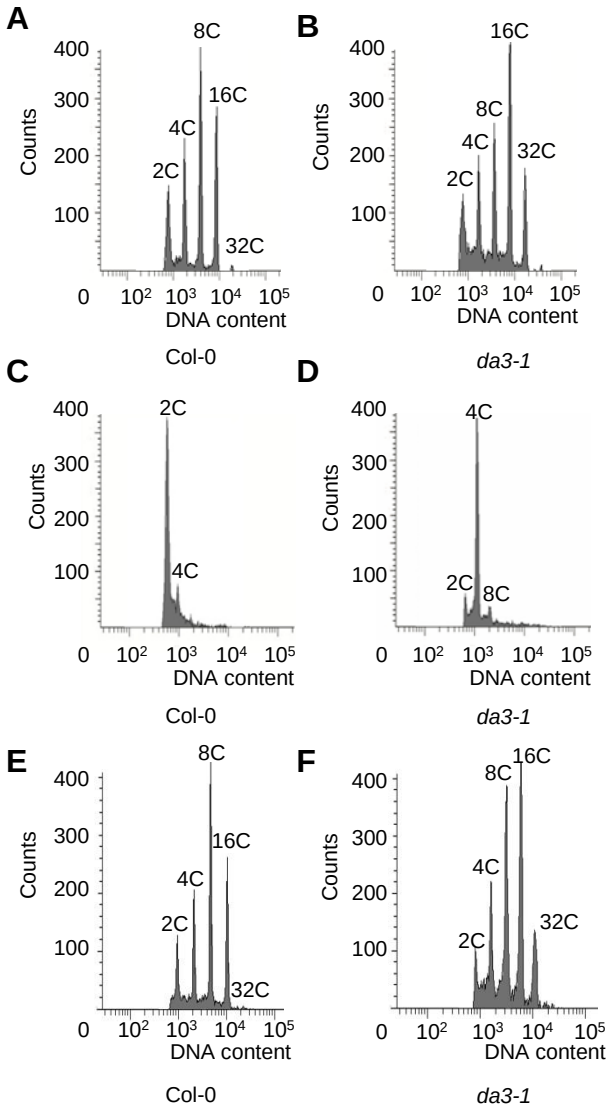
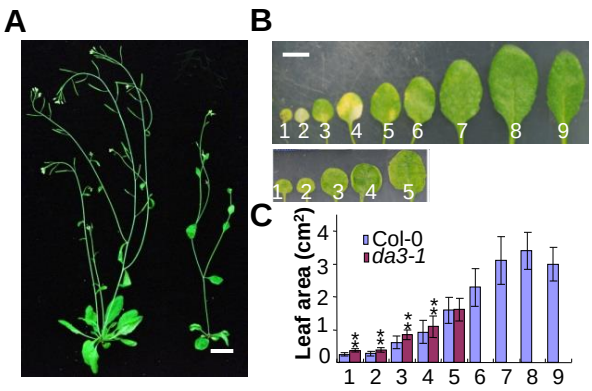


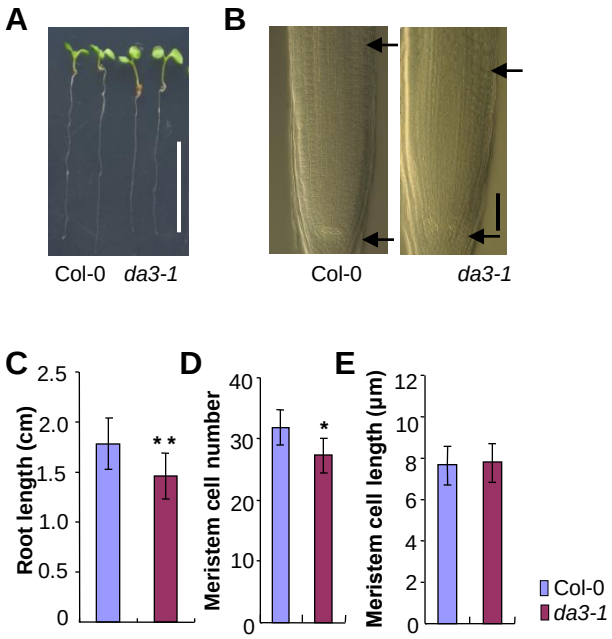
Supplemental Figure 1. *da3-1* Influences Cell and Organ Growth.
(A) to **(C)** Cotyledon area, cotyledon length and cotyledon width of 10-day-old Col-0 and *da3-1* seedlings (*n* = 60).
(C) to **(E)** Petal area, petal length and petal width of Col-0 and *da3-1* flowers (Stage 14) (*n* = 50).
Values in **(A)** to **(E)** are given as means ± SD. ******P<0.01 compared with the wild type (Student's *t* test).



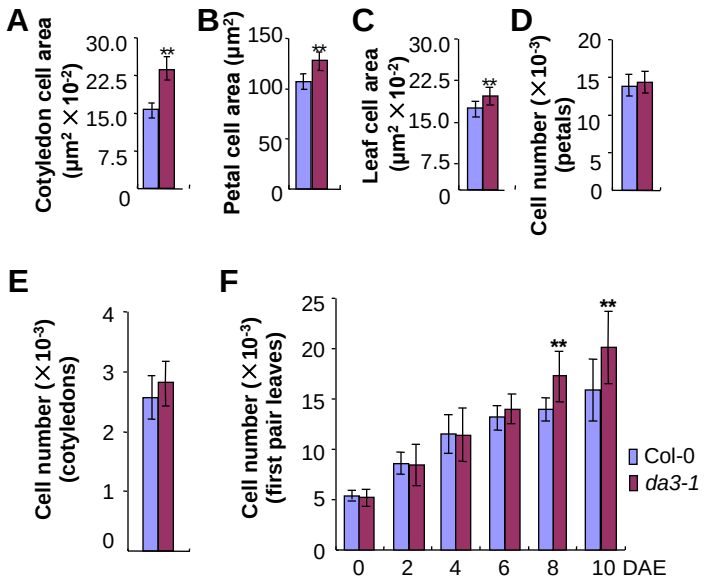
Supplemental Figure 2. *da3-1* Shows Increased Ploidy Levels.
Flow cytometric analysis of Col-0 and *da3-1* cotyledons **(A** and **B)**, petals (stage 14) **(C** and **D)** and leaves **(E** and **F)**.



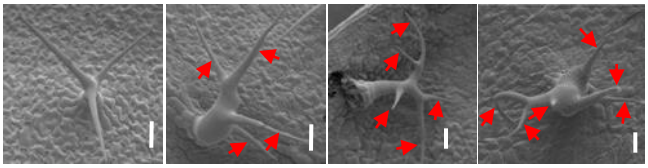
Supplemental Figure 3. *da3-1* Affects Plant Growth.
(A) 37-day-old plants of Col-0 (left) and *da3-1* (right).
(B) Rosette leaves of Col-0 and *da3-1*. The top row of images shows rosette leaves of Col-0, and the bottom row of images indicates rosette leaves of *da3-1*.
(C) The average area of Col-0 and *da3-1* rosette leaves. 37-day-old plants were used to measure leaf area. Values are given as means ± SD (*n* = 15). **P<0.01 compared with the wild type (Student's *t* test).
Bars= 1 cm in **(A)** and **(B).**



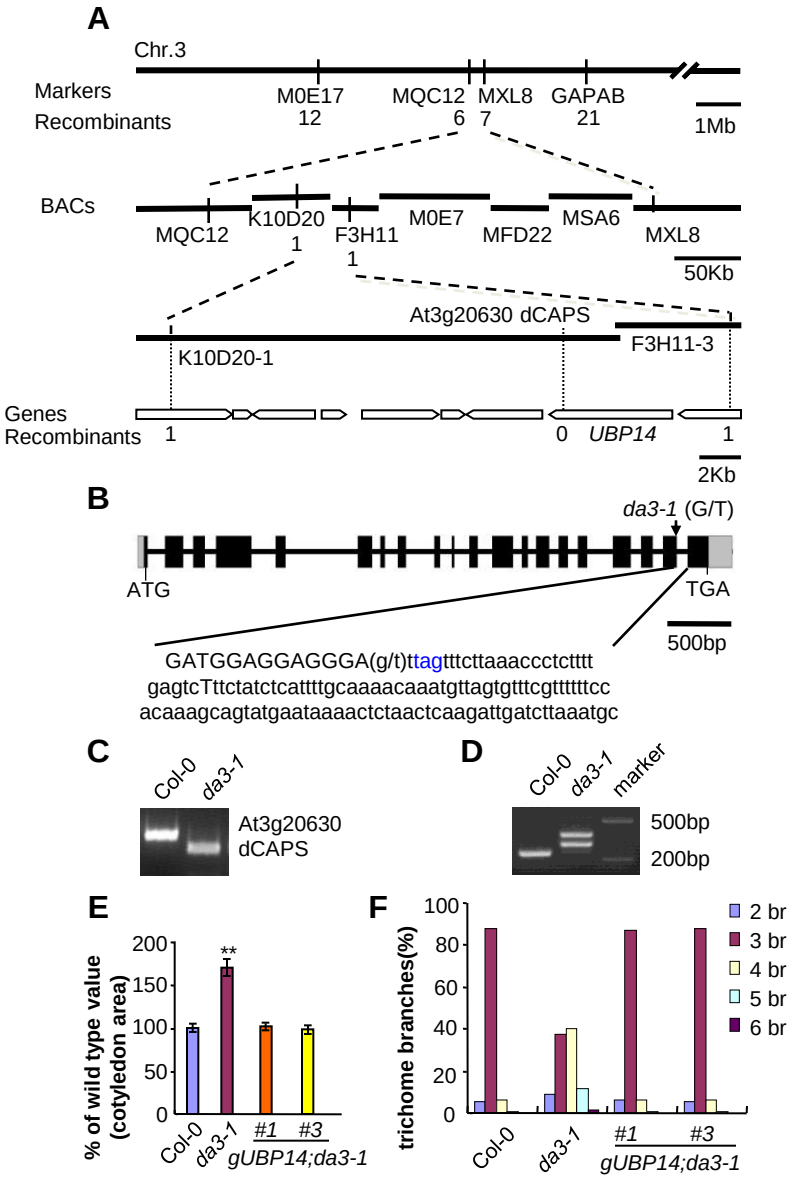
Supplemental Figure 4. *da3-1* Influences Root Growth.
(A) 7-day-old Col-0 and *da3-1* seedlings.
(B) Root meristems of 7-day-old Col-0 and *da3-1* seedlings.
(C) Root length of 7-day-old Col-0 and *da3-1* seedlings (*n* = 40). .
(D) Number of cortical cells in Col-0 and *da3-1* root meristems (*n* = 50).
(E) Length of cortical cells in Col-0 and *da3-1* root meristems (*n* = 50).
Values in **(C)** to **(E)** are given as means ± SD.
* P<0.05 and ** P<0.01 compared with the wild type (Student's *t* test).
Bars = 1 cm in **(A)** and 50 μm in **(B)**.



Supplemental Figure 5. *da3-1* Influences Cell Size and Cell Number.
(A) The average area of cells in cotyledons of Col-0 and *da3-1*. Thirty-five cotyledons were used to measure cotyledon cell area (*n* = 35).
(B) The average area of cells in petals of Col-0 and *da3-1*. Thirty-five petals were used to measure cotyledon cell area (*n* = 35).
(C) The average area of cells in first pair of leaves of Col-0 and *da3-1*. Twenty-eight leaves were used to measure cotyledon cell area (*n* = 28).
(D) The calculated number of cells in Col-0 and *da3-1* petals. Thirty-five petals were used to calculate cell number (*n* = 35).
(E) The calculated number of cells in Col-0 and *da3-1* cotyledons. Thirty-five cotyledons were used to calculate cell number (*n* = 35).
(F) The calculated number of cells in the first pair of Col-0 and *da3-1* leaves over time after emergence (DAE). Thirty leaves at each time point were used to calculate cell number (*n* = 30). Values in **(A)** to **(F)** are given as means ± SD. ******P<0.01 compared with the wild type (Student's *t* test).



Supplemental Figure 6. *da3-1* Increases the Number of Trichome Branches.
Trichomes on the first pair of Col-0 and *da3-1* leaves. The red arrows indicate the branches of trichomes. Bars = 50 μm.



Supplemental Figure 7. Identification and Molecular Characterization of *UBP14/DA3.*

(A) Mapping of the *da3-1* mutation. The *da3-1* mutation was mapped in the region between markers F3H11-3 and K10D20-1. The open arrows indicate the genes in the mapping region.

(B) The *DA3/UBP14* gene structure. The start codon (ATG) and the stop codon (TGA) are indicated. Closed boxes indicate the coding sequence, open boxes indicate the 5' and 3' untranslated regions, and lines between boxes indicate introns. The capital letters represent the exon sequence, and the small letters indicate the intron sequence. The mutation site (g/t) of *da3-1* is shown. The mutation in *da3-1* affects the splicing of *UBP14*, resulting in the premature stop codon (tag) (blue).

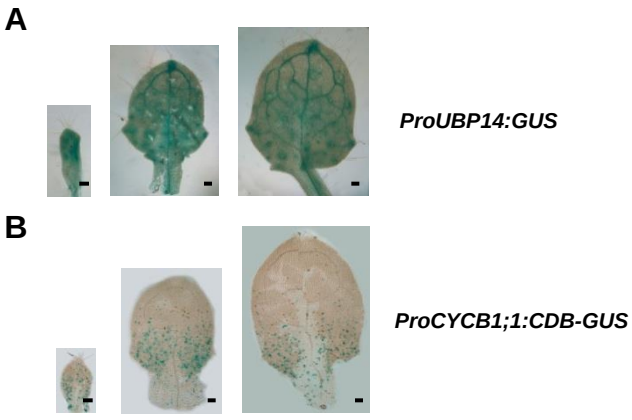
(C) The mutation in the *da3-1* allele produces the *Apo*I site that is used to develop the AT3G20630 dCAPS marker.

(D) RT-PCR analysis of *UBP14* in Col-0 and *da3-1* seedlings. The *da3-1* mutation causes two main transcripts, resulting in a premature stop codon at the same position (blue letter in **B**).

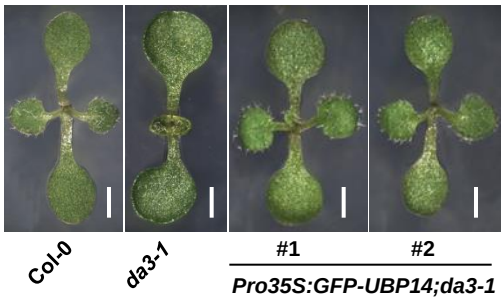
(E) The average area of Col-0, *da3-1*, *gUBP14;da3-1#1* and *gUBP14;da3-1#3* cotyledons (n = 50).

(F) Trichome branch (br) distribution of Col-0, *da3-1*, *gUBP14;da3-1#1* and *gUBP14;da3-1#3* first pair of leaves at 15 days after germination (DAG) (n = 200).

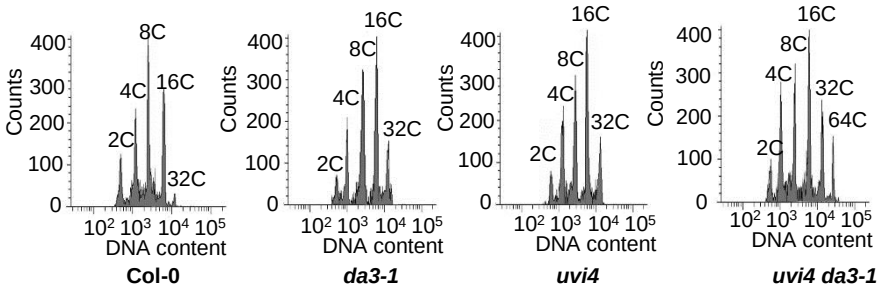
Values in **(E)** are given as means ± SD relative to the respective wild-type values, set at 100%. **P<0.01 compared with the wild type (Student's t-test).



Supplemental Figure 8. *UBP14* is Expressed in both the Proliferation and Expansion Phases during Leaf Development.
(A) Histochemical analysis of GUS activity in the developing rosette leaves of *ProUBP14: GUS* transgenic plants.
(B) Histochemical analysis of GUS activity in the developing rosette leaves of *ProCYCB1;1:CDB-GUS* transgenic plants.
Bars = 100 μm in **(A)** and **(B)**.

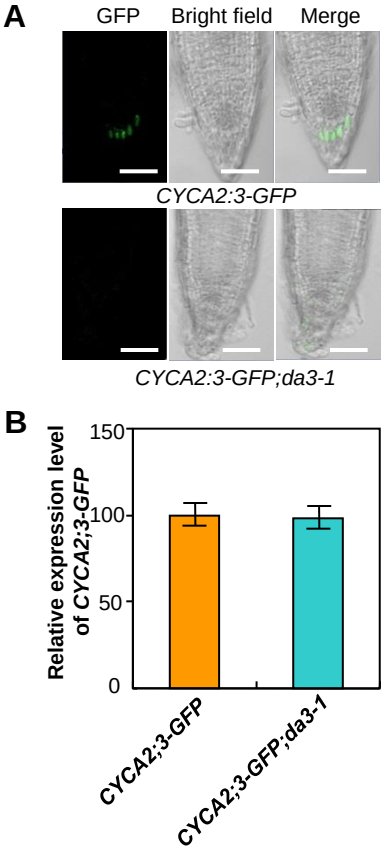


Supplemental Figure 9. Overexpression of *GFP-DA3* Complements the Phenotypes of *da3-1*.
10-day-old seedlings of Col-0, *da3-1*, *Pro35S:GFP-UBP14;da3-1*#1 and *Pro35S:GFP-UBP14;da3-1#2*.
Bars = 1 mm.

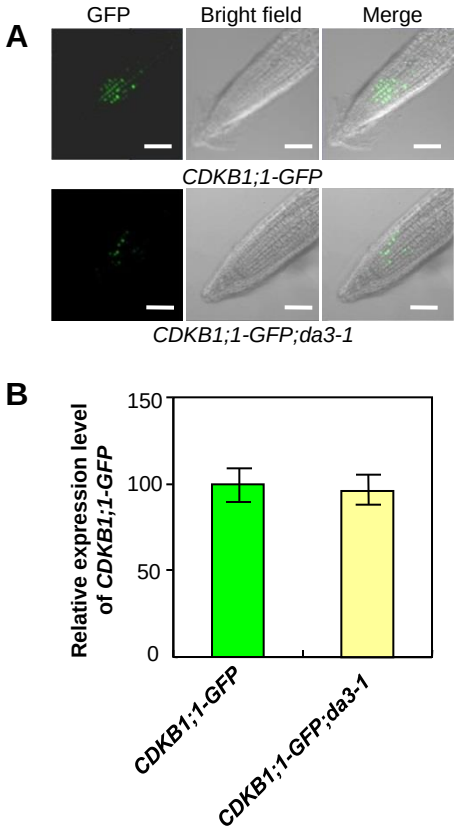


Supplemental Figure 10. *UBP14* Acts Genetically with *UVI4* to Regulate Endoreduplication.

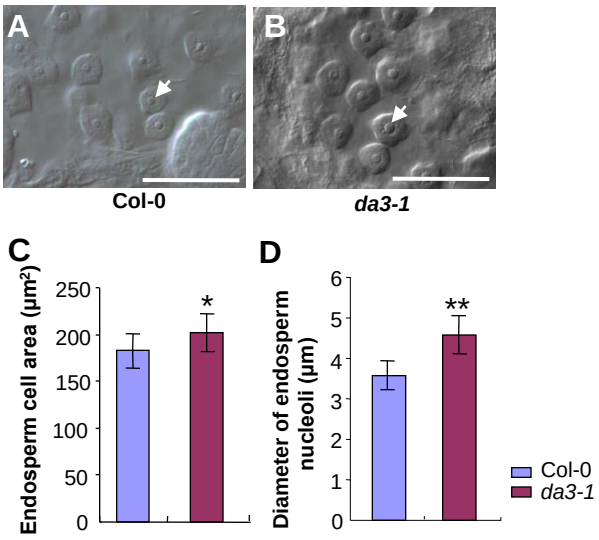
Flow cytometric analysis of Col-0, *da3-1, uvi4* and *uvi4 da3-1* first pair leaves.



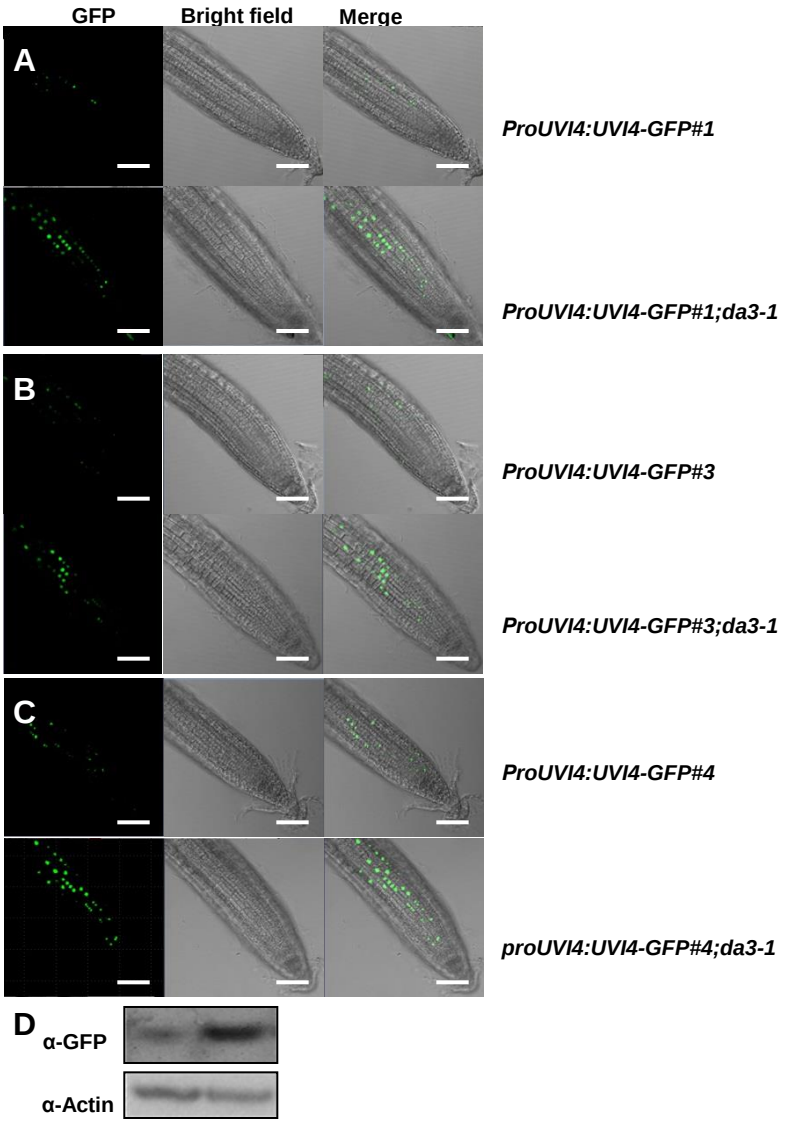
Supplemental Figure 11. UBP14 Modulates the Stability of CYCA2;3.
(A) Confocal images of induced CYCA2;3-GFP in Col-0 or *da3-1* mutant root meristems. The top row of images shows the CYCA2;3-GFP signal in wild-type root meristems, and the bottom row of images indicates the CYCA2;3-GFP signal in *da3-1* root meristems. GFP fluorescence of CYCA2;3-GFP (left), bright field (middle) and merged (right) images are shown. Bars = 50 μm.
(B) After *CYCA2;3-GFP* and *CYCA2;3-GFP;da3-1* seedlings were induced with the inducer, expression of *CYCA2;3-GFP* was detected using quantitative real-time RT-PCR. Data shown are means ± SD of three biological replicates.



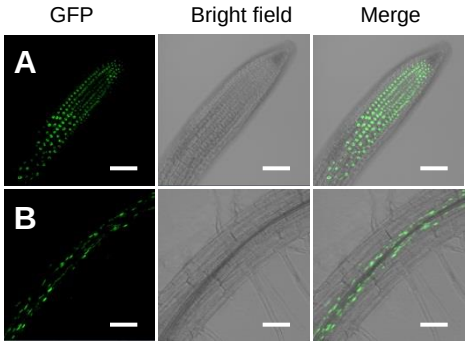
Supplemental Figure 12. UBP14 Modulates the Stability of CDKB1;1.
(A) Confocal images of CDKB1;1-GFP in wild-type or *da3-1*mutant root meristems. The top row of images shows the CDKB1;1-GFP signal in *CDKB1;1-GFP* root meristems, and the bottom row of images indicates the CDKB1;1-GFP signal in *CDKB1;1-GFP;da3-1* root meristems. GFP fluorescence of CDKB1;1-GFP (left), bright field (middle) and merged (right) images are shown. Bars = 50 μm.
(B) Expression of *CDKB1;1-GFP* was detected using quantitative real-time RT-PCR. Data shown are means ± SD of three biological replicates.



Supplemental Figure 13. The Effect of *da3-1* on Endosperm.
(A) and **(B)** The endosperm in Col-0 and *da3-1* seeds at the heart stage. The arrows indicate the nucleoli.
(C) The average area of endosperm cells in Col-0 and *da3-1* seeds at the heart stage (*n* = 80).
(D) The average diameter of endosperm nucleoli in Col-0 and *da3-1* seeds at the heart stage (*n* = 80).
Values are given as means ± SD. *P<0.05 and **P<0.01 compared with the wild type (Student's t-test).
Bars= 50 μm in **(A)** and **(B)**.



Supplemental Figure 14. The *da3-1* Mutation Influences the Levels of UVI4 Proteins.
(A) Confocal images of UVI4-GFP in *ProUVI4:UVI4-GFP#1* and *ProUVI4:UVI4-GFP#1;da3-1* root meristems. The top row of images shows the UVI4-GFP signal in *ProUVI4:UVI4-GFP#1* root meristems, and the bottom row of images indicates the UVI4-GFP signal in *ProUVI4:UVI4-GFP#1;da3-1* root meristems. GFP fluorescence of UVI4-GFP (left), bright field (middle) and merged (right) images are shown.
(B) Confocal images of UVI4-GFP in *ProUVI4:UVI4-GFP#3* and *ProUVI4:UVI4-GFP#3;da3-1* root meristems. The top row of images shows the UVI4-GFP signal in *ProUVI4:UVI4-GFP#3* root meristems, and the bottom row of images indicates the UVI4-GFP signal in *ProUVI4:UVI4-GFP#3;da3-1* root meristems. GFP fluorescence of UVI4-GFP (left), bright field (middle) and merged (right) images are shown.
(C) Confocal images of UVI4-GFP in *ProUVI4:UVI4-GFP#4* and *ProUVI4:UVI4-GFP#4;da3-1* root meristems. The top row of images shows the UVI4-GFP signal in *ProUVI4:UVI4-GFP#4* root meristems, and the bottom row of images indicates the UVI4-GFP signal in *ProUVI4:UVI4-GFP#4;da3-1* root meristems. GFP fluorescence of UVI4-GFP (left), bright field (middle) and merged (right) images are shown.
(D) The *da3-1* mutation increases the level of UVI4-GFP. Total proteins from *ProUVI4:UVI4-GFP#4* (left lane) and *ProUVI4:UVI4-GFP#4;da3-1* (right lane) seedlings were subjected to immunoblot assays using anti-GFP and anti-Actin (as loading control) antibodies.
Bars = 50 μm in **(A)** to **(C)**.



Supplemental Figure 15. UBP14 is Expressed in Roots.
(A) and **(B)** UBP14 expression was monitored by *ProUBP14:UBP14-GFP* transgene expression. GFP fluorescence of UBP14-GFP in root meristem **(A)** and differentiated regions **(B)** of *ProUBP14:UBP14-GFP* transgenic plants. GFP fluorescence of UBP14-GFP (left), bright field (middle) and merged (right) images are shown
Bars = 50 μm in **(A)** and **(B)**.

Supplemental Table 1. Primers Used in this Study.

Primer Name	Primers
PCR-based markers developed for *DA3/UBP14* mapping in this study	
GAPAB-F	TCCTGAGAATTCAGTGAAACCC
GAPAB-R	CACCATGGCTTCGGTTACTT
MXL8-F	GTAGCCCAAAGCCGTACAG
MXL8-R	GAGATGCGTTTCACCTACAA
MQC12-1F	GCCTACAGAAAAACGAACAGG
MQC12-1R	CAATTTCTCCGGGAAAGGTA
MOE17-1F	CGGGTGAAATCCTACATATAACAA
MOE17-1R	AAGATGGCTATCACCAATATGAAA
K10D20-1F	GAATACACCGCTCACAGCAG
K10D20-1R	ATCCATGCGGGTATGAAGAC
F3H11-3F	CATGATGATCTCCCATAGCTTC
F3H11-3R	CCACAATCTGAGAAGACACAACA
dCAPS marker for *DA3/UBP14*	
DA3d-F2	ACTCCGGCTCAAAGTGGATTACCAGATGGAGGAGGAA
DA3d-R2	GAGTTTTATTCATACTGCTTTGTGGA
PCR products were digested with *Apo*I.	
Primers for T-DNA identification	
SALK_083656-LP	AAGACTCGGTATGTGTGACCG
SALK_083656-RP	CGTGGACTGTAGGATTCTTGC
SALK_086463-LP	CTCACGATCTGTTCGTTTTCC
SALK_086463-RP	AGAAGCTGATCTCCCAAGAGG
Lba1	TGGTTCACGTAGTGGGCCATCG
Primers for constructs	
UBP14genome-F	GTGTGCAGACGAGTGTTCCGTTCC
UBP14genome-R	ATCAAGCCGCTGAAAGAAGTAGACATCA
UBP14CDS-F	ATGGAGCTCCTCCGATCCAAC
UBP14CDS-R	TCAATCAAGC CGCTGAAAG
UBP14pro-F	GTGTGCAGACGAGTGTTCCGTTCC
UBP14pro-R	AGGGTTTTTGCGAAATCGGCGAAA
UBP14CDSM-R	ACTCCCTCCTCCATCTGGTAATCCA
UBP14MBP-F	TAC GTA GGA TCCATGGAGCTCCTCCGATCCAAC
UBP14MBP-R	CTG CAG GTC GACTCAATCAAGC CGCTGAAAG
UBP14MBP-MR	CTGCAGGTC GACACTCCCTCCTCCATCTGGTAATCCA
UBP14UMBP-F	TACGTAGGA TCCAGCCACATGCGTAGCAAAGGACTC
UBP14UMBP-R	CTGCAG GTCGACTCATTTCCCTCCTCCATCTGGT
UBP14dUMBP-F	GCGCAGCCCGTGGCAAACCCTAATGCATCT
UBP14dUMBP-R	AGATGCATTAGGGTTTGCCACGGGCTGCGC
UBQ14-F	ATGCAGATCTTTGTTAAGACTCTCAC

UBQ14-R	TTAGAAACCA CCACGGAGCC TTAGC
UBQ10-F	CGCGGATCC ATGCAGATCT TTGTTAAGAC TCTC
UBQ10-R	CGCAAGCTTG TTAGAAACCACCACGAAGACGCA
CCS52A1GST-F	GAATTCCCGGGTATGGAAGAAGAAGATCCTACAGCA
CCS52A1GST-R	CGA TGC GGCCGCTCACCGAATTGTTGTTCTACCAAA
UVI4GST-F	CCGGAATTCATGCCAGAAGCACGAGATCGAATAG
UVI4GST-R	CGCGTCGACTCATCGCATCGACATTAGCGTCCTAAC
CCS52A1MBP-F	TGCTCTAGAATGGAAGAAGAAGATCCTACAGCAA
CCS52A1MBP -R	CCCAAGCTTTCACCGAATT GTTGTTCTAC CAAA
Myc-CCS52A1-F	CGGGGTACCCATGGAAGAAG AAGATCCTAC AG
Myc-CCS52A1-R	ATCGAGCTCTCACCGAATT GTTGTTCTAC CAAAG
Myc-UVI4-F	CGGGGTACCCATGCCAGAAGCACGAGATCGAAT
Myc-UVI4-R	CGCGGATCCTCATCGCATCGACATTAGCGTCC
CCS52A1CDS-F	ATGGAAGAAG AAGATCCTACAG
CCS52A1CDS-R	TCACCGAATT GTTGTTCTAC CAAAG
UVI4CDS-F	ATGCCAGAAGCACGAGATCGAAT
UVI4CDS-R	TCATCGCATCGACATTAGCGTCC
UVI4107-F	CAAGAATTAAATCAATGAAAC
UVI4107-R	TCGCATCGACATTAGCGTCCTAAC
Primers for RT-PCR and QRT-PCR	
ACTIN2-F	GAAATCACAGCACTTGCACC
ACTIN2-R	AAGCCTTTGATCTTGAGAGC
QRTUBP14N-F	AAGTTAATTAGTGAACATGC
QRTUBP14N-R	TTTCTTCCACAGAGAATC
RTUBP14-F	ACCAATCTCCCACCAGACATCTG
RTUBP14-R	TCAATCAAGCCGCTGAAAGAAG
GFP-F	ACGCCGCCGTCTTCGATGTTGT
GFP-R	GTGCTTCTCCCGTTACCCTGAT