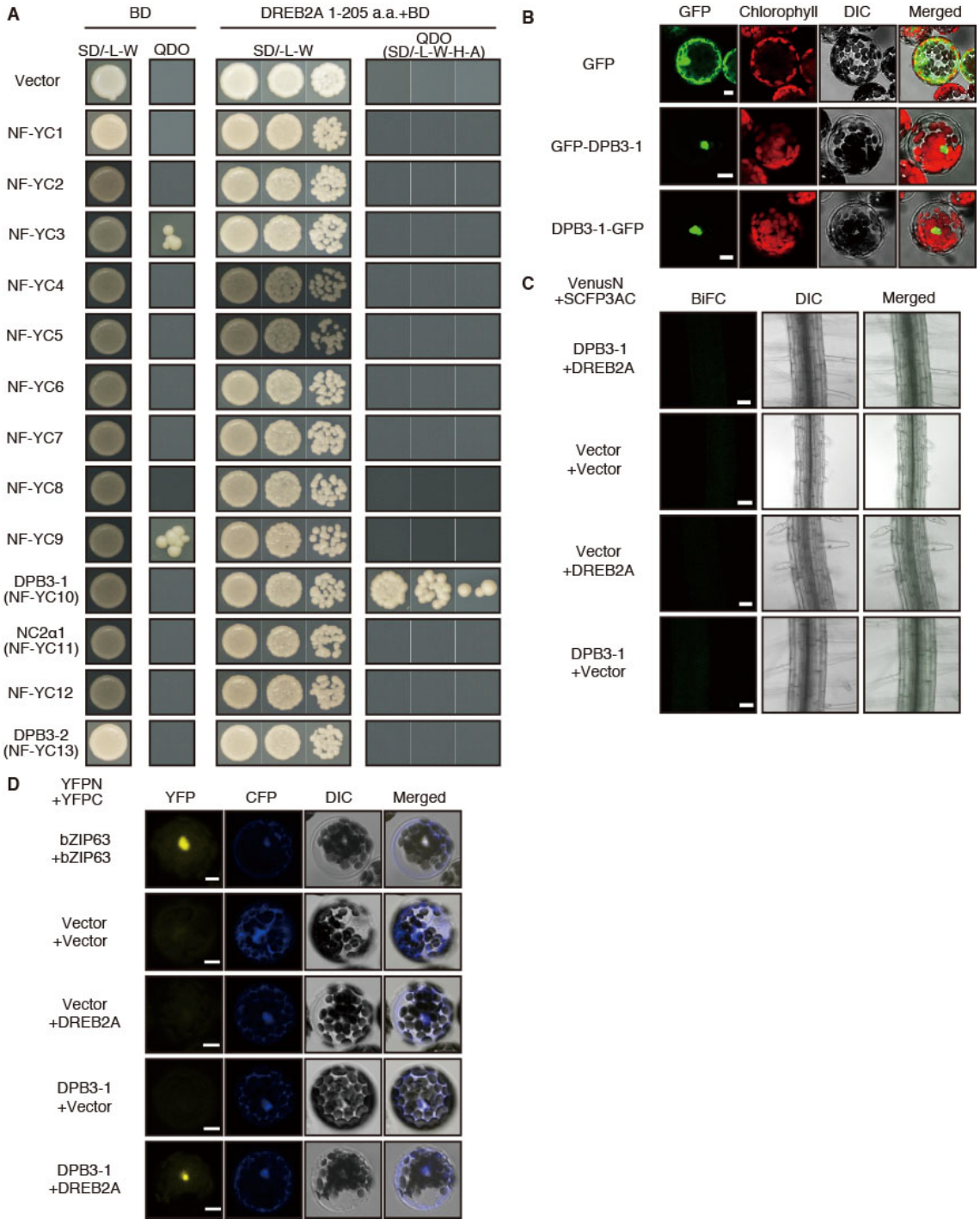


Supplemental Figure 1. Analysis of the Interactions between DREB2A and H2A-Like Proteins, and Verification of the DREB2A-DPB3-1 Interaction by the BiFC System in Transgenic *Arabidopsis* under the Control Condition or in Mesophyll Protoplasts.

(A) The growth of yeast cells harboring H2A-like proteins fused to the GAL4 activation domain (AD) on the non-selective medium SD/-L-W or the selective medium SD-L-W-H-Ade (QDO) was tested. The DREB2A fragment was expressed as a fusion protein with the GAL4 DNA-binding domain (BD).

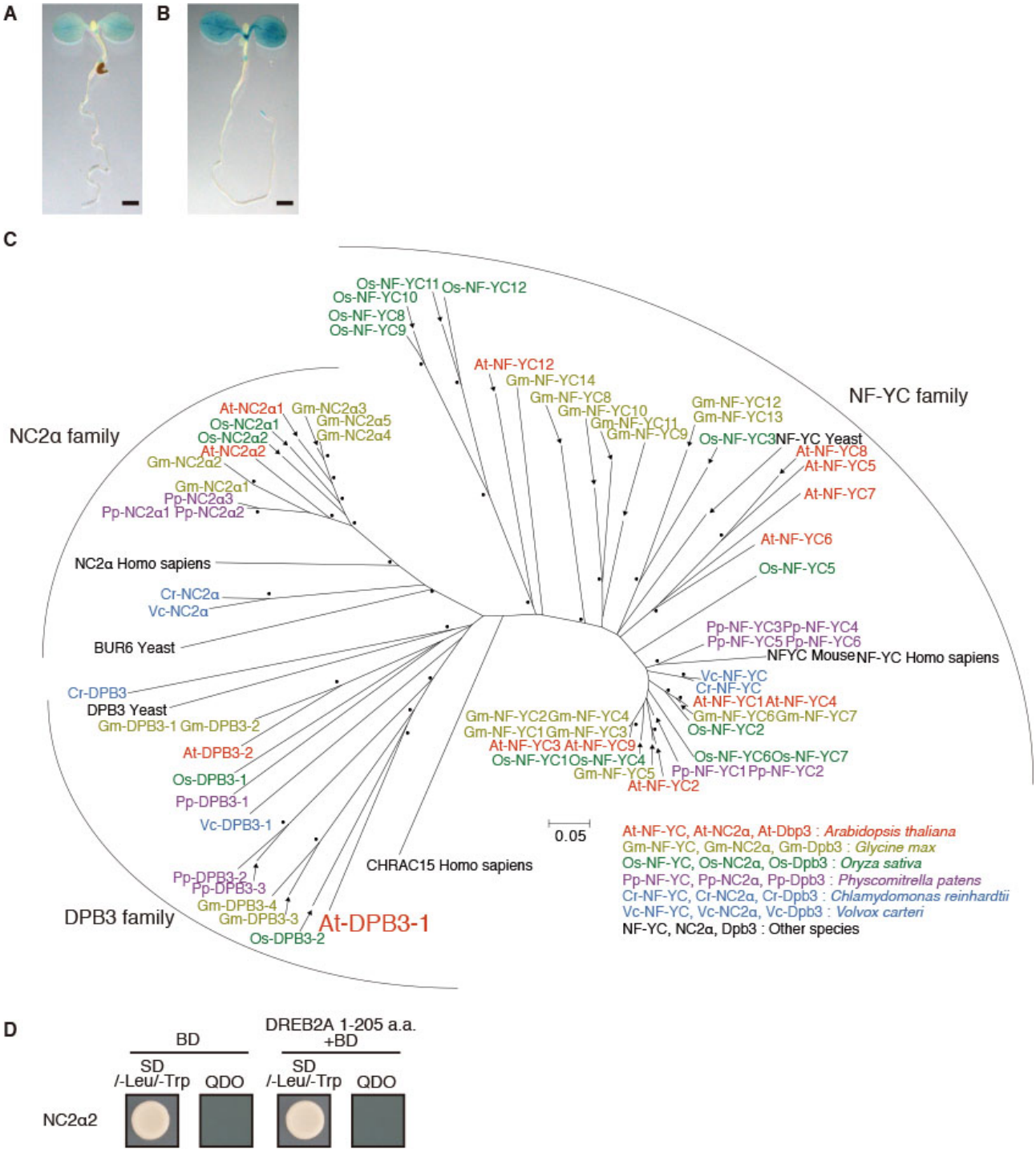
(B) Nuclear localization of DPB3-1 fused to the N- or C-terminal end of sGFP in *Arabidopsis*

Supplemental Figure 1 (continued).

mesophyll protoplasts. The construct that expressed each fusion protein was transfected into *Arabidopsis* mesophyll protoplasts. Differential interference contrast (DIC) images, confocal images of GFP, confocal images of chlorophyll fluorescence, and merged images are shown. Scale bars represent 10 μm.

(C) *In vivo* DREB2A-DPB3-1 interaction in transgenic plants under the non-stress condition. The roots of the transgenic plants used in Figure 1E were observed under the non-stress condition. Confocal images of BiFC fluorescence (left), DIC images (middle), and merged images (right) are shown. Scale bars represent 50 μm.

(D) Verification of the DREB2A-DPB3-1 interaction by the BiFC system in *Arabidopsis* mesophyll protoplasts. Two constructs that expressed a fusion protein of DREB2A and the C-terminal half of YFP (YFP^C-DREB2A) or a fusion protein of DPB3-1 and the N-terminal half of YFP (YFP^N-DPB3-1) were transfected into *Arabidopsis* mesophyll protoplasts under the control of the *35S* promoter. The empty vectors in combination with each fusion construct were also transfected. A construct that expressed CFP under the control of the *35S* promoter was co-transfected to indicate transfected protoplasts. The transcription factor bZIP63, which forms a dimer, was used as a positive control (Walter et al., 2004). The transfected protoplasts were treated with 25 μM MG132 for 2 h in the dark. DIC images, confocal images of YFP and CFP fluorescence, and merged images are shown. Scale bars represent 10 μm.



Supplemental Figure 2. Expression Patterns of *DPB3-1* and a Phylogenetic Tree of the H2A-Like HFD-Containing Proteins.

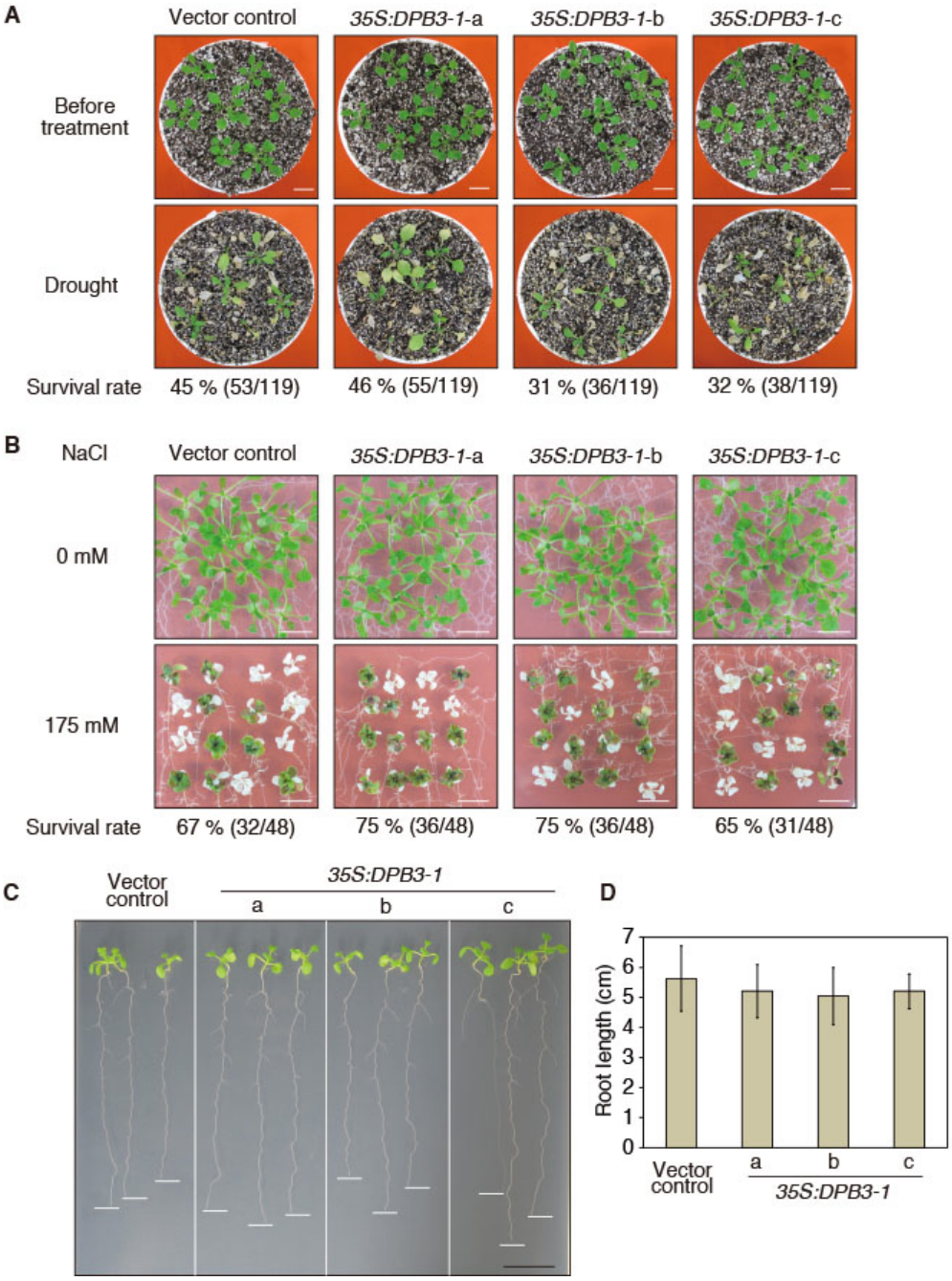
(A) and **(B)** GUS staining of seven-day-old *DPB3-1pro*:*GUS* transgenic plants under the control condition **(A)** and the heat stress condition (37°C, 5 h) **(B)**. Scale bars represent 1 mm.

(C) Phylogenetic tree of H2A-like HFD-containing proteins based on amino acids sequences of the conserved domain. The peptide sequences of the H2A-like proteins for *Glycine max*, *Oryza sativa*, *Physcomitrella patens*, *Chlamydomonas reinhardtii* and *Volvox*

Supplemental Figure 2 (continued).

carteri were obtained from Phytozome (Phytozome v9.1, http://www.phytozome.net/). A consensus tree from 1000 bootstrap samplings is shown, and a dot indicates a node that was supported with a bootstrap value > 50. The scale bar indicates the substitution rate per residue.

(D) The growth of yeast cells harboring NC2α2 proteins fused to the GAL4 activation domain (AD) on the non-selective medium SD/-L-W or the selective medium SD-L-W-H-Ade (QDO) was tested. DREB2A was expressed as a fusion protein with the GAL4 DNA-binding domain (BD).



Supplemental Figure 3. Stress Tolerance and Root Growth of *DPB3-1*-Overexpressing *Arabidopsis.*

Drought stress tolerance of the *DPB3-1*-overexpressing plants. Seedlings were grown on agar medium for 14 days and then on soil for five days. Water was withheld for two weeks. The survival rates presented below the photographs were determined after three days of recovery in the well-watered condition. The numbers in the parentheses indicate the number of individuals that survived over the number of tested individuals. Scale bars represent 1 cm. The average survival rates were calculated using the results of six replicate experiments. More than twenty plants (seven plants/pot) were tested in each experiment. The data were evaluated using one-way ANOVA. No significant differences were detected

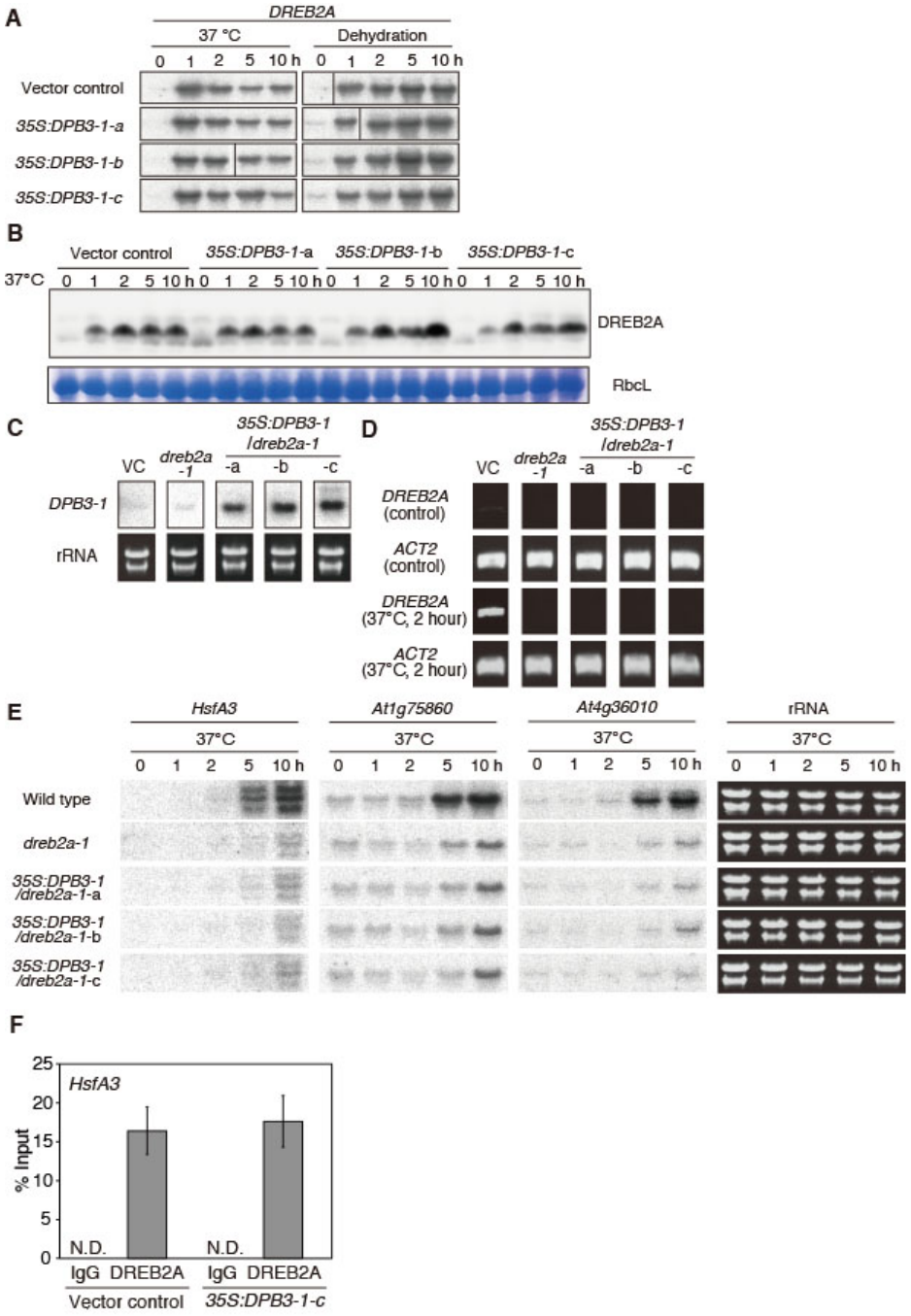
Supplemental Figure 3 (continued).

($p > 0.05$).

(B) High salt stress tolerance of the *DPB3-1*-overexpressing plants. Seedlings were grown on solid GM for 9 days and then transferred onto 0.8% agar plates (0.5 × MS medium) supplemented with or without 175 mM NaCl. They were grown for approximately nine to ten days after the transfer at 22°C. Scale bars represent 1 cm. Average survival rates were calculated using the results of three replicate experiments. Sixteen plants were tested in each experiment. The data were evaluated using one-way ANOVA, and no significant differences were detected ($p > 0.05$).

(C) Root growth of the *DPB3-1*-overexpressing plants under the control conditions. Seedlings were grown on solid GM for 3 days and then in square Petri dishes containing 35 mL of 1.2% solid medium (0.5 × MS medium) for an additional seven days. Photographs of 10-day-old plants are shown. The white bars indicate the positions of the root tips. The black scale bar represents 1 cm.

(D) Average root lengths of plants grown as in **(C)**. The error bars indicate SD (n = 28). The data were evaluated using one-way ANOVA, and no significant differences were detected ($p > 0.05$).



Supplemental Figure 4. Expression Analysis of the Heat Stress-Inducible Genes in *35S*:*DPB3-1/dreb2a-1* Plants, and Effect of the DPB3-1 Subunit on the Accumulation Level or DNA-Binding Activity of DREB2A.

(A) Expression levels of *DREB2A* during heat and dehydration stress in the vector control and *35S*:*DPB3-1* plants. Ethidium bromide staining of rRNA bands to demonstrate equal loading is shown in the Figure 4A.

(B) Accumulation levels of the DREB2A protein in the *DPB3-1*-overexpressing plants. Total proteins extracted from the heat stress-treated plants were analyzed by immunoblotting using the DREB2A-specific antibody (upper panel). The rubisco large subunit (rbcL) visualized by Coomassie staining is shown as a loading control (lower panel).

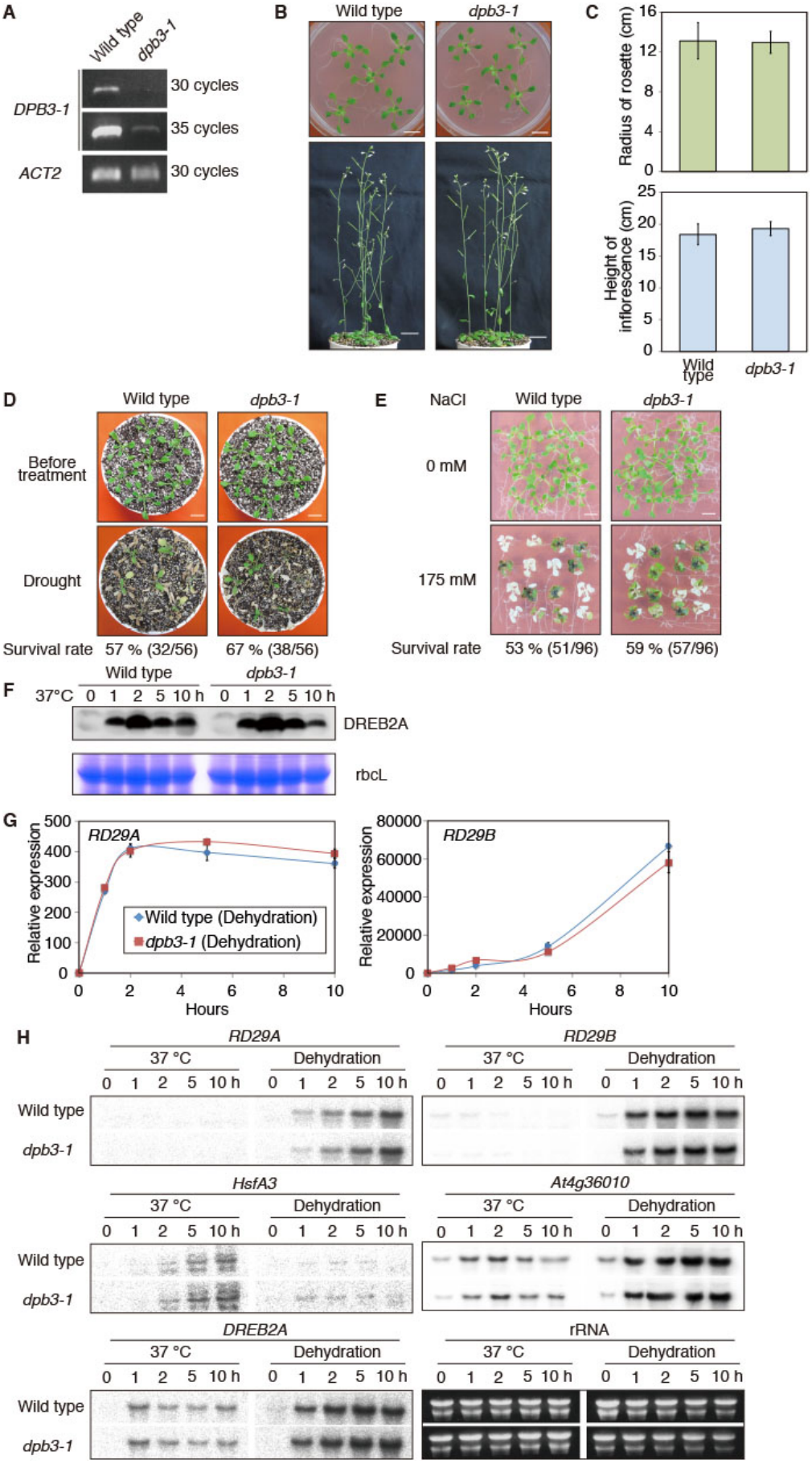
Supplemental Figure 4 (continued).

(C) Expression levels of *DPB3-1* mRNA in the wild type, *dreb2a-1* mutant and three transgenic lines overexpressing *DPB3-1* in *dreb2a-1* mutant (*35S*:*DPB3-1*/*dreb2a-1*).

(D) RT-PCR analysis of the expression levels of *DREB2A* in the wild type, *dreb2a-1* and *35S:DPB3-1*/*dreb2a-1* plants under the control and heat stress conditions. *ACTIN2* was used as an internal control. The primers used for PCR are shown in Supplemental Table 5.

(E) Expression levels of several heat stress-inducible genes downstream of DREB2A during heat stress in the wild-type, *dreb2a-1* and *35S*:*DPB3-1*/*dreb2a-1* plants. Ethidium bromide staining of rRNA bands is shown to demonstrate equal loading.

(F) ChIP-PCR assays of the *HsfA3* promoter region were performed using the vector control and *DPB3-1*-overexpressing plants. The values represent the means from triplicate biological repeats, and the error bars indicate SD. The results show the recovery of immunoprecipitated material using the DREB2A-specific antibody (IP) or IgG (negative control), as a percentage of the input DNA. The data were evaluated using Student's t-test, and no significant differences were detected between the two plants ($p > 0.05$).



Supplemental Figure 5.

Supplemental Figure 5 (continued). Additional Analysis of the *dpb3-1* Mutant.

(A) RT-PCR analysis of the expression levels of *DPB3-1* in the wild type and the *dpb3-1* mutant. The results after 30 and 35 PCR cycles are shown. *Actin* was used as an internal control. The primers used for PCR are shown in Supplemental Table 5.

(B) Growth of the *dpb3-1* mutant under the control condition. The analysis was performed as described in Figure 5B. Scale bars represent 1 cm.

(C) Average radius of the rosette and height of the inflorescence calculated from the plants shown in **(B)**. Error bars indicate SD (n = 25). The data were evaluated using one-way ANOVA, and no significant differences were detected ($p > 0.05$).

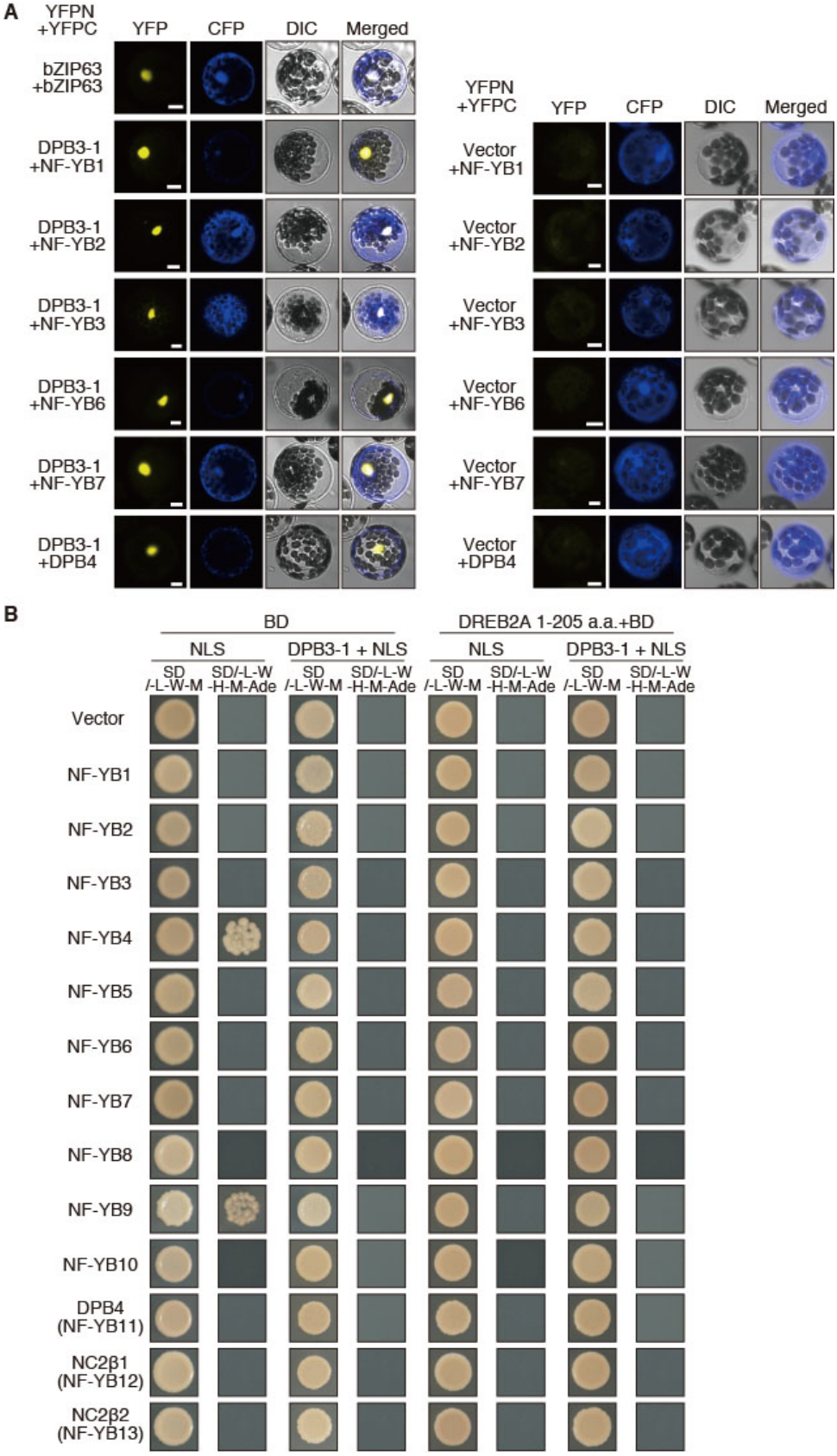
(D) Drought stress tolerance of the *dpb3-1* mutant. The analysis was performed as described in Supplemental Figure 5A. Scale bars represent 1 cm. The data were evaluated using one-way ANOVA, and no significant differences were detected ($p > 0.05$).

(E) High salinity stress tolerance of the *dpb3-1* mutant. The analysis was performed as described in Figure Supplemental Figure 5B. Scale bars represent 1 cm. The data were evaluated using one-way ANOVA, and no significant differences were detected ($p > 0.05$).

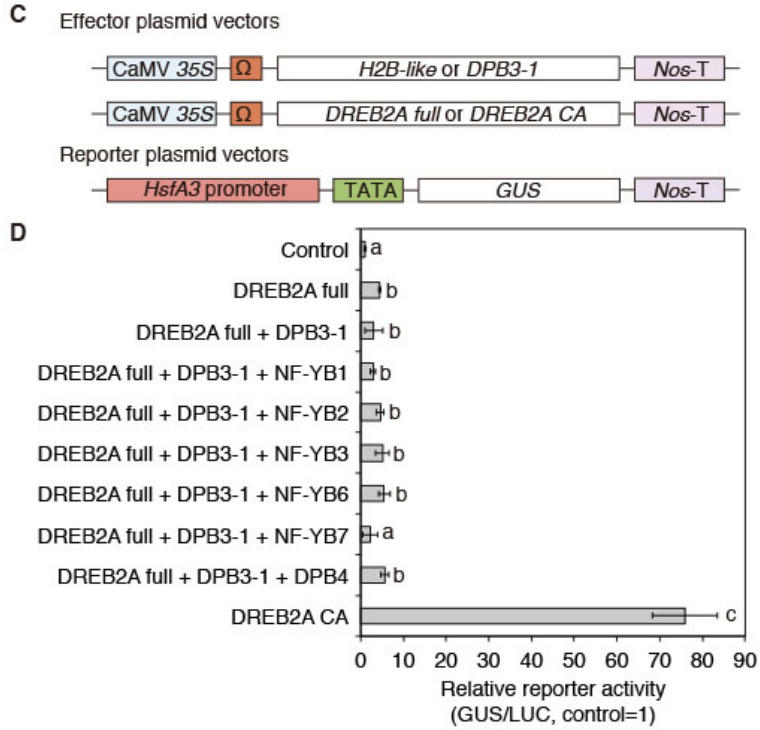
(F) Accumulation level of the DREB2A protein in the *dpb3-1* mutant. The analysis was performed as described in Supplemental Figure 4B.

(G) Quantitative RT-PCR analysis of the expression levels of two dehydration-inducible genes during dehydration stress in the *dpb3-1* mutant. The expression level of each gene in the wild-type plant under the control condition was defined as 1.0. The values represent means from triplicate measurements, and the error bars indicate SD. The data at each time point were evaluated using one-way ANOVA, and no significant differences were detected ($p > 0.05$).

(H) Expression levels of several genes downstream of DREB2A and the *DREB2A* gene during dehydration or heat stress in 14-day-old wild-type and *dpb3-1* mutant plants. Ethidium bromide staining of rRNA bands is shown to demonstrate equal loading.



Supplemental Figure 6.



Supplemental Figure 6 (continued). Confirmation of the Interaction between DPB3-1 and H2B-Like Proteins in Protoplasts, and Analysis of the Interaction between DREB2A and Dimers Composed of DPB3-1 and H2B-Like Proteins, and Effect of the Dimers on the Transcriptional Activity of DREB2A.

(A) Verification of the interaction between DPB3-1 and H2B-like proteins using the BiFC system in *Arabidopsis* mesophyll protoplasts. Two constructs that expressed a fusion protein of DPB3-1 and the N-terminal half of YFP (YFP^N-DPB3-1) or a fusion protein of six H2B-like proteins and the C-terminal half of YFP (YFP^c-DPB3-1) under the control of the *35S* promoter were transfected into *Arabidopsis* mesophyll protoplasts. The empty vectors were also transfected in combination with each fusion construct. A construct that expressed CFP under the control of the *35S* promoter was co-transfected to indicate transfection of the protoplasts. The transcription factor bZIP63, which forms a dimer, was used as a positive control (Walter et al., 2004). DIC images, confocal images of YFP and CFP fluorescence, and merged images are shown. Scale bars represent 10 μm.

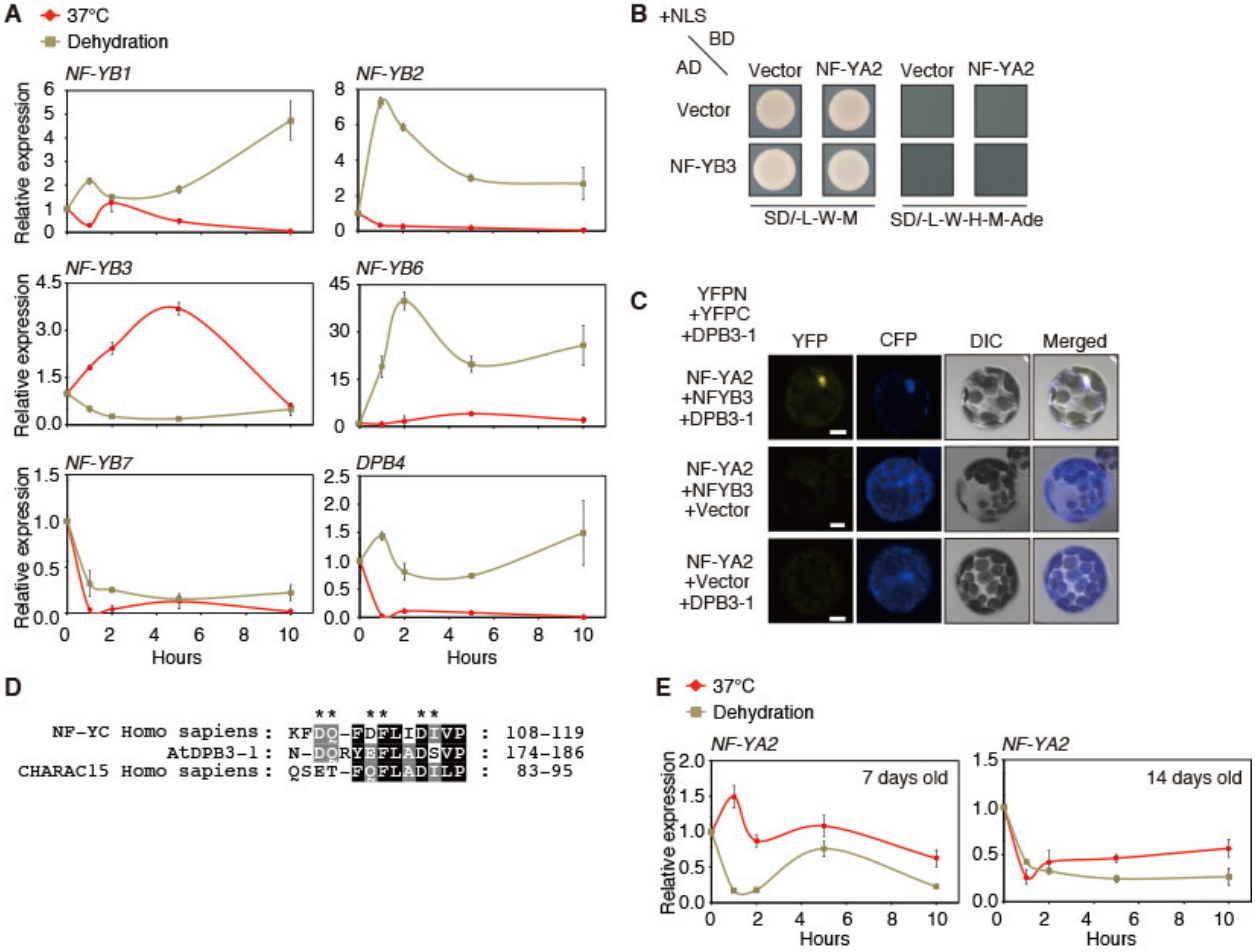
(B) The growth of yeast cells harboring H2B-like proteins fused to the GAL4 activation domain (AD), the N-terminal region of DREB2A fused to the GAL4 DNA-binding domain (BD), and DPB3-1 fused to a nuclear localization signal (NLS) on selective medium (SD/-L-W-H-M-Ade) or nonselective medium (SD/-L-W-M).

(C) Schematic diagram of the effector and reporter constructs for the transactivation experiment. The *HsfA3* 1-kb promoter:*GUS* fusion gene was used as the reporter. The plasmids containing the *CaMV 35S* promoter and the tobacco mosaic virus Ω sequence fused to the coding sequence of H2B-like proteins, DPB3-1, full-length DREB2A or

Supplemental Figure 6 (continued).

DREB2A CA were cotransfected into protoplasts. *Nos*-T indicates the terminator sequence of the gene for nopaline synthetase.

(D) Transactivation of the *HsfA3* 1-kb promoter:*GUS* reporter gene by full-length DREB2A and various dimers of a H2B-like protein and DPB3-1. Values indicate means from assays performed in triplicate, and the bars indicate the SD. The letters next to the bars indicate significant differences between the construct combinations ($p < 0.05$ according to Tukey's multiple range test). The *35S*:*LUC* plasmid was also cotransfected in each experiment as an internal control.



Supplemental Figure 7. Expression Analysis of *NF-YA2* and *H2B-like* Genes under Stress Conditions in 7-day-old Plants, and Interaction among NF-YA2, NF-YB3 and DPB3-1.

(A) Quantitative RT-PCR analysis of the expression levels of the H2B-like genes during heat and dehydration stress in 7-day-old plants. The expression level of each gene under the control condition was defined as 1.0. The error bars indicate SD (n = 3).

(B) The growth of yeast cells harboring NF-YB3 fused to the GAL4 activation domain (AD) and NF-YA2 fused to the GAL4 DNA-binding domain (BD) on selective medium (SD/-L-W-H-M-Ade) or nonselective medium (SD/-L-W-M).

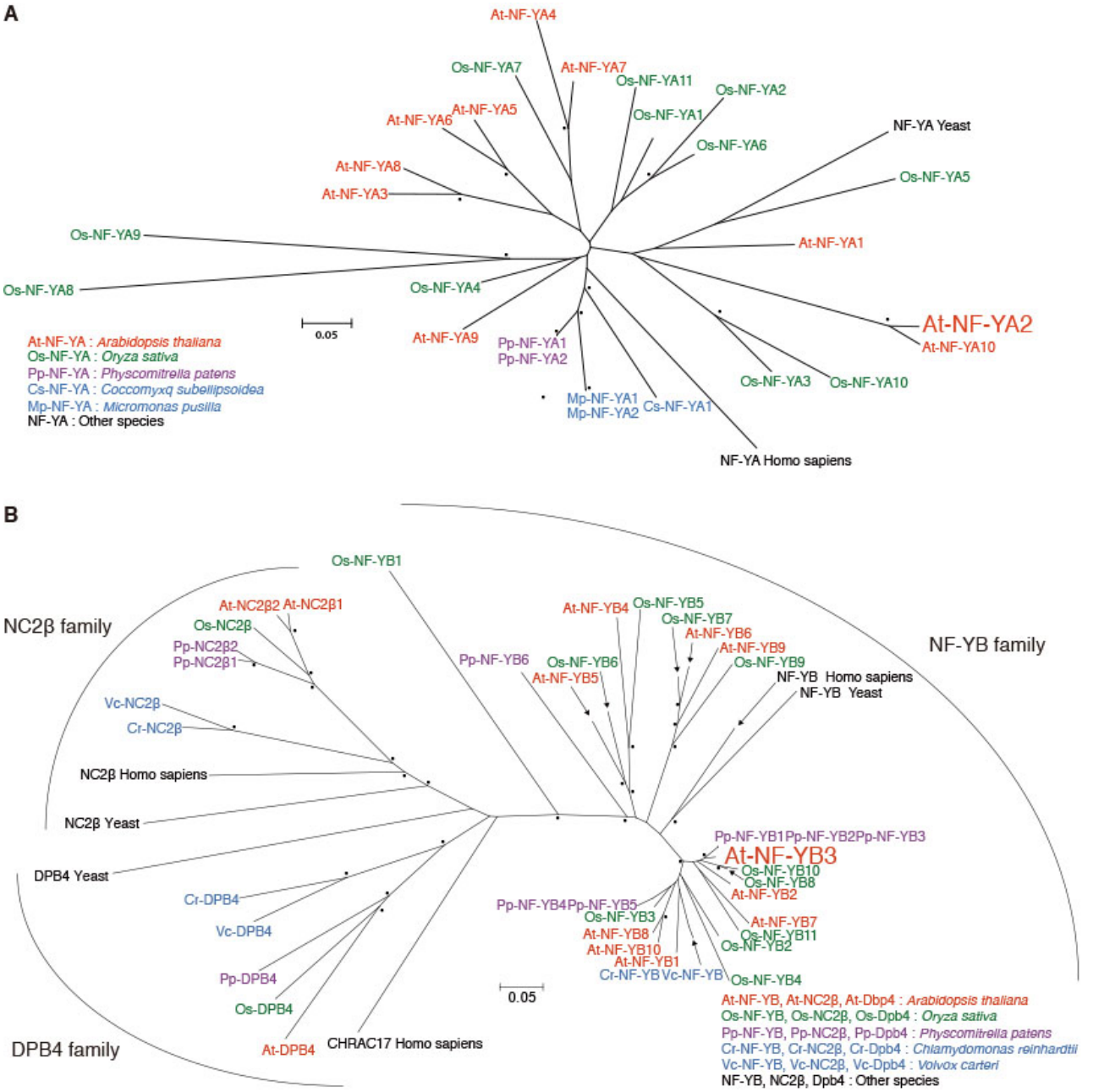
(C) Verification of the interaction among NF-YA2, NF-YB3 and DPB3-1 using the BiFC system in *Arabidopsis* mesophyll protoplasts. Three constructs that expressed (1) a fusion protein of NF-YA2 and the N-terminal half of YFP (YFP^N-NF-YA2), (2) a fusion protein of NF-YB3 and the C-terminal half of YFP (YFP^c-NF-YB3), and (3) DPB3-1 under the control of the *35S* promoter were transfected into *Arabidopsis* mesophyll protoplasts. Corresponding empty vectors were transfected for the control experiments. A construct that expressed CFP under the control of the *35S* promoter was co-transfected to indicate transfection of the protoplasts. DIC images, confocal images of YFP and CFP fluorescence, and merged images are shown. The YFP signal indicates that DPB3-1 expression is

Supplemental Figure 7 (continued).

necessary for the interaction between NF-YA2 and NF-YB3. Scale bars represent 10 μm.

(D) Alignment of the conserved amino acid sequences in H2A-like HFD-containing proteins. The sequences of the conserved regions in the H2A-like proteins are shown. Asterisks indicate residues involved in the trimerization of NF-Y. The CHRAC15 protein in humans is a homolog of the corresponding protein in *Arabidopsis*, DPB3-1. Numbers on the right side correspond to the actual amino acid sequence numbers of each protein.

(E) Quantitative RT-PCR analysis of the expression levels of the NF-YA2 genes during heat and dehydration stress in 7-day-old and 14-day-old plants. The expression level of each gene under the control condition was defined as 1.0. The error bars indicate SD (n = 3).



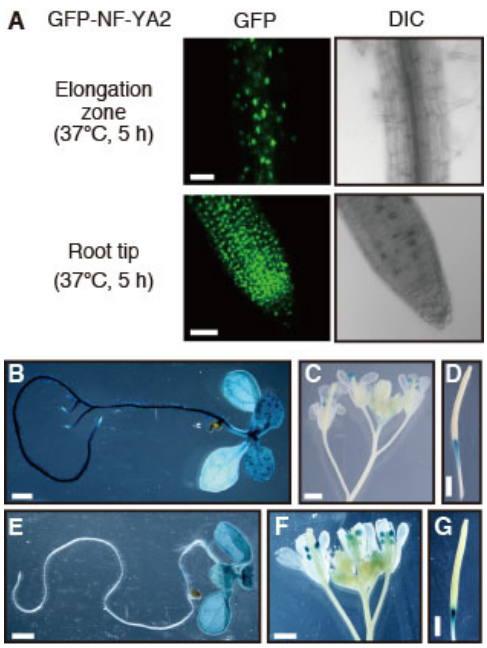
Supplemental Figure 8. Phylogenetic Trees of the NF-YA and H2B-Like HFD-Containing Proteins.

(A) Phylogenetic tree of NF-YA family proteins based on amino acids sequences of the conserved domain. The peptide sequences of the NF-YA family proteins from *Oryza sativa*, *Physcomitrella patens*, *Coccomyxa subellipsoidea* and *Micromonas pusilla* were obtained from Phytozome (Phytozome v9.1, http://www.phytozome.net/). A consensus tree from 1000 bootstrap samplings is shown, and a dot indicates a node that was supported with a bootstrap value > 50. The scale bar indicates the substitution rate per residue.

(B) Phylogenetic tree of H2B-like HFD-containing proteins based on amino acid sequences of the conserved domain. The peptide sequences of the H2B-like proteins for *Oryza sativa*, *Physcomitrella patens*, *Chlamydomonas reinhardtii* and *Volvox carteri* were

Supplemental Figure 8 (continued).

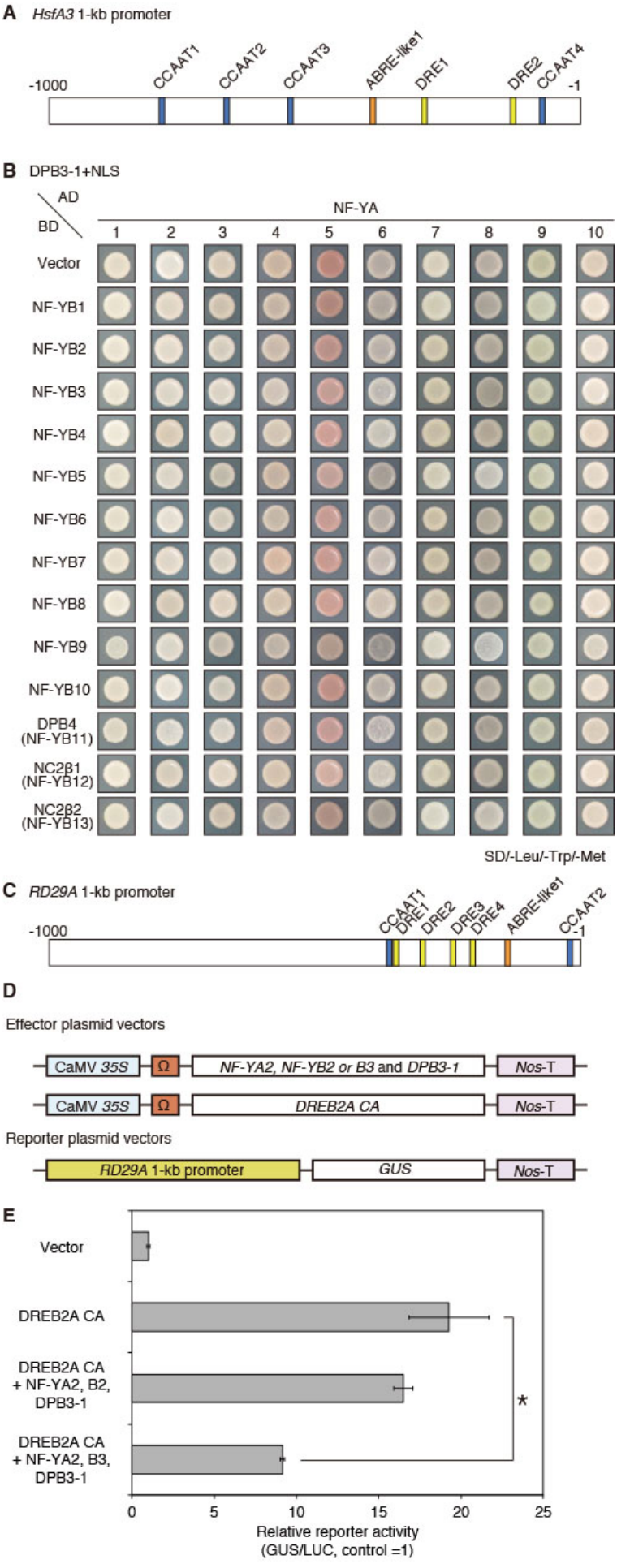
obtained from Phytozome (Phytozome v9.1, http://www.phytozome.net/). A consensus tree from 1000 bootstrap samplings is shown, and a dot indicates a node that was supported with a bootstrap value > 50. The scale bar indicates the substitution rate per residue.



Supplemental Figure 9. Subcellular Localization of NF-YA2 under Heat Stress Conditions, and Additional Analysis of the Tissue-Specific Expression Patterns of *NF-YA2* and *NF-YB3*.

(A) Nuclear localization of sGFP-NF-YA2 under heat stress conditions. The root tissues of *35S:sGFP-NF-YA2* plants were observed under a microscope after 5 hours of heat stress. Confocal images of GFP fluorescence and differential interference contrast (DIC) images are shown. Scale bars represent 100 μm.

(B) to **(G)** GUS staining of *NF-YA2*$_{pro}$:*GUS* transgenic plants (**[B]** to **[D]**) and *NF-YB3*$_{pro}$:*GUS* transgenic plants (**[E]** to **[G]**) at different growth stages. Whole seedlings of 10-day-old (**[B]** and **[E]**) plants and flowers (**[C]** and **[F]**) and siliques (**[D]** and **[G]**) from seven-week-old plants are shown. Scale bars represent 1 mm.



Supplemental Figure 10. Schematic Diagram of the *HsfA3* 1-kb and *RD29A* 1-kb Promoter, and Promoter-Specific Effect of the Trimer Composed of NF-YA2, NF-YB3 and DPB3-1, and Yeast Three-Hybrid Assay on Nonselective Medium.

(A) Schematic diagram of the *HsfA3* 1-kb promoter. The positions of the DREs, CCAAT boxes and ABRE-like motif on the promoter are indicated.

(B) Yeast three-hybrid assay to identify candidate NF-Y trimers containing DPB3-1. The growth of yeast cells harboring H2B-like proteins fused to the GAL4 DNA-binding domain (BD), NF-YA family proteins fused to the GAL4 activation domain (AD), and DPB3-1 fused to a nuclear localization signal (NLS) on nonselective medium (SD/-L-W-M) are shown.

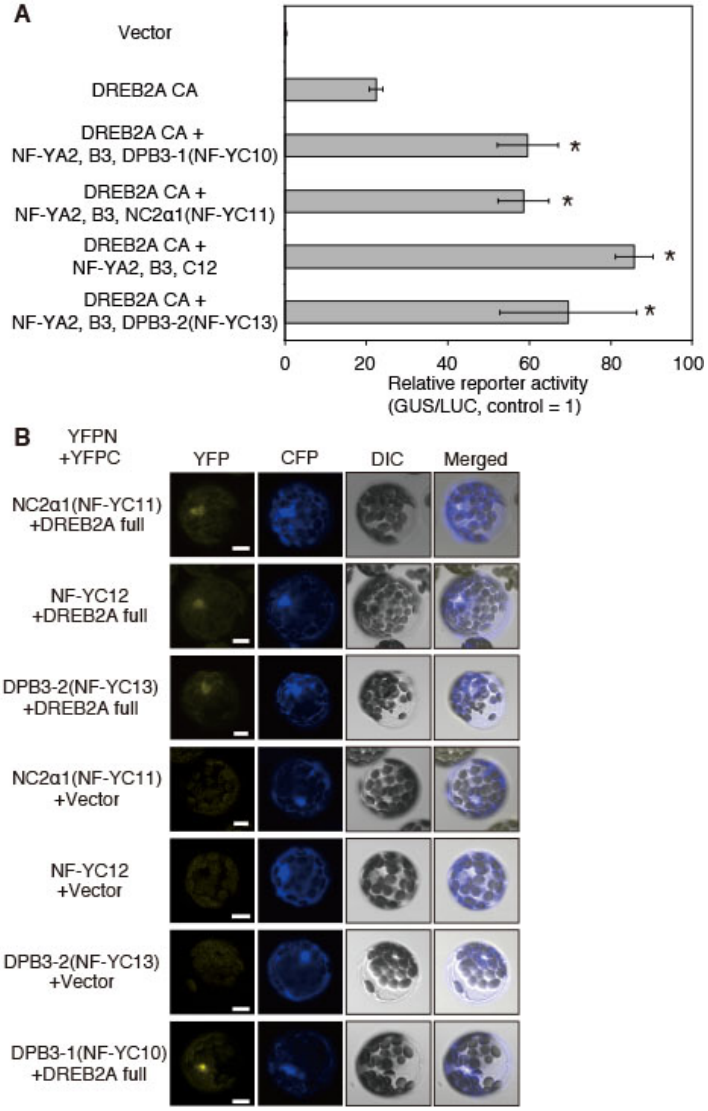
(C) Schematic diagram of the *RD29A* 1-kb promoter. The positions of the DREs, CCAAT boxes and ABRE-like motif on the promoter are indicated.

(D) Schematic diagram of the effector and reporter constructs for the transactivation experiment. The *RD29A* 1kb-promoter:*GUS* fusion gene was used as the reporter. The plasmids containing the *CaMV 35S*

Supplemental Figure 10 (continued).

promoter and the tobacco mosaic virus Ω sequence fused to *NF-Y2A, NF-YB3, DPB3-1* or *DREB2A CA* coding sequence were cotransfected into protoplasts.

(E) Transactivation of the *RD29A* 1-kb promoter:*GUS* reporter gene by DREB2A CA and trimer of NF-YA2, NF-YB3 and DPB3-1. The *35S*:*LUC* plasmid was also cotransfected in each experiment as an internal control. The asterisks (*) indicate significantly low differences between the reporter activities ($p < 0.05$ according to Student's t-test).



Supplemental Figure 11. The Effect of Other H2A-Like Proteins on the Reporter Activity with DREB2A, and Interaction between H2A-Like Proteins and DREB2A in Protoplasts.

(A) Transactivation of the *HsfA3* 1-kb promoter:*GUS* reporter gene by DREB2A CA and trimer of NF-YA2, NF-YB3 and H2A-like proteins. The *35S*:*LUC* plasmid was also cotransfected in each experiment as an internal control. Asterisks (*) indicate significantly high differences between the reporter activities ($p < 0.05$ according to a Bonferroni-corrected Student's t-test)

(B) Analysis of the interaction between DREB2A and H2A-like proteins using the BiFC system in *Arabidopsis* mesophyll protoplasts. Two constructs that expressed a fusion protein of DREB2A and the C-terminal half of YFP (YFP^C-DREB2A) or a fusion protein of H2A-like protein and the N-terminal half of YFP (YFP^N-H2A-like protein) were transfected into *Arabidopsis* mesophyll protoplasts under the control of the *35S* promoter. The empty vectors were also transfected in combination with each fusion construct. A construct that expressed CFP under the control of the *35S* promoter was co-transfected to indicate transfection of the protoplasts. The transfected protoplasts were treated with 25 μM MG132 for 2 h in the dark. The YFP^c-DPB3-1(NF-YC10) protein was used as a positive control. DIC images, confocal images of YFP and CFP fluorescence, and merged images are shown. Scale bars represent 10 μm.

Supplemental Table 1. Gene Names and Accession Numbers of the H2A-Like HFD-Containing Proteins.

Protein families in *Arabidopsis thaliana*, *Glycine max* (soybean), *Oryza sativa* (rice), *Physcomitrella patens*, *Chlamydomonas reinhardtii* and *Volvox carteri* were identified on the basis of the amino acid sequences of the conserved domain (Panther:10252). The proteins were numbered according to their locations in the phylogenetic tree.

Arabidopsis thaliana			*Glycine max*		*Oryza sativa*			*Physcomitrella patens*		*Chlamydomonas reinhardtii*		*Volvox carteri*	
Gene name	Generic name	Other name	Gene name	Generic name	Gene name	Generic name	Other name	Gene name	Generic name	Gene name	Generic name	Gene name	Generic name
AT3G48590	NF-YC1		Glyma10g29690	Gm--NF-YC1	LOC_Os02g07450	Os-NF-YC1	HAP5A	Pp1s409_32V6	Pp-NF-YC1	Cre12.g556400.t1.1	Cr-NF-YC	Vocar20009899m.g	Vc-NF-YC
AT1G56170	NF-YC2		Glyma19g42460	Gm--NF-YC2	LOC_Os03g14669	Os-NF-YC2	HAP5C	Pp1s51_318V6	Pp-NF-YC2	Cre16.g680050.t1.1	Cr-NC2α	Vocar20000027m.g	Vc-NC2α
AT1G54830	NF-YC3		Glyma20g37620	Gm--NF-YC3	LOC_Os04g58680	Os-NF-YC3	HAP5G	Pp1s370_63V6	Pp-NF-YC3	Cre03.g193900.t1.1	Cr-DPB3	Vocar20003435m.g	Vc-DPB3
AT5G63470	NF-YC4		Glyma03g39910	Gm--NF-YC4	LOC_Os06g45640	Os-NF-YC4	HAP5B	Pp1s315_9V6	Pp-NF-YC4				
AT5G50490	NF-YC5		Glyma08g17630	Gm--NF-YC5	LOC_Os08g10560	Os-NF-YC5	HAP5F	Pp1s159_32V6	Pp-NF-YC5				
AT5G50480	NF-YC6		Glyma06g17780	Gm--NF-YC6	LOC_Os08g38780	Os-NF-YC6	HAP5D	Pp1s158_8V6	Pp-NF-YC6				
AT5G50470	NF-YC7		Glyma04g37290	Gm--NF-YC7	LOC_Os09g30310	Os-NF-YC7	HAP5E	Pp1s112_139V6	Pp-NC2α1				
AT5G27910	NF-YC8		Glyma13g27790	Gm--NF-YC8	LOC_Os01g39850	Os-NF-YC8		Pp1s35_42V6	Pp-NC2α2				
AT1G08970	NF-YC9		Glyma08g15700	Gm--NF-YC9	LOC_Os01g01290	Os-NF-YC9		Pp1s143_36V6	Pp-NC2α3				
AT1G07980	DPB3-1	NF-YC10	Glyma13g27780	Gm--NF-YC10	LOC_Os01g24460	Os-NF-YC10		Pp1s37_218V6	Pp-DPB3-1				
AT3G12480	NC2α1	NF-YC11	Glyma13g27770	Gm--NF-YC11	LOC_Os10g11580	Os-NF-YC11		Pp1s329_24V6	Pp-DPB3-2				
AT5G38140	NF-YC12		Glyma13g35980	Gm--NF-YC12	LOC_Os05g23910	Os-NF-YC12		Pp1s149_89V6	Pp-DPB3-3				
AT5G43250	DPB3-2	NF-YC13	Glyma12g34510	Gm--NF-YC13	LOC_Os11g34200	Os-NC2α1							

Arabidopsis thaliana			*Glycine max*		*Oryza sativa*			*Physcomitrella patens*		*Chlamydomonas reinhardtii*		*Volvox carteri*	
Gene name	Generic name	Other name	Gene name	Generic name	Gene name	Generic name	Other name	Gene name	Generic name	Gene name	Generic name	Gene name	Generic name
AT5G19490	NC2α2		Glyma02g09860	Gm--NF-YC14	LOC_Os05g41450	Os-NC2α2							
			Glyma14g04320	Gm--NC2α1	LOC_Os01g08790	Os-DPB3-1							
			Glyma02g44500	Gm--NC2α2	LOC_Os03g63530	Os-DPB3-2							
			Glyma06g46850	Gm--NC2α3									
			Glyma15g36170	Gm--NC2α4									
			Glyma13g25860	Gm--NC2α5									
			Glyma18g01040	Gm--DPB3-1									
			Glyma11g37130	Gm--DPB3-2									
			Glyma12g07390	Gm--DPB3-3									
			Glyma11g20740	Gm--DPB3-4									

Supplemental Table 2. GO analysis of the Genes Upregulated in *DPB3-1*-Overexpressing Plants under Heat Stress.

GO analysis was performed using the MAPMAN tool (http://mapman.mpimp-golm.mpg.de/general/ora/ora.shtml). The terms that are significantly enriched compared with all *Arabidopsis* genes are listed ($p < 0.0001$). The count refers to the number of genes that are categorized into that term among the upregulated in *DPB3-1*-overexpressing plants. The background refers to the number of total *Arabidopsis* genes categorized under that term.

BIN	Binname	Count	Background	p value
16.5.1	secondary metabolism.sulfur-containing.glucosinolates	3	59	9.37E-04
20.2	stress.abiotic	9	442	1.42E-05
20.2.1	stress.abiotic.heat	6	186	3.29E-05
27.3.23	RNA.regulation of transcription.HSF,Heat-shock transcription factor family	3	23	5.56E-05

Supplemental Table 3. Gene Names and Accession Numbers of the NF-YA Family Proteins.

Protein families in *Arabidopsis thaliana*, *Oryza sativa* (rice), *Physcomitrella patens*, *Coccomyxa subellipsoidea* and *Micromonas pusilla* were identified on the basis of the amino acid sequences of the conserved domain (Pfam:02045). The proteins were numbered according to their locations in the phylogenetic tree.

Arabidopsis thaliana		*Oryza sativa*			*Physcomitrella patens*		*Coccomyxa subellipsoidea* C-169		*Micromonas pusilla* CCMP1545	
Gene name	Generic name	Gene name	Generic name	Other name	Gene name	Generic name	Gene name	Generic name	Gene name	Generic name
AT5G12840	NF-YA1	LOC_Os03g07880	Os-NF-YA1	HAP2C	Pp1s42 174V6	Pp-NF-YA1	60947	Cs-NF-YA1	195698	Mp-NF-YA1
AT3G05690	NF-YA2	LOC_Os03g29760	Os-NF-YA2	HAP2E	Pp1s31 299V6	Pp-NF-YA2			106430	Mp-NF-YA2
AT1G72830	NF-YA3	LOC_Os03g44540	Os-NF-YA3	HAP2H						
AT2G34720	NF-YA4	LOC_Os03g48970	Os-NF-YA4	HAP2D						
AT1G54160	NF-YA5	LOC_Os07g06470	Os-NF-YA5	HAP2J						
AT3G14020	NF-YA6	LOC_Os07g41720	Os-NF-YA6	HAP2G						
AT1G30500	NF-YA7	LOC_Os08g09690	Os-NF-YA7	HAP2A						
AT1G17590	NF-YA8	LOC_Os10g25850	Os-NF-YA8	HAP2I						
AT3G20910	NF-YA9	LOC_Os12g41880	Os-NF-YA9	HAP2B						
AT5G06510	NF-YA10	LOC_Os12g42400	Os-NF-YA10	HAP2F						
		LOC_Os02g53620	Os-NF-YA11							

Supplemental Table 4. Gene Names and Accession Numbers of the H2B-Like HFD-Containing Family Proteins.

Protein families in *Arabidopsis thaliana*, *Oryza sativa* (rice), *Physcomitrella patens*, *Chlamydomonas reinhardtii* and *Volvox carteri* were identified on the basis of the amino acid sequences of the conserved domain (Panther:11064). The proteins were numbered according to their locations in the phylogenetic tree.

Arabidopsis thaliana			*Oryza sativa*			*Physcomitrella patens*		*Chlamydomonas reinhardtii*		*Volvox carteri*	
Gene name	Generic name	Other name	Gene name	Generic name	Other name	Gene name	Generic name	Gene name	Generic name	Gene name	Generic name
AT2G38880	NF-YB1		LOC_Os02g49410	Os-NF-YB1	HAP3K	Pp1s302_35V6	Pp-NF-YB1	Cre02.g079200.t1.2	Cr-NF-YB	Vocar20010774m.g	Vc-NF-YB
AT2G47810	NF-YB2		LOC_Os01g61810	Os-NF-YB2	HAP3A	Pp1s83_179V6	Pp-NF-YB2	Cre17.g739450.t1.3	Cr-NC2β	Vocar20003887m.g	Vc-NC2β
AT1G09030	NF-YB3		LOC_Os05g38820	Os-NF-YB3	HAP3B	Pp1s462_7V6	Pp-NF-YB3	Cre07.g341800.t1.2	Cr-DPB4	Vocar20006871m.g	Vc-DPB4
AT2G37060	NF-YB4		LOC_Os05g49780	Os-NF-YB4	HAP3C	Pp1s25_10V6	Pp-NF-YB4				
AT2G13570	NF-YB5		LOC_Os01g70880	Os-NF-YB5	HAP3J	Pp1s25_89V6	Pp-NF-YB5				
AT3G53340	NF-YB6		LOC_Os01g70890	Os-NF-YB6	HAP3G	Pp1s148_126V6	Pp-NF-YB6				
AT5G47670	NF-YB7		LOC_Os02g49370	Os-NF-YB7	HAP3E	Pp1s181_25V6	Pp-NC2β1				
AT5G47640	NF-YB8		LOC_Os03g29970	Os-NF-YB8	HAP3I	Pp1s288_38V6	Pp-NC2β2				
AT1G21970	NF-YB9		LOC_Os06g17480	Os-NF-YB9	HAP3D	Pp1s217_34V6	Pp-DPB4				
AT4G14540	NF-YB10		LOC_Os07g41580	Os-NF-YB10	HAP3F						
AT5G23090	DPB4	NF-YB11	LOC_Os08g07740	Os-NF-YB11	HAP3H						
AT5G08190	NC2β1	NF-YB12	LOC_Os08g29500	Os-NC2β							
AT2G27470	NC2β2	NF-YB13	LOC_Os09g39490	Os-DPB4							

Supplemental Table 5. Sequences of the Primers Used in This Study.

Target gene	LocusID	Oligonucleotide name	Sequence (5' to 3')
Primers used for cloning of coding or promoter sequences			
DPB3-1	At1g07980	NFYC10_F_XbaI	GCTCTAGAGATGGTGTCGTCAAAGAA
		NFYC10_R_XhoI	ATCTCGAGTCAGCCTGCATCTGTCAT
		NFYC10_F_XbaI_2	CGTCTAGAATGGTGTCGTCAAAGAA
		NFYC10_R_XhoI_2	ATCTCGAGTCCGCCTGCATCTGTCAT
		NFYC10_F_BamHI	ATGGATCCATGGTGTCGTCAAAGAA
		NFYC10_R_PstI	ATCTGCAGTCAGCCTGCATCTGTCAT
		NFYC10_F_NotI	ATGCGGCCGCTATGGTGTCGTCAAAGAA
		NFYC10_R_NotI	ATGCGGCCGCTCAGCCTGCATCTGTCAT
DPB3-1 promoter	At1g07980	NFYC10p_F_SacI	GCGAGCTCTTAGGGAGAAGAAGATCCAACAAC
		NFYC10p_R_PstI	GCCTGCAGTAATTTTTTAGAACTACAGTATGTTTCACCC
DREB2A	At5g05410	DREB2A_F_SpeI	CGACTAGTATGGCAGTTTATGATCAGAGTG
		DREB2A_R_ClaI	CGATCGATTAAGTTCTCCAGATCCAAG
		DREB2A_F_EcoRI	GGGGAATTCATGGCAGTTTATGATC
		DREB2A205_R_PstI	GGGCTGCAGCTAAAACTCGCTCAGCCA
		DREB2A135_R_PstI	TTTCTGCAGCTAAGGGAAATTAAGACGAGCC
		DREB2A165_R_PstI	TTTCTGCAGCTACTCTGTTTTCACATGAACAC
		DREB2A180_R_PstI	GGGCTGCAGCTACGGCTCCACTCCACC
		DREB2A136_F_EcoRI	GGGGAATTCCGGTCTGATGCGTCTGAG
		DREB2A77_R_PstI	ATCTGCAGACATCGGCTATTCTCTGGTCCTCC
		DREB2A78_F_EcoRI	GCGAATTCAGTTTCAGAGGAGTTAGGCAAAGGA
NF-YC1	AT3G48590	NFYC1_F_EcoRI	GTGAATTCATGGATACCAACAACCAGCAA
		NFYC1_R_ClaI	ATAGCGATTTAACCTTGGCCGTCGAGAT
NF-YC2	AT1G56170	NFYC2_F_EcoRI	AGGAATTCATGGAGCAGTCAGAAGAGGG
		NFYC2_R_XhoI	GTCTCGAGTTAAGACTCATCAGGGTGTTGC
NF-YC3	AT1G54830	NFYC3_F_EcoRI	GCGAATTCATGGATCAACAAGGACAATC
		NFYC3_R_XhoI	ATCTCGAGCTAATTGTCAGGATCCTGCTGC
NF-YC4	AT5G63470	NFYC4_F_ClaI	GTATCGATGCATGGACAATAACAACAACAACAACAACC
		NFYC4_R_XhoI	ATCTCGAGTCAACCTTGGCTATCGAGATTACCAT
NF-YC5	AT5G50490	NFYC5_F_EcoRI	ATGAATTCATGGAGAACAACAACAACAACCACCAACAGC
		NFYC5_R_XhoI	ATCTCGAGTTAATTCCCACCGTTTCCTCCATTTGC
NF-YC6	AT5G50480	NFYC6_F_EcoRI	ATGAATTCATGGCTGAGAACAACAACAACAACGG

Target gene	LocusID	Oligonucleotide name	Sequence (5' to 3')
		Primers used for cloning of coding or promoter sequences	
NF-YC6	AT5G50480	NFYC6_R_XhoI	ATCTCGAGTCAATTTCCGCCGCCGTTTCCTC
NF-YC7	AT5G50470	NFYC7_F_EcoRI	GCGAATTCATGGAAGAGAACAACGGCAAC
		NFYC7_R_XhoI	ATCTCGAGTCAATTACCGCCGCTGCTTC
NF-YC8	AT5G27910	NFYC8_F_EcoRI	GTGAATTCATGGAGAACAACAACGGCA
		NFYC8_R_XhoI	ATCTCGAGTTAGTTTCCGTCGTCACCTCC
NF-YC9	AT1G08970	NFYC9_F_EcoRI	ATGAATTCATGGATCAACAAGACCATGGACAG
		NFYC9_R_XhoI	ATCTCGAGCTAATTTTCCTGGTCAGGTTGG
NC2α1	AT3G12480	NFYC11_F_EcoRI	CCGAATTCATGAGGAAGAAGCTCGATAC
		NFYC11_R_XhoI	CGCTCGAGTTAGCCTTCTTCGTCATAATC
		NFYC11_F_SmaI	ATCCCGGGAAATGAGGAAGAAGCTCGATACTCGGT
		NFYC11_R_XhoI_2	CGCTCGAGTAAGCCTTCTTCGTCATAATC
		NFYC11_F_SalI	ATGTCGACATGAGGAAGAAGCTCGATACTCGGT
NF-YC12	AT5G38140	NFYC12_F_EcoRI	CTGAATTCATGAGGAGGCCAAAGTCATC
		NFYC12_R_XhoI	ATCTCGAGTCACTGGAGATCACAGTTGAGG
		NFYC12_F_SmaI	ATCCCGGGTAATGAGGAGGCCAAAGTCATC
		NFYC12_R_XhoI_2	GCCTCGAGTAACTGGAGATCACAGTTGAGG
		NFYC12_F_SalI	ATGTCGACATGAGGAGGCCAAAGTCATC
DPB3-2	AT5G43250	NFYC13_F_EcoRI	CGGAATTCATGGAGGAAGAAGAAGGAT
		NFYC13_R_XhoI	ATCTCGAGTTAGGCTGAATCAGTCTTTGCT
		NFYC13_F_BamHI	GCGGATCCTATGGAGGAAGAAGAAGGAT
		NFYC13_R_XhoI_2	ATCTCGAGTAAGGCTGAATCAGTCTTTGCT
		NFYC13_F_BamHI_2	GCGGATCCATGGAGGAAGAAGAAGGAT
NC2α2	AT5G19490	NFYC14_F_SmaI	ATCCCGGGTATGAAGAAGAAGCTCCAGACACGTT
		NFYC14_R_XhoI	CCCTCGAGTCACTCTTGGTCTATGCTTTCTTC
NF-YB1	AT2G38880	NFYB1_F_BamHI	ATGGATCCATATGGCGGATACGCCTTCG
		NFYB1_R_XhoI	ATCTCGAGTTACCAGCTCGGCATTTCTTCACC
		NFYB1_F_XbaI	ATTCTAGACATGGCGGATACGCCTTCG
		NFYB1_R_XhoI_2	ATCTCGAGTAACCAGCTCGGCATTTCTTCACC
		NFYB1_F_XbaI_2	ATTCTAGAATGGCGGATACGCCTTCG
NF-YB2	AT2G47810	NFYB2_F_ClaI	CGATCGATATATGGGGGATTCCGACAGG
		NFYB2_R_XhoI	ATCTCGAGTTAAGTCCTTGTCCTACCGGAGGC
		NFYB2_F_XbaI	CGTCTAGAGATGGGGGATTCCGACAGG
		NFYB2_R_XhoI_2	ATCTCGAGTAAAGTCCTTGTCCTACCGGAGGC

		NFYB2_F_XbaI_2	CGTCTAGAATGGGGGATTCCGACAGG
Target gene	LocusID	Oligonucleotide name	Sequence (5' to 3')
Primers used for cloning of coding or promoter sequences			
NF-YB3	AT1G09030	NFYB3_F_ClaI	ATATCGATACATGGCGGATTCGGACAACG
		NFYB3_R_XhoI	CGCTCGAGTTAAGAAAAATGATGGGAA
		NFYB3_F_XbaI	ATTCTAGAGATGGCGGATTCGGACAACG
		NFYB3_R_XhoI_2	CGCTCGAGTAAAGAAAAATGATGGGAA
		NFYB3_F_XbaI_2	ATTCTAGAATGGCGGATTCGGACAACG
NF-YB4	AT2G37060	NFYB4_F_ClaI	CGATCGATGCATGACAGACGAAGATAGATTG
		NFYB4_R_XhoI	ATCTCGAGTCAACGGGCCGAGGAGC
NF-YB5	AT2G13570	NFYB5_F_ClaI	CGATCGATACATGGCGGGGAATTATCAT
		NFYB5_R_XhoI	CGCTCGAGTTAATTATCTGGCGAGGATTTAG
		NFYB5_F_XbaI	GCTCTAGAGATGGCGGGGAATTATCAT
NF-YB6	AT3G53340	NFYB6_F_ClaI	ATATCGATACATGGAACGTGGAGGCTTC
		NFYB6_R_XhoI	CGCTCGAGTCAGTACTTATGTTGTTGAGTCG
		NFYB6_F_XbaI	ATTCTAGAGATGGCAGAGGGCAGTATGCGTC
		NFYB6_R_XhoI_2	CGCTCGAGTAAGTACTTATGTTGTTGAGTCG
		NFYB6_F_XbaI_2	ATTCTAGAATGGCAGAGGGCAGTATGCGTC
NF-YB7	AT5G47670	NFYB7_F_ClaI	ATATCGATACATGACTGAGGAGAGCCCAGAAGAAG
		NFYB7_R_XhoI	CGCTCGAGTCACCAGTGAATTGAATCAATGT
		NFYB7_F_XbaI	ATTCTAGAGATGACTGAGGAGAGCCCAGAAGAAG
		NFYB7_R_XhoI_2	CGCTCGAGTAACCAGTGAATTGAATCAATGT
		NFYB7_F_XbaI_2	ATTCTAGAATGACTGAGGAGAGCCCAGAAGAAG
NF-YB8	AT5G47640	NFYB8_F_ClaI	ATATCGATACATGGCGGAGTCGCAGG
		NFYB8_R_XhoI	ATCTCGAGCTAGTCTGTTCCCGGCATTG
NF-YB9	AT1G21970	NFYB9_F_ClaI	ATATCGATATATGGAACGTGGAGCTCCCTTC
		NFYB9_R_XhoI	CGCTCGAGTCACTTATACTGACCATAAT
		NFYB9_F_XbaI	GCTCTAGAGATGACCAGCTCAGTCGTA
NF-YB10	AT4G14540	NFYB10_F_BamHI	CGGGATCCATATGGCCGAATCGCAAAC
		NFYB10_R_XhoI	ATCTCGAGCTACTCTGTGCCCGGCATTTGA
DPB4	AT5G23090	NFYB11_F_ClaI	GCATCGATACATGGAGTCGGAGAAAGTGG
		NFYB11_R_XhoI	CGCTCGAGTCATTCATCTTCTTCATCACTC
		NFYB11_F_XbaI	GCTCTAGAGATGGAGTCGGAGAAAGTGG
		NFYB11_R_XhoI_2	CGCTCGAGTCCTTCATCTTCTTCATCACTC
		NFYB11_F_XbaI_2	GCTCTAGAATGGAGTCGGAGAAAGTGG

NC2β1	AT5G08190	NFYB12_F_EcoRI	GCGAATTCATGGATCCGATGGATATAGTTGG
		NFYB12_R_ClaI	GCATCGATTTAGCTTTGTAGACTTGTTTGTTG
Target gene	LocusID	Oligonucleotide name	Sequence (5' to 3')
		Primers used for cloning of coding or promoter sequences	
NC2β2	AT2G27470	NFYB13_F_ClaI	GCATCGATACATGGATCCAATGGATATAGTCG
		NFYB13_R_XhoI	ATCTCGAGTTAGCTTTGCGGACTTCTCTGGTC
NF-YA1	AT5G12840	NFYA1_F_SmaI	ATCCCGGGTATGCAATCAAAACCGGGAAGAG
		NFYA1_R_SalI	ATGTCGACTTATGGTGCACCAGAAGAATTCAGGG
		NFYA1_F_XbaI	GCTCTAGAGATGCAATCAAAACCGGGAAGAG
		NFYA1_R_XhoI	ATCTCGAGTTATGGTGCACCAGAAGAATTCAGGG
NF-YA2	AT3G05690	NFYA2_F_SmaI	ATCCCGGGTATGGCTATGCAAACTGTGAGA
		NFYA2_R_SalI	ATGTCGACTCAGGTTTTGAAATTGCAGCAG
		NFYA2_F_XbaI	GCTCTAGAGATGGCTATGCAAACTGTGAGA
		NFYA2_R_XhoI	ATCTCGAGTCAGGTTTTGAAATTGCAGCAG
		NFYA2_F_XbaI_2	ATTCTAGAATGGCTATGCAAACTGTGAGA
		NFYA2_R_XhoI_2	ATCTCGAGTCCGGTTTTGAAATTGCAGCAG
NF-YA3	AT1G72830	NFYA3_F_SmaI	ATCCCGGGTATGATGCATCAGATGTTGA
		NFYA3_R_SalI	GCGTCGACTCAGATATGGACAGAGAAATGG
NF-YA4	AT2G34720	NFYA4_F_BamHI	GCGGATCCGTATGACTTCTTCAGTACATGA
		NFYA4_R_PstI	GCCTGCAGTCAAGATCTACCATTAGGACCAG
		NFYA4_F_XbaI	GCTCTAGAGATGACTTCTTCAGTACATGA
		NFYA4_R_XhoI	ATCTCGAGTCAAGATCTACCATTAGGACCAG
NF-YA5	AT1G54160	NFYA5_F_BamHI	GCGGATCCGTATGCAAGTGTTTCAAAGGA
		NFYA5_R_PstI	GCCTGCAGTCAAGTCCCTGACATGAGA
NF-YA6	AT3G14020	NFYA6_F_BamHI	GCGGATCCGTATGCAAGAGTTCCATAGTAGC
		NFYA6_R_PstI	GCCTGCAGTCACATGAGGACTGAGACATGG
NF-YA7	AT1G30500	NFYA7_F_BamHI	GCGGATCCGTATGACTTCTTCAATCCATGA
		NFYA7_R_PstI	GCCTGCAGTCAAGATGTACCACTAGAAGCAG
		NFYA7_F_XbaI	GCTCTAGAGATGACTTCTTCAATCCATGA
		NFYA7_R_XhoI	ATCTCGAGTCAAGATGTACCACTAGAAGCAG
NF-YA8	AT1G17590	NFYA8_F_BamHI	GCGGATCCGCATGGATAAGAAAGTTTCATTTACTA
		NFYA8_R_PstI	GCCTGCAGTCAGATATGGACAGAGAAATGG
NF-YA9	AT3G20910	NFYA9_F_SmaI	ATCCCGGGTATGGGAATTGAAGACATGC
		NFYA9_R_SalI	GCGTCGACTCATTTAATGGCTAGACGAGCTT
NF-YA10	AT5G06510	NFYA10_F_SmaI	ATCCCGGGTATGCAAACTGAGGAGCTTTTGTCGC

		NFYA10_R_SalI	CGTCGACTCATATATTAAGTTTGCAGCAGCCA
NF-YA2 promoter	AT3G05690	NFYA2p_F_PstI	GCCTGCAGGTTTCTGAAGCTCGTTAGTCG
		NFYA2p_R_XhoI	ATCTCGAGCTCCAAATTCCAATTACAAAAAGTG
Target gene	LocusID	Oligonucleotide name	Sequence (5' to 3')
		Primers used for cloning of coding or promoter sequences	
NF-YB3 promoter	AT1G09030	NFYB3p_F_PstI	GCCTGCAGACTCTCAAAAATCGCCAAGAT
		NFYB3p_R_XhoI	GCCTCGAGCTTTAGATCGAGGAGACAAAAGGT
HsfA3 promoter	At5g03720	HsfA3p_F_SpeI	GCACTAGTAAACAATGTGAGGGATA
		HsfA3p_R_PstI	GGGCTGCAGTTGATATAGTAGAAAA
		HsfA3p1_F_SacI	GGGGAGCTCTGGACTATAAACCAACAGAAA
		HsfA3p2_F_SacI	TTTGAGCTCATAGTCAACTATTTTTGCCTTCGC
		HsfA3p3_F_SacI	TTTGAGCTCTGAAAAAGGAAACACGAAAAGCG
		HsfA3p4_F_SacI	GGGGAGCTCTACTTCCTTCCCTAAACCT
		HsfA3p3M_F	AGTGAGAGAGAGAGTGAGAAAAAAAGGTGTGTGTGATAATTAGGG
RD29A promoter	At5g52310	RD29Ap_F_XbaI	CCCTCTAGACATTTAATCTGAGTCC
		RD29Ap_R_PstI	GGGCTGCAGTTTCCAAAGATTTTTT
		Primers used for genotyping of T-DNA insertion mutant	
DPB3-1	At1g07980	NFYC10_F_XbaI	Described above
		NFYC10_R_XhoI	Described above
DREB2A	At5g05410	dreb2a-1_F	GCTTCTTGAGCAGTAGGGAAAGTA
		dreb2a-1_R	CGAAAAAGCTACACACAAGAAGAA
T-DNA		SALK_LBb1.3	ATTTTGCCGATTTCGGAAC
		GABI_o8409	ATATTGACCATCATACTCATTGC
		Primers used for qRT-PCR	
Hsp17.A-CI	At1g59860	Hsp17.A-CI_RT-PCR_F	CTGGGTCTTGACTTTGTGTGTG
		Hsp17.A-CI_RT-PCR_R	TGTCACACAAGTTACTAGCTTCCA
HsfA2	At2g26150	HsfA2_RT-PCR_F	TGGGATTCTCATAAGTTCTCAACA
		HsfA2_RT-PCR_R	TGGATCAATCTTTCTGAATCCAT
HsfA7A	At3g51910	HsfA7A_RT-PCR_F	GCTCTAGAATGATGAACCCGTTTCTCCCG
		HsfA7A_RT-PCR_R	TCCCCCGGGTTAGGAGGTGGAAGCCAAAC
HsfA7B	At3g63350	HsfA7B_RT-PCR_F	AGCAGATTTTCGAGCAGAAGAGA
		HsfA7B_RT-PCR_R	TGCTCCACCTCTTCCATTTTGAT
HsfA3	At5g03720	HsfA3_RT-PCR_F	TTCGCTAACGAGGCTTTCC
		HsfA3_RT-PCR_R	CCTCAGTAGGTGACCCTT
HsfA3promoter	At5g03720	HsfA3promoter_RT-PCR_F	GAGAGCTAAGTGAAGCTGCAAGGA

		HsfA3promoter_RT-PCR_R	TCGTCATCATGTTCCATTGATT
GSTU20	At1g78370	GSTU20_RT-PCR_F	CACACACTCGCTTGTTCACG
		GSTU20_RT-PCR_R	TCGCCATTGCTATAGGATCTC
DPB3-1	At1g07980	NF-YC10_RT-PCR_F	GTCAACAAAGCCACGGAGAT
Target gene	LocusID	Oligonucleotide name	Sequence (5' to 3')
		Primers used for qRT-PCR	
DPB3-1	At1g07980	NF-YC10_RT-PCR_R	ATGCCTCTTTCCCATTCCTC
At4g36010	At4g36010	At4g36010_RT-PCR_F	CTTGTGGCGGAGCTGATTAC
		At4g36010_RT-PCR_R	CCTTCGTTGCACTCTTCACA
DREB2A	At5g05410	DREB2A_RT-PCR_F	CAGTGTTGCCAACGGTTCAT
		DREB2A_RT-PCR_R	AAACGGAGGTATTCCGTAGTTGAG
RD29A	At5g52310	RD29A_RT-PCR_F	TGGATCTGAAGAACGAATCTGATATC
		RD29A_RT-PCR_R	GGTCTTCCCTTCGCCAGAA
RD29B	At5g52300	RD29B_RT-PCR_F	GGAGAGAGCAGAGAGGCTCA
		RD29B_RT-PCR_R	CCGTTGACCACCGAGATAGT
18S rRNA		18S rRNA_RT-PCR_F	AAACGGCTACCACATCCAAG
		18S rRNA_RT-PCR_R	CCTCCAATGGATCCTCGTTA
NF-YB1	AT2G38880	NFYB1_RT-PCR_F	AGTGATTAAGAACAATCGCCAAA
		NFYB1_RT-PCR_R	CACTGATCTCTAATTTCCCATGC
NF-YB2	AT2G47810	NFYB2_RT-PCR_F	TATCATGTGATAGAACGAACATTGG
		NFYB2_RT-PCR_R	TTTACACAGCCTCAAAATCTAAACC
NF-YB3	AT1G09030	NFYB3_RT-PCR_F	GGAGACAAGGCGATAAGGAAG
		NFYB3_RT-PCR_R	GATGTCCCATCGTAGTCACCA
NF-YB6	AT3G53340	NFYB6_RT-PCR_F	AAGTTTAAGCGAAAACAATGCTG
		NFYB6_RT-PCR_R	CCACAAGACAGATCAGATGAAAA
NF-YB7	AT5G47670	NFYB7_RT-PCR_F	CTCTCATCATCATCCTTCTCCAT
		NFYB7_RT-PCR_R	GCAATGATTTAGGAGAGAAAGCA
DPB4	AT5G23090	NFYB11_RT-PCR_F	GGATCTTCATCCACTACCTCTCC
		NFYB11_RT-PCR_R	CCTTAAACACATCATCAGCCTTC
NF-YA2	AT3G05690	NFYA2_RT-PCR_F	CCGAGATGGCTTCCTAACAA
		NFYA2_RT-PCR_R	GAAAGATATGTTCACAGATGGAGTG
		Primers used for ChIP-PCR	
HsfA3	At5g03720	HsfA3promoter_RT-PCR_F	Described above
		HsfA3promoter_RT-PCR_R	Described above
At1g75860	At1g75860	At1g75860_ChIP_F	CGGACCGAGCCAGTAGTCGTC

		At1g75860_ChIP_R	GGGGGAGAAGATAGCTAAGCGCG
HsfA2	At2g26150	HsfA2_ChIP_F	AGAGAAAAATTGTGCAGCAGGT
		HsfA2_ChIP_R	CGCCAGAAAAAGCCTACTAAAA
18S rDNA		18S rRNA_RT-PCR_F	Described above
		18S rRNA_RT-PCR_R	Described above
Primers used for construction of vectors			
		Myc-N/SpeI	AAAACTAGTTATGGAACAGAAGCTTATTTCAGAGG
		Myc-C/XbaI	AAATCTAGAAGATCCTCCTCTGAAATAAGCTTCTG
		3xFlag-N/SpeI	AAAACTAGTTATGGACTACAAAGACCATGACGG
		3xFlag-C/XbaI	AAATCTAGACCCTTGTCATCGTCATCCTTGT
		StrepII-N/SpeI	AAAACTAGTTATGTGGTCTCATCCTCAATTCGAG
		StrepII-C/XbaI	AAATCTAGACCCTTCTCGAATTGAGGATGAGACC