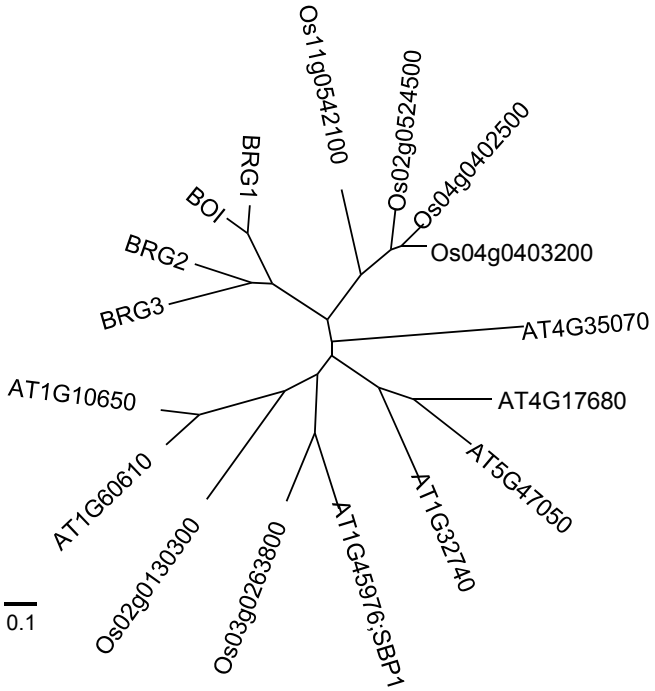
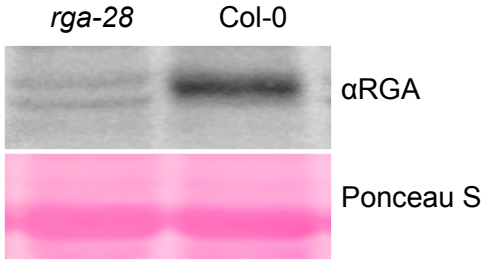
A

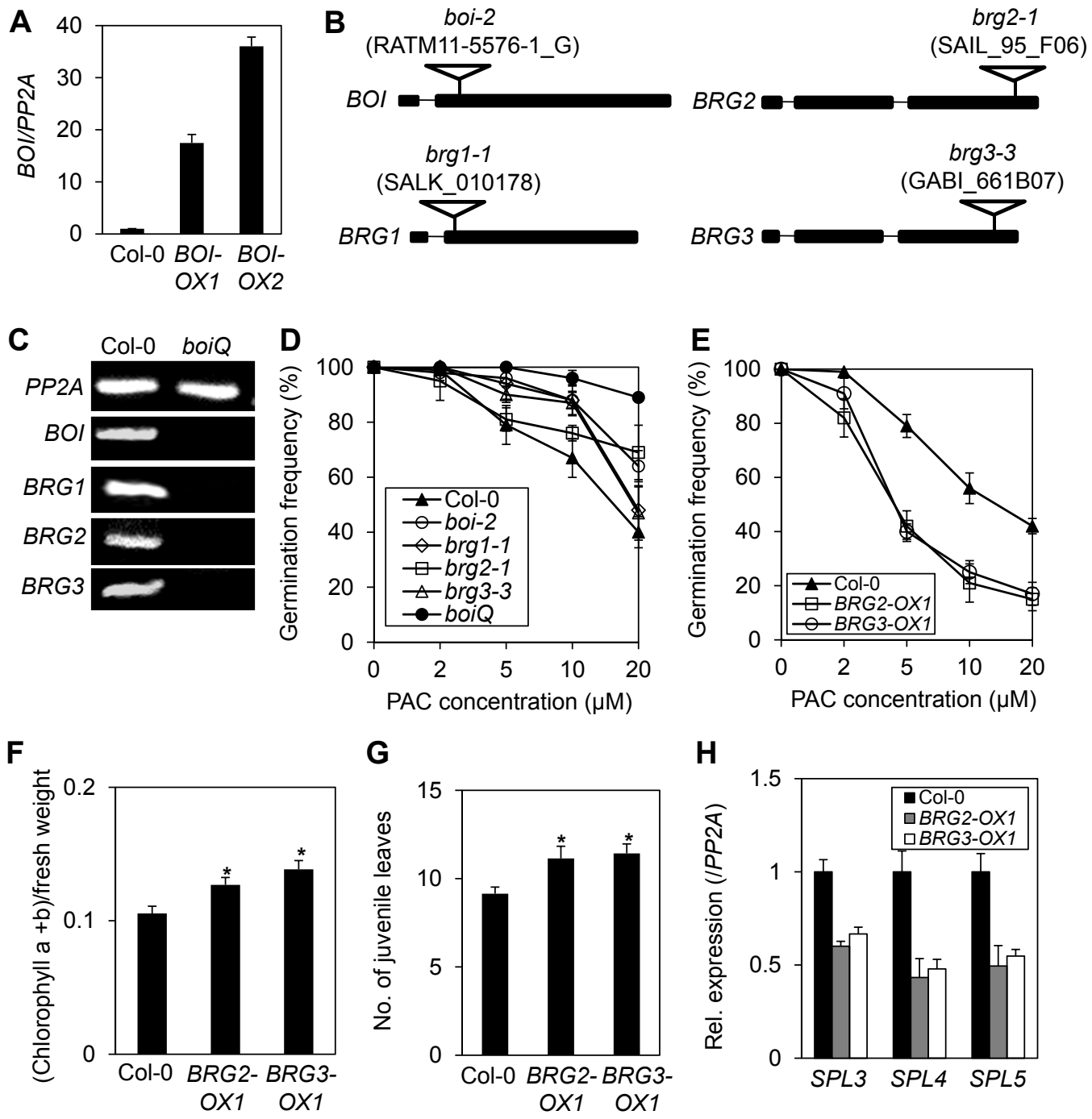
B



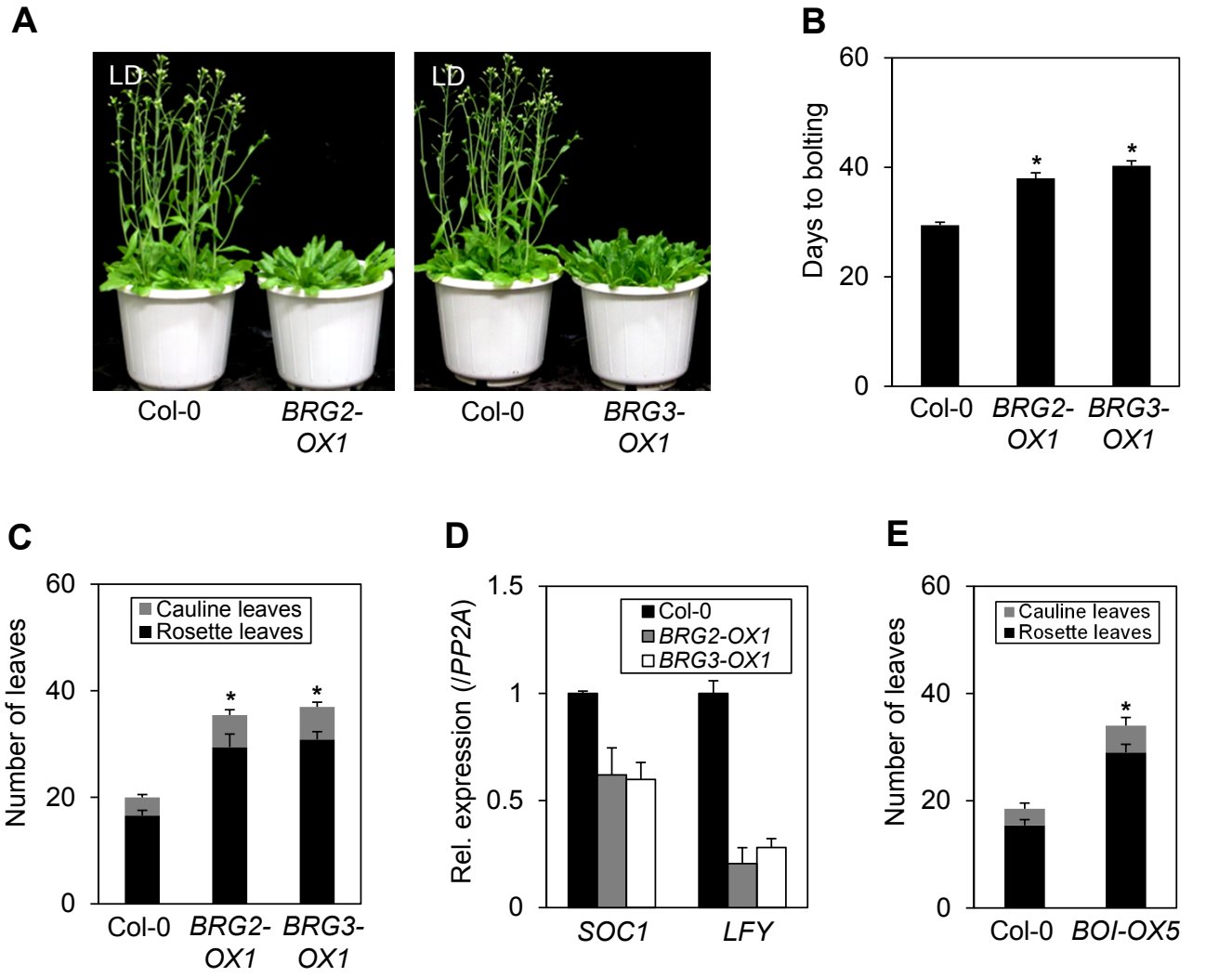
Supplemental Figure 1. Amino acid alignment of the four BOIs (A) and a neighbor-joining tree showing the relationships among the BOIs and their *Arabidopsis* and rice homologs (B). Sequence alignment was generated by Clustal W multiple alignment tool of BioEdit (www.mbio.ncsu.edu/bioedit/bioedit.html) and the phylogenetic tree was generated by MEGA5 program (www.megasoftware.net). The evolutionary distances were computed using the Poisson correction method. The scale bar indicates the evolutionary distance of 0.1 amino acid substitution per position.; * indicates zinc-coordinating Cys or His residues.



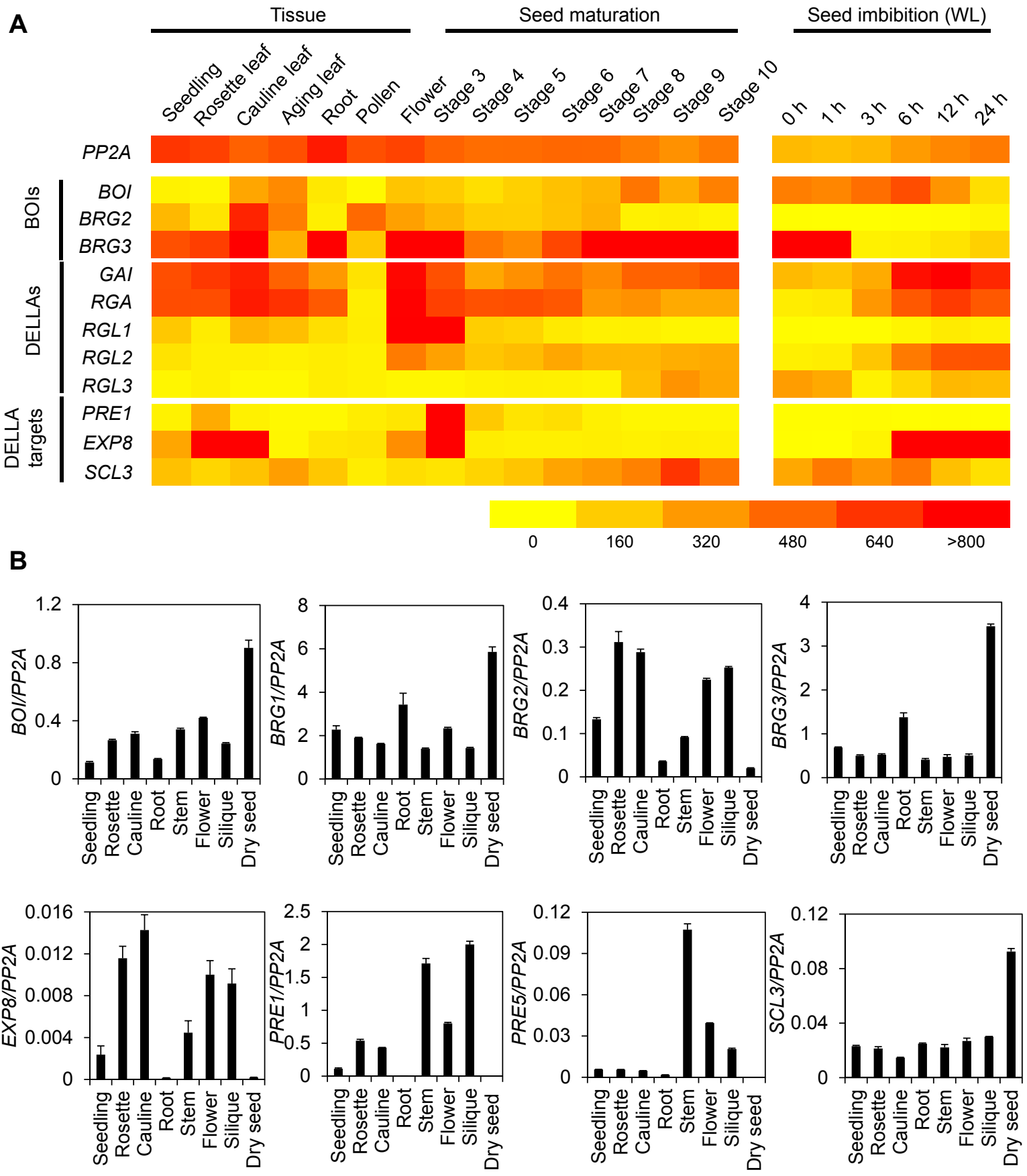
Supplemental Figure 2. The specificity of RGA antibody. 7-day-old white light-grown seedlings of the *rga-28* and Col-0 were used for the analysis of RGA antibody.



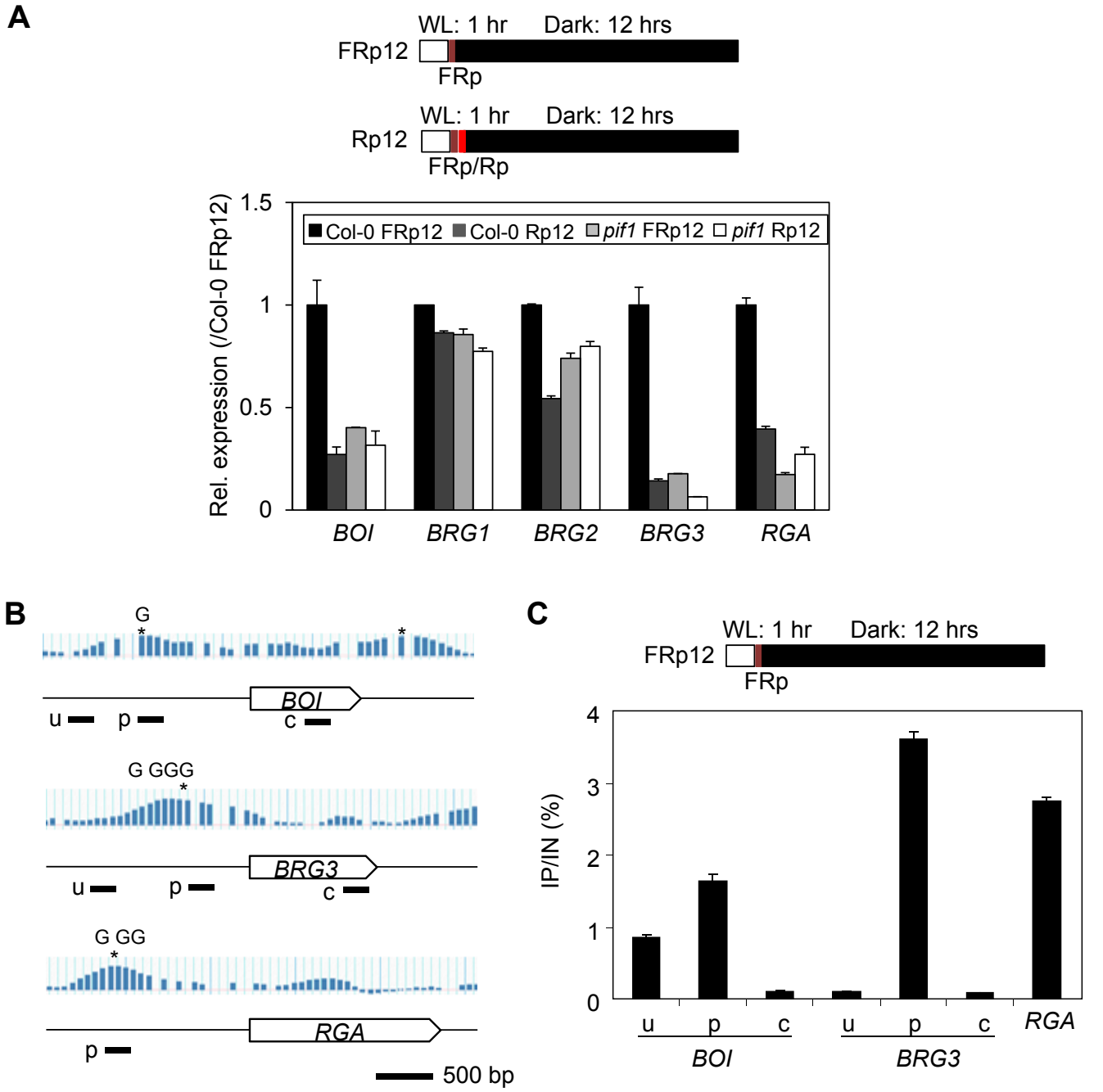
Supplemental Figure 3. BOI family members redundantly inhibit GA responses. (A) *BOI* mRNA expression levels in the two *BOI*-overexpressing lines. *BOI* mRNA levels (endogenous + transgenic) were determined in 7-day-old seedlings grown under LD (SD, n=3). (B) T-DNA insertion mutants of *BOI* family members. Exons are indicated by filled rectangles and T-DNAs are by inverted triangles. (C) The full-length *BOI* mRNAs are not detected in the *boi* quadruple mutant (*boiQ*) seedlings, as determined by RT-PCR. (D) Germination frequencies of single and quadruple mutants of *BOI* family members in the presence of PAC (SD, n=3). (E) Decreased germination frequencies of *BRG2*- and *BRG3*-overexpressing lines in the presence of PAC (SD, n=3). (F) Increased chlorophyll accumulation by *BRG2*- and *BRG3*-overexpressing lines (SD, n=6; *, $p<0.05$, Student's t-test). (G) Delayed juvenile-to-adult phase transition in *BRG2*- and *BRG3*-overexpressing lines (SD, n=10; *, $p<0.05$, Student's t-test). (H) Decreased expression of *SPL* mRNAs in *BRG2*- and *BRG3*-overexpressing lines. 17-day-old plants were sampled for expression analysis at the 12th hour of light (SD, n=3 biological replicates).



Supplemental Figure 4. Overexpression of *BRGs* inhibit flowering and mRNA expression of *SOC1* and *LFY*. (A) Delayed flowering in *BRG2*- and *BRG3*-overexpressing plants under the LD condition. Pictures were taken at 5 weeks. (B) Quantification of bolting days in *BRG2*- and *BRG3*-overexpressing plants under the LD condition (SD, n=10; *, $p<0.05$, Student's t-test). (C) Quantification of rosette leaves and cauline leaves in *BRG2*- and *BRG3*-overexpressing plants under the LD condition (SD, n=10; *, $p<0.05$, Student's t-test). (D) Decreased expression of *SOC1* and *LFY* mRNAs in *BRG2*- and *BRG3*-overexpressing lines under the LD condition. 17-day-old plants were sampled for expression analysis at the 12th hour of light (SD, n=3 biological replicates). (E) Quantification of rosette leaves and cauline leaves in *BOI-OX5* plants under the LD condition (SD, n=10; *, $p<0.05$, Student's t-test).



Supplemental Figure 5. Expression patterns of *BOI*s, *DELLA*s, and their target genes analyzed by the BAR expression browser and visualized by the BAR heatmapper tool (http://bar.utoronto.ca) (A) or by quantitative RT-PCR (SD, n=3) (B).



Supplemental Figure 6. Direct regulation of *BOI* and *BRG3* expression by PIF1. (A) Repression of *BOI* and *BRG3* mRNA expression by PIF1 during seed germination. Upper diagrams indicate light irradiation scheme for FRp12 and Rp12. Each mRNA level is presented relative to that of Col-0 FRp12 (SD, n=3). (B) Diagrams showing PIF1 ChIP-Chip signals around *BOI*, *BRG3*, and *RGA*. Vertical blue bars indicate PIF1 signal intensities; * indicates a PIF1 binding site; G indicates G-box elements; and underlines with u, p, and c indicate the amplicons used for ChIP-PCR. (C) Enrichment of *BOI* and *BRG3* promoter fragments by PIF1 ChIP-PCR. The upper diagram indicates light irradiation scheme. The *RGA* promoter was used as a PIF1-binding positive control (SD, n=3).

Supplemental Table 1. Primers used in this study.

Name	Forward primer	Restriction site	Reverse primer	Restriction site	Purposes
pETM_MCS	TATGACTAGTTCTAGAGAATTCCCCGGGCCTAGGCTC GAGTCGGATCCCGTCGACA	SpeI-XbaI-EcoRI-XmaI-AvrII-XhoI-BamHI-SalI	TCGATGTCGACGGGATCCGACTCGAGCCTAGGCCCGGG GAATTCTCTAGAACTAGTCA		Adapter ligation pET29a: NdeI/XhoI
pGADM_MCS	//	//	//		Adapter ligation pGADT7: NdeI/XhoI
pGBKM_MCS	//	//	//		Adapter ligation pGBKT7: NdeI/SalI
pMALM_MCS	AATTGTCTAGAGAATTCCCCGGGCCTAGGCTCGAGTC GGATCCCG	XbaI-EcoRI-XmaI-AvrII-XhoI-BamHI-SalI	TCGACGGGATCCGACTCGAGCCTAGGCCCGGGGAATTCT CTAGAC		Adapter ligation pMAL-c2X: EcoRI/SalI
phNIL_MCS	CTAGAACTAGTCCCGGGCCTAGGCTCGAGTCGGATCC CGTCGACTAATTGATTAAGAGCT	XbaI-SpeI-XmaI-AvrII-XhoI-BamHI-SalI-SacI	CTTAATCAATTAGTCGACGGGATCCGACTCGAGCCTAGG CCCGGGACTAGTT		Adapter ligation pCAMBIA1300: XbaI/SacI
3XFLAG	GTGTACTAGTatgGGAGGTGGCAGCGTCGAGATGG	SpeI	GGGTCTAGACCCCCCCTCGACTTTATCGTCA	SmaI	phNF construction
BOI	GTGTCCTAGGatgGCTGTTCAAGCTCATCACATG	AvrII	GTGTGGATCCGGAGAAGACATGTTAACATGCACA	BamHI	Cloning
BRG1	GTGTGTTCTAGAatgGCTGTTGAAGCAAGACACA	XbaI	GTGTGTGTCGACTGATGACATGTTAACATGTACA	SalI	Cloning
BRG2	GTGTGTTCTAGAatgGCCGTCGATGCTCACCATC	XbaI	GTGTGTGTCGACAGATGACATGTTGACATGAACG	SalI	Cloning
BRG3	GTGTGAATTCatgGCCGTTGAAGCTCACCATCTA	EcoRI	GTGTCTCGAGAGAGGAAAGATTAACATGTAGACT	XhoI	Cloning
BOIdC	GTGTCCTAGGatgGCTGTTCAAGCTCATCACATG	AvrII	GTGTGGATCCAGCGGTTGGAAACGTTTCGAGT	BamHI	Cloning
RGA	GAGTCTAGAatgAAGAGAGATCATCACCAAT	XbaI	GAGGGATCCCCGTACGCCGCCGTCGAG AG	BamHI	Cloning
GAI	GAGTCTAGAatgAAGAGAGATCATCATCATC	XbaI	GAGGGATCCCCATTGGTGGAGAGTTTCCA	BamHI	Cloning
RGL1	GAGTCTAGAatgAAGAGAGAGCACAACCA	XbaI	GAGGGATCCCCTTCCACACGATTGATTCG	BamHI	Cloning
RGL2	GAGCCTAGGatgAAGAGAGGATACGGAG	AvrII	GAGAGATCTCCGGCGAGTTTCCACGCCGA	BglII	Cloning
RGL3	GTGTACTAGTatgAAACGAAGCCATCAAGAAACG	SpeI	GTGTGTCGACCCGCCGCAACTCCGCCGCTAGTTT	SalI	Cloning
boi-2	ATGGCTGTTCAAGCTCATCACAT		AGAAGACATGTTAACATGCAC		Genotyping
brg1-1	TAAATAGCATTTATGCACGGG		CGCCAGATCTGATTCTCTACG		Genotyping
brg2-1	CGTCTGTCTTCCACGCTCTAC		ACGTAAGTTTTGCATCAACGG		Genotyping
brg3-3	AATCCCACCGATCCTCTTATG		TCAAGCTTGTGAAAAGTGACG		Genotyping
BOI	TGCTCAACTCGAAACGTTTCC		ACCAACACACTCGCTTCTCTC		RT-qPCR
BRG1	CGTCGTCCTTTGGTTGAAGAAGC		AGCCGACGATCCACAAACCGTA		RT-qPCR
BRG2	GAACGAAGAGGACGATGCGGA		TCCTCCCCACAGTTTCTACACA		RT-qPCR
BRG3	GAGGCGCAGGATACGAAAAAGATG		CTAAGAGGAAAGATTAACATGTAG		RT-qPCR
SOC1	TCGCCAGCTCCAATATGCAAGATAC		CGATTGAGCATGTTCCTATGCCTTC		RT-qPCR
LFY	TACGCTCTCCACTGCCTAGAC		AGACGGCGTCTATATCCCAGC		RT-qPCR
SPL3	TGAGAAGAAGCAAAGCGGAA		TATCCGCGGTACAACTCTCG		RT-qPCR
SPL4	GTAGCATCAATCGTGGTGGC		CTTCGCTCATTGTGTCCAGC		RT-qPCR
SPL5	ATGCAGCAGGTTTCATGAGC		GCCTGACCCTTCTCCAAAAC		RT-qPCR
EXP8	CATGTATGAAGAAAGGAGGAATAAG		AACTGCCAATTAGAAGGAGCCACG		RT-qPCR
PRE1	CAGCCTCGAAAGTATTGCAAG		TTCTAATAACGGCGGCTTCAG		RT-qPCR
PRE5	TCGAATGCTTCGAGGATCTCC		CAGAGTCAAGAAGCTGCGACA		RT-qPCR
SCL3	CAGCTGAGGCACGTGAGAATGAT		ACCACCATGACCTTTGGAGACAAAC		RT-qPCR
PP2A	TATCGGATGACGATTCTTCGTGCAG		GCTTGGTCGACTATCGGAATGAGAG		RT-qPCR
BOIu	TTGCTACTTGCGAATTACTTGC		TCTTTTGACTCGTATCTCGTC		ChIP-qPCR
BOIp	CACGCTTCTCACGTGCAACTTA		GCCATGTCATCTTCCACCGT		ChIP-qPCR
BOIc	TGCTCAACTCGAAACGTTTCC		ACCAACACACTCGCTTCTCTC		ChIP-qPCR
BRG3u	ATGGAGCTGACTTGATTGGTT G		ATGACCTATGTGAGACTGTGAC		ChIP-qPCR
BRG3p	GTCCTCCAACGGATAAGCAAG		GGCTCATGTGACAAGACTTGC		ChIP-qPCR
BRG3c	GAGGCGCAGGATACGAAAAAGATG		CTAAGAGGAAAGATTAACATGTAG		ChIP-qPCR
EXP8	CCCATTCCTTCCATTTGTAGATTC		GGAGGAATAATACGGATATAATTG		ChIP-qPCR
PRE1	CTCTCTTGTGGTCCATTGGCCTA		ATCGGCTATGTCTATGTGGCAAG		ChIP-qPCR
PRE5	TCGGATCAACCACAAACTTCCTAG		GTGCATGTCACTAAAAGGCAATAC		ChIP-qPCR
SCL3	GCCTCAGCCTCATCTCTTTT		GGAATCATGACTATATATTTCTACATCA		ChIP-qPCR
PIL1	ATGAATCACGCGGCATTC		ACGTGAGCGGAAAGAACC		ChIP-qPCR
RGA	GTGACGTAACATGACAATATAACAT		CTAAAACGGTAGGGACCGAGTCTG		ChIP-qPCR

* Underlined are restriction enzyme sites. Start codon (atg) is in lowercase.

Supplemental Table 2. Vectors used in this study.

Name	Transgenic lines and protein name	Plant selection	Usage
phNF-BOI	*BOI-OX3*, *BOI-OX4*, FLAG-BOI	Hygromycin	Transgenic, transient
pbFLAG2-BOI	*BOI-OX5*	Phosphinothricin	Transgenic
pBARH8-BOI	*BOI-OX1*, *BOI-OX2*	Phosphinothricin	Transgenic
phNF-BRG2	*BRG2-OX1*	Hygromycin	Transgenic
phNF-BRG3	*BRG3-OX1*	Hygromycin	Transgenic
phNF-BOIdC	*BOIdC-OX1*, *BOIdC-OX2*	Hygromycin	Transgenic
pbFLAG2-GFP	*GFP-OX*	Phosphinothricin	Transgenic
phNF-GFP	FLAG-GFP	Hygromycin	Transient
pMALM-RGA	MBP-RGA	n/a	Pull-down
pMALM-GAI	MBP-GAI	n/a	Pull-down
pMALM-RGL2	MBP-RGL2	n/a	Pull-down
pETM-BOI	BOI-His	n/a	Antibody production
pGADM-RGA	AD-RGA	n/a	Yeast two-hybrid
pGADM-GAI	AD-GAI	n/a	Yeast two-hybrid
pGADM-RGL1	AD-RGL1	n/a	Yeast two-hybrid
pGADM-RGL2	AD-RGL2	n/a	Yeast two-hybrid
pGADM-RGL3	AD-RGL3	n/a	Yeast two-hybrid
pGBKM-BOI	BD-BOI	n/a	Yeast two-hybrid
pGBKM-BRG1	BD-BRG1	n/a	Yeast two-hybrid
pGBKM-BRG2	BD-BRG2	n/a	Yeast two-hybrid
pGBKM-BRG3	BD-BRG3	n/a	Yeast two-hybrid

* n/a : not applicable.