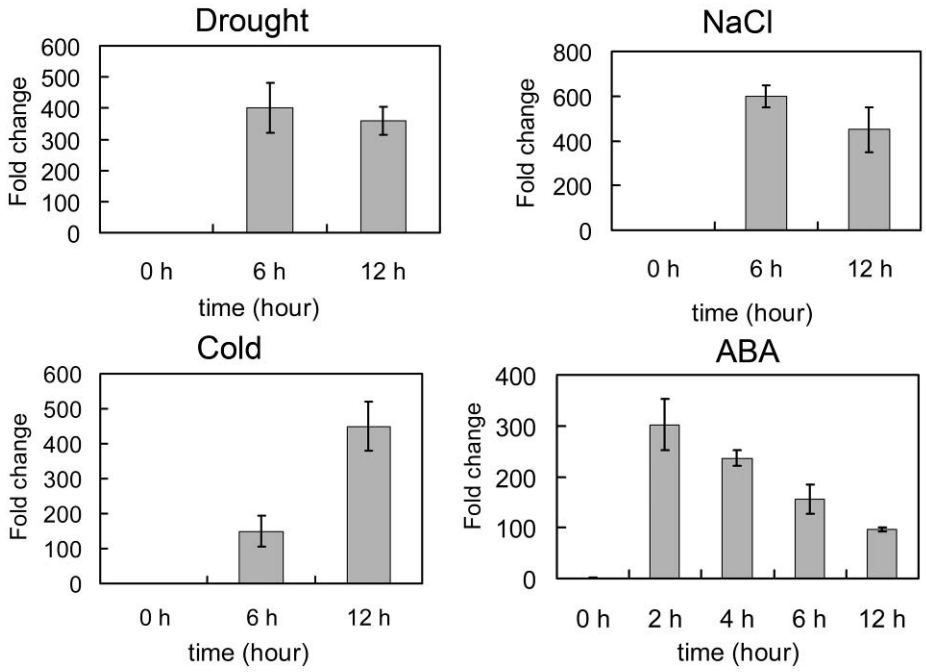
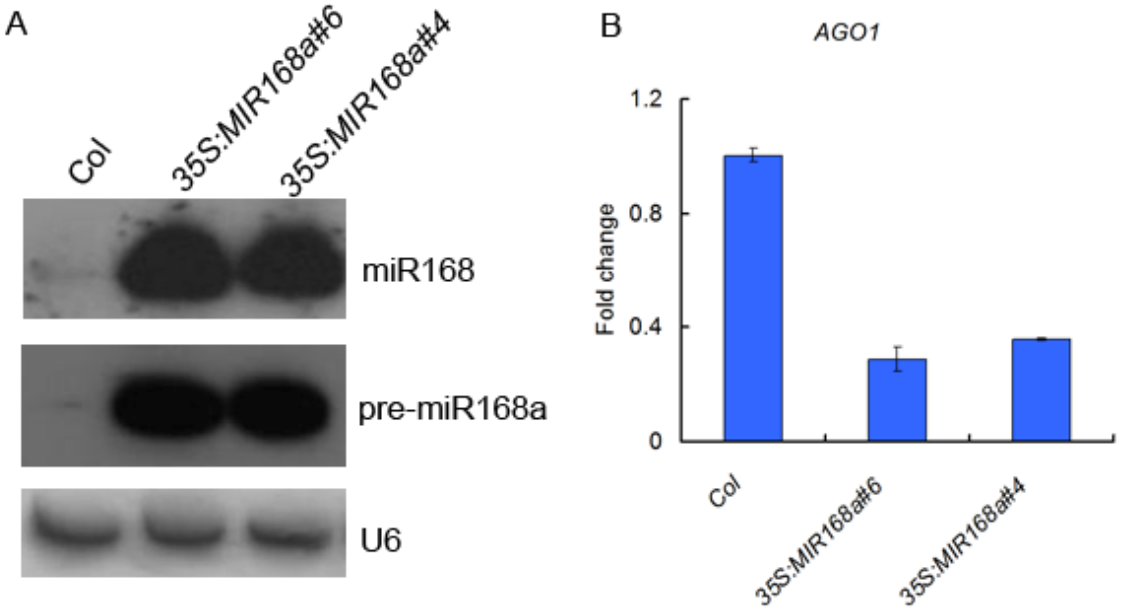
SUPPLEMENTAL DATA

Fig.S1



Supplemental Figure 1. qRT-PCR analysis of *RD29A* mRNA under ABA and abiotic stress treatments. The expression levels were normalized to that of *TUBULIN4*, and the expression level in the wild type (Col) without any treatment was set to 1.0. These experiments were repeated three times independently and error bars denote SD.

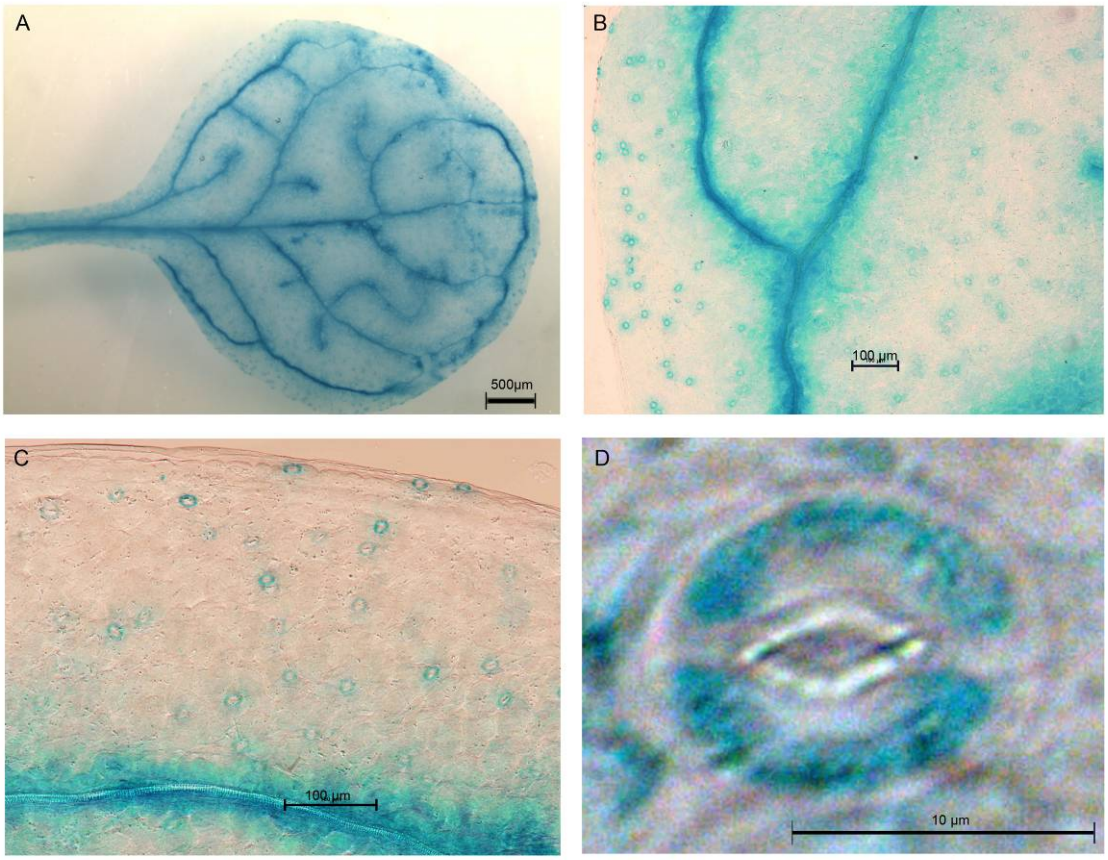
Fig.S2



Supplemental Figure 2. Expression analysis of mature miR168, pre-miR168a and *AGO1* mRNA in the wild type (Col) and *MIR168a* overexpression lines.

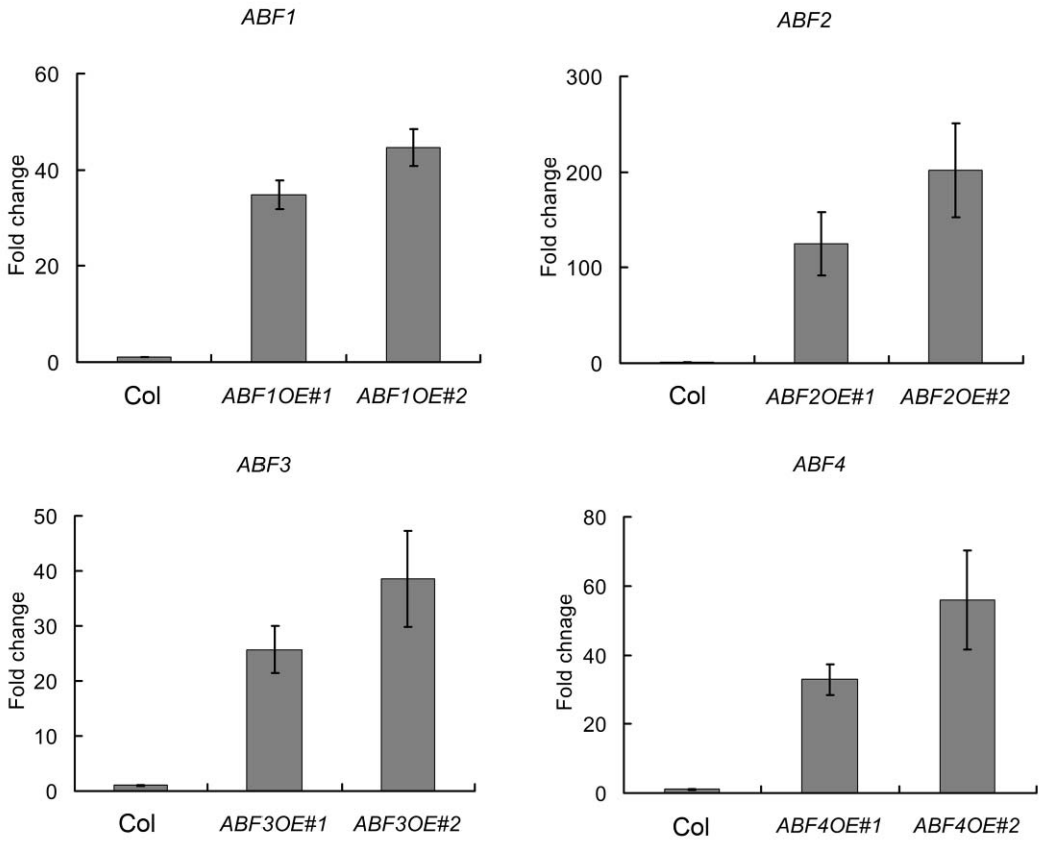
(A) Northern blot analysis of mature miR168 and pre-miR168a expression in the wild type (Col) and *MIR168a* overexpression lines. (B) qRT-PCR analysis of *AGO1* mRNA in the wild type (Col) and *MIR168a* overexpression lines. The expression levels were normalized to that of *TUBULIN4*, and the expression level in the wild type (Col) was set to 1.0. These experiments were repeated three times independently and similar results were observed. Error bars denote SD.

Fig.S3



Supplemental Figure 3. Histochemical GUS staining in the guard cells of *pMIR168a:GUS* transgenic plants.

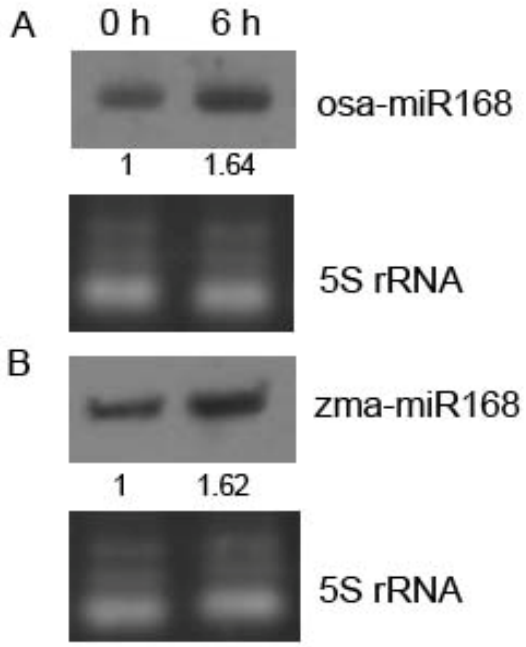
Fig.S4



Supplemental Figure 4. qRT-PCR analysis of *ABF1, ABF2, ABF3* and *ABF4* transcript levels in overexpression lines.

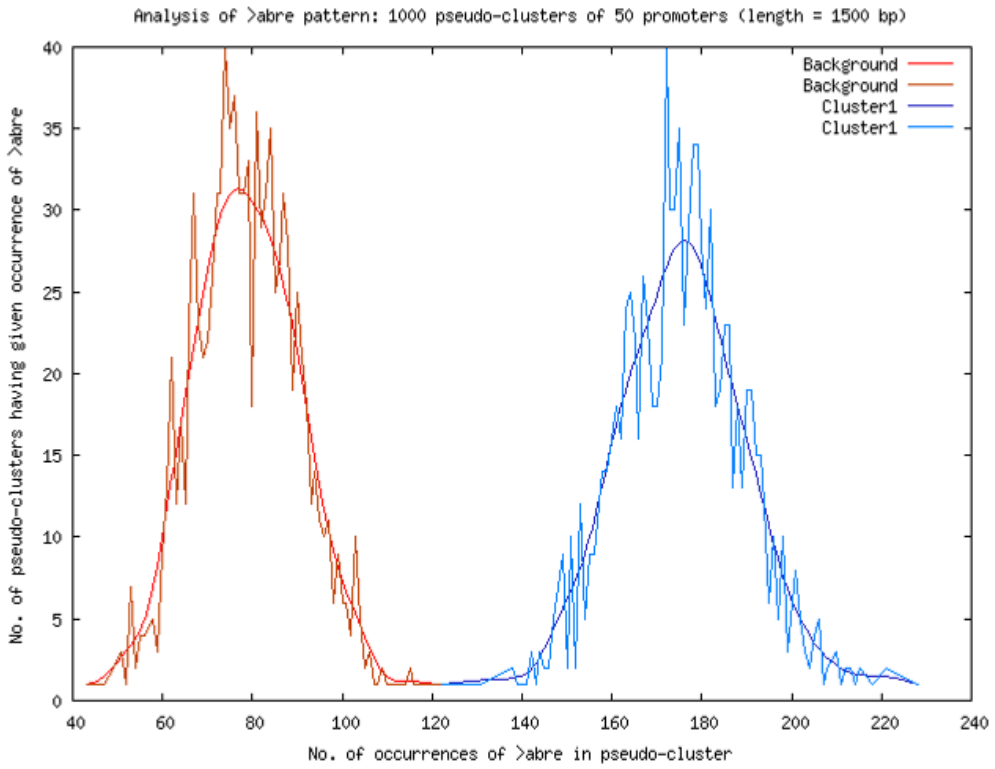
The data show that the expressions of *ABF1* (A), *ABF2* (B), *ABF3* (C) and *ABF4* (D) were enhanced in these transgenic lines, respectively. The expression levels were normalized to that of *TUBULIN4*, and the expression level in the wild-type (Col) was set to 1.0. These experiments were repeated three times independently and error bars denote SD.

Fig. S5



Supplemental Figure 5. Northern blot analysis of mature miR168 in 2-week-old seedlings of (A) *Oryza sativa* and (B) *Zea mays* with or without ABA treatment. These experiments were repeated three times and similar results were observed. Numbers below the blot figures show the relative abundance compared to the control of 5S rRNA, the level of each target in non-treated wild type was set to 1.

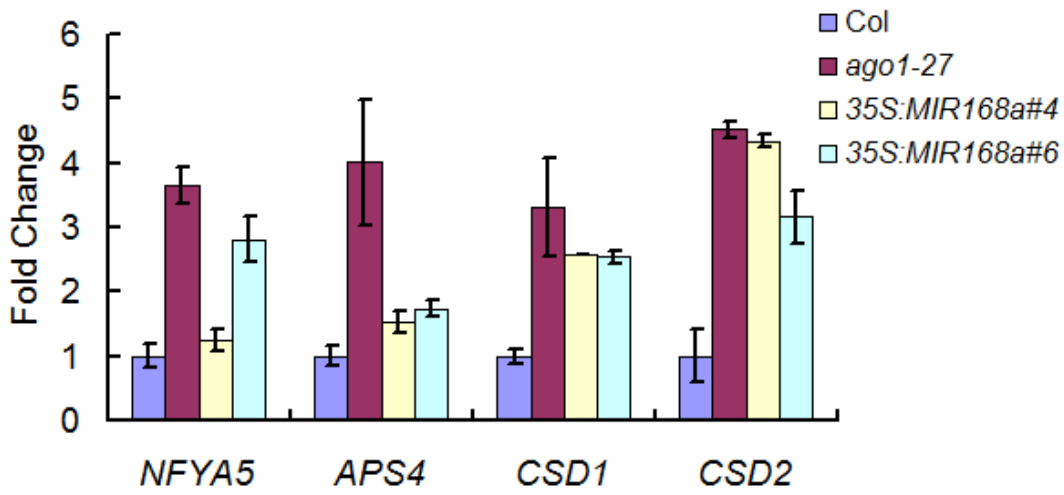
Fig. S6



Supplemental Figure 6. POBO output interface.

We performed the ABRE scan in every known promoter in the genome of *Arabidopsis* which was considered to be the background data in POBO.

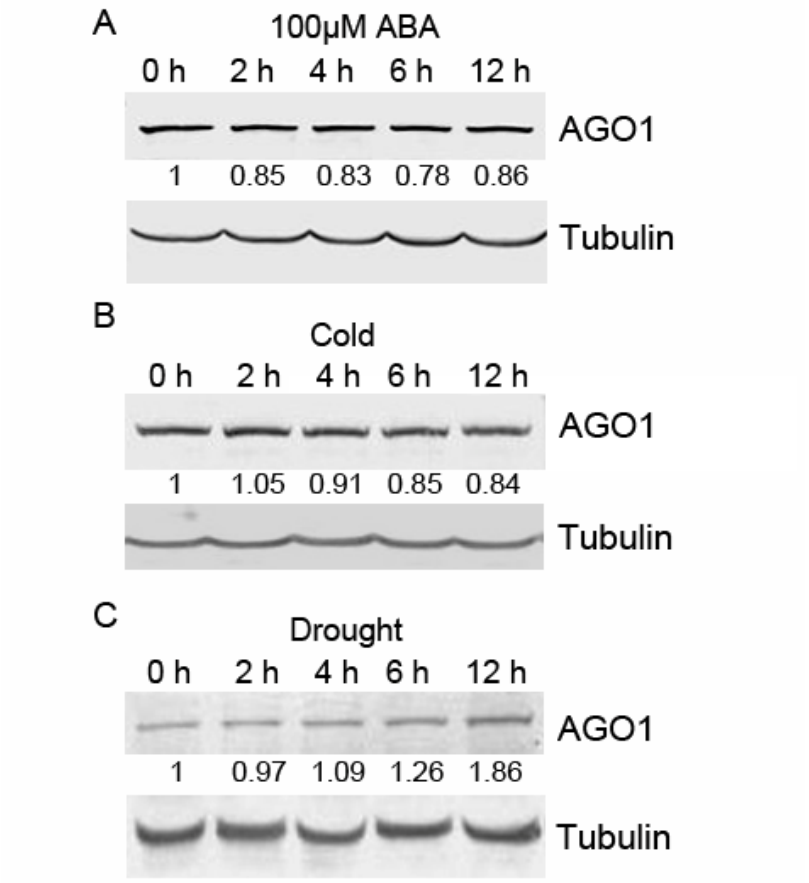
Fig. S7



Supplemental Figure 7. qRT-PCR analysis of miRNA targets in *ago1-27* and *35S:MIR168a* lines.

To confirm the data of the previous microarray analysis, the expressions of selected targets involved in ABA or stress response were determined by qRT-PCR in *ago1-27* and *35S:MIR168a* lines. The expression levels were normalized to that of *TUBULIN4*, and the expression level in the wild type (Col) was set to 1.0. These experiments were repeated three times independently and error bars denote SD.

Fig. S8



Supplemental Figure 8. Western Blot analysis of AGO1 in response to ABA, cold and drought.

Compared with the non-treated control, AGO1 protein level displays only subtle changes in response to ABA (A) and cold (B), and a slight increase under the drought treatment (C). These experiments were repeated three times and similar results were observed. Numbers below the blot figures show the relative abundance compared to the control β-Tubulin, and the level of AGO1 in non-treated wild type was set to 1.

Supplemental Table 1. Putative miR168 in 15 species.

Supplemental Table 2. 2Kb upstream sequences of *MIR168* in 10 species.

Supplemental Table 3. The putative transcription start sites of *MIR168* genes.

Supplemental Table 4. Candidate ABRE sites in the promoters of *MIR168* genes.

Supplemental Table 5. Primers and probers used in this article.