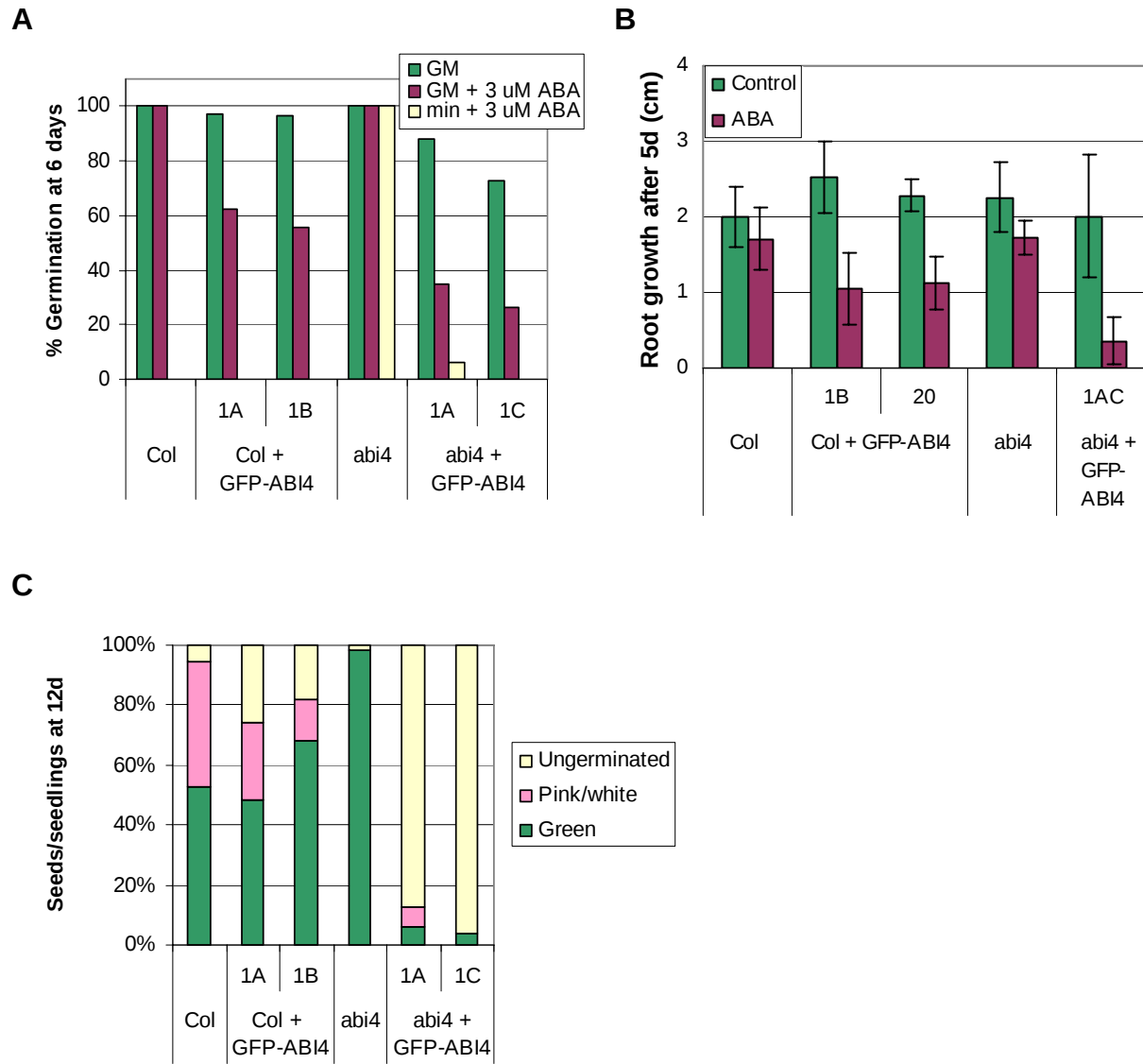


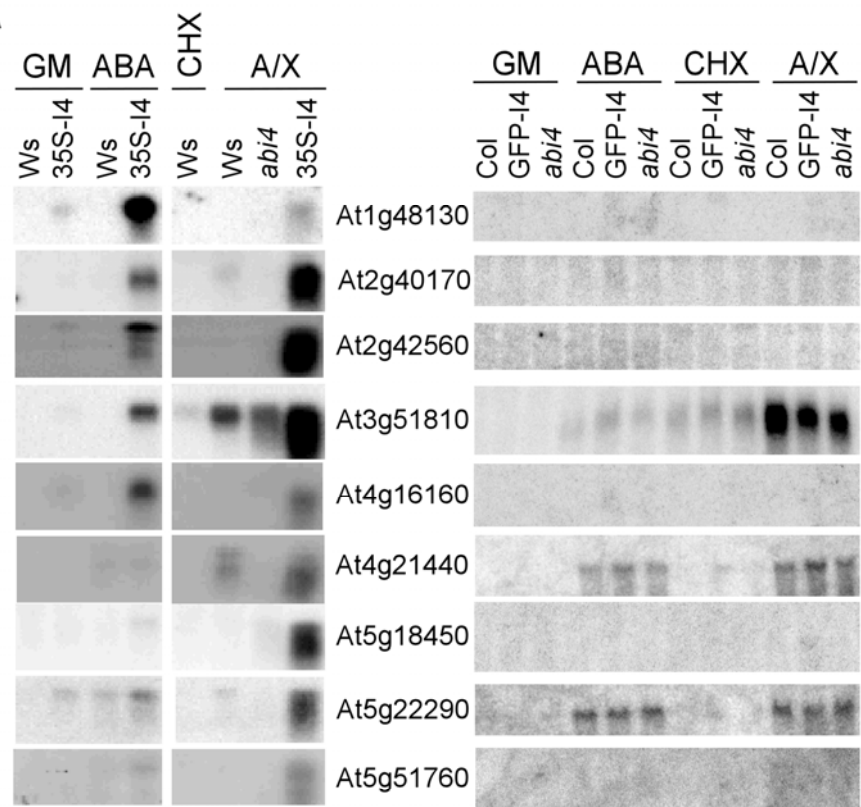


Supp. Fig. 1. Functional tests of 35S:GFP:ABI4 transgene, scoring enhanced ABA sensitivity in wild-type Col background and complementation of ABA resistance due to *abi4-1* mutation. (A) Germination (radicle emergence) at 6 days post stratification on the indicated media. (B) Root growth of seedlings transferred at 2d post stratification from GM to fresh GM with or without 3 μ M ABA, scored after an additional 5d growth. (C) Sugar sensitivity of seedling growth, as reflected in reduced growth and increased anthocyanin accumulation on minimal medium supplemented with 4% Glc.

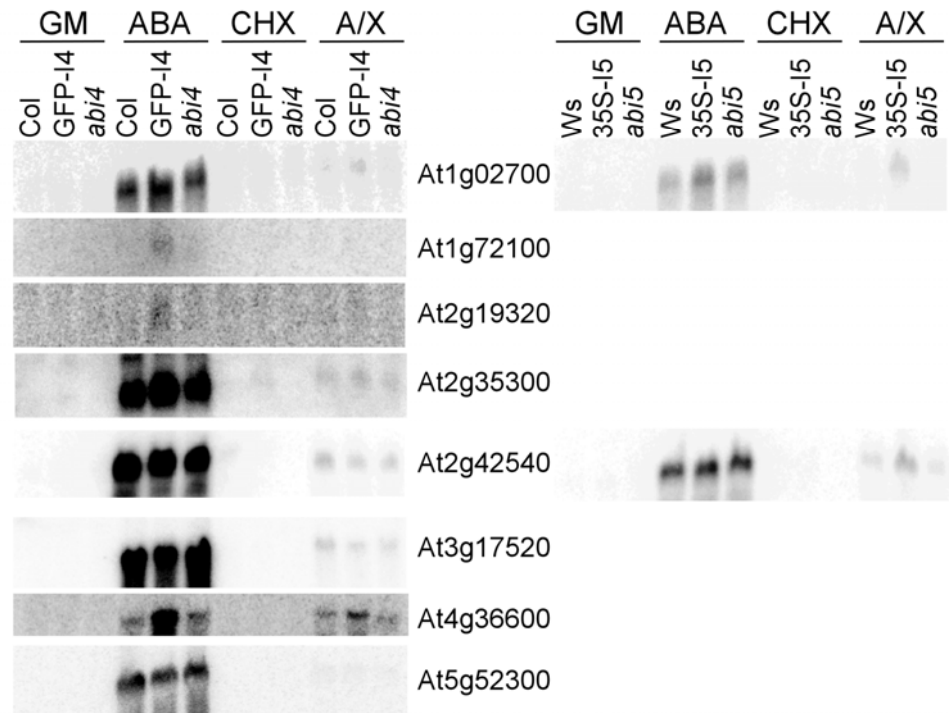
The 1B line of Col + 35S:GFP:ABI4 was used for subsequent studies of gene expression. Note that, although more sensitive to ABA than the wild-type line, this is much less sensitive than the previously reported 35S:ABI4 line #114A, which showed complete inhibition of root growth by 3 μ M ABA (Söderman et al. 2000) and strong Glc hypersensitivity (Finkelstein et al. 2002).

Supplemental Figure 2

A

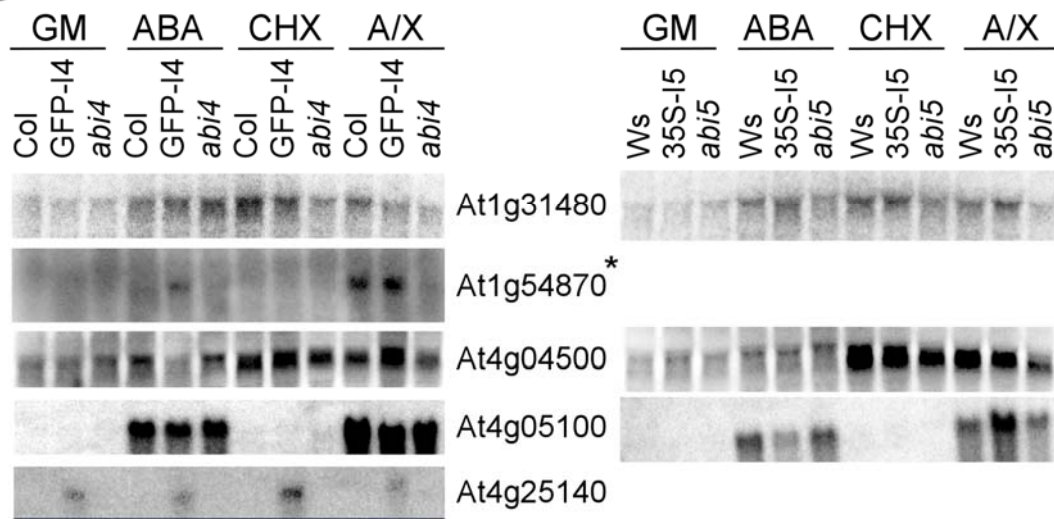


B



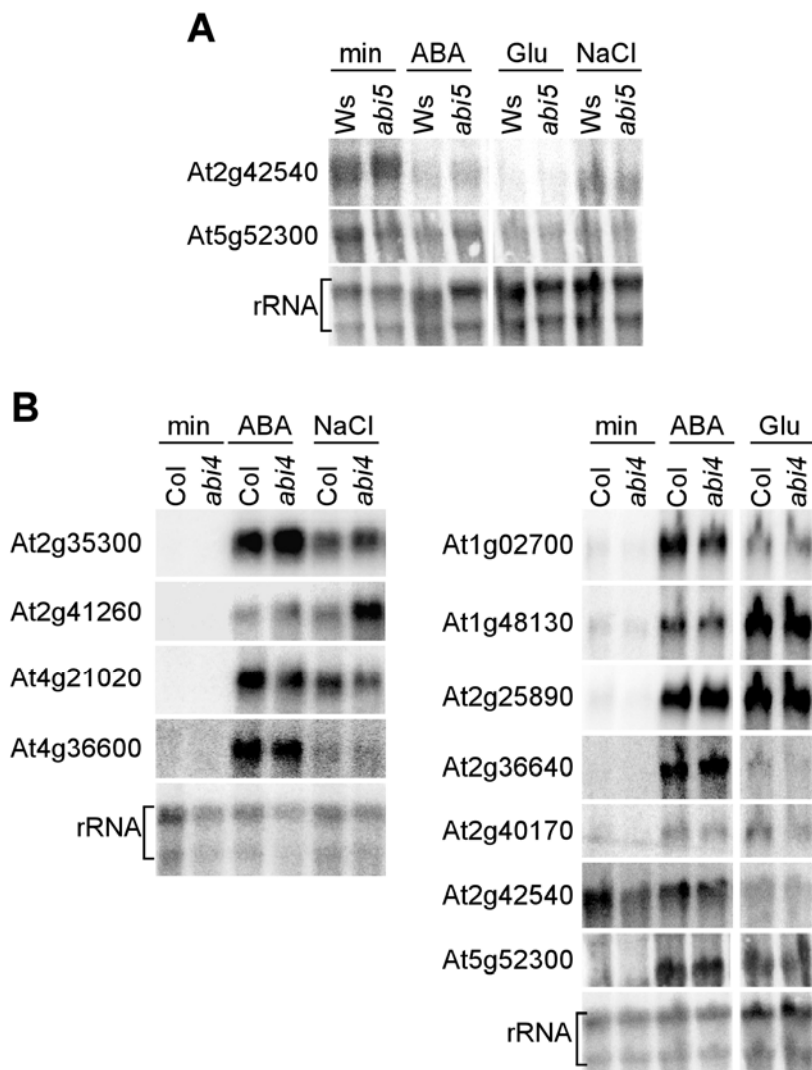
Supplementary Fig 2 cont

C

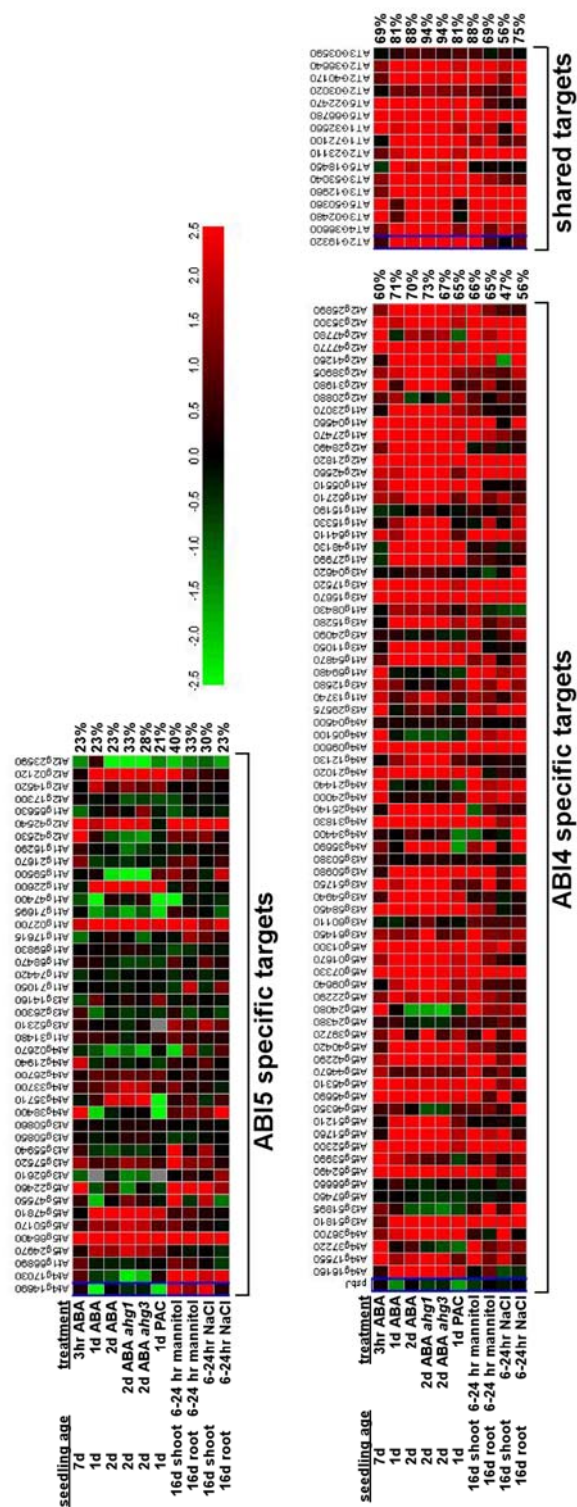


Supp. Fig. 2. RNA gel blot tests of ectopic ABI-dependent ABA induction A) Certain ABI4 targets are only induced in original 35S-ABI4 lines. Seeds were germinated for 11 days on GM media, then transferred for four hours to GM media with or without 50 μ M ABA (ABA), 20 μ M cycloheximide (CHX) or both ABA and cycloheximide (A/X). Seedlings were harvested, RNA was extracted and transcripts were analyzed by Northern blot. Overexpression lines included the original 35S-ABI4 line (35S-I4, on left) and the 35S-GFP-ABI4 line (GFP-I4, on right). B) Indirect targets of ABA/ABI induction. Transcripts were analyzed as described in (A). C) Genes whose induction is not dependent on ABA treatment and/or ABI overexpression. Asterisks indicate genes in (C) whose expression matches microarray results.

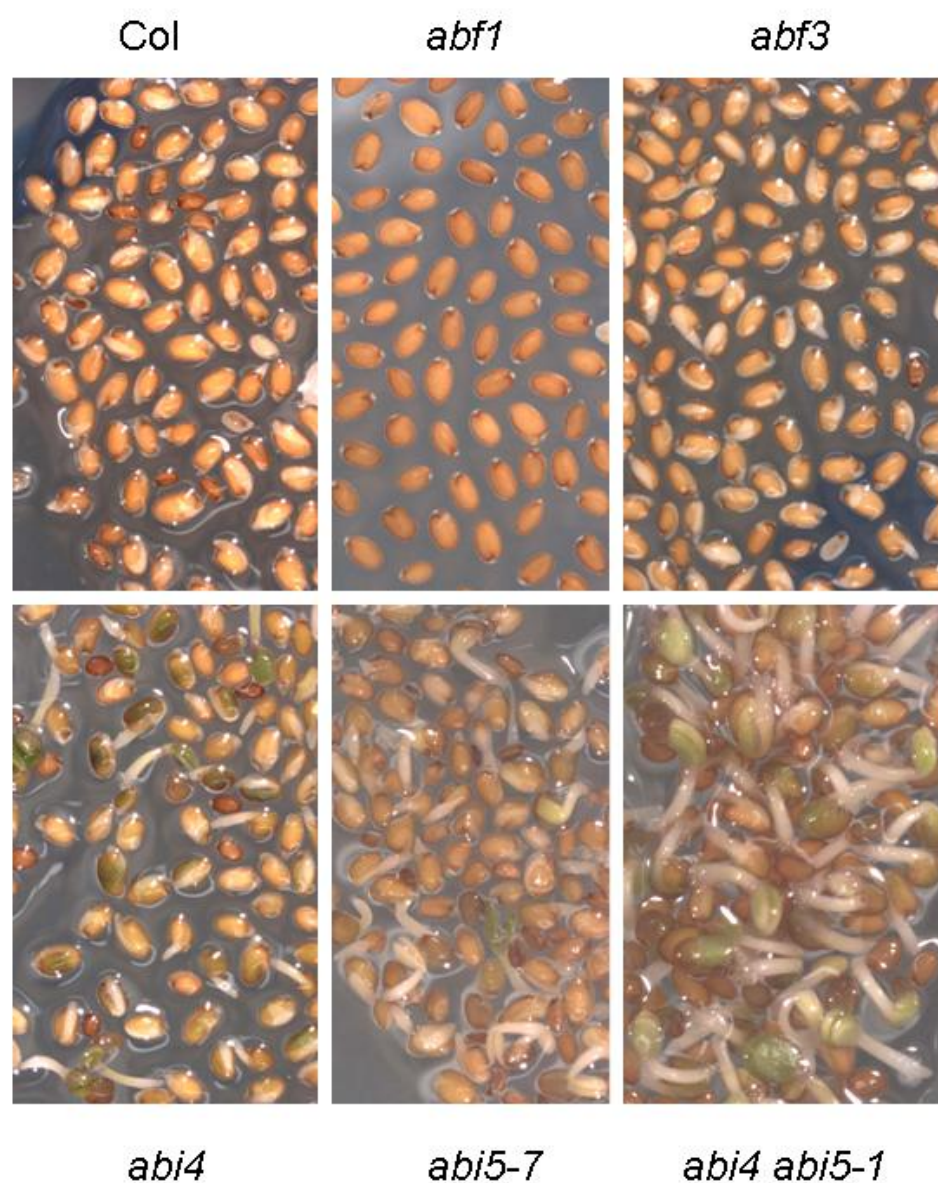
Supplementary Figure 3



Supp. Fig. 3. RNA gel blot tests of ABA- and stress-regulated gene expression at 1d post stratification. Genes showing minimal or no change between wild type and *abi* response to ABA or stress.

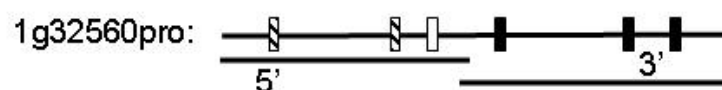
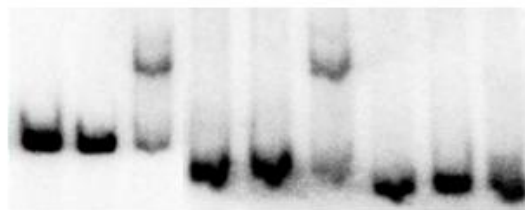


Supp. Fig. 4. Co-regulation of ABI4 target set, but not ABI5 target set by ABA and stress treatments. Genevestigator (Hruz et al. 2008) was used to analyze previously published microarrays. For each condition, the percent of genes in a target set that were induced at least two fold is indicated.

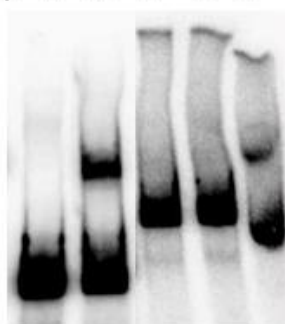


Supplementary Figure 5. Germination and seedling growth of *abi*, *abf* monogenic and double mutant lines. Comparison of wild-type, *abi4*, *abi5-7*, *abf1*, *abf3*, and *abi4 abi5-1* seeds after 3d post-stratification on GM supplemented with 5 μ M ABA.

1g32560pro:	Full			5'			3'		
GST	-	+	-	-	+	-	-	+	-
GST-ABI4	-	-	+	-	-	+	-	-	+



4g16160pro:	5'Hf		3'Dde		
GST	-	-	-	+	-
GST-ABI4	-	+	-	-	+



CCAC
 CACCG (CE1-like)
 YACGTG (ABRE)

Supplementary Fig. 6. ABI4 binding sites within promoter fragments. Binding is limited to portion of At1g32560 promoter containing consensus ABI4 binding site identified in maize. At4g16160 promoter does not include any known ABI4 binding sites, but does bind ABI4.