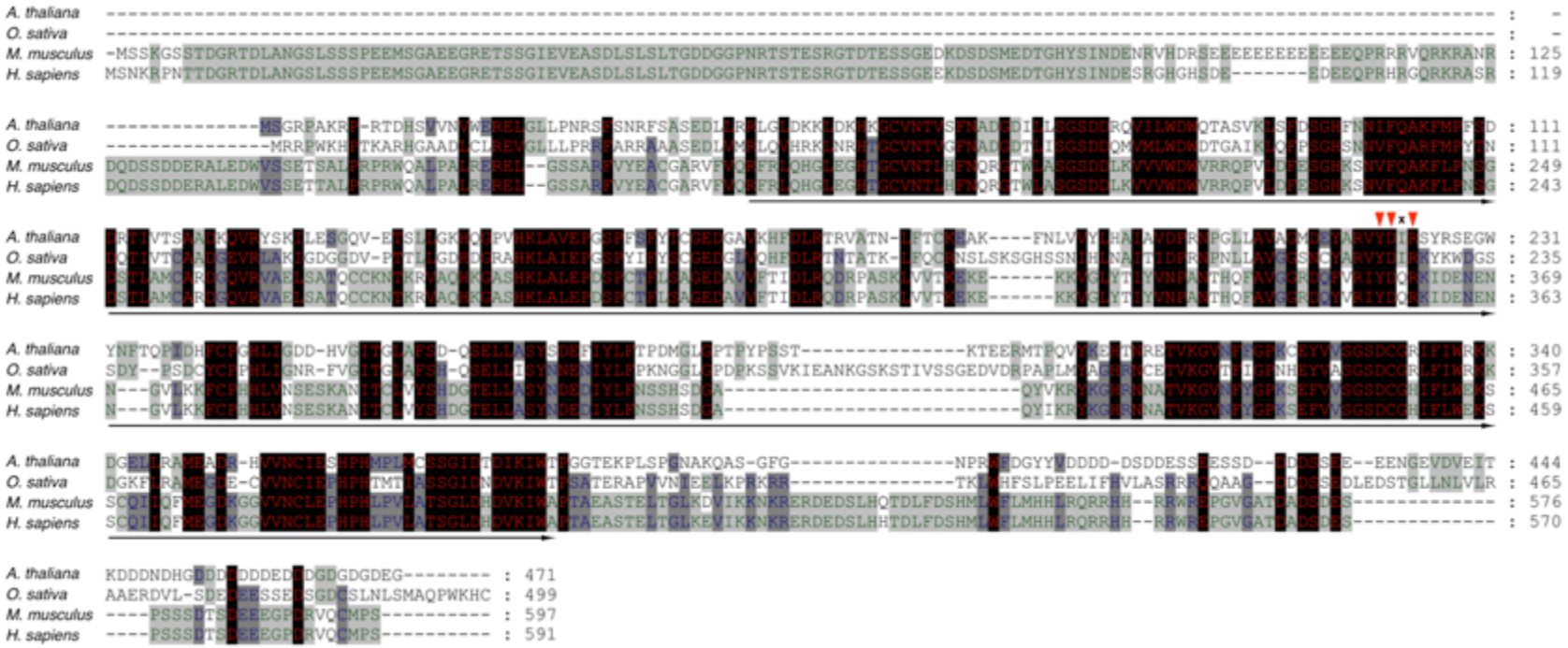
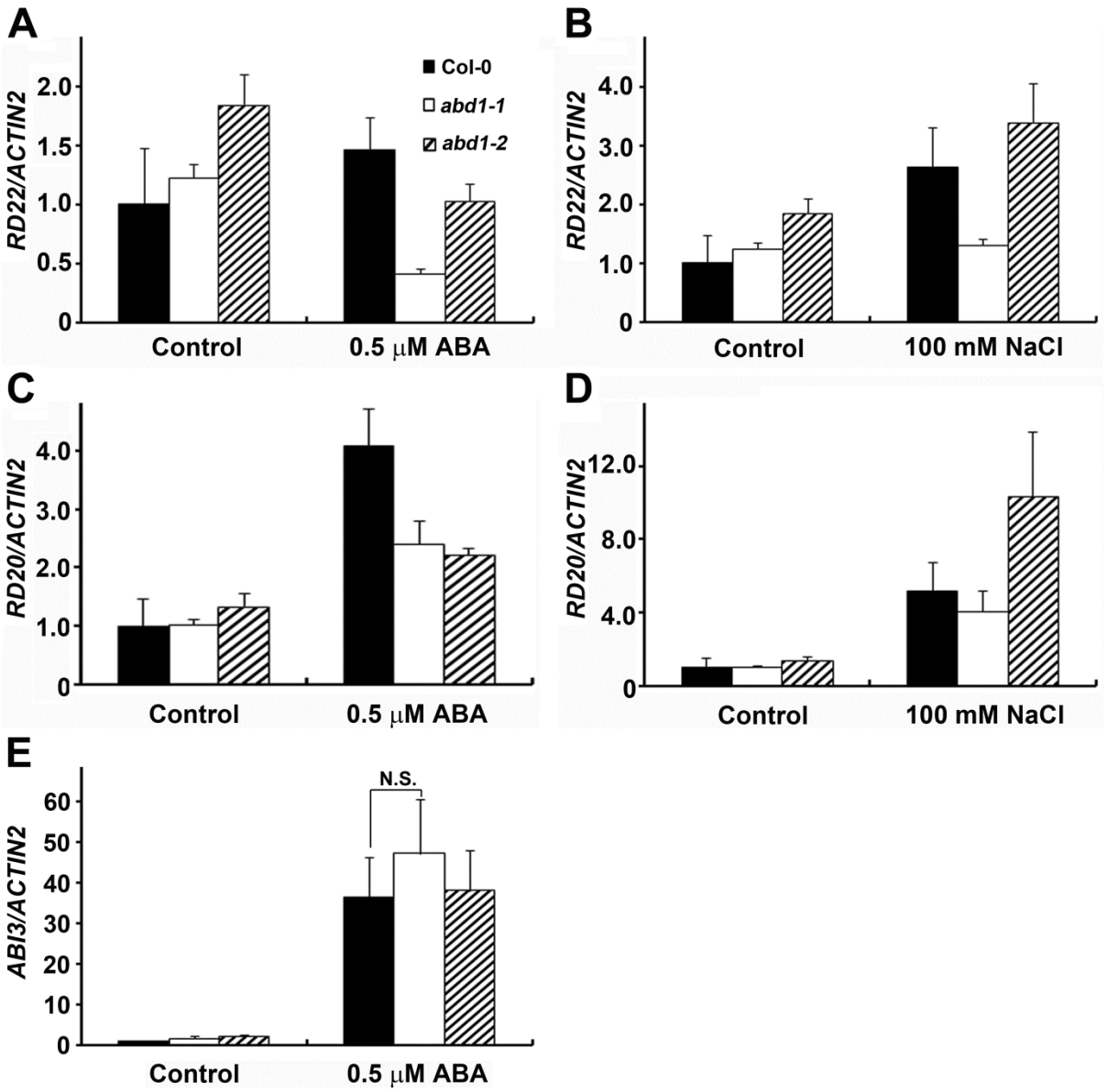
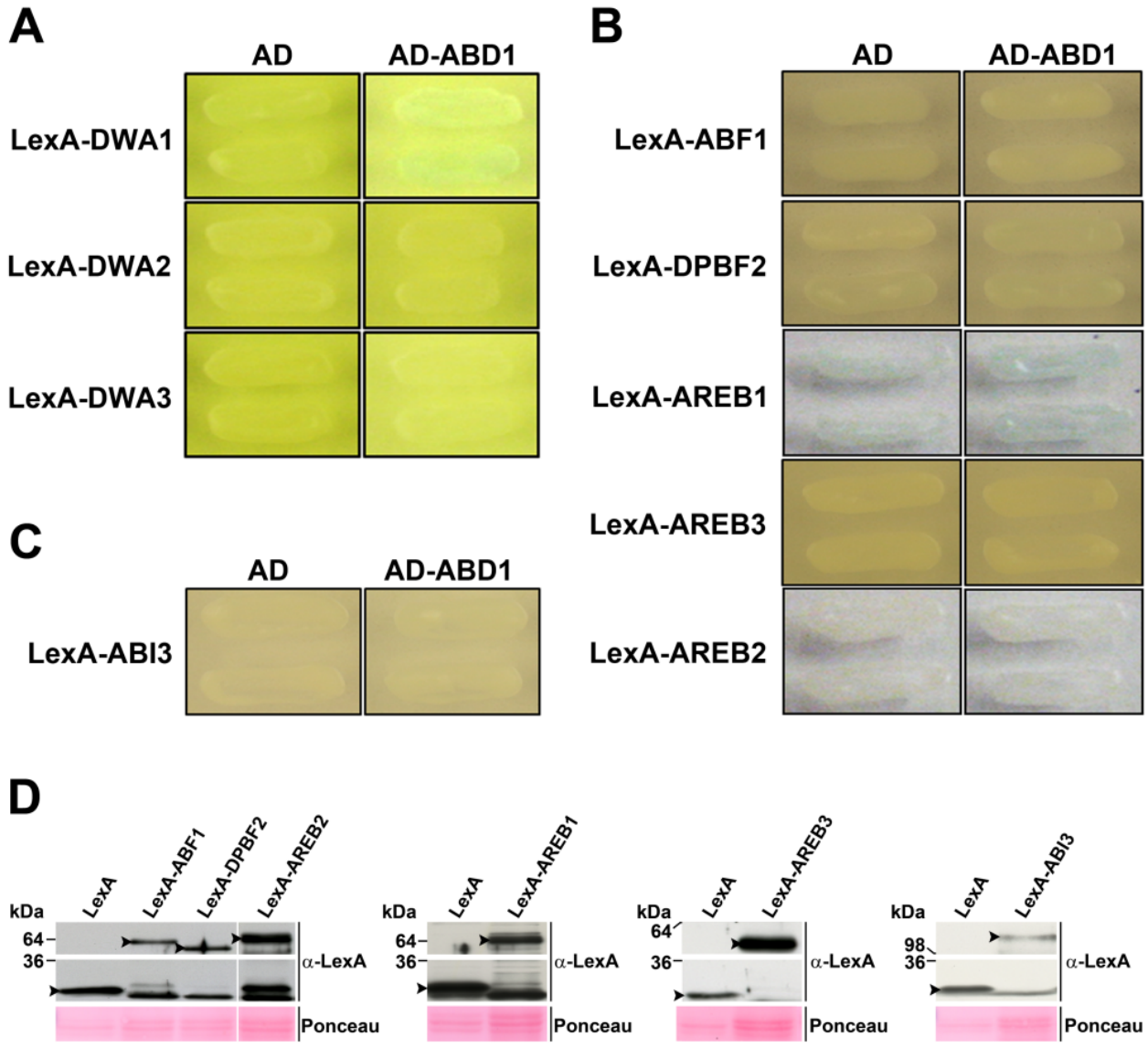


Supplemental Figure 1. Protein alignment of ABD1 from other model organisms.
The alignment was performed with *H. sapiens* DCAF8, *M. musculus* DCAF8 and *O. sativa* Os10g0544500. The WD40 domains are underlined. The red triangles indicate the WDxR motif within the WD40 domain and “x” stands for an undefined amino acid. The shading mode indicates the level of conservation, with red letters in black shading corresponding to a high level of conservation (100%), blue letters in dark gray shading corresponding to a moderate level of conservation (80%) and green letters in light gray shading corresponding to a low level of conservation (60%).



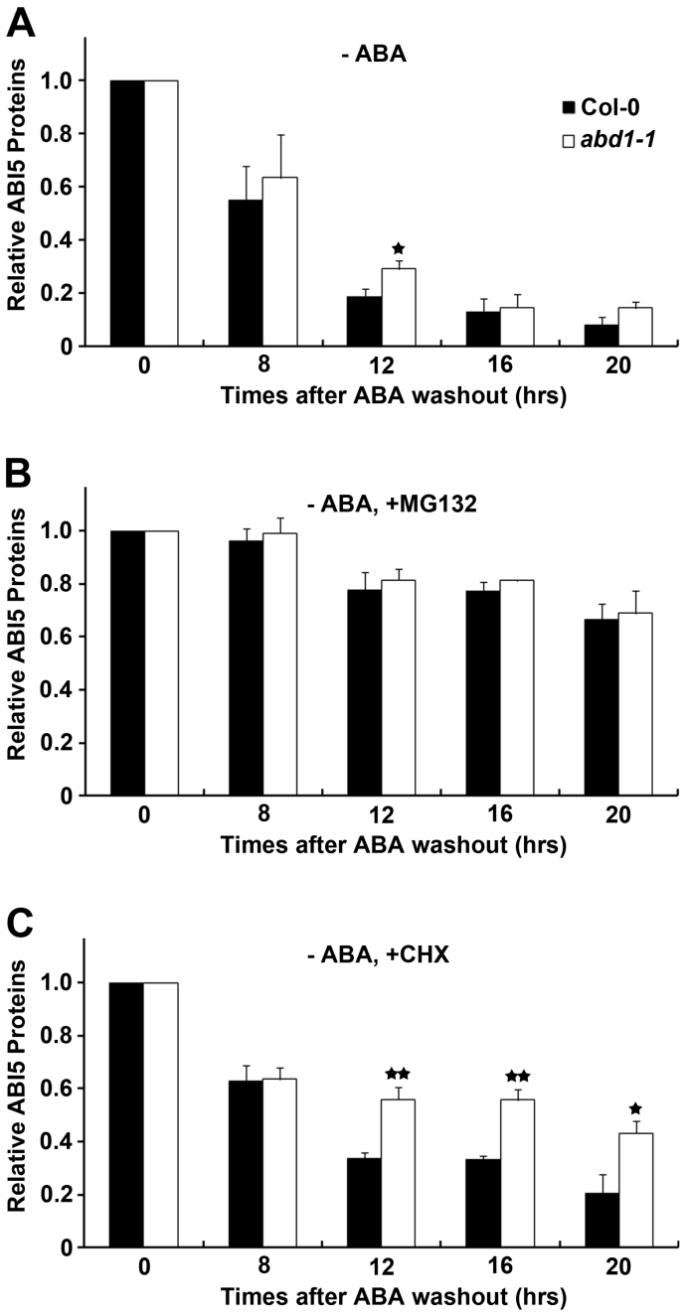
Supplemental Figure 2. *abd1-1* and *abd1-2* seedlings have no change in expression of RD20 and RD22 after ABA and NaCl treatment.

7-day-old Col-0 wt, *abd1-1* and *abd1-2* seeds were grown in the absence or presence of 0.5 μM ABA or 100 mM NaCl. mRNA levels were determined by quantitative real-time PCR analysis. Relative amounts of transcripts were normalized to the levels of *ACTIN2* within the same sample. **(A)** *RD22* after ABA treatment. **(B)** *RD22* after NaCl treatment. **(C)** *RD20* after ABA treatment. **(D)** *RD20* after NaCl treatment. **(E)** *ABI3* after ABA treatment. Results are from three biological replicates and values represent mean ± SD (n=9). N.S., not significant.



Supplemental Figure 3. ABD1 does not directly interact with DWA proteins, ABI5 homologs or ABI3 by yeast two hybrid assays.

Assays were performed with ABD1 protein as prey and various ABA responsive proteins as bait to monitor their interactions. Empty vector was used as a negative control. Yeast were grown in the presence of X-gal for 15 hours, after which images were taken. **(A)** Interaction between ABD1 and DWA1, DWA2, or DWA3. **(B)** Interaction between ABD1 and the five most closely related ABI5 homologs: ABF1, DPBF2, AREB1, AREB3 and AREB1. **(C)** Interaction between ABD1 and ABI3. **(D)** Immunoblots of the target fusion proteins in the yeast two hybrid assays in **(B)** and **(C)**. The LexA fusions were detected by anti-LexA antibodies and the expression of these proteins are indicated by the arrows. Empty LexA vector was used as a negative control. Ponceau S staining was used as a loading control. A total of 15 µg of protein was loaded in each lane.



Supplemental Figure 4. Quantification of ABI5 protein degradation after ABA removal.

Immunoblot assays shown in Figure 9 were quantified showing relative amounts of ABI5 protein in Col-0 wt and *abd1-1* seeds that were treated with 5 μM ABA in white light for 3 days, and then harvested at the indicated times after the removal of ABA with either being washed out with **(A)** liquid media, **(B)** liquid media supplemented with the proteasome inhibitor MG132 (50 μM) or **(C)** the protein synthesis inhibitor CHX (100 μM). Relative amounts of ABI5 protein were normalized to the levels of RPN6 within the same sample. Values are means ± SD (n=3). Significant difference was determined by a Student's t-test; single or double stars indicate a P values of $P<0.03$ or $P<0.004$, respectively.

Supplemental Tables

Supplemental Table 1. List of primers used for genotyping and RT-PCR analysis.

Name	T-DNA Line	Forward Primer (5'-3')	Reverse Primer (5'-3')	Genotyping[a]	RT-PCR
ABD1 (*At4g38480*)	SALK_051074 (*abd1-1*)	GAAAAGGCCGAGGACCGACCAT	CTGTCATCAGAACCAGAAAG	FP1+RP1 (F/LBb1.3)	FP1+RP1
ABD1 (*At4g38480*)	SAIL_648_G02 (*abd1-2*)	CTTTCTGGTTCTGATGACAGA	ATGTCTGTCTGCTTCCATGG	FP2+RP2 (F/LB3)	FP2+RP2
		GAAAAGGCCGAGGACCGACCAT	TATTATTGAAGTGGCCGGAA		FP1+RP3
LBb1.3		ATTTTGCCGATTTCGGAAC			
LB3		TAGCATCTGAATTTCATAACCAATCTCGATACAC			
RPN6		AAGGCACGATAGATCTGCAGA	TCGAGGGTAGCCGAGTAGAT		

[a] primer sets for confirmation of homo- or heterozygous lines

Supplemental Table 2. List of primers used in quantitative real-time PCR analysis.

Name	Forward Primer (5'-3')	Reverse Primer (5'-3')
ABD1	TGGGTCTCTTACCCAATCGCAGTT	CAGAAGCAGTCTGCCAATCCCAAA
RD29A	GGAGGAGAAGAAGAGAAGAA	TAAAGCTCCTTCTGCACCGG
RD29B	ACGGAAACATCGGACTGG	TCCGTTGACCACCGAGAT
RD22	TTCGGAAGAAGCGGAGAT	CAGTGGAAACAGCCCTGA
RD20	CGTTTCAAACAAAGTTGAATGGATAC	TTAGTGCTTGTTTGCGAGAATTGGCC
ABI5	AACATGCATTGGCGGAGT	TTGTGCCCTTGACTTCAAACT
ABI3	TCTTGAATGGGTCCAAAC	AGGGTTTTGAAATGGATC
ACTIN 2	CAAGGCCGAGTATGATGAGG	GAAACGCAGACGTAAGTAAAAAC

Supplemental Table 3. List of primers used for LCI analysis.

Name	Forward Primer (5'-3')	Reverse Primer (5'-3')
*ABD1_Kpn*I_cLUC	GGGGTACCATGAGTGGAAGGCCGGCG	GGGGTACCTCATCCCTCATCCCCATCCCC
*ABI5_Kpn*I_nLUC	GGGGTACCATGGTAACTAGAGAAACGAAGTTG	GGGGTACCGAGTGGACAACTCGGGTTC

Supplemental Table 4. List of primers used for yeast two-hybrid analysis.

Name	Sequence (5'-3')
*ABD1_Eco*RI_Forward	GGGAATTCTCATCCCTCATCCCCATC
*ABD1_Eco*RI_Reverse	CGGAATTCATGAGGGAAGGCCGGC
*AREB1_Eco*RI_Forward	CCGGAATTCATGGATGGTAGTATGAATTTGGGG
*AREB1_Not*I_Reverse	AAGGAAAAAAGCGGCCGCTCACCAAGGTCCCGACTC
*AREB2_Eco*RI_Forward	CCGGAATTCATGGGAACTCACATCAATTTCAAC
*AREB2_Not*I_Reverse	AAGGAAAAAAGCGGCCGCTCACCATGGTCCGGTTAATGTCC
*DWA1_Eco*RI_Forward	CGGAATTCATGTACGGAGACGCTACAAAC
*DWA1_Eco*RI_Reverse	CGGAATTCTTACAATGAACTGCTACGAA
*DWA2_Xho*I_Forward	CCGCTCGAGATGCAAGGAGGATCATCGGG
*DWA2_Xho*I_Reverse	CCGCTCGAGCTATCTTCTTGGCAGGAAAG
*DWA3_Eco*RI_Forward	CGGAATTCATGGCGAAGCGTGGTTATAA
*DWA3_Eco*RI_Reverse	CGGAATTCCTATGGTGTTTGAAGAACTA
*ABI5_Eco*RI_Forward	CGGAATTCGGATGGTAACTAGAGAAACGAAG
*ABI5_Eco*RI_Reverse	CGGAATTCTTAGAGTGGACAACTCGGGT
*ABF1_Bam*HI_Forward	CGGGATCCCGATGGGTACTCACATTGATATCAAC
*ABF1_Not*I_Reverse	AAGGAAAAAAGCGGCCGCTCACCTTCTTACCACGGACC
*DPBF2_Bam*HI_Forward	CGGGATCCCGATGTCGGTTTTCGAATCGGAGACTTCG
*DPBF2_Not*I_Reverse	AAGGAAAAAAGCGGCCGCTTACCACCCGGCACTGGCCA
*AREB3_Bam*HI_Forward	CGGGATCCCGATGGATTCTCAGAGGGGTATTG
*AREB3_Not*I_Reverse	AAGGAAAAAAGCGGCCGCTCAGAAAGGAGCCGAGCTTG
*ABI3_Bam*HI_Forward	CGGGATCCCGATGAAAAGCTTGCATGTGGCG
*ABI3_Not*I_Reverse	AAGGAAAAAAGCGGCCGCTCATTTAACAGTTTGAGAAGTTGG

Supplemental Table 5. List of primers used for BiFC assay.

Name	Sequence (5'-3')
*ABD1_Not*I_ pSY728_Forward	TTGCGGCCGCAAATGAGTGGAAGGCCGGCGAAA
*ABD1_Not*I_ pSY728_Reverse	TTGCGGCCGCTTTCCCTCATCCCCATCCCCAT
*ABI5_Bam*HI_ pSY735_Forward	CGGGATCCCGATGGTAACTAGAGAAACGAAGTTG
*ABI5_Bam*HI_ pSY735_Reverse	CGGGATCCTTAGAGTGGACAACTCGGGTTC
*DDB1a-Not*I_ pSY738_Forward	TTGCGGCCGCAAATGAGCTCATGGAACTACGTTG
*DDB1a-Not*I_ pSY738_Reverse	TTGCGGCCGCTTGTGAAGCCTAGTGAGTTCTTCAA