

**Figure S1.** Hierarchical clustering analysis of differentially expressed Arabidopsis seed-to-seedling transition transcripts. 19,130 transcripts, which showed a significant level of differential expression at, at least, one stage, were clustered hierarchically, following the Bayesian Estimation of Temporal Regulation method. Horizontal lines point out the expression pattern of each gene, with the seed-to-seedling transition stages in the different columns. Seed-to-seedling stages: DS – dry seeds; 6H – six hours imbibed; TR – testa rupture; RP – radicle protrusion; RH – root hair; GC – greening cotyledons; and OC – cotyledons fully opened.

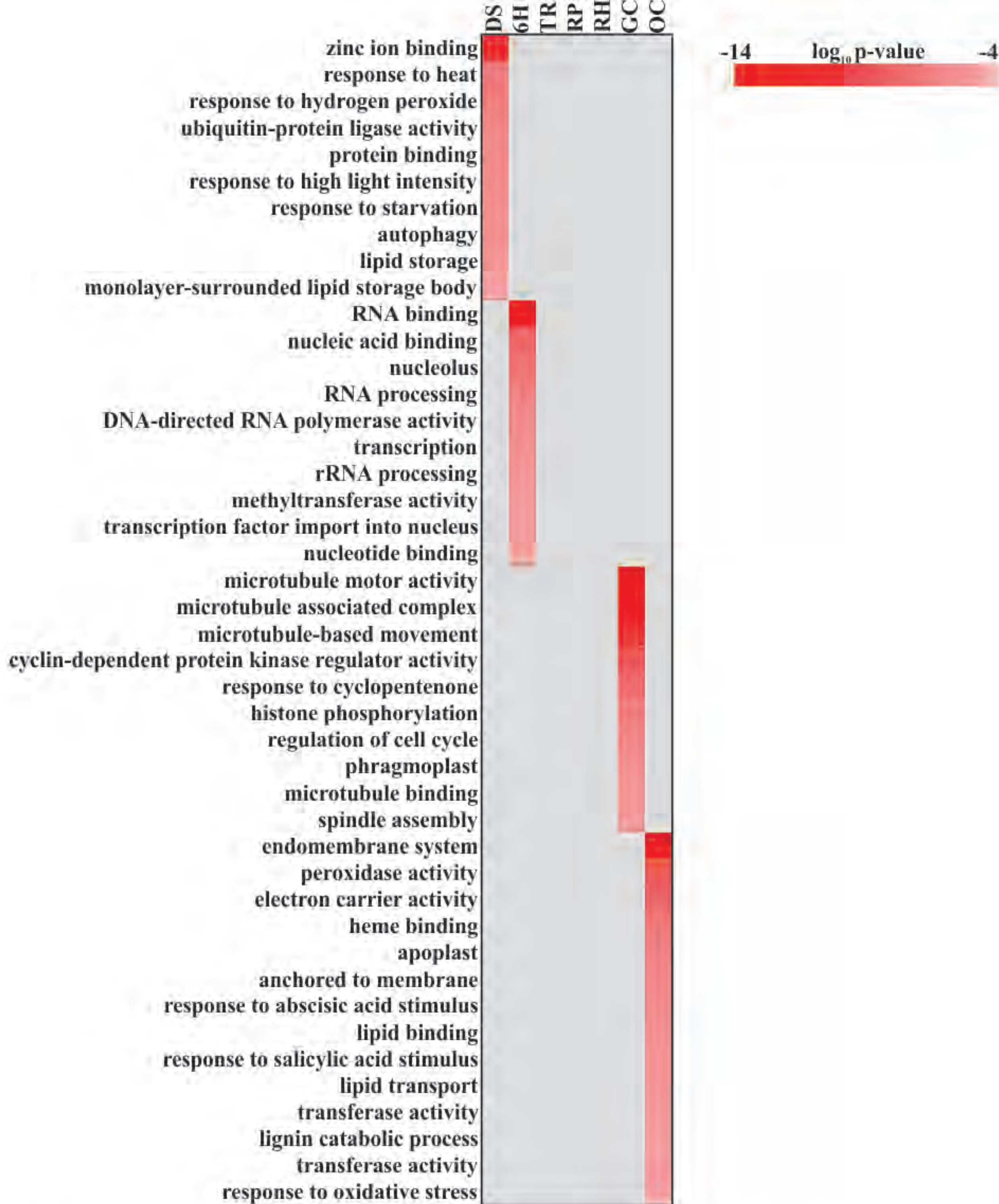


**Number of down-regulated genes**

	mRNA						
	DS	6H	TR	RP	RH	GC	OC
DS		4895	6139	6598	7039	7510	8069
6H	7192		5600	6839	7590	8043	8691
TR	7787	4768		840	4337	6068	7519
RP	7827	5551	1107		1596	4283	6603
RH	8013	6098	3601	1824		1543	5383
GC	8019	6410	4626	3490	1407		2515
OC	7825	6555	5414	4789	4081	3272	

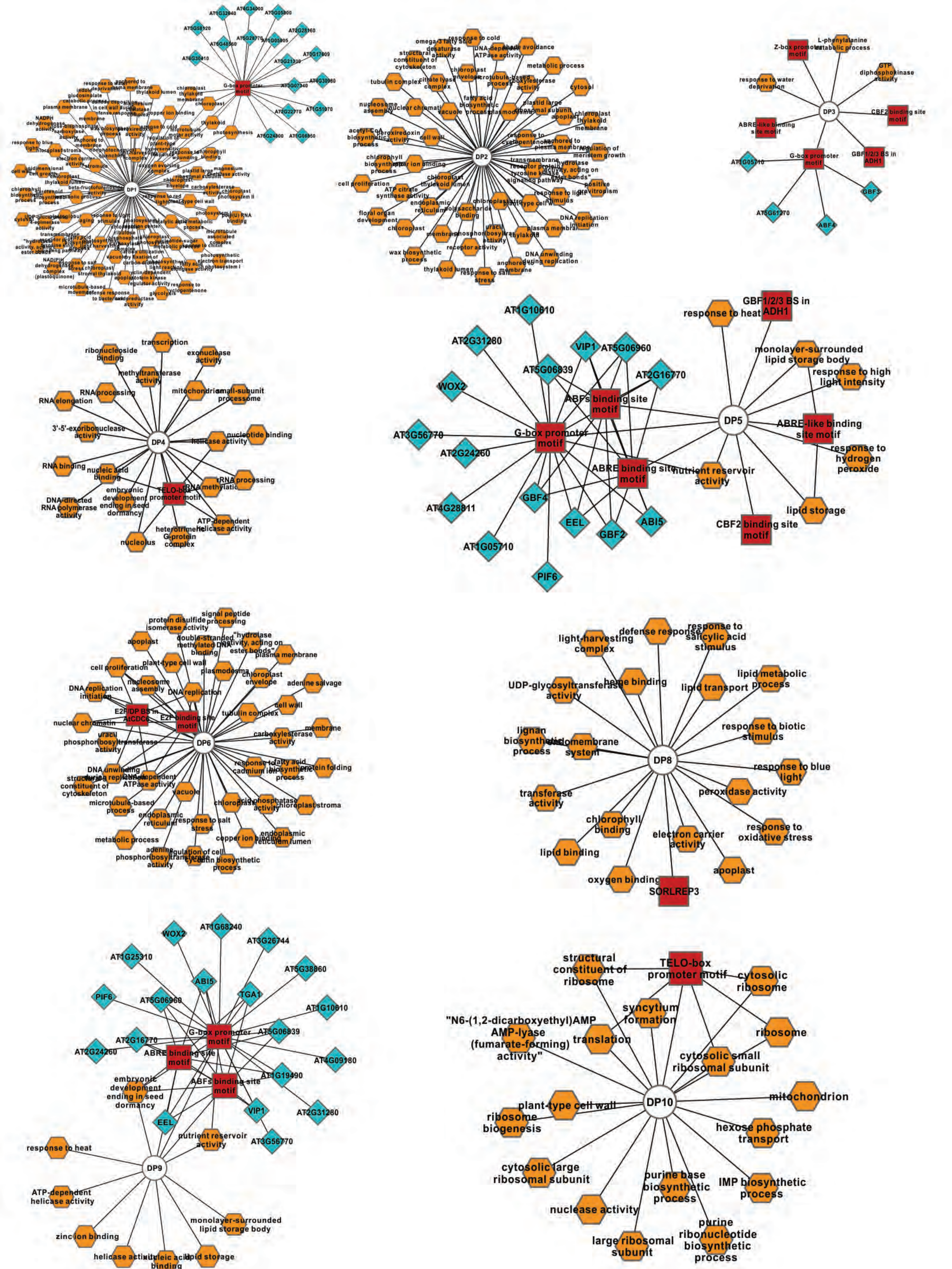
**Figure S2.** Overview of changes in transcript levels across seed-to-seedling developmental stages. Number of transcripts significantly different in abundance between all combinations of the different morphological developmental stages.





**Figure S3.** Heat map showing the P value significance of GO enrichment terms for peak-transcript sets (Supplemental Table S2). GO terms listed are for biological process or/and cellular components that were overrepresented in peak-transcripts for each stage. *P* values were calculated by their hypergeometric distribution.





**Figure S4.** Transcriptional modules predicting regulation of the seed-to-seedling transition. DNA motifs (red rectangles) and GO terms (orange octagons) that are significantly overrepresented ( $P < 0.001$ ) within the peak-transcripts sets (open ellipses) together with co-expressed transcription factors (light-blue diamonds).  $P$  values were calculated by their hypergeometric distribution.



wt

*athb13-1*

*athb13-2*

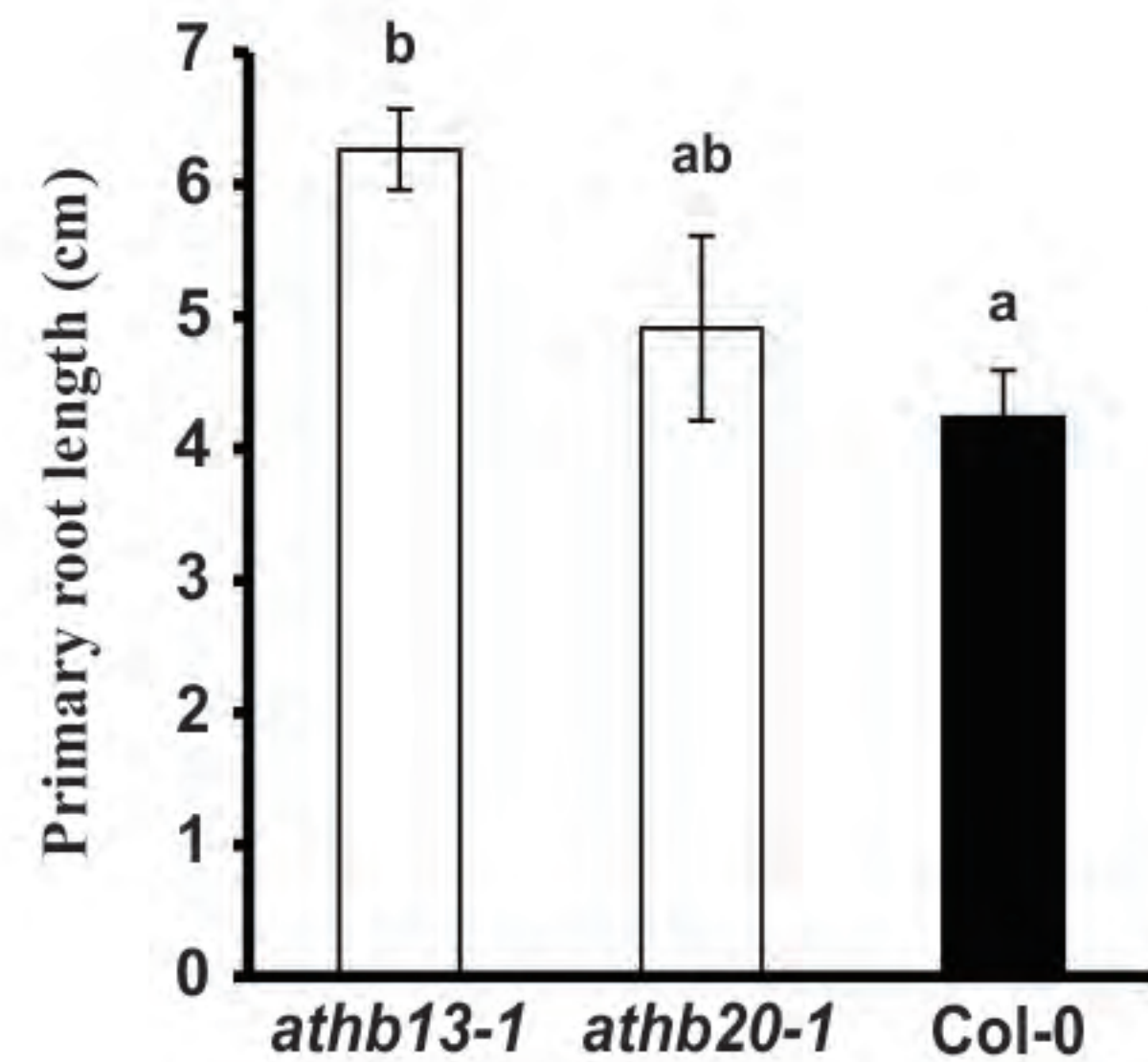
*athb13-1*  
+*AtHB13* (1)

*athb13-1*  
+*AtHB13* (2)



**Figure S5.** Illustrative plates of wild type (Col-0), two *AtHB13* mutant lines (*athb13-1* and *athb13-2*) and two complemented lines (*athb13-1*+*AtHB13* lines 1 and 2), 15 days after transfer to MS medium.



**A****B**

**Figure S6.** An independent experiment of root growth phenotype of mutant lines (*athb13-1* and *athb20-1*) and wild type (Col-0). **A.** Roots were scanned at 15 days after transfer to MS medium. **B.** Primary root length comparison at 15 days after transfer to MS medium. Statistical analyses of the mean values were performed using R statistical language (R Development Core Team, 2011) and letters denote significant differences with a Student's t-test ( $P < 0.01$ ,  $n=27$ ).