

**Figure S1.** Genotyping of the *myb74* T-DNA insertion line. **A.** Diagram showing the gene structure of *MYB74* (At4g05100). The location of the T-DNA insertion in exon 3 has been confirmed by sequencing. The arrows indicate the position and orientation of the primers used for genotyping. ATG, start codon; TAA, stop codon. **B.** PCR zygosity analysis of *myb74*. One T-DNA and three gene specific primers were used in the following combinations for genotyping: (1) myb74\_RP and myb74\_LP and (2) myb74\_RP and myb74\_LP2, flanking the T-DNA insertion. (3) myb74\_RP and LBb3.1 and (4) myb74\_LP and LBb3.1, comprising the T-DNA left boarder primer and one gene specific primer. In the lane, (5) we used the myb74\_RP and myb74\_LP to confirm homozygosity. **C.** Phenotype of wild-type (Col-0) and *myb74* mutant plants grown for 2 weeks on ½ MS plates under control conditions. **D.** Quantitative RT-PCR analysis of *MYB74* expression in *myb74* relative to *MYB74* expression levels in wild-type Arabidopsis. Corresponding primer sequences can be found in **Supplementary Table S1**.

Figure S2:



**Figure S2.** Phenotypic analysis of plants conditionally overexpressing *MYB74*. **A.** Relative fresh weights of the aerial parts of 4 weeks old wild-type control plants (Col-0) and the two MYB740e lines. The average weight of the Col-0 plants was set as 100%. **B.** To determine the relative dry weight, the same plants were dried in an oven at 60°C for 48 h, before the weight was again assessed. The experiment was carried out in triplicate with cohorts of n = 50 individual plants per genotype. **C.** Quantitative analysis of primary root length in seven daysold wild-type (Col-0), MYB740e-1, and MYB740e-2 plants under control conditions (n = 25). The bar plots represent the means  $\pm$  SEs of the compared genotypes. Asterisks refer to significant differences between the corresponding wild-type control and the tested MYB740e lines. Student's t-test: \*\* $p \le 0.01$ , \*\*\* $p \le 0.001$ .

## Figure S3:





## B IAA vs Ctrl in wt

## IAM vs Ctrl in ami1

	<i>–log</i> 10(q-value)											<i>–log</i> 10(q-value)			
Term name	Term ID	$\mathbf{p}_{\mathrm{adj}}$	Q		8	16	Term name	Term ID	$\mathbf{p}_{adj}$	Ŷ	14	4	28		
response to hormone	GO:0009725	1.093×10 <sup>-16</sup>					response to stimulus	GO:0050896	4.433×10 <sup>-26</sup>			1.0	ſ .		
response to endogenous stimulus	GO:0009719	2.607×10-16					response to oxygen-containing compound	GO:1901700	1.237×10-22						
response to auxin	GO:0009733	6.529×10 <sup>-14</sup>					response to abiotic stimulus	GO:0009628	4.376×10-21						
cellular response to hormone stimulus	GO:0032870	1.385×10-13					response to chemical	GO:0042221	1.199×10 <sup>-20</sup>						
response to organic substance	GO:0010033	3.594×10 <sup>-13</sup>					response to water deprivation	GO:0009414	4.395×10 <sup>-17</sup>						
cellular response to endogenous stimulus	GO:0071495	4.002×10 <sup>-13</sup>					response to water	GO:0009415	1.134×10 <sup>-16</sup>				1		
response to chemical	GO:0042221	7.423×10 <sup>-13</sup>					response to organic substance	GO:0010033	2.481×10 <sup>-16</sup>						
hormone-mediated signaling pathway	GO:0009755	1.432×10-11					response to acid chemical	GO:0001101	2.441×10 <sup>-15</sup>						
cellular response to chemical stimulus	GO:0070887	1.776×10-11					response to hormone	GO:0009725	8.908×10 <sup>-14</sup>						
cellular response to organic substance	GO:0071310	2.155×10-11					response to lipid	GO:0033993	9.637×10 <sup>-14</sup>						
response to stimulus	GO:0050896	1.379×10-7					response to stress	GO:0006950	1.249×10 <sup>-13</sup>						
cellular response to auxin stimulus	GO:0071365	9.000×10-7					response to endogenous stimulus	GO:0009719	4.133×10 <sup>-13</sup>						
cellular response to ethylene stimulus	GO:0071369	1.021×10-6					response to karrikin	GO:0080167	1.520×10 <sup>-12</sup>						
response to ethylene	GO:0009723	2.654×10-6					response to inorganic substance	GO:0010035	3.657×10 <sup>-10</sup>						
ethylene-activated signaling pathway	GO:0009873	8.941×10 <sup>-6</sup>					response to light stimulus	GO:0009416	6.389×10 <sup>-9</sup>						
biological regulation	GO:0065007	2.104×10-5					response to alcohol	GO:0097305	1.599×10 <sup>-8</sup>						
signaling	GO:0023052	2.346×10-5					response to radiation	GO:0009314	2.108×10 <sup>-8</sup>						
cellular response to stimulus	GO:0051716	3.296×10 <sup>-5</sup>					response to abscisic acid	GO:0009737	3.279×10 <sup>-8</sup>						
cell communication	GO:0007154	4.861×10 <sup>-5</sup>					response to osmotic stress	GO:0006970	4.113×10 <sup>-8</sup>						
auxin-activated signaling pathway	GO:0009734	4.998×10-5					response to wounding	GO:0009611	1.916×10 <sup>-7</sup>						
signal transduction	GO:0007165	5.290×10 <sup>-5</sup>					flavonoid biosynthetic process	GO:0009813	2.043×10 <sup>-7</sup>						
							secondary metabolic process	GO:0019748	2.454×10-7						
							secondary metabolite biosynthetic process	GO:0044550	3.998×10 <sup>-7</sup>						
							flavonoid metabolic process	GO:0009812	9.054×10 <sup>-7</sup>						
							response to cold	GO:0009409	1.356×10 <sup>-6</sup>						
							response to external stimulus	GO:0009605	2.088×10 <sup>-6</sup>						
							glucosinolate biosynthetic process	GO:0019761	2.123×10 <sup>-6</sup>						
							S-glycoside biosynthetic process	GO:0016144	2.123×10 <sup>-6</sup>						
							glycosinolate biosynthetic process	GO:0019758	2.123×10 <sup>-6</sup>						
							cellular response to stimulus	GO:0051716	2.288×10 <sup>-6</sup>						
							cell communication	GO:0007154	2.904×10 <sup>-6</sup>						
							glycosyl compound biosynthetic process	GO:1901659	8.632×10 <sup>-6</sup>						
							cellular response to light stimulus	GO:0071482	1.649×10 <sup>-5</sup>						
							response to temperature stimulus	GO:0009266	1.689×10 <sup>-5</sup>						
							cellular response to environmental stimulus	GO:0104004	2.859×10 <sup>-5</sup>						
							cellular response to abiotic stimulus	GO:0071214	2.859×10 <sup>-5</sup>						
							cellular response to radiation	GO:0071478	3.604×10 <sup>-5</sup>						
The colors for log scale:							response to jasmonic acid	GO:0009753	3.718×10 <sup>-5</sup>						
							anthocyanin-containing compound metabolic process	GO:0046283	5.251×10 <sup>-5</sup>						
							response to fatty acid	GO:0070542	5.283×10 <sup>-5</sup>						
0 5 10 15 20 25 30 35 4	40 45 ≤ 50						pigment metabolic process	GO:0042440	7.439×10 <sup>-5</sup>						



the tow compared conditions. Color and length of the bars indicate the significance of the identified GO terms. The color code use to differentiate the significance levels is given at the bottom of the figure. The bars only show terms with a significance score  $-log_{10}(q-value) \ge 5$ .

Okushima, Y., Mitina, I., Quach, H.L., and Theologis, A. (2005). AUXIN RESPONSE FACTOR 2 (ARF2): a pleiotropic developmental regulator. *Plant J.* 43(1), 29-46. doi: 10.1111/j.1365-313X.2005.02426.x.



**Figure S4.** Phylogenetic analysis of the subgroup 11 members of Arabidopsis thaliana R2R3 MYB transcription factor proteins. **A.** Phylogram showing a Neighbor joining tree inferred using the CLC Main Workbench v7.9.2 (Qiagen, Hilden, Germany) with default settings. **B.** Primary amino acid sequence percent identity matrix calculated using the Clustal Omega online tool (https://www.ebi.ac.uk/Tools/msa/clustalo/).