

Supporting Table 5. GWAS results for loci selected as interesting *de novo* candidate genes.

Locus	Gene name	Kruskal-Wallis -log ₁₀ P-value				EMMA -log ₁₀ P-value				Differential regulation	Pattern category*
		High R:FR	Low R:FR	Response	Corrected	High R:FR	Low R:FR	Response	Corrected		
AT1G09530	<i>PIF3</i>	3.49	0.99	5.10	4.12	1.41	0.98	2.76	4.26	TRUE	3
AT1G09540	<i>MYB61</i>	3.49	0.99	5.10	4.12	1.41	0.98	2.76	4.26	FALSE	3
AT1G09570	<i>PHYA</i>	3.49	0.99	5.10	3.57	1.41	0.98	2.76	3.79	TRUE	3
AT1G10170	<i>NFXL1</i>	3.01	1.43	4.91	5.34	3.18	1.93	3.68	6.13	TRUE	3
AT1G10210	<i>MPK1</i>	3.01	2.59	4.91	5.34	3.18	1.59	3.68	6.13	FALSE	3
AT1G10240	<i>FRS11</i>	3.48	2.82	4.91	5.34	1.68	1.59	3.23	6.13	FALSE	3
AT1G15050	<i>IAA34</i>	2.72	2.61	5.31	3.14	0.90	1.98	2.82	3.25	FALSE	3
AT1G19350	<i>BES1</i>	6.07	5.77	3.87	1.87	2.63	2.55	1.51	1.17	FALSE	1
AT1G48410	<i>AGO1</i>	5.14	4.54	4.16	2.81	2.15	2.38	2.80	2.19	FALSE	1
AT1G69640	<i>SBH1</i>	2.21	2.10	1.51	1.55	3.93	4.86	1.66	3.93	TRUE	1
AT2G18790	<i>PHYB</i>	5.09	2.77	6.18	1.84	2.56	1.56	3.97	1.91	TRUE	2
AT2G26990	<i>FUS12</i>	2.59	3.54	1.25	1.99	3.58	4.50	1.25	1.58	FALSE	1
AT2G27050	<i>EIL1</i>	1.15	2.74	1.25	2.82	2.68	1.28	4.14	1.92	TRUE	3
AT2G28190	<i>CSD2</i>	3.49	1.61	5.07	3.50	1.36	1.54	2.61	2.73	TRUE	3
AT2G28200	none	2.39	1.61	5.07	3.50	0.99	1.54	1.77	2.73	TRUE	3
AT2G32250	<i>FRS2</i>	7.05	2.88	4.95	2.53	2.59	2.20	2.94	1.90	FALSE	1
AT2G32410	<i>AXL</i>	5.12	2.23	3.49	1.46	1.84	1.60	2.33	1.45	FALSE	1
AT2G32440	<i>KAO1</i>	5.12	2.23	3.98	2.29	1.84	1.32	2.33	1.03	FALSE	1
AT2G32460	<i>MYB101</i>	5.12	2.23	3.98	2.29	1.84	1.32	2.33	1.03	FALSE	1
AT2G35300	<i>LEA18</i>	2.47	2.75	2.67	2.35	4.14	4.60	1.00	1.97	TRUE	1
AT2G46530	<i>ARF11</i>	5.87	4.43	4.42	2.05	2.25	2.03	3.14	1.85	TRUE	1
AT3G01220	<i>ATHB20</i>	5.09	4.64	3.15	1.59	1.41	1.80	1.91	1.83	FALSE	1
AT3G05800	<i>AIF1</i>	1.97	1.75	2.43	3.06	2.85	5.19	2.05	3.62	TRUE	1
AT3G12580	<i>HSP70</i>	5.40	3.66	5.31	1.45	2.98	1.52	3.27	1.56	TRUE	2
AT3G12630	none	6.42	4.23	5.51	1.45	3.28	2.28	2.55	1.56	TRUE	2
AT3G12830	<i>SAP5</i>	4.19	5.14	3.68	2.60	2.23	2.32	2.12	2.15	FALSE	1
AT3G15540	<i>IAA19</i>	7.05	6.15	3.73	0.73	4.84	4.41	2.31	0.87	TRUE	1
AT3G15570	none	7.05	6.15	3.73	0.88	4.84	4.41	2.65	1.01	FALSE	1
AT3G23210	<i>bHLH34</i>	6.05	3.56	3.70	4.08	2.83	3.28	2.47	3.86	TRUE	1
AT3G25880	none	3.96	4.32	3.10	1.85	4.06	5.32	1.85	2.35	FALSE	1
AT3G25890	none	3.96	3.67	3.10	1.85	4.06	5.32	2.04	1.81	TRUE	1
AT3G59470	none	5.36	4.87	2.44	1.67	2.97	2.63	1.83	1.35	FALSE	1
AT3G59900	<i>ARGOS</i>	5.91	3.71	3.27	1.70	2.90	2.05	1.74	1.23	TRUE	1
AT4G01120	<i>GBF2</i>	5.51	1.71	6.31	3.97	1.80	1.31	3.53	3.87	FALSE	2
AT4G01350	none	4.58	2.21	5.69	4.03	2.02	1.43	3.55	3.86	FALSE	3
AT4G01480	<i>PPa5</i>	3.75	2.47	6.00	4.43	1.98	1.09	5.53	4.04	TRUE	3
AT4G08810	<i>SUB1</i>	4.60	4.89	2.71	1.57	4.33	3.08	2.34	1.07	FALSE	1
AT4G16780	<i>ATHB-2</i>	3.39	2.16	3.19	1.82	4.02	4.89	2.27	1.55	TRUE	1
AT4G19990	<i>FRS1</i>	3.21	3.45	1.94	2.19	4.22	3.87	2.01	1.74	FALSE	1
AT4G26150	<i>CGA1</i>	5.30	3.93	4.62	2.14	7.08	5.86	2.76	1.35	TRUE	1
AT4G26200	<i>ACS7</i>	5.30	3.93	4.62	2.47	7.08	5.86	2.76	1.35	TRUE	1
AT4G32280	<i>IAA29</i>	5.14	1.73	5.68	1.69	1.39	1.51	1.61	1.24	TRUE	2
AT4G32980	<i>ATH1</i>	5.21	1.11	7.43	3.08	3.61	1.31	4.93	2.66	FALSE	2
AT4G35230	<i>BSK1</i>	2.30	2.08	6.00	3.68	3.07	2.80	3.13	3.47	FALSE	3
AT5G01990	none	5.01	3.13	3.81	1.70	3.23	1.78	3.19	1.36	FALSE	1
AT5G35840	<i>PHYC</i>	4.83	3.23	4.57	3.64	2.02	1.81	4.18	3.42	FALSE	3
AT5G43700	<i>ATAUX2-11</i>	3.38	3.26	3.07	2.96	3.38	4.51	1.93	2.71	TRUE	1
AT5G43890	<i>YUC5</i>	3.38	2.40	3.79	2.89	2.61	1.57	4.13	2.59	TRUE	3
AT5G44110	<i>ABC121</i>	1.38	2.52	3.78	5.41	1.70	1.91	2.86	4.70	FALSE	3
AT5G51810	<i>GA20OX2</i>	4.22	4.55	3.21	2.23	3.80	4.47	1.28	1.77	TRUE	1
AT5G57090	<i>EIR1</i>	5.46	1.57	6.05	2.53	3.91	2.11	3.26	1.70	FALSE	2
AT5G57360	<i>ZTL</i>	4.73	2.56	5.13	2.03	2.82	2.42	3.33	1.84	FALSE	3
AT5G63870	<i>PP7</i>	3.26	1.72	5.49	3.56	1.40	1.85	1.84	1.93	FALSE	3

*Significance pattern categories: 1=general control of hypocotyl height, 2=control of shade avoidance via hypocotyl height, 3=specific control of shade avoidance response.