

Note 1:**Statistical Analysis of Array Data:**

The experimental design consisted of four treatments with four replications per treatment, for a total of sixteen chips. The treatment categories were untreated wild type (Wt), untreated *pk1* mutant (Pk1), uniconazole-P treated wild type (Uwt) and uniconazole-P treated *pk1* mutant (Upkl). The Affymetrix® analysis reported two values for each gene: the average difference call and the absolute analysis or presence/absence call (Affymetrix Microarray Suite v. 4.0).

Differences in gene expression were evaluated in paired comparisons (Pk1 vs. Wt and Upkl vs. Uwt). A *t*-test was generated for each gene pair using the Cyber-T (Long et al., 2001) web interface (<http://genex.ncgr.org/genex/cybert>). Probability values were generated with and without the Bonferroni correction for multiple comparisons. For the Bonferroni correction, the experiment-wide false positive rate (the probability of declaring an expression difference significant by chance alone) was set at 0.25. The set of genes examined in this paper occurred in the intersection of all of those genes that met criteria $p < 0.05$ without the Bonferroni correction for the two comparisons (Pk1 vs. Wt $p < 0.05$ □ Upkl vs. Uwt $p < 0.05$). 293 genes in total met these selection criteria. Those genes for which the corresponding transcript level is elevated two-fold or more in *pk1* seeds in both the absence and presence of uniconazole-P are listed in Table 1a (56 in total). The remaining 237 genes are listed in Table 1b. In addition, we include here the list of genes that occur in the intersection of all of those genes that met criteria $p < 0.05$ without the Bonferroni correction for the two comparisons (Pk1 vs. Upkl $p < 0.05$ □ Wt vs. Uwt $p < 0.05$) in Table 2, and the list of genes that occur in the intersection of all of those genes that met criteria $p < 0.05$ without the Bonferroni correction for the three comparisons (Wt vs. Upkl $p < 0.05$ □ Pk1 vs. Upkl $p < 0.05$ □ Uwt vs. Upkl $p < 0.05$) in Table 3.

Note 2:**Supplementary information for qRT-PCR:**

Oligonucleotide primer sequences and primer concentrations used for qRT-PCR are available in Table 4. Relative expression values of genes were calculated from critical threshold values as described in ABI User Bulletin #2, part # 4303859B available at http://docs.appliedbiosystems.com/search.taf?_UserReference=6E00E667F6CFB2C43DE24701. Tables 5 through 10 list the critical threshold values for Figures 1, 3, 4, 5, 6, and 7 respectively from the manuscript.

Long, A.D., Mangalam, H.J., Chan, B.Y., Toller, L., Hatfield, G.W. and Baldi, P. (2001) Improved statistical inference from DNA microarray data using analysis of variance and a Bayesian statistical framework. Analysis of global gene expression in *Escherichia coli* K12. *J Biol Chem* **276**, 19937-19944.

Table 1a. Genes that exhibit *PKL*-dependent transcription based on the criteria (*Pkl* vs. *Wt* $p < 0.05$ □ *Upkl* vs. *Uwt* $p < 0.05$) and for which the corresponding transcript level is elevated two-fold or more in *pkl* seeds in both the absence and presence of uniconazole-P.

Wt=Wild type, Pkl=*pickle* mutant, Uwt=uniconazole-P treated wild type, Upkl= uniconazole-P treated *pickle* mutant; Mean= mean value for a given treatment, SD= standard deviation of the mean for a given treatment
Putative identification and Class represent a manual annotation based on computer derived Gene ontologies available at TAIR in conjunction with BLAST results from the non-redundant GenBank protein database
Class designations are analogous to those presented by White et. al. 2000, Plant Physiology 124 :1582-1594; Data is sorted by the ratio of Pkl/Wt; This data set contains 56 genes

Affy Code	AGI Code	Pkl Mean	Pkl SD	Wt Mean	Wt SD	Pkl/Wt	Upkl Mean	Upkl SD	Uwt Mean	Uwt SD	Upkl/Uwt	Class	Putative Identification/Function	Potential Role in Embryos	Citation
13276_at	\NULL	480	89	33	111	14.75	352	135	20	66	17.84	UF	\NULL		
12902_at	At3g54180	304	59	30	161	10.13	293	69	19	84	15.61	CDC	cdc2b/cell cycle control		
14550_at	At4g23690	213	53	27	67	7.90	225	89	69	75	3.25	D	disease response		
15996_at	At3g16430	2586	485	357	1395	7.25	3489	128	381	989	9.17	D	jasmonate inducible isolog	Defense	Plant Physiology 103:703
15357_at	At4g33560	2712	185	401	1655	6.77	2285	178	342	335	6.69	UF	unknown		
18464_at	At2g43480	168	44	27	48	6.33	165	70	53	30	3.14	OX	Ascorbate peroxidase		
12763_s_at	At2g05520	512	90	89	298	5.75	402	163	22	137	18.71	D	atGRP3/cell wall, signaling	Somatic embryogenesis	Plant Mol Biol 28:39
13278_f_at	At5g12030	630	223	137	140	4.62	491	56	20	26	25.19	CHP	HSP17.6A/heat shock protein	Dessiccation	Plant Physiology 122:1099
16014_at	At1g75750	1730	236	377	873	4.59	2050	188	311	609	6.59	UF	GASA1/gibberellin response	maturation	Plant Mol Biol 36:871
14383_at	At1g09460	322	158	82	63	3.93	446	188	85	48	5.27	CW	glucanase		
16238_at	At4g16480	562	164	162	133	3.48	745	203	107	94	6.96	MT	sugar transporter		
20438_at	At1g10370	1217	218	361	563	3.38	1386	157	320	123	4.33	OX	GST 30		
12151_at	At2g43150	10084	3613	3057	4262	3.30	10809	851	1554	1763	6.96	CW	putative extensin		
17909_at	At1g62480	2029	522	625	583	3.25	1935	170	676	186	2.86	UF	unknown		
15971_s_at	At3g16410	13774	2954	4335	4451	3.18	16642	1052	3949	905	4.21	D	lectin/myrosinase binding	Defense	Plant Physiology 103:703
13277_i_at	\NULL	3589	1146	1165	1019	3.08	3050	316	660	350	4.62	UF	\NULL		
16487_at	At2g25450	482	170	160	78	3.02	462	135	216	74	2.14	UF	dioxigenase		
13275_f_at	At3g46230	1163	380	385	342	3.02	857	49	157	157	5.45	CHP	HSP	Dessiccation	Plant Physiology 122:1099
17413_s_at	At5g64120	1896	284	630	773	3.01	2847	382	489	1112	5.82	OX	Ascorbate peroxidase		
12781_at	At1g13930	968	227	337	228	2.87	1730	228	349	685	4.96	UF	unknown		
13438_at	At4g08685	2249	427	812	1002	2.77	1776	35	754	132	2.36	L	pollen allergen-related/unknown		
12349_s_at	At2g37040	1338	221	492	541	2.72	1936	168	421	343	4.60	SEM	PAL1		
20060_at	At1g10370	1837	350	695	847	2.64	2134	155	708	365	3.01	OX	GST 30		
13880_s_at	At4g25900	810	197	313	272	2.59	791	88	256	190	3.10	C	Apospory related/carbohydrate metabol.	Somatic embryogenesis	Proc XVII Grass Cong 2:1033
20097_at	At1g65340	1302	296	510	477	2.55	1499	219	441	201	3.40	OX	CYP96A3		
18663_s_at	At4g24130	921	334	365	283	2.53	948	85	255	130	3.72	UF	unknown		
17003_at	At2g39900	875	179	351	289	2.49	918	118	369	108	2.49	T	AtWLM2/transcription factor	Transcription	This study
14863_at	At1g23750	769	136	309	301	2.49	1152	118	346	260	3.33	UF	unknown		
17782_at	At4g15480	616	183	249	46	2.48	627	115	278	101	2.26	SEM	UDP-glucosyl transferase		
15983_at	At4g27140	2191	779	884	441	2.48	2989	134	370	311	8.08	SP	2s1 albumin precursor	Storage Reserves	
20323_at	At2g29500	393	96	162	120	2.43	303	103	68	95	4.49	CHP	HSP 20 alpha crystallin	Dessiccation	Plant Physiology 122:1099
13680_at	At1g55020	4941	1157	2055	2045	2.40	5126	577	1918	1027	2.67	L	lipoxigenase		
19597_s_at	At4g17260	430	63	179	123	2.40	489	118	200	61	2.45	C	Lactate dehydrogenase LDH1		
14090_i_at	At2g15830	372	39	155	61	2.40	224	71	86	65	2.62	UF	unknown		
15981_at	At3g16420	30967	6321	12976	7081	2.39	39616	2439	16150	3365	2.45	D	Jacalin type lectin	Defense	Plant Physiology 103:703
18584_at	At1g10970	2642	320	1126	799	2.35	2339	163	1095	523	2.14	MT	ZIP4 zinc transporter		
16893_at	At4g31550	656	178	284	193	2.31	713	98	315	190	2.27	T	WRKY11/transcription factor		
20024_s_at	At2g35810	2727	362	1181	877	2.31	2653	201	1033	335	2.57	UF	unknown		
16513_at	At2g04780	3059	557	1330	793	2.30	2765	278	1105	212	2.50	CW	FLA7(arabinogalactan)/cell wall, signaling	Somatic embryogenesis	Phys Plant 114:637
19907_at	At2g17320	390	131	172	115	2.26	442	129	157	27	2.82	C	panthothenate kinase		
15193_s_at	At2g30870	9046	1184	4012	3190	2.25	8628	628	3640	865	2.37	OX	ERD13/dehydration induced GST		
16031_at	At5g01600	6218	1245	2768	2195	2.25	8266	658	2457	1673	3.36	MT	ATFER1/iron metabolism		
17771_at	At1g26830	421	102	189	127	2.22	350	34	174	112	2.01	CDC	E3 ubiquitin ligase SCF complex subunit Cullin		
15868_at	At2g22080	640	177	288	102	2.22	514	130	207	60	2.49	UF	En/Spm like transposon protein		
12587_at	At2g22770	1881	134	850	785	2.21	1867	151	910	573	2.05	T	bHLH transcription factor		
20420_at	At4g19810	1077	151	498	352	2.16	1477	122	465	263	3.18	CW	glycosyl hydrolase family 18		
19683_at	At1g62500	654	85	303	110	2.16	1617	81	596	471	2.71	CW	proline rich cell wall protein		
19699_i_at	At4g23420	411	67	193	75	2.13	368	118	154	63	2.38	C	possible dehydrogenase		
14066_at	At2g35880	718	186	341	108	2.11	659	83	320	131	2.06	UF	unknown		
19998_at	At2g30520	792	142	379	267	2.09	959	249	289	171	3.32	STD	RPT2/phototropism		
15633_s_at	At3g23000	287	3	140	60	2.06	282	62	103	93	2.74	STD	ATSRPK1/osmolarity stress		
13288_s_at	At5g11260	404	32	197	57	2.05	401	42	134	66	2.98	T	HY5/light response transcriptional control		
20054_at	At1g03420	1206	188	597	365	2.02	1234	230	559	105	2.21	UF	unknown		
19490_at	At1g10550	1423	336	705	226	2.02	1117	153	486	197	2.30	C	xyloglucan endotransglycosylase		
17832_at	At2g16060	4064	559	2032	1213	2.00	3212	389	1512	328	2.12	OX	HB1/hemoglobin		
18929_s_at	At5g13930	31844	3707	15954	9363	2.00	38565	2520	17649	7231	2.19	D	CHS/responsive to light, defense response		

C=carbohydrate metabolism, CDC=cell division cycle, CHP=Chaperonin/heat shock protein/folding, CW= Cell wall, D= Defense response, L=Lipid metabolism, MT=membrane/transporter/receptor, OX=oxygen detoxifying enzyme/peroxidase
SEM= secondary metabolism, SP=Storage protein, STD= signal transduction, T=Transcription factors, UF=unknown function

Red text was validated by qRT-PCR, Blue text was present on the array of Girke et. al. 2000, Plant Physiology 124 :1570-1581 (the relative transcript level of all three genes was observed to be unchanged in embryos).

Table 1b. Genes that exhibit *PKL*-dependent transcription based on the criteria (*Pkl* vs. *Wt* $p < 0.05$ \square *Upkl* vs. *Uwt* $p < 0.05$) and for which the corresponding transcript level is not elevated two-fold or more in *pkl* seeds in both the absence and presence of uniconazole-P.

Wt=Wild type, Pkl= *pickle* mutant, Uwt=uniconazole-P treated wild type, Upkl= uniconazole-P treated *pickle* mutant
Mean= mean value for a given treatment, SD= standard deviation of the mean for a given treatment
Putative identification represents the annotation as available through TAIR
Ratios are given for specific treatment comparisons and data was sorted by the ratio of Pkl/Uwt
This data set contains 237 genes

Affy Code	AGI Code	Pkl Mean	Pkl SD	Wt Mean	Wt SD	Pkl/Wt	Upkl Mean	Upkl SD	Uwt Mean	Uwt SD	Upkl/Uwt	Putative Identification
16426_at	At1g72730	1172	232	572	314	2.05	1397	263	723	291	1.93	putative Eukaryotic initiation factor 4A
18807_at	At1g13170	324	53	136	43	2.39	220	47	116	41	1.89	putative oxysterol-binding protein
20360_at	At1g58290	264	99	120	24	2.2	237	68	125	21	1.89	glutamyl-tRNA reductase, putative
16523_s_at	At1g08830	14217	1819	6957	4270	2.04	11688	1912	6264	1724	1.87	superoxidase dismutase
19424_at	At1g24280	1163	178	565	239	2.06	1027	191	566	122	1.82	glucose-6-phosphate 1-dehydrogenase
12769_at	At2g37170	664	73	247	178	2.69	558	61	329	158	1.7	aquaporin (plasma membrane intrinsic protein 2B)
13822_s_at	At2g31540	-167	29	-21	51	8.02	-16	53	-137	53	0.12	putative GDSL-motif lipase hydrolase
14976_at	At2g24190	52	32	9	11	6.15	138	144	-78	64	-1.77	putative carbonyl reductase
13279_at	At5g12020	588	357	70	167	8.43	601	147	-165	205	-3.64	heat shock protein 17.6-II
19979_at	At1g67330	543	144	55	317	9.95	1132	76	-13	308	-87.1	unknown protein
14720_s_at	At1g35720	692	204	82	256	8.47	786	73	-3	212	-314.3	Ca2+-dependent membrane-binding protein annexin
13078_at	At2g47650	2354	446	1188	391	1.98	2823	57	1188	289	2.38	putative dTDP-glucose 4-6-dehydratase
14073_at	At1g54410	1577	447	799	401	1.97	1379	395	740	221	1.86	water stress-induced protein, putative
15614_s_at	At4g30270	4197	767	2126	707	1.97	4364	539	1953	1079	2.24	endoxyloglucan transferase (meri5B)
18703_at	At2g07711	387	85	198	63	1.96	394	90	100	133	3.93	pseudogene
13219_at	At3g54420	419	126	215	33	1.95	391	90	141	126	-2.77	class IV chitinase (CHIV)
16015_at	At1g74470	1016	134	521	295	1.95	1405	102	503	116	2.8	geranylgeranyl reductase
13908_s_at	At4g20860	1412	259	736	206	1.92	1465	137	723	382	2.03	berberine bridge enzyme - like protein
20640_s_at	At1g42970	782	87	410	171	1.91	892	126	366	219	2.44	glyceraldehyde-3-phosphate dehydrogenase
16423_at	At2g30570	2502	408	1316	694	1.9	2694	639	1562	589	1.73	photosystem II reaction center 6.1KD protein
17739_at	At5g51810	329	79	173	77	1.9	1521	216	519	231	2.93	gibberellin 20-oxidase (emb CAA58294.1)
13254_at	At4g17190	3431	332	1835	563	1.87	3422	437	2329	381	1.47	farnesyl-pyrophosphate synthetase FPS2
14018_at	At1g09750	2414	469	1290	372	1.87	3802	102	1450	204	2.62	hypothetical protein
14039_at	At2g19590	12609	1969	6757	3089	1.87	11436	1152	5102	1689	2.24	1-aminocyclopropane-1-carboxylate oxidase
14117_at	At4g37410	3246	804	1736	636	1.87	3057	271	1571	463	1.95	cytochrome P450 monooxygenase - like protein
15985_at	At5g64100	16755	2207	9063	4176	1.85	17824	729	9735	3834	1.83	peroxidase ATP3a (emb CAA67340.1)
16008_i_at	At2g47730	3594	459	1952	1098	1.84	4701	127	2533	853	1.86	glutathione S-transferase (GST6)
16288_at	At2g17720	551	57	304	69	1.81	797	64	391	51	2.04	putative prolyl 4-hydroxylase, alpha subunit
16035_at	At5g02380	39437	3171	21854	11089	1.8	34438	1552	19889	2810	1.73	metallothionein 2b
13119_at	At1g78570	2742	436	1532	774	1.79	3313	220	1378	605	2.4	dTDP-glucose 4,6-dehydratase, putative
17070_at	At1g18250	2648	345	1485	769	1.78	2846	369	1783	320	1.6	pathogenesis-related group 5 protein, putative
13609_at	At4g22010	3136	264	1769	499	1.77	3518	348	2519	148	1.4	pectinesterase like protein
17697_at	At2g46740	1269	168	719	416	1.77	839	147	628	71	1.34	unknown protein
19127_at	At2g03750	258	55	146	72	1.77	481	60	190	109	2.53	putative steroid sulfotransferase
12932_s_at	At5g57090	3068	484	1747	937	1.76	2629	390	1813	366	1.45	auxin transport protein EIR1 (gb AAC39513.1)
18660_at	At4g17670	443	108	253	72	1.75	458	23	97	115	4.72	\NULL
15990_at	At3g55800	639	102	367	115	1.74	843	78	504	214	1.67	sedoheptulose-bisphosphatase precursor
13201_at	At5g54740	1777	366	1028	423	1.73	1987	205	638	231	3.11	2S storage protein-like
12515_at	At2g39700	1354	114	787	319	1.72	1336	193	986	181	1.35	putative expansin
20616_at	At2g32560	4529	859	2633	988	1.72	3550	354	1323	570	2.68	unknown protein
18939_at	At1g30490	186	49	109	13	1.71	194	39	106	57	1.83	HD-Zip protein
16605_s_at	At5g08640	2638	349	1553	454	1.7	3460	208	1707	997	2.03	flavonol synthase (FLS) (sp Q96330)
12786_at	At1g78660	2353	263	1400	270	1.68	2703	198	1629	520	1.66	gamma glutamyl hydrolase, putative
19448_s_at	At1g70710	2172	477	1295	71	1.68	2717	378	1359	135	2	endo-1,4-beta-glucanase
20317_at	At1g48480	637	107	380	94	1.68	556	119	302	94	1.84	protein kinase, putative
16949_s_at	At4g12880	3501	373	2106	1016	1.66	3410	306	2002	544	1.7	blue copper-binding protein, 15K (lamin)
17255_at	At2g25980	1901	174	1142	371	1.66	2687	286	1645	234	1.63	similar to jasmonate-inducible proteins from Brass
16977_at	At4g40060	6328	1814	3853	376	1.64	4886	406	2514	585	1.94	homeodomain - like protein
16637_s_at	At4g14890	1674	121	1026	513	1.63	1784	183	960	406	1.86	Expressed protein
16974_at	At4g15160	2427	693	1492	265	1.63	4823	207	1987	324	2.43	cell wall protein like
19815_at	At1g14210	1400	97	859	392	1.63	1359	151	813	247	1.67	ribonuclease
14729_s_at	At3g26650	2901	231	1793	648	1.62	3067	303	2140	587	1.43	glyceraldehyde 3-phosphate dehydrogenase A subunit
18991_s_at	At3g27660	3497	976	2173	318	1.61	5719	170	1509	476	3.79	oleosin isoform
20155_s_at	At4g26130	794	142	492	76	1.61	1180	122	371	194	3.18	uncharacterized protein
19217_at	At1g05510	484	109	304	67	1.6	815	92	184	145	4.42	hypothetical protein
13441_at	At4g30996	2047	262	1285	274	1.59	1720	242	1219	204	1.41	Expressed protein
13887_s_at	At2g33620	796	60	500	204	1.59	750	114	388	98	1.93	AT-hook DNA-binding protein (AHP1)
16429_at	At1g07890	21484	1412	13520	4773	1.59	18807	1668	11704	2222	1.61	L-ascorbate peroxidase
16432_g_at	At2g38530	18489	2367	11617	4304	1.59	15087	3699	9228	1521	1.63	putative nonspecific lipid-transfer protein
16493_at	At1g54010	69667	9110	44121	11408	1.58	77370	6349	51669	10945	1.5	myrosinase-associated protein, putative
13118_f_at	At1g75480	3260	246	2074	739	1.57	3715	340	2383	307	1.56	pseudogene, gamma-glutamyl hydrolase
13218_s_at	At1g20620	1785	222	1141	364	1.57	2985	291	995	356	3	catalase 3
16009_s_at	At2g47730	3090	213	1962	679	1.57	4436	316	2436	735	1.82	glutathione S-transferase (GST6)
13177_at	At4g12720	377	75	242	37	1.56	367	71	203	56	1.81	growth factor like protein
14547_at	At4g03190	750	102	480	117	1.56	691	7	544	34	1.27	F-box protein GRR1-like protein 1, AtFBL18
15672_s_at	At2g22470	1365	288	882	228	1.55	1022	128	599	157	1.7	unknown protein
20321_s_at	At1g73190	3291	563	2121	407	1.55	5887	136	1850	414	3.18	tonoplast intrinsic protein, alpha (alpha-TIP)
14118_i_at	\NULL	930	236	605	73	1.54	902	104	558	139	1.62	\NULL
15189_s_at	At2g42840	49015	7668	32013	10521	1.53	49516	4005	32518	8225	1.52	En Spm-like transposon protein
18232_at	At2g23910	1385	36	905	265	1.53	1285	129	894	143	1.44	putative cinnamoyl CoA reductase
12741_at	At4g38970	3393	486	2247	576	1.51	4405	357	2670	662	1.65	putative fructose-bisphosphate aldolase
12966_s_at	At4g34590	676	91	447	126	1.51	751	87	502	66	1.5	bZIP transcription factor ATB2
14080_at	At4g37470	3798	540	2517	449	1.51	3416	540	2147	292	1.59	putative protein
14504_s_at	At2g28200	1046	54	691	177	1.51	1032	92	547	384	1.89	putative zinc-finger protein
15451_at	At5g64620	2231	199	1482	246	1.51	3497	215	1728	522	2.02	invertase inhibitor homolog (emb CAA73335.1)

Table 1b. (cont'd)

18622_g_at	At4g23710	1866	230	1245	363	1.5	1478	146	1064	147	1.39	V-ATPase subunit G (vag2 gene)
20529_at	At4g16500	10375	1059	6916	2335	1.5	9933	1346	5069	650	1.96	cysteine proteinase inhibitor like protein
12167_at	At3g51670	956	170	643	130	1.49	1074	75	626	144	1.72	putative protein
13240_f_at	At3g16770	5117	523	3426	454	1.49	4774	953	2518	888	1.9	AP2 domain containing protein RAP2.3
16038_s_at	At5g66400	10814	2439	7270	913	1.49	14005	1041	6178	652	2.27	dehydrin RAB18-like protein (sp P30185)
18311_at	At1g53840	760	163	509	58	1.49	1026	30	434	105	2.37	pectinesterase, putative
13052_s_at	At1g47670	2428	472	1643	234	1.48	2713	324	1574	340	1.72	lysine and histidine specific transporter, putative
15111_s_at	At2g06850	6573	834	4441	1390	1.48	6200	541	4833	313	1.28	putative endoxylglucan glycosyltransferase
16598_s_at	At1g70370	1957	221	1325	179	1.48	2441	202	1753	136	1.39	aromatic rich glycoprotein, putative
17488_at	At2g25810	983	79	665	183	1.48	934	35	613	153	1.52	putative aquaporin (tonoplast intrinsic protein)
18090_s_at	At4g28750	634	38	428	43	1.48	610	63	358	96	1.71	photosystem I subunit PSI-E - like protein
17009_at	At4g31340	5195	1069	3543	263	1.47	4922	353	3139	588	1.57	putative protein
15834_at	At2g07000	547	40	374	101	1.46	583	66	459	75	1.27	unknown protein
16517_at	At5g13630	636	29	436	117	1.46	908	159	459	236	1.98	cobalamin biosynthesis protein
18159_at	At1g27680	794	75	547	91	1.45	834	30	636	79	1.31	ADP-glucose pyrophosphorylase, putative
20238_at	At3g13790	8931	1966	6182	717	1.44	10366	1951	6959	1471	1.49	beta-fructofuranosidase 1
17938_at	At5g65360	11571	652	8100	2192	1.44	11248	1082	8265	1556	1.36	histone H3 (sp P05203)
12752_s_at	At4g21960	1694	291	1191	205	1.42	2840	388	1794	369	1.58	peroxidase prxr1
15594_s_at	At5g07440	2636	204	1859	202	1.42	2040	321	1510	99	1.35	glutamate dehydrogenase 2
13197_r_at	At4g27170	9181	1867	6598	342	1.39	7165	1690	4816	464	1.49	NWMIJ4 - 2S albumin 4 precursor
19839_at	At2g28790	7119	1097	5137	837	1.39	11500	1194	5630	1783	2.04	putative thaumatin
14962_at	At1g04520	848	72	615	91	1.38	998	194	672	86	1.49	unknown protein
15126_s_at	At2g31360	6472	659	4687	716	1.38	6436	458	4855	309	1.33	delta 9 desaturase
12817_g_at	At1g78830	1456	123	1060	185	1.37	1602	326	924	300	1.73	hypothetical protein
17523_s_at	At3g53610	892	67	650	79	1.37	930	128	486	115	1.91	GTPase AtRAB8
12792_s_at	At2g45180	20395	1239	15005	3720	1.36	26965	1366	15778	3530	1.71	unknown protein
14921_at	At2g20930	1612	201	1183	250	1.36	1614	139	1356	126	1.19	unknown protein
13573_at	At4g37550	1037	101	766	96	1.35	1625	201	975	301	1.67	formamidase - like protein
12421_at	At4g26650	1329	168	993	43	1.34	1371	90	942	232	1.46	hnRNP-like protein
13137_at	At2g31380	5256	573	3911	722	1.34	6337	50	3877	293	1.63	putative CONSTANS-like B-box zinc finger protein
15551_at	At4g26910	1517	111	1136	211	1.34	1480	282	942	264	1.57	putative dihydroipoamide succinyltransferase
18581_at	At2g29340	442	40	331	43	1.34	689	147	314	173	2.2	putative tropinone reductase
18933_at	At2g40300	1552	151	1163	171	1.34	1728	160	1411	169	1.22	putative ferritin
20156_at	At3g52470	9267	596	6961	1169	1.33	6916	720	5018	610	1.38	putative protein
12171_at	At3g52500	1353	194	1026	152	1.32	1977	58	937	166	2.11	expressed protein
13116_at	At2g20760	4390	628	3338	547	1.32	4383	450	2825	266	1.55	unknown protein
20385_at	At1g32200	1663	203	1257	231	1.32	1581	303	1115	178	1.42	glycerol-3-phosphate acyltransferase
12779_f_at	At1g54000	10543	824	8062	986	1.31	13738	463	8632	463	1.59	myosinase-associated protein, putative
13154_s_at	At2g43590	7975	999	6106	610	1.31	6533	474	4157	1266	1.57	putative endochitinase
16044_s_at	At1g55670	562	74	431	11	1.31	685	121	507	62	1.35	photosystem I subunit V precursor, putative
14421_at	At2g24290	889	101	690	125	1.29	987	104	641	126	1.54	unknown protein
18330_at	At4g23850	1675	244	1306	162	1.28	1787	198	1078	197	1.66	acyl-CoA synthetase - like protein
16631_s_at	At2g34470	2348	114	1882	252	1.25	2469	141	2012	309	1.23	putative urease accessory protein
15988_at	At5g44340	13437	1279	10959	1243	1.23	14534	551	11554	925	1.26	tubulin beta-4 chain (sp P24636)
17382_at	At2g36290	2328	238	1906	67	1.22	2647	242	1889	451	1.4	unknown protein
13089_at	At2g27860	15799	1311	13448	711	1.17	15251	365	13347	1074	1.14	putative dTDP-glucose 4-6-dehydratase
16504_at	At4g13930	16945	1430	14566	1288	1.16	17859	1823	13803	688	1.29	hydroxymethyltransferase
17878_at	At4g19410	3545	160	3075	84	1.15	3882	95	3205	327	1.21	putative pectinacetyltransferase protein
16902_at	At2g21620	2041	57	1879	107	1.09	2466	373	1945	160	1.27	unknown protein
12796_s_at	At2g26250	5787	301	6403	151	0.9	5375	281	6607	121	0.81	beta-ketoacyl-CoA synthase (FIDDLEHEAD)
15902_at	At1g10180	707	43	833	51	0.85	751	95	947	88	0.79	unknown protein
19930_at	At5g08620	2489	163	2924	191	0.85	2429	243	3310	482	0.73	RNA helicase (emb CAA09212.1)
16069_s_at	At1g23860	5408	602	6420	497	0.84	5419	1842	7772	402	0.7	splicing factor, putative
16102_s_at	At4g57610	3839	409	4569	388	0.84	3521	861	4713	184	0.75	adenylosuccinate synthetase
17463_at	At1g79530	6158	460	7330	534	0.84	6570	664	8183	541	0.8	glyceraldehyde-3-phosphate dehydrogenase, putative
17924_at	At5g07340	3832	285	4612	364	0.83	3277	412	4489	574	0.73	calnexin homolog
18002_at	At5g52470	13490	1403	16207	1598	0.83	13467	2234	17638	2288	0.76	fibrillarin 1 AtFib1 SKIP7
20639_at	At4g37910	7645	256	9341	413	0.82	7778	638	9687	779	0.8	heat shock protein 70 like protein
12613_at	At2g34750	2157	261	2678	234	0.81	2203	360	2749	31	0.8	unknown protein
12794_at	At2g37270	12846	1799	15782	975	0.81	11535	2130	16462	328	0.7	40S ribosomal protein S5
13560_at	At1g16270	1750	219	2149	224	0.81	1968	15	2213	148	0.89	putative Ser Thr protein kinase
14531_at	At4g02680	2004	224	2465	274	0.81	2167	226	2797	164	0.77	hypothetical protein
14688_at	At2g37490	986	111	1212	123	0.81	1198	151	1421	42	0.84	unknown protein
15082_at	At1g15140	1036	72	1289	105	0.8	989	234	1352	143	0.73	unknown protein
18010_s_at	At3g54110	9378	923	11781	327	0.8	8602	394	11138	459	0.77	uncoupling protein (ucp PUMP)
19407_at	NULL	697	103	868	74	0.8	574	148	801	104	0.72	NULL
20344_at	At2g15090	2206	280	2770	200	0.8	1498	443	2364	182	0.63	putative fatty acid elongase
19190_g_at	At4g38580	7037	497	8956	1384	0.79	5804	612	8325	782	0.7	farnesylated protein (ATFP6)
18369_at	At4g16390	1554	107	2002	334	0.78	1523	370	2218	313	0.69	salt-inducible protein homolog
19471_at	At4g32300	698	92	893	128	0.78	727	78	520	113	1.4	S-receptor kinase -like protein
12002_at	At4g02940	1597	174	2082	324	0.77	1311	415	2016	51	0.65	hypothetical protein
13896_at	At1g60140	424	72	553	57	0.77	500	85	670	36	0.75	trehalose-6-phosphate synthase, putative
18713_at	At4g02930	11658	2242	15083	1603	0.77	10684	1140	13951	741	0.77	mitochondrial elongation factor Tu
16025_s_at	At4g28520	3846	589	5051	741	0.76	9037	808	5008	892	1.8	12S cruciferin seed storage protein
18716_at	At1g75830	52560	12729	69549	3490	0.76	36233	11721	58869	668	0.62	unknown protein
19670_at	At4g10450	10795	1119	14248	1176	0.76	10260	1875	14505	934	0.71	putative ribosomal protein L9, cytosolic
12485_at	At4g32520	3420	512	4588	532	0.75	3155	281	4629	261	0.68	glycine hydroxymethyltransferase (EC 2.1.2.1) - li
14416_at	At2g14880	3754	440	4998	727	0.75	4409	199	5622	471	0.78	unknown protein
16451_at	At3g58610	17563	1682	23414	1568	0.75	19012	1073	22716	769	0.84	ketol-acid reductoisomerase
20314_s_at	At4g11240	2192	137	2933	212	0.75	2278	373	3182	166	0.72	protein phosphatase type 1 PP1BG
13592_g_at	At4g21810	2611	413	3548	506	0.74	2117	698	3769	252	0.56	putative protein
14126_s_at	At4g34740	2829	491	3804	387	0.74	2808	680	4260	304	0.66	amidophosphoribosyltransferase 2 precursor

Table 1b. (cont'd)

14651_at	At1g23820	9616	1748	12963	1420	0.74	10191	2764	14264	473	0.71	putative spermidine synthase
15143_s_at	At4g11840	385	70	521	36	0.74	547	88	416	34	1.31	putative phospholipase D-gamma
18280_at	At1g21000	1359	209	1843	315	0.74	1498	190	2095	158	0.71	unknown protein
18659_at	At5g45350	1670	278	2262	389	0.74	1618	172	2202	110	0.73	unknown protein
18710_at	At5g11770	7567	1389	10193	780	0.74	7897	786	10310	394	0.77	NADH dehydrogenase (ubiquinone)
12484_g_at	At2g37690	1285	215	1763	284	0.73	1423	116	1862	216	0.76	putative phosphoribosylaminoimidazole carboxylase
15928_at	At1g49510	1010	188	1384	128	0.73	1103	192	1449	115	0.76	unknown protein
17484_at	At1g17020	8205	1908	11166	1055	0.73	6529	2454	11904	1206	0.55	SRG1-like protein
19227_at	At4g13830	1305	106	1798	361	0.73	1166	109	1653	112	0.71	DnaJ-like protein
19830_at	At2g15690	2640	615	3611	303	0.73	2733	390	3972	417	0.69	Expressed protein
20041_at	At1g49850	910	212	1250	157	0.73	868	114	1137	65	0.76	RING-H2 finger protein RHY1a
13292_at	At1g04550	549	122	758	81	0.72	576	239	978	67	0.59	putative auxin-induced protein, IAA12
13868_at	At1g15440	1789	260	2487	398	0.72	1760	293	2763	319	0.64	hypothetical protein
15155_s_at	At1g43170	22569	4001	31328	1146	0.72	23090	1683	28886	2510	0.8	ribosomal protein
15179_s_at	At3g01120	5362	624	7405	1471	0.72	5321	491	7508	667	0.71	putative cystathionine gamma-synthase
12251_at	At2g34930	1659	345	2341	380	0.71	1453	700	2572	109	0.56	putative disease resistance protein
13467_at	At3g47420	2195	169	3098	484	0.71	1892	742	3132	266	0.6	putative protein
15578_s_at	At2g27050	870	145	1220	111	0.71	782	133	1123	114	0.7	ethylene-insensitive3-like1 (EIL1)
13237_at	At4g33510	1664	332	2426	310	0.69	1821	551	2822	126	0.65	2-dehydro-3-deoxyphosphoheptonate aldolase
13561_at	NULL	1363	214	1968	310	0.69	1128	128	1679	131	0.67	NULL
14384_at	At2g35040	2812	275	4065	475	0.69	2885	686	4124	492	0.7	putative phosphoribosylaminoimidazolecarboxamide f
16290_at	At4g04940	874	166	1260	116	0.69	769	178	1323	126	0.58	putative WD-repeat membrane protein
19124_i_at	At1g14920	657	198	957	138	0.69	620	51	765	32	0.81	signal response protein (GAI)
20005_s_at	At2g47990	2556	556	3690	605	0.69	2200	368	3224	414	0.68	unknown protein
20668_at	At2g45240	1623	319	2366	175	0.69	1823	267	2311	195	0.79	putative methionine aminopeptidase
12268_at	At4g13910	4761	907	6991	253	0.68	4522	477	6309	1036	0.72	putative disease resistance protein
14381_at	At2g02810	342	36	501	121	0.68	319	54	473	52	0.68	unknown protein
19915_at	At2g32070	1523	173	2237	397	0.68	1451	154	1918	167	0.76	putative CCR4-associated factor
13591_at	At4g21810	1522	456	2288	340	0.67	1392	421	2219	186	0.63	putative protein
14945_at	At4g25620	431	33	648	122	0.67	399	80	585	93	0.68	putative protein
17426_at	At1g78080	927	138	1393	283	0.67	585	209	1126	125	0.52	AP2 domain containing protein, putative
19376_at	At2g17760	634	81	948	199	0.67	527	153	845	105	0.62	putative chloroplast nucleoid DNA-binding protein
20507_at	At4g22720	765	187	1157	152	0.66	805	164	1335	88	0.6	glycoprotein endopeptidase - like protein
16086_s_at	At2g16570	2653	718	4080	595	0.65	2399	880	4512	245	0.53	amidophosphoribosyltransferase
17178_at	At1g20910	374	54	574	38	0.65	326	118	511	81	0.64	hypothetical protein
11996_at	At2g39020	3405	821	5358	1077	0.64	3991	521	5475	390	0.73	unknown protein
12436_at	At4g27680	620	157	975	43	0.64	744	125	1008	14	0.74	putative protein
15421_at	At4g01410	866	261	1360	206	0.64	746	135	986	124	0.76	putative hypersensitive response protein
15647_s_at	At4g14680	899	174	1412	189	0.64	816	224	1193	49	0.68	ATP-sulfurylase
14077_at	At4g08950	2290	632	3650	484	0.63	1426	494	2723	391	0.52	putative phi-1-like phosphate-induced protein
18596_at	At1g62570	1792	338	2847	492	0.63	1453	341	2356	147	0.62	flavin-containing monooxygenase, putative
15186_s_at	At1g62180	1344	346	2167	375	0.62	1110	363	1804	163	0.62	5-adenylylphosphosulfate reductase, putative
16062_s_at	At4g25470	2177	375	3517	162	0.62	2394	552	3580	292	0.67	DRE CRT-binding protein DREB1C
13355_at	At5g07360	765	200	1264	336	0.61	996	204	1377	111	0.72	putative amidase
15674_at	At3g25585	913	277	1490	248	0.61	881	243	1568	59	0.56	aminoalcoholphosphotransferase, putative
16045_at	At4g15390	11396	2617	18532	4185	0.61	12724	953	17977	1598	0.71	HSR201 like protein
18696_s_at	At1g62180	780	223	1273	286	0.61	607	178	989	58	0.61	5-adenylylphosphosulfate reductase, putative
12072_at	At4g25170	1279	350	2122	238	0.6	1353	122	1775	130	0.76	putative protein
15178_s_at	At4g14130	2728	967	4700	578	0.58	2181	465	5138	173	0.42	xyloglucan endotransglycosylase-related protein XT
13099_s_at	At1g22710	2729	542	4777	847	0.57	2424	1062	4903	140	0.49	putative sucrose transport protein, SUC2
15109_s_at	At1g12110	1919	512	3429	571	0.56	1690	319	3607	229	0.47	putative NPK1-related protein kinase 2
12169_i_at	At4g33960	683	355	1245	281	0.55	693	401	1529	70	0.45	putative protein
14367_at	At1g60190	673	351	1274	249	0.53	589	133	1067	61	0.55	hypothetical protein
20517_at	At5g59430	298	124	557	137	0.53	346	163	628	85	0.55	telomere repeat-binding protein
17545_s_at	At4g37580	2825	1511	5606	996	0.5	2186	2084	5597	478	0.39	probable N-acetyltransferase hookless 1
18250_at	At5g16990	142	45	281	68	0.5	178	52	292	32	0.61	quinone oxidoreductase - like protein
20450_at	At5g24150	1927	1049	3879	853	0.5	1450	760	3989	309	0.36	squalene monooxygenase
12166_i_at	At4g04830	763	377	1570	410	0.49	637	202	1612	82	0.4	putative protein
20117_at	At4g16370	395	169	801	223	0.49	361	99	886	46	0.41	isp4 like protein
14789_at	At2g15010	520	216	1073	298	0.48	656	96	1104	106	0.59	putative thionin
12946_at	At1g15110	140	29	298	65	0.47	148	57	225	18	0.66	putative phosphatidylserine synthase
19878_at	At4g08290	2194	1392	4764	1298	0.46	1361	540	3838	328	0.35	nodulin-like protein
20175_at	At2g28420	5336	2609	11477	3119	0.46	5276	1522	14491	866	0.36	unknown protein
20283_at	NULL	414	308	894	154	0.46	742	326	1349	164	0.55	NULL
19516_at	At1g54730	185	115	469	77	0.39	319	82	509	58	0.63	integral membrane protein, putative
16667_at	At3g48130	140	147	389	116	0.36	17	25	361	117	0.05	ribosomal protein L13 homolog
18235_at	At1g27020	127	135	361	127	0.35	142	71	540	88	0.26	unknown protein
16896_s_at	At2g41260	929	956	3092	889	0.33	933	594	3008	154	0.31	late embryogenesis abundant M17 protein
19548_at	At2g15050	121	134	447	81	0.27	91	98	388	93	0.24	putative lipid transfer protein
19051_at	At2g36970	42	26	159	76	0.26	117	61	237	28	0.49	putative glucosyltransferase
17572_s_at	At1g64780	161	279	668	96	0.24	189	244	1147	155	0.16	ammonium transporter, putative
19720_at	At1g22690	-27	96	-208	52	0.13	-27	45	-159	40	0.17	putative gibberellin-regulated protein
12869_s_at	At4g11880	55	75	-81	29	-0.68	22	72	-130	51	-0.17	MADS-box protein AGL14
17024_s_at	At1g64900	48	56	-59	65	-0.81	319	64	12	57	27.72	cytochrome p450, putative
13231_at	At1g32210	49	57	-52	45	-0.94	-7	16	88	25	-0.07	defender against cell death protein, putative
19794_at	At2g45490	81	89	-71	26	-1.14	39	46	-69	34	-0.56	putative protein kinase
16699_at	At2g31100	48	12	-34	55	-1.44	-62	28	21	9	-2.96	putative lipase
18204_at	At4g35030	40	4	-15	21	-2.69	-25	32	46	39	-0.54	protein kinase - like
17953_at	At4g01480	265	184	-46	49	-5.8	136	153	-128	98	-1.07	putative inorganic phosphatase
16034_at	At1g32060	285	45	-10	131	-29.23	428	72	-39	147	-10.97	phosphoribulokinase precursor

Table 2. Genes that exhibit uniconazole-P-dependent transcription based on the criteria (Pkl vs. Upkl $p < 0.05$ Wt vs. Uwt $p < 0.05$)

Wt=Wild type, Pkl= pickle mutant, Uwt=uniconazole-P treated wild type, Upkl= uniconazole-P treated pickle mutant
 Mean = mean value for a given treatment, SD= standard deviation of the mean for a given treatment
 Ratios are given for specific treatment comparisons and Data was sorted by the ratio of Uwt/Wt
 This data set contains 69 genes

Affy Code	AGI Code	Wt Mean	Wt SD	Uwt Mean	UwtSD	p value Wt v Uwt	Uwt/Wt	Pkl Mean	Pkl SD	Upkl Mean	Upkl SD	p value Pkl v Upkl	Upkl/Pkl	Putative Identification
12788_at	At1g23130	-15.75	19.31	-105.00	18.20	5.00E-04	6.67	-44.50	38.42	-126.75	25.25	1.20E-02	2.85	unknown protein
13822_s_at	At2g31540	-20.75	28.92	-137.00	53.20	8.60E-03	6.60	-166.50	51.18	-16.25	52.65	6.00E-03	0.10	putative GDSL-motif lipase hydrolase
20027_at	At1g50420	170.75	113.54	911.50	157.05	3.00E-04	5.34	201.25	31.47	1347.00	187.30	0.00E+00	6.69	scarecrow-like 3
19085_at	At2g37060	65.75	61.55	200.25	23.64	6.50E-03	3.05	111.25	19.26	23.00	38.45	6.00E-03	0.21	putative CCAAT-box binding transcription factor
17739_at	At5g51810	173.00	78.97	518.50	216.37	2.40E-02	3.00	328.75	76.87	1520.75	230.88	0.00E+00	4.63	gibberellin 20-oxidase (emb CAA58294.1)
17299_s_at	At4g25420	165.75	111.82	495.50	94.62	4.10E-03	2.99	185.25	76.37	850.00	248.67	2.00E-03	4.59	gibberellin 20-oxidase - Arabidopsis thaliana
13516_at	At4g18690	112.25	75.01	286.50	103.36	3.42E-02	2.55	215.25	104.35	594.50	107.61	2.00E-03	2.76	putative protein
12368_at	At5g07200	1413.25	500.10	3386.00	381.23	8.00E-04	2.40	525.25	442.45	3780.25	252.68	0.00E+00	7.20	gibberellin 20-oxidase
12103_at	At1g20890	98.25	85.38	233.50	65.37	4.56E-02	2.38	178.50	66.92	275.00	39.21	4.70E-02	1.54	unknown protein
18350_at	At4g35390	194.00	95.84	401.75	120.53	3.57E-02	2.07	156.25	61.86	352.75	119.50	2.70E-02	2.26	putative protein
19683_at	At1g62500	302.75	85.06	596.25	80.72	2.40E-03	1.97	653.50	110.00	1616.50	470.66	7.00E-03	2.47	putative proline-rich cell wall protein (pir IS529)
12881_s_at	NULL	1124.00	103.71	2160.25	633.69	1.80E-02	1.92	1676.50	299.81	2883.00	506.52	6.00E-03	1.72	NULL
17549_at	At1g15550	925.50	108.89	1739.00	273.95	1.50E-03	1.88	667.75	295.86	1986.75	254.00	1.00E-03	2.98	gibberellin 3 beta-hydroxylase, putative
18439_s_at	At3g26570	729.50	117.12	1249.50	263.64	1.13E-02	1.71	855.25	182.03	1246.00	192.99	2.60E-02	1.46	phosphate transporter, putative
17310_at	At3g51810	2999.00	413.49	5033.00	874.08	5.60E-03	1.68	3032.25	277.66	8118.00	501.98	0.00E+00	2.66	embryonic abundant protein AtEm1
14097_at	At2g47770	1482.00	161.84	2325.50	149.13	3.00E-04	1.57	1469.75	103.53	2940.50	576.17	2.00E-03	3.00	unknown protein
20375_at	At1g48130	793.00	198.58	1198.00	238.12	4.00E-02	1.51	764.75	86.84	2787.25	827.11	3.00E-03	2.64	peroxidoxin
12752_s_at	At4g21960	1191.25	290.70	1794.00	388.23	4.74E-02	1.51	1693.75	205.16	2839.50	368.73	2.00E-03	1.68	peroxidase prx1
12538_at	At1g11580	4539.00	1366.07	6614.25	872.36	4.29E-02	1.46	4418.00	736.67	6599.25	394.86	2.00E-03	1.49	pectin methyltransferase, putative
17255_at	At2g25980	1142.00	174.10	1645.25	285.60	2.37E-02	1.44	1901.00	370.55	2686.50	233.84	1.20E-02	1.41	similar to jasmonate-inducible proteins from Brass
18022_at	At5g40760	219.25	44.66	315.50	49.18	2.74E-02	1.44	281.25	77.89	436.50	74.74	2.80E-02	1.55	glucose-6-phosphate dehydrogenase
15068_at	At2g29660	510.00	98.86	732.50	69.19	1.02E-02	1.44	469.00	126.16	644.75	49.56	4.10E-02	1.37	unknown protein
17038_s_at	At2g36640	707.00	84.83	1011.50	119.58	6.00E-03	1.43	519.25	63.02	841.00	202.00	2.30E-02	1.62	late embryogenesis abundant protein (ATECP63)
16503_at	At5g35630	311.75	79.96	443.00	50.23	3.20E-02	1.42	425.00	181.21	797.50	108.61	1.20E-02	1.88	glutamate-ammonia ligase (EC 6.3.1.2) precursor, c
12777_i_at	At1g54000	12508.25	994.29	17700.25	2732.06	1.18E-02	1.42	14460.25	2208.00	21379.75	3780.66	2.00E-02	1.48	myrosinase-associated protein, putative
12459_i_at	At2g15400	613.50	87.24	849.50	168.76	4.75E-02	1.38	618.50	111.37	867.75	51.89	7.00E-03	1.40	DNA-directed RNA polymerase II, third largest subu
15131_s_at	At1g28330	2919.50	367.98	4002.00	323.10	4.50E-03	1.37	3133.25	415.69	4790.25	538.84	3.00E-03	1.53	dormancy-associated protein, putative
16598_s_at	At1g70370	1325.25	221.15	1752.50	201.98	2.91E-02	1.32	1956.75	178.51	2440.50	136.00	5.00E-03	1.25	aromatic rich glycoprotein, putative
18872_at	At3g17520	1759.50	152.95	2285.50	282.54	1.69E-02	1.30	1473.75	199.83	2457.00	414.06	5.00E-03	1.67	unknown protein
18073_g_at	At4g03280	1719.00	183.47	2216.75	249.11	1.82E-02	1.29	2037.25	238.35	2459.25	204.29	3.60E-02	1.21	putative component of cytochrome B6-F complex
15938_at	At4g33100	289.25	43.58	373.00	33.93	2.30E-02	1.29	414.25	137.07	222.50	45.67	3.80E-02	0.54	putative protein
15949_s_at	At2g39730	686.00	44.50	883.00	70.80	3.30E-03	1.29	724.50	59.43	1025.75	166.96	1.50E-02	1.42	hypothetical protein
16168_s_at	At2g14260	709.00	81.41	904.75	84.99	1.59E-02	1.28	572.25	212.81	970.50	191.70	3.20E-02	1.70	proline iminopeptidase
17568_at	At3g25860	2080.00	267.75	2619.50	236.01	2.33E-02	1.26	2199.50	159.03	2543.50	30.70	5.00E-03	1.16	dihydroliipoamide S-acetyltransferase
16009_s_at	At2g47730	1962.25	212.82	2435.50	315.65	4.74E-02	1.24	3089.50	678.65	4435.75	735.10	3.60E-02	1.44	glutathione S-transferase (GST6)
18685_at	At4g30950	2799.00	69.69	3455.25	474.10	3.38E-02	1.23	2919.75	239.95	3338.50	222.86	4.30E-02	1.14	chloroplast omega-6 fatty acid desaturase (fad6)
13629_s_at	At2g38120	3446.00	194.36	2970.25	312.81	4.16E-02	0.86	2912.75	492.58	2188.75	201.13	3.50E-02	0.75	unknown protein
18946_at	At5g39580	8397.00	774.42	6730.75	563.51	1.31E-02	0.80	8011.50	1063.13	6401.50	482.43	3.30E-02	0.80	peroxidase ATP24a
18706_s_at	At2g14750	2307.75	153.96	1822.00	133.03	3.10E-03	0.79	2629.00	197.13	2103.50	218.02	1.20E-02	0.80	putative adenosine phosphosulfate kinase
16495_at	At5g66040	3410.25	400.37	2614.75	85.50	8.10E-03	0.77	4480.25	778.84	2940.50	292.40	1.00E-02	0.66	senescence-associated protein
15194_s_at	At5g15230	14574.25	2532.56	11060.00	822.55	3.86E-02	0.76	18371.50	4589.06	10965.25	1324.82	2.10E-02	0.76	GASA4
19459_at	At4g36880	37492.25	4168.40	28158.00	5808.82	4.01E-02	0.75	37121.75	5522.94	28046.00	3444.45	3.20E-02	0.60	cysteine proteinase
16087_s_at	At3g08730	1918.00	342.17	1422.00	105.25	3.24E-02	0.74	1704.50	87.87	1190.75	143.89	1.00E-03	0.70	putative ribosomal-protein S6 kinase (ATPK6)
12523_at	At1g69530	52336.75	5313.38	38006.25	7107.05	1.79E-02	0.73	41144.25	7919.06	27232.00	4673.30	2.30E-02	0.66	expansin (At-EXP1)
20156_at	At3g52470	6960.50	596.30	5017.50	719.51	6.00E-03	0.72	9267.25	1169.20	6915.75	609.90	1.20E-02	0.75	putative protein
20605_at	At1g27150	527.50	104.13	376.75	34.06	3.32E-02	0.71	482.25	33.77	375.75	66.97	3.00E-02	0.78	unknown protein
18339_at	At4g01450	3611.50	615.34	2541.75	227.21	1.72E-02	0.70	3453.25	406.14	2153.75	424.53	4.00E-03	0.62	predicted protein of unknown function
15483_s_at	At2g46650	1421.50	67.88	948.50	106.66	3.00E-04	0.67	1824.00	223.90	1243.50	234.60	1.20E-02	0.68	putative cytochrome b5
14019_at	At2g17280	1411.25	125.88	934.00	232.84	1.13E-02	0.66	1215.25	235.71	724.25	96.11	8.00E-03	0.60	unknown protein
15355_at	At4g21560	1527.00	310.76	997.50	220.99	3.21E-02	0.65	1168.50	79.58	962.00	85.86	1.20E-02	0.82	putative protein
14620_at	At5g17990	684.00	115.45	444.75	132.19	3.44E-02	0.65	592.50	52.11	439.25	81.34	1.90E-02	0.74	anthranilate phosphoribosyltransferase, chloroplas
19737_at	At1g01580	478.75	33.34	309.75	95.30	1.55E-02	0.65	527.50	94.09	737.00	77.71	1.40E-02	1.40	hypothetical protein
20487_at	At4g34810	826.75	110.02	525.50	59.16	2.90E-03	0.64	1030.75	249.16	619.75	131.55	2.70E-02	0.60	putative protein
16438_at	At1g03870	3353.75	701.33	2127.50	650.53	4.27E-02	0.63	3869.00	425.81	2979.00	411.69	2.40E-02	0.77	unknown protein
17577_g_at	At1g23080	1101.75	235.69	689.50	60.79	1.47E-02	0.63	1377.50	213.70	966.75	181.42	3.20E-02	0.72	putative auxin transport protein
13793_at	At4g26790	852.25	137.18	530.75	107.10	1.02E-02	0.62	820.25	91.08	575.50	138.33	2.50E-02	0.70	putative APG protein
12150_at	At2g44080	822.75	58.05	504.75	133.42	4.70E-03	0.61	1002.50	209.27	541.00	51.27	5.00E-03	0.54	unknown protein
15997_s_at	At1g20440	6094.50	1295.56	3679.00	657.63	1.59E-02	0.60	8179.75	1594.37	5439.25	417.41	1.60E-02	0.66	hypothetical protein
17960_at	At1g65310	726.75	270.26	321.25	71.18	2.73E-02	0.44	1121.75	204.27	539.25	120.31	3.00E-03	0.48	xyloglucan endotransglycosylase, putative
12512_at	At2g44220	219.25	42.16	82.75	54.87	7.60E-03	0.38	60.25	36.47	139.75	35.40	2.00E-02	2.32	hypothetical protein
19565_at	At3g02885	732.25	217.48	221.25	127.37	6.70E-03	0.30	590.50	216.52	264.50	154.75	5.00E-02	0.45	Expressed protein
16440_at	At2g40000	275.00	112.09	80.50	90.61	3.56E-02	0.29	280.50	76.97	132.25	68.66	2.80E-02	0.47	putative nematode-resistance protein
14413_at	At4g02860	145.50	23.56	39.25	53.69	1.10E-02	0.27	82.50	80.43	209.00	21.62	2.30E-02	2.53	putative protein
13854_at	At2g28830	125.00	28.25	3.25	40.48	2.60E-03	0.03	68.25	42.90	-21.75	30.38	1.40E-02	-0.32	hypothetical protein
16231_at	At3g57730	74.50	52.36	-35.00	60.96	3.44E-02	-0.47	-9.00	78.03	153.00	73.72	2.30E-02	-17.00	putative protein
16699_at	At2g31100	-33.50	11.73	20.75	28.24	1.21E-02	-0.62	48.25	54.96	-61.50	9.47	8.00E-03	-1.27	putative lipase
18204_at	At4g35030	-14.75	4.27	45.50	31.72	9.30E-03	-3.08	39.75	20.58	-24.75	39.08	2.70E-02	-0.62	protein kinase - like
18848_at	At2g01840	-24.00	79.03	90.75	43.57	4.39E-02	-3.78	8.50	37.19	79.25	39.51	4.00E-02	9.32	putative non-LTR retroelement reverse transcriptas
15298_at	At2g04810	-19.00	60.04	180.25	123.80	2.75E-02	-9.49	-80.50	56.60	52.50	71.29	2.70E-02	-0.65	hypothetical

Table 3. Genes that exhibit uniconazole-P-dependent and *PKL*-dependent transcription based on the criteria (Wt vs. Upkl $p < 0.05$ \square Pkl vs. Upkl $p < 0.05$ \square Uwt vs. Upkl $p < 0.05$).

Wt=Wild type, Pkl= pickle mutant, Uwt=uniconazole-P treated wild type, Upkl= uniconazole-P treated pickle mutant
Mean = mean value for a given treatment, SD= standard deviation of the mean for a given treatment
Ratios are given for specific treatment comparisons and Data was sorted by the ratio of Upkl/Pkl
There are 88 genes here

Affy Code	AGI Code	Pkl Mean	Pkl SD	Wt Mean	Wt SD	Upkl Mean	Upkl SD	Uwt Mean	Uwt SD	p value pkl v Upkl	p value Upkl v Wt	p value Upkl v Uwt	Upkl/Wt	Upkl/Pkl	Upkl/Uwt	Putative Identification
17024_s_at	At1g64900	47.50	64.54	-58.75	55.83	318.75	56.59	11.50	63.98	7.82E-04	8.10E-05	4.33E-04	-5.43	6.71	27.72	cytochrome p450, putative
20027_at	At1g50420	201.25	31.47	170.75	113.54	1347.00	187.30	911.50	157.05	5.10E-06	2.58E-05	1.09E-02	7.89	6.69	1.48	scarecrow-like 3
13449_at	At4g36700	215.00	60.23	179.50	86.16	1206.00	204.91	357.75	226.70	3.77E-05	4.77E-05	1.60E-03	6.72	5.61	3.37	globulin-like protein
17739_at	At5g51810	328.75	76.87	173.00	78.97	1520.75	230.88	518.50	216.37	2.77E-05	1.29E-05	9.35E-04	8.79	4.63	2.93	gibberellin 20-oxidase (emb CAA58294.1)
17299_s_at	At4g25420	185.25	76.37	165.75	111.82	850.00	248.67	495.50	94.62	1.41E-03	1.83E-03	3.52E-02	5.13	4.59	1.72	gibberellin 20-oxidase - Arabidopsis thaliana
19031_at	At2g10010	-32.00	41.43	-6.00	35.92	-131.00	16.99	-54.75	28.95	4.13E-03	6.83E-04	3.71E-03	21.83	4.09	2.39	putative TNP2-like transposon protein
15280_at	At2g19900	109.00	52.31	108.00	41.85	409.00	73.48	165.50	100.88	4.76E-04	3.03E-04	6.01E-03	3.79	3.75	2.47	malate oxidoreductase (malic enzyme)
20347_s_at	At1g48130	764.75	86.84	793.00	198.58	2787.25	827.11	1198.00	238.12	7.53E-04	1.17E-03	5.55E-03	3.51	3.64	2.33	peroxiredoxin
17282_s_at	At3g51810	642.50	96.62	726.25	136.65	1957.25	135.52	820.25	206.52	3.98E-06	1.87E-05	9.93E-04	2.70	3.05	2.39	embryonic abundant protein AtEm1
20196_at	At1g08630	124.25	116.72	59.50	44.43	343.75	51.59	133.75	106.38	1.48E-02	1.62E-04	1.24E-02	5.78	2.77	2.57	unknown protein
13516_at	At4g18690	215.25	104.35	112.25	75.01	594.50	107.61	286.50	103.36	2.47E-03	2.97E-04	6.76E-03	5.30	2.76	2.08	putative protein
15708_at	At2g34700	91.00	64.82	63.00	43.38	251.25	67.89	108.25	61.28	1.48E-02	3.35E-03	2.14E-02	3.99	2.76	2.32	putative proline-rich glycoprotein
17310_at	At3g51810	3032.25	277.66	2999.00	413.49	8118.00	501.98	5033.00	874.08	1.50E-06	7.91E-06	1.23E-03	2.71	2.68	1.61	embryonic abundant protein AtEm1
19683_at	At1g62500	653.50	110.00	302.75	85.06	1616.50	470.66	596.25	80.72	3.77E-03	4.72E-04	2.39E-03	5.34	2.47	2.71	putative proline-rich cell wall protein (pir IS529)
20535_at	At2g28490	819.00	137.65	681.50	122.40	1992.50	73.10	836.50	143.90	1.37E-05	4.26E-06	1.54E-05	2.92	2.43	2.38	putative seed storage protein (vicilin-like)
18714_at	At5g51210	1464.75	618.94	1163.00	428.04	3543.75	823.25	1894.75	586.95	6.09E-03	1.10E-03	1.36E-02	3.05	2.42	1.87	oleosin-like
16025_s_at	At4g28520	3845.50	740.86	5050.75	588.94	9036.75	891.59	5007.75	807.57	1.36E-04	2.52E-04	6.17E-04	1.79	2.35	1.80	12S cruciferin seed storage protein
19979_at	At1g67330	542.50	317.16	54.50	143.53	1132.25	308.13	-13.00	76.03	4.28E-02	3.58E-04	9.29E-05	20.78	2.09	-87.10	unknown protein
13199_r_at	NULL	7591.25	665.41	7691.75	560.11	15518.25	2423.02	9914.00	2824.89	2.52E-04	2.27E-04	2.31E-02	2.02	2.04	1.57	NULL
15117_at	At1g44575	710.25	465.40	418.75	342.64	1420.50	305.36	436.75	164.46	5.98E-02	8.12E-03	9.95E-04	3.39	2.00	3.25	photosystem II 22kDa protein, putative
16974_at	At4g15160	2427.25	264.78	1492.00	692.82	4823.00	324.41	1987.00	207.32	2.35E-05	4.09E-04	6.03E-06	3.23	1.99	4.23	cell wall protein like
16503_at	At5g35630	425.00	181.21	311.75	79.96	797.50	108.61	443.00	50.23	1.56E-02	2.98E-04	7.42E-04	2.56	1.88	1.80	glutamate-ammonia ligase (EC 6.3.1.2) precursor, c
19127_at	At2g03750	257.50	71.86	145.50	54.76	481.00	109.47	190.00	59.54	1.29E-02	1.15E-03	2.78E-03	3.31	1.87	2.53	putative steroid sulfotransferase
17775_at	At1g61800	2764.50	190.45	2447.75	294.64	5045.75	532.83	2628.75	743.86	1.06E-04	1.03E-04	4.28E-03	2.06	1.83	1.92	glucose-6-phosphate phosphate-translocator precursor
20321_s_at	At1g73190	3291.00	406.59	2120.50	562.91	5887.00	413.58	1850.25	136.11	1.29E-04	9.70E-05	5.03E-07	2.78	1.79	3.18	tonoplast intrinsic protein, alpha (alpha-TIP)
16053_l_at	At1g02920	1185.75	272.13	860.75	402.76	2000.75	202.18	636.00	165.74	4.11E-03	4.02E-03	4.96E-05	2.32	1.69	3.15	glutathione S-transferase, putative
15199_s_at	At5g20960	3567.75	1182.36	3658.50	777.77	6017.25	551.02	4327.25	903.79	1.33E-02	6.10E-03	2.27E-02	1.56	1.69	1.39	aldehyde oxidase AAO1
19217_at	At1g05510	484.25	87.40	303.50	108.82	815.25	144.79	184.25	91.53	5.09E-03	1.21E-03	2.57E-04	2.69	1.68	4.42	hypothetical protein
12752_s_at	At4g21960	1693.75	205.16	1191.25	290.70	2839.50	368.73	1794.00	388.23	1.33E-03	3.86E-04	8.26E-03	2.38	1.68	1.58	peroxidase prx1
13218_s_at	At1g20620	1785.00	363.66	1140.50	221.51	2985.25	358.80	995.00	291.09	4.37E-03	1.11E-04	2.07E-04	2.62	1.67	3.00	catalsase 3
18991_s_at	At3g27660	3497.00	317.99	2173.25	976.01	5718.75	475.76	1509.00	169.73	1.95E-04	1.36E-03	9.51E-07	2.63	1.64	3.79	oleosin isoform
15965_at	At3g16460	2535.50	932.97	1163.25	848.34	4134.50	652.73	1265.25	117.79	4.84E-02	2.37E-03	2.59E-05	3.56	1.63	3.27	putative lectin
19839_at	At2g28790	7118.50	836.81	5137.00	1096.72	11500.00	1782.90	5629.75	1194.50	2.49E-03	5.77E-04	1.47E-03	2.24	1.62	2.04	putative thaumatin
15198_at	At1g76090	735.75	99.57	604.75	86.08	1183.50	52.95	642.50	149.31	1.85E-04	3.94E-05	7.29E-04	1.96	1.61	1.84	S-adenosyl-methionine-sterol-C-methyltransferase,
13144_at	At2g35860	536.75	109.55	467.00	122.49	855.25	107.46	570.25	166.44	6.53E-03	3.39E-03	3.21E-02	1.83	1.59	1.50	unknown protein
14018_at	At1g09750	2413.50	372.18	1289.50	468.52	3801.50	204.31	1449.50	101.56	9.65E-04	2.11E-04	4.65E-07	2.95	1.58	2.62	hypothetical protein
15451_at	At5g64620	2230.75	246.26	1482.00	199.20	3496.75	522.33	1727.50	215.41	3.65E-03	1.81E-04	4.52E-04	2.36	1.57	2.02	invertase inhibitor homolog (emb CAA73335.1)
13573_at	At4g37550	1037.25	96.47	765.50	100.92	1625.00	301.30	974.75	200.97	3.67E-03	8.22E-04	9.61E-03	2.12	1.57	1.67	formamidase - like protein
18022_at	At5g40760	281.25	77.89	219.25	44.66	436.50	74.74	315.50	49.18	2.76E-02	2.21E-03	3.47E-02	1.99	1.55	1.38	glucose-6-phosphate dehydrogenase
17492_at	At1g80340	2862.00	391.24	2336.75	378.98	4379.25	266.10	2578.00	552.08	1.14E-03	2.32E-04	1.64E-03	1.87	1.53	1.70	gibberellin 3 beta-hydroxylase
15131_s_at	At1g28330	3133.25	415.69	2919.50	367.98	4790.25	537.84	4002.00	323.10	2.56E-03	9.76E-04	4.29E-02	1.64	1.53	1.20	domoyancy-associated protein, putative
16575_s_at	At5g40420	4969.00	903.06	4006.00	360.50	7588.75	678.57	4059.00	1444.84	4.72E-03	5.13E-05	8.91E-03	1.89	1.53	1.87	oleosin
18560_at	At1g62510	9129.00	1087.94	7810.25	1504.38	13928.50	1913.00	8850.50	1451.99	4.11E-03	2.49E-03	6.62E-03	1.78	1.53	1.57	similar to 14kD proline-rich protein DC2.15 precursor
20383_at	At2g26640	280.50	58.60	205.75	70.73	424.25	37.29	173.50	137.87	6.51E-03	1.78E-03	1.64E-02	2.06	1.51	2.45	putative beta-ketocacyl-CoA synthase
20155_s_at	At4g26130	794.25	76.03	492.00	142.11	1180.25	193.81	371.00	122.40	8.87E-03	1.15E-03	3.60E-04	2.40	1.49	3.18	uncharacterized protein
12171_at	At3g52500	1352.50	152.12	1025.50	194.34	1976.75	165.63	936.75	58.12	1.46E-03	3.48E-04	1.14E-05	1.93	1.46	2.11	expressed protein
13621_g_at	At4g37560	614.50	126.21	661.25	65.27	896.50	34.65	655.00	72.83	5.85E-03	9.71E-04	1.11E-03	1.36	1.46	1.37	formamidase - like protein
17543_s_at	At5g25900	2881.00	414.91	2780.00	387.47	4170.25	312.57	3264.50	348.21	3.22E-03	1.82E-03	8.12E-03	1.50	1.45	1.28	cytochrome P450 GA3
16288_at	At2g17220	551.00	69.49	303.75	57.42	796.50	51.44	391.25	64.37	1.41E-03	1.59E-05	7.64E-05	2.62	1.45	2.04	putative prolyl 4-hydroxylase, alpha subunit
16009_s_at	At2g47730	3089.50	678.65	1962.25	212.82	4435.75	735.10	2435.50	315.65	4.50E-02	3.25E-04	1.88E-03	2.26	1.44	1.82	glutathione S-transferase (GST6)
20341_at	At2g29750	314.00	78.27	300.25	26.32	447.75	55.73	257.50	121.66	1.89E-02	2.81E-03	3.18E-02	1.48	1.43	1.74	putative flavonol 3-O-glucosyltransferase
17255_at	At2g25980	1901.00	370.55	1142.00	174.10	2686.50	233.84	1645.25	285.60	1.52E-02	3.79E-05	1.45E-03	2.35	1.41	1.63	similar to jasmonate-inducible proteins from Brass
19737_at	At1g01580	527.50	94.09	478.75	33.34	737.00	77.71	309.75	95.30	1.45E-02	7.03E-04	5.57E-04	1.54	1.40	2.38	hypothetical protein
14383_at	At1g09460	322.00	63.10	82.00	157.82	446.25	47.55	84.75	188.39	2.07E-02	7.62E-03	1.30E-02	5.44	1.39	5.27	unknown protein
16015_at	At1g74470	1015.50	295.23	521.25	134.46	1404.50	115.95	502.50	102.21	6.27E-02	7.86E-05	2.67E-05	2.69	1.38	2.80	geranylgeranyl reductase
15983_at	At4g27140	2190.50	441.42	884.25	778.65	2988.75	311.33	370.00	133.95	3.04E-02	4.19E-03	1.98E-06	3.38	1.36	8.08	NWMI1 - 2S albumin 1 precursor
12185_at	At1g54860	844.75	148.42	613.75	155.59	1143.50	131.69	647.00	79.07	2.51E-02	2.07E-03	5.14E-04	1.86	1.35	1.77	unknown protein
18311_at	At1g53840	759.75	58.12	509.25	163.37	1025.75	105.40	433.50	29.54	4.16E-03	2.09E-03	2.18E-05	2.01	1.35	2.37	pectinesterase, putative
12792_s_at	At2g45180	20395.25	3719.83	15004.75	1239.28	26965.00	3530.13	15777.50	1365.51	4.80E-02	2.91E-04	5.06E-04	1.80	1.32	1.71	unknown protein
13011_at	At4g38430	961.25	142.40	776.00	53.25	1260.50	149.98	948.75	133.10	2.51E-02	5.76E-04	2.01E-02	1.62	1.31	1.33	putative protein
18297_at	At5g11720	499.25	93.88	348.50	111.51	650.75	76.93	258.2								

Table 4. Primer information for qRT-PCR.

Text Designation	Gene Name	AGI Code	Oligonucleotide Primer Sequences		Primer number (JOPR###)		Concentrations Used (nM)	
			Forward primer sequence	Reverse primer sequence	Forward	Reverse	Forward	Reverse
18s ribosomal	18s ribosomal		TCCTAGTAAGCGCGAGTCATCA	CGAACACTTCACCGGATCAT	862	863	900	900
LEC1	LEC1	At1g21970	AAGCCGGCATTCCGTTAAT	GGTCGTCGGGTCAAGATGAA	868	869	300	50
LEC2	LEC2	At1g28300	CCATCCCTAACGATCTCATGGA	TCATCGGATGAACCCACGTA	870	871	300	900
ABI3	ABI3	At3g24650	TTACCCACGTCGCTTTGCTT	CAGGGATGGAAACCAGAAAAGA	877	878	900	300
Unknown2	At2g35810	At2g35810	CGGTGGAAGTGAATCTGATACCA	AGAGATCCAATTGAGCGTCGTT	883	884	900	900
Glucanase	At1g09460	At1g09460	GTTGCACCGCTGTTGTCT	CTTGCCACACACCAGCTT	885	886	300	900
Apospory	At4g25900	At4g25900	TCTTCAAATCCTCATTGGATGATC	ACCACCTCCTTTGCCATCAC	887	888	900	900
Unknown3	At1g03420	At1g03420	TCCGGTGTCTCCATTTCCA	TGCACTCCAGAACTTTCAAATCA	889	890	300	300
FLA7	FLA7	At2g04780	TTCGCTTTCGGAATTCAAGAA	AAGGAGATTGACCACCAGCAAA	895	896	300	900
FUS3	FUS3	At3g26790	GGTACTGGCCAAACAACAATAGC	CTAGCTGCAGACCATGAGCATT	897	898	900	900
GASA1	GASA1	At1g75750	TCCAACCTCGTCCAGGCTGAT	GCACTCCACAATCGATCTTC	909	910	300	300
HB1	HB1	At2g16060	ACCAATTCCTGCTGAGCAAAA	TGATTCACAACACATGACAAAAACA	911	912	900	300
HSP17.6A	HSP17.6A	At5g12030	CACCCGGATGCGTACGTT	GGACCTGAATCTCATCTCCTTTGA	913	914	300	300
AtWLIM2	At2g39900	At2g39900	GGAAAGCCAGTGTTACCATAAATCTT	AGAGCTGCATAGTTCGATGGAGATA	915	916	900	900
atGRP3	atGRP3	At2g05520	GGCATCTTCTGCCACAGTGAA	CATTGTCACCGTAGCCACGTT	925	926	900	900
Unknown1	At1g62480	At1g62480	CCGTCTCCGAGTCTCTTCCA	CGACCAAATCTTTAGTTGTTACTTCGA	927	928	900	900
WRKY	At4g31550	At4g31550	CCACCGTCTAGTGTAACACTCGAT	GCTCGGCCTCTTAGCTTT	929	930	300	300
WUSCHEL	WUSCHEL	At2g17950	AAGTATGGCCAATCGGAAGTTC	CCGGCGTAAGAGCTAGTTCAGA	979	980	900	900
AGL15	AGL15	AT5G13790	AAAAGGAAAAGTAGGACCCAGAA	AATTTTAGGGTTTTTTCATGATACC	975	976	900	900
SERK1	AtSERK1	At1g71830	TCTTGACAGCTGGGATCCT	ACTGTTCTCGTTGTTGCAAGTGA	977	978	900	900

Table 5. Critical threshold values for Figure 1. “QPCR Group” refers to 96-well plate the reaction was carried out on. “Gene” and “AGI Code” indicates the gene analyzed and the corresponding AGI number. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype”, “Tissue”, and “Growth Conditions” all refer to the sample analyzed, as also described in Figure 1 and associated text.

QPCR Group	Gene	AGI Code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
1	18s		12.19	0.083	Wt Columbia	Germinating seeds	MS+0.01% Methanol
1	18s		11.69	0.128	pk1	Germinating seeds	MS+0.01% Methanol
1	18s		12.06	0.026	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
1	18s		11.20	0.074	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
2	18S		12.46	0.138	Wt Columbia	Germinating seeds	MS+0.01% Methanol
2	18S		11.81	0.198	pk1	Germinating seeds	MS+0.01% Methanol
2	18S		11.98	0.150	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
2	18S		11.21	0.168	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	18S		16.81	0.212	pk1	Germinating seeds	MS+0.01% Methanol
3	18S		14.61	0.146	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	18S		17.56	0.079	Wt Columbia	Germinating seeds	MS+0.01% Methanol
3	18S		15.55	0.181	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
2	ABI3	At3g24650	24.45	2.228	Wt Columbia	Germinating seeds	MS+0.01% Methanol
2	ABI3	At3g24650	25.97	0.570	pk1	Germinating seeds	MS+0.01% Methanol
2	ABI3	At3g24650	25.33	0.088	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
2	ABI3	At3g24650	24.64	0.134	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	AGL15	At5g13790	34.13	0.742	pk1	Germinating seeds	MS+0.01% Methanol
3	AGL15	At5g13790	35.92	0.381	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	AGL15	At5g13790	34.97	1.798	Wt Columbia	Germinating seeds	MS+0.01% Methanol
3	AGL15	At5g13790	32.67	0.557	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	AtSERK1	At1g71830	35.00	0.520	pk1	Germinating seeds	MS+0.01% Methanol
3	AtSERK1	At1g71830	36.27	0.116	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	AtSERK1	At1g71830	35.58	0.925	Wt Columbia	Germinating seeds	MS+0.01% Methanol
3	AtSERK1	At1g71830	32.86	0.787	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
2	FUS3	At3g26790	32.58	1.336	Wt Columbia	Germinating seeds	MS+0.01% Methanol
2	FUS3	At3g26790	32.48	1.598	pk1	Germinating seeds	MS+0.01% Methanol
2	FUS3	At3g26790	32.11	1.015	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
2	FUS3	At3g26790	30.20	0.153	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
1	LEC1	At1g21970	32.65	0.346	Wt Columbia	Germinating seeds	MS+0.01% Methanol
1	LEC1	At1g21970	33.38	0.434	pk1	Germinating seeds	MS+0.01% Methanol
1	LEC1	At1g21970	30.05	0.448	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
1	LEC1	At1g21970	29.30	0.286	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
1	LEC2	At1g28300	32.60	0.422	Wt Columbia	Germinating seeds	MS+0.01% Methanol
1	LEC2	At1g28300	32.79	0.451	pk1	Germinating seeds	MS+0.01% Methanol
1	LEC2	At1g28300	29.38	0.280	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
1	LEC2	At1g28300	28.48	0.256	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	WUSCHEL	At2g17950	29.31	0.193	pk1	Germinating seeds	MS+0.01% Methanol
3	WUSCHEL	At2g17950	28.42	0.184	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
3	WUSCHEL	At2g17950	30.48	0.416	Wt Columbia	Germinating seeds	MS+0.01% Methanol
3	WUSCHEL	At2g17950	28.44	0.288	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole

Table 6. Critical threshold values for Figure 3. “QPCR Group” refers to 96-well plate the reaction was carried out on. “Gene” and “AGI Code” indicates the gene analyzed and the corresponding AGI number. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype”, “Tissue”, and “Growth Conditions” all refer to the sample analyzed, as also described in Figure 3 and associated text.

QPCR Group	Gene	AGI Code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
4	18s		13.34	0.148	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	18s		15.25	0.126	pk1	Germinating seeds	MS+0.01% Methanol
4	18s		14.44	0.568	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	18s		16.17	0.029	Wt Columbia	Germinating seeds	MS+0.01% Methanol
5	18s		14.48	0.123	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	18s		16.37	0.098	pk1	Germinating seeds	MS+0.01% Methanol
5	18s		15.57	0.132	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	18s		17.34	0.029	Wt Columbia	Germinating seeds	MS+0.01% Methanol
6	18s		11.16	0.069	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
6	18s		12.09	0.091	pk1	Germinating seeds	MS+0.01% Methanol
6	18s		11.71	0.089	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
6	18s		12.28	0.155	Wt Columbia	Germinating seeds	MS+0.01% Methanol
7	18S		11.21	0.168	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
7	18S		11.81	0.198	pk1	Germinating seeds	MS+0.01% Methanol
7	18S		11.98	0.150	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
7	18S		12.46	0.138	Wt Columbia	Germinating seeds	MS+0.01% Methanol
5	Apospory	At4g25900	27.65	0.086	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Apospory	At4g25900	28.84	0.212	pk1	Germinating seeds	MS+0.01% Methanol
5	Apospory	At4g25900	30.51	0.271	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Apospory	At4g25900	32.35	0.336	Wt Columbia	Germinating seeds	MS+0.01% Methanol
7	atGRP3	At2g05520	26.75	0.037	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
7	atGRP3	At2g05520	26.40	0.196	pk1	Germinating seeds	MS+0.01% Methanol
7	atGRP3	At2g05520	29.47	0.514	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
7	atGRP3	At2g05520	30.19	0.021	Wt Columbia	Germinating seeds	MS+0.01% Methanol
6	AtWLM2	At2g39900	26.97	0.151	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
6	AtWLM2	At2g39900	27.30	0.166	pk1	Germinating seeds	MS+0.01% Methanol
6	AtWLM2	At2g39900	29.17	0.204	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
6	AtWLM2	At2g39900	29.34	0.122	Wt Columbia	Germinating seeds	MS+0.01% Methanol
5	FLA7	At2g04780	28.88	0.122	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	FLA7	At2g04780	31.08	0.609	pk1	Germinating seeds	MS+0.01% Methanol
5	FLA7	At2g04780	30.91	0.636	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	FLA7	At2g04780	32.83	0.833	Wt Columbia	Germinating seeds	MS+0.01% Methanol
6	GASA1	At1g75750	25.80	0.208	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
6	GASA1	At1g75750	25.65	0.162	pk1	Germinating seeds	MS+0.01% Methanol
6	GASA1	At1g75750	28.96	0.127	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
6	GASA1	At1g75750	29.72	0.417	Wt Columbia	Germinating seeds	MS+0.01% Methanol
5	Glucanase	At1g09460	29.39	0.210	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Glucanase	At1g09460	31.03	0.192	pk1	Germinating seeds	MS+0.01% Methanol
5	Glucanase	At1g09460	31.33	0.353	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Glucanase	At1g09460	32.79	0.442	Wt Columbia	Germinating seeds	MS+0.01% Methanol
4	HB1	At2g16060	26.20	0.122	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	HB1	At2g16060	27.93	0.722	pk1	Germinating seeds	MS+0.01% Methanol
4	HB1	At2g16060	28.86	0.339	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	HB1	At2g16060	29.97	0.178	Wt Columbia	Germinating seeds	MS+0.01% Methanol
4	HSP17.6A	At5g12030	27.02	0.136	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	HSP17.6A	At5g12030	27.92	0.226	pk1	Germinating seeds	MS+0.01% Methanol
4	HSP17.6A	At5g12030	29.56	0.321	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	HSP17.6A	At5g12030	31.27	0.917	Wt Columbia	Germinating seeds	MS+0.01% Methanol
4	Unknown1	At1g62480	25.80	0.314	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	Unknown1	At1g62480	27.24	0.167	pk1	Germinating seeds	MS+0.01% Methanol
4	Unknown1	At1g62480	28.73	0.386	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	Unknown1	At1g62480	30.92	0.731	Wt Columbia	Germinating seeds	MS+0.01% Methanol
5	Unknown2	At2g35810	28.32	0.068	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Unknown2	At2g35810	30.22	0.341	pk1	Germinating seeds	MS+0.01% Methanol
5	Unknown2	At2g35810	30.93	0.354	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Unknown2	At2g35810	33.27	0.415	Wt Columbia	Germinating seeds	MS+0.01% Methanol
5	Unknown3	At1g03420	29.71	0.302	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Unknown3	At1g03420	31.36	0.103	pk1	Germinating seeds	MS+0.01% Methanol
5	Unknown3	At1g03420	29.94	0.125	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
5	Unknown3	At1g03420	32.03	0.362	Wt Columbia	Germinating seeds	MS+0.01% Methanol
4	WRKY	At4g31550	26.41	0.089	pk1	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	WRKY	At4g31550	27.88	0.377	pk1	Germinating seeds	MS+0.01% Methanol
4	WRKY	At4g31550	27.62	0.109	Wt Columbia	Germinating seeds	MS+ 10 ⁻⁸ M Uniconazole
4	WRKY	At4g31550	29.21	0.312	Wt Columbia	Germinating seeds	MS+0.01% Methanol

Table 7. Critical threshold values for Figure 4. “QPCR Group” refers to 96-well plate the reaction was carried out on. “Gene” and “AGI Code” indicates the gene analyzed and the corresponding AGI number. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype”, “Tissue”, and “Growth Conditions” all refer to the sample analyzed, as also described in Figure 4 and associated text.

QPCR Group	Gene	AGI Code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
8	18S		12.82	0.127	Wt Columbia	Leaves	32 day old plants in soil
9	18S		12.73	0.006	Wt Columbia	Leaves	32 day old plants in soil
8	Apospory	At4g25900	27.15	0.142	Wt Columbia	Leaves	32 day old plants in soil
8	atGRP3	At2g05520	21.40	0.105	Wt Columbia	Leaves	32 day old plants in soil
8	AtWLIM2	At2g39900	29.85	0.275	Wt Columbia	Leaves	32 day old plants in soil
8	FUS3	At3g26790	37.57	1.688	Wt Columbia	Leaves	32 day old plants in soil
8	GASA1	At1g75750	26.13	0.078	Wt Columbia	Leaves	32 day old plants in soil
9	HSP17.6A	At5g12030	34.88	0.297	Wt Columbia	Leaves	32 day old plants in soil
8	Unknown1	At1g62480	29.18	0.136	Wt Columbia	Leaves	32 day old plants in soil
8	Unknown2	At2g35810	29.09	0.129	Wt Columbia	Leaves	32 day old plants in soil
10	18S		13.71	0.133	Wt Columbia	Roots	32 day old plants in soil
11	18S		11.32	0.026	Wt Columbia	Roots	32 day old plants in soil
10	Apospory	At4g25900	27.31	0.789	Wt Columbia	Roots	32 day old plants in soil
10	atGRP3	At2g05520	28.41	0.168	Wt Columbia	Roots	32 day old plants in soil
10	AtWLIM2	At2g39900	31.05	0.176	Wt Columbia	Roots	32 day old plants in soil
10	FUS3	At3g26790	38.38	1.867	Wt Columbia	Roots	32 day old plants in soil
10	GASA1	At1g75750	26.17	0.061	Wt Columbia	Roots	32 day old plants in soil
11	HSP17.6A	At5g12030	29.96	0.299	Wt Columbia	Roots	32 day old plants in soil
10	Unknown1	At1g62480	25.29	0.038	Wt Columbia	Roots	32 day old plants in soil
10	Unknown2	At2g35810	29.59	0.136	Wt Columbia	Roots	32 day old plants in soil
12	18s		11.90	0.106	Wt Columbia	Siliques	32 day old plants in soil
13	18s		12.87	0.221	Wt Columbia	Siliques	32 day old plants in soil
14	18s		12.79	0.137	Wt Columbia	Siliques	32 day old plants in soil
15	18s		12.82	0.104	Wt Columbia	Siliques	32 day old plants in soil
15	Apospory	At4g25900	27.25	0.148	Wt Columbia	Siliques	32 day old plants in soil
14	atGRP3	At2g05520	26.20	0.300	Wt Columbia	Siliques	32 day old plants in soil
15	AtWLIM2	At2g39900	27.49	0.242	Wt Columbia	Siliques	32 day old plants in soil
13	FUS3	At3g26790	34.98	0.690	Wt Columbia	Siliques	32 day old plants in soil
14	GAST1	At1g75750	24.66	0.064	Wt Columbia	Siliques	32 day old plants in soil
15	HSP17.6A	At5g12030	34.75	0.764	Wt Columbia	Siliques	32 day old plants in soil
15	Unknown1	At1g62480	24.65	0.068	Wt Columbia	Siliques	32 day old plants in soil
12	Unknown2	At2g35810	28.16	0.112	Wt Columbia	Siliques	32 day old plants in soil

Table 8. Critical threshold values for Figure 5. “QPCR Group” refers to 96-well plate the reaction was carried out on. “Gene” and “AGI Code” indicates the gene analyzed and the corresponding AGI number. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype”, “Tissue”, and “Growth Conditions” all refer to the sample analyzed, as also described in Figure 5 and associated text.

QPCR Group	Gene	AGI Code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
17	18s		12.58	0.134	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
17	18s		14.17	0.087	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
18	18s		12.77	0.225	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
18	18s		14.28	0.148	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
19	18s		12.83	0.172	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
19	18s		14.36	0.067	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	18s		13.05	0.103	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	18s		14.33	0.057	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
21	18s		10.64	0.038	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
21	18s		12.24	0.058	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	Apospory	At4g25900	24.88	0.076	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	Apospory	At4g25900	26.16	0.026	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
19	atGRP3	At2g05520	28.55	0.454	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
19	atGRP3	At2g05520	27.05	0.197	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	AtWLIM2	At2g39900	27.02	0.284	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	AtWLIM2	At2g39900	29.59	0.307	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
18	FUS3	At3g26790	37.43	3.106	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
18	FUS3	At3g26790	28.10	0.079	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
19	GASA1	At1g75750	23.75	0.093	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
19	GASA1	At1g75750	26.63	0.070	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	HSP17.6A	At5g12030	33.75	0.744	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	HSP17.6A	At5g12030	31.46	0.650	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
17	LEC1	At1g21970	36.85	2.841	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
17	LEC1	At1g21970	29.68	0.244	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
21	LEC2	At1g28300	38.20	1.260	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
21	LEC2	At1g28300	29.70	0.506	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	Unknown1	At1g62480	24.46	0.082	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
20	Unknown1	At1g62480	26.27	0.099	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8
17	Unknown2	At2g35810	25.45	0.171	Wt Columbia	Roots	3wk on MS+Cytokinin after 4d on MS+U8
17	Unknown2	At2g35810	28.27	0.180	<i>pkl</i>	Roots	3wk on MS+Cytokinin after 4d on MS+U8

Table 9. Critical threshold values for Figure 6. “QPCR Group” refers to 96-well plate the reaction was carried out on. “Gene” and “AGI Code” indicates the gene analyzed and the corresponding AGI number. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype”, “Tissue”, and “Growth Conditions” all refer to the sample analyzed, as also described in Figure 6 and associated text.

QPCR Group	Gene	AGI Code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
22	18S		12.82	0.127	Wt Columbia	Leaves	32 day old plants in soil
22	18S		12.93	0.137	pkl	Leaves	32 day old plants in soil
23	18S		12.73	0.006	Wt Columbia	Leaves	32 day old plants in soil
23	18S		13.20	0.070	pkl	Leaves	32 day old plants in soil
22	Apospory	At4g25900	27.15	0.142	Wt Columbia	Leaves	32 day old plants in soil
22	Apospory	At4g25900	26.82	0.160	pkl	Leaves	32 day old plants in soil
22	atGRP3	At2g05520	21.40	0.105	Wt Columbia	Leaves	32 day old plants in soil
22	atGRP3	At2g05520	21.81	0.177	pkl	Leaves	32 day old plants in soil
22	AtWLIM2	At2g39900	29.85	0.275	Wt Columbia	Leaves	32 day old plants in soil
22	AtWLIM2	At2g39900	29.23	0.175	pkl	Leaves	32 day old plants in soil
22	FUS3	At3g26790	37.57	1.688	Wt Columbia	Leaves	32 day old plants in soil
22	FUS3	At3g26790	35.11	0.919	pkl	Leaves	32 day old plants in soil
22	GASA1	At1g75750	26.13	0.078	Wt Columbia	Leaves	32 day old plants in soil
22	GASA1	At1g75750	24.20	0.386	pkl	Leaves	32 day old plants in soil
23	HSP17.6A	At5g12030	34.88	0.297	Wt Columbia	Leaves	32 day old plants in soil
23	HSP17.6A	At5g12030	37.96	0.431	pkl	Leaves	32 day old plants in soil
22	LEC2	At1g28300	34.57	0.494	Wt Columbia	Leaves	32 day old plants in soil
22	LEC2	At1g28300	34.58	1.092	pkl	Leaves	32 day old plants in soil
22	Unknown1	At1g62480	29.18	0.136	Wt Columbia	Leaves	32 day old plants in soil
22	Unknown1	At1g62480	27.72	0.135	pkl	Leaves	32 day old plants in soil
22	Unknown2	At2g35810	29.09	0.129	Wt Columbia	Leaves	32 day old plants in soil
22	Unknown2	At2g35810	28.47	0.159	pkl	Leaves	32 day old plants in soil

Table 10. Critical threshold values for Figure 7. “QPCR Group” refers to 96-well plate the reaction was carried out on. “Gene” and “AGI Code” indicates the gene analyzed and the corresponding AGI number. “Average CT” is average critical threshold of three measurements, and “STDEV CT” is the standard deviation associated with the average critical threshold. “Genotype”, “Tissue”, and “Growth Conditions” all refer to the sample analyzed, as also described in Figure 7 and associated text.

QPCR Group	Gene	AGI Code	Average CT	STDEV CT	Genotype	Tissue	Growth Conditions
24	18S		19.37	0.112	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	18S		15.65	0.157	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	18S		20.68	0.078	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	18S		15.24	0.051	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	18S		12.46	0.083	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	18S		12.22	0.066	pk1	36 h Germinating seeds	MS+0.01% Methanol
30	18S		25.36	0.272	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
31	18S		17.67	0.107	pk1	12 h Germinating seeds	MS+0.01% Methanol
32	18S		25.10	0.115	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
33	18S		17.04	0.080	pk1	24 h Germinating seeds	MS+0.01% Methanol
34	18S		14.21	0.026	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
35	18S		15.54	0.055	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	Apospory	At4g25900	35.55	0.243	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	Apospory	At4g25900	33.55	0.349	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	Apospory	At4g25900	34.62	1.147	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	Apospory	At4g25900	30.01	0.140	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	Apospory	At4g25900	28.18	0.315	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	Apospory	At4g25900	26.17	0.131	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	atGRP3	At2g05520	37.30	1.119	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	atGRP3	At2g05520	35.96	0.860	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	atGRP3	At2g05520	34.28	0.121	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	atGRP3	At2g05520	31.94	0.122	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	atGRP3	At2g05520	27.83	0.196	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	atGRP3	At2g05520	27.94	0.080	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	AtWLMIM2	At2g39900	38.56	2.494	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	AtWLMIM2	At2g39900	35.71	0.751	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	AtWLMIM2	At2g39900	36.34	1.089	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	AtWLMIM2	At2g39900	32.16	0.186	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	AtWLMIM2	At2g39900	29.43	0.167	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	AtWLMIM2	At2g39900	28.32	0.262	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	FUS3	At3g26790	38.87	1.249	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	FUS3	At3g26790	35.23	0.433	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	FUS3	At3g26790	39.33	1.155	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	FUS3	At3g26790	35.62	1.730	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	FUS3	At3g26790	35.22	0.697	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	FUS3	At3g26790	33.10	0.269	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	GASA1	At1g75750	39.00	1.726	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	GASA1	At1g75750	34.49	1.397	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	GASA1	At1g75750	37.67	2.022	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	GASA1	At1g75750	32.47	0.553	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	GASA1	At1g75750	28.38	0.121	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	GASA1	At1g75750	25.05	0.032	pk1	36 h Germinating seeds	MS+0.01% Methanol
30	HSP17.6A	At5g12030	33.00	0.110	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
31	HSP17.6A	At5g12030	26.68	0.241	pk1	12 h Germinating seeds	MS+0.01% Methanol
32	HSP17.6A	At5g12030	35.20	0.014	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
33	HSP17.6A	At5g12030	29.31	0.159	pk1	24 h Germinating seeds	MS+0.01% Methanol
34	HSP17.6A	At5g12030	29.88	0.169	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
35	HSP17.6A	At5g12030	28.22	0.274	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	LEC1	At1g21970	35.10	0.232	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	LEC1	At1g21970	34.71	0.864	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	LEC1	At1g21970	37.16	2.576	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	LEC1	At1g21970	32.67	0.260	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	LEC1	At1g21970	34.70	0.386	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	LEC1	At1g21970	30.59	0.095	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	LEC2	At1g28300	40.00	0.000	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	LEC2	At1g28300	34.04	0.502	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	LEC2	At1g28300	38.92	1.871	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	LEC2	At1g28300	31.59	0.370	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	LEC2	At1g28300	32.81	0.403	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	LEC2	At1g28300	29.79	0.085	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	Unknown1	At1g62480	37.27	0.877	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	Unknown1	At1g62480	34.47	0.260	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	Unknown1	At1g62480	36.81	1.702	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	Unknown1	At1g62480	30.76	0.262	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	Unknown1	At1g62480	28.26	0.156	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	Unknown1	At1g62480	26.31	0.061	pk1	36 h Germinating seeds	MS+0.01% Methanol
24	Unknown2	At2g35810	36.35	0.638	Wt Columbia	12 h Germinating seeds	MS+0.01% Methanol
25	Unknown2	At2g35810	33.80	0.390	pk1	12 h Germinating seeds	MS+0.01% Methanol
26	Unknown2	At2g35810	35.17	0.241	Wt Columbia	24 h Germinating seeds	MS+0.01% Methanol
27	Unknown2	At2g35810	31.21	0.257	pk1	24 h Germinating seeds	MS+0.01% Methanol
28	Unknown2	At2g35810	29.22	0.151	Wt Columbia	36 h Germinating seeds	MS+0.01% Methanol
29	Unknown2	At2g35810	27.53	0.150	pk1	36 h Germinating seeds	MS+0.01% Methanol