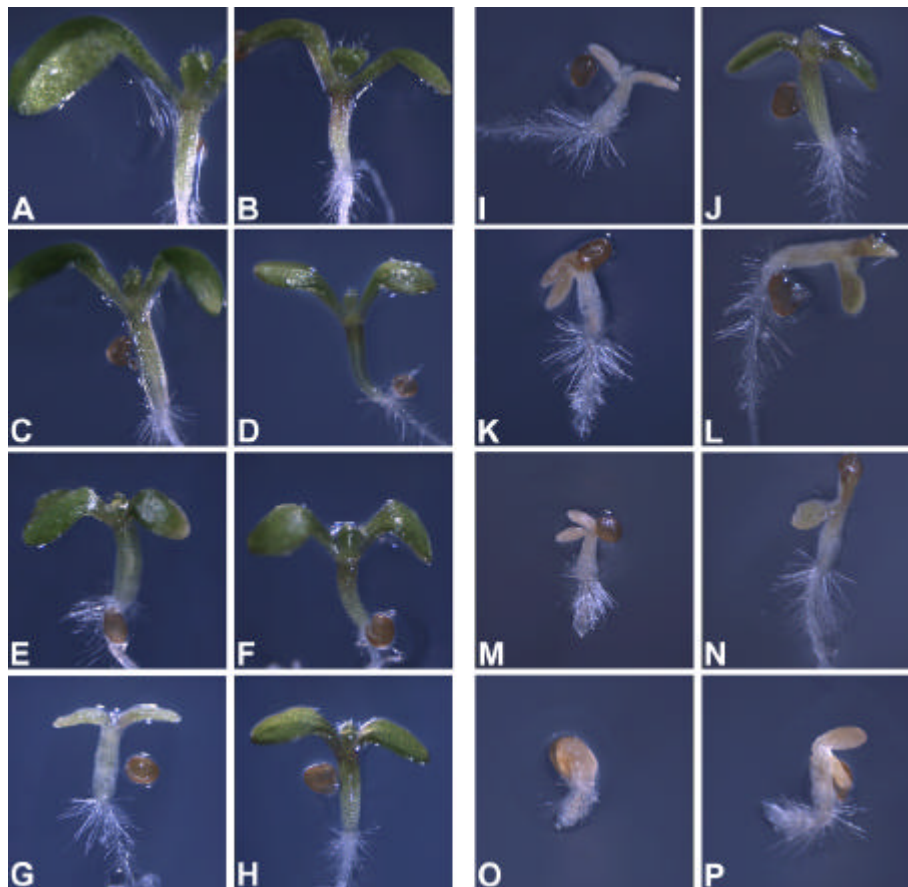


Supplemental Materials

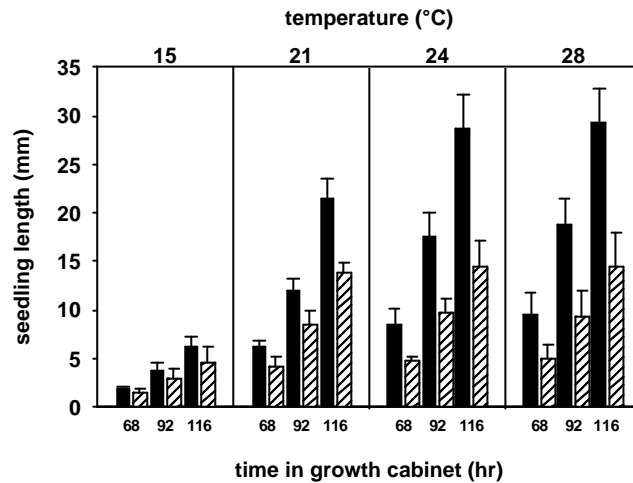
Supplemental Figure 1. Representative phenotypes of six day old wild type and *txr1* mutant seedlings grown in the presence of 0 – 1600 nM thaxtomin on vertical agar plates.

Wild type (**A, C, E, G, I, K, M, O**) and *txr1* mutant seedlings (**B, D, F, H, J, L, N, P**) were grown in the presence of (**A, B**) 0 nM, (**C, D**) 12 nM, (**E, F**) 25 nM, (**G, H**) 50 nM, (**I, J**) 200 nM, (**K, L**) 400 nM, (**M, N**) 800 nM and (**O, P**) 1600 nM thaxtomin.



Supplemental Figure 2. Growth of wild type and *txr1* mutant seedlings in response to different temperatures.

Each bar represents the mean \pm standard deviation of the lengths of 15 seedlings grown in Percival chambers on vertical agar plates. Wild type is shown in black and *txr1* mutant in crosshatched bars. The lengths of the seedlings were determined at three different times (68, 92 and 116 hours) after transfer to growth cabinets set at four different temperatures (15, 21, 24 and 28°C).



Supplemental Table 1. Expression profiles of genes that are significantly induced (arithmetic mean value >1) or repressed (arithmetic mean value <1) in *txr1* mutants compared to wild type plants.

Analysis was performed using a 14,300-element DNA microarray. Data points were first filtered to remove those with net (Channel 1, Cy3) or normalized net (Channel 2, Cy5) spot intensities = 500 and data points flagged as dubious. The table lists 50 genes with an expression ratio that was =2.5 standard deviation away from the mean of the $\log_2(\text{ratio})$ value of data points from the same slide, in each of the two slides (exp 1 and 2). The primary data sets may be viewed and downloaded from the Stanford Microarray Database (<http://genome-www5.stanford.edu/MicroArray/SMD/>, Experiment ID # 21779 and 21780).

Gene Code	Putative Function	Arithmetic Mean	Log2 values Mean	Log2 values Std. Dev.
At2g21640	hypothetical protein	3,252	1,702	1,143
At2g03760	steroid sulfotransferase	2,863	1,518	0,466
At5g54100	stomatin-like	2,366	1,243	0,037
At3g01600	hypothetical protein	2,328	1,219	0,069
At2g03130	50S ribosomal protein L7/L12	2,327	1,219	0,663
At4g27585	stomatin-like	2,208	1,143	0,517
At5g55200	chaperone GrpE-like protein	2,202	1,139	0,191
At3g29185	hypothetical protein	2,138	1,096	0,020
At5g43450	1-aminocyclopropane-1-carboxylate oxidase	2,093	1,066	0,296
At5g50160	FRO1 and FRO2-like protein	2,088	1,062	0,287
At3g27780	myb transcription factor	2,006	1,004	0,051
At5g56350	pyruvate kinase	1,989	0,992	0,107
At3g45730	hypothetical protein	1,979	0,985	0,045
At4g15760	hypothetical protein	1,966	0,975	0,156
At1g17580	myosin, putative	1,931	0,950	0,322
At5g19550	aspartate aminotransferase Asp2	1,893	0,921	0,125
At4g27210	hypothetical protein	1,888	0,917	0,035
At2g36790	putative glucosyl transferase	1,869	0,902	0,095
At1g05680	indole-3-acetate beta-glucosyltransferase-like	1,815	0,860	0,164
At5g42060	hypothetical protein	1,798	0,846	0,066
At2g15750	putative non-LTR retroelement reverse transcriptase	1,794	0,844	0,059
At5g36230	H. sapiens protein of unknown function	1,794	0,844	0,276
At3g27770	hypothetical protein	1,767	0,821	0,066
At1g70310	spermidine synthase	1,720	0,782	0,071
At1g69370	chorismate mutase	1,706	0,771	0,013
At1g70560	putative alliinase	1,703	0,769	0,172
At1g80130	hypothetical protein	1,697	0,763	0,168
At2g36530	enolase (2-phospho-D-glycerate hydroylase)	1,686	0,754	0,136
At5g49560	hypothetical protein	1,665	0,736	0,115
At1g52600	microsomal signal peptidase 21 KD subunit	1,641	0,715	0,075
At2g47480	hypothetical protein	0,606	-0,724	0,141
At1g22530	hypothetical protein	0,596	-0,746	0,124
At4g15940	similarity to 2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	0,592	-0,756	0,127
At5g64570	beta-xylosidase	0,579	-0,788	0,185
At5g49360	xylosidase	0,577	-0,794	0,097
At3g16240	delta tonoplast integral protein	0,567	-0,820	0,053
At1g53750	26S proteasome ATPase subunit	0,562	-0,832	0,032
At4g19420	putative pectinacetylesterase	0,556	-0,848	0,307
At5g24770	vegetative storage protein Vsp2	0,527	-0,924	0,415
At2g36620	ribosomal protein L24	0,521	-0,941	0,311
At5g14120	nodulin-like protein	0,517	-0,952	0,012
At5g59310	nonspecific lipid-transfer protein precursor	0,517	-0,953	0,323
At4g15210	beta-amylase	0,502	-0,994	0,057
At2g43550	putative trypsin inhibitor	0,474	-1,077	0,182
At5g61440	thioredoxin-like 3	0,447	-1,163	0,363
At1g75750	hypothetical protein	0,430	-1,218	0,047
At2g02990	ribonuclease 1	0,426	-1,231	0,156
At2g38770	hypothetical protein	0,325	-1,620	0,249
At1G75750	hypothetical protein	0,299	-1,741	0,077
At5g24240	ubiquitin	0,280	-1,838	0,069