Supporting Information

Supplemental Materials and Methods

Plant material. Seeds of *Arabidopsis thaliana* were sown on 0.8 % agar-water in clear plastic boxes (8 x 5 x 2 cm), stratified 5-7 d at 5 ºC in darkness and transferred to simulated sunlight (photoperiod 8 h) at 20 ºC for 2 d, before the light or shade treatments. The mutants are listed in Table S3. *Glycine max* (soybean) cv. BIOSOJA 4.70 (Bioceres) was sown on moist cotton and transplanted after germination to 330-cm^3 pots containing perlite, vermiculite and sphagnum peat moss (1: 1: 2) watered with 2% Hakaphos R (COMPO).

Generation of transgenic line. The *pPIF4:PIF4-GFP* construct, was generated by amplifying a genomic fragment corresponding to the 2.47 kb promoter region upstream of the ATG and the *PIF4* coding region lacking the stop codon, using the forward primer CACCCAGTACGCATCCAATCTTCTC and the reverse primer TCCGTGGTCCAAACGAGAACCGTC. This PCR product was cloned into the pENTR^{TM}/D-TOPO vector and sequenced for the absence of mutations, to be then mobilized into the pGWB4 cassette in the pPZP221 vector, by LR clonase (Invitrogene) recombination. Transgenic lines bearing this construct were obtained by floral dip infiltration of *pif4-101* mutants and selection in gentamycin containing media. Seedlings displaying nuclear fluorescence by the PIF4-GFP protein were then brought to homozygosis.

Shade intensity. Simulated shade treatments started at the beginning of the photoperiod of the indicated day. In the glasshouse (soybean experiments), photoperiod was 10.5 h and the presence of neighbors was simulated by a means of a 30-cm tall and 10-cm diameter green plastic tube (Lee filters, 089) placed around each soybean plant. A clear filter (Lee Filters, 130) was used as the sunlight controls. Under controlled conditions, simulated sunlight (red / far-red ratio = 1.14, photosynthetically active radiation= 95 µmol.m^{-2}.s^{-1}) was provided by a combination of fluorescent (Osram L30W/10) and halogen (Philips NR63 40W) lamps in addition to a clear and a diffusing filter (Lee Filters, 130 and

216). To produce two levels of simulated shade (red / far-red ratios= 0.45 and 0.19, photosynthetically active radiation= 37 and 26 µmol.m^{-2}.s^{-1}, respectively) the clear filter was replaced by a green filter (Lee filters, 089) with or without perforations to allow the penetration of unfiltered light. The light fields were characterized with a spectroradiometer (Ocean Optics, USB4000) (Fig. S9). To obtain a biologically-meaningful integral measure of the shade intensity, we first calculated the terms corresponding to the activity of phyB and the activity of the other photo-receptors from the denominator of the growth equation used by Legris et al. (1) by using each light condition as input. Then we calculated the inverse of these values because there is an inverse relationship between shade and photoreceptor activity. The resulting values were 0.18 for simulated sunlight, 0.25 for weak shade and 0.27 for strong shade. Since simulated shade is conceptually no shade, we subtracted 0.18 to have the final values of shade intensity: 0 for simulated sunlight, 0.07 for weak shade and 0.09 for intense shade.

Gene expression in soybean. Samples were harvested on liquid nitrogen between 3 and 4 h after the beginning of the photoperiod. Total RNA was extracted with Trizol Reagent (Invitrogen) following the manufacturer's protocols. To estimate the concentration and quality of samples we used a NanoDrop 2000c (Thermo Scientific) and the Agilent 2100 Bioanalyzer (Agilent Technologies) with the Agilent RNA 6000 NanoKit, respectively. The preparation of the libraries and the paired-end sequencing with an Illumina HiSeq 1500 were performed at INDEAR, Argentina. Three replicates for each treatment and tissue were sequenced.

Sequence reads were mapped to the *Glycine max* Ensembl Gm01 genome using TopHat 2.1.1 (2) with default parameters, except maximum intron length, which was set at 5,000. Count tables for different feature levels were obtained from BAM files, using custom R scripts, and the Ensembl Gm01 transcriptome. Before differential expression analysis, we discarded genes with fewer than 10 reads per condition. Paired comparisons were performed separately for each tissue using the control condition never exposed to shade as reference (i.e., six contrasts). Differential gene expression was analyzed using the edgeR package version 3.18.1 (3), and the resulting P values were adjusted using a false discovery rate (FDR) criterion (4). Genes with FDR values lower than 0.05 were considered as differentially expressed.

The analysis of the full list of genes obtained from the above samples and additional experimental conditions will be presented separately. Given the focus of the current work, the analysis here is restricted to auxin-related genes. A list of 516 *Glycine max* auxin-related genes was built-up by merging annotation data from the Pantherdb, Phytozome and the Soybase data bases (5–7). Differential expression values for each gene in all six paired comparisons were extracted using custom R scripts, then a hierarchical clustering analysis was performed using the hclust R package (8). Clusters were plotted in a heat-map using the pheatmap R package (9).

Gene expression in *Arabidopsis*. Samples were harvested in liquid nitrogen 3 h after the beginning of day 4. Total RNA was extracted with the Spectrum Plant Total RNA Kit (Sigma-Aldrich) and subjected to a DNAse treatment with RQ1 RNase-Free DNase (Promega). cDNA derived from this RNA was synthesized using Invitrogen SuperScript III and an oligo-dT primer. The synthesized cDNAs were amplified with FastStart Universal SYBRGreen Master (Roche) using the 7500 Real Time PCR System (Applied Biosystems, available from Invitrogen). *The UBIQUITIN-CONJUGATING ENZYME 2 (UBC2)* gene was used as the normalization control (10). The primers used for amplification are listed in Table S4.

Meta-analysis of gene expression in *Arabidopsis*. We obtained gene expression data for *IAA19* (AT3G15540), IAA29 (AT4G32280), and *IAA17/AXR3* (AT1G04250) in *Arabidopsis* seedlings either exposed to light signals simulating neighbors (natural shade, simulated shade or low red / far-red ratios) (11–14) or to auxin treatments (15–20) from publicly available data. Expression data were normalized to the control of each experiment, averaged for the different experiments and analyzed by ANOVA to compare the response of different *Aux/IAAs*.

Measurement of growth rates. We photographed the plants with a digital camera and measured internode, petioles or hypocotyl lengths using an image processing software (21). Growth was measured between 9:00 and 13:00 local time for soybean and between 0 and 3 h after the beginning of the photoperiod of day 4 (except when stated otherwise) for *Arabidopsis*.

Growth models. To investigate whether growth patterns can be accounted for by the dynamics of selected receptor / signaling components we fitted the data to models of this structure:

$$G \;=\; \frac{G_0}{(\beta_0 + \beta_1 x_1} + \beta_2 x_2 + \cdots + \beta_n x_n + \epsilon)$$

Where G is the rate of hypocotyl growth, G_0 is the maximum rate, and the denominator includes the explanatory variables, which represent the components that either repress ($\beta > 0$) or promote ($\beta < 0$) growth. For model selection we considered two levels that were analyzed separately for specific purposes: PIFs and auxin perception/ signaling.

We observed three different patterns of PIF4 dynamics, which depended on the tissues examined. Therefore, for the PIF level, we wanted to evaluate which one of these patterns showed the best correlation with growth and we independently parameterized three versions of the model. The first version assumes that PIF activity is elevated by the early exposure to shade and remains elevated if shade is persistent (the pattern observed for PIF4 in epidermal and sub-epidermal hypocotyl tissues). The second version assumes that PIF activity is elevated by early shade and further elevated by persistent shade (the pattern observed for PIF4 in the vascular tissues of the hypocotyl). The third version assumes that PIF activity is elevated by early shade and then decreases under persistent shade (the pattern observed for PIF4 in the cotyledons). The four continuous explanatory variables were PIF3, PIF4, PIF5 and PIF7. These variables were respectively set to zero in the *pif3*, *pif4*, *pif5* and *pif7* mutants. As a proxy for PIF activity in the presence of wild-type alleles we used the values reported in Fig. 3 for PIF4 in the epidermal and sub-epidermal hypocotyl tissues (version 1), in the vascular tissues of the hypocotyl (version 2) and in the cotyledons (version 3). The version of the model that better captured the variability was defined by comparing the modulus of the difference between observed and predicted averages for each genotype and condition (relative to the ones predicted) by means of one-way-ANOVA followed by Bonferroni post tests. We also provide the Chi square values for each model variant. The second variant was the one showing the best goodness of fit. In this case, the four explanatory variables were significant (PIF3: $P < 0.005$, PIF4: $P < 0.0001$), PIF5: $P < 0.0001$ and PIF7: $P < 0.0001$) and their four coefficients were negative, indicating growth promotion by PIFs. As indicated above, we gave PIF3, PIF5 and PIF7 the same values of activity used for PIF4. Although we do not claim that each one of them followed the same temporal patterns of activity as PIF4, this approach was followed to capture the observed genetic redundancy (stronger effect of multiple mutations than expected from the additive effect of single mutations), particularly when the plants were exposed to shade during day 3. The latter suggests that PIF4 was not the only growth-promoting factor of this level of analysis that enhanced its activity under persistent shade.

For the auxin level we wanted to evaluate the impact on growth of the dynamics of perception /signaling components observed under persistent shade. For this purpose, we independently parameterized two versions of the model, one in which the continuous predictors assumed the values generated by CS conditions at PS=0 (i.e., only CS were taken into account), and the other where the predictors assumed the values generated by the different CS and PS conditions (Fig. S10). The version of the model that better captured the variability was defined by comparing the modulus of the difference between observed and predicted averages for each genotype and condition (relative to the ones predicted) by means of a *t* test. We also provide the Chi square values for each model variant. When the goodness of fit of the model based on PS and CS conditions outperformed the model that only incorporated the effect of CS, we concluded that the growth changes caused by PS in the levels of the receptor / signaling component were significant. The nine explanatory variables were IAA19 (P <0.0001), IAA29 (P <0.0001), AXR3 (P <0.0001), *axr3 x* PS *x* CS (P <0.0001), AXR2 (P <0.0001), MIR393A (P= 0.0857), MIR393B (P= 0.0030), TIR1 plus AFB2 (P <0.0001) and ARF6 (P <0.0001). IAA19, IAA29, AXR2, and TIR1 plus AFB2, had negative coefficients, indicating that they promote growth. AXR3, *axr3 x* PS *x* CS, MIR393A, MIR393B and ARF6 had positive coefficients, indicating that they inhibit growth. As proxies for IAA19 and IAA29 activity, TIR1 plus AFB2 activity and ARF6 activity we used *IAA19* and *IAA29* expression data (Fig. 4A), GUS staining driven by the *pTIR1:TIR1-GUS* and *pTIR1:AFB2-GUS* transgenes (Fig. 4B) and nuclear fluorescence driven by the *pARF6:ARF6-GFP* transgene (Fig. 4F). In the model variant based only on CS conditions we used the respective values observed for plants grown under simulated sunlight on day 3, irrespectively of the actual growth conditions on that day. For these variables the values were set to zero in the loss-of-function mutants and multiplied by two in the gain-of-function mutants. The variables AXR3, AXR2, MIR393A and MIR393B were used as categorical predictors to account for the effect of mutations and the values were set to one for the wild-type alleles, zero for the loss-of function mutant alleles and two for the gain of function alleles. The *axr3* x PS *x* CS interaction term reflects the stronger inhibitory effect observed in the *axr3* mutant when the wild-type plants had a higher growth rate due to more intense CS and PS. It was calculated as the product of CS by PS intensity for the *axr3* mutant and set to zero for the rest of the genotypes.

Confocal microscopy. Confocal fluorescence images were taken with an LSM5 Pascal (Zeiss) or LSM510 Meta (Zeiss) laser scanning microscope with a Plan-Apochromat 40×/1.2 objective lens. For chloroplast visualization, probes were excited with a He-Ne laser (λ = 543 nm) and fluorescence was detected using an LP560 filter. For visualization of GFP/YFP fusion proteins and DII-VENUS, probes were excited with an Argon laser (λ = 488 nm) and fluorescence was detected using a BP 505-530 and BP 505-570 filter respectively. To visualize PIF4 in the vascular tissue we used a LSM710 (Zeiss). Objective: 20x W, Laser 488nm.

Indole-acetic-acid abundance. Samples were harvested in liquid nitrogen 3 h after the beginning of day 4. Indole-3-acetic acid was quantified by the stable isotope dilution method on an Agilent 7890A/5975C XL GC-MS operated in selected ion monitoring mode, equipped with a 0.25 mm × 30 m DB-5MS column (0.25 μm film) using pulsed splitless injection as described (22).

Protein blot. Total protein was extracted in extraction buffer (50 mM Tris/HCl pH 7.5, 100 mM EDTA, 1 mM 1,4-dithiothreitol, 0.1% Triton X-100 and Protease Inhibitor Cocktail, Roche) and quantified using the Bio-Rad Protein Assay (Bio-Rad). β-mercaptoethanol was added immediately before loading aliquots containing equal amounts of protein in polyacrylamide gels for electrophoresis. Immunodetection of PIF4-HA and TIR-myc was performed by using anti-HA (12CA5 Roche, Madison, USA) and anti-myc (Sigma, USA), respectively. Anti-mouse-HRP was used as secondary antibody (Invitrogen) and the Amersham ECL Prime Western Blotting Detection Reagent kit (GE Healthcare, Little Chalfont, UK) was used for detection. Ponceau staining was used to visually check equal loading.

GUS staining. Seedlings were fixed in 90% (v/v) acetone at -20 °C for 1 h, washed twice in 50 mM sodium phosphate buffer pH 7.0 and incubated in staining buffer [50 mM Na phosphate (pH 7.0), 5 mM EDTA, 0.1% (v/v) Triton X-100, 5 mM K4Fe(CN)6, 0.5 mM

K3Fe (CN)6 and 1 mg/ml X-Gluc (GBT)] at 37 °C from 2 h to overnight. Bright-field images were taken using a Zeiss Axioplan imaging 2 microscope with an Axiocam HRC CCD camera (Zeiss) using the Axiovision program (version 4.2).

Fluorometric GUS activity assay. To measure GUS activity in seedling extracts, 50 mg of transgenic seedlings (100-150 seedlings) were frozen in liquid Nitrogen and protein was then extracted in MUG extraction buffer (50 mM Na phosphate buffer, pH 7.4, 0.1% SDS, 0.1% Triton X-100, 10 mM b-mercaptoethanol, and 10 mM EDTA). Protein concentration was determined by Bradford assay. Fifty micrograms of protein extract were incubated in 150 µl of MUG assay buffer (1mM MUG (Duchefa) in GUS extraction buffer from 1 h to 12 h at 37°C. The enzyme reaction was stopped in 0.3M NaCO3.Fluorescence was measured using a Fluoroskan Acsent microwell fluorometer (Thermo Electron Company, Vantaa, Finland) and calculated as nanomolar MU per minute per microgram of protein.

Dexamethasone induction. Seeds were sown as described above but on a filter paper placed on top of the 0.8 % agar-water in the plastic boxes and the seedlings were grown under the simulated sunlight conditions described above. On day 3, Col-0 and *pDEX:TIR1-myc* seedlings were transferred to plastic boxes containing 0.8% agar-water supplemented with 100 µM Dexamethasone (Dex) and protein level and growth rate were analyzed on day 4.

Agroinfiltration and transient activation assays. The *pIAA17:LUC* reporter construct was generated by amplifying a genomic fragment corresponding to a 2.4 kb promoter region upstream of the ATG of *IAA17* and cloning the PCR product into the pDONR207 vector by incubation with BP clonase (Invitrogen),which was subsequently mobilized into the pGWB435 destination vector (23) by LR clonase II reaction (Invitrogen). In order to obtain the IAA19 and PIF4 effector constructs, the IAA19 and PIF4 ORFs without stop codon were amplified and cloned into pENTR TM /D-TOPO vector and subsequently mobilized by LR clonase II reaction into the pABinGFP vector (24) to generate the β-estradiol inducible IAA19-GFP and PIF4-GFP fusions, respectively. Primers used for these constructions are included in Table S5. The empty pABinGFP vector, IAA19 and PIF4 effector constructs were transformed into the *Agrobacterium tumefaciens* GV3101 strain and used to co-infiltrate *Nicotiana benthamiana* leaves together with an Agrobacteria strain bearing the pIAA17:LUC+ reporter and the p19 protein, used as a suppressor of gene silencing (25). *Agrobacterium* strains containing the p*IAA17:LUC*+ fusion were diluted in 10 mM MES pH 5.5, 10 mM $MgSO_4$ and 150 μM acetosyringone at an OD_{600} ratio of 0.2, while those containing the p19 protein, the empty pABinGFP vector, or the IAA19-GFP or PIF4-GFP effector constructs were diluted to an OD_{600} of 0.4. After incubation for 3 h at room temperature, equal volumes of the reporter, empty vector/ effector vector, and p19 cells were pooled and used for infiltration of *N. benthamiana* leaves. Leaves were sprayed with 20 μM β-estradiol 24 h post infiltration. For *in vivo* imaging of LUC activity, leaves were sprayed with 20 μM β-estradiol 24 h post infiltration and the following day were observed in a luminescence chamber in the presence of 0.02 mg/mL D-luciferin (Promega) in MS media. For time course LUC activity studies, leaf disks were taken two days after infiltration and incubated in the presence of 0.02 mg/mL D-luciferin (Promega) in MS salt media (mock) or MS salt media supplemented with 10 μM β-estradiol. LUC activity was measured every hour by using a LB-960 microplate luminometer (Berthold Technologies), using Mikrowin 2000 (version 4.29) software.

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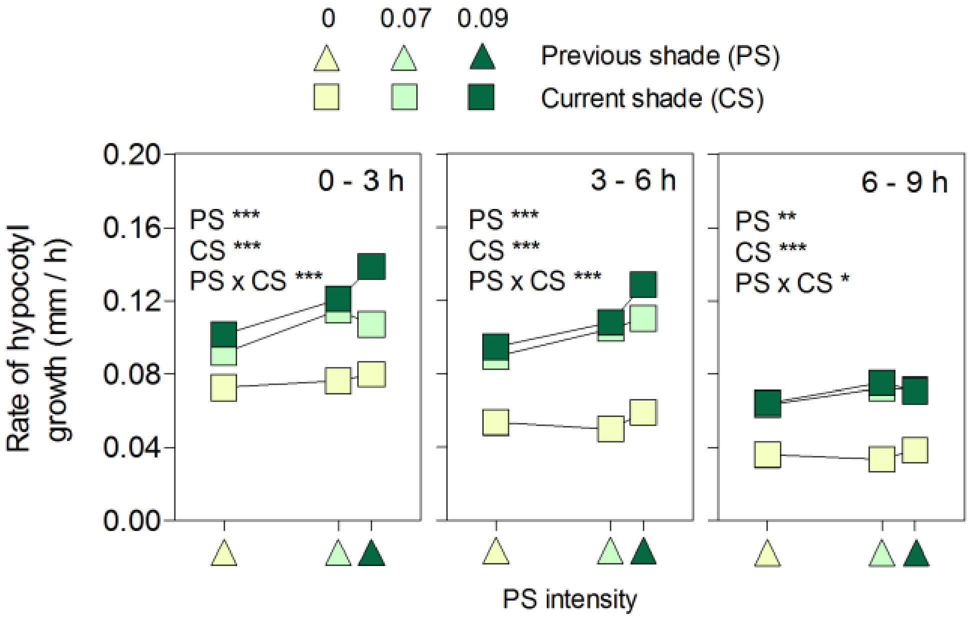

Fig. S1. Effect of current shade (CS) and previous shade (PS) conditions on the rate of growth at different times of the day. Hypocotyl growth rate of Arabidopsis seedlings during day 4 (0-3, 3-6 and 3-9 h after the beginning of the photoperiod) as affected by current (day 4) and previous (day 3, abscissas) simulated sunlight or shade conditions. A numerical estimate of shade intensity is provided above the plot. Means ±SE of 220 seedlings (smaller than the symbols). *, P <0.05; **, P <0.01; ***, P <0.001.

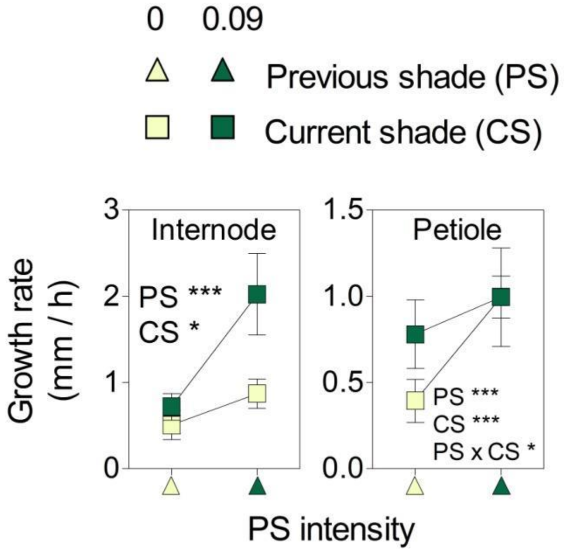

Fig. S2. Persistent shade reinforces shade avoidance in soybean. Glasshouse cultivated soybean plants with the first trifoliate leaf expanded were transferred to simulated shade (low red / far-red, low irradiance) or left as controls. The following day, half of the plants of each group were transferred to the opposite condition, to obtain plants subjected to all possible combinations of current shade (CS) and previous shade (PS). A numerical estimate of shade intensity is provided above the plot. The growth rate of the stem (internode between the unifoliate and first trifoliate leaf) and petioles (first trifoliate leaf) was then measured. In both organs growth promotion was strongly reinforced when plants had been subjected to simulated shade during the previous day (note significant effects of PS or PS x CS interaction). Means ±SE of 21 plants. *, $P < 0.05$; ***, $P < 0.001$.

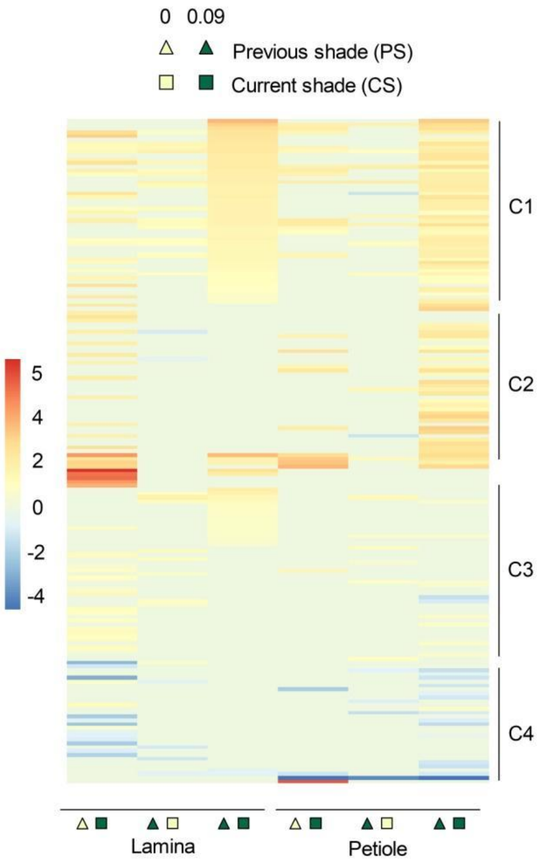

Fig. S3. Persistent shade reinforces auxin-related gene expression in soybean. Glasshouse cultivated soybean plants were exposed to all possible combinations of current shade (CS) and previous shade (PS) as described in Fig. S2. A numerical estimate of shade intensity is provided above the plot. The petiole and lamina of the first soybean trifoliate leaf were harvested for RNAseq (3 biological replicates) and differential expression analyses focused on auxin-related genes (Table S1), as these genes typically respond to neighbor signals (26). Four large clusters of genes with statistically significant responses to CS and/or PS were identified. The log2 fold change compared to the sunlight control (CS= 0, PS= 0) is indicated by the color scale. The control was used for fold-change calculations is therefore not included in the clustering analysis. Clusters 1 and 2 include genes whose expression was increased in the petiole, particularly when exposed to persistent shade (for cluster 1 this was also the case in the lamina). Genes with similarity to *Arabidopsis Aux/IAAs* were found to be over-represented in cluster 1 (42 %, Chi-square test: P < 0.00001), including four genes with homology to *MASSUGU 2* (*MSG2)/IAA19* (only present in this cluster). *YUC8* was present in cluster 2 and most *SMALL AUXIN UPREGULATED (SAUR)*-like genes were represented in clusters 1 and 2 (92 %, Chi-square test: P <0.01). These observations indicate that prolonged shade not only enhances the physiological growth response but also the auxin-related molecular signature. Genes whose expression was only moderately increased or decreased in response to shade were grouped in clusters 3 and 4, respectively.

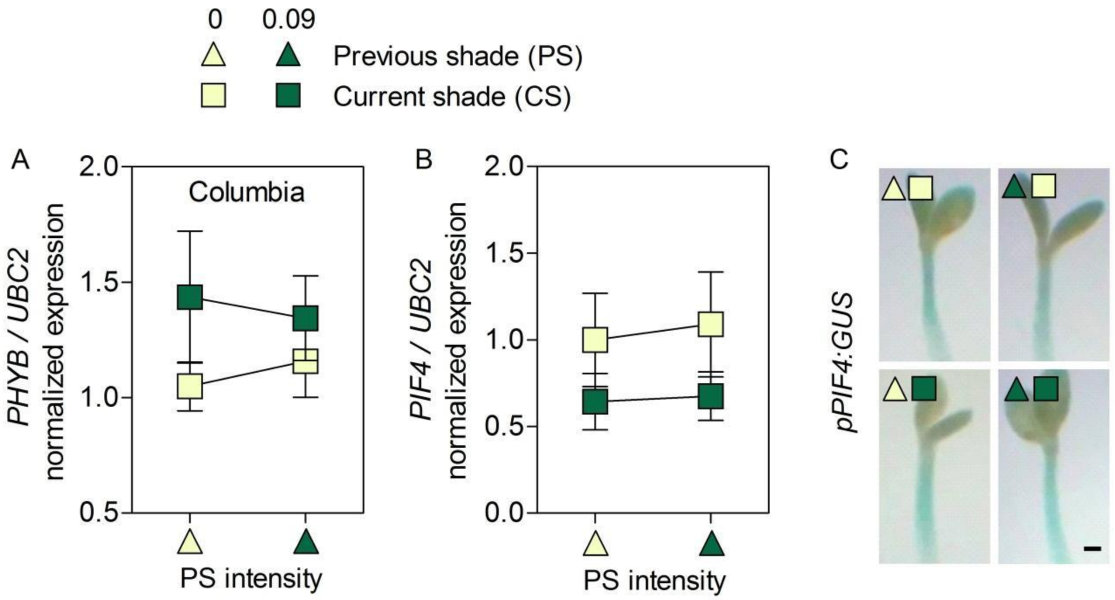

Fig. S4. Persistent shade does not significantly affect the expression of the *PHYB* or *PIF4* genes. *Arabidopsis* seedlings were exposed to different shade conditions during day 3 (previous shade, PS) followed by different shade conditions during the first 3 h of day 4 (current shade, CS) and harvested at the end of these 3 h. A, *PHYB*. B-C, *PIF4*. A-B, Real-Time PCR data. Means ±SE of 3 biological replicates. C, Representative seedlings stained by GUS activity, Bar= 100 µm.

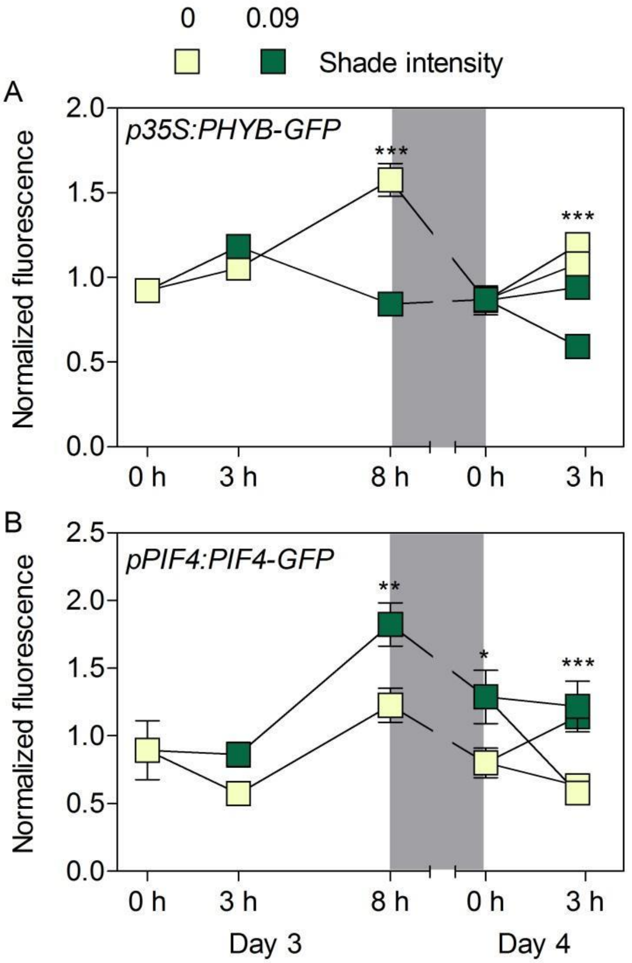

Fig. S5. Kinetics of nuclear phyB and PIF4 abundance in the epidermis and first sub-epidermal cell layers of the hypocotyl of *Arabidopsis* seedlings. A. Fluorescence driven by the *p35S:PHYB-YFP* transgene (27). B. Fluorescence driven by the *pPIF4:PIF4-GFP* transgene. Means ±SE (whenever larger than the symbols) of 30-40 biological replicates. Data shown for 3 h of day 4 are the same data included in Fig. 3A (phyB) and Fig. 4A (PIF4, hypocotyl epidermal and first sub-epidermal cell layers).

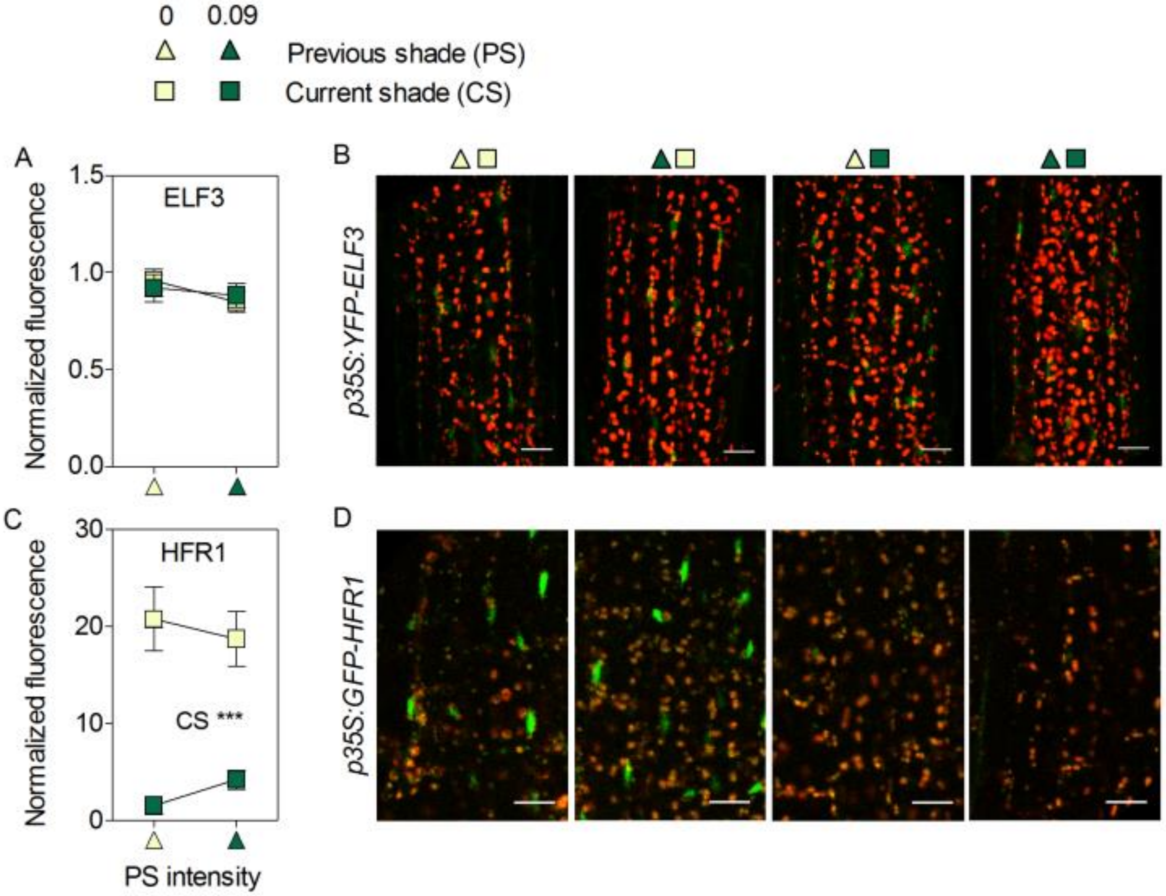

Fig. S6. Dynamics of the negative regulators of PIF4 activity ELF3 and HFR1. Nuclear fluorescence driven by the *p35S:YFP-ELF3* (A) and *p35S:GFP-HFR1* (C) transgenes in epidermal and sub-epidermal cells of the hypocotyl in *Arabidopsis* seedlings as affected by current shade (CS) and previous shade (PS). A, C, Means ±SE of 20-35 seedlings. B, D, Representative images. ***, $P < 0.001$. Bar= 20 µm.

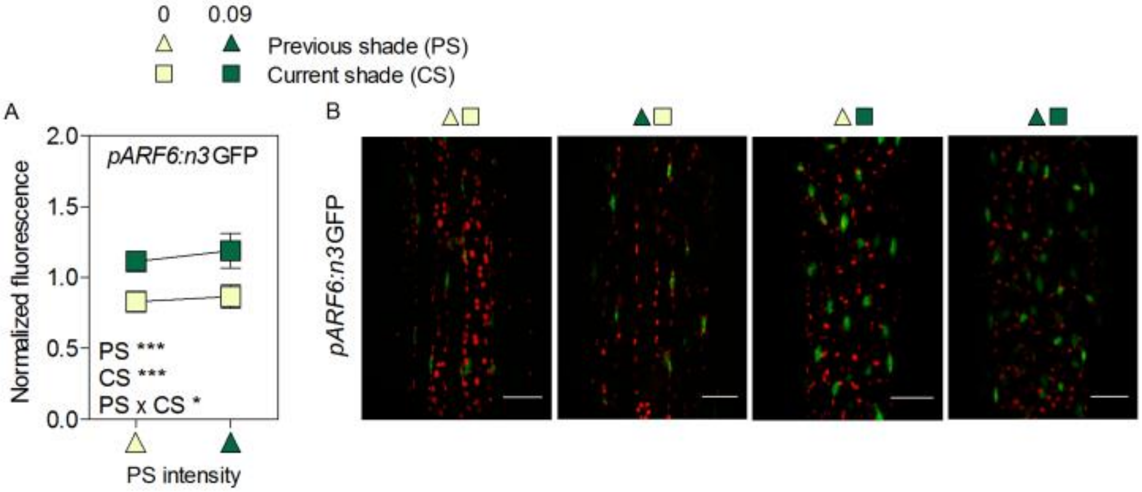

Fig. S7. The expression of the *ARF6* promoter is enhanced by shade. A, **F**luorescence driven by the *pARF6-n3GFP* transgene in epidermal and sub-epidermal cells of the hypocotyl in *Arabidopsis* seedlings as affected by current shade (CS) and previous shade (PS). Means ±SE of 36 seedlings. B, representative images. *, $P < 0.05$; ***, $P < 0.001$. Bar= 35 µm.

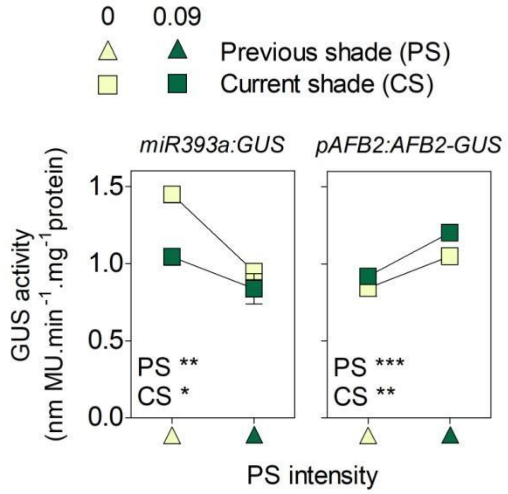

Fig. S8. Persistent shade modifies auxin perception and signaling to promote growth. GUS activity driven by the *pMIR393a:GUS* or the *pAFB2:AFB2-GUS* transgene is enhanced by prolonged shade. Means ±SE (whenever larger than the symbols) of 3 biological replicates. *, P <0.05; **, P <0.01; ***, P <0.001.

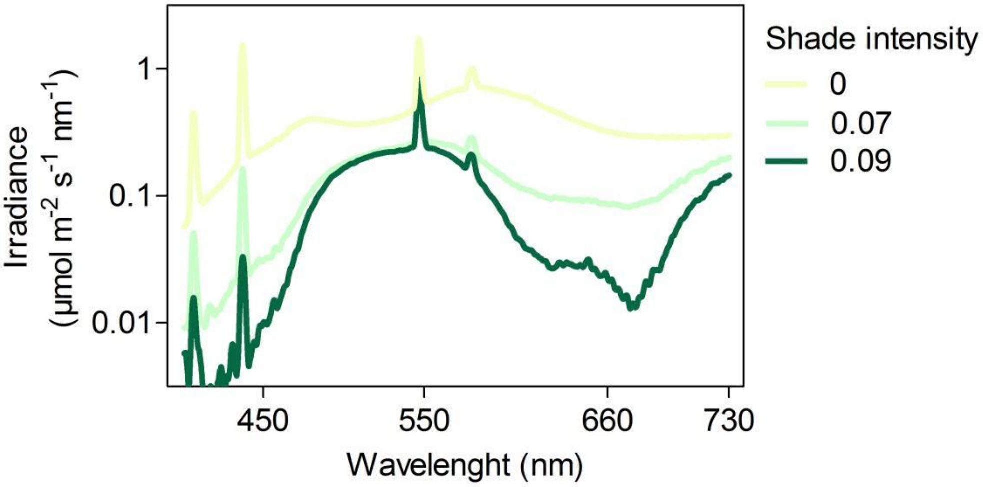

Fig. S9. Spectral photon distribution of the light used in experiments with *Arabidopsis* under controlled conditions. The photon irradiance is shown in log scale. Shade intensity= 0 corresponds to simulated sunlight.

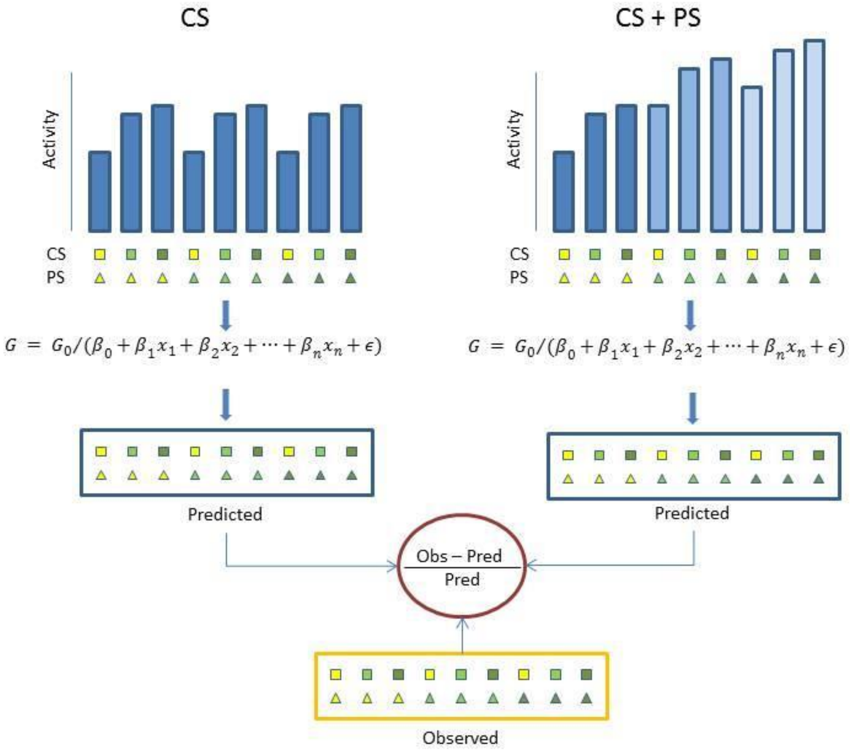

Fig. S10. Protocol used to evaluate the statistical significance of the changes in activity of different components of the auxin network caused by previous shade (PS) conditions. A model was parameterized either using the activities established by the different degrees of current shade (CS) ignoring PS conditions or the activities established by the corresponding combination of CS and PS (CS+PS). The moduli of the difference between observed and predicted data (relative to predicted) were compared by *t* tests.

Table S1. Expression pattern of auxin-related genes in the leaf and petiole of soybean plants grown in the glasshouse and exposed either to sunlight or to simulated shadelight during the day of harvest and the previous day (four combinations of current and previous shade conditions). The log2 fold-change between a given shade condition and the controls that remained under sunlight both days is indicated when significant at a false discovery rate <XXXX

C= Cluster number.
log2 fold change= 0,0 indicates that it is statistically not significantly different from 0

○ Sunlight during harvest day
● Shadelight during harvest day
△ Sunlight during the day before harvest
▲ Shadelight during the day before harvest

			Leaf				Petiole			
ID	**Description**	**C**	△○	△●	▲○	▲●	△○	△●	▲○	▲●
GLYMA12G14670	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	1	0,0	0,0	0,0	3,4	0,0	0,0	0,0	2,9
GLYMA12G15110	SAUR-like auxin-responsive protein family	1	0,0	0,0	0,0	2,8	0,0	1,6	1,5	2,5
GLYMA12G03890	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	1	0,0	0,0	0,0	2,4	0,0	1,8	0,0	2,4
GLYMA11G03850	HAT2, Homeobox-leucine zipper protein 4 (HB-4) / HD-ZIP protein	1	0,0	2,5	0,7	2,2	0,0	1,4	0,0	1,8
GLYMA17G12080	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	2,8	0,0	2,2	0,0	0,0	0,0	0,0
GLYMA02G16090	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	0,0	0,0	2,2	0,0	0,0	0,0	1,2
GLYMA19G34380	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	1,2	1,3	2,0	0,0	0,0	0,0	2,1
GLYMA19G34370	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	1,1	1,2	2,0	0,0	1,4	0,0	1,5
GLYMA03G31530	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	1,1	1,5	2,0	0,0	1,1	0,9	1,9
GLYMA12G14606	SAUR-like auxin-responsive protein family	1	0,0	0,0	0,0	1,9	0,0	0,0	0,0	2,1
GLYMA06G43430	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	1,5	0,0	1,9	0,0	0,0	0,0	2,1
GLYMA08G22190	IAA19, MSG2, indole-3-acetic acid inducible 19	1	0,0	2,4	1,3	1,8	0,0	0,0	0,0	1,2
GLYMA15G01560	(1 of 4) PTHR31734:SF12 - AUXIN-RESPONSIVE PROTEIN IAA19-RELATED	1	0,0	0,0	0,0	1,8	0,0	1,5	1,8	2,4

GLYMA09G20580	(1 of 19) K13947 - auxin efflux carrier family (PIN)	1	0,0	1,6	1,0	1,8	0,0	1,8	0,0	1,0
GLYMA03G31520	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	0,8	1,2	1,7	0,0	1,4	0,0	1,7
GLYMA12G03960	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,7	0,0	0,0	0,0	1,6
GLYMA15G01550	(1 of 2) PTHR31734:SF34 - AUXIN-RESPONSIVE	1	0,0	0,0	1,6	1,7	0,0	1,8	1,9	1,7
GLYMA12G03930	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	1	0,0	0,0	1,0	1,6	0,0	0,0	0,0	1,8
GLYMA09G35520	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,6	0,0	0,0	0,0	1,7
GLYMA17G15380	ATHB-2, ATHB2, HAT4, HB-2, homeobox protein 2	1	0,0	2,2	0,0	1,6	0,0	0,0	-1,2	1,3
GLYMA06G43270	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	1,2	0,0	1,6	0,0	0,0	0,0	2,2
GLYMA12G03920	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,5	0,0	0,0	0,0	1,7
GLYMA06G43350	SAUR-like auxin-responsive protein family	1	0,0	0,0	0,0	1,5	0,0	0,0	0,0	1,6
GLYMA02G16080	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	0,8	1,1	1,5	0,0	0,0	0,0	1,6
GLYMA07G22340	Auxin efflux carrier component-K7L258	1	0,0	1,4	0,0	1,4	0,0	0,0	0,0	0,8
GLYMA08G16500	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,4	0,0	0,0	1,4	2,1
GLYMA07G03840	(1 of 4) PTHR31734:SF12 - AUXIN-RESPONSIVE PROTEIN IAA19-RELATED	1	0,0	1,6	1,1	1,4	0,0	1,9	0,0	1,4
GLYMA13G43780	(1 of 4) PTHR31734:SF12 - AUXIN-RESPONSIVE PROTEIN IAA19-RELATED	1	0,0	0,0	1,1	1,4	0,0	1,9	1,4	2,4
GLYMA20G35280	(1 of 4) PTHR31734:SF11 - AUXIN-RESPONSIVE PROTEIN IAA1-RELATED	1	0,0	0,0	0,7	1,4	0,0	1,2	0,0	1,4
GLYMA13G18910	(1 of 4) PTHR31734:SF6 - AUXIN-RESPONSIVE PROTEIN IAA10-RELATED	1	0,0	0,0	0,0	1,4	0,0	0,9	0,0	1,1
GLYMA09G35570	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,3	0,0	0,0	0,0	1,6
GLYMA10G03720	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	0,8	0,8	1,3	0,0	0,0	0,0	1,9
GLYMA02G16071	(1 of 3) PTHR31734:SF30 - AUXIN-RESPONSIVE PROTEIN IAA14-RELATED	1	0,0	0,7	0,9	1,3	0,0	0,0	0,9	1,7

GLYMA06G43150	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,3	0,0	0,0	0,0	1,4
GLYMA06G43380	SAUR-like auxin-responsive protein family	1	0,0	0,0	0,0	1,3	0,0	0,0	0,0	1,7
GLYMA10G03710	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	1	0,0	0,0	0,9	1,2	0,0	1,3	0,0	1,6
GLYMA06G11540	LAX3, like AUX1 3	1	0,0	1,2	0,0	1,2	0,0	0,0	0,0	1,1
GLYMA09G35460	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	1,1	0,0	1,1	0,0	0,0	0,0	2,4
GLYMA09G35510	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	1,1	0,0	0,0	0,0	1,7
GLYMA04G43150	(1 of 2) PTHR22950:SF3 - AUXIN TRANSPORTER-LIKE PROTEIN 2-RELATED	1	0,0	1,0	0,0	1,0	0,0	0,0	0,0	1,0
GLYMA09G14090	ATCIPK6, CIPK6, SIP3, SNRK3.14, SOS3-interacting	1	0,0	0,0	0,8	1,0	0,0	0,0	1,0	1,4
GLYMA01G00510	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor (Auxin_resp)	1	0,0	1,3	0,0	1,0	0,0	0,0	0,0	0,9
GLYMA09G35620	(1 of 4) PTHR31374:SF41 - AUXIN-INDUCED PROTEIN-LIKE-RELATED	1	0,0	0,0	0,0	1,0	0,0	0,0	0,0	0,9
GLYMA13G17270	(1 of 4) PTHR31384:SF21 - AUXIN RESPONSE FACTOR 19-RELATED	1	0,0	2,3	0,0	0,9	0,0	0,0	0,0	0,0
GLYMA09G35580	(1 of 252) PF02519 - Auxin responsive protein	1	0,0	0,0	0,0	0,8	0,0	0,0	0,0	1,7
GLYMA20G35270	(1 of 3) PTHR31734:SF30 - AUXIN-RESPONSIVE PROTEIN IAA14-RELATED	1	0,0	0,0	0,0	0,8	0,0	0,0	0,0	0,9
GLYMA03G09100	(1 of 5) PTHR22950:SF256 - AUXIN TRANSPORTER PROTEIN 1-RELATED	1	0,0	2,0	0,0	0,8	0,0	0,0	0,0	0,0
GLYMA10G32340	IAA14, SLR, indole-3-acetic acid inducible 14	1	0,0	0,0	0,0	0,6	0,0	0,0	0,0	1,7
GLYMA06G00950	SAUR-like auxin-responsive protein family	2	0,0	2,0	0,0	0,0	0,0	0,0	0,0	2,5
GLYMA09G35430	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,7
GLYMA09G08350	ARF11, ARF19, IAA22, auxin response factor 19	2	0,0	1,8	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA19G42060	(1 of 4) PTHR33565:SF1 - DORMANCY/AUXIN ASSOCIATED PROTEIN	2	0,0	2,3	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G27800	AILP1, ATAILP1, Aluminium induced protein with YGL and LRDR motifs	2	0,0	1,6	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G02760	SAUR-like auxin-responsive protein family	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,3
GLYMA12G03830	SAUR-like auxin-responsive protein family	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,5
GLYMA04G00920	(1 of 4) PTHR31374:SF41 - AUXIN-INDUCED PROTEIN-LIKE-RELATED	2	0,0	1,8	-0,9	0,0	0,0	0,0	0,0	1,9
GLYMA06G00841	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	1,4	0,0	2,1
GLYMA09G35560	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,0
GLYMA12G15360	MAX2, ORE9, PPS, RNI-like superfamily protein	2	0,0	1,6	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G17400	SAUR-like auxin-responsive protein family	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,9
GLYMA07G02080	IAA27, PAP2, phytochrome-associated protein 2	2	0,0	0,0	0,0	0,0	0,0	2,4	0,0	2,3
GLYMA02G44040	B73, CHL6, CNX, CNX1, SIR4, molybdopterin biosynthesis CNX1 protein / molybdenum cofactor biosynthesis enzyme CNX1 (CNX1)	2	0,0	1,9	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G03990	(1 of 4) PTHR31374:SF41 - AUXIN-INDUCED PROTEIN-LIKE-RELATED	2	0,0	0,0	-0,6	0,0	0,0	0,0	0,0	1,3
GLYMA05G02863	ATBT2, BT2, BTB and TAZ domain protein 2	2	0,0	1,5	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G32330	IAA3, SHY2, AUX/IAA transcriptional regulator family	2	0,0	0,0	0,0	0,0	0,0	1,2	0,0	1,2
GLYMA09G35540	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	2	0,0	0,0	0,0	0,0	0,0	2,1	0,0	2,4
GLYMA08G21740	(1 of 4) PTHR31734:SF5 - AUXIN-RESPONSIVE	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,2
GLYMA06G47960	CNX7, SIR5, co-factor for nitrate, reductase and xanthine dehydrogenase 7	2	0,0	1,8	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G35290	SAUR-like auxin-responsive protein family	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,5
GLYMA06G43505	SAUR-like auxin-responsive protein family	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,1

GLYMA04G36040	TAR2, tryptophan aminotransferase related 2	2	0,0	0,0	0,0	0,0	0,0	0,0	1,2	1,5
GLYMA09G35600	SAUR-like auxin-responsive protein family	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,1
GLYMA09G14560	BT1, BTB and TAZ domain	2	0,0	1,6	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G19100	YUC8, Flavin-binding monooxygenase family protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,0
GLYMA12G03840	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,6
GLYMA17G15200	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,1
GLYMA12G03810	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,4
GLYMA06G00851	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,7
GLYMA12G14760	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,1
GLYMA12G29720	(1 of 5) PTHR31384:SF27 - AUXIN RESPONSE FACTOR 10-RELATED	2	0,0	1,6	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G15090	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	2	0,0	0,0	0,0	0,0	0,0	1,8	0,0	2,8
GLYMA12G03880	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,6
GLYMA09G08490	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	2	0,0	1,7	0,0	0,0	0,0	0,0	-1,2	0,0
GLYMA06G43181	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	1,7
GLYMA06G43190	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,5
GLYMA09G35440	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	2,5	0,0	0,0	0,0	0,0	0,0	2,2
GLYMA09G35400	(1 of 252) PF02519 - Auxin responsive protein	2	0,0	0,0	0,0	0,0	0,0	0,0	0,0	2,3
GLYMA09G35420	(1 of 252) PF02519 - Auxin responsive protein	5	0,0	4,0	0,0	3,2	0,0	2,5	0,0	2,5
GLYMA06G07130	IAA29, indole-3-acetic acid inducible 29	5	0,0	2,1	0,0	1,5	0,0	3,0	1,1	2,1
GLYMA04G07040	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	5	0,0	2,7	0,0	1,4	0,0	3,0	0,0	1,7
GLYMA09G35390	(1 of 252) PF02519 - Auxin responsive protein	5	0,0	2,7	0,0	0,0	0,0	3,3	0,0	2,6

GLYMA20G38100	(1 of 4) PTHR33565:SF1 - DORMANCY/AUXIN ASSOCIATED PROTEIN	6	0,0	5,9	0,0	2,4	0,0	0,0	0,0	0,0
GLYMA10G29190	(1 of 4) PTHR33565:SF1 - DORMANCY/AUXIN ASSOCIATED PROTEIN	6	0,0	4,6	0,0	1,8	0,0	0,0	0,0	0,0
GLYMA13G31060	(1 of 8) PF05564 - Dormancy/auxin associated protein (Auxin_repressed)	6	0,0	4,7	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G08300	(1 of 8) PF05564 - Dormancy/auxin associated protein (Auxin_repressed)	6	0,0	3,9	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G12120	ILL6, IAA-leucine resistant (ILR)-like gene 6	6	0,0	3,4	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G29435	CVP2, DNAse I-like superfamily protein	3	0,0	0,0	0,0	1,7	0,0	0,0	0,0	0,0
GLYMA03G39450	(1 of 4) PTHR33565:SF1 - DORMANCY/AUXIN ASSOCIATED PROTEIN	3	0,0	0,0	0,9	1,6	0,0	0,0	0,0	0,0
GLYMA13G43800	AXR3, IAA17, AUX/IAA transcriptional regulator family protein	3	0,0	0,0	1,5	1,2	0,0	0,0	1,2	0,0
GLYMA09G33630	(1 of 4) PTHR31734:SF24 - AUXIN-RESPONSIVE	3	0,0	0,0	1,0	1,0	0,0	0,0	0,0	0,7
GLYMA03G17450	(1 of 5) PTHR31384:SF1 - AUXIN RESPONSE FACTOR 12-RELATED	3	0,0	0,0	0,0	0,8	0,0	0,0	0,0	0,0
GLYMA02G40650	(1 of 6) PTHR31384:SF2 - AUXIN RESPONSE FACTOR 8	3	0,0	0,0	0,0	0,7	0,0	0,0	0,0	0,0
GLYMA20G36790	(1 of 4) PTHR31734:SF28 - AUXIN-RESPONSIVE PROTEIN IAA16	3	0,0	0,0	0,0	0,7	0,0	0,0	0,0	0,0
GLYMA01G25270	(1 of 5) PTHR31384:SF1 - AUXIN RESPONSE FACTOR 12-RELATED	3	0,0	0,0	0,0	0,7	0,0	0,0	0,0	0,0
GLYMA13G30750	(1 of 4) PTHR31384:SF5 - AUXIN RESPONSE FACTOR 3	3	0,0	0,0	0,0	0,7	0,0	0,0	0,0	0,0
GLYMA12G09860	ATE2FB, E2F1, E2FB, E2F transcription factor 1	3	0,0	0,0	0,0	0,7	0,0	0,0	0,0	0,0
GLYMA07G15640	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor	3	0,0	1,0	0,0	0,6	0,0	0,0	0,0	0,0
GLYMA03G41920	(1 of 3) PTHR31384:SF17 - AUXIN RESPONSE FACTOR 11-RELATED	3	0,0	0,0	0,0	0,6	0,0	0,0	0,0	0,0

GLYMA19G36571	(1 of 20) PF02362//PF06507 - B3 DNA binding domain (B3) // Auxin response factor	3	0,0	0,0	0,0	0,6	0,0	0,0	0,7	0,7
GLYMA08G01100	(1 of 4) PTHR31384:SF8 - AUXIN RESPONSE FACTOR 2	3	0,0	0,0	0,0	0,6	0,0	0,0	0,0	0,0
GLYMA10G30440	(1 of 4) PTHR31734:SF28 - AUXIN-RESPONSIVE	3	0,0	0,0	0,0	0,6	0,0	0,0	0,0	0,0
GLYMA07G16810	Probable glutathione S-transferase-HSP26-A	3	0,0	0,0	0,0	0,0	0,0	0,0	1,1	0,0
GLYMA15G09750	(1 of 4) PTHR31384:SF3 - AUXIN RESPONSE FACTOR 6	3	0,0	0,0	1,2	0,0	0,0	0,0	0,0	0,0
GLYMA08G10550	ARF6, auxin response factor 6	3	0,0	1,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G32040	ARF16, auxin response factor 16	3	0,0	0,0	1,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G30700	Auxin efflux carrier component-PIN4b	3	0,0	0,0	0,0	0,0	0,0	0,0	0,6	0,0
GLYMA05G36430	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor	3	0,0	0,6	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G01760	Auxin efflux carrier component-LOC100802247	3	0,0	0,7	0,0	0,0	0,0	1,3	0,0	0,0
GLYMA10G06080	(1 of 20) PF02362//PF06507 - B3 DNA binding domain (B3) // Auxin response factor	3	0,0	0,0	0,6	0,0	0,0	0,0	0,0	0,0
GLYMA12G08110	ARF10, auxin response factor 10	3	0,0	0,9	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G38260	(1 of 4) PTHR31734:SF18 - AUXIN-RESPONSIVE	3	0,0	0,0	0,0	0,0	0,0	0,0	0,9	0,5
GLYMA01G02350	(1 of 4) PTHR31734:SF24 - AUXIN-RESPONSIVE	3	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,6
GLYMA07G17810	(1 of 5) PTHR22950:SF256 - AUXIN TRANSPORTER PROTEIN 1-RELATED	3	0,0	0,6	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G27280	AFB3, auxin signaling F-box 3	3	0,0	1,3	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G02210	ATIPS2, ATMIPS2, MIPS2, myo-inositol-1-phosphate synthase 2	3	0,0	0,0	0,5	0,0	0,0	0,0	0,0	0,0
GLYMA15G02350	(1 of 4) PTHR31734:SF2 - AUXIN-RESPONSIVE PROTEIN IAA18-RELATED	3	0,0	1,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G11030	Uncharacterized protein-LOC100775721	3	0,0	0,8	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA10G04610	(1 of 4) PTHR31734:SF6 - AUXIN-RESPONSIVE PROTEIN IAA10-RELATED	3	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,8
GLYMA06G17320	(1 of 4) PTHR31384:SF8 - AUXIN RESPONSE FACTOR 2	3	0,0	0,8	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G09550	(1 of 4) PTHR31734:SF18 - AUXIN-RESPONSIVE	3	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,6
GLYMA06G06850	ATSK21, BIN2, DWF12, SK21, UCU1, Protein kinase superfamily protein	3	0,0	0,7	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G40030	(1 of 5) PTHR31384:SF27 - AUXIN RESPONSE FACTOR 10-RELATED	3	0,0	1,1	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G09390	(1 of 5) PTHR31651:SF5 - AUXIN EFFLUX CARRIER FAMILY PROTEIN-RELATED	3	0,0	0,8	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G43410	DSPTP1E, IBR5, indole-3-butyric acid response 5	3	0,0	0,9	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G04000	SAUR-like auxin-responsive protein family	3	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,8
GLYMA09G00490	AtETR1, EIN1, ETR, ETR1, Signal transduction histidine kinase, hybrid-type, ethylene	3	0,0	1,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G08960	CHY1, beta-hydroxyisobutyryl-CoA hydrolase 1	3	0,0	0,5	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G37070	(1 of 4) PTHR31734:SF24 - AUXIN-RESPONSIVE	3	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,5
GLYMA18G42640	(1 of 5) PTHR22950:SF256 - AUXIN TRANSPORTER PROTEIN 1-RELATED	3	0,0	0,0	0,0	0,0	0,0	0,0	0,8	0,0
GLYMA06G47520	ATPHB3, PHB3, prohibitin 3	4	0,0	-2,5	0,7	0,0	0,0	0,0	0,0	0,0
GLYMA16G21930	Auxin efflux carrier family protein	4	0,0	-1,1	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G01601	ELF3, PYK20, hydroxyproline-rich glycoprotein family protein	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-1,4
GLYMA06G45120	(1 of 4) PTHR31901:SF10 - AUXIN-RESPONSIVE GH3 FAMILY PROTEIN	4	0,0	0,0	1,0	0,0	0,0	0,0	0,0	-1,0
GLYMA17G33985	ENP, MAB4, NPY1, Phototropic-responsive NPH3 family protein	4	0,0	0,0	0,0	0,0	0,0	0,0	-0,7	-1,3
GLYMA15G15220	(1 of 1) PF00400//PF00439//PF06507 - WD domain, G-beta repeat (WD40) // Bromodomain (Bromodomain) // Auxin	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-0,6
GLYMA18G12660	ATRHM1, RHM1, ROL1, rhamnose biosynthesis 1	4	0,0	-2,7	0,0	0,0	0,0	0,0	0,0	-1,1

GLYMA13G07250	Putative uncharacterized protein-LOC100783522	4	0,0	0,6	-0,6	0,0	0,0	0,0	0,0	0,0
GLYMA20G35180	ATMYB15, ATY19, MYB15, myb domain protein 15	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-1,2
GLYMA10G02440	GH3.9, putative indole-3-acetic acid-amido synthetase GH3.9	4	0,0	0,0	0,0	0,0	0,0	-2,0	0,0	0,0
GLYMA13G20530	ABCB1, ATPGP1, PGP1, ATP binding cassette subfamily B1	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-0,8
GLYMA04G08910	ATCCD8, CCD8, MAX4, carotenoid cleavage	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-1,0
GLYMA13G43050	IAA26, PAP1, phytochrome-associated protein 1	4	0,0	0,0	0,0	0,0	0,0	0,0	-0,8	0,0
GLYMA07G16170	(1 of 5) PTHR31384:SF1 - AUXIN RESPONSE FACTOR 12-RELATED	4	0,0	1,1	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G01800	(1 of 4) PTHR31734:SF2 - AUXIN-RESPONSIVE PROTEIN IAA18-RELATED	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,8
GLYMA03G31340	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	4	0,0	0,0	0,0	0,0	0,0	0,0	-1,3	-1,0
GLYMA13G20540	ATNUP160, NUP160, SAR1, SUPPRESSOR OF AUXIN RESISTANCE1	4	0,0	-1,9	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G29280	(1 of 5) PTHR31384:SF20 - AUXIN RESPONSE FACTOR 4	4	0,0	-0,7	0,0	0,0	0,0	0,0	0,0	-0,8
GLYMA16G27440	UGT74E2, Uridine diphosphate glycosyltransferase 74E2	4	0,0	-2,1	0,0	0,0	0,0	0,0	0,0	-1,4
GLYMA11G20490	(1 of 5) PTHR31384:SF27 - AUXIN RESPONSE FACTOR 10-RELATED	4	0,0	0,7	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G09650	(1 of 4) PTHR31734:SF18 - AUXIN-RESPONSIVE	4	0,0	-0,7	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G22460	AMP-dependent synthetase and ligase family protein	4	0,0	-0,8	0,0	0,0	0,0	0,0	0,0	-0,5
GLYMA16G06333	ASB1, TRP4, WEI7, anthranilate synthase beta subunit 1	4	0,0	-0,8	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G30900	(1 of 3) PTHR23130:SF95 - AUXIN-RESPONSIVE	4	0,0	-2,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G07320	Putative uncharacterized protein-LOC100790426	4	0,0	0,0	-1,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G31970	Uncharacterized protein-LOC100820508	4	0,0	-0,8	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G16890	Uncharacterized protein-LOC100801817	4	0,0	-1,7	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G05530	(1 of 4) PTHR31374:SF35 - AUXIN-INDUCED PROTEIN-	4	0,0	0,0	-1,1	0,0	0,0	0,0	0,0	0,0

GLYMA08G03141	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-1,1
GLYMA04G33720	ATMYB94, ATMYBCP70, MYB94, myb domain protein 94	4	0,0	0,0	0,0	0,0	0,0	0,0	0,0	-1,2
GLYMA11G20020	AMP-dependent synthetase and ligase family protein	4	0,0	0,0	0,0	-0,6	0,0	0,0	0,0	0,0
GLYMA18G03270	AMT1, ASA1, JDL1, TRP5, WEI2, anthranilate synthase alpha subunit 1	4	0,0	0,0	-0,6	-0,7	0,0	-1,1	0,0	-1,0
GLYMA01G43880	ATCHS, CHS, TT4, Chalcone and stilbene synthase family	7	0,0	0,0	0,0	0,0	0,0	-4,0	-3,6	-4,1
GLYMA07G04850	(1 of 252) PF02519 - Auxin responsive protein	8	0,0	0,0	0,0	0,0	0,0	5,2	0,0	0,0
GLYMA12G02570	Uncharacterized protein-LOC100777785	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G06290	Uncharacterized protein-LOC100789273	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G27900	Auxin efflux carrier component-PIN6B	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G13500	Auxin efflux carrier component-I1L2C6	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G00390	Auxin efflux carrier component-LOC100499638	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G49080	Auxin efflux carrier component-LOC100779697	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G10270	Uncharacterized protein-LOC100803097	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G09470	Uncharacterized protein-LOC100792133	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G02560	Uncharacterized protein-I1LPF2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G00870	Uncharacterized protein-LOC100810179	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G30900	Auxin efflux carrier component-LOC100802041	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G35460	Uncharacterized protein-LOC100815995	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G16870	Auxin efflux carrier component-LOC100789817	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G06460	Auxin efflux carrier component-PIN2b	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G06970	Auxin efflux carrier component-GLYMA_09G061800	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G27270	Uncharacterized protein-LOC100815218	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA07G34190	Auxin efflux carrier component-LOC100785146	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G34730	Uncharacterized protein-LOC100804154	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G47630	Auxin efflux carrier component-LOC100784879	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G12370	Uncharacterized protein-I1JE79	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G05900	Auxin efflux carrier component-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G18440	Uncharacterized protein-LOC100814176	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G36960	Uncharacterized protein-LOC100795488	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G23180	Auxin efflux carrier component-PIN11A	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G28130	Auxin efflux carrier component-PIN10B	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G25690	Auxin efflux carrier component-LOC100781239	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G35960	Uncharacterized protein-LOC100783059	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G35970	Uncharacterized protein-LOC100779470	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G18241	Uncharacterized protein-GLYMA_15G168100	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G01391	Uncharacterized protein-K7N0P2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G10260	Uncharacterized protein-LOC100802572	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G09461	Uncharacterized protein-GLYMA_11G089200	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G41072	Uncharacterized protein-GLYMA_06G262200	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G11550	Auxin efflux carrier component-PIN4a	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G09043	Uncharacterized protein-LOC100818269	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G09026	Uncharacterized protein-GLYMA_13G038400	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G28050	Uncharacterized protein-LOC100800464	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G07280	Uncharacterized protein-LOC100787244	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G38700	Auxin efflux carrier component-LOC100788225	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G37561	Auxin efflux carrier component-LOC100801456	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G45520	ATMYB14, MYB14, MYB14AT, myb domain protein 14	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA10G06610	ATEIN2, CKR1, EIN2, ERA3, ORE2, ORE3, PIR2, NRAMP metal ion transporter family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G09010	ATMIXTA, ATMYB16, MYB16, myb domain protein 16	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G09750	BRL2, VH1, BRI1-like 2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G07940	AJH2, CSN5, CSN5B, COP9-signalosome 5B	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G26860	IAA33, indole-3-acetic acid inducible 33	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G00291	AXR5, IAA1, indole-3-acetic acid inducible	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G09760	AIR12, auxin-responsive family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G49177	MIF1, mini zinc finger 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G36190	Auxin efflux carrier family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G29110	PDLZ2, PLDP2, PLDZETA2, phospholipase D P2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G04310	YUC2, Flavin-binding monooxygenase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G42320	AXR4, RGR, RGR1, alpha/beta-Hydrolases superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G11705	ATAVP3, AtVHP1;1, AVP-3, AVP1, Inorganic H pyrophosphatase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G10840	AtMYB93, MYB93, myb domain protein 93	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G09100	ATHB-8, ATHB8, HB-8, homeobox gene 8	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G13270	TGH, SWAP (Suppressor-of-White-APricot)/surp domain-containing protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G42790	ATCPL2, CPL2, carboxyl-terminal domain (ctd)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G23205	Auxin-responsive GH3 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G35620	ATMYB44, ATMYBR1, MYB44, MYBR1, myb domain protein r1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G42030	AtMYB109, MYB109, myb domain protein 109	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G06830	RCE1, RUB1 conjugating	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G40090	ATBT4, BT4, BTB and TAZ domain protein 4	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G11730	NOV, Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA11G02390	ACS6, ATACS6, 1-aminocyclopropane-1-carboxylic acid (acc) synthase 6	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G40530	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G02800	ATCUL1, AXR6, CUL1, cullin 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G20900	SMAP1, small acidic protein 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G33831	DRB1, HYL1, dsRNA-binding domain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G37660	AMI1, ATAMI1, ATTOC64-I, TOC64-I, amidase 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G07710	SRS1, STY1, Lateral root primordium (LRP) protein-related	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G00570	ATCAND1, CAND1, ETA2, HVE, TIP120, cullin-associated and neddylation dissociated	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G03863	ABCG37, ATPDR9, PDR9, PIS1, pleiotropic drug resistance	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G23430	COP3, HLS1, UNS2, Acyl-CoA N-acyltransferases (NAT) superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G38800	DRN-LIKE, DRNL, ESR2, SOB2, DORNROSCHEN-like	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G03920	VIK, VH1-interacting kinase	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G43450	IAA16, indoleacetic acid-induced protein 16	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G09290	AIR3, Subtilisin-like serine endopeptidase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G38370	IAA20, indole-3-acetic acid inducible 20	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G40540	ARF5, IAA24, MP, Transcriptional factor B3 family protein / auxin-responsive factor	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G41730	EMB30, GN, VAN7, sec7 domain-containing protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G04761	LEC2, AP2/B3-like transcriptional factor family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G11260	SLOMO, F-box family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G29720	AGO1, Stabilizer of iron transporter SufD /	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G20180	YUC3, YUCCA 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G09140	AUX1, MAP1, PIR1, WAV5, Transmembrane amino acid transporter family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA13G22750	BDL, IAA12, AUX/IAA transcriptional regulator family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G40340	PK3AT, WAG1, WAG 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G05070	ATTBP3, ATTRB2, TBP3, TRB2, Homeodomain-like/winged-helix DNA-binding family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G03020	myb-like transcription factor family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G06911	APP1, ATAPP1, aminopeptidase P1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G06690	PRHA, pathogenesis related homeodomain protein A	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G36220	ATSNX1, SNX1, sorting nexin 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G05520	CYP711A1, MAX1, cytochrome P450, family 711, subfamily A, polypeptide 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G13373	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G38410	ATMES17, MES17, methyl esterase 17	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G33420	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G24100	IAA9, indole-3-acetic acid	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G21680	AUR3, BRU6, GH3-2, GH3.2, YDK1, Auxin-responsive GH3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G40270	ARF1, auxin response factor 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G03640	ATR4, CYP83B1, RED1, RNT1, SUR2, cytochrome P450, family 83, subfamily B, polypeptide 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G38550	AGD3, SFC, VAN3, ARF GTPase-activating protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G08070	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G39380	ACT7, actin 7	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G00295	5PTASE13, AT5PTASE13, Endonuclease/exonuclease/phosphatase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G39780	GH3.1, Auxin-responsive GH3 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G05440	PNC1, peroxisomal adenine nucleotide carrier 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G37215	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA06G37381	ABCG36, ATABCG36, ATPDR8, PDR8, PEN3, ABC-2 and Plant PDR ABC-type transporter family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G03900	LRP1, Lateral root primordium (LRP) protein-related	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G24090	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G19670	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G05300	ABCB19, ATABCB19, ATMDR1, ATMDR11, ATPGP19, MDR1, MDR11, PGP19, ATP binding cassette subfamily B19	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G40760	Auxin efflux carrier family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G35500	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G27336	FUS3, AP2/B3-like transcriptional factor family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G33381	ATNDPK2, NDPK IA, NDPK IA IA, NDPK1A, NDPK2, nucleoside diphosphate kinase 2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G01501	ADA2B, PRZ1, homolog of yeast ADA2 2B	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G36880	ARAC1, ATGP2, ATRAC1, ATROP3, ROP3, Arabidopsis RAC-like 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G05093	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G23590	ATMCB1, MBP1, MCB1, RPN10, regulatory particle non-ATPase 10	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G17750	IAA31, indole-3-acetic acid inducible 31	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G45640	DFL1, GH3.6, Auxin-responsive GH3 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G51450	CDC27b, HBT, CDC27 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G44310	FIN219, JAR1, Auxin-responsive GH3 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G15850	AS1, ATMYB91, ATPHAN, MYB91, myb-like HTH transcriptional regulator family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA02G06970	OBP1, OBF binding protein 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G39440	ACL5, S-adenosyl-L-methionine-dependent methyltransferases superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G00830	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G46210	AXR1, NAD(P)-binding Rossmann-fold superfamily	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G00870	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G36360	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G35630	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G35950	PBP1, pinoid-binding protein 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G00880	MOS3, NUP96, PRE, SAR3, SUPPRESSOR OF AUXIN RESISTANCE 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G32993	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G11890	DFL2, GH3-10, Auxin-responsive GH3 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G20670	YUC6, Flavin-binding monooxygenase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G40360	RSL2, ROOT HAIR DEFECTIVE 6-LIKE 2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G16061	AJH1, CSN5A, JAB1, COP9 signalosome 5A	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G18600	WAG2, Protein kinase superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G51061	ASA1, BIG, CRM1, DOC1, LPR1, TIR3, UMB1, auxin transport protein (BIG)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G33770	TTL3, VIT, tetratricopetide-repeat thioredoxin-like 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G08130	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G34031	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G02600	ATMYB30, MYB30, myb domain protein 30	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G19960	Homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G02250	Homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA14G35690	ATPURC, PUR7, PURC, purin 7	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G07200	Homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G42260	LHY, LHY1, Homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G10280	AIR9, Outer arm dynein light chain 1 protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G14266	ATCCD7, CCD7, MAX3, carotenoid cleavage	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G43150	ATSGT1B, EDM1, ETA3, RPR1, SGT1B, phosphatase-related	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G17300	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G04845	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G19320	Auxin efflux carrier family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G17680	FQR1, flavodoxin-like quinone reductase 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G38180	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G15820	YUC4, Flavin-binding monooxygenase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G00490	HCT, hydroxycinnamoyl-CoA shikimate/quinate hydroxycinnamoyl transferase	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G12981	ATPEX5, PEX5, peroxin 5	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G42080	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G05220	ARF7, BIP, IAA21, IAA23, IAA25, MSG1, NPH4, TIR5, Transcriptional factor B3 family protein / auxin-responsive factor	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G07730	WAT1, Walls Are Thin 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G03270	ATMPK1, MPK1, mitogen-activated protein kinase 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G12180	AAE18, acyl-activating enzyme 18	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G27881	IAA30, indole-3-acetic acid inducible 30	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G43350	ARF17, auxin response factor 17	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA07G03180	TPL, WSIP1, Transducin family protein / WD-40 repeat family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G17880	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G10280	ATGGT-IB, GGB, PGGT-I, Prenyltransferase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G41230	ATRUB1, NEDD8, RUB1, related to ubiquitin 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G41260	ANAC009, FEZ, NAC (No Apical Meristem) domain transcriptional regulator superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G49490	AAR3, Domain of unknown function (DUF298)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G41250	ATMYB61, MYB61, myb domain protein 61	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G24240	ARF3, ETT, Transcriptional factor B3 family protein / auxin-responsive factor AUX/IAA-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G47240	ABI3, SIS10, AP2/B3-like transcriptional factor family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G15910	TCTP, translationally controlled tumor protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G04240	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G07980	Duplicated homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G30590	GDG1, GH3.12, PBS3, WIN3, Auxin-responsive GH3 family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G49290	ATHB20, HB20, homeobox protein 20	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G38390	ATHB40, HB-5, HB40, homeobox protein 40	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G25580	IAA32, MEE10, indole-3-acetic acid inducible 32	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G29190	ABR, PID, Protein kinase superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G06360	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G39420	TIR1, F-box/RNI-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G16870	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA20G35415	AGG2, G-protein gamma subunit	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G35180	IAA13, auxin-induced protein 13	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G01300	IBR1, SDRA, indole-3-butyric acid response 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G53900	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G01941	EXGT-A1, EXT, XTH4, xyloglucan	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G07400	RGLG2, RING domain ligase2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G30310	ATMKK7, BUD1, MKK7, MKK7, MAP kinase kinase 7	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G43730	LOP1, TRN1, tornado 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G01150	TCH4, XTH22, Xyloglucan endotransglucosylase/hydrolase family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G20380	ATGLB3, GLB3, hemoglobin 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G03390	ATTRB1, TRB1, telomere repeat binding factor 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G06720	CHD3, CHR6, GYM, PKL, SSL2, chromatin remodeling factor CHD3 (PICKLE)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G32810	Auxin efflux carrier family protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G03340	SAV3, TAA1, WEI8, tryptophan aminotransferase of Arabidopsis	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G15420	NDL1, N-MYC downregulated-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G25050	ATSEH, SEH, soluble epoxide hydrolase	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G40800	RVE1, Homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G18470	anac021, ANAC022, NAC1, NAC domain containing protein 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G05860	CYP79B2, cytochrome P450, family 79, subfamily B,	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G32150	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G09975	ARF8, ATARF8, auxin response factor 8	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G40440	ILL3, IAA-leucine-resistant (ILR1)-like 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G30421	RGLG1, RING domain ligase1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G05620	APM1, ATAPM1, aminopeptidase M1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA10G03610	AGG1, ATAGG1, GG1, Ggamma-subunit 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G40381	ARGOS, auxin-regulated gene involved in organ size	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G08690	RPN12a, regulatory particle non-ATPase 12A	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G05560	Homeodomain-like superfamily protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G08465	5PTASE11, AT5PTASE11, inositol polyphosphate 5-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G00370	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G10750	ATRBX1, HRT1, RBX1, ROC1, RING-box 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G09060	CCA1, circadian clock	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G20133	ABCB4, ATPGP4, MDR4, PGP4, ATP binding cassette	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G26200	AFB2, auxin signaling F-box 2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G03350	WOX5, WUSCHEL related homeobox 5	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G16640	SAUR-like auxin-responsive protein family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G35180	BRX, NLM9, DZC (Disease resistance/zinc finger/chromosome condensation-like region) domain	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G01420	ATWRKY23, WRKY23, WRKY DNA-binding protein 23	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G00460	ABA3, ACI2, ATABA3, LOS5, SIR3, molybdenum cofactor sulfurase (LOS5) (ABA3)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G45100	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G01390	(1 of 6) PTHR23130:SF80 - AUXIN-INDUCED IN ROOT CULTURES PROTEIN 12	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G29400	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G39740	(1 of 2) PTHR10992:SF773 - PROTEIN AUXIN RESPONSE 4	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA05G04760	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G00220	(1 of 3) PTHR31384:SF28 - AUXIN RESPONSE FACTOR 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G29410	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G27580	(1 of 4) PTHR31384:SF3 - AUXIN RESPONSE FACTOR 6	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G20382	(1 of 20) PF02362//PF06507 - B3 DNA binding domain (B3) // Auxin response factor	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G15230	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G20374	(1 of 5) PTHR31384:SF27 - AUXIN RESPONSE FACTOR 10-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G00895	(1 of 1) PTHR31929:SF2 - AUXIN-RESPONSIVE FAMILY PROTEIN-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA0079s003	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G29430	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA0079s002	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G07560	(1 of 5) PTHR31384:SF20 - AUXIN RESPONSE FACTOR 4	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G39630	(1 of 6) PTHR23130:SF80 - AUXIN-INDUCED IN ROOT CULTURES PROTEIN 12	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G05510	(1 of 20) K14487 - auxin responsive GH3 gene family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G38540	(1 of 4) PTHR31384:SF8 - AUXIN RESPONSE FACTOR 2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G00260	(1 of 4) PTHR31734:SF11 - AUXIN-RESPONSIVE PROTEIN IAA1-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA07G05770	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G14350	(1 of 1) PF03105//PF03321 - SPX domain (SPX) // GH3 auxin-responsive promoter (GH3)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G40760	(1 of 4) PTHR31734:SF28 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G24110	(1 of 4) PTHR31374:SF35 - AUXIN-INDUCED PROTEIN-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G16181	(1 of 5) PTHR31384:SF1 - AUXIN RESPONSE FACTOR 12-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G03480	(1 of 5) PTHR31374:SF56 - AUXIN-REGULATED PROTEIN-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G14720	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G29320	(1 of 4) PTHR31384:SF3 - AUXIN RESPONSE FACTOR 6	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G40180	(1 of 5) PTHR31384:SF1 - AUXIN RESPONSE FACTOR 12-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G01510	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G32410	(1 of 20) K14487 - auxin responsive GH3 gene family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G40310	(1 of 5) PTHR31384:SF20 - AUXIN RESPONSE FACTOR 4	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G38000	(1 of 20) K14487 - auxin responsive GH3 gene family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G17380	(1 of 6) PTHR31374:SF22 - AUXIN-RESPONSIVE PROTEIN-LIKE PROTEIN-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G41640	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G17581	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G41640	(1 of 2) PTHR31734:SF29 - AUXIN-RESPONSIVE PROTEIN IAA32-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G20050	(1 of 6) PTHR31374:SF16 - AUXIN-RESPONSIVE FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA07G06060	(1 of 3) PTHR31384:SF17 - AUXIN RESPONSE FACTOR 11-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA06G04000	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G36710	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G22260	(1 of 3) PTHR23130:SF95 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G14686	(1 of 5) PTHR31374:SF56 - AUXIN-REGULATED PROTEIN-	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G36390	(1 of 4) PTHR31734:SF18 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G14800	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G04760	(1 of 2) PTHR31734:SF3 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G15910	(1 of 5) PTHR31384:SF20 - AUXIN RESPONSE FACTOR 4	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G25650	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G28550	(1 of 3) PTHR31384:SF28 - AUXIN RESPONSE FACTOR 1	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G37550	(1 of 4) PTHR31901:SF10 - AUXIN-RESPONSIVE GH3 FAMILY PROTEIN	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G08540	(1 of 4) PTHR31384:SF5 - AUXIN RESPONSE FACTOR 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G11200	(1 of 20) K14487 - auxin responsive GH3 gene family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G16330	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G42045	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G03500	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA19G36781	(1 of 6) PTHR31374:SF16 - AUXIN-RESPONSIVE FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G02410	(1 of 3) PTHR31384:SF19 - AUXIN RESPONSE FACTOR 17	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G03900	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G07630	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G32451	(1 of 4) PTHR31734:SF6 - AUXIN-RESPONSIVE PROTEIN IAA10-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA02G01010	(1 of 4) PTHR31734:SF15 - AUXIN-RESPONSIVE PROTEIN IAA20-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G32300	(1 of 4) PTHR31384:SF5 - AUXIN RESPONSE FACTOR 3	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G12240	(1 of 6) PTHR23130:SF80 - AUXIN-INDUCED IN ROOT CULTURES PROTEIN 12	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G18080	(1 of 20) K14487 - auxin responsive GH3 gene family (GH3)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G18040	(1 of 20) K14487 - auxin responsive GH3 gene family	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G32570	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G32910	(1 of 4) PTHR31901:SF10 - AUXIN-RESPONSIVE GH3 FAMILY PROTEIN	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G08480	(1 of 6) PTHR31374:SF22 - AUXIN-RESPONSIVE PROTEIN-LIKE PROTEIN-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G06427	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G02040	(1 of 4) PTHR31734:SF5 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G14560	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G35470	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA04G00840	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G01170	(1 of 6) PTHR23130:SF80 - AUXIN-INDUCED IN ROOT CULTURES PROTEIN 12	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G33730	(1 of 3) PTHR31384:SF19 - AUXIN RESPONSE FACTOR 17	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G14580	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G34180	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G39340	(1 of 17) K14486 - auxin response factor (K14486, ARF)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA01G36030	(1 of 5) PTHR31651:SF5 - AUXIN EFFLUX CARRIER FAMILY PROTEIN-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G43310	(1 of 4) PTHR31734:SF5 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA20G01290	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G35320	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G01390	(1 of 2) PTHR33565:SF3 - DORMANCY/AUXIN ASSOCIATED FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G03650	(1 of 36) PF02309//PF02362//PF06507 - AUX/IAA family (AUX_IAA) // B3 DNA binding domain (B3) // Auxin response factor	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA04G37760	(1 of 4) PTHR31384:SF8 - AUXIN RESPONSE FACTOR 2	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA09G35410	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA0101s002	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G31940	(1 of 6) PTHR31384:SF2 - AUXIN RESPONSE FACTOR 8	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA16G02650	(1 of 3) PTHR31384:SF17 - AUXIN RESPONSE FACTOR 11-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G15040	(1 of 252) PF02519 - Auxin responsive protein (Auxin_inducible)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA16G02350	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA13G39800	(1 of 6) PTHR31374:SF16 - AUXIN-RESPONSIVE FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G15030	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA15G19980	(1 of 4) PTHR31384:SF21 - AUXIN RESPONSE FACTOR 19-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G40970	(1 of 4) PTHR31734:SF15 - AUXIN-RESPONSIVE PROTEIN IAA20-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G04070	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA14G38940	(1 of 6) PTHR31384:SF2 - AUXIN RESPONSE FACTOR 8	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA17G37580	(1 of 3) PTHR31384:SF10 - AUXIN RESPONSE FACTOR 5	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G16874	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G14960	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA11G03720	(1 of 16) PF05703 - Auxin canalisation (Auxin_canalis)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA03G01700	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G15110	(1 of 6) PTHR31384:SF2 - AUXIN RESPONSE FACTOR 8	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA08G45940	(1 of 3) PTHR23130:SF95 - AUXIN-RESPONSIVE	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G04810	(1 of 2) PTHR33565:SF3 - DORMANCY/AUXIN ASSOCIATED FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA05G35640	(1 of 53) K14484 - auxin-responsive protein IAA (IAA)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

GLYMA12G14940	(1 of 252) PF02519 - Auxin responsive protein	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G24368	(1 of 3) PTHR31384:SF10 - AUXIN RESPONSE FACTOR 5	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA12G08420	(1 of 6) PTHR31374:SF16 - AUXIN-RESPONSIVE FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA07G33210	(1 of 8) PTHR34052:SF1 - AUXIN RESPONSE FACTOR 30-RELATED	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA19G21600	(1 of 2) PTHR31419:SF2 - AUXIN EFFLUX CARRIER FAMILY PROTEIN	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G35360	(1 of 2) PTHR31374:SF45 - AUXIN-RESPONSIVE FAMILY	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA18G05330	(1 of 6) PTHR31384:SF2 - AUXIN RESPONSE FACTOR 8	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0
GLYMA10G35481	(1 of 20) PF02362//PF06507 - B3 DNA binding domain (B3) // Auxin response factor (Auxin_resp)	-	0,0	0,0	0,0	0,0	0,0	0,0	0,0	0,0

Table S2. Average rate of hypocotyl growth (mm / h) in Arabidopsis seedlings of the indicated genotype as affected by different combinations of previous shade (PS) and current shade (CS).

The rates are highlighted in red and blue when higher or lower than the rate of the Col wild type respectively.

L= loss-of-function mutant. G= gain-of-function mutant

The significance compred to the Col wild type is indicated (NS= not significant)

PS		0	0	0	0.07	0.07	0.07	0.09	0.09	0.09	
CS		0	0.07	0.09	0	0.07	0.09	0	0.07	0.09	
Col	--	0.052	0.072	0.076	0.060	0.088	0.095	0.066	0.102	0.119	
phyB	L	0.077	0.111	0.123	0.073	0.083	0.113	0.070	0.100	0.101	<0.0001
pif3	L	0.033	0.042	0.051	0.053	0.086	0.100	0.066	0.102	0.114	<0.0001
pif4	L	0.033	0.038	0.049	0.050	0.078	0.074	0.056	0.079	0.108	<0.0001
pif5	L	0.040	0.048	0.055	0.057	0.073	0.087	0.061	0.086	0.097	<0.0001
pif7-1	L	0.013	0.021	0.019	0.032	0.058	0.062	0.029	0.031	0.054	<0.0001
pif7-2	L	0.013	0.020	0.021	0.026	0.049	0.058	0.024	0.043	0.043	<0.0001
pif3 pif4	L	0.033	0.037	0.047	0.041	0.063	0.061	0.052	0.069	0.096	<0.0001
pif4 pif5	L	0.029	0.034	0.048	0.040	0.061	0.063	0.053	0.068	0.083	<0.0001
pif3 pif4 pif5	L	0.033	0.046	0.053	0.052	0.051	0.058	0.055	0.065	0.101	<0.0001
iaa19 (msg2)	G	0.090	0.129	0.140	0.111	0.159	0.147	0.086	0.144	0.157	<0.0001
iaa29	L	0.027	0.046	0.038	0.030	0.078	0.085	0.044	0.091	0.074	<0.0001
iaa17 (axr3)	G	0.026	0.015	0.012	0.017	0.016	0.015	0.015	0.010	0.012	<0.0001
iaa7 (axr2)	G	0.062	0.094	0.103	0.082	0.116	0.123	0.081	0.103	0.160	<0.0001
iaa14 (slr)	G	0.035	0.048	0.078	0.057	0.123	0.125	0.064	0.092	0.145	NS
iaa30	L	0.042	0.056	0.057	0.062	0.098	0.127	0.075	0.113	0.156	NS
MIR393a	L	0.057	0.072	0.062	0.064	0.103	0.095	0.078	0.144	0.174	0.0001
MIR393b	L	0.054	0.097	0.072	0.070	0.081	0.105	0.091	0.153	0.185	<0.0001
MIR393ab	L	0.058	0.093	0.077	0.091	0.106	0.181	0.075	0.178	0.154	<0.0001
tir1 afb2	L	0.045	0.061	0.055	0.055	0.058	0.060	0.056	0.098	0.078	<0.0001
arf6	L	0.077	0.138	0.121	0.076	0.131	0.177	0.086	0.170	0.161	<0.0001
arf7	L	0.045	0.095	0.101	0.052	0.091	0.096	0.052	0.103	0.099	NS
arf6 arf7	L	0.057	0.112	0.120	0.057	0.114	0.131	0.070	0.105	0.109	<0.0001
arf6 arf8	L	0.089	0.123	0.129	0.092	0.099	0.158	0.099	0.158	0.179	<0.0001

Table S3. Mutant and transgenic lines used in this study. All the lines are in the Columbia background except for *35S:PHYB-YFP*, which is in Landsberg *erecta*.

Mutants

phyB-9 (28)
pif3-3 (this allele is listed as *pif3-7* in single and multiple mutants in ABRC) (29)
pif4-101 (30)
pif5-3 (pil6-1) (31)
pif3-3 pif4-2 (32)
pif4-101 pif5-3 (30)
pif3-3 pif4-1 pif5 (32)
pif7-1, (33)
pif7-2 , (33)
sav3-1 (34)
iaa29 (35)
iaa30 (36)
iaa19 (msg2-1) (37)
iaa7 (axr2-1) (38)
iaa14 (slr1-1) (39)
iaa17 (axr3-1) (40)
mir393a-1 (41)
mir393b-1 (42)
mir393a-1 mir393b-1 (41)
tir1-1 afb2-3 (43)
arf6-1 (44)
arf7-1 (45)
nph4-1 arf6-2 Kindly provided by Jason Reed (Biology Department | UNC Chapel Hill)
arf6-1 arf8-2 (44)

Transgenic lines

pIAA19:GUS (37)
p35S:PHYB-YFP (27)
pPIF4:GUS, (35)
pPIF4:PIF4-GFP, this paper
pPIF4:PIF4-HA in *pif4 pif5* (46)
pSUC2:PIF4 (47)
pTIR1:TIR1-GUS (48)
pAFB2:AFB2-GUS (48)
pAFB2:AFB2m-GUS (48)
pMIR393A:GUS (48)
pMIR393B:GUS (48)
pDR5:GUS mir393ab (41)
pDEX:TIR1-myc (49)
DII-VENUS (50)
pARF6:ARF6-GFP (51)
pARF6-n3GFP (51)
p35S:YFP-ELF3 (52)
p35S:GFP-HFR1 (53)

Table S4. Primers used for real-time PCR. Fw: Forward, Rv: reverse.

PHYB
Fw TGGAAATGAAGATGATGGGAGCAATG
Rv GCAGCGAGAAGAAGTGTGATGG

PIF4
Fw ACTTCTCCTCCCACTTCTTCTCAAC
Rv TGGACTTAGGCTTAACCGTCTCTG

IAA19
Fw GGCAGAGAAGATGATGAAGAAGAG
Rv TCAGCGTCACCACCAGATG

IAA29
Fw CGAGGGTGCTGCGTCTTGTTTG
Rv CACGATGATGATACGGGCAATGATGG

UBC
Fw AGAATGCTTGGAGTCCTGCTTG
Rv ACATTTGTGCCATTGAATTGAACCC

Table S5. Primers used for transient activation assays. Fw: Forward, Rv: reverse.

pIAA17

Fw GGGGACAAGTTTGTACAAAAAAGCAGGCTGAGTTGTGGCCTTGTATTGTC
Rv GGGGACCACTTTGTACAAGAAAGCTGGGTCGACACTGCCCATCATtattaac

eIAA19

Fw CACCATGGAGAAGGAAGGACTCGGG
Rv CTCGTCTACTCCTCTAGGCTGC

ePIF4

Fw CACCATGGAACACCAAGGTTGG
Rv TCCGTGGTCCAAACGAGAACCGTC