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Note

Gene expression profile of *Arabidopsis* plants that overexpress *ZEITLUPE/LOV KELCH PROTEIN1*: up-regulation of auxin-inducible genes in hypocotyls

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Abstract ZEITLUPE (ZTL) is a blue-light photoreceptor with an F-box motif in *Arabidopsis thaliana*. The molecular mechanisms underlying the ZTL-dependent control of the circadian rhythm and repression of photoperiodic flowering are relatively well characterized. ZTL also positively regulates hypocotyl elongation under light, but the molecular mechanisms remain unknown. Using microarray analysis, we showed that 194 genes, including 17 *SMALL AUXIN UP RNA* (*SAUR*) genes (*SAUR9*, *15*, *16*, *19*, *20*, *22–24*, *28*, *29*, *61–67*) and two *AUXIN/INDOLE-3-ACETIC ACID* (*AUX/IAA*) genes (*IAA7*, *29*), were up-regulated and 283 genes were down-regulated in *ZTL*-overexpressing *Arabidopsis* seedlings. The results were confirmed for *SAUR22*, *23*, and *IAA29* by real-time quantitative reverse-transcription PCR. Application of the polar auxin transport inhibitor *N*-1-naphthylphthalamic acid (NPA), the auxin antagonist α-(phenyl ethyl-2-one)-indole-3-acetic acid (PEO-IAA), or the auxin biosynthesis inhibitor 5-(4-chlorophenyl)-4*H*-1,2,4-triazole-3-thiol (YUCASIN) inhibited hypocotyl elongation enhanced in *ZTL*-overexpressing seedlings. Our data suggest the involvement of auxin and auxin-inducible genes, including *SAUR*s and *IAA*s, in hypocotyl elongation in *ZTL*-overexpressing seedlings.

Key words: *Arabidopsis thaliana*, auxin, hypocotyl elongation, SAUR, ZEITLUPE.

Arabidopsis ZEITLUPE (ZTL) or LOV KELCH PROTEIN1 is a blue-light photoreceptor F-box protein (Kiyosue and Wada 2000; Somers et al. 2000). ZTL determines the period of circadian oscillation by regulating polyubiquitination and subsequent degradation of two circadian clock proteins, TIMING OF CAB EXPRESSION1 (TOC1) (Más et al. 2003) and PSEUDO RESPONSE REGULATOR (PRR)5 (Kiba et al. 2007). ZTL represses photoperiodic flowering by inhibiting the function of the GIGANTEA (GI)–FLAVIN BINDING, KELCH REPEAT, F-BOX1 (FKF1) complex (Imaizumi et al. 2005; Kim et al. 2013; Sawa et al. 2007; Song et al. 2012; Takase et al. 2011). Another function of ZTL is to promote hypocotyl elongation in light-grown plants. *ZTL*-overexpressing plants have elongated hypocotyls under blue, red, or white light, whereas *ztl* mutants have shorter hypocotyls under red or white light (Kevei et al. 2006; Kiyosue and Wada 2000; Nelson et al 2000; Somers et al. 2000). In the dark, hypocotyl length of both *ZTL*-overexpressing and knock-out seedlings is the same as that of control plants (Kevei et al. 2006; Kiyosue and Wada 2000; Nelson et al. 2000; Somers et al. 2000). Although the molecular mechanisms of ZTL function in circadian rhythm determination and photoperiodic flowering are relatively well characterized, the effect of ZTL on hypocotyl elongation still remains underexplored. To identify the genes that may enhance hypocotyl elongation caused by *ZTL*-overexpression under white light, we performed microarray and real-time PCR analyses.

First, seeds of two independent *ZTL*-overexpressing lines, *ZTL*ox1 and *ZTL*ox2 (Kiyosue and Wada 2000), and wild-type Columbia accession (Col) were surface-sterilized with 0.1% (v/v) sodium hypochlorite, sown on 1.5% (w/v) agar containing 1/2-basal-salt Murashige and Skoog medium and incubated at 4°C for 7 days in the dark and then at 22°C for 8 days under continuous white light ($80\,\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$). Scion Image software (http://www.mediafire.com/download/2tmpv0gibwcwwv1/Scion+Image.zip) was used to measure the hypocotyl length. Under white light, the lengths of hypocotyls of the *ZTL*-

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Abbreviations: AUX/IAA, auxin/indole-3-acetic acid; EIR1, ETHYLENE INSENSITIVE ROOT1; ERF1, ETHYLENE RESPONSE FACTOR1; FKF1, FLAVIN-BINDING KELCH REPEAT F-BOX 1; PRR, PSEUDO RESPONSE REGULATOR; SAUR, SMALL AUXIN UP RNA; TOC1, TIMING OF CAB EXPRESSION1; ZTL, ZEITLUPE.

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overexpressing plants were significantly greater than those of the wild type (Figure S1), in line with previous reports (Kiyosue and Wada 2000; Nelson et al. 2000).

Next, we grew *ZTL*ox1, *ZTL*ox2, and wild-type Col seedlings (two biological replicates: Col1 and Col2) axenically under continuous white light ($80\,\mu\text{mol}\cdot\text{m}^{-2}\cdot\text{s}^{-1}$) for 8 days and isolated total RNA with an RNeasy Plant Mini Kit (Qiagen, Valencia, CA, USA). The RNA quality was checked using an Agilent 2100 Bioanalyzer platform (Agilent Technologies, Böblingen, Germany). Single-color hybridization of *Arabidopsis* RNA to Agilent Whole *Arabidopsis* Genome Oligo Microarrays 4×44 K V4 (G2519F-021169) (Agilent Technologies) was performed for each sample by Miltenyi Biotec KK (Tokyo, Japan) as previously described (Miyazaki et al. 2015). Briefly, hybridization was performed according to the Agilent 60-mer oligo microarray processing protocol using an Agilent Gene Expression Hybridization Kit (Agilent Technologies). To produce Cy3-labeled cRNA, the RNA samples were amplified and labeled using an Agilent Low Input Quick Amp Labeling Kit (Agilent Technologies) following the manufacturer's protocol. The Cy3-labeled fragmented cRNA ($1.65\,\mu$g) in hybridization buffer was hybridized overnight (17 h, 65°C) to Agilent Whole *Arabidopsis* Genome Oligo Microarrays 4×44 K V4 in a hybridization chamber and oven as recommended by Agilent. Fluorescence signals were detected using an Agilent Microarray Scanner System (Agilent Technologies). The Agilent Feature Extraction Software (FES,10.7.3.1) was used to read out and process the microarray image files. For determination of differential gene expression FES derived output data files were further analyzed using the Rosetta Resolver gene expression data analysis system (Rosetta Biosoftware, Rosetta Inpharmatics, Seattle, WA, USA).

A total of 194 genes were up-regulated (fold change >2; $p<0.01$) and 283 genes were down-regulated (fold change <0.5; $p<0.01$) in both *ZTL*-overexpressing lines (Figure 1). These up-regulated genes are listed in Table S1 and down-regulated genes in Table S2. Up-regulation of *ZTL* in *ZTL*-overexpressing lines (AT5G57360; 30-fold in *ZTL*ox1 and 40-fold in *ZTL*ox2) validated this microarray analysis. The up-regulation of clock genes *PRR3* (AT5G60100; 6.4-fold in *ZTL*ox1, 6.5-fold in *ZTL*ox2), *PRR5* (AT5G24470; 2.5-fold in *ZTL*ox1, 2.1-fold in *ZTL*ox2), *PRR7* (AT5G02810; two probes: 5.4- and 4.9-fold in *ZTL*ox1; 3.0- and 3.4-fold in *ZTL*ox2), *PRR9* (AT2G46790; 6.5-fold in *ZTL*ox1, 3.5-fold in *ZTL*ox2), and *GI* (AT1G22770; two probes: 4.4- and 2.5-fold in *ZTL*ox1; 2.8- and 3.5-fold in *ZTL*ox2) in *ZTL*-overexpressing plants was consistent with the involvement of ZTL in circadian clock regulation. The down-regulation of flowering time genes *CONSTANS* (AT5G15840; −5.5-fold in *ZTL*ox1, −2.1-fold in *ZTL*ox2) and *FLOWERING LOCUS T* (AT1G65480; −9.2-fold in *ZTL*ox1, −8.7-fold in *ZTL*ox2) was consistent with the involvement of ZTL in flowering time regulation. Pathway analysis of up-regulated and down-regulated genes with the Gene Functional Classification Tool in DAVID Bioinformatics Resources 6.7 (http://david.abcc.ncifcrf.gov/home.jsp) classified them into several groups (Tables S3, S4). Among the down-regulated genes, those involved in flavonoid biosynthesis (11 genes) were detected as the group with the smallest *p*-value (1.21E-10; Table S3). Among the up-regulated genes, those involved in the response to auxin (19 genes) were detected as the group with the smallest *p*-value (4.03E-11; Table S4). The latter group included 17 *SMALL AUXIN UP RNA* (*SAUR*) genes (*SAUR9*, *15*, *16*, *19, 20, 22–24*, *28*, *29*, and *61–67*) and 2 *AUXIN/INDOLE-3-ACETIC ACID* (*AUX/IAA*) genes (*IAA7* and *29*) (Table 1).

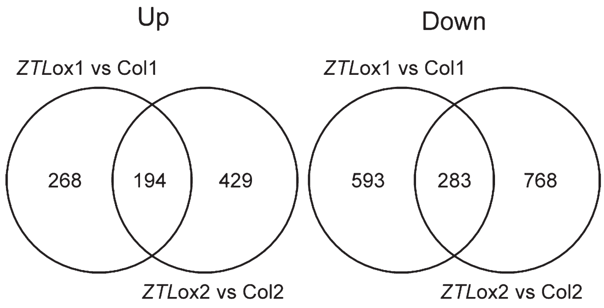

Figure 1. Venn diagrams showing the number of genes differentially expressed in *ZTL*-overexpressing seedlings (*ZTL*ox1 and *ZTL*ox2) in comparison with wild-type Columbia seedlings (Col1 and Col2). A total of 194 genes were up-regulated (fold change >2; $p<0.01$) in both *ZTL*-overexpressing lines in comparison with Col. A total of 283 genes were down-regulated (fold change <0.5; $p<0.01$) in both *ZTL*-overexpressing lines in comparison with Col.

We performed real-time quantitative reverse-transcription PCR (qRT-PCR) to confirm the up-regulation of *SAUR22*, *SAUR23*, and *IAA29* in hypocotyls of 8-day-old *ZTL*-overexpressing plants in comparison with wild-type plants grown as for microarray analysis. RNA was isolated from hypocotyls with RNAiso Plus (Takara, Otsu, Japan). The reverse transcription reaction was performed with an oligo dT primer and a PrimeScript II 1st Strand cDNA Synthesis Kit (Takara). PCR was performed with SYBR Premix Ex Taq II (Takara) and a StepOnePlus Real-Time PCR System (Life Technologies, Carlsbad, CA). The PCR primers are listed in Table S5. The expression level of *Actin2* (*ACT2*) was used to normalize the expression levels of the target genes. The expression of *SAUR22*, *SAUR23*, and *IAA29* was significantly higher (>5 fold) in both *ZTL*-overexpressing lines in comparison with wild-type plants, which confirms that these genes are up-regulated in the hypocotyls of *ZTL*-overexpressing seedlings (Figure 2).

To evaluate the role of auxin in enhanced hypocotyl

Table 1. Genes up-regulated in *ZTL*-overexpressing seedlings in comparison with control seedlings identified with the Gene Functional Classification Tool within DAVID Bioinformatics Resources 6.7.

Array Element	Gene locus	Gene name	*ZTL*ox1 vs Col1		*ZTL*ox2 vs Col2	
			Fold Change	*p*-value	Fold Change	*p*-value
A_84_P196504	AT5G18010	SAUR19	10.30	4.25.E-19	8.82	1.98.E-18
A_84_P141269	AT5G18050	SAUR22	6.57	6.53.E-17	10.64	2.37.E-19
A_84_P94979	AT5G18060	SAUR23	6.10	2.64.E-16	7.23	2.49.E-17
A_84_P147028	AT5G18020	SAUR20	5.02	7.33.E-15	6.68	1.05.E-16
A_84_P272980	AT5G18080	SAUR24	4.36	1.14.E-13	4.37	1.16.E-13
A_84_P15930	AT1G29460	SAUR65	4.04	4.03.E-13	4.07	5.71.E-13
A_84_P537376	AT1G29420	SAUR61	3.92	1.21.E-06	3.73	7.00.E-03
A_84_P16734	AT4G38850	SAUR15	3.89	1.47.E-10	4.49	4.67.E-09
A_84_P12944	AT4G36110	SAUR9	3.54	2.60.E-03	2.21	1.96.E-03
A_84_P19713	AT1G29450	SAUR64	2.98	3.56.E-10	4.53	4.19.E-14
A_84_P20189	AT3G03830	SAUR28	2.76	1.82.E-08	2.10	4.00.E-05
A_84_P55550	AT4G32280	IAA29	2.69	2.72.E-07	4.86	8.81.E-14
A_84_P11207	AT1G29500	SAUR66	2.63	7.87.E-09	2.85	1.15.E-09
A_84_P17680	AT4G38860	SAUR16	2.49	3.18.E-08	3.33	3.03.E-11
A_84_P21135	AT3G03820	SAUR29	2.31	4.74.E-07	8.00	5.41.E-16
A_84_P279980	AT1G29440	SAUR63	2.29	2.64.E-07	2.98	3.62.E-10
A_84_P22555	AT1G29510	SAUR67	2.23	5.26.E-07	3.12	1.54.E-10
A_84_P760471	AT3G23050	IAA7	2.21	1.65.E-06	2.06	9.12.E-06
A_84_P10257	AT1G29430	SAUR62	2.01	9.40.E-04	3.78	5.00.E-05

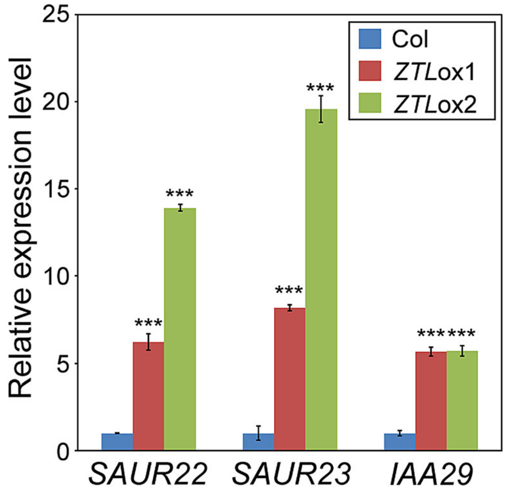

Figure 2. Expression of *SAUR22*, *SAUR23*, and *IAA29* in hypocotyls of wild-type Columbia (Col) and two *ZTL*-overexpressing seedlings (*ZTL*ox1 and *ZTL*ox2) quantified by real-time quantitative reverse-transcription PCR. The expression levels were normalized by using the levels of actin transcript (*ACT2*). The values for *ZTL*ox1 and *ZTL*ox2 are shown relative to wild-type Col. Error bars represent standard deviation ($n=3$; technical repeats); *** $p<0.001$ (Student's *t*-test) in comparison with wild-type Col.

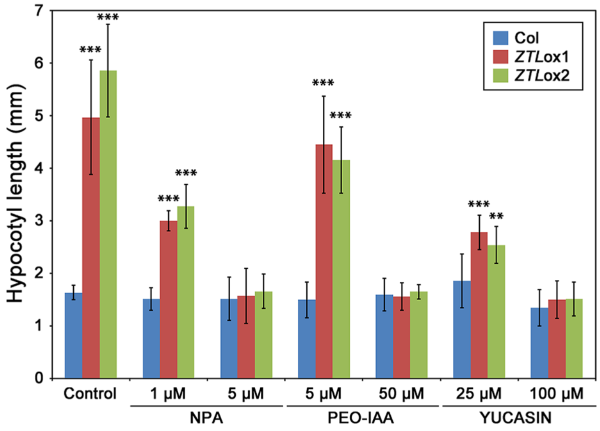

Figure 3. Inhibition of hypocotyl elongation by auxin inhibitors. Seedlings were grown under continuous white light for 8 days on 1.5% (w/v) agar containing 1/2-basal-salt Murashige and Skoog medium with 1% (v/v) dimethyl-sulfoxide (DMSO) in the absence or presence of indicated concentrations of *N*-1-naphthylphthalamic acid (NPA), *α*-(phenyl ethyl-2-one)-indole-3-acetic acid (PEO-IAA), or 5-(4-chlorophenyl)-4*H*-1,2,4-triazole-3-thiol (YUCASIN). Error bars represent standard deviation ($n=5$–10); ** $p<0.01$, *** $p<0.001$ (Student's *t*-test) in comparison with wild-type Col.

elongation in *ZTL*-overexpressing seedlings, we used three auxin inhibitors. Col, *ZTL*ox1, and *ZTL*ox2 seedlings were grown as above in the absence or presence of the auxin transport inhibitor *N*-1-naphthylphthalamic acid (NPA), the auxin antagonist *α*-(phenyl ethyl-2-one)-indole-3-acetic acid (PEO-IAA), or the auxin biosynthesis inhibitor 5-(4-chlorophenyl)-4*H*-1,2,4-triazole-3-thiol (YUCASIN). In the presence of 1 μM NPA, 5 μM PEO-IAA, or 25 μM YUCASIN, the hypocotyl length of *ZTL*-overexpressing seedlings was reduced, although their hypocotyls were still significantly longer than those of Col (Figure 3). Enhanced hypocotyl elongation in *ZTL*-overexpressing seedlings was completely inhibited by 5 μM NPA, 50 μM PEO-IAA, or 100 μM YUCASIN. These results strongly suggest the involvement of auxin in the enhancement of hypocotyl elongation in *ZTL*-overexpressing seedlings.

Auxin regulates the expression of a large number of genes involved in growth, development, and differentiation (Abel and Theologis 1996), including the *AUX/IAA* and *SAUR* families of the early (primary) auxin-inducible genes (Hagen and Guilfoyle 2002; Woodward and Bartel 2005). *AUX/IAA* genes encode transcriptional repressors and function in negative-feedback pathways to attenuate auxin responses (Tiwari et al. 2001). The expression of *SAUR* genes is usually associated with tissue elongation (Franklin et al. 2011; Roig-Villanova et al. 2007). The sequences of SAUR19–24 are highly identical to each other, and these six genes are located in a tandem array on chromosome 5, which suggests their functional redundancy (Hagen and Guilfoyle 2002). Plants overexpressing *SAUR19* have longer hypocotyls than wild-type plants under continuous light (Franklin et al. 2011), and plants overexpressing a *GFP-SAUR19*, *21*, *23*, or *24* fusion gene also have elongated hypocotyls under long-day conditions (Spartz et al. 2012). SAUR19 stimulates plasma membrane H^+-ATPase by inhibiting the activity of type 2C protein phosphatases, which leads to cell expansion via an acid-growth mechanism (Spartz et al. 2014). It is noteworthy that the expression of *SAUR22* and *SAUR23* in *ZTL*ox2 was higher than that in *ZTL*ox1 and the hypocotyls of *ZTL*ox2 were longer than those of *ZTL*ox1 (Figures 2, S1).

Auxin transcriptionally activates the expression of genes for expansins, which are involved in cell wall loosening necessary for growth (Cosgrove 2000). The up-regulation of the expression of genes for expansins A8 (AT2G40610; two probes: 2.9- and 2.7-fold in *ZTL*ox1; 4.5- and 3.9-fold in *ZTL*ox2; Table S1) and A11 (AT1G20190; 2.4-fold in *ZTL*ox1, 2.5-fold in *ZTL*ox2; Table S1) might contribute to hypocotyl elongation in *ZTL*-overexpressing seedlings grown under light.

We also observed up-regulation of the expression of genes for gibberellin 20-oxidase (GA5) (AT4G25420; 2.2-fold in *ZTL*ox1, 5.0-fold in *ZTL*ox2; Table S1) and a gibberellin-regulated protein (AT5G14920; two probes: 2.3-fold for both probes in *ZTL*ox1; 5.6- and 5.0-fold in *ZTL*ox2; Table S1). Two genes involved in ethylene signaling were down-regulated (Table S2): *ETHYLENE RESPONSE FACTOR1* (*ERF1*) (AT3G23240; −2.3-fold in *ZTL*ox1, −2.5-fold in *ZTL*ox2) and *ETHYLENE INSENSITIVE ROOT1* (*EIR1*) (AT5G57090; −2.8-fold in both *ZTL*ox1 and *ZTL*ox2). These data suggest *ZTL*-dependent changes in gibberellin and ethylene signaling. Gibberellins stimulate cell elongation in *Arabidopsis* hypocotyls, whereas ethylene predominantly inhibits cell elongation, although it can also stimulate elongation under certain conditions (Cowling and Harberd 2007; Vandenbussche et al. 2007). The up-regulation of gibberellin-related genes and the down-regulation of ethylene-related genes in *ZTL*-overexpressing seedlings indicate that these hormones may also contribute to the effect of ZTL on hypocotyl elongation.

We found that expression of the gene for phytochrome-interacting factor (PIF) 4 was up-regulated in *ZTL*-overexpressing seedlings (AT2G43010; 4.2-fold in *ZTL*ox1, 3.1-fold in *ZTL*ox2; Table S1). PIF4 is a basic helix-loop-helix transcription factor that promotes hypocotyl elongation by activating the expression of genes involved in auxin biosynthesis, auxin signaling components, cell wall loosening, and cell expansion (Hornitschek et al. 2012; Leivar and Quail 2011; de Lucas and Prat 2014; Sun et al. 2013). Therefore, the up-regulation of *PIF4* might lead to elevation of auxin biosynthesis and up-regulation of *SAUR*s in *ZTL*-overexpressing seedlings. The expression of *PIF4* is diurnally regulated by the evening complex (EC), which consists of EARLY FLOWERING (ELF)3, ELF4, and LUX ARRHYTHMO (LUX)/PHYTOCLOCK1 (PCL1) (Nusinow et al. 2011). The expression of EC genes is under circadian control; EC binds to the *PIF4* promoter to repress *PIF4* (Nusinow et al. 2011). Plants overexpressing *ZTL* show very short circadian rhythm or arrhythmicity under continuous light (Somers et al. 2004), which may reduce the EC amount, activity, or both. If so, this might be a reason for the up-regulation of *PIF4* and enhancement of hypocotyl elongation in *ZTL*-overexpressing seedlings grown under light. Further study is necessary to evaluate the role of PIF4 and EC in ZTL-mediated hypocotyl elongation.

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Table S1. Genes up-regulated in *ZTL*-overexpressing seedlings in comparison with control seedlings.

			ZTL ox1 vs Col1			*ZTL* ox2 vs Col2		
Array element	Gene locus	Annotation	Log(Ratio)	Fold Change	P-value	Log(Ratio)	Fold Change	P-value
A_84_P750390	AT1G68800	BRC2/TCP12 (BRANCHED2); transcription factor	1.823	66.564	8.9.E-22	1.420	26.280	1.7.E-18
A_84_P22137	AT3G19350	polyadenylate-binding protein-related / PABP-related	1.646	44.247	3.6.E-20	1.211	16.256	2.1.E-17
A_84_P23534	AT5G57360	ZTL (ZEITLUPE); ubiquitin-protein ligase	1.481	30.267	4.3.E-22	1.599	39.682	1.9.E-22
A_84_P562254	AT1G66060	binding	1.405	25.395	1.2.E-21	1.152	14.189	2.7.E-20
A_84_P10613	AT2G42530	COR15B	1.378	23.886	1.0.E-21	0.996	9.900	3.7.E-19
A_84_P13270	AT1G70220	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G24050.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40953.1); contains domain UNCHARACTERIZED	1.360	22.912	2.5.E-20	1.621	41.786	4.3.E-20
A_84_P761927	AT3G33528	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G07526.3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G07526.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G07526.1)	1.217	16.464	5.3.E-18	1.158	14.403	2.1.E-17
A_84_P196694	AT5G44430	PDF1.2c (plant defensin 1.2c)	1.198	15.777	9.0.E-21	0.941	8.734	1.4.E-18
A_84_P23852	AT2G42540	COR15A (COLD-REGULATED 15A)	1.188	15.427	1.0.E-20	0.821	6.618	4.7.E-17
A_84_P239215	AT2G26010	PDF1.3 (plant defensin 1.3)	1.183	15.237	1.1.E-20	0.945	8.808	1.3.E-18
A_84_P592566	AT1G69470	unknown protein	1.149	14.080	7.8.E-10	1.051	11.233	5.4.E-08
A_84_P17513	AT3G55580	regulator of chromosome condensation (RCC1) family protein	1.058	11.419	8.3.E-19	0.660	4.573	1.5.E-13
A_84_P310613	AT2G26020	PDF1.2b (plant defensin 1.2b)	1.055	11.360	1.1.E-19	0.901	7.954	4.3.E-18
A_84_P196504	AT5G18010	auxin-responsive protein, putative	1.013	10.296	4.2.E-19	0.946	8.822	2.0.E-18
A_84_P137009	AT5G44420	PDF1.2 (Low-molecular-weight cysteine-rich 77)	0.992	9.822	4.1.E-19	0.985	9.656	5.9.E-19
A_84_P50100	AT3G55240	Overexpression leads to PEL (Pseudo-Etiolation in Light) phenotype.	0.988	9.736	4.4.E-19	0.922	8.360	2.3.E-18
A_84_P767684	AT5G33395	transposable element gene	0.987	9.703	2.2.E-06	1.041	11.002	9.8.E-10
A_84_P757222	AT2G16367	Encodes a defensin-like (DEFL) family protein.	0.979	9.521	3.0.E-06	0.533	3.414	1.4.E-07
A_84_P20655	AT5G45830	DOG1 (DELAY OF GERMINATION 1)	0.976	9.466	1.1.E-18	0.733	5.407	3.2.E-15
A_84_P798436	AT1G80130	binding	0.941	8.726	1.4.E-18	0.856	7.177	1.5.E-17
A_84_P16114	AT1G09350	ATGOLS3 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 3); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	0.935	8.611	1.7.E-18	0.621	4.181	1.4.E-13
A_84_P20425	AT4G12480	pEARLI 1; lipid binding	0.921	8.333	2.4.E-18	1.001	10.012	3.4.E-19
A_84_P18533	AT4G12470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	0.910	8.135	3.2.E-18	0.942	8.746	1.4.E-18
A_84_P833384	AT5G45830	DOG1 (DELAY OF GERMINATION 1)	0.907	8.079	1.8.E-17	0.814	6.523	1.3.E-15
A_84_P761198	AT3G27283	Encodes a defensin-like (DEFL) family protein.	0.904	8.012	6.0.E-05	0.931	8.535	2.0.E-05
A_84_P22552	AT5G47130	Bax inhibitor-1 family / BI-1 family	0.889	7.752	5.5.E-16	0.959	9.100	1.8.E-14
A_84_P598557	AT5G57380	VIN3 (VERNALIZATION INSENSITIVE 3); protein binding / zinc ion binding	0.884	7.657	1.3.E-04	0.817	6.554	8.4.E-04
A_84_P811782	AT2G31980	cysteine proteinase inhibitor-related	0.870	7.413	1.1.E-17	0.700	5.011	4.5.E-15
A_84_P23964	AT2G31980	cysteine proteinase inhibitor-related	0.864	7.311	1.3.E-17	0.721	5.265	1.8.E-15
A_84_P11230	AT5G54190	PORA (Protochlorophyllide reductase A); oxidoreductase/ protochlorophyllide reductase	0.852	7.120	3.2.E-04	0.934	8.586	2.0.E-05
A_84_P167173	AT4G25480	DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription activator/ transcription factor	0.850	7.084	7.9.E-15	0.465	2.920	1.1.E-09
A_84_P141269	AT5G18050	auxin-responsive protein, putative	0.818	6.573	6.5.E-17	1.027	10.643	2.4.E-19
A_84_P126821	AT2G46790	PRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription regulator	0.816	6.548	2.4.E-15	0.549	3.543	2.6.E-10
A_84_P96276	AT5G60100	PRR3 (PSEUDO-RESPONSE REGULATOR 3); transcription regulator	0.803	6.355	8.8.E-17	0.812	6.490	6.6.E-17
A_84_P94979	AT5G18060	auxin-responsive protein, putative	0.786	6.105	2.6.E-16	0.859	7.226	2.5.E-17
A_84_P792258	AT4G01080	no_match	0.766	5.841	8.7.E-14	0.726	5.325	2.4.E-12
A_84_P15628	AT3G57240	BG3 (BETA-1,3-GLUCANASE 3); hydrolase, hydrolyzing O-glycosyl compounds	0.760	5.756	1.2.E-14	0.427	2.675	1.0.E-05
A_84_P724799	AT1G67105	other RNA	0.754	5.678	5.2.E-16	0.499	3.155	8.6.E-11
A_84_P21826	AT1G10770	invertase/pectin methylesterase inhibitor family protein	0.753	5.659	2.5.E-15	0.789	6.146	6.5.E-16
A_84_P242573	AT5G54470	zinc finger (B-box type) family protein	0.752	5.649	4.0.E-15	0.647	4.433	1.0.E-13
A_84_P297344	23240;AT5G2	[AT5G23240, DNAJ heat shock N-terminal domain-containing protein];[AT5G23235, pseudogene, antisense mRNA to genes At5g23230 and At5g23240, blastp match of 34% identity and 7.4e-17 P-value to OMNI|TM0133 isochorismatase-related protein {Thermotoga maritima	0.730	5.366	1.3.E-15	0.608	4.059	2.6.E-13
A_84_P820553	AT5G02810	PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator	0.729	5.355	2.3.E-15	0.477	2.996	6.1.E-10
A_84_P21360	69570;AT1G	[AT1G69570, Dof-type zinc finger domain-containing protein];[AT1G69572, other RNA]	0.711	5.139	2.7.E-15	0.406	2.547	1.6.E-08
A_84_P103016	AT4G12500	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	0.708	5.102	3.1.E-15	0.806	6.404	7.8.E-17
A_84_P766729	AT5G57340	similar to hypothetical protein MtrDRAFT_AC155282g59v2 [Medicago truncatula]	0.707	5.092	7.1.E-03	0.461	2.891	8.9.E-03
A_84_P11360	AT1G52040	MBP1 (MYROSINASE-BINDING PROTEIN 1)	0.703	5.049	4.8.E-15	0.468	2.935	5.0.E-10
A_84_P147028	AT5G18020	auxin-responsive protein, putative	0.701	5.018	7.3.E-15	0.825	6.680	1.0.E-16
A_84_P21494	AT5G02810	PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator	0.695	4.949	5.3.E-15	0.537	3.442	9.6.E-12
A_84_P581126	46790;AT2G4	[AT2G46790, PRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription regulator];[AT2G46670, pseudo-response regulator, putative / timing of CAB expression 1-like	0.693	4.937	2.9.E-07	0.503	3.186	4.0.E-05
A_84_P152798	;AT5G18020;	[AT5G18030, auxin-responsive protein, putative];[AT5G18020, auxin-responsive protein, putative];[AT5G18080, auxin-responsive protein, putative]	0.683	4.814	1.3.E-14	0.729	5.360	2.0.E-15
A_84_P11710	AT1G53080	legume lectin family protein	0.682	4.813	5.0.E-14	0.573	3.744	2.8.E-12
A_84_P577170	AT5G64190	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G40390.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO41445.1)	0.662	4.595	9.8.E-14	0.402	2.525	3.5.E-08
A_84_P14317	AT1G69830	AMY3/ATAMY3 (ALPHA-AMYLASE-LIKE 3); alpha-amylase	0.661	4.585	2.2.E-14	0.670	4.674	1.5.E-14
A_84_P118712	AT1G56300	DNAJ heat shock N-terminal domain-containing protein	0.652	4.489	3.3.E-14	0.565	3.673	2.2.E-12
A_84_P788885	AT1G56300	DNAJ heat shock N-terminal domain-containing protein	0.646	4.426	4.3.E-14	0.598	3.959	4.3.E-13
A_84_P18969	AT1G22770	GI (GIGANTEA); binding	0.640	4.369	5.8.E-14	0.444	2.780	1.7.E-09
A_84_P751876	AT1G11803	pseudogene, auxin responsive protein, blastp match of 74% identity and 1.2e-15 P-value to GP|3043536|dbj|BAA25434.1||AB000708 SAUR {Raphanus sativus}	0.640	4.363	3.0.E-05	0.726	5.324	3.6.E-06
A_84_P272980	AT5G18080	auxin-responsive protein, putative	0.640	4.361	1.1.E-13	0.641	4.374	1.2.E-13
A_84_P15807	AT4G36450	ATMPK14 (MITOGEN-ACTIVATED PROTEIN KINASE 14); MAP kinase/ kinase	0.639	4.358	2.4.E-13	0.523	3.333	6.4.E-11
A_84_P18698	AT5G17320	HDG9 (HOMEODOMAIN GLABROUS9); DNA binding / sequence-specific DNA binding / transcription factor	0.632	4.281	4.2.E-08	0.375	2.373	1.5.E-04
A_84_P753024	AT1G67265	DVL3/RTFL21 (ROTUNDIFOLIA LIKE 21)	0.630	4.268	1.0.E-13	0.542	3.483	8.4.E-12
A_84_P848817	AT5G10760	aspartyl protease family protein	0.621	4.174	2.4.E-06	0.777	5.981	4.4.E-10
A_84_P162983	AT2G43010	PIF4 (PHYTOCHROME INTERACTING FACTOR 4); DNA binding / transcription factor	0.620	4.171	1.4.E-13	0.494	3.121	9.7.E-11
A_84_P291304	AT1G29395	COR414-TM1 (cold regulated 414 thylakoid membrane 1)	0.611	4.087	2.2.E-13	0.560	3.630	2.8.E-12
A_84_P15930	AT1G29460	auxin-responsive protein, putative	0.607	4.043	4.0.E-13	0.609	4.066	5.7.E-13
A_84_P804296	AT4G16080	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45940.1); contains InterPro domain Protein of unknown function DUF295 (InterPro:IPR005174)	0.606	4.034	8.8.E-04	0.750	5.617	1.3.E-04
A_84_P157735	AT3G51400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35720.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23715.1); contains InterPro domain Protein of unknown function DUF241, plant (InterPro:IPR004320)	0.604	4.017	3.4.E-13	0.548	3.531	6.3.E-12
A_84_P14898	AT5G10760	aspartyl protease family protein	0.601	3.992	2.0.E-12	0.738	5.467	3.5.E-15
A_84_P537376	AT1G29420	similar to SAUR68 (SMALL AUXIN UPREGULATED 68) [Arabidopsis thaliana] (TAIR:AT1G29510.1); similar to auxin-responsive protein [Brassica rapa] (GB:ABV89665.1); contains InterPro domain Auxin responsive SAUR protein (InterPro:IPR003676)	0.593	3.917	1.2.E-06	0.572	3.728	7.0.E-03
A_84_P16734	AT4G38850	SAUR_AC1 (SMALL AUXIN UP RNA 1 FROM ARABIDOPSIS THALIANA ECOTYPE	0.590	3.890	1.5.E-10	0.652	4.487	4.7.E-09
A_84_P506389	AT1G58320	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G35525.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42113.1); contains InterPro domain Protein of unknown function Cys-rich (InterPro:IPR006461)	0.585	3.844	9.2.E-12	0.520	3.314	4.7.E-11
A_84_P845206	AT1G06450	CCR4-NOT transcription complex protein, putative	0.578	3.784	2.2.E-06	0.597	3.951	5.5.E-08
A_84_P850999	AT1G20620	CAT3 (CATALASE 3); catalase	0.574	3.751	3.4.E-11	0.585	3.847	1.2.E-10
A_84_P12310	AT1G76960	unknown protein	0.572	3.734	3.8.E-12	0.378	2.387	1.1.E-07
A_84_P788781	AT1G09080	BIP3; ATP binding	0.571	3.727	1.1.E-04	0.558	3.611	2.2.E-04
A_84_P17660	AT4G33490	aspartic-type endopeptidase/ pepsin A	0.566	3.677	2.1.E-12	0.648	4.441	4.1.E-14
A_84_P769604	26146;AT5G2	[AT5G26146, other RNA];[AT5G26150, protein kinase family protein]	0.557	3.607	8.4.E-08	0.374	2.365	8.0.E-05
A_84_P22010	AT2G45550	CYP76C4 (cytochrome P450, family 76, subfamily C, polypeptide 4); oxygen binding	0.554	3.578	8.5.E-03	0.478	3.005	3.2.E-03
A_84_P14823	AT4G33720	pathogenesis-related protein, putative	0.551	3.559	5.4.E-08	0.422	2.643	5.8.E-04
A_84_P12944	AT4G36110	auxin-responsive protein, putative	0.549	3.540	2.6.E-03	0.345	2.212	2.0.E-03
A_84_P191914	AT2G21320	zinc finger (B-box type) family protein	0.541	3.479	1.5.E-08	0.413	2.591	8.5.E-06
A_84_P19525	AT4G27310	zinc finger (B-box type) family protein	0.539	3.457	8.7.E-12	0.372	2.354	1.2.E-07
A_84_P808697	AT2G05100	LHCB2.1 (Photosystem II light harvesting complex gene 2.1); chlorophyll binding	0.529	3.384	1.5.E-11	0.312	2.050	4.2.E-06
A_84_P17808	AT5G43440	2-oxoglutarate-dependent dioxygenase, putative	0.526	3.359	1.7.E-11	0.447	2.800	1.4.E-09
A_84_P826714	AT1G52000	jacalin lectin family protein	0.526	3.357	1.8.E-11	0.436	2.727	2.9.E-09
A_84_P185784	AT2G39920	acid phosphatase class B family protein	0.525	3.352	1.8.E-11	0.592	3.912	5.8.E-13
A_84_P19369	AT3G47500	CDF3 (CYCLING DOF FACTOR 3); DNA binding / protein binding / transcription factor	0.525	3.349	1.8.E-11	0.402	2.523	2.0.E-08
A_84_P10439	AT1G09080	BIP3; ATP binding	0.523	3.336	1.2.E-09	0.571	3.724	1.4.E-10
A_84_P150068	AT2G43140	DNA binding / transcription factor	0.515	3.271	3.4.E-11	0.364	2.311	2.8.E-07
A_84_P23654	AT1G52000	jacalin lectin family protein	0.511	3.241	3.9.E-11	0.515	3.271	3.2.E-11
A_84_P600468	AT1G20620	CAT3 (CATALASE 3); catalase	0.508	3.219	1.4.E-10	0.703	5.047	3.0.E-14

A_84_P861072	AT3G26740	CCL (CCR-LIKE)	0.502	3.175	6.4.E-11	0.619	4.162	1.5.E-13
A_84_P560548	AT2G01310	contains domain PTHR10177 (PTHR10177); contains domain PTHR10177:SF6	0.502	3.174	2.6.E-08	0.312	2.052	4.6.E-04
A_84_P750244	AT1G69140	pseudogene, hypothetical protein	0.501	3.169	1.6.E-09	0.948	8.864	3.2.E-18
A_84_P13813	AT4G18650	transcription factor-related	0.499	3.153	4.4.E-06	0.702	5.031	3.4.E-13
A_84_P16781	AT1G06460	ACD32.1 (ALPHA-CRYSTALLIN DOMAIN 31.2)	0.488	3.073	1.4.E-10	0.516	3.284	2.9.E-11
A_84_P806842	AT3G26740	CCL (CCR-LIKE)	0.487	3.066	1.5.E-10	0.604	4.017	3.2.E-13
A_84_P761641	AT3G55734	MIR393B; miRNA	0.484	3.050	8.5.E-04	0.510	3.236	9.0.E-03
A_84_P100746	AT3G28220	meprin and TRAF homology domain-containing protein / MATH domain-containing protein	0.483	3.044	1.8.E-10	0.577	3.778	1.2.E-12
A_84_P241663	AT3G58540	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06190.1)	0.482	3.033	3.4.E-09	0.360	2.289	2.2.E-06
A_84_P814968	AT1G06460	ACD32.1 (ALPHA-CRYSTALLIN DOMAIN 31.2)	0.479	3.012	2.3.E-10	0.546	3.513	6.0.E-12
A_84_P838362	AT2G43140	DNA binding / transcription factor	0.475	2.984	4.8.E-10	0.413	2.589	9.9.E-08
A_84_P21085	AT2G22980	SCPL13; serine carboxypeptidase	0.474	2.981	3.0.E-10	0.436	2.728	2.8.E-09
A_84_P19713	AT1G29450	auxin-responsive protein, putative	0.474	2.980	3.6.E-10	0.656	4.532	4.2.E-14
A_84_P852921	AT3G26740	CCL (CCR-LIKE)	0.474	2.980	3.0.E-10	0.579	3.794	1.1.E-12
A_84_P788748	AT1G13470	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13520.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42040.1); contains InterPro domain Protein of unknown function DUF1262 (InterPro:IPR010683)	0.473	2.975	8.0.E-05	0.373	2.362	1.1.E-04
A_84_P758477	AT2G30424	DNA binding	0.473	2.971	3.2.E-10	0.586	3.852	7.9.E-13
A_84_P22510	AT5G28230	pseudogene, similar to glucose-6-phosphate/phosphate-translocator precursor, contains similarity to glucose-6-phosphate/phosphate-translocator precursors; blastp match of 78% identity and 1.6e-75 P-value to GP|2997591|gb|AAC08525.1||AF020814 glucose-6-phosphate/phosphate-translocator precursor {Pisum sativum}	0.470	2.953	2.0.E-05	0.436	2.730	3.0.E-05
A_84_P753286	AT1G31173	MIR167D; miRNA	0.469	2.944	1.1.E-07	0.607	4.046	3.4.E-10
A_84_P806966	AT2G40610	ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	0.467	2.929	5.3.E-10	0.658	4.548	6.2.E-14
A_84_P831724	AT5G44010	similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD21667.1); similar to Os02g0814600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048494.1)	0.458	2.869	6.4.E-09	0.319	2.083	1.0.E-05
A_84_P589589	AT5G46600	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G17970.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G46610.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO63429.1); contains InterPro domain Protein of unknown function UPF0005 (InterPro:IPR006214)	0.457	2.863	4.5.E-06	0.352	2.251	1.5.E-04
A_84_P757683	AT2G10606	MIR396A; miRNA	0.457	2.862	6.9.E-09	0.357	2.277	1.6.E-06
A_84_P72294	AT5G11610	exostosin family protein	0.456	2.860	1.0.E-09	0.359	2.284	3.4.E-07
A_84_P819980	AT3G52180	no_match	0.454	2.845	1.0.E-09	0.535	3.430	1.1.E-11
A_84_P12369	AT1G10760	SEX1 (STARCH EXCESS 1)	0.454	2.841	9.8.E-10	0.539	3.457	8.6.E-12
A_84_P16468	AT3G26740	CCL (CCR-LIKE)	0.453	2.836	1.0.E-09	0.515	3.273	3.1.E-11
A_84_P564785	AT1G14250	nucleoside phosphatase family protein / GDA1/CD39 family protein	0.451	2.824	3.1.E-09	0.818	6.577	9.3.E-17
A_84_P14029	AT5G44440	FAD-binding domain-containing protein	0.445	2.784	4.0.E-05	1.079	11.985	2.9.E-15
A_84_P132345	AT4G32340	binding	0.443	2.774	1.9.E-09	0.577	3.777	1.3.E-12
A_84_P14905	AT1G18350	ATMKK7 (MAP KINASE KINASE7); kinase	0.443	2.773	1.8.E-06	0.701	5.027	1.2.E-06
A_84_P20189	AT3G03830	auxin-responsive protein, putative	0.441	2.757	1.8.E-08	0.323	2.104	4.0.E-05
A_84_P20842	AT1G04650	similar to unnamed protein product [Vitis vinifera] (GB:CAO71563.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN72207.1)	0.440	2.757	5.9.E-09	0.482	3.037	7.0.E-10
A_84_P11569	AT2G40610	ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	0.439	2.746	3.1.E-09	0.596	3.944	2.4.E-12
A_84_P10923	AT3G62550	universal stress protein (USP) family protein	0.435	2.724	2.8.E-09	0.752	5.654	5.3.E-16
A_84_P819992	AT4G32340	binding	0.432	2.704	3.4.E-09	0.637	4.337	6.5.E-14
A_84_P79045	AT1G06980	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G30230.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO21365.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN59819.1)	0.431	2.697	4.0.E-05	0.406	2.545	8.0.E-05
A_84_P542830	AT2G03310	unknown protein	0.431	2.695	4.3.E-09	0.458	2.870	1.1.E-09
A_84_P55550	AT4G32280	IAA29 (indoleacetic acid-induced protein 29); transcription factor	0.430	2.693	2.7.E-07	0.687	4.860	8.8.E-14
A_84_P188764	G04330;AT4G0	[AT4G04330, similar to unnamed protein product [Vitis vinifera] (GB:CAO69665.1)];[AT4G04320, malonyl-CoA decarboxylase family protein]	0.428	2.682	4.2.E-09	0.570	3.719	1.7.E-12
A_84_P806687	AT1G20620	CAT3 (CATALASE 3); catalase	0.428	2.678	4.5.E-09	0.806	6.404	8.2.E-17
A_84_P827080	AT4G04330	similar to unnamed protein product [Vitis vinifera] (GB:CAO69665.1)	0.426	2.669	5.1.E-09	0.561	3.636	3.2.E-12
A_84_P109442	AT3G52180	ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	0.424	2.653	5.6.E-09	0.515	3.272	3.1.E-11
A_84_P558998	AT3G42800	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54200.1); similar to expressed protein [Olimarabidopsis pumila] (GB:ABA18092.1)	0.422	2.644	1.7.E-08	0.497	3.140	3.2.E-09
A_84_P11207	AT1G29500	auxin-responsive protein, putative	0.420	2.633	7.9.E-09	0.454	2.847	1.2.E-09
A_84_P591378	AT5G44565	unknown protein	0.419	2.624	7.7.E-09	0.392	2.468	3.7.E-08
A_84_P144039	AT5G40720	similar to zinc finger (C3HC4-type RING finger) family protein [Arabidopsis thaliana] (TAIR:AT3G27330.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14626.1); contains InterPro domain Protein of unknown function DUF23 (InterPro:IPR008166)	0.418	2.617	9.5.E-08	0.314	2.062	3.0.E-05
A_84_P868153	AT1G73470	similar to unnamed protein product [Vitis vinifera] (GB:CAO68549.1)	0.417	2.615	8.0.E-09	0.396	2.491	2.8.E-08
A_84_P837093	AT1G14280	PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)	0.417	2.613	9.4.E-09	0.322	2.100	2.6.E-06
A_84_P18886	AT1G20620	CAT3 (CATALASE 3); catalase	0.416	2.608	8.6.E-09	0.701	5.020	4.0.E-15
A_84_P561544	AT2G45560	CYP76C1 (cytochrome P450, family 76, subfamily C, polypeptide 1); heme binding / iron ion binding / monooxygenase	0.415	2.600	9.3.E-09	0.504	3.193	5.7.E-11
A_84_P189624	AT1G70890	MLP43 (MLP-LIKE PROTEIN 43)	0.412	2.580	1.1.E-08	0.437	2.736	2.5.E-09
A_84_P785715	AT2G22540	SVP (SHORT VEGETATIVE PHASE); transcription factor	0.409	2.567	1.3.E-08	0.428	2.679	4.4.E-09
A_84_P560726	AT3G13980	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54200.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN69469.1)	0.409	2.562	2.1.E-08	0.543	3.490	1.3.E-11
A_84_P580907	AT1G53035	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G15358.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69750.1)	0.407	2.554	1.5.E-08	0.535	3.426	1.1.E-11
A_84_P586034	AT5G44010	similar to unknown protein [Oryza sativa (japonica cultivar-group)] (GB:BAD21667.1); similar to Os02g0814600 [Oryza sativa (japonica cultivar-group)] (GB:NP_001048494.1)	0.406	2.548	4.3.E-07	0.378	2.388	2.0.E-06
A_84_P816130	AT1G10070	ATBCAT-2; branched-chain-amino-acid transaminase/ catalytic	0.403	2.528	2.3.E-07	0.406	2.548	1.0.E-05
A_84_P12575	AT2G23030	SNRK2-9/SNRK2.9 (SNF1-RELATED PROTEIN KINASE 2.9); kinase	0.401	2.516	2.2.E-08	0.304	2.014	6.5.E-06
A_84_P839149	AT1G22770	GI (GIGANTEA); binding	0.401	2.515	2.8.E-08	0.538	3.453	1.6.E-11
A_84_P771152	AT1G20620	CAT3 (CATALASE 3); catalase	0.400	2.514	2.2.E-08	0.590	3.892	6.2.E-13
A_84_P23100	AT3G15570	phototropic-responsive NPH3 family protein	0.400	2.512	2.3.E-08	0.527	3.362	2.0.E-11
A_84_P11816	AT3G50120	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G50150.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G50130.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G50170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71911.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN59797.1); contains InterPro domain Protein of unknown function DUF247, plant (InterPro:IPR004158)	0.400	2.511	4.3.E-07	0.462	2.896	5.4.E-09
A_84_P787782	AT1G73470	no_match	0.399	2.505	3.1.E-08	0.388	2.446	6.0.E-08
A_84_P503493	AT5G49015	Expressed protein	0.398	2.502	2.5.E-08	0.331	2.142	1.4.E-06
A_84_P230339	AT2G22540	SVP (SHORT VEGETATIVE PHASE); transcription factor	0.398	2.499	2.6.E-08	0.424	2.655	5.4.E-09
A_84_P17680	AT4G38860	auxin-responsive protein, putative	0.397	2.492	3.2.E-08	0.522	3.325	3.0.E-11
A_84_P16821	AT5G24470	PRR5 (PSEUDO-RESPONSE REGULATOR 5); transcription regulator	0.396	2.490	2.8.E-08	0.329	2.131	1.6.E-06
A_84_P852182	AT1G20620	CAT3 (CATALASE 3); catalase	0.395	2.484	3.0.E-08	0.783	6.073	1.7.E-16
A_84_P862359	AT3G52180	ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	0.395	2.482	3.2.E-08	0.542	3.487	7.5.E-12
A_84_P571542	AT4G12900	gamma interferon responsive lysosomal thiol reductase family protein / GILT family protein	0.393	2.473	3.6.E-08	0.771	5.899	3.8.E-16
A_84_P195094	AT1G73470	similar to unnamed protein product [Vitis vinifera] (GB:CAO68549.1)	0.388	2.446	4.5.E-08	0.368	2.335	1.5.E-07
A_84_P867415	AT1G73470	similar to unnamed protein product [Vitis vinifera] (GB:CAO68549.1)	0.388	2.444	4.6.E-08	0.378	2.386	8.5.E-08
A_84_P12234	AT5G16030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02500.1); similar to hypothetical protein [Cleome spinosa] (GB:ABD96956.1)	0.388	2.443	4.6.E-08	0.483	3.040	1.8.E-10
A_84_P19479	AT1G17460	TRFL3 (TRF-LIKE 3); DNA binding / transcription factor	0.387	2.439	5.6.E-08	0.462	2.899	8.8.E-10
A_84_P790487	AT5G44565	unknown protein	0.386	2.434	5.6.E-08	0.387	2.438	5.1.E-08
A_84_P20046	AT1G14280	PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)	0.385	2.426	5.5.E-08	0.331	2.142	1.4.E-06
A_84_P21915	AT1G20190	ATEXPA11 (ARABIDOPSIS THALIANA EXPANSIN A11)	0.382	2.413	6.5.E-08	0.398	2.499	2.8.E-08
A_84_P502546	AT5G35525	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G14870.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42338.1); contains InterPro domain Protein of unknown function Cys-rich (InterPro:IPR006461)	0.380	2.398	1.8.E-06	0.355	2.266	9.0.E-06
A_84_P806696	AT1G20620	CAT3 (CATALASE 3); catalase	0.379	2.395	7.7.E-08	0.754	5.678	5.0.E-16
A_84_P16574	AT3G57260	BGL2 (PATHOGENESIS-RELATED PROTEIN 2); glucan 1,3-beta-glucosidase/ hydrolase, hydrolyzing O-glycosyl compounds	0.379	2.395	8.8.E-07	0.640	4.369	3.0.E-12
A_84_P10174	AT5G11150	ATVAMP713 (Arabidopsis thaliana vesicle-associated membrane protein 713)	0.378	2.386	8.5.E-08	0.442	2.766	1.9.E-09
A_84_P806743	AT1G20620	CAT3 (CATALASE 3); catalase	0.378	2.385	8.5.E-08	0.755	5.683	4.8.E-16
A_84_P20959	AT1G75900	family II extracellular lipase 3 (EXL3)	0.377	2.383	9.1.E-08	0.626	4.226	1.1.E-13
A_84_P12921	AT4G30650	hydrophobic protein, putative / low temperature and salt responsive protein, putative	0.377	2.382	8.8.E-08	0.468	2.941	4.2.E-10

A_84_P10332	AT5G66110	metal ion binding	0.377	2.381	1.4.E-07	0.506	3.208	2.8.E-10
A_84_P761538	AT3G22142	structural constituent of cell wall	0.376	2.377	2.0.E-25	0.791	6.185	0.0.E+00
A_84_P14450	AT2G28900	OEP16 (OUTER ENVELOPE PROTEIN 16); P-P-bond-hydrolysis-driven protein transmembrane transporter	0.375	2.373	9.7.E-08	0.560	3.628	2.9.E-12
A_84_P21014	AT2G05530	glycine-rich protein	0.375	2.373	5.9.E-06	0.412	2.580	5.0.E-07
A_84_P806732	AT1G20620	CAT3 (CATALASE 3); catalase	0.375	2.369	1.0.E-07	0.760	5.751	4.0.E-16
A_84_P549629	AT5G58140	PHOT2 (NON PHOTOTROPIC HYPOCOTYL 1-LIKE); kinase	0.374	2.367	6.5.E-06	0.488	3.078	1.0.E-05
A_84_P23180	AT3G53800	armadillo/beta-catenin repeat family protein	0.374	2.365	1.1.E-07	0.639	4.351	6.4.E-14
A_84_P806759	AT1G20620	CAT3 (CATALASE 3); catalase	0.373	2.360	1.1.E-07	0.784	6.084	1.6.E-16
A_84_P20058	AT2G30420	myb family transcription factor	0.372	2.354	6.7.E-07	0.490	3.093	2.7.E-08
A_84_P69244	AT2G45560	CYP76C1 (cytochrome P450, family 76, subfamily C, polypeptide 1); heme binding / iron ion binding / monooxygenase	0.372	2.353	1.8.E-07	0.582	3.818	2.5.E-12
A_84_P22976	AT2G36270	ABI5 (ABA INSENSITIVE 5); DNA binding / transcription activator/ transcription factor	0.371	2.351	1.8.E-07	0.398	2.502	4.3.E-08
A_84_P809730	AT5G14920	gibberellin-regulated family protein	0.371	2.348	1.3.E-07	0.747	5.587	8.0.E-16
A_84_P842922	AT3G13980	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G54200.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN69469.1)	0.364	2.315	3.1.E-07	0.333	2.154	1.9.E-06
A_84_P790043	AT3G07390	no_match	0.364	2.312	2.3.E-03	0.613	4.107	1.0.E-05
A_84_P21135	AT3G03820	auxin-responsive protein, putative	0.364	2.311	4.7.E-07	0.903	8.002	5.4.E-16
A_84_P131456	AT5G14920	gibberellin-regulated family protein	0.362	2.302	2.1.E-07	0.703	5.042	3.7.E-15
A_84_P16857	AT5G41890	GDSL-motif lipase/hydrolase family protein	0.362	2.301	6.8.E-03	0.359	2.287	1.5.E-04
A_84_P279980	AT1G29440	auxin-responsive family protein	0.360	2.291	2.6.E-07	0.474	2.979	3.6.E-10
A_84_P21864	AT1G73805	calmodulin binding	0.359	2.287	3.0.E-07	0.332	2.149	1.6.E-06
A_84_P811729	AT2G33830	dormancy/auxin associated family protein	0.357	2.275	2.9.E-07	0.469	2.944	4.0.E-10
A_84_P255590	AT4G23870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11020.1)	0.355	2.266	3.2.E-07	0.325	2.114	1.9.E-06
A_84_P597910	AT1G68870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G26210.1)	0.355	2.265	1.7.E-06	0.438	2.743	2.3.E-08
A_84_P750656	AT1G53160	SPL4 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4); DNA binding	0.354	2.261	1.0.E-05	0.395	2.482	1.0.E-05
A_84_P789621	AT1G24148	other RNA	0.353	2.255	2.3.E-06	0.417	2.613	2.0.E-07
A_84_P768857	AT5G44572	unknown protein	0.353	2.252	3.8.E-07	0.443	2.773	1.8.E-09
A_84_P719823	AT1G11362	enzyme inhibitor/ pectinesterase	0.352	2.251	1.8.E-03	0.595	3.938	2.3.E-04
A_84_P839042	AT1G11925	Encodes a Stigma-specific Stig1 family protein	0.350	2.241	1.0.E-05	0.522	3.330	4.4.E-10
A_84_P22555	AT1G29510	SAUR68 (SMALL AUXIN UPREGULATED 68)	0.349	2.233	5.3.E-07	0.495	3.125	1.5.E-10
A_84_P825225	AT5G65080	AGL68/MAF5 (MADS AFFECTING FLOWERING 5); transcription factor	0.349	2.233	9.1.E-04	0.507	3.211	6.0.E-05
A_84_P16678	AT4G25420	GA5 (GA REQUIRING 5); gibberellin 20-oxidase/ gibberellin 3-beta-dioxygenase	0.348	2.229	3.5.E-06	0.703	5.044	1.1.E-13
A_84_P814887	AT1G75900	family II extracellular lipase 3 (EXL3)	0.347	2.224	5.2.E-07	0.624	4.204	1.2.E-13
A_84_P811724	AT2G33830	dormancy/auxin associated family protein	0.347	2.223	5.2.E-07	0.420	2.628	7.0.E-09
A_84_P834622	AT1G02300	cathepsin B-like cysteine protease, putative	0.346	2.217	5.9.E-07	0.348	2.229	5.3.E-07
A_84_P765839	38825;AT4G3	[AT4G38825, similar to auxin-responsive protein, putative [Arabidopsis thaliana] (TAIR:AT5G18030.1); similar to auxin-induced protein-like [Brassica rapa] (GB:ABL97983.1); contains InterPro domain Auxin responsive SAUR protein (InterPro:IPR003676)];[AT4G38820, unknown protein]	0.346	2.216	7.3.E-07	1.021	10.498	3.3.E-16
A_84_P299810	AT1G11925	Encodes a Stigma-specific Stig1 family protein	0.345	2.215	1.4.E-06	0.466	2.925	9.8.E-10
A_84_P760471	AT3G23050	IAA7 (AUXIN RESISTANT 2)	0.345	2.212	1.7.E-06	0.313	2.055	9.1.E-06
A_84_P15583	AT3G46970	ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups	0.344	2.207	6.3.E-07	0.407	2.551	1.5.E-08
A_84_P844205	AT4G23160	protein kinase family protein	0.344	2.206	9.5.E-03	0.424	2.656	5.7.E-03
A_84_P856901	AT5G16030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G02500.1); similar to hypothetical protein [Cleome spinosa] (GB:ABD96956.1)	0.340	2.190	8.0.E-07	0.474	2.978	3.3.E-10
A_84_P838988	AT5G26570	PWD (PHOSPHOGLUCAN WATER DIKINASE); catalytic	0.337	2.173	1.7.E-06	0.402	2.525	5.4.E-08
A_84_P519104	AT3G25717	DVL6/RTFL16 (ROTUNDIFOLIA LIKE 16)	0.336	2.168	1.0.E-06	0.378	2.390	8.2.E-08
A_84_P841512	AT3G28370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28350.1); similar to hypothetical protein OsI_021564 [Oryza sativa (indica cultivar-group)] (GB:EAZ00332.1)	0.335	2.165	1.2.E-06	0.503	3.183	9.6.E-11
A_84_P148558	AT5G64490	binding	0.334	2.156	4.6.E-06	0.362	2.302	2.2.E-06
A_84_P235073	AT1G73870	zinc finger (B-box type) family protein	0.333	2.152	1.2.E-06	0.482	3.031	2.1.E-10
A_84_P17108	AT1G71000	DNAJ heat shock N-terminal domain-containing protein	0.333	2.151	8.9.E-03	0.693	4.930	1.4.E-14
A_84_P14446	AT2G19190	FRK1 (FLG22-INDUCED RECEPTOR-LIKE KINASE 1); kinase	0.330	2.136	1.8.E-06	0.359	2.285	3.3.E-07
A_84_P833578	AT3G04960	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G27980.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71037.1); contains InterPro domain Molecular chaperone, heat shock protein, Hsp40, DnaJ (InterPro:IPR015609)	0.330	2.136	2.0.E-05	0.544	3.498	8.7.E-09
A_84_P80689	AT5G62720	integral membrane HPP family protein	0.329	2.134	1.5.E-06	0.422	2.640	6.3.E-09
A_84_P577078	AT5G35480	unknown protein	0.327	2.123	1.7.E-06	0.419	2.623	7.7.E-09
A_84_P13568	AT2G33830	dormancy/auxin associated family protein	0.324	2.110	2.0.E-06	0.369	2.336	1.5.E-07
A_84_P115312	AT3G47860	apolipoprotein D-related	0.322	2.099	2.3.E-06	0.509	3.230	4.3.E-11
A_84_P105486	AT3G28370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28350.1); similar to hypothetical protein OsI_021564 [Oryza sativa (indica cultivar-group)] (GB:EAZ00332.1)	0.322	2.097	2.4.E-06	0.441	2.758	2.1.E-09
A_84_P23021	AT2G29090	CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2); oxygen binding	0.321	2.096	6.7.E-06	0.652	4.484	6.1.E-13
A_84_P289354	AT2G15890	MEE14 (maternal effect embryo arrest 14)	0.320	2.087	2.6.E-06	0.347	2.223	5.2.E-07
A_84_P555946	AT1G18265	contains InterPro domain Protein of unknown function DUF593 (InterPro:IPR007656)	0.319	2.083	3.0.E-05	0.350	2.240	1.0.E-05
A_84_P813465	AT2G15890	MEE14 (maternal effect embryo arrest 14)	0.318	2.079	2.9.E-06	0.323	2.104	2.2.E-06
A_84_P16577	AT1G21520	unknown protein	0.318	2.077	3.3.E-06	0.386	2.433	5.7.E-08
A_84_P754400	AT1G24148	other RNA	0.315	2.067	6.9.E-06	0.365	2.317	5.9.E-07
A_84_P17209	AT1G31690	copper ion binding	0.315	2.063	6.0.E-06	0.370	2.342	4.0.E-07
A_84_P812392	AT4G33720	pathogenesis-related protein, putative	0.313	2.058	3.2.E-03	0.541	3.472	1.1.E-03
A_84_P79415	AT2G18300	basic helix-loop-helix (bHLH) family protein	0.313	2.057	3.9.E-06	0.436	2.731	2.8.E-09
A_84_P20612	AT5G26570	PWD (PHOSPHOGLUCAN WATER DIKINASE); catalytic	0.312	2.052	4.0.E-06	0.536	3.439	9.8.E-12
A_84_P55630	AT1G02300	cathepsin B-like cysteine protease, putative	0.312	2.050	4.2.E-06	0.352	2.248	4.0.E-07
A_84_P521683	AT2G46970	PIL1 (PHYTOCHROME INTERACTING FACTOR 3-LIKE 1); transcription factor	0.312	2.049	5.3.E-04	0.744	5.545	4.7.E-12
A_84_P847330	AT3G46970	ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups	0.310	2.041	6.8.E-06	0.529	3.384	4.1.E-11
A_84_P761148	AT3G22886	MIR167A; miRNA	0.310	2.040	3.0.E-03	0.344	2.208	6.5.E-03
A_84_P802615	AT5G62360	invertase/pectin methylesterase inhibitor family protein	0.308	2.034	5.2.E-06	0.337	2.174	9.8.E-07
A_84_P847119	AT5G62360	invertase/pectin methylesterase inhibitor family protein	0.307	2.028	5.5.E-06	0.348	2.226	5.0.E-07
A_84_P164883	AT5G42900	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G33980.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN75496.1)	0.306	2.025	5.7.E-06	0.679	4.773	1.1.E-14
A_84_P13577	AT1G36940	unknown protein	0.304	2.014	6.6.E-06	0.350	2.238	4.4.E-07
A_84_P242433	AT3G25020	disease resistance family protein	0.304	2.013	2.0.E-05	0.398	2.503	3.1.E-07
A_84_P17881	AT5G62360	invertase/pectin methylesterase inhibitor family protein	0.304	2.012	6.7.E-06	0.312	2.050	4.1.E-06
A_84_P10257	AT1G29430	auxin-responsive family protein	0.303	2.008	9.4.E-04	0.578	3.783	5.0.E-05
A_84_P103276	AT5G02160	unknown protein	0.301	2.001	7.7.E-06	0.430	2.693	3.8.E-09

Table S2. Genes down-regulated in *ZTL*-overexpressing seedlings in comparison with control seedlings.

			ZTL ox1 vs Col1			*ZTL* ox2 vs Col2		
Array Element	Gene locus	Annotation	Log(Ratio)	Fold Change	P-value	Log(Ratio)	Fold Change	P-value
A_84_P24087	AT3G45060	ATNRT2.6 (Arabidopsis thaliana high affinity nitrate transporter 2.6); nitrate transmembrane transporter	−1.91092	−81.45552	1.73E−22	−0.46996	−2.95094	1.40E−07
A_84_P16501	AT3G13784	ATCWINV5 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 5); hydrolase, hydrolyzing O-glycosyl compounds	−1.66453	−46.18788	4.43E−21	−0.50619	−3.20771	0.00022
A_84_P16247	AT1G12610	DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / transcription factor	−1.45302	−28.38036	1.46E−18	−0.44953	−2.8153	1.87E−09
A_84_P11439	AT1G52560	26.5 kDa class I small heat shock protein-like (HSP26.5-P)	−1.26726	−18.50388	3.09E−19	−0.7041	−5.05942	6.98E−14
A_84_P13966	AT5G14650	polygalacturonase, putative / pectinase, putative	−1.22831	−16.91665	7.52E−14	−0.316	−2.07016	0.00466
A_84_P712672	AT3G15210	no_match	−1.13283	−13.5777	1.85E−11	−0.38668	−2.436	6.49E−08
A_84_P842527	AT5G42800	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase	−1.0818	−12.07266	6.77E−17	−0.57148	−3.72802	3.34E−10
A_84_P233899	AT5G66780	similar to unknown [Ammopiptanthus mongolicus] (GB:AAW33981.1)	−0.98072	−9.56572	9.25E−08	−0.86696	−7.36146	1.21E−06
A_84_P507728	AT4G23496	SP1L5 (SPIRAL1-LIKE5)	−0.9711	−9.35623	2.29E−18	−0.87966	−7.57981	2.25E−17
A_84_P21851	AT1G66370	MYB113 (myb domain protein 113); DNA binding / transcription factor	−0.96928	−9.31698	1.73E−07	−0.72691	−5.33227	3.61E−15
A_84_P825033	AT1G58120; AT1G58122	[AT1G58120, similar to unnamed protein product [Vitis vinifera] (GB:CAO61619.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN74009.1)];[AT1G58122, CPuORF45 (Conserved peptide upstream open reading frame 45)]	−0.96716	−9.27177	1.10E−09	−1.12904	−13.45992	4.53E−11
A_84_P17055	AT1G65480	FT (FLOWERING LOCUS T)	−0.96479	−9.2213	1.99E−07	−0.93973	−8.70416	1.16E−06
A_84_P146938	AT1G02450	NIMIN-1/NIMIN1; protein binding	−0.94512	−8.81298	5.89E−07	−0.72416	−5.29858	1.62E−11
A_84_P20780	AT1G03940; AT1G03495	[AT1G03940, transferase family protein];[AT1G03495, transferase]	−0.93459	−8.60191	7.56E−17	−0.55851	−3.61833	4.82E−11
A_84_P578638	AT4G01240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G05390.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO39658.1); contains domain SSF53335 (SSF53335)	−0.91702	−8.26074	1.18E−07	−0.5615	−3.64337	0.00257
A_84_P17806	AT5G42800	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase	−0.91342	−8.19254	3.10E−18	−0.62066	−4.17507	1.46E−13
A_84_P825539	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	−0.90575	−8.0492	3.68E−06	−0.89021	−7.76631	2.61E−15
A_84_P76184	AT5G24110	WRKY30 (WRKY DNA-binding protein 30); transcription factor	−0.90351	−8.00772	1.56E−15	−1.19413	−15.63618	1.85E−20
A_84_P15503	AT3G22830	AT-HSFA6B (Arabidopsis thaliana heat shock transcription factor A6B); DNA binding / transcription factor	−0.89466	−7.84629	1.75E−11	−0.91224	−8.17038	1.84E−15
A_84_P823530	AT1G19640	JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase	−0.87496	−7.49832	0.00002	−1.14851	−14.07699	1.35E−11
A_84_P173441	AT3G61920	similar to unnamed protein product [Vitis vinifera] (GB:CAO24317.1)	−0.87432	−7.48725	4.26E−08	−0.30416	−2.01445	0.00025
A_84_P17898	AT5G66670	Identical to UPF0496 protein At5g66670 [Arabidopsis Thaliana] (GB:Q9LVR3); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66660.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO22906.1); contains InterPro domain Protein of unknown function DUF677 (InterPro:IPR007749)	−0.87012	−7.41512	0.00002	−0.46284	−2.90296	9.24E−06
A_84_P269530	AT3G29430	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative	−0.86573	−7.34051	0.00002	−0.9036	−8.00939	6.24E−06
A_84_P17688	AT4G14695	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22310.1); similar to unknown [Populus trichocarpa] (GB:ABK93494.1); contains InterPro domain Protein of unknown function UPF0041 (InterPro:IPR005336)	−0.85114	−7.09803	8.45E−07	−0.68891	−4.88549	0.00474
A_84_P826417	AT5G24110	WRKY30 (WRKY DNA-binding protein 30); transcription factor	−0.84755	−7.03965	7.42E−12	−1.11179	−12.93577	1.44E−19
A_84_P23924	AT2G18150	peroxidase, putative	−0.83855	−6.89519	6.34E−17	−0.38332	−2.41723	1.97E−07
A_84_P13518	AT1G19640	JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase	−0.83645	−6.86191	3.02E−15	−1.1445	−13.94755	3.10E−19
A_84_P16901	AT5G54060	UF3GT (UDP-GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE); transferase, transferring glycosyl groups	−0.83475	−6.83522	1.31E−16	−0.52613	−3.35841	3.06E−11
A_84_P19609	AT5G05390	LAC12 (laccase 12); copper ion binding / oxidoreductase	−0.83305	−6.80844	3.12E−16	−0.40149	−2.52049	2.47E−08
A_84_P16488	AT3G20590	non-race specific disease resistance protein, putative	−0.82944	−6.75217	5.30E−06	−0.73143	−5.38809	9.89E−07
A_84_P189924	AT4G13280	ATTPS12/TPS12 (TERPENOID SYNTHASE12); cyclase	−0.82675	−6.71042	6.65E−17	−0.49275	−3.10993	2.11E−10
A_84_P544235	AT5G28237	tryptophan synthase, beta subunit, putative	−0.82276	−6.64909	0.0001	−1.00054	−10.01241	4.05E−18
A_84_P163603	AT4G05095	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G04650.1); similar to putative AP endonuclease/reverse transcriptase [Brassica napus] (GB:AAM82604.1)	−0.81393	−6.51521	0.00013	−0.35332	−2.25591	0.00481
A_84_P12885	AT4G22880	LDOX (TANNIN DEFICIENT SEED 4)	−0.81323	−6.50468	3.26E−16	−0.52556	−3.35398	4.45E−11
A_84_P210018	AT4G10560	MEE53 (maternal effect embryo arrest 53); protein binding / zinc ion binding	−0.81308	−6.50256	0.00008	−0.63653	−4.33045	0.00056
A_84_P16037	AT1G56650	PAP1 (PRODUCTION OF ANTHOCYANIN PIGMENT 1); DNA binding / transcription factor	−0.79871	−6.29087	1.50E−14	−0.53718	−3.44494	1.18E−11
A_84_P13969	AT5G17220	ATGSTF12 (GLUTATHIONE S-TRANSFERASE 26); glutathione transferase	−0.78396	−6.08085	1.82E−16	−0.52232	−3.32906	2.18E−11
A_84_P831728	AT5G17220	ATGSTF12 (GLUTATHIONE S-TRANSFERASE 26); glutathione transferase	−0.77901	−6.01184	8.20E−15	−0.47451	−2.98203	1.79E−09
A_84_P197194	AT4G22870	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative	−0.77719	−5.98669	6.79E−16	−0.50486	−3.19787	9.16E−11
A_84_P790750	AT3G62990	no_match	−0.76438	−5.81279	1.29E−07	−0.94666	−8.84425	1.24E−10
A_84_P532079	AT1G47510	endonuclease/exonuclease/phosphatase family protein	−0.76344	−5.8002	2.16E−11	−0.73695	−5.45699	1.29E−15
A_84_P13657	AT3G29590	AT5MAT; O-malonyltransferase/ transferase	−0.76224	−5.78415	3.31E−14	−0.349	−2.23355	7.91E−06
A_84_P757840	AT2G05995	other RNA	−0.75659	−5.70936	4.45E−14	−0.80874	−6.43782	1.10E−14
A_84_P15113	AT1G71520	AP2 domain-containing transcription factor, putative	−0.75255	−5.65649	1.45E−15	−0.4625	−2.90067	6.94E−10
A_84_P62840	AT4G14690	ELIP2 (EARLY LIGHT-INDUCIBLE PROTEIN 2); chlorophyll binding	−0.75187	−5.64765	5.43E−16	−0.78302	−6.06761	1.78E−16
A_84_P265780	AT5G15840	CO (CONSTANS); transcription factor/ zinc ion binding	−0.74423	−5.54925	5.82E−15	−0.31817	−2.08052	0.0021
A_84_P517162	AT2G20630	protein phosphatase 2C, putative / PP2C, putative	−0.74222	−5.52357	4.18E−10	−0.42188	−2.64169	3.40E−08
A_84_P750187	AT1G65680	ATEXPB2 (ARABIDOPSIS THALIANA EXPANSIN B2)	−0.73286	−5.40581	5.34E−08	−0.83365	−6.81795	0.00001
A_84_P210278	AT1G66700	PXMT1; S-adenosylmethionine-dependent methyltransferase	−0.72954	−5.36469	1.34E−13	−1.32586	−21.17674	1.87E−21
A_84_P551607	AT1G61810	BGLU45; hydrolase, hydrolyzing O-glycosyl compounds	−0.72822	−5.3483	0.0002	−0.72094	−5.25948	0.00004
A_84_P18908	AT1G33760	AP2 domain-containing transcription factor, putative	−0.72301	−5.28462	0.00002	−0.58954	−3.88637	2.28E−12
A_84_P11557	AT2G25820	transcription factor	−0.7228	−5.28207	0.00019	−0.55811	−3.615	1.12E−10
A_84_P788197	AT2G32550	rcd1-like cell differentiation family protein	−0.72139	−5.26487	6.05E−07	−0.48897	−3.08297	0.00021
A_84_P23516	AT5G51990	CBF4/DREB1D (C- REPEAT-BINDING FACTOR 4); DNA binding / transcription activator/ transcription factor	−0.72103	−5.2605	0.00253	−0.4204	−2.63267	7.63E−07
A_84_P20179	AT2G40100	LHCB4.3 (LIGHT HARVESTING COMPLEX PSII); chlorophyll binding	−0.71172	−5.14901	2.58E−15	−0.55159	−3.56114	4.41E−12
A_84_P582920	AT2G45760	BAP2 (BON ASSOCIATION PROTEIN 2)	−0.71036	−5.13282	3.76E−07	−0.58161	−3.81602	4.28E−12
A_84_P14853	AT4G15480	UGT84A1; UDP-glycosyltransferase/ sinapate 1-glucosyltransferase/ transferase, transferring glycosyl groups	−0.70429	−5.06157	4.31E−15	−0.89526	−7.85713	5.71E−18
A_84_P511021	AT2G42660	myb family transcription factor	−0.69747	−4.98276	0.00003	−0.89055	−7.77227	1.82E−13
A_84_P599083	AT3G42550	aspartyl protease family protein	−0.69109	−4.9101	0.0052	−0.89333	−7.82213	8.65E−06
A_84_P16077	AT1G05100	MAPKKK18 (Mitogen-activated protein kinase kinase kinase 18); kinase	−0.68985	−4.89608	6.30E−12	−0.5799	−3.80101	1.72E−12
A_84_P544251	AT5G38700	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40081.1)	−0.68967	−4.89402	2.48E−07	−0.50625	−3.20814	5.66E−10
A_84_P563250	AT2G26400	ARD/ATARD3 (ACIREDUCTONE DIOXYGENASE); acireductone dioxygenase [iron(II)-requiring]/ heteroglycan binding / metal ion binding	−0.68385	−4.82892	1.00E−14	−0.57568	−3.76423	1.48E−12
A_84_P11109	AT5G07570	glycine/proline-rich protein	−0.68338	−4.82367	1.80E−07	−0.57802	−3.7846	1.69E−08
A_84_P20925	AT1G66550	WRKY67 (WRKY DNA-binding protein 67); transcription factor	−0.67325	−4.71243	0.00786	−0.75509	−5.68966	9.75E−15
A_84_P18113	AT1G76640	calmodulin-related protein, putative	−0.67197	−4.69859	3.69E−11	−0.57418	−3.75131	1.65E−12
A_84_P792228	AT3G22490	late embryogenesis abundant protein, putative / LEA protein, putative	−0.66164	−4.58815	0.00246	−0.91047	−8.13705	3.09E−08
A_84_P786320	AT5G35935	transposable element gene	−0.66136	−4.58519	4.53E−14	−1.13895	−13.77037	5.68E−20
A_84_P11217	AT5G50260	cysteine proteinase, putative	−0.65852	−4.5553	8.50E−13	−0.41999	−2.63018	1.63E−08
A_84_P22793	AT1G15610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15630.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN70531.1)	−0.65568	−4.52566	2.11E−07	−0.33872	−2.1813	4.42E−06
A_84_P21945	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	−0.65348	−4.50281	6.38E−07	−0.83062	−6.77054	1.74E−15
A_84_P845171	AT5G42800	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reductase	−0.63965	−4.3616	7.36E−14	−0.56692	−3.68914	2.27E−12
A_84_P258120	AT1G75830	LCR67/PDF1.1 (Low-molecular-weight cysteine-rich 67)	−0.63541	−4.31922	4.20E−13	−0.92644	−8.44198	2.03E−17
A_84_P831396	AT1G20310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76070.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN83887.1)	−0.63469	−4.31207	0.00006	−0.44392	−2.77918	2.69E−08
A_84_P13030	AT5G18910	protein kinase family protein	−0.62424	−4.20962	0.00314	−0.40527	−2.54253	0.00456
A_84_P67354	AT5G63580	flavonol synthase, putative	−0.62054	−4.17388	2.55E−12	−0.56649	−3.68544	1.61E−09
A_84_P13963	AT5G13930	ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase	−0.62032	−4.17176	1.43E−13	−0.6746	−4.72717	1.22E−14
A_84_P561097	AT5G46295	unknown protein	−0.6187	−4.15622	4.98E−13	−0.82397	−6.66764	5.18E−17
A_84_P181974	AT1G20310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76070.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN83887.1)	−0.61421	−4.11346	8.73E−10	−0.41656	−2.60949	1.45E−08
A_84_P17872	AT5G60520	late embryogenesis abundant protein-related / LEA protein-related	−0.61212	−4.09376	3.00E−13	−0.5199	−3.31056	1.22E−10
A_84_P848499	AT5G35935	transposable element gene	−0.6063	−4.03924	5.03E−13	−1.20447	−16.01297	1.96E−20
A_84_P16137	AT1G10530	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G60010.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40951.1)	−0.60236	−4.00272	0.00003	−0.40213	−2.52422	0.00056
A_84_P11148	AT5G24080	protein kinase family protein	−0.60003	−3.98135	3.28E−07	−0.78795	−6.13692	1.51E−16
A_84_P11046	AT4G34410	AP2 domain-containing transcription factor, putative	−0.59189	−3.90744	1.93E−10	−0.63174	−4.28289	8.96E−14
A_84_P16282	AT2G43480	peroxidase, putative	−0.59169	−3.90561	1.00E−06	−0.80999	−6.45633	4.16E−07
A_84_P757120	AT2G12646	similar to zinc-binding protein, putative [Arabidopsis thaliana] (TAIR:AT3G60670.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO67744.1); contains InterPro domain Protein of unknown function DUF597 (InterPro:IPR006734)	−0.58888	−3.88045	4.46E−10	−0.463	−2.90401	2.04E−07
A_84_P11901	AT1G06100	fatty acid desaturase family protein	−0.58838	−3.876	6.93E−12	−0.6074	−4.04946	2.85E−13

A_84_P18335	AT3G02480	ABA-responsive protein-related	-0.58731	-3.86646	2.15E-12	-0.4252	-2.66194	5.77E-09
A_84_P836925	AT5G35935	no_match	-0.58283	-3.82677	6.93E-12	-1.15498	-14.2882	1.21E-18
A_84_P16253	AT1G15460	ATBOR4/BOR4; anion exchanger	-0.58064	-3.80747	0.00872	-0.47856	-3.00998	2.88E-06
A_84_P23404	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	-0.58038	-3.80526	1.11E-12	-0.68954	-4.89257	7.24E-15
A_84_P21760	AT1G03940	transferase family protein	-0.57365	-3.74669	1.27E-07	-0.38329	-2.41708	0.00001
A_84_P701336	AT2G42760	similar to unnamed protein product [Vitis vinifera] (GB:CAO69913.1)	-0.57316	-3.74246	0.00083	-0.51189	-3.25004	0.00016
A_84_P825767	AT1G56250	ATPP2-B14 (Phloem protein 2-B14); carbohydrate binding	-0.56882	-3.70524	1.46E-06	-0.37269	-2.3588	1.74E-06
A_84_P818529	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	-0.56671	-3.68732	2.25E-12	-0.6937	-4.93969	6.07E-15
A_84_P761070	AT3G19184	DNA binding	-0.55565	-3.59459	7.06E-09	-0.37563	-2.37484	0.00007
A_84_P14146	AT1G56680	glycoside hydrolase family 19 protein	-0.55477	-3.58733	4.03E-12	-0.52477	-3.34789	2.21E-11
A_84_P594418	AT2G17660	nitrate-responsive NOI protein, putative	-0.55351	-3.57691	4.08E-11	-0.36715	-2.32888	2.72E-07
A_84_P19861	AT1G64480	CBL8 (CALCINEURIN B-LIKE PROTEIN 5)	-0.55192	-3.56385	8.03E-07	-0.32942	-2.13509	0.00003
A_84_P12863	AT4G13420	HAK5 (High affinity K+ transporter 5); potassium ion transmembrane transporter	-0.55179	-3.56282	1.23E-11	-0.568	-3.6983	3.10E-12
A_84_P15944	AT5G50790	nodulin MtN3 family protein	-0.54719	-3.52524	2.36E-11	-0.4379	-2.74093	1.21E-07
A_84_P174401	AT4G16820	lipase class 3 family protein	-0.54632	-3.51821	1.58E-08	-0.41588	-2.60544	1.58E-08
A_84_P73804	AT5G62165	AGL42 (AGAMOUS LIKE 42); transcription factor	-0.5434	-3.4946	2.49E-10	-0.65816	-4.55152	1.07E-13
A_84_P19294	AT1G26380	FAD-binding domain-containing protein	-0.54098	-3.47523	1.26E-11	-0.96129	-9.14734	8.99E-19
A_84_P100606	AT1G02810	pectinesterase family protein	-0.53855	-3.45579	9.63E-12	-0.35627	-2.27125	3.12E-07
A_84_P607864	AT3G02885	GASA5 (GAST1 PROTEIN HOMOLOG 5)	-0.53717	-3.44484	1.35E-11	-0.32562	-2.1165	2.83E-06
A_84_P818534	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen binding	-0.53634	-3.43825	2.28E-06	-1.09394	-12.41473	2.96E-10
A_84_P12815	AT3G62760	ATGSTF13 (Arabidopsis thaliana Glutathione S-transferase (class phi) 13); glutathione	-0.53569	-3.43312	3.16E-11	-0.46536	-2.91983	2.42E-09
A_84_P11248	AT5G59220	protein phosphatase 2C, putative / PP2C, putative	-0.53332	-3.41442	9.01E-11	-0.49627	-3.13523	9.22E-11
A_84_P824281	AT1G66700	PXMT1; S-adenosylmethionine-dependent methyltransferase	-0.52743	-3.36848	1.61E-08	-1.31808	-20.80057	2.24E-21
A_84_P10627	AT2G20880	AP2 domain-containing transcription factor, putative	-0.52665	-3.36237	2.96E-06	-0.58782	-3.87096	7.99E-13
A_84_P573393	AT4G27654	unknown protein	-0.52415	-3.34312	1.56E-10	-0.42086	-2.63547	6.69E-09
A_84_P12058	AT5G08640	FLS (FLAVONOL SYNTHASE)	-0.51703	-3.28873	2.78E-11	-0.66206	-4.59262	2.12E-14
A_84_P790512	AT1G22460	no_match	-0.5164	-3.28398	0.00035	-0.79114	-6.18213	0.00003
A_84_P760622	AT3G56275	pseudogene of unknown protein	-0.5123	-3.25311	7.29E-09	-0.44712	-2.79978	1.87E-09
A_84_P17724	AT5G07190	ATS3 (ARABIDOPSIS THALIANA SEED GENE 3)	-0.50991	-3.2353	5.71E-08	-0.77803	-5.99833	2.08E-09
A_84_P17423	AT3G26610	polygalacturonase, putative / pectinase, putative	-0.50726	-3.21558	7.02E-11	-0.31158	-2.04919	6.36E-06
A_84_P173571	AT1G73165	CLE1 (CLAVATA3/ESR-RELATED 1); receptor binding	-0.50619	-3.20768	0.00293	-0.52371	-3.33969	0.00002
A_84_P22064	AT2G16230	glycosyl hydrolase family 17 protein	-0.49735	-3.14302	1.88E-08	-0.58611	-3.85574	7.52E-07
A_84_P19028	AT1G74930	ORA47; DNA binding / transcription factor	-0.49548	-3.12955	1.52E-07	-0.53746	-3.44712	1.06E-11
A_84_P155845	AT2G47950	unknown protein	-0.49312	-3.1126	1.32E-10	-0.40375	-2.53367	1.87E-08
A_84_P842252	AT1G19640	JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate O-methyltransferase	-0.49294	-3.11128	0.00003	-0.70919	-5.11908	1.04E-09
A_84_P860810	AT3G08770	LTP6 (Lipid transfer protein 6); lipid binding	-0.49114	-3.09841	1.16E-10	-0.33872	-2.1813	8.53E-07
A_84_P16314	AT2G22590	glycosyltransferase family protein	-0.48989	-3.08951	1.03E-09	-0.57619	-3.76871	6.88E-12
A_84_P10966	AT4G11610	C2 domain-containing protein	-0.4892	-3.0846	3.36E-07	-0.56743	-3.69344	3.90E-06
A_84_P848759	AT4G28410	aminotransferase-related	-0.48324	-3.04256	0.00015	-0.41476	-2.59874	0.00229
A_84_P10196	AT5G22300	NIT4 (NITRILASE 4)	-0.48318	-3.04218	1.81E-10	-0.67582	-4.74041	1.18E-14
A_84_P18100	AT1G69930	ATGSTU11 (Arabidopsis thaliana Glutathione S-transferase (class tau) 11); glutathione	-0.48249	-3.03733	2.25E-10	-0.47416	-2.97961	3.15E-10
A_84_P813812	AT3G08770	LTP6 (Lipid transfer protein 6); lipid binding	-0.47989	-3.01919	2.17E-10	-0.32457	-2.11139	1.96E-06
A_84_P833880	AT1G54890	late embryogenesis abundant protein-related / LEA protein-related	-0.47879	-3.01152	2.34E-09	-0.82733	-6.71947	1.09E-13
A_84_P231939	AT1G61800	GPT2 (glucose-6-phosphate/phosphate translocator 2); antiporter/ glucose-6-phosphate transmembrane transporter	-0.47855	-3.0099	6.35E-10	-1.04638	-11.12709	1.35E-19
A_84_P19271	AT3G09680	40S ribosomal protein S23 (RPS23A)	-0.47767	-3.00383	0.00004	-0.36724	-2.32936	0.00997
A_84_P12766	AT3G51240; AT3G51238	[AT3G51240, F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase];[AT3G51238, other RNA]	-0.47712	-2.99999	2.55E-10	-0.70283	-5.04466	3.71E-15
A_84_P23972	AT2G23630	SKS16 (SKU5 Similar 16); copper ion binding / pectinesterase	-0.47532	-2.98756	4.07E-10	-0.40941	-2.5669	3.15E-08
A_84_P521598	AT2G22760	basic helix-loop-helix (bHLH) family protein	-0.47458	-2.98252	5.34E-07	-0.38327	-2.41694	7.17E-08
A_84_P828648	AT2G34020	calcium ion binding	-0.4737	-2.97644	4.32E-10	-0.48039	-3.0227	3.12E-10
A_84_P525365	AT3G57500	similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:AAO19376.1)	-0.47367	-2.97629	1.12E-09	-0.30687	-2.02708	9.37E-06
A_84_P13764	AT3G44830	lecithin:cholesterol acyltransferase family protein / LACT family protein	-0.47322	-2.97318	0.00032	-1.06235	-11.54376	3.13E-18
A_84_P255680	AT5G05960	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-0.47232	-2.96705	3.34E-10	-0.32935	-2.13476	1.48E-06
A_84_P149258	AT2G23050	phototropic-responsive NPH3 family protein	-0.47154	-2.96167	4.42E-10	-0.44585	-2.79156	2.07E-09
A_84_P292024	AT4G03292	nucleic acid binding	-0.47102	-2.95814	8.68E-07	-0.30908	-2.03742	0.0015
A_84_P59930	AT1G15150	MATE efflux family protein	-0.47029	-2.95317	4.84E-08	-0.32841	-2.13017	0.00004
A_84_P15222	AT1G65060	4CL3 (4-coumarate:CoA ligase 3); 4-coumarate-CoA ligase	-0.46908	-2.94494	4.34E-10	-0.50604	-3.20655	5.39E-11
A_84_P11143	AT5G22570	WRKY38 (WRKY DNA-binding protein 38); transcription factor	-0.46853	-2.94121	7.21E-09	-0.64144	-4.37962	1.01E-13
A_84_P19175	AT2G19050	GDSL-motif lipase/hydrolase family protein	-0.46794	-2.93724	0.00001	-0.51021	-3.23747	2.96E-06
A_84_P836638	AT1G52060	similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:AT1G52070.1); similar to jasmonate inducible protein [Brassica napus] (GB:CAA72271.1); contains InterPro domain Mannose-binding lectin (InterPro:IPR001229)	-0.46731	-2.93301	8.66E-10	-0.65991	-4.56996	1.55E-09
A_84_P513731	AT3G12955	auxin-responsive protein-related	-0.46628	-2.92606	6.33E-09	-0.51379	-3.26429	7.04E-10
A_84_P20248	AT3G23230	ethylene-responsive factor, putative	-0.46605	-2.92452	2.29E-06	-0.76821	-5.8642	2.66E-15
A_84_P16900	AT5G53820	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G38760.1); similar to pollen coat protein [Brassica oleracea] (GB:CAA63531.1); contains domain PTHR23241:SF11 (PTHR23241:SF11); contains domain PTHR23241 (PTHR23241)	-0.46519	-2.91869	1.00E-08	-0.32153	-2.09669	0.00005
A_84_P788340	AT2G26310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G63170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO43896.1); contains InterPro domain Chalcone isomerase-like (InterPro:IPR016087)	-0.46412	-2.9115	0.00003	-0.35864	-2.2837	0.0001
A_84_P807539	AT3G51240; AT3G51238	[AT3G51240, F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase];[AT3G51238, other RNA]	-0.46296	-2.90372	6.28E-10	-0.70757	-5.1	3.35E-15
A_84_P762507	AT3G25573	unknown protein	-0.46278	-2.90256	0.00013	-0.93656	-8.64084	1.42E-17
A_84_P840120	AT3G62990	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G47950.1)	-0.46243	-2.90025	1.29E-07	-1.10431	-12.71467	1.49E-15
A_84_P22732	AT1G08860	BON3 (BONZAI 3)	-0.46187	-2.89649	0.00116	-0.73886	-5.481	4.84E-12
A_84_P23604	AT1G54890	late embryogenesis abundant protein-related / LEA protein-related	-0.46172	-2.89548	6.31E-10	-0.72064	-5.2558	1.95E-15
A_84_P15083	AT5G19520	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein	-0.45995	-2.88372	7.06E-10	-0.45972	-2.88215	7.28E-10
A_84_P23103	AT3G14940	ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpyruvate carboxylase	-0.45994	-2.88363	6.77E-10	-0.46044	-2.88698	6.57E-10
A_84_P824903	AT5G22460	esterase/lipase/thioesterase family protein	-0.45328	-2.83978	4.14E-09	-0.33745	-2.17496	3.58E-06
A_84_P556217	AT2G38995	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G37300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48523.1); contains InterPro domain Protein of unknown function UPF0089 (InterPro:IPR004255); contains InterPro domain Protein of unknown function DUF1298 (InterPro:IPR009721)	-0.45308	-2.83845	5.34E-07	-0.46537	-2.91994	2.93E-09
A_84_P12272	AT2G04025	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13620.1)	-0.44891	-2.81134	5.71E-08	-0.47608	-2.99279	1.08E-07
A_84_P22110	AT3G08770	LTP6 (Lipid transfer protein 6); lipid binding	-0.44787	-2.80463	1.36E-09	-0.34293	-2.20257	6.65E-07
A_84_P14597	AT3G30460	zinc finger (C3HC4-type RING finger) family protein	-0.44745	-2.80191	6.56E-06	-0.36376	-2.31076	0.00069
A_84_P827147	AT1G61800	GPT2 (glucose-6-phosphate/phosphate translocator 2); antiporter/ glucose-6-phosphate transmembrane transporter	-0.44588	-2.79176	8.51E-08	-1.07798	-11.96678	1.00E-19
A_84_P13934	AT5G05270	chalcone-flavanone isomerase family protein	-0.443	-2.77334	1.84E-09	-0.56317	-3.65736	2.47E-12
A_84_P23070	AT3G22740	HMT3 (Homocysteine S-methyltransferase 3); homocysteine S-methyltransferase	-0.443	-2.77332	1.90E-09	-0.32594	-2.11809	1.83E-06
A_84_P19749	AT5G57090	EIR1 (ETHYLENE INSENSITIVE ROOT 1); auxin:hydrogen symporter/ transporter	-0.44226	-2.76857	7.31E-09	-0.45027	-2.82013	9.43E-09
A_84_P532174	AT1G78815	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G16910.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN63025.1); contains InterPro domain Protein of unknown function DUF640 (InterPro:IPR006936)	-0.44066	-2.75839	1.89E-07	-0.31381	-2.05972	0.00032
A_84_P18422	AT1G48470	GLN1;5 (GLUTAMINE SYNTHETASE 1;5); glutamate-ammonia ligase	-0.44053	-2.7576	0.00878	-0.45303	-2.83811	0.00004
A_84_P19131	AT2G23910	cinnamoyl-CoA reductase-related	-0.44028	-2.75599	4.23E-09	-0.45328	-2.83978	1.50E-09
A_84_P752662	AT1G12064	similar to hypothetical protein [Vitis vinifera] (GB:CAN77938.1)	-0.4383	-2.74348	0.00034	-0.46464	-2.91503	0.00069
A_84_P10202	AT5G24070	peroxidase family protein	-0.43801	-2.74161	1.84E-08	-0.34947	-2.23601	6.03E-06
A_84_P13172	AT5G67080	MAPKKK19 (Mitogen-activated protein kinase kinase kinase 19); kinase	-0.43543	-2.72543	4.35E-09	-0.64815	-4.44782	4.11E-14
A_84_P845967	AT5G22570	WRKY38 (WRKY DNA-binding protein 38); transcription factor	-0.43504	-2.72295	4.21E-09	-0.66098	-4.58126	2.44E-14
A_84_P22742	AT1G10400	UDP-glycosyltransferase/ transferase, transferring glycosyl groups	-0.43237	-2.70629	1.25E-08	-0.46684	-2.92981	2.28E-09
A_84_P503304	AT4G25860	oxysterol-binding family protein	-0.43161	-2.70154	6.87E-06	-0.31008	-2.0421	0.00021
A_84_P18104	AT1G74500	bHLH family protein	-0.43131	-2.69967	6.67E-09	-0.59536	-3.93875	1.37E-12
A_84_P756427	AT2G27420	cysteine proteinase, putative	-0.43014	-2.69238	0.00958	-0.8904	-7.76971	1.72E-06
A_84_P21200	AT3G23060	zinc finger (C3HC4-type RING finger) family protein	-0.42989	-2.69084	0.00014	-0.97229	-9.38192	2.10E-13
A_84_P253555	AT4G14090	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-0.4292	-2.6866	5.57E-09	-0.35405	-2.25971	4.36E-07
A_84_P196584	AT3G48650	pseudogene, At14a-related protein, similar to At14a (GI:11994571 and GI:11994573) (Arabidopsis thaliana)	-0.42893	-2.68488	0.00009	-0.39566	-2.48692	8.01E-08
A_84_P528434	AT5G56960	basic helix-loop-helix (bHLH) family protein	-0.42594	-2.66649	0.00572	-1.17722	-15.03909	2.36E-12
A_84_P10687	AT2G43880	polygalacturonase, putative / pectinase, putative	-0.42531	-2.66265	5.45E-09	-0.62192	-4.18716	1.64E-13
A_84_P10395	AT1G19050	ARR7 (RESPONSE REGULATOR 7); transcription regulator/ two-component response regulator	-0.42259	-2.64602	6.60E-09	-0.40929	-2.56622	1.35E-08
A_84_P12917	AT4G29880	protein binding	-0.42219	-2.64353	0.00191	-0.66191	-4.59099	0.00279

A_84_P567920	AT3G57950	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G42180.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN83225.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23380.1)	-0.42148	-2.63926	1.29E-06	-0.33381	-2.1568	0.00006
A_84_P23633	AT1G43910	AAA-type ATPase family protein	-0.42108	-2.6368	6.60E-09	-0.33706	-2.17298	9.48E-07
A_84_P598333	AT4G22640	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22666.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G22666.2); contains InterPro domain Bifunctional inhibitor/plant lipid transfer protein/seed storage (InterPro:IPR016140)	-0.41909	-2.62476	0.00065	-0.37294	-2.36017	0.00004
A_84_P612389	AT3G24240	leucine-rich repeat transmembrane protein kinase, putative	-0.41748	-2.61502	2.33E-08	-0.32123	-2.09523	4.76E-06
A_84_P17663	AT4G34320	Identical to UPF0496 protein At4g34320 [Arabidopsis Thaliana] (GB:Q9SYZ7); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G34330.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47666.1); contains InterPro domain Protein of unknown function DUF677 (InterPro:IPR007749)	-0.41705	-2.61248	1.58E-07	-0.32457	-2.11138	8.15E-06
A_84_P11239	AT5G56840	DNA-binding family protein	-0.41686	-2.61133	9.68E-09	-0.51226	-3.25282	4.13E-11
A_84_P16071	AT1G33750	terpene synthase/cyclase family protein	-0.41585	-2.60524	2.06E-08	-0.40036	-2.51398	6.72E-08
A_84_P188424	AT5G15800	SEP1 (SEPALLATA1); DNA binding / transcription factor	-0.41521	-2.60144	0.00589	-0.67174	-4.69609	0.0009
A_84_P17163	AT1G73160	glycosyl transferase family 1 protein	-0.41466	-2.5981	4.06E-07	-0.51467	-3.27093	3.81E-08
A_84_P96556	AT1G19900	glyoxal oxidase-related	-0.41399	-2.59412	1.14E-08	-0.33123	-2.14405	1.40E-06
A_84_P19702	AT5G44110	POP1	-0.41388	-2.59347	1.01E-08	-0.54482	-3.50609	6.44E-12
A_84_P521593	AT2G20515	similar to unnamed protein product [Vitis vinifera] (GB:CAO40634.1)	-0.41082	-2.57526	1.44E-08	-0.35233	-2.25079	4.83E-07
A_84_P839599	AT1G73160	glycosyl transferase family 1 protein	-0.41058	-2.57385	3.61E-08	-0.47733	-3.00148	1.72E-09
A_84_P18265	AT2G18480	mannitol transporter, putative	-0.40989	-2.56975	2.28E-08	-0.31493	-2.06506	4.75E-06
A_84_P11446	AT1G15520	ATPDR12/PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	-0.40669	-2.5509	1.59E-08	-1.18412	-15.27991	1.11E-20
A_84_P101676	AT4G14980	DC1 domain-containing protein	-0.40597	-2.54663	9.09E-07	-0.35064	-2.24205	0.00011
A_84_P817725	AT1G78140	methyltransferase-related	-0.40546	-2.54369	0.00266	-0.84105	-6.935	0.00006
A_84_P755918	AT2G34020	calcium ion binding	-0.40459	-2.53858	5.46E-08	-0.39994	-2.51154	8.66E-08
A_84_P579358	AT3G01516	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G14690.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14758.1)	-0.4032	-2.53045	2.57E-08	-0.4435	-2.77654	2.89E-09
A_84_P11919	AT4G13620	AP2 domain-containing transcription factor, putative	-0.40309	-2.52981	1.56E-07	-0.61128	-4.08581	2.95E-12
A_84_P566998	AT3G49540	unknown protein	-0.40184	-2.52255	0.00005	-0.67401	-4.72069	2.49E-11
A_84_P14242	AT1G79330	AMC6/ATMC5/ATMCP2B (TYPE-II METACASPASES); caspase/ cysteine-type endopeptidase	-0.40107	-2.51808	0.00002	-0.32134	-2.09574	0.00003
A_84_P10297	AT5G57980	eukaryotic rpb5 RNA polymerase subunit family protein	-0.40051	-2.51483	8.19E-08	-0.47551	-2.98891	4.15E-09
A_84_P24148	AT3G59010	pectinesterase family protein	-0.39707	-2.49501	2.87E-08	-0.39934	-2.50809	2.36E-08
A_84_P13060	AT5G37800	basic helix-loop-helix (bHLH) family protein	-0.39406	-2.47777	0.00016	-0.32321	-2.10478	0.00984
A_84_P511862	AT2G32550	rcd1-like cell differentiation family protein	-0.39333	-2.47361	3.43E-06	-0.41859	-2.62176	4.59E-07
A_84_P513890	AT4G11780	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G23020.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60407.1)	-0.39321	-2.47292	3.78E-07	-0.73135	-5.38702	7.71E-13
A_84_P594570	AT3G15240	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G53900.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO39314.1); contains domain gb def: At3g15240 (PTHR13902:SF3); contains domain SERINE/THREONINE-PROTEIN KINASE WNK (WITH NO LYSINE)-RELATED (PTHR13902)	-0.39304	-2.47196	3.50E-08	-0.4087	-2.56274	1.41E-08
A_84_P140389	AT2G03505	glycosyl hydrolase family protein 17	-0.3909	-2.45978	4.37E-08	-0.5063	-3.20849	5.78E-11
A_84_P589734	AT1G13610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G30380.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15341.1); contains InterPro domain Alpha/beta hydrolase fold-1 (InterPro:IPR000073)	-0.39081	-2.45927	0.00197	-0.3636	-2.30994	0.00931
A_84_P15447	AT2G25980	jacalin lectin family protein	-0.39063	-2.45825	4.88E-08	-0.38206	-2.41025	9.14E-08
A_84_P12847	AT1G06120	fatty acid desaturase family protein	-0.39042	-2.45709	1.81E-07	-0.45744	-2.86709	5.35E-09
A_84_P23514	AT5G51500	pectinesterase family protein	-0.39028	-2.45629	3.83E-06	-0.55515	-3.59044	2.98E-07
A_84_P14475	AT1G30080	glycosyl hydrolase family 17 protein	-0.38903	-2.44924	1.70E-07	-0.40957	-2.56783	4.20E-08
A_84_P22215	AT3G49630	2-oxoacid-dependent oxidase, putative	-0.38884	-2.44816	0.00034	-0.58279	-3.82639	0.00235
A_84_P21863	AT1G50090	aminotransferase class IV family protein	-0.38555	-2.4297	0.00008	-0.42995	-2.69121	7.56E-06
A_84_P18059	AT1G22480	plastocyanin-like domain-containing protein	-0.38316	-2.41637	0.00001	-0.40789	-2.55793	7.48E-08
A_84_P14693	AT3G59750	receptor lectin kinase, putative	-0.38275	-2.41406	2.86E-06	-0.35655	-2.27274	1.04E-06
A_84_P763163	AT4G01770	RGXT1 (RHAMNOGALACTURONAN XYLOSYLTRANSFERASE 1); UDP-xylosyltransferase	-0.38101	-2.40441	0.00002	-0.4772	-3.00055	0.00016
A_84_P583210	AT4G33550	lipid binding	-0.38065	-2.40245	9.87E-08	-0.40024	-2.5133	2.34E-08
A_84_P187744	AT3G48300	CYP71A23 (cytochrome P450, family 71, subfamily A, polypeptide 23); oxygen binding	-0.37948	-2.39598	0.00004	-0.32579	-2.11735	0.00161
A_84_P825764	AT1G56240	no_match	-0.37579	-2.37567	0.00535	-0.3088	-2.03609	0.00034
A_84_P13250	AT1G52060	similar to jacalin lectin family protein [Arabidopsis thaliana] (TAIR:AT1G52070.1); similar to jasmonate inducible protein [Brassica napus] (GB:CAA72271.1); contains InterPro domain Mannose-binding lectin (InterPro:IPR001229)	-0.37466	-2.36951	1.16E-07	-0.57881	-3.79145	4.14E-11
A_84_P16823	AT1G01060	LHY (LATE ELONGATED HYPOCOTYL); DNA binding / transcription factor	-0.37458	-2.36908	1.03E-07	-0.53969	-3.46487	8.47E-12
A_84_P786039	AT3G49130	RNA binding	-0.37453	-2.36881	0.00092	-0.41674	-2.61062	3.94E-07
A_84_P14137	AT5G13170	nodulin MtN3 family protein	-0.37281	-2.35945	0.00285	-0.49624	-3.13504	9.13E-06
A_84_P12926	AT4G31870	ATGPX7 (GLUTATHIONE PEROXIDASE 7); glutathione peroxidase	-0.37155	-2.35261	2.66E-06	-0.79249	-6.2014	1.67E-15
A_84_P849853	AT1G67865	unknown protein	-0.37066	-2.3478	1.28E-07	-0.60814	-4.05644	2.56E-13
A_84_P822840	AT3G11340	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-0.37004	-2.34446	1.69E-07	-0.4285	-2.68222	4.95E-09
A_84_P21194	AT3G23240	ATERF1/ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	-0.36929	-2.34037	6.86E-07	-0.39557	-2.4864	4.21E-08
A_84_P159165	AT1G17030	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G47010.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G47010.1); similar to Os05g0272800 [Oryza sativa (japonica cultivar-group)] (GB:NP_001055066.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48013.1)	-0.36818	-2.33444	2.59E-07	-0.32305	-2.104	3.07E-06
A_84_P814936	AT4G30210	ATR2 (ARABIDOPSIS P450 REDUCTASE 2)	-0.368	-2.33346	2.02E-07	-0.40789	-2.55796	1.48E-08
A_84_P23770	AT1G48750; AT1G48760	[AT1G48750, protease inhibitor/seed storage/lipid transfer protein (LTP) family protein];[AT1G48760, DELTA-ADR (DELTA-ADAPTIN); clathrin binding]	-0.3671	-2.32863	1.58E-07	-0.32166	-2.09732	2.33E-06
A_84_P762464	AT3G25795	other RNA	-0.36652	-2.3255	0.00002	-0.54941	-3.54333	2.20E-10
A_84_P799181	AT1G05660	polygalacturonase, putative / pectinase, putative	-0.36488	-2.31675	0.00065	-0.44658	-2.79627	0.00622
A_84_P17584	AT1G17380	JAZ5/TIFY11A (JASMONATE-ZIM-DOMAIN PROTEIN 5)	-0.36375	-2.31072	0.00002	-0.47003	-2.95141	5.16E-10
A_84_P16770	AT5G04970	pectinesterase, putative	-0.36346	-2.3092	3.29E-07	-0.50391	-3.19091	5.73E-10
A_84_P18072	AT1G72520	lipoxygenase, putative	-0.36248	-2.30398	3.06E-07	-0.69179	-4.91807	6.03E-15
A_84_P790687	AT3G23470	cyclopropane-fatty-acyl-phospholipid synthase	-0.36246	-2.3039	1.33E-06	-0.67245	-4.70376	3.26E-12
A_84_P576362	AT1G13620	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G04025.1)	-0.35796	-2.28012	0.00002	-0.44964	-2.81602	2.86E-07
A_84_P18989	AT1G16420	ATMC8 (METACASPASE 8); caspase	-0.35688	-2.27449	3.43E-07	-0.54241	-3.48667	1.01E-11
A_84_P22880	AT1G31950	terpene synthase/cyclase family protein	-0.35394	-2.25911	6.81E-07	-0.60635	-4.03974	1.32E-12
A_84_P537901	AT4G28410	aminotransferase-related	-0.35231	-2.25064	6.12E-07	-0.37606	-2.37715	1.50E-07
A_84_P13758	AT3G62280	carboxylesterase	-0.35188	-2.24845	4.27E-07	-0.36243	-2.30374	2.36E-07
A_84_P15043	AT5G62340	invertase/pectin methylesterase inhibitor family protein	-0.34965	-2.2369	4.48E-07	-0.57362	-3.74648	1.43E-12
A_84_P595141	AT1G30135	JAZ8/TIFY5A (JASMONATE-ZIM-DOMAIN PROTEIN 8)	-0.34909	-2.23404	3.57E-06	-0.4651	-2.91809	5.80E-10
A_84_P834894	AT2G18550	ATHB21/HB-2 (homeobox-2); DNA binding / transcription factor	-0.34857	-2.23135	0.0002	-0.60386	-4.01665	1.49E-10
A_84_P789317	AT3G56275	pseudogene of unknown protein	-0.34852	-2.2311	5.64E-06	-0.47954	-3.01679	2.73E-10
A_84_P842669	AT1G29720	protein kinase family protein	-0.34826	-2.22979	5.64E-07	-0.38381	-2.42	6.83E-08
A_84_P18334	AT3G06490	MYB108 (MYB DOMAIN PROTEIN 108); DNA binding / transcription factor	-0.34485	-2.21235	3.10E-06	-0.39137	-2.46249	4.82E-08
A_84_P12725	AT3G28510	AAA-type ATPase family protein	-0.34453	-2.21069	1.97E-06	-0.69639	-4.97038	6.29E-15
A_84_P222749	AT4G33800	similar to hypothetical protein [Vitis vinifera] (GB:CAN66218.1)	-0.34445	-2.21031	0.0002	-0.35156	-2.24679	0.00001
A_84_P10265	AT5G48650	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RRM)-containing	-0.34336	-2.20474	1.15E-06	-0.34526	-2.21444	9.64E-07
A_84_P500468	AT3G29780	RALFL27 (RALF-LIKE 27)	-0.34253	-2.20052	7.04E-07	-0.33768	-2.17609	9.22E-07
A_84_P19611	AT5G05900	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-0.34236	-2.19967	1.74E-06	-0.43734	-2.7374	5.91E-09
A_84_P13407	AT1G18590	sulfotransferase family protein	-0.34209	-2.19833	7.00E-07	-0.35176	-2.24779	3.94E-07
A_84_P14595	AT3G20110	CYP705A20 (cytochrome P450, family 705, subfamily A, polypeptide 20); oxygen binding	-0.34048	-2.1902	8.02E-07	-0.57289	-3.74019	1.58E-12
A_84_P17815	AT5G45200	disease resistance protein (TIR-NBS-LRR class), putative	-0.34037	-2.18964	0.00002	-0.31683	-2.07411	0.00005
A_84_P592130	AT4G33905	peroxisomal membrane protein 22 kDa, putative	-0.33948	-2.18515	0.00231	-0.78514	-6.09731	4.47E-16
A_84_P501581	AT5G06080	LBD33 (LOB DOMAIN-CONTAINING PROTEIN 33)	-0.33862	-2.18083	0.00003	-0.33746	-2.17502	7.81E-06
A_84_P14195	AT1G52070	jacalin lectin family protein	-0.33796	-2.1775	8.97E-07	-0.38686	-2.43704	5.54E-08
A_84_P18818	AT5G60530	late embryogenesis abundant protein-related / LEA protein-related	-0.33764	-2.17589	9.28E-07	-0.34561	-2.2162	6.16E-07
A_84_P576622	AT2G32200	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32210.1); similar to unknown [Populus trichocarpa] (GB:ABK92801.1)	-0.3374	-2.17471	1.93E-06	-0.58886	-3.88026	6.69E-13
A_84_P11345	AT1G17750	leucine-rich repeat transmembrane protein kinase, putative	-0.33669	-2.17118	2.49E-06	-0.35177	-2.24788	4.92E-07
A_84_P857969	AT4G37430	CYP91A2 (CYTOCHROME P450 MONOOXYGENASE 91A2); oxygen binding	-0.33505	-2.16297	3.15E-06	-0.35059	-2.24175	7.76E-07
A_84_P831446	AT5G17780	hydrolase, alpha/beta fold family protein	-0.33459	-2.16069	1.64E-06	-0.30396	-2.01354	0.00001
A_84_P14013	AT5G40000	AAA-type ATPase family protein	-0.33419	-2.15869	0.00619	-0.39491	-2.48259	9.51E-08
A_84_P752277	AT1G66570; AT5G43610	[AT1G66570, ATSUC7 (SUCROSE-PROTON SYMPORTER 7); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen ion symporter];[AT5G43610, ATSUC6 (SUCROSE-PROTON SYMPORTER 6); carbohydrate transmembrane transporter/ sucrose:hydrogen symporter/ sugar:hydrogen ion symporter]	-0.33339	-2.15472	0.00147	-0.72212	-5.27374	6.98E-13

A_84_P19565	AT4G37430	CYP91A2 (CYTOCHROME P450 MONOOXYGENASE 91A2); oxygen binding	−0.33311	−2.15335	1.23E−06	−0.37235	−2.35695	1.18E−07
A_84_P545036	AT4G39795	senescence−associated protein−related	−0.33179	−2.14678	1.99E−06	−0.43183	−2.70289	3.93E−09
A_84_P10354	AT1G27940	PGP13 (P−GLYCOPROTEIN 13); ATPase, coupled to transmembrane movement of substances	−0.33021	−2.13899	0.00023	−0.53443	−3.42315	1.17E−10
A_84_P17762	AT5G23030	TET12 (TETRASPANIN12)	−0.33013	−2.13862	3.65E−06	−0.36087	−2.29547	3.40E−07
A_84_P802975	AT4G17340	DELTA−TIP2/TIP2;2 (tonoplast intrinsic protein 2;2); water channel	−0.33011	−2.13852	1.42E−06	−0.39129	−2.46201	3.76E−08
A_84_P10804	AT1G26770	ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A10)	−0.3295	−2.13549	1.49E−06	−0.31769	−2.07822	2.94E−06
A_84_P558829	AT2G29350	SAG13 (Senescence−associated gene 13); oxidoreductase	−0.32828	−2.12949	0.0072	−0.94742	−8.85967	1.53E−18
A_84_P831307	AT1G32450	proton−dependent oligopeptide transport (POT) family protein	−0.32817	−2.12896	3.25E−06	−0.31826	−2.08094	8.74E−06
A_84_P14717	AT4G01630	ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN A17)	−0.32781	−2.1272	1.75E−06	−0.35124	−2.24513	5.02E−07
A_84_P79425	AT5G20820	auxin−responsive protein−related	−0.32726	−2.1245	1.73E−06	−0.44297	−2.7731	1.84E−09
A_84_P19141	AT2G47460	ATMYB12/MYB12 (MYB DOMAIN PROTEIN 12); DNA binding / transcription activator/ transcription factor	−0.3269	−2.12273	1.89E−06	−0.61935	−4.16241	1.77E−13
A_84_P149248	AT1G21120	O−methyltransferase, putative	−0.32643	−2.12045	1.79E−06	−0.33306	−2.15307	1.20E−06
A_84_P787902	AT3G46250; AT3G46270	[AT3G46250, pseudogene, similar to leaf senescence−associated receptor−like protein kinase, serine/threonine−specific receptor protein kinase, Arabidopsis thaliana, PIR:S71277; blastp match of 31% identity and 2.8e−15 P−value to GP|9837280|gb|AAG00510.1||AF285172 leaf senescence−associated receptor−like protein kinase {Phaseolus vulgaris}];[AT3G46270, receptor protein kinase−related]	−0.32462	−2.11162	2.61E−06	−0.30891	−2.03662	5.89E−06
A_84_P22048	AT2G18550	ATHB21/HB−2 (homeobox−2); DNA binding / transcription factor	−0.32349	−2.10613	0.00001	−0.45251	−2.83471	3.49E−09
A_84_P762771	AT3G52561	unknown protein	−0.32342	−2.10583	0.00001	−0.401	−2.51769	7.95E−08
A_84_P150278	AT2G34610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G30190.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG12037.1)	−0.3234	−2.10573	3.48E−06	−0.53171	−3.4018	1.58E−11
A_84_P799508	AT1G02220	ANAC003 (Arabidopsis NAC domain containing protein 3); transcription factor	−0.32272	−2.10245	2.52E−06	−0.5255	−3.35352	1.90E−11
A_84_P857567	AT4G30170	peroxidase, putative	−0.32267	−2.10218	2.29E−06	−0.36815	−2.33427	1.67E−07
A_84_P182054	AT5G37690	GDSL−motif lipase/hydrolase family protein	−0.32181	−2.09804	2.34E−06	−0.33252	−2.15039	1.24E−06
A_84_P288500	AT3G47710	bHLH family protein	−0.32176	−2.09779	0.00015	−0.73142	−5.38786	7.14E−11
A_84_P21046	AT2G38600	acid phosphatase class B family protein	−0.32088	−2.09352	3.69E−06	−0.46383	−2.90958	6.05E−10
A_84_P22181	AT3G28210	PMZ; zinc ion binding	−0.32065	−2.09242	2.52E−06	−0.36445	−2.31446	1.86E−07
A_84_P230859	AT3G22550	senescence−associated protein−related	−0.32034	−2.09094	2.66E−06	−0.37308	−2.36091	1.16E−07
A_84_P869736	AT5G62165	AGL42 (AGAMOUS LIKE 42); transcription factor	−0.31861	−2.0826	0.00006	−0.51699	−3.28843	2.81E−10
A_84_P63350	AT1G29720	protein kinase family protein	−0.31584	−2.06938	4.91E−06	−0.4262	−2.66807	7.66E−09
A_84_P833808	AT1G17420	LOX3 (Lipoxygenase 3); iron ion binding / lipoxygenase/ metal ion binding / oxidoreductase, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of	−0.31582	−2.06926	3.42E−06	−0.58941	−3.88513	6.43E−13
A_84_P245475	AT2G25460	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04860.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN68625.1); contains InterPro domain C2 calcium−dependent membrane targeting (InterPro:IPR000008)	−0.31546	−2.06757	5.87E−06	−0.35003	−2.23887	4.68E−07
A_84_P76404	AT4G00080	UNE11 (unfertilized embryo sac 11); pectinesterase inhibitor	−0.31531	−2.06686	3.43E−06	−0.4378	−2.74029	2.48E−09
A_84_P22381	AT4G31320	auxin−responsive protein, putative / small auxin up RNA (SAUR_C)	−0.31527	−2.06665	4.47E−06	−0.36064	−2.29423	3.83E−07
A_84_P823058	AT3G04630	WDL1 (WVD2−LIKE 1)	−0.31453	−2.06314	5.73E−06	−0.31428	−2.06196	4.66E−06
A_84_P12677	AT3G23630	ATIPT7 (Arabidopsis thaliana isopentenyltransferase 7); transferase, transferring alkyl or aryl (other than methyl) groups	−0.31347	−2.05812	0.00029	−0.35999	−2.29084	0.00001
A_84_P10500	AT1G15640	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15620.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN70531.1)	−0.31286	−2.05525	0.00002	−0.46593	−2.92367	1.34E−09
A_84_P16270	AT1G33610	leucine−rich repeat family protein	−0.30896	−2.03684	0.00003	−0.42798	−2.67906	3.11E−06
A_84_P835471	AT2G34080	cysteine proteinase, putative	−0.30866	−2.03545	7.55E−06	−0.52284	−3.33304	3.79E−11
A_84_P543604	AT1G47400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G47395.1)	−0.30764	−2.03068	6.17E−06	−0.7919	−6.19301	1.51E−16
A_84_P23409	AT5G10130	pollen Ole e 1 allergen and extensin family protein	−0.30652	−2.02543	9.23E−06	−0.48864	−3.08063	8.20E−10
A_84_P22377	AT4G30430	TET9 (TETRASPANIN9)	−0.30613	−2.02362	0.00089	−0.3647	−2.31581	6.68E−07
A_84_P24008	AT3G04320	endopeptidase inhibitor	−0.30547	−2.02055	6.36E−06	−0.67486	−4.72997	1.54E−14
A_84_P557480	AT5G15725	unknown protein	−0.30505	−2.01858	0.00059	−0.61729	−4.1428	0.00001
A_84_P573814	AT1G59171	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G58936.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G58643.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G59312.1); contains InterPro domain Protein of unknown function DUF941 (InterPro:IPR009286)	−0.30431	−2.01518	0.00093	−0.33124	−2.14409	0.00008
A_84_P17313	AT2G37770	aldo/keto reductase family protein	−0.30411	−2.01423	6.59E−06	−0.61219	−4.09439	2.11E−13
A_84_P20772	AT5G04370	NAMT1; S−adenosylmethionine−dependent methyltransferase	−0.3036	−2.01185	0.00001	−0.3925	−2.46887	4.90E−08
A_84_P577990	AT5G44570	unknown protein	−0.30304	−2.00927	0.00176	−0.60065	−3.987	7.29E−13
A_84_P11789	AT3G43250	cell cycle control protein−related	−0.30265	−2.00749	0.00325	−0.42642	−2.66945	7.45E−09
A_84_P11200	AT5G45920	carboxylesterase	−0.30242	−2.00639	8.65E−06	−0.34905	−2.23385	5.45E−07
A_84_P567338	AT5G55570	heat shock protein binding / unfolded protein binding	−0.30104	−2.00005	0.00001	−0.42111	−2.63703	1.51E−08

Table S3. Pathway analysis of genes down-regulated in *ZTL*-overexpressors performed with the Gene Functional Classification Tool in DAVID Bioinformatics Resources 6.7.

Annotation Cluster 1: Enrichment Score: 7.660176315895672

Term	Count	%	PValue
flavonoid biosynthetic process	11	4.489796	1.21E-10
flavonoid metabolic process	11	4.489796	2.58E-10
phenylpropanoid metabolic process	15	6.122449	1.48E-09
secondary metabolic process	20	8.163265	5.99E-08
phenylpropanoid biosynthetic process	12	4.897959	7.54E-08
cellular amino acid derivative metabolic process	16	6.530612	1.74E-07
cellular amino acid derivative biosynthetic process	13	5.306122	6.96E-07
aromatic compound biosynthetic process	13	5.306122	2.06E-06

Annotation Cluster 2: Enrichment Score: 4.8640217871452025

Term	Count	%	PValue
flavonoid biosynthetic process	11	4.489796	1.21E-10
flavonoid metabolic process	11	4.489796	2.58E-10
anthocyanin biosynthetic process	4	1.632653	1.19E-04
anthocyanin metabolic process	4	1.632653	3.50E-04
pigment biosynthetic process	4	1.632653	0.059527
pigment metabolic process	4	1.632653	0.084623

Annotation Cluster 3: Enrichment Score: 3.577382072650882

Term	Count	%	PValue
response to endogenous stimulus	28	11.42857	1.70E-06
response to organic substance	31	12.65306	2.22E-06
response to ethylene stimulus	13	5.306122	1.23E-05
transcription	30	12.2449	5.08E-05
response to hormone stimulus	23	9.387755	1.33E-04
ethylene mediated signaling pathway	9	3.673469	3.55E-04
two-component signal transduction system (phosphorelay)	10	4.081633	4.01E-04
response to carbohydrate stimulus	9	3.673469	0.001003
cellular response to hormone stimulus	13	5.306122	0.001588
hormone-mediated signaling	13	5.306122	0.001588
regulation of transcription	35	14.28571	0.001967
intracellular signaling cascade	18	7.346939	0.002879
regulation of transcription, DNA-dependent	22	8.979592	0.003476
regulation of RNA metabolic process	22	8.979592	0.003706

Annotation Cluster 4: Enrichment Score: 3.2353612172106825

Term	Count	%	PValue
response to UV	7	2.857143	9.19E-05
response to light stimulus	15	6.122449	2.97E-04
response to radiation	15	6.122449	4.18E-04
response to abiotic stimulus	22	8.979592	0.010034

Annotation Cluster 5: Enrichment Score: 1.9675766001400188

Term	Count	%	PValue
regulation of anthocyanin biosynthetic process	3	1.22449	0.00442
regulation of flavonoid biosynthetic process	3	1.22449	0.008702
regulation of anthocyanin metabolic process	3	1.22449	0.009974
regulation of secondary metabolic process	3	1.22449	0.035145

Annotation Cluster 6: Enrichment Score: 1.7606299652332218

Term	Count	%	PValue
cell wall modification	7	2.857143	0.002615
external encapsulating structure organization	8	3.265306	0.030836
cell wall organization	7	2.857143	0.06481

Annotation Cluster 7: Enrichment Score: 1.1809446630620486

Term	Count	%	PValue
response to far red light	4	1.632653	0.010184
response to red light	3	1.22449	0.111796
response to red or far red light	4	1.632653	0.251675

Annotation Cluster 8: Enrichment Score: 0.7446376091400814

Term	Count	%	PValue
response to oxidative stress	8	3.265306	0.027992
response to reactive oxygen species	5	2.040816	0.055332
response to hydrogen peroxide	4	1.632653	0.117843
cellular response to reactive oxygen species	3	1.22449	0.253278
cellular response to oxidative stress	3	1.22449	0.257067
oxygen and reactive oxygen species metabolic process	3	1.22449	0.306275
response to inorganic substance	7	2.857143	0.476071
cellular response to stress	5	2.040816	0.637024

Annotation Cluster 9: Enrichment Score: 0.5391032334165797

Term	Count	%	PValue
organic acid biosynthetic process	8	3.265306	0.124756
carboxylic acid biosynthetic process	8	3.265306	0.124756
fatty acid biosynthetic process	4	1.632653	0.221805
cellular amino acid biosynthetic process	4	1.632653	0.290393
amine biosynthetic process	4	1.632653	0.346308
fatty acid metabolic process	4	1.632653	0.374193
lipid biosynthetic process	6	2.44898	0.418754
nitrogen compound biosynthetic process	4	1.632653	0.894487

Annotation Cluster 10: Enrichment Score: 0.37690502440290247

Term	Count	%	PValue
transmembrane receptor protein tyrosine kinase signaling pathwa	3	1.22449	0.384197
enzyme linked receptor protein signaling pathway	3	1.22449	0.384197
cell surface receptor linked signal transduction	3	1.22449	0.501393

Annotation Cluster 11: Enrichment Score: 0.21246079467630907

Term	Count	%	PValue
growth	4	1.632653	0.461355
cell growth	3	1.22449	0.645776
regulation of cell size	3	1.22449	0.675135
regulation of cellular component size	3	1.22449	0.702504

Annotation Cluster 12: Enrichment Score: 0.07072851963326712

Term	Count	%	PValue
flower development	3	1.22449	0.689065
reproductive structure development	6	2.44898	0.873657
reproductive developmental process	6	2.44898	0.920814
post-embryonic development	6	2.44898	0.9404

Annotation Cluster 13: Enrichment Score: 0.045019450030184975

Term	Count	%	PValue
protein amino acid phosphorylation	9	3.673469	0.860406
phosphate metabolic process	10	4.081633	0.91216
phosphorus metabolic process	10	4.081633	0.912609
phosphorylation	9	3.673469	0.92228

Table S4. Pathway analysis of genes up-regulated in *ZTL*-overexpressors performed with the Gene Functional Classification Tool in DAVID Bioinformatics Resources 6.7.

Annotation Cluster 1: Enrichment Score: 8.026434844463541

Term	Count	%	PValue
response to auxin stimulus	19	11.80124	4.03E-11
response to endogenous stimulus	26	16.14907	2.59E-08
response to hormone stimulus	25	15.52795	3.01E-08
response to organic substance	27	16.77019	2.49E-07

Annotation Cluster 2: Enrichment Score: 7.700409336795261

Term	Count	%	PValue
response to abiotic stimulus	31	19.25466	1.17E-09
response to temperature stimulus	17	10.55901	6.08E-09
response to cold	12	7.453416	1.11E-06

Annotation Cluster 3: Enrichment Score: 4.057457021955261

Term	Count	%	PValue
response to red or far red light	10	6.21118	4.39E-06
response to light stimulus	15	9.31677	7.73E-06
response to radiation	15	9.31677	1.13E-05
red or far red light signaling pathway	6	3.726708	1.06E-04
intracellular signaling cascade	10	6.21118	0.127068

Annotation Cluster 4: Enrichment Score: 3.005851716823043

Term	Count	%	PValue
response to red or far red light	10	6.21118	4.39E-06
response to red light	5	3.10559	7.57E-04
post-embryonic development	9	5.590062	0.288941

Annotation Cluster 5: Enrichment Score: 2.1461282184755133

Term	Count	%	PValue
circadian rhythm	6	3.726708	9.23E-06
rhythmic process	6	3.726708	2.88E-05
regulation of circadian rhythm	3	1.863354	0.006785
regulation of transcription	25	15.52795	0.010854
transcription	16	9.937888	0.056232
two-component signal transduction system (phosphorelay)	5	3.10559	0.077141
regulation of transcription, DNA-dependent	11	6.832298	0.279358
regulation of RNA metabolic process	11	6.832298	0.285047

Annotation Cluster 6: Enrichment Score: 1.4573214047782048

Term	Count	%	PValue
response to fungus	10	6.21118	0.004958
defense response	16	9.937888	0.008209
defense response to fungus	9	5.590062	0.009175
cell killing	4	2.484472	0.372049
killing of cells of another organism	4	2.484472	0.372049

Annotation Cluster 7: Enrichment Score: 1.2193856300758492

Term	Count	%	PValue
starch metabolic process	4	2.484472	0.001962
starch catabolic process	3	1.863354	0.003967
cellular polysaccharide catabolic process	3	1.863354	0.005289
glucan catabolic process	3	1.863354	0.0333
cellular glucan metabolic process	4	2.484472	0.063432
glucan metabolic process	4	2.484472	0.100167
polysaccharide catabolic process	3	1.863354	0.103065
cellular polysaccharide metabolic process	4	2.484472	0.104684
polysaccharide metabolic process	4	2.484472	0.218409

cellular carbohydrate catabolic process	3	1.863354	0.289049
carbohydrate catabolic process	3	1.863354	0.444369
macromolecule catabolic process	4	2.484472	0.883978

Annotation Cluster 8: Enrichment Score: 1.0067600602344602

Term	Count	%	PValue
systemic acquired resistance	3	1.863354	0.023041
defense response, incompatible interaction	4	2.484472	0.033789
innate immune response	4	2.484472	0.329742
immune response	4	2.484472	0.366024

Annotation Cluster 9: Enrichment Score: 0.3579734088771785

Term	Count	%	PValue
developmental growth involved in morphogenesis	3	1.863354	0.318941
unidimensional cell growth	3	1.863354	0.318941
developmental growth	3	1.863354	0.382969
cell morphogenesis	3	1.863354	0.454283
cell growth	3	1.863354	0.468965
regulation of cell size	3	1.863354	0.497622
cellular component morphogenesis	3	1.863354	0.509274
regulation of cellular component size	3	1.863354	0.525292
growth	3	1.863354	0.543169

Annotation Cluster 10: Enrichment Score: 0.35013923663701424

Term	Count	%	PValue
flower development	4	2.484472	0.24369
regulation of post-embryonic development	3	1.863354	0.286323
post-embryonic development	9	5.590062	0.288941
reproductive structure development	7	4.347826	0.452165
reproductive developmental process	7	4.347826	0.549398
seed development	3	1.863354	0.831547
fruit development	3	1.863354	0.850066

Annotation Cluster 11: Enrichment Score: 0.1271781828743214

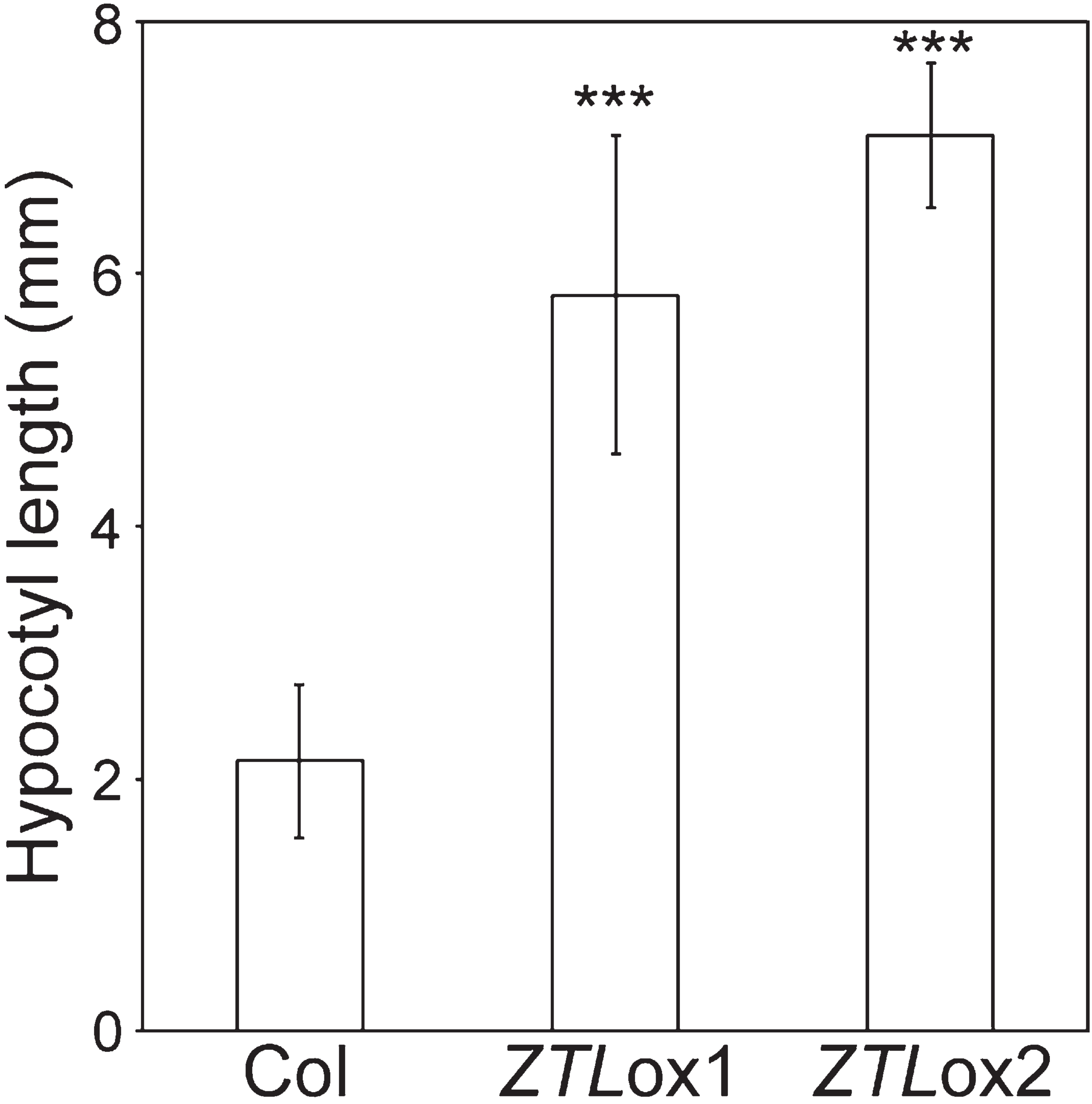
Term	Count	%	PValue
response to cadmium ion	3	1.863354	0.697609
response to inorganic substance	4	2.484472	0.764793
response to metal ion	3	1.863354	0.778591

Annotation Cluster 12: Enrichment Score: 0.06411649297992181

Term	Count	%	PValue
phosphate metabolic process	8	4.968944	0.838337
phosphorus metabolic process	8	4.968944	0.838929
phosphorylation	7	4.347826	0.874631
protein amino acid phosphorylation	6	3.726708	0.90067

Table S5. PCR primers used for expression analysis.

Genes	Forward sequence	Reverse sequence
ACT2	5’-GGTAACATTGTGCTCAGTGGTGG-3’	5’-AACGACCTTAATCTTCATGCTGC-3’
SAUR22	5’-CCTTCTTTCAAGCTCTGCTCAGT-3’	5’-TTGGAGCCGAGAAGTCACATT-3’
SAUR23	5’-AGTGTACGTAGGAGAGAGCCAGAA-3’	5’-ATCGGATGATCGAACCCAAA-3’
IAA29	5’-CTTCCAAGGGAAAGAGGGTGAC-3’	5’-TTCCGCAAAGATCTTCCATGTAAC-3’



Supplemental Figure S1. Hypocotyl length of *ZTL*-overexpressing (*ZTL*ox1 and *ZTL*ox2) and wild-type Columbia (Col) *Arabidopsis thaliana* seedlings. Seeds were incubated for 7 days in the dark on 1.5% (w/v) agar containing 1/2-basal-salt Murashige and Skoog medium at 4°C, and then exposed to continuous white light (80 $\mu mol \cdot m^{-2} \cdot s^{-1}$) for 8 days at 22°C. Error bars represent standard deviation (n = 15–16); ***$P < 0.001$ (Student's *t*-test) in comparison with wild-type Col.