A study on the mechanism of ZEITLUPE regulated hypocotyl elongation in *Arabidopsis thaliana*

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CONTENTS

Chapter 1

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

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 poly ubiquitination and subsequent degradation of two circadian clock proteins, TIMING OF CAB EXPRESSION1 (TOC1) (Mas 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 realtime 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 μmol・m−2・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* 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 μmol・m−2・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, Boblingen, 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 μg) 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 downregulated 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 downregulated 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).

We performed real-time quantitative reverse transcription PCR (qRT-PCR) to confirm the upregulation 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 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 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.

			ZTL ox1 vsCol1		*ZTL* ox2 vs Col2	
Array Element	Gene locus	Gene name	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	SAUR68	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

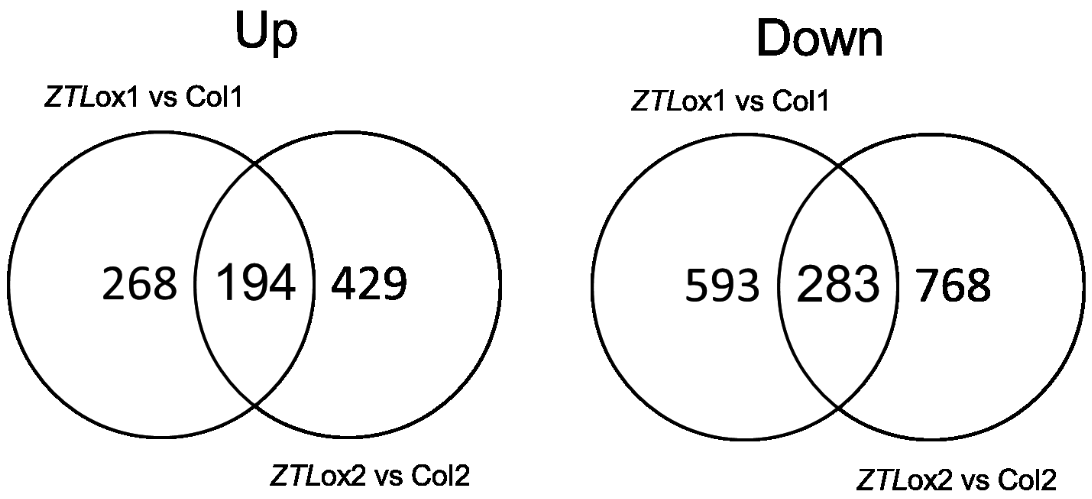


Figure 1. Venn diagrams showing the number of genes differentially expressed in *ZTL*-overexpressing seedlings (*ZTL*ox1 and *ZTL*ox2) in comparison with wild-type Columbia seedlings (Col1 and Col2). A total of 194 genes were up-regulated (fold change >2; p<0.01) in both *ZTL*-overexpressing lines in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

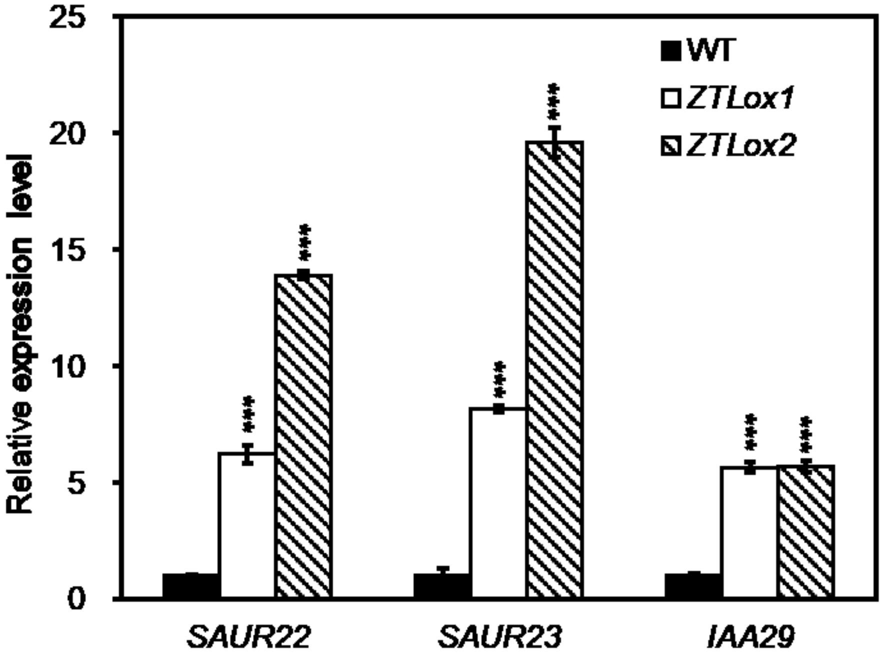


Figure 2. Expression of *SAUR22*, *SAUR23*, and *IAA29* in hypocotyls of wild-type Columbia (Col) and two *ZTL*-overexpressing seedlings (*ZTL*ox1 and *ZTL*ox2) quantified by real-time quantitative reverse transcription PCR. The expression levels were normalized by using the levels of actin transcript (*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.

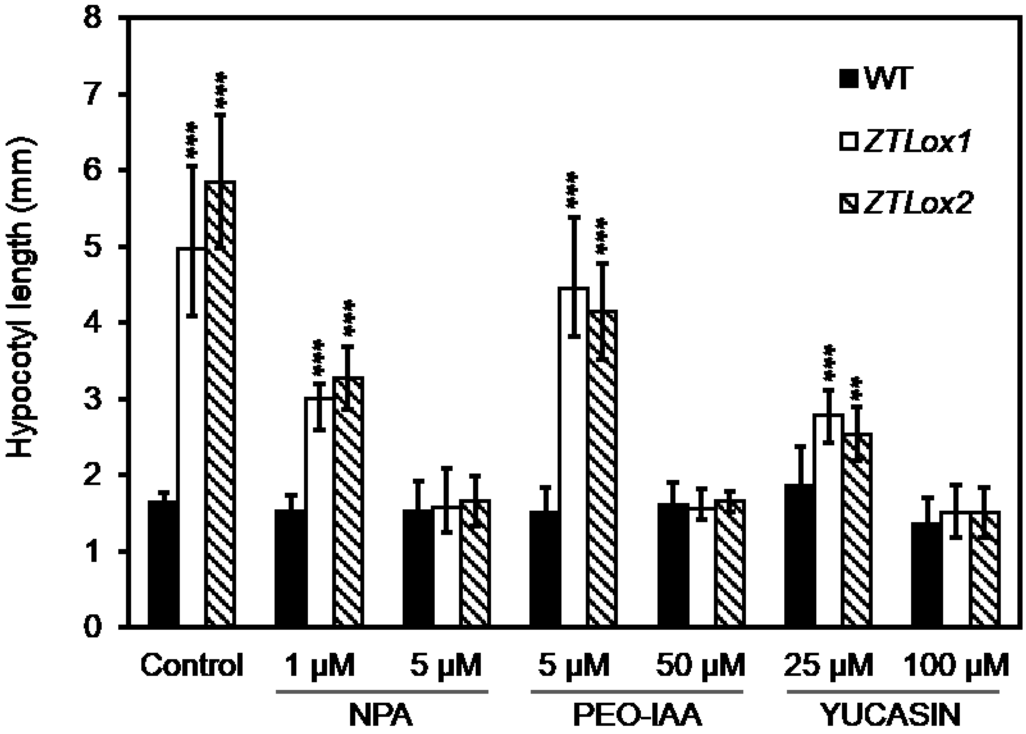


Figure 3. Inhibition of hypocotyl elongation by auxin inhibitors. Seedlings were grown under continuous white light for 8 days on 1.5% (w/v) agar containing 1/2-basal-salt Murashige and Skoog medium with 1% (v/v) dimethyl-sulfoxide (DMSO) in the absence or presence of indicated concentrations of N-1-naphthylphthalamic acid (NPA), α-(phenyl ethyl-2-one)-indole-3-acetic acid (PEO-IAA), or 5-(4-chlorophenyl)-4H-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.

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	8.88.E-22	1.420	26.280	1.71.E-18
A_84_P22137	AT3G19350	polyadenylate-binding protein-related / PABP-related	1.646	44.247	3.64.E-20	1.211	16.256	2.14.E-17
A_84_P23534	AT5G57360	ZTL (ZEITLUPE); ubiquitin-protein ligase	1.481	30.267	4.27.E-22	1.599	39.682	1.94.E-22
A_84_P562254	AT1G66060	binding	1.405	25.395	1.21.E-21	1.152	14.189	2.73.E-20
A_84_P10613	AT2G42530	COR15B	1.378	23.886	1.04.E-21	0.996	9.900	3.74.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 (PTHR13542)	1.360	22.912	2.47.E-20	1.621	41.786	4.27.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	5.32.E-18	1.158	14.403	2.12.E-17
A_84_P196694	AT5G44430	PDF1.2c (plant defensin 1.2c)	1.198	15.777	8.98.E-21	0.941	8.734	1.40.E-18
A_84_P23852	AT2G42540	COR15A (COLD-REGULATED 15A)	1.188	15.427	1.04.E-20	0.821	6.618	4.71.E-17
A_84_P239215	AT2G26010	PDF1.3 (plant defensin 1.3)	1.183	15.237	1.12.E-20	0.945	8.808	1.27.E-18
A_84_P592566	AT1G69470	unknown protein	1.149	14.080	7.85.E-10	1.051	11.233	5.39.E-08
A_84_P17513	AT3G55580	regulator of chromosome condensation (RCC1) family protein	1.058	11.419	8.29.E-19	0.660	4.573	1.55.E-13
A_84_P310613	AT2G26020	PDF1.2b (plant defensin 1.2b)	1.055	11.360	1.05.E-19	0.901	7.954	4.33.E-18
A_84_P196504	AT5G18010	SAUR19	1.013	10.296	4.25.E-19	0.946	8.822	1.98.E-18
A_84_P137009	AT5G44420	PDF1.2 (Low-molecular-weight cysteine-rich 77)	0.992	9.822	4.13.E-19	0.985	9.656	5.90.E-19
A_84_P50100	AT3G55240	Overexpression leads to PEL (Pseudo-Etiolation in Light) phenotype.	0.988	9.736	4.42.E-19	0.922	8.360	2.31.E-18
A_84_P767684	AT5G33395	transposable element gene	0.987	9.703	2.21.E-06	1.041	11.002	9.83.E-10
A_84_P757222	AT2G16367	Encodes a defensin-like (DEFL) family protein.	0.979	9.521	3.00.E-06	0.533	3.414	1.45.E-07
A_84_P20655	AT5G45830	DOG1 (DELAY OF GERMINATION 1)	0.976	9.466	1.13.E-18	0.733	5.407	3.23.E-15
A_84_P798436	AT1G80130	binding	0.941	8.726	1.42.E-18	0.856	7.177	1.54.E-17
A_84_P16114	AT1G09350	ATGOLS3 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 3); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	0.935	8.611	1.70.E-18	0.621	4.181	1.39.E-13
A_84_P20425	AT4G12480	pEARLI 1; lipid binding	0.921	8.333	2.40.E-18	1.001	10.012	3.39.E-19
A_84_P18533	AT4G12470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	0.910	8.135	3.18.E-18	0.942	8.746	1.40.E-18
A_84_P833384	AT5G45830	DOG1 (DELAY OF GERMINATION 1)	0.907	8.079	1.76.E-17	0.814	6.523	1.32.E-15
A_84_P761198	AT3G27283	Encodes a defensin-like (DEFL) family protein.	0.904	8.012	6.00.E-05	0.931	8.535	2.00.E-05
A_84_P22552	AT5G47130	Bax inhibitor-1 family / BI-1 family	0.889	7.752	5.45.E-16	0.959	9.100	1.75.E-14
A_84_P598557	AT5G57380	VIN3 (VERNALIZATION INSENSITIVE 3); protein binding / zinc ion bindin	0.884	7.657	1.30.E-04	0.817	6.554	8.40.E-04
A_84_P811782	AT2G31980	cysteine proteinase inhibitor-related	0.870	7.413	1.15.E-17	0.700	5.011	4.53.E-15
A_84_P23964	AT2G31980	cysteine proteinase inhibitor-related	0.864	7.311	1.25.E-17	0.721	5.265	1.78.E-15
A_84_P11230	AT5G54190	PORA (Protochlorophyllide reductase A); oxidoreductase/ protochlorophyllid	0.852	7.120	3.20.E-04	0.934	8.586	2.00.E-05
A_84_P167173	AT4G25480	DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription activator/ transcription factor	0.850	7.084	7.91.E-15	0.465	2.920	1.11.E-09
A_84_P141269	AT5G18050	SAUR22	0.818	6.573	6.53.E-17	1.027	10.643	2.37.E-19
A_84_P126821	AT2G46790	PRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription regulator	0.816	6.548	2.40.E-15	0.549	3.543	2.62.E-10
A_84_P96276	AT5G60100	PRR3 (PSEUDO-RESPONSE REGULATOR 3); transcription regulator	0.803	6.355	8.85.E-17	0.812	6.490	6.62.E-17
A_84_P94979	AT5G18060	SAUR23	0.786	6.105	2.64.E-16	0.859	7.226	2.49.E-17
A_84_P792258	AT4G01080	no_match	0.766	5.841	8.69.E-14	0.726	5.325	2.36.E-12
A_84_P15628	AT3G57240	BG3 (BETA-1,3-GLUCANASE 3); hydrolase, hydrolyzing O-glycosyl compou	0.760	5.756	1.22.E-14	0.427	2.675	1.00.E-05
A_84_P724799	AT1G67105	other RNA	0.754	5.678	5.23.E-16	0.499	3.155	8.61.E-11
A_84_P21826	AT1G10770	invertase/pectin methylesterase inhibitor family protein	0.753	5.659	2.47.E-15	0.789	6.146	6.46.E-16
A_84_P242573	AT5G54470	zinc finger (B-box type) family protein	0.752	5.649	3.97.E-15	0.647	4.433	1.00.E-13
A_84_P297344	AT5G23240 AT5G23235	[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 MSB8}]	0.730	5.366	1.27.E-15	0.608	4.059	2.57.E-13
A_84_P820553	AT5G02810	PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator	0.729	5.355	2.26.E-15	0.477	2.996	6.10.E-10
A_84_P21360	AT1G69570 AT1G69572	[AT1G69570, Dof-type zinc finger domain-containing protein];[AT1G69572,	0.711	5.139	2.71.E-15	0.406	2.547	1.59.E-08
A_84_P103016	AT4G12500	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	0.708	5.102	3.06.E-15	0.806	6.404	7.78.E-17
A_84_P766729	AT5G57340	similar to hypothetical protein MtrDRAFT_AC155282g59v2 [Medicago trunca	0.707	5.092	7.08.E-03	0.461	2.891	8.90.E-03
A_84_P11360	AT1G52040	MBP1 (MYROSINASE-BINDING PROTEIN 1)	0.703	5.049	4.79.E-15	0.468	2.935	5.00.E-10
A_84_P147028	AT5G18020	SAUR20	0.701	5.018	7.33.E-15	0.825	6.680	1.05.E-16
A_84_P21494	AT5G02810	PRR7 (PSEUDO-RESPONSE REGULATOR 7); transcription regulator	0.695	4.949	5.25.E-15	0.537	3.442	9.60.E-12

A_84_P15807	AT4G36450	ATMPK14 (MITOGEN-ACTIVATED PROTEIN KINASE 14); MAP kinase/ k	0.639	4.358	2.43.E-13	0.523	3.333	6.36.E-11
A_84_P18698	AT5G17320	HDG9 (HOMEODOMAIN GLABROUS9); DNA binding / sequence-specific DNA binding / transcription factor	0.632	4.281	4.20.E-08	0.375	2.373	1.50.E-04
A_84_P753024	AT1G67265	DVL3/RTFL21 (ROTUNDIFOLIA LIKE 21)	0.630	4.268	1.05.E-13	0.542	3.483	8.41.E-12
A_84_P848817	AT5G10760	aspartyl protease family protein	0.621	4.174	2.39.E-06	0.777	5.981	4.41.E-10
A_84_P162983	AT2G43010	PIF4 (PHYTOCHROME INTERACTING FACTOR 4); DNA binding / transcr	0.620	4.171	1.44.E-13	0.494	3.121	9.69.E-11
A_84_P291304	AT1G29395	COR414-TM1 (cold regulated 414 thylakoid membrane 1)	0.611	4.087	2.19.E-13	0.560	3.630	2.85.E-12
A_84_P15930	AT1G29460	SAUR65	0.607	4.043	4.03.E-13	0.609	4.066	5.71.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	8.80.E-04	0.750	5.617	1.30.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	3.44.E-13	0.548	3.531	6.29.E-12
A_84_P14898	AT5G10760	aspartyl protease family protein	0.601	3.992	2.02.E-12	0.738	5.467	3.46.E-15
A_84_P537376	AT1G29420	SAUR61	0.593	3.917	1.21.E-06	0.572	3.728	7.00.E-03
A_84_P16734	AT4G38850	SAUR15	0.590	3.890	1.47.E-10	0.652	4.487	4.67.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	9.16.E-12	0.520	3.314	4.74.E-11
A_84_P845206	AT1G06450	CCR4-NOT transcription complex protein, putative	0.578	3.784	2.15.E-06	0.597	3.951	5.51.E-08
A_84_P850999	AT1G20620	CAT3 (CATALASE 3); catalase	0.574	3.751	3.37.E-11	0.585	3.847	1.16.E-10
A_84_P12310	AT1G76960	unknown protein	0.572	3.734	3.76.E-12	0.378	2.387	1.10.E-07
A_84_P788781	AT1G09080	BIP3; ATP binding	0.571	3.727	1.10.E-04	0.558	3.611	2.20.E-04
A_84_P17660	AT4G33490	aspartic-type endopeptidase/ pepsin A	0.566	3.677	2.13.E-12	0.648	4.441	4.06.E-14
A_84_P769604	AT5G26146 AT5G26150	[AT5G26146, other RNA];[AT5G26150, protein kinase family protein]	0.557	3.607	8.40.E-08	0.374	2.365	8.00.E-05
A_84_P22010	AT2G45550	CYP76C4 (cytochrome P450, family 76, subfamily C, polypeptide 4); oxygen	0.554	3.578	8.53.E-03	0.478	3.005	3.19.E-03
A_84_P14823	AT4G33720	pathogenesis-related protein, putative	0.551	3.559	5.38.E-08	0.422	2.643	5.80.E-04
A_84_P12944	AT4G36110	SAUR9	0.549	3.540	2.60.E-03	0.345	2.212	1.96.E-03
A_84_P191914	AT2G21320	zinc finger (B-box type) family protein	0.541	3.479	1.52.E-08	0.413	2.591	8.53.E-06
A_84_P19525	AT4G27310	zinc finger (B-box type) family protein	0.539	3.457	8.70.E-12	0.372	2.354	1.20.E-07
A_84_P808697	AT2G05100	LHCB2.1 (Photosystem II light harvesting complex gene 2.1); chlorophyll bin	0.529	3.384	1.47.E-11	0.312	2.050	4.24.E-06
A_84_P17808	AT5G43440	2-oxoglutarate-dependent dioxygenase, putative	0.526	3.359	1.72.E-11	0.447	2.800	1.44.E-09
A_84_P826714	AT1G52000	jacalin lectin family protein	0.526	3.357	1.85.E-11	0.436	2.727	2.89.E-09
A_84_P185784	AT2G39920	acid phosphatase class B family protein	0.525	3.352	1.82.E-11	0.592	3.912	5.81.E-13
A_84_P19369	AT3G47500	CDF3 (CYCLING DOF FACTOR 3); DNA binding / protein binding / transcri	0.525	3.349	1.81.E-11	0.402	2.523	2.00.E-08
A_84_P10439	AT1G09080	BIP3; ATP binding	0.523	3.336	1.16.E-09	0.571	3.724	1.44.E-10
A_84_P150068	AT2G43140	DNA binding / transcription factor	0.515	3.271	3.42.E-11	0.364	2.311	2.79.E-07
A_84_P23654	AT1G52000	jacalin lectin family protein	0.511	3.241	3.92.E-11	0.515	3.271	3.16.E-11
A_84_P600468	AT1G20620	CAT3 (CATALASE 3); catalase	0.508	3.219	1.38.E-10	0.703	5.047	2.98.E-14
A_84_P861072	AT3G26740	CCL (CCR-LIKE)	0.502	3.175	6.39.E-11	0.619	4.162	1.50.E-13
A_84_P560548	AT2G01310	contains domain PTHR10177 (PTHR10177); contains domain PTHR10177:SF	0.502	3.174	2.64.E-08	0.312	2.052	4.60.E-04
A_84_P750244	AT1G69140	pseudogene, hypothetical protein	0.501	3.169	1.61.E-09	0.948	8.864	3.18.E-18
A_84_P13813	AT4G18650	transcription factor-related	0.499	3.153	4.41.E-06	0.702	5.031	3.38.E-13
A_84_P16781	AT1G06460	ACD32.1 (ALPHA-CRYSTALLIN DOMAIN 31.2)	0.488	3.073	1.42.E-10	0.516	3.284	2.86.E-11
A_84_P806842	AT3G26740	CCL (CCR-LIKE)	0.487	3.066	1.49.E-10	0.604	4.017	3.15.E-13
A_84_P761641	AT3G55734	MIR393B; miRNA	0.484	3.050	8.50.E-04	0.510	3.236	8.95.E-03
A_84_P100746	AT3G28220	meprin and TRAF homology domain-containing protein / MATH domain-con	0.483	3.044	1.77.E-10	0.577	3.778	1.18.E-12
A_84_P241663	AT3G58540	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06190.1)	0.482	3.033	3.37.E-09	0.360	2.289	2.16.E-06
A_84_P814968	AT1G06460	ACD32.1 (ALPHA-CRYSTALLIN DOMAIN 31.2)	0.479	3.012	2.31.E-10	0.546	3.513	5.98.E-12
A_84_P838362	AT2G43140	DNA binding / transcription factor	0.475	2.984	4.79.E-10	0.413	2.589	9.92.E-08
A_84_P21085	AT2G22980	SCPL13; serine carboxypeptidase	0.474	2.981	3.02.E-10	0.436	2.728	2.77.E-09
A_84_P19713	AT1G29450	SAUR64	0.474	2.980	3.56.E-10	0.656	4.532	4.19.E-14
A_84_P852921	AT3G26740	CCL (CCR-LIKE)	0.474	2.980	3.00.E-10	0.579	3.794	1.07.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	8.00.E-05	0.373	2.362	1.10.E-04
A_84_P758477	AT2G30424	DNA binding	0.473	2.971	3.24.E-10	0.586	3.852	7.89.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	2.00.E-05	0.436	2.730	3.00.E-05

A_84_P14029	AT5G44440	FAD-binding domain-containing protein	0.445	2.784	4.00.E-05	1.079	11.985	2.87.E-15
A_84_P132345	AT4G32340	binding	0.443	2.774	1.90.E-09	0.577	3.777	1.35.E-12
A_84_P14905	AT1G18350	ATMKK7 (MAP KINASE KINASE7); kinase	0.443	2.773	1.81.E-06	0.701	5.027	1.16.E-06
A_84_P20189	AT3G03830	SAUR28	0.441	2.757	1.82.E-08	0.323	2.104	4.00.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	5.87.E-09	0.482	3.037	7.02.E-10
A_84_P11569	AT2G40610	ATEXPA8 (ARABIDOPSIS THALIANA EXPANSIN A8)	0.439	2.746	3.15.E-09	0.596	3.944	2.44.E-12
A_84_P10923	AT3G62550	universal stress protein (USP) family protein	0.435	2.724	2.82.E-09	0.752	5.654	5.26.E-16
A_84_P819992	AT4G32340	binding	0.432	2.704	3.43.E-09	0.637	4.337	6.53.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	4.00.E-05	0.406	2.545	8.00.E-05
A_84_P542830	AT2G03310	unknown protein	0.431	2.695	4.32.E-09	0.458	2.870	1.12.E-09
A_84_P55550	AT4G32280	IAA29 (indoleacetic acid-induced protein 29); transcription factor	0.430	2.693	2.72.E-07	0.687	4.860	8.81.E-14
A_84_P188764	AT4G04330 AT4G04320	[AT4G04330, similar to unnamed protein product [Vitis vinifera] (GB:CAO69665.1)];[AT4G04320, malonyl-CoA decarboxylase family protein]	0.428	2.682	4.24.E-09	0.570	3.719	1.70.E-12
A_84_P806687	AT1G20620	CAT3 (CATALASE 3); catalase	0.428	2.678	4.49.E-09	0.806	6.404	8.25.E-17
A_84_P827080	AT4G04330	similar to unnamed protein product [Vitis vinifera] (GB:CAO69665.1)	0.426	2.669	5.13.E-09	0.561	3.636	3.20.E-12
A_84_P109442	AT3G52180	ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	0.424	2.653	5.56.E-09	0.515	3.272	3.14.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	1.70.E-08	0.497	3.140	3.17.E-09
A_84_P11207	AT1G29500	SAUR66	0.420	2.633	7.87.E-09	0.454	2.847	1.15.E-09
A_84_P591378	AT5G44565	unknown protein	0.419	2.624	7.73.E-09	0.392	2.468	3.66.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	9.49.E-08	0.314	2.062	3.00.E-05
A_84_P868153	AT1G73470	similar to unnamed protein product [Vitis vinifera] (GB:CAO68549.1)	0.417	2.615	8.00.E-09	0.396	2.491	2.80.E-08
A_84_P837093	AT1G14280	PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)	0.417	2.613	9.37.E-09	0.322	2.100	2.63.E-06
A_84_P18886	AT1G20620	CAT3 (CATALASE 3); catalase	0.416	2.608	8.60.E-09	0.701	5.020	4.04.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	9.33.E-09	0.504	3.193	5.70.E-11
A_84_P189624	AT1G70890	MLP43 (MLP-LIKE PROTEIN 43)	0.412	2.580	1.13.E-08	0.437	2.736	2.53.E-09
A_84_P785715	AT2G22540	SVP (SHORT VEGETATIVE PHASE); transcription factor	0.409	2.567	1.29.E-08	0.428	2.679	4.38.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	2.07.E-08	0.543	3.490	1.32.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	1.48.E-08	0.535	3.426	1.08.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	4.33.E-07	0.378	2.388	1.96.E-06
A_84_P816130	AT1G10070	ATBCAT-2; branched-chain-amino-acid transaminase/ catalytic	0.403	2.528	2.29.E-07	0.406	2.548	1.00.E-05
A_84_P12575	AT2G23030	SNRK2-9/SNRK2.9 (SNF1-RELATED PROTEIN KINASE 2.9); kinase	0.401	2.516	2.17.E-08	0.304	2.014	6.49.E-06
A_84_P839149	AT1G22770	GI (GIGANTEA); binding	0.401	2.515	2.76.E-08	0.538	3.453	1.60.E-11
A_84_P771152	AT1G20620	CAT3 (CATALASE 3); catalase	0.400	2.514	2.21.E-08	0.590	3.892	6.17.E-13
A_84_P23100	AT3G15570	phototropic-responsive NPH3 family protein	0.400	2.512	2.33.E-08	0.527	3.362	1.98.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	4.30.E-07	0.462	2.896	5.36.E-09
A_84_P787782	AT1G73470	no_match	0.399	2.505	3.07.E-08	0.388	2.446	5.99.E-08
A_84_P503493	AT5G49015	Expressed protein	0.398	2.502	2.50.E-08	0.331	2.142	1.37.E-06
A_84_P230339	AT2G22540	SVP (SHORT VEGETATIVE PHASE); transcription factor	0.398	2.499	2.56.E-08	0.424	2.655	5.44.E-09
A_84_P17680	AT4G38860	SAUR16	0.397	2.492	3.18.E-08	0.522	3.325	3.03.E-11
A_84_P16821	AT5G24470	PRR5 (PSEUDO-RESPONSE REGULATOR 5); transcription regulator	0.396	2.490	2.82.E-08	0.329	2.131	1.56.E-06
A_84_P852182	AT1G20620	CAT3 (CATALASE 3); catalase	0.395	2.484	3.02.E-08	0.783	6.073	1.72.E-16
A_84_P862359	AT3G52180	ATPTPKIS1/DSP4/SEX4 (STARCH-EXCESS 4); polysaccharide binding / protein tyrosine/serine/threonine phosphatase	0.395	2.482	3.18.E-08	0.542	3.487	7.54.E-12
A_84_P571542	AT4G12900	gamma interferon responsive lysosomal thiol reductase family protein / GILT	0.393	2.473	3.59.E-08	0.771	5.899	3.78.E-16
A_84_P195094	AT1G73470	similar to unnamed protein product [Vitis vinifera] (GB:CAO68549.1)	0.388	2.446	4.46.E-08	0.368	2.335	1.47.E-07
A_84_P867415	AT1G73470	similar to unnamed protein product [Vitis vinifera] (GB:CAO68549.1)	0.388	2.444	4.55.E-08	0.378	2.386	8.48.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	4.58.E-08	0.483	3.040	1.84.E-10
A_84_P19479	AT1G17460	TRFL3 (TRF-LIKE 3); DNA binding / transcription factor	0.387	2.439	5.60.E-08	0.462	2.899	8.83.E-10
A_84_P790487	AT5G44565	unknown protein	0.386	2.434	5.56.E-08	0.387	2.438	5.13.E-08
A_84_P20046	AT1G14280	PKS2 (PHYTOCHROME KINASE SUBSTRATE 2)	0.385	2.426	5.51.E-08	0.331	2.142	1.36.E-06

A_84_P806732	AT1G20620	CAT3 (CATALASE 3); catalase	0.375	2.369	1.01.E-07	0.760	5.751	4.00.E-16
A_84_P549629	AT5G58140	PHOT2 (NON PHOTOTROPIC HYPOCOTYL 1-LIKE); kinase	0.374	2.367	6.49.E-06	0.488	3.078	1.00.E-05
A_84_P23180	AT3G53800	armadillo/beta-catenin repeat family protein	0.374	2.365	1.07.E-07	0.639	4.351	6.45.E-14
A_84_P806759	AT1G20620	CAT3 (CATALASE 3); catalase	0.373	2.360	1.11.E-07	0.784	6.084	1.64.E-16
A_84_P20058	AT2G30420	myb family transcription factor	0.372	2.354	6.70.E-07	0.490	3.093	2.68.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	1.75.E-07	0.582	3.818	2.45.E-12
A_84_P22976	AT2G36270	ABI5 (ABA INSENSITIVE 5); DNA binding / transcription activator/ transcrip	0.371	2.351	1.76.E-07	0.398	2.502	4.34.E-08
A_84_P809730	AT5G14920	gibberellin-regulated family protein	0.371	2.348	1.34.E-07	0.747	5.587	7.96.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	3.08.E-07	0.333	2.154	1.87.E-06
A_84_P790043	AT3G07390	no_match	0.364	2.312	2.25.E-03	0.613	4.107	1.00.E-05
A_84_P21135	AT3G03820	SAUR29	0.364	2.311	4.74.E-07	0.903	8.002	5.41.E-16
A_84_P131456	AT5G14920	gibberellin-regulated family protein	0.362	2.302	2.14.E-07	0.703	5.042	3.74.E-15
A_84_P16857	AT5G41890	GDSL-motif lipase/hydrolase family protein	0.362	2.301	6.79.E-03	0.359	2.287	1.50.E-04
A_84_P279980	AT1G29440	SAUR63	0.360	2.291	2.64.E-07	0.474	2.979	3.62.E-10
A_84_P21864	AT1G73805	calmodulin binding	0.359	2.287	3.05.E-07	0.332	2.149	1.56.E-06
A_84_P811729	AT2G33830	dormancy/auxin associated family protein	0.357	2.275	2.90.E-07	0.469	2.944	4.05.E-10
A_84_P255590	AT4G23870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G11020.1)	0.355	2.266	3.24.E-07	0.325	2.114	1.93.E-06
A_84_P597910	AT1G68870	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G26210.1)	0.355	2.265	1.65.E-06	0.438	2.743	2.33.E-08
A_84_P750656	AT1G53160	SPL4 (SQUAMOSA PROMOTER BINDING PROTEIN-LIKE 4); DNA bindi	0.354	2.261	1.00.E-05	0.395	2.482	1.00.E-05
A_84_P789621	AT1G24148	other RNA	0.353	2.255	2.30.E-06	0.417	2.613	2.04.E-07
A_84_P768857	AT5G44572	unknown protein	0.353	2.252	3.76.E-07	0.443	2.773	1.81.E-09
A_84_P719823	AT1G11362	enzyme inhibitor/ pectinesterase	0.352	2.251	1.78.E-03	0.595	3.938	2.30.E-04
A_84_P839042	AT1G11925	Encodes a Stigma-specific Stig1 family protein	0.350	2.241	1.00.E-05	0.522	3.330	4.39.E-10
A_84_P22555	AT1G29510	SAUR68 (SMALL AUXIN UPREGULATED 68)	0.349	2.233	5.26.E-07	0.495	3.125	1.54.E-10
A_84_P825225	AT5G65080	AGL68/MAF5 (MADS AFFECTING FLOWERING 5); transcription factor	0.349	2.233	9.10.E-04	0.507	3.211	6.00.E-05
A_84_P16678	AT4G25420	GA5 (GA REQUIRING 5); gibberellin 20-oxidase/ gibberellin 3-beta-dioxygen	0.348	2.229	3.55.E-06	0.703	5.044	1.10.E-13
A_84_P814887	AT1G75900	family II extracellular lipase 3 (EXL3)	0.347	2.224	5.24.E-07	0.624	4.204	1.23.E-13
A_84_P811724	AT2G33830	dormancy/auxin associated family protein	0.347	2.223	5.22.E-07	0.420	2.628	7.04.E-09
A_84_P834622	AT1G02300	cathepsin B-like cysteine protease, putative	0.346	2.217	5.91.E-07	0.348	2.229	5.34.E-07
A_84_P765839	AT4G38825 AT4G38820	[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	7.26.E-07	1.021	10.498	3.28.E-16
A_84_P299810	AT1G11925	Encodes a Stigma-specific Stig1 family protein	0.345	2.215	1.42.E-06	0.466	2.925	9.75.E-10
A_84_P760471	AT3G23050	IAA7 (AUXIN RESISTANT 2)	0.345	2.212	1.65.E-06	0.313	2.055	9.12.E-06
A_84_P15583	AT3G46970	ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups	0.344	2.207	6.33.E-07	0.407	2.551	1.50.E-08
A_84_P844205	AT4G23160	protein kinase family protein	0.344	2.206	9.49.E-03	0.424	2.656	5.66.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	7.96.E-07	0.474	2.978	3.33.E-10
A_84_P838988	AT5G26570	PWD (PHOSPHOGLUCAN WATER DIKINASE); catalytic	0.337	2.173	1.68.E-06	0.402	2.525	5.41.E-08
A_84_P519104	AT3G25717	DVL6/RTFL16 (ROTUNDIFOLIA LIKE 16)	0.336	2.168	1.01.E-06	0.378	2.390	8.21.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	1.24.E-06	0.503	3.183	9.64.E-11
A_84_P148558	AT5G64490	binding	0.334	2.156	4.58.E-06	0.362	2.302	2.20.E-06
A_84_P235073	AT1G73870	zinc finger (B-box type) family protein	0.333	2.152	1.22.E-06	0.482	3.031	2.08.E-10
A_84_P17108	AT1G71000	DNAJ heat shock N-terminal domain-containing protein	0.333	2.151	8.89.E-03	0.693	4.930	1.45.E-14
A_84_P14446	AT2G19190	FRK1 (FLG22-INDUCED RECEPTOR-LIKE KINASE 1); kinase	0.330	2.136	1.80.E-06	0.359	2.285	3.25.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	2.00.E-05	0.544	3.498	8.71.E-09
A_84_P80689	AT5G62720	integral membrane HPP family protein	0.329	2.134	1.50.E-06	0.422	2.640	6.28.E-09
A_84_P577078	AT5G35480	unknown protein	0.327	2.123	1.73.E-06	0.419	2.623	7.73.E-09
A_84_P13568	AT2G33830	dormancy/auxin associated family protein	0.324	2.110	2.00.E-06	0.369	2.336	1.45.E-07
A_84_P115312	AT3G47860	apolipoprotein D-related	0.322	2.099	2.28.E-06	0.509	3.230	4.27.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	2.37.E-06	0.441	2.758	2.14.E-09
A_84_P23021	AT2G29090	CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2); oxyge	0.321	2.096	6.71.E-06	0.652	4.484	6.09.E-13
A_84_P289354	AT2G15890	MEE14 (maternal effect embryo arrest 14)	0.320	2.087	2.63.E-06	0.347	2.223	5.24.E-07
A_84_P555946	AT1G18265	contains InterPro domain Protein of unknown function DUF593 (InterPro:IP	0.319	2.083	3.00.E-05	0.350	2.240	1.00.E-05
A_84_P813465	AT2G15890	MEE14 (maternal effect embryo arrest 14)	0.318	2.079	2.90.E-06	0.323	2.104	2.15.E-06

A_84_P847330	AT3G46970	ATPHS2/PHS2 (ALPHA-GLUCAN PHOSPHORYLASE 2); phosphorylase/ transferase, transferring glycosyl groups	0.310	2.041	6.75.E-06	0.529	3.384	4.08.E-11
A_84_P761148	AT3G22886	MIR167A; miRNA	0.310	2.040	2.97.E-03	0.344	2.208	6.53.E-03
A_84_P802615	AT5G62360	invertase/pectin methylesterase inhibitor family protein	0.308	2.034	5.24.E-06	0.337	2.174	9.78.E-07
A_84_P847119	AT5G62360	invertase/pectin methylesterase inhibitor family protein	0.307	2.028	5.47.E-06	0.348	2.226	5.04.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	5.74.E-06	0.679	4.773	1.05.E-14
A_84_P13577	AT1G36940	unknown protein	0.304	2.014	6.58.E-06	0.350	2.238	4.43.E-07
A_84_P242433	AT3G25020	disease resistance family protein	0.304	2.013	2.00.E-05	0.398	2.503	3.05.E-07
A_84_P17881	AT5G62360	invertase/pectin methylesterase inhibitor family protein	0.304	2.012	6.69.E-06	0.312	2.050	4.14.E-06
A_84_P10257	AT1G29430	SAUR62	0.303	2.008	9.40.E-04	0.578	3.783	5.00.E-05
A_84_P103276	AT5G02160	unknown protein	0.301	2.001	7.69.E-06	0.430	2.693	3.78.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	-1.911	-81.456	1.73.E-22	-0.470	-2.951	1.40.E-07
A_84_P16501	AT3G13784	ATCWINV5 (ARABIDOPSIS THALIANA CELL WALL INVERTASE 5); hydrolase, hydrolyzing O-glycosyl compounds	-1.665	-46.188	4.43.E-21	-0.506	-3.208	2.20.E-04
A_84_P16247	AT1G12610	DDF1 (DWARF AND DELAYED FLOWERING 1); DNA binding / transcripti	-1.453	-28.380	1.46.E-18	-0.450	-2.815	1.87.E-09
A_84_P11439	AT1G52560	26.5 kDa class I small heat shock protein-like (HSP26.5-P)	-1.267	-18.504	3.09.E-19	-0.704	-5.059	6.98.E-14
A_84_P13966	AT5G14650	polygalacturonase, putative / pectinase, putative	-1.228	-16.917	7.52.E-14	-0.316	-2.070	4.66.E-03
A_84_P712672	AT3G15210	no_match	-1.133	-13.578	1.85.E-11	-0.387	-2.436	6.49.E-08
A_84_P842527	AT5G42800	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reducta	-1.082	-12.073	6.77.E-17	-0.571	-3.728	3.34.E-10
A_84_P233899	AT5G66780	similar to unknown [Ammopiptanthus mongolicus] (GB:AAW33981.1)	-0.981	-9.566	9.25.E-08	-0.867	-7.361	1.21.E-06
A_84_P507728	AT4G23496	SP1L5 (SPIRAL1-LIKE5)	-0.971	-9.356	2.29.E-18	-0.880	-7.580	2.25.E-17
A_84_P21851	AT1G66370	MYB113 (myb domain protein 113); DNA binding / transcription factor	-0.969	-9.317	1.73.E-07	-0.727	-5.332	3.61.E-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)]	-0.967	-9.272	1.10.E-09	-1.129	-13.460	4.53.E-11
A_84_P17055	AT1G65480	FT (FLOWERING LOCUS T)	-0.965	-9.221	1.99.E-07	-0.940	-8.704	1.16.E-06
A_84_P146938	AT1G02450	NIMIN-1/NIMIN1; protein binding	-0.945	-8.813	5.89.E-07	-0.724	-5.299	1.62.E-11
A_84_P20780	AT1G03940 AT1G03495	[AT1G03940, transferase family protein];[AT1G03495, transferase]	-0.935	-8.602	7.56.E-17	-0.559	-3.618	4.82.E-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)	-0.917	-8.261	1.18.E-07	-0.562	-3.643	2.57.E-03
A_84_P17806	AT5G42800	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reducta	-0.913	-8.193	3.10.E-18	-0.621	-4.175	1.46.E-13
A_84_P825539	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	-0.906	-8.049	3.68.E-06	-0.890	-7.766	2.61.E-15
A_84_P76184	AT5G24110	WRKY30 (WRKY DNA-binding protein 30); transcription factor	-0.904	-8.008	1.56.E-15	-1.194	-15.636	1.85.E-20
A_84_P15503	AT3G22830	AT-HSFA6B (Arabidopsis thaliana heat shock transcription factor A6B); DNA binding / transcription factor	-0.895	-7.846	1.75.E-11	-0.912	-8.170	1.84.E-15
A_84_P823530	AT1G19640	JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate	-0.875	-7.498	2.00.E-05	-1.149	-14.077	1.35.E-11
A_84_P173441	AT3G61920	similar to unnamed protein product [Vitis vinifera] (GB:CAO24317.1)	-0.874	-7.487	4.26.E-08	-0.304	-2.014	2.50.E-04
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)	-0.870	-7.415	2.00.E-05	-0.463	-2.903	9.24.E-06
A_84_P269530	AT3G29430	geranylgeranyl pyrophosphate synthase, putative / GGPP synthetase, putative / farnesyltranstransferase, putative	-0.866	-7.341	2.00.E-05	-0.904	-8.009	6.24.E-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)	-0.851	-7.098	8.45.E-07	-0.689	-4.885	4.74.E-03
A_84_P826417	AT5G24110	WRKY30 (WRKY DNA-binding protein 30); transcription factor	-0.848	-7.040	7.42.E-12	-1.112	-12.936	1.44.E-19
A_84_P23924	AT2G18150	peroxidase, putative	-0.839	-6.895	6.34.E-17	-0.383	-2.417	1.97.E-07
A_84_P13518	AT1G19640	JMT (JASMONIC ACID CARBOXYL METHYLTRANSFERASE); jasmonate	-0.836	-6.862	3.02.E-15	-1.145	-13.948	3.10.E-19
A_84_P16901	AT5G54060	UF3GT (UDP-GLUCOSE:FLAVONOID 3-O-GLUCOSYLTRANSFERASE); transferase, transferring glycosyl groups	-0.835	-6.835	1.31.E-16	-0.526	-3.358	3.06.E-11
A_84_P19609	AT5G05390	LAC12 (laccase 12); copper ion binding / oxidoreductase	-0.833	-6.808	3.12.E-16	-0.401	-2.520	2.47.E-08
A_84_P16488	AT3G20590	non-race specific disease resistance protein, putative	-0.829	-6.752	5.30.E-06	-0.731	-5.388	9.89.E-07
A_84_P189924	AT4G13280	ATTPS12/TPS12 (TERPENOID SYNTHASE12); cyclase	-0.827	-6.710	6.65.E-17	-0.493	-3.110	2.11.E-10
A_84_P544235	AT5G28237	tryptophan synthase, beta subunit, putative	-0.823	-6.649	1.00.E-04	-1.001	-10.012	4.05.E-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)	-0.814	-6.515	1.30.E-04	-0.353	-2.256	4.81.E-03
A_84_P12885	AT4G22880	LDOX (TANNIN DEFICIENT SEED 4)	-0.813	-6.505	3.26.E-16	-0.526	-3.354	4.45.E-11
A_84_P210018	AT4G10560	MEE53 (maternal effect embryo arrest 53); protein binding / zinc ion binding	-0.813	-6.503	8.00.E-05	-0.637	-4.330	5.60.E-04
A_84_P16037	AT1G56650	PAP1 (PRODUCTION OF ANTHOCYANIN PIGMENT 1); DNA binding / tra	-0.799	-6.291	1.50.E-14	-0.537	-3.445	1.18.E-11
A_84_P13969	AT5G17220	ATGSTF12 (GLUTATHIONE S-TRANSFERASE 26); glutathione transferase	-0.784	-6.081	1.82.E-16	-0.522	-3.329	2.18.E-11
A_84_P831728	AT5G17220	ATGSTF12 (GLUTATHIONE S-TRANSFERASE 26); glutathione transferase	-0.779	-6.012	8.20.E-15	-0.475	-2.982	1.79.E-09
A_84_P197194	AT4G22870	leucoanthocyanidin dioxygenase, putative / anthocyanidin synthase, putative	-0.777	-5.987	6.79.E-16	-0.505	-3.198	9.16.E-11
A_84_P790750	AT3G62990	no_match	-0.764	-5.813	1.29.E-07	-0.947	-8.844	1.24.E-10
A_84_P532079	AT1G47510	endonuclease/exonuclease/phosphatase family protein	-0.763	-5.800	2.16.E-11	-0.737	-5.457	1.29.E-15

A_84_P599083	AT3G42550	aspartyl protease family protein	-0.691	-4.910	5.20.E-03	-0.893	-7.822	8.65.E-06
A_84_P16077	AT1G05100	MAPKKK18 (Mitogen-activated protein kinase kinase kinase 18); kinase	-0.690	-4.896	6.30.E-12	-0.580	-3.801	1.72.E-12
A_84_P544251	AT5G38700	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G02170.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40081.1)	-0.690	-4.894	2.48.E-07	-0.506	-3.208	5.66.E-10
A_84_P563250	AT2G26400	ARD/ATARD3 (ACIREDUCTONE DIOXYGENASE); acireductone dioxygenase [iron(II)-requiring]/ heteroglycan binding / metal ion binding	-0.684	-4.829	1.00.E-14	-0.576	-3.764	1.48.E-12
A_84_P11109	AT5G07570	glycine/proline-rich protein	-0.683	-4.824	1.80.E-07	-0.578	-3.785	1.69.E-08
A_84_P20925	AT1G66550	WRKY67 (WRKY DNA-binding protein 67); transcription factor	-0.673	-4.712	7.86.E-03	-0.755	-5.690	9.75.E-15
A_84_P18113	AT1G76640	calmodulin-related protein, putative	-0.672	-4.699	3.69.E-11	-0.574	-3.751	1.65.E-12
A_84_P792228	AT3G22490	late embryogenesis abundant protein, putative / LEA protein, putative	-0.662	-4.588	2.46.E-03	-0.910	-8.137	3.09.E-08
A_84_P786320	AT5G35935	transposable element gene	-0.661	-4.585	4.53.E-14	-1.139	-13.770	5.68.E-20
A_84_P11217	AT5G50260	cysteine proteinase, putative	-0.659	-4.555	8.50.E-13	-0.420	-2.630	1.63.E-08
A_84_P22793	AT1G15610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G15630.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN70531.1)	-0.656	-4.526	2.11.E-07	-0.339	-2.181	4.42.E-06
A_84_P21945	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	-0.653	-4.503	6.38.E-07	-0.831	-6.771	1.74.E-15
A_84_P845171	AT5G42800	DFR (DIHYDROFLAVONOL 4-REDUCTASE); dihydrokaempferol 4-reducta	-0.640	-4.362	7.36.E-14	-0.567	-3.689	2.27.E-12
A_84_P258120	AT1G75830	LCR67/PDF1.1 (Low-molecular-weight cysteine-rich 67)	-0.635	-4.319	4.20.E-13	-0.926	-8.442	2.03.E-17
A_84_P831396	AT1G20310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76070.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN83887.1)	-0.635	-4.312	6.00.E-05	-0.444	-2.779	2.69.E-08
A_84_P13030	AT5G18910	protein kinase family protein	-0.624	-4.210	3.14.E-03	-0.405	-2.543	4.56.E-03
A_84_P67354	AT5G63580	flavonol synthase, putative	-0.621	-4.174	2.55.E-12	-0.566	-3.685	1.61.E-09
A_84_P13963	AT5G13930	ATCHS/CHS/TT4 (CHALCONE SYNTHASE); naringenin-chalcone synthase	-0.620	-4.172	1.43.E-13	-0.675	-4.727	1.22.E-14
A_84_P561097	AT5G46295	unknown protein	-0.619	-4.156	4.98.E-13	-0.824	-6.668	5.18.E-17
A_84_P181974	AT1G20310	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G76070.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN83887.1)	-0.614	-4.113	8.73.E-10	-0.417	-2.609	1.45.E-08
A_84_P17872	AT5G60520	late embryogenesis abundant protein-related / LEA protein-related	-0.612	-4.094	3.00.E-13	-0.520	-3.311	1.22.E-10
A_84_P848499	AT5G35935	transposable element gene	-0.606	-4.039	5.03.E-13	-1.204	-16.013	1.96.E-20
A_84_P16137	AT1G10530	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G60010.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO40951.1)	-0.602	-4.003	3.00.E-05	-0.402	-2.524	5.60.E-04
A_84_P11148	AT5G24080	protein kinase family protein	-0.600	-3.981	3.28.E-07	-0.788	-6.137	1.51.E-16
A_84_P11046	AT4G34410	AP2 domain-containing transcription factor, putative	-0.592	-3.907	1.93.E-10	-0.632	-4.283	8.96.E-14
A_84_P16282	AT2G43480	peroxidase, putative	-0.592	-3.906	1.00.E-06	-0.810	-6.456	4.16.E-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)	-0.589	-3.880	4.46.E-10	-0.463	-2.904	2.04.E-07
A_84_P11901	AT1G06100	fatty acid desaturase family protein	-0.588	-3.876	6.93.E-12	-0.607	-4.049	2.85.E-13
A_84_P18335	AT3G02480	ABA-responsive protein-related	-0.587	-3.866	2.15.E-12	-0.425	-2.662	5.77.E-09
A_84_P836925	AT5G35935	no_match	-0.583	-3.827	6.93.E-12	-1.155	-14.288	1.21.E-18
A_84_P16253	AT1G15460	ATBOR4/BOR4; anion exchanger	-0.581	-3.807	8.72.E-03	-0.479	-3.010	2.88.E-06
A_84_P23404	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen bind	-0.580	-3.805	1.11.E-12	-0.690	-4.893	7.24.E-15
A_84_P21760	AT1G03940	transferase family protein	-0.574	-3.747	1.27.E-07	-0.383	-2.417	1.00.E-05
A_84_P701336	AT2G42760	similar to unnamed protein product [Vitis vinifera] (GB:CAO69913.1)	-0.573	-3.742	8.30.E-04	-0.512	-3.250	1.60.E-04
A_84_P825767	AT1G56250	ATPP2-B14 (Phloem protein 2-B14); carbohydrate binding	-0.569	-3.705	1.46.E-06	-0.373	-2.359	1.74.E-06
A_84_P818529	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen bind	-0.567	-3.687	2.25.E-12	-0.694	-4.940	6.07.E-15
A_84_P761070	AT3G19184	DNA binding	-0.556	-3.595	7.06.E-09	-0.376	-2.375	7.00.E-05
A_84_P14146	AT1G56680	glycoside hydrolase family 19 protein	-0.555	-3.587	4.03.E-12	-0.525	-3.348	2.21.E-11
A_84_P594418	AT2G17660	nitrate-responsive NOI protein, putative	-0.554	-3.577	4.08.E-11	-0.367	-2.329	2.72.E-07
A_84_P19861	AT1G64480	CBL8 (CALCINEURIN B-LIKE PROTEIN 5)	-0.552	-3.564	8.03.E-07	-0.329	-2.135	3.00.E-05
A_84_P12863	AT4G13420	HAK5 (High affinity K+ transporter 5); potassium ion transmembrane transpo	-0.552	-3.563	1.23.E-11	-0.568	-3.698	3.10.E-12
A_84_P15944	AT5G50790	nodulin MtN3 family protein	-0.547	-3.525	2.36.E-11	-0.438	-2.741	1.21.E-07
A_84_P174401	AT4G16820	lipase class 3 family protein	-0.546	-3.518	1.58.E-08	-0.416	-2.605	1.58.E-08
A_84_P73804	AT5G62165	AGL42 (AGAMOUS LIKE 42); transcription factor	-0.543	-3.495	2.49.E-10	-0.658	-4.552	1.07.E-13
A_84_P19294	AT1G26380	FAD-binding domain-containing protein	-0.541	-3.475	1.26.E-11	-0.961	-9.147	8.99.E-19
A_84_P100606	AT1G02810	pectinesterase family protein	-0.539	-3.456	9.63.E-12	-0.356	-2.271	3.12.E-07
A_84_P607864	AT3G02885	GASA5 (GAST1 PROTEIN HOMOLOG 5)	-0.537	-3.445	1.35.E-11	-0.326	-2.117	2.83.E-06
A_84_P818534	AT5G07990	TT7 (TRANSPARENT TESTA 7); flavonoid 3'-monooxygenase/ oxygen bind	-0.536	-3.438	2.28.E-06	-1.094	-12.415	2.96.E-10
A_84_P12815	AT3G62760	ATGSTF13 (Arabidopsis thaliana Glutathione S-transferase (class phi) 13); gl	-0.536	-3.433	3.16.E-11	-0.465	-2.920	2.42.E-09
A_84_P11248	AT5G59220	protein phosphatase 2C, putative / PP2C, putative	-0.533	-3.414	9.01.E-11	-0.496	-3.135	9.22.E-11
A_84_P824281	AT1G66700	PXMT1; S-adenosylmethionine-dependent methyltransferase	-0.527	-3.368	1.61.E-08	-1.318	-20.801	2.24.E-21
A_84_P10627	AT2G20880	AP2 domain-containing transcription factor, putative	-0.527	-3.362	2.96.E-06	-0.588	-3.871	7.99.E-13
A_84_P573393	AT4G27654	unknown protein	-0.524	-3.343	1.56.E-10	-0.421	-2.635	6.69.E-09
A_84_P12058	AT5G08640	FLS (FLAVONOL SYNTHASE)	-0.517	-3.289	2.78.E-11	-0.662	-4.593	2.12.E-14
A_84_P790512	AT1G22460	no_match	-0.516	-3.284	3.50.E-04	-0.791	-6.182	3.00.E-05
A_84_P760622	AT3G56275	pseudogene of unknown protein	-0.512	-3.253	7.29.E-09	-0.447	-2.800	1.87.E-09
A_84_P17724	AT5G07190	ATS3 (ARABIDOPSIS THALIANA SEED GENE 3)	-0.510	-3.235	5.71.E-08	-0.778	-5.998	2.08.E-09
A_84_P17423	AT3G26610	polygalacturonase, putative / pectinase, putative	-0.507	-3.216	7.02.E-11	-0.312	-2.049	6.36.E-06

A_84_P833880	AT1G54890	late embryogenesis abundant protein-related / LEA protein-related	-0.479	-3.012	2.34.E-09	-0.827	-6.719	1.09.E-13
A_84_P231939	AT1G61800	GPT2 (glucose-6-phosphate/phosphate translocator 2); antiporter/ glucose-6-phosphate transmembrane transporter	-0.479	-3.010	6.35.E-10	-1.046	-11.127	1.35.E-19
A_84_P19271	AT3G09680	40S ribosomal protein S23 (RPS23A)	-0.478	-3.004	4.00.E-05	-0.367	-2.329	9.97.E-03
A_84_P12766	AT3G51240 AT3G51238	[AT3G51240, F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase];[	-0.477	-3.000	2.55.E-10	-0.703	-5.045	3.71.E-15
A_84_P23972	AT2G23630	SKS16 (SKU5 Similar 16); copper ion binding / pectinesterase	-0.475	-2.988	4.07.E-10	-0.409	-2.567	3.15.E-08
A_84_P521598	AT2G22760	basic helix-loop-helix (bHLH) family protein	-0.475	-2.983	5.34.E-07	-0.383	-2.417	7.17.E-08
A_84_P828648	AT2G34020	calcium ion binding	-0.474	-2.976	4.32.E-10	-0.480	-3.023	3.12.E-10
A_84_P525365	AT3G57500	similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:A	-0.474	-2.976	1.12.E-09	-0.307	-2.027	9.37.E-06
A_84_P13764	AT3G44830	lecithin:cholesterol acyltransferase family protein / LACT family protein	-0.473	-2.973	3.20.E-04	-1.062	-11.544	3.13.E-18
A_84_P255680	AT5G05960	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-0.472	-2.967	3.34.E-10	-0.329	-2.135	1.48.E-06
A_84_P149258	AT2G23050	phototropic-responsive NPH3 family protein	-0.472	-2.962	4.42.E-10	-0.446	-2.792	2.07.E-09
A_84_P292024	AT4G03292	nucleic acid binding	-0.471	-2.958	8.68.E-07	-0.309	-2.037	1.50.E-03
A_84_P59930	AT1G15150	MATE efflux family protein	-0.470	-2.953	4.84.E-08	-0.328	-2.130	4.00.E-05
A_84_P15222	AT1G65060	4CL3 (4-coumarate:CoA ligase 3); 4-coumarate-CoA ligase	-0.469	-2.945	4.34.E-10	-0.506	-3.207	5.39.E-11
A_84_P11143	AT5G22570	WRKY38 (WRKY DNA-binding protein 38); transcription factor	-0.469	-2.941	7.21.E-09	-0.641	-4.380	1.01.E-13
A_84_P19175	AT2G19050	GDSL-motif lipase/hydrolase family protein	-0.468	-2.937	1.00.E-05	-0.510	-3.237	2.96.E-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)	-0.467	-2.933	8.66.E-10	-0.660	-4.570	1.55.E-09
A_84_P513731	AT3G12955	auxin-responsive protein-related	-0.466	-2.926	6.33.E-09	-0.514	-3.264	7.04.E-10
A_84_P20248	AT3G23230	ethylene-responsive factor, putative	-0.466	-2.925	2.29.E-06	-0.768	-5.864	2.66.E-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)	-0.465	-2.919	1.00.E-08	-0.322	-2.097	5.00.E-05
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)	-0.464	-2.912	3.00.E-05	-0.359	-2.284	1.00.E-04
A_84_P807539	AT3G51240 AT3G51238	[AT3G51240, F3H (TRANSPARENT TESTA 6); naringenin 3-dioxygenase];[	-0.463	-2.904	6.28.E-10	-0.708	-5.100	3.35.E-15
A_84_P762507	AT3G25573	unknown protein	-0.463	-2.903	1.30.E-04	-0.937	-8.641	1.42.E-17
A_84_P840120	AT3G62990	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G47950.1)	-0.462	-2.900	1.29.E-07	-1.104	-12.715	1.49.E-15
A_84_P22732	AT1G08860	BON3 (BONZAI 3)	-0.462	-2.896	1.16.E-03	-0.739	-5.481	4.84.E-12
A_84_P23604	AT1G54890	late embryogenesis abundant protein-related / LEA protein-related	-0.462	-2.895	6.31.E-10	-0.721	-5.256	1.95.E-15
A_84_P15083	AT5G19520	mechanosensitive ion channel domain-containing protein / MS ion channel domain-containing protein	-0.460	-2.884	7.06.E-10	-0.460	-2.882	7.28.E-10
A_84_P23103	AT3G14940	ATPPC3 (PHOSPHOENOLPYRUVATE CARBOXYLASE 3); phosphoenolpy	-0.460	-2.884	6.77.E-10	-0.460	-2.887	6.57.E-10
A_84_P824903	AT5G22460	esterase/lipase/thioesterase family protein	-0.453	-2.840	4.14.E-09	-0.337	-2.175	3.58.E-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)	-0.453	-2.838	5.34.E-07	-0.465	-2.920	2.93.E-09
A_84_P12272	AT2G04025	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G13620.1)	-0.449	-2.811	5.71.E-08	-0.476	-2.993	1.08.E-07
A_84_P22110	AT3G08770	LTP6 (Lipid transfer protein 6); lipid binding	-0.448	-2.805	1.36.E-09	-0.343	-2.203	6.65.E-07
A_84_P14597	AT3G30460	zinc finger (C3HC4-type RING finger) family protein	-0.447	-2.802	6.56.E-06	-0.364	-2.311	6.90.E-04
A_84_P827147	AT1G61800	GPT2 (glucose-6-phosphate/phosphate translocator 2); antiporter/ glucose-6-phosphate transmembrane transporter	-0.446	-2.792	8.51.E-08	-1.078	-11.967	1.00.E-19
A_84_P13934	AT5G05270	chalcone-flavanone isomerase family protein	-0.443	-2.773	1.84.E-09	-0.563	-3.657	2.47.E-12
A_84_P23070	AT3G22740	HMT3 (Homocysteine S-methyltransferase 3); homocysteine S-methyltransfera	-0.443	-2.773	1.90.E-09	-0.326	-2.118	1.83.E-06
A_84_P19749	AT5G57090	EIR1 (ETHYLENE INSENSITIVE ROOT 1); auxin:hydrogen symporter/ trans	-0.442	-2.769	7.31.E-09	-0.450	-2.820	9.43.E-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)	-0.441	-2.758	1.89.E-07	-0.314	-2.060	3.20.E-04
A_84_P18422	AT1G48470	GLN1;5 (GLUTAMINE SYNTHETASE 1;5); glutamate-ammonia ligase	-0.441	-2.758	8.78.E-03	-0.453	-2.838	4.00.E-05
A_84_P19131	AT2G23910	cinnamoyl-CoA reductase-related	-0.440	-2.756	4.23.E-09	-0.453	-2.840	1.50.E-09
A_84_P752662	AT1G12064	similar to hypothetical protein [Vitis vinifera] (GB:CAN77938.1)	-0.438	-2.743	3.40.E-04	-0.465	-2.915	6.90.E-04
A_84_P10202	AT5G24070	peroxidase family protein	-0.438	-2.742	1.84.E-08	-0.349	-2.236	6.03.E-06
A_84_P13172	AT5G67080	MAPKKK19 (Mitogen-activated protein kinase kinase kinase 19); kinase	-0.435	-2.725	4.35.E-09	-0.648	-4.448	4.11.E-14
A_84_P845967	AT5G22570	WRKY38 (WRKY DNA-binding protein 38); transcription factor	-0.435	-2.723	4.21.E-09	-0.661	-4.581	2.44.E-14
A_84_P22742	AT1G10400	UDP-glycosyltransferase/ transferase, transferring glycosyl groups	-0.432	-2.706	1.25.E-08	-0.467	-2.930	2.28.E-09
A_84_P503304	AT4G25860	oxysterol-binding family protein	-0.432	-2.702	6.87.E-06	-0.310	-2.042	2.10.E-04
A_84_P18104	AT1G74500	bHLH family protein	-0.431	-2.700	6.67.E-09	-0.595	-3.939	1.37.E-12

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)	-0.419	-2.625	6.50.E-04	-0.373	-2.360	4.00.E-05
A_84_P612389	AT3G24240	leucine-rich repeat transmembrane protein kinase, putative	-0.417	-2.615	2.33.E-08	-0.321	-2.095	4.76.E-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)	-0.417	-2.612	1.58.E-07	-0.325	-2.111	8.15.E-06
A_84_P11239	AT5G56840	DNA-binding family protein	-0.417	-2.611	9.68.E-09	-0.512	-3.253	4.13.E-11
A_84_P16071	AT1G33750	terpene synthase/cyclase family protein	-0.416	-2.605	2.06.E-08	-0.400	-2.514	6.72.E-08
A_84_P188424	AT5G15800	SEP1 (SEPALLATA1); DNA binding / transcription factor	-0.415	-2.601	5.89.E-03	-0.672	-4.696	9.00.E-04
A_84_P17163	AT1G73160	glycosyl transferase family 1 protein	-0.415	-2.598	4.06.E-07	-0.515	-3.271	3.81.E-08
A_84_P96556	AT1G19900	glyoxal oxidase-related	-0.414	-2.594	1.14.E-08	-0.331	-2.144	1.40.E-06
A_84_P19702	AT5G44110	POP1	-0.414	-2.593	1.01.E-08	-0.545	-3.506	6.44.E-12
A_84_P521593	AT2G20515	similar to unnamed protein product [Vitis vinifera] (GB:CAO40634.1)	-0.411	-2.575	1.44.E-08	-0.352	-2.251	4.83.E-07
A_84_P839599	AT1G73160	glycosyl transferase family 1 protein	-0.411	-2.574	3.61.E-08	-0.477	-3.001	1.72.E-09
A_84_P18265	AT2G18480	mannitol transporter, putative	-0.410	-2.570	2.28.E-08	-0.315	-2.065	4.75.E-06
A_84_P11446	AT1G15520	ATPDR12/PDR12 (PLEIOTROPIC DRUG RESISTANCE 12); ATPase, coupled to transmembrane movement of substances	-0.407	-2.551	1.59.E-08	-1.184	-15.280	1.11.E-20
A_84_P101676	AT4G14980	DC1 domain-containing protein	-0.406	-2.547	9.09.E-07	-0.351	-2.242	1.10.E-04
A_84_P817725	AT1G78140	methyltransferase-related	-0.405	-2.544	2.66.E-03	-0.841	-6.935	6.00.E-05
A_84_P755918	AT2G34020	calcium ion binding	-0.405	-2.539	5.46.E-08	-0.400	-2.512	8.66.E-08
A_84_P579358	AT3G01516	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G14690.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO14758.1)	-0.403	-2.530	2.57.E-08	-0.444	-2.777	2.89.E-09
A_84_P11919	AT4G13620	AP2 domain-containing transcription factor, putative	-0.403	-2.530	1.56.E-07	-0.611	-4.086	2.95.E-12
A_84_P566998	AT3G49540	unknown protein	-0.402	-2.523	5.00.E-05	-0.674	-4.721	2.49.E-11
A_84_P14242	AT1G79330	AMC6/ATMC5/ATMCP2B (TYPE-II METACASPASES); caspase/ cysteine-ty	-0.401	-2.518	2.00.E-05	-0.321	-2.096	3.00.E-05
A_84_P10297	AT5G57980	eukaryotic rpb5 RNA polymerase subunit family protein	-0.401	-2.515	8.19.E-08	-0.476	-2.989	4.15.E-09
A_84_P24148	AT3G59010	pectinesterase family protein	-0.397	-2.495	2.87.E-08	-0.399	-2.508	2.36.E-08
A_84_P13060	AT5G37800	basic helix-loop-helix (bHLH) family protein	-0.394	-2.478	1.60.E-04	-0.323	-2.105	9.84.E-03
A_84_P511862	AT2G32550	rcd1-like cell differentiation family protein	-0.393	-2.474	3.43.E-06	-0.419	-2.622	4.59.E-07
A_84_P513890	AT4G11780	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G23020.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN60407.1)	-0.393	-2.473	3.78.E-07	-0.731	-5.387	7.71.E-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)	-0.393	-2.472	3.50.E-08	-0.409	-2.563	1.41.E-08
A_84_P140389	AT2G03505	glycosyl hydrolase family protein 17	-0.391	-2.460	4.37.E-08	-0.506	-3.208	5.78.E-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)	-0.391	-2.459	1.97.E-03	-0.364	-2.310	9.31.E-03
A_84_P15447	AT2G25980	jacalin lectin family protein	-0.391	-2.458	4.88.E-08	-0.382	-2.410	9.14.E-08
A_84_P12847	AT1G06120	fatty acid desaturase family protein	-0.390	-2.457	1.81.E-07	-0.457	-2.867	5.35.E-09
A_84_P23514	AT5G51500	pectinesterase family protein	-0.390	-2.456	3.83.E-06	-0.555	-3.590	2.98.E-07
A_84_P14475	AT1G30080	glycosyl hydrolase family 17 protein	-0.389	-2.449	1.70.E-07	-0.410	-2.568	4.20.E-08
A_84_P22215	AT3G49630	2-oxoacid-dependent oxidase, putative	-0.389	-2.448	3.40.E-04	-0.583	-3.826	2.35.E-03
A_84_P21863	AT1G50090	aminotransferase class IV family protein	-0.386	-2.430	8.00.E-05	-0.430	-2.691	7.56.E-06
A_84_P18059	AT1G22480	plastocyanin-like domain-containing protein	-0.383	-2.416	1.00.E-05	-0.408	-2.558	7.48.E-08
A_84_P14693	AT3G59750	receptor lectin kinase, putative	-0.383	-2.414	2.86.E-06	-0.357	-2.273	1.04.E-06
A_84_P763163	AT4G01770	RGXT1 (RHAMNOGALACTURONAN XYLOSYLTRANSFERASE 1); UDP-	-0.381	-2.404	2.00.E-05	-0.477	-3.001	1.60.E-04
A_84_P583210	AT4G33550	lipid binding	-0.381	-2.402	9.87.E-08	-0.400	-2.513	2.34.E-08
A_84_P187744	AT3G48300	CYP71A23 (cytochrome P450, family 71, subfamily A, polypeptide 23); oxyge	-0.379	-2.396	4.00.E-05	-0.326	-2.117	1.61.E-03
A_84_P825764	AT1G56240	no_match	-0.376	-2.376	5.35.E-03	-0.309	-2.036	3.40.E-04
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)	-0.375	-2.370	1.16.E-07	-0.579	-3.791	4.14.E-11
A_84_P16823	AT1G01060	LHY (LATE ELONGATED HYPOCOTYL); DNA binding / transcription facto	-0.375	-2.369	1.03.E-07	-0.540	-3.465	8.47.E-12
A_84_P786039	AT3G49130	RNA binding	-0.375	-2.369	9.20.E-04	-0.417	-2.611	3.94.E-07
A_84_P14137	AT5G13170	nodulin MtN3 family protein	-0.373	-2.359	2.85.E-03	-0.496	-3.135	9.13.E-06
A_84_P12926	AT4G31870	ATGPX7 (GLUTATHIONE PEROXIDASE 7); glutathione peroxidase	-0.372	-2.353	2.66.E-06	-0.792	-6.201	1.67.E-15
A_84_P849853	AT1G67865	unknown protein	-0.371	-2.348	1.28.E-07	-0.608	-4.056	2.56.E-13
A_84_P822840	AT3G11340	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-0.370	-2.344	1.69.E-07	-0.429	-2.682	4.95.E-09
A_84_P21194	AT3G23240	ATERF1/ERF1 (ETHYLENE RESPONSE FACTOR 1); DNA binding / transcription activator/ transcription factor	-0.369	-2.340	6.86.E-07	-0.396	-2.486	4.21.E-08

A_84_P537901	AT4G28410	aminotransferase-related	-0.352	-2.251	6.12.E-07	-0.376	-2.377	1.50.E-07
A_84_P13758	AT3G62280	carboxylesterase	-0.352	-2.248	4.27.E-07	-0.362	-2.304	2.36.E-07
A_84_P15043	AT5G62340	invertase/pectin methylesterase inhibitor family protein	-0.350	-2.237	4.48.E-07	-0.574	-3.746	1.43.E-12
A_84_P595141	AT1G30135	JAZ8/TIFY5A (JASMONATE-ZIM-DOMAIN PROTEIN 8)	-0.349	-2.234	3.57.E-06	-0.465	-2.918	5.80.E-10
A_84_P834894	AT2G18550	ATHB21/HB-2 (homeobox-2); DNA binding / transcription factor	-0.349	-2.231	2.00.E-04	-0.604	-4.017	1.49.E-10
A_84_P789317	AT3G56275	pseudogene of unknown protein	-0.349	-2.231	5.64.E-06	-0.480	-3.017	2.73.E-10
A_84_P842669	AT1G29720	protein kinase family protein	-0.348	-2.230	5.64.E-07	-0.384	-2.420	6.83.E-08
A_84_P18334	AT3G06490	MYB108 (MYB DOMAIN PROTEIN 108); DNA binding / transcription factor	-0.345	-2.212	3.10.E-06	-0.391	-2.462	4.82.E-08
A_84_P12725	AT3G28510	AAA-type ATPase family protein	-0.345	-2.211	1.97.E-06	-0.696	-4.970	6.29.E-15
A_84_P222749	AT4G33800	similar to hypothetical protein [Vitis vinifera] (GB:CAN66218.1)	-0.344	-2.210	2.00.E-04	-0.352	-2.247	1.00.E-05
A_84_P10265	AT5G48650	nuclear transport factor 2 (NTF2) family protein / RNA recognition motif (RR	-0.343	-2.205	1.15.E-06	-0.345	-2.214	9.64.E-07
A_84_P500468	AT3G29780	RALFL27 (RALF-LIKE 27)	-0.343	-2.201	7.04.E-07	-0.338	-2.176	9.22.E-07
A_84_P19611	AT5G05900	UDP-glucoronosyl/UDP-glucosyl transferase family protein	-0.342	-2.200	1.74.E-06	-0.437	-2.737	5.91.E-09
A_84_P13407	AT1G18590	sulfotransferase family protein	-0.342	-2.198	7.00.E-07	-0.352	-2.248	3.94.E-07
A_84_P14595	AT3G20110	CYP705A20 (cytochrome P450, family 705, subfamily A, polypeptide 20); oxy	-0.340	-2.190	8.02.E-07	-0.573	-3.740	1.58.E-12
A_84_P17815	AT5G45200	disease resistance protein (TIR-NBS-LRR class), putative	-0.340	-2.190	2.00.E-05	-0.317	-2.074	5.00.E-05
A_84_P592130	AT4G33905	peroxisomal membrane protein 22 kDa, putative	-0.339	-2.185	2.31.E-03	-0.785	-6.097	4.47.E-16
A_84_P501581	AT5G06080	LBD33 (LOB DOMAIN-CONTAINING PROTEIN 33)	-0.339	-2.181	3.00.E-05	-0.337	-2.175	7.81.E-06
A_84_P14195	AT1G52070	jacalin lectin family protein	-0.338	-2.178	8.97.E-07	-0.387	-2.437	5.54.E-08
A_84_P18818	AT5G60530	late embryogenesis abundant protein-related / LEA protein-related	-0.338	-2.176	9.28.E-07	-0.346	-2.216	6.16.E-07
A_84_P576622	AT2G32200	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32210.1); similar to unknown [Populus trichocarpa] (GB:ABK92801.1)	-0.337	-2.175	1.93.E-06	-0.589	-3.880	6.69.E-13
A_84_P11345	AT1G17750	leucine-rich repeat transmembrane protein kinase, putative	-0.337	-2.171	2.49.E-06	-0.352	-2.248	4.92.E-07
A_84_P857969	AT4G37430	CYP91A2 (CYTOCHROME P450 MONOOXYGENASE 91A2); oxygen bindi	-0.335	-2.163	3.15.E-06	-0.351	-2.242	7.76.E-07
A_84_P831446	AT5G17780	hydrolase, alpha/beta fold family protein	-0.335	-2.161	1.64.E-06	-0.304	-2.014	1.00.E-05
A_84_P14013	AT5G40000	AAA-type ATPase family protein	-0.334	-2.159	6.19.E-03	-0.395	-2.483	9.51.E-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]	-0.333	-2.155	1.47.E-03	-0.722	-5.274	6.98.E-13
A_84_P19565	AT4G37430	CYP91A2 (CYTOCHROME P450 MONOOXYGENASE 91A2); oxygen bindi	-0.333	-2.153	1.23.E-06	-0.372	-2.357	1.18.E-07
A_84_P545036	AT4G39795	senescence-associated protein-related	-0.332	-2.147	1.99.E-06	-0.432	-2.703	3.93.E-09
A_84_P10354	AT1G27940	PGP13 (P-GLYCOPROTEIN 13); ATPase, coupled to transmembrane movem	-0.330	-2.139	2.30.E-04	-0.534	-3.423	1.17.E-10
A_84_P17762	AT5G23030	TET12 (TETRASPANIN12)	-0.330	-2.139	3.65.E-06	-0.361	-2.295	3.40.E-07
A_84_P802975	AT4G17340	DELTA-TIP2/TIP2;2 (tonoplast intrinsic protein 2;2); water channel	-0.330	-2.139	1.42.E-06	-0.391	-2.462	3.76.E-08
A_84_P10804	AT1G26770	ATEXPA10 (ARABIDOPSIS THALIANA EXPANSIN A10)	-0.330	-2.135	1.49.E-06	-0.318	-2.078	2.94.E-06
A_84_P558829	AT2G29350	SAG13 (Senescence-associated gene 13); oxidoreductase	-0.328	-2.129	7.20.E-03	-0.947	-8.860	1.53.E-18
A_84_P831307	AT1G32450	proton-dependent oligopeptide transport (POT) family protein	-0.328	-2.129	3.25.E-06	-0.318	-2.081	8.74.E-06
A_84_P14717	AT4G01630	ATEXPA17 (ARABIDOPSIS THALIANA EXPANSIN A17)	-0.328	-2.127	1.75.E-06	-0.351	-2.245	5.02.E-07
A_84_P79425	AT5G20820	auxin-responsive protein-related	-0.327	-2.125	1.73.E-06	-0.443	-2.773	1.84.E-09
A_84_P19141	AT2G47460	ATMYB12/MYB12 (MYB DOMAIN PROTEIN 12); DNA binding / transcription activator/ transcription factor	-0.327	-2.123	1.89.E-06	-0.619	-4.162	1.77.E-13
A_84_P149248	AT1G21120	O-methyltransferase, putative	-0.326	-2.120	1.79.E-06	-0.333	-2.153	1.20.E-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]	-0.325	-2.112	2.61.E-06	-0.309	-2.037	5.89.E-06
A_84_P22048	AT2G18550	ATHB21/HB-2 (homeobox-2); DNA binding / transcription factor	-0.323	-2.106	1.00.E-05	-0.453	-2.835	3.49.E-09
A_84_P762771	AT3G52561	unknown protein	-0.323	-2.106	1.00.E-05	-0.401	-2.518	7.95.E-08
A_84_P150278	AT2G34610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G30190.1); similar to unnamed protein product [Tetraodon nigroviridis] (GB:CAG12037.1)	-0.323	-2.106	3.48.E-06	-0.532	-3.402	1.58.E-11
A_84_P799508	AT1G02220	ANAC003 (Arabidopsis NAC domain containing protein 3); transcription facto	-0.323	-2.102	2.52.E-06	-0.526	-3.354	1.90.E-11
A_84_P857567	AT4G30170	peroxidase, putative	-0.323	-2.102	2.29.E-06	-0.368	-2.334	1.67.E-07
A_84_P182054	AT5G37690	GDSL-motif lipase/hydrolase family protein	-0.322	-2.098	2.34.E-06	-0.333	-2.150	1.24.E-06
A_84_P288500	AT3G47710	bHLH family protein	-0.322	-2.098	1.50.E-04	-0.731	-5.388	7.14.E-11
A_84_P21046	AT2G38600	acid phosphatase class B family protein	-0.321	-2.094	3.69.E-06	-0.464	-2.910	6.05.E-10
A_84_P22181	AT3G28210	PMZ; zinc ion binding	-0.321	-2.092	2.52.E-06	-0.364	-2.314	1.86.E-07
A_84_P230859	AT3G22550	senescence-associated protein-related	-0.320	-2.091	2.66.E-06	-0.373	-2.361	1.16.E-07
A_84_P869736	AT5G62165	AGL42 (AGAMOUS LIKE 42); transcription factor	-0.319	-2.083	6.00.E-05	-0.517	-3.288	2.81.E-10
A_84_P63350	AT1G29720	protein kinase family protein	-0.316	-2.069	4.91.E-06	-0.426	-2.668	7.66.E-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 oxygen	-0.316	-2.069	3.42.E-06	-0.589	-3.885	6.43.E-13
		similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04860.1);						

A_84_P543604	AT1G47400	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G47395.1)	-0.308	-2.031	6.17.E-06	-0.792	-6.193	1.51.E-16
A_84_P23409	AT5G10130	pollen Ole e 1 allergen and extensin family protein	-0.307	-2.025	9.23.E-06	-0.489	-3.081	8.20.E-10
A_84_P22377	AT4G30430	TET9 (TETRASPANIN9)	-0.306	-2.024	8.90.E-04	-0.365	-2.316	6.68.E-07
A_84_P24008	AT3G04320	endopeptidase inhibitor	-0.305	-2.021	6.36.E-06	-0.675	-4.730	1.54.E-14
A_84_P557480	AT5G15725	unknown protein	-0.305	-2.019	5.90.E-04	-0.617	-4.143	1.00.E-05
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)	-0.304	-2.015	9.30.E-04	-0.331	-2.144	8.00.E-05
A_84_P17313	AT2G37770	aldo/keto reductase family protein	-0.304	-2.014	6.59.E-06	-0.612	-4.094	2.11.E-13
A_84_P20772	AT5G04370	NAMT1; S-adenosylmethionine-dependent methyltransferase	-0.304	-2.012	1.00.E-05	-0.393	-2.469	4.90.E-08
A_84_P577990	AT5G44570	unknown protein	-0.303	-2.009	1.76.E-03	-0.601	-3.987	7.29.E-13
A_84_P11789	AT3G43250	cell cycle control protein-related	-0.303	-2.007	3.25.E-03	-0.426	-2.669	7.45.E-09
A_84_P11200	AT5G45920	carboxylesterase	-0.302	-2.006	8.65.E-06	-0.349	-2.234	5.45.E-07
A_84_P567338	AT5G55570	heat shock protein binding / unfolded protein binding	-0.301	-2.000	1.00.E-05	-0.421	-2.637	1.51.E-08

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

Annotation Cluster 1: Enrichment Score: 7.660176315895672			
Term	Count	%	PValue
flavonoid biosynthetic process	11	4.490	1.21.E-10
flavonoid metabolic process	11	4.490	2.58.E-10
phenylpropanoid metabolic process	15	6.122	1.48.E-09
secondary metabolic process	20	8.163	5.99.E-08
phenylpropanoid biosynthetic process	12	4.898	7.54.E-08
cellular amino acid derivative metabolic process	16	6.531	1.74.E-07
cellular amino acid derivative biosynthetic process	13	5.306	6.96.E-07
aromatic compound biosynthetic process	13	5.306	2.06.E-06
Annotation Cluster 2: Enrichment Score: 4.8640217871452025			
Term	Count	%	PValue
flavonoid biosynthetic process	11	4.490	1.21.E-10
flavonoid metabolic process	11	4.490	2.58.E-10
anthocyanin biosynthetic process	4	1.633	1.19.E-04
anthocyanin metabolic process	4	1.633	3.50.E-04
pigment biosynthetic process	4	1.633	5.95.E-02
pigment metabolic process	4	1.633	8.46.E-02
Annotation Cluster 3: Enrichment Score: 3.577382072650882			
Term	Count	%	PValue
response to endogenous stimulus	28	11.429	1.70.E-06
response to organic substance	31	12.653	2.22.E-06
response to ethylene stimulus	13	5.306	1.23.E-05
transcription	30	12.245	5.08.E-05
response to hormone stimulus	23	9.388	1.33.E-04
ethylene mediated signaling pathway	9	3.673	3.55.E-04
two-component signal transduction system (phosphorelay)	10	4.082	4.01.E-04
response to carbohydrate stimulus	9	3.673	1.00.E-03
cellular response to hormone stimulus	13	5.306	1.59.E-03

Annotation Cluster 4: Enrichment Score: 3.2353612172106825			
Term	Count	%	PValue
response to UV	7	2.857	9.19.E-05
response to light stimulus	15	6.122	2.97.E-04
response to radiation	15	6.122	4.18.E-04
response to abiotic stimulus	22	8.980	1.00.E-02

Annotation Cluster 5: Enrichment Score: 1.9675766001400188			
Term	Count	%	PValue
regulation of anthocyanin biosynthetic process	3	1.224	4.42.E-03
regulation of flavonoid biosynthetic process	3	1.224	8.70.E-03
regulation of anthocyanin metabolic process	3	1.224	9.97.E-03
regulation of secondary metabolic process	3	1.224	3.51.E-02

Annotation Cluster 6: Enrichment Score: 1.7606299652332218			
Term	Count	%	PValue
cell wall modification	7	2.857	2.61.E-03
external encapsulating structure organization	8	3.265	3.08.E-02
cell wall organization	7	2.857	6.48.E-02

Annotation Cluster 7: Enrichment Score: 1.1809446630620486			
Term	Count	%	PValue
response to far red light	4	1.633	1.02.E-02
response to red light	3	1.224	1.12.E-01
response to red or far red light	4	1.633	2.52.E-01

Annotation Cluster 8: Enrichment Score: 0.7446376091400814			
Term	Count	%	PValue
response to oxidative stress	8	3.265	2.80.E-02
response to reactive oxygen species	5	2.041	5.53.E-02
response to hydrogen peroxide	4	1.633	1.18.E-01
cellular response to reactive oxygen species	3	1.224	2.53.E-01
cellular response to oxidative stress	3	1.224	2.57.E-01

Annotation Cluster 9: Enrichment Score: 0.5391032334165797			
Term	Count	%	PValue
organic acid biosynthetic process	8	3.265	1.25.E-01
carboxylic acid biosynthetic process	8	3.265	1.25.E-01
fatty acid biosynthetic process	4	1.633	2.22.E-01
cellular amino acid biosynthetic process	4	1.633	2.90.E-01
amine biosynthetic process	4	1.633	3.46.E-01
fatty acid metabolic process	4	1.633	3.74.E-01
lipid biosynthetic process	6	2.449	4.19.E-01
nitrogen compound biosynthetic process	4	1.633	8.94.E-01

Annotation Cluster 10: Enrichment Score: 0.37690502440290247			
Term	Count	%	PValue
transmembrane receptor protein tyrosine kinase signaling path	3	1.224	3.84.E-01
enzyme linked receptor protein signaling pathway	3	1.224	3.84.E-01
cell surface receptor linked signal transduction	3	1.224	5.01.E-01

Annotation Cluster 11: Enrichment Score: 0.21246079467630907			
Term	Count	%	PValue
growth	4	1.633	4.61.E-01
cell growth	3	1.224	6.46.E-01
regulation of cell size	3	1.224	6.75.E-01
regulation of cellular component size	3	1.224	7.03.E-01

Annotation Cluster 12: Enrichment Score: 0.07072851963326712			
Term	Count	%	PValue
flower development	3	1.224	6.89.E-01
reproductive structure development	6	2.449	8.74.E-01
reproductive developmental process	6	2.449	9.21.E-01
post-embryonic development	6	2.449	9.40.E-01

Annotation Cluster 13: Enrichment Score: 0.045019450030184975			
Term	Count	%	PValue

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

Annotation Cluster 1: Enrichment Score: 4.525889916481404			
Term	Count	%	PValue
response to endogenous stimulus	24	15.894	3.31.E-08
response to hormone stimulus	23	15.232	4.49.E-08
response to auxin stimulus	14	9.272	2.24.E-07
response to organic substance	25	16.556	2.39.E-07
intracellular signaling cascade	13	8.609	4.56.E-03
hormone-mediated signaling	9	5.960	6.58.E-03
cellular response to hormone stimulus	9	5.960	6.58.E-03
auxin mediated signaling pathway	4	2.649	3.96.E-02
Annotation Cluster 2: Enrichment Score: 3.866677277370593			
Term	Count	%	PValue
response to light stimulus	13	8.609	4.17.E-05
response to radiation	13	8.609	5.78.E-05
response to abiotic stimulus	20	13.245	1.80.E-04
response to red or far red light	7	4.636	7.88.E-04
Annotation Cluster 3: Enrichment Score: 1.8837448032489852			
Term	Count	%	PValue
photoperiodism	4	2.649	2.14.E-03
response to gibberellin stimulus	5	3.311	7.24.E-03
photoperiodism, flowering	3	1.987	2.35.E-02
vegetative to reproductive phase transition	3	1.987	8.01.E-02
Annotation Cluster 4: Enrichment Score: 1.778121309358034			
Term	Count	%	PValue
reproductive structure development	12	7.947	7.07.E-03
reproductive developmental process	12	7.947	1.42.E-02
post-embryonic development	11	7.285	4.62.E-02

Annotation Cluster 6: Enrichment Score: 1.7606299652332218			
Term	Count	%	PValue
cell wall modification	7	2.857	2.61.E-03
external encapsulating structure organization	8	3.265	3.08.E-02
cell wall organization	7	2.857	6.48.E-02

Annotation Cluster 7: Enrichment Score: 1.1809446630620486			
Term	Count	%	PValue
response to far red light	4	1.633	1.02.E-02
response to red light	3	1.224	1.12.E-01
response to red or far red light	4	1.633	2.52.E-01

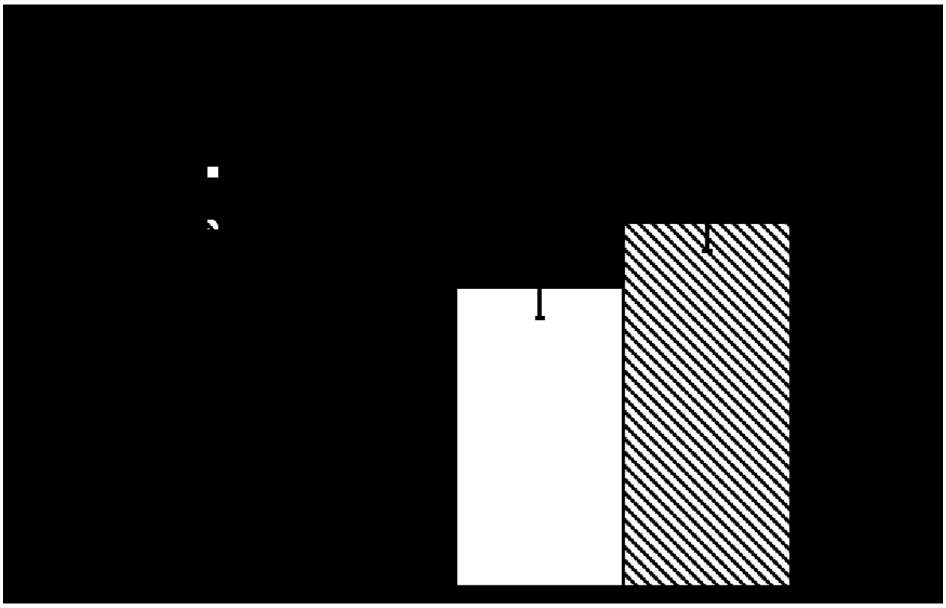
Annotation Cluster 8: Enrichment Score: 0.7446376091400814			
Term	Count	%	PValue
response to oxidative stress	8	3.265	2.80.E-02
response to reactive oxygen species	5	2.041	5.53.E-02
response to hydrogen peroxide	4	1.633	1.18.E-01
cellular response to reactive oxygen species	3	1.224	2.53.E-01
cellular response to oxidative stress	3	1.224	2.57.E-01
oxygen and reactive oxygen species metabolic process	3	1.224	3.06.E-01
response to inorganic substance	7	2.857	4.76.E-01
cellular response to stress	5	2.041	6.37.E-01

Annotation Cluster 9: Enrichment Score: 0.5391032334165797			
Term	Count	%	PValue
organic acid biosynthetic process	8	3.265	1.25.E-01
carboxylic acid biosynthetic process	8	3.265	1.25.E-01
fatty acid biosynthetic process	4	1.633	2.22.E-01
cellular amino acid biosynthetic process	4	1.633	2.90.E-01
amine biosynthetic process	4	1.633	3.46.E-01
fatty acid metabolic process	4	1.633	3.74.E-01
lipid biosynthetic process	6	2.449	4.19.E-01
nitrogen compound biosynthetic process	4	1.633	8.94.E-01

Annotation Cluster 11: Enrichment Score: 0.21246079467630907			
Term	Count	%	PValue
growth	4	1.633	4.61.E-01
cell growth	3	1.224	6.46.E-01
regulation of cell size	3	1.224	6.75.E-01
regulation of cellular component size	3	1.224	7.03.E-01
Annotation Cluster 12: Enrichment Score: 0.07072851963326712			
Term	Count	%	PValue
flower development	3	1.224	6.89.E-01
reproductive structure development	6	2.449	8.74.E-01
reproductive developmental process	6	2.449	9.21.E-01
post-embryonic development	6	2.449	9.40.E-01
Annotation Cluster 13: Enrichment Score: 0.045019450030184975			
Term	Count	%	PValue
protein amino acid phosphorylation	9	3.673	8.60.E-01
phosphate metabolic process	10	4.082	9.12.E-01
phosphorus metabolic process	10	4.082	9.13.E-01
phosphorylation	9	3.673	9.22.E-01

Table S5. PCR primers used for expression analysis.

Gene	Primer sequence
ACT2_F	GGTAACATTGTGCTCAGTGGTGG
ACT2_R	AACGACCTTAATCTTCATGCTGC
SAUR22_F	CCTTCTTTCAAGCTCTGCTCAGT
SAUR22_R	TTGGAGCCGAGAAGTCACATT
SAUR23_F	AGTGTACGTAGGAGAGAGCCAGAA
SAUR23_R	ATCGGATGATCGAACCCAAA
IAA29_F	CTTCCAAGGGAAAGAGGGTGAC
IAA29_R	TTCCGCAAAGATCTTCCATGTAAC



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 µmol·m^{-2}·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.

Chapter 2

Gene expression profile of *zeitlupe/lov kelch protein1* T-DNA insertion mutants in *Arabidopsis thaliana*: Down regulation of auxin-inducible genes in hypocotyls

Abstract

Elongation of hypocotyl cells has been studied as a model for elucidating the contribution of cellular expansion to plant organ growth. ZEITLUPE (ZTL) or LOV KELCH PROTEIN1 (LKP1) is a positive regulator of warmth-induced hypocotyl elongation under white light in *Arabidopsis*, although the molecular mechanisms by which it promotes hypocotyl cell elongation remain unknown. Microarray analysis showed that 134 genes were upregulated and 204 genes including 15 auxin-inducible genes were downregulated in the seedlings of 2 *ztl* T-DNA insertion mutants grown under warm conditions with continuous white light. Application of a polar auxin transport inhibitor, an auxin antagonist or an auxin biosynthesis inhibitor inhibited hypocotyl elongation of control seedlings to the level observed with the *ztl* mutant. Our data suggest the involvement of auxin and auxin-inducible genes in ZTL-mediated hypocotyl elongation.

Key words: *Arabidopsis thaliana*, Arabidopsis thaliana, auxin, high temperature, hypocotyl elongation, microarray, SAUR, ZEITLUPE

Plants use light not only as an energy source but also as an environmental cue for growth and development.[1,2] Numerous genes and proteins are involved in the perception and transduction of environmental light signals, including photoreceptors.[1,2] ZEITLUPE (ZTL)/LOV KELCH PROTEIN1 (LKP1) is a blue-light photoreceptor harbouring an F-box in *Arabidopsis*.[3-5] ZTL determines the period of circadian oscillation, regulates photoperiodic flowering and promotes hypocotyl elongation under light.[3-6] The molecular mechanisms of circadian oscillation and flowering-time control have been relatively well studied, whereas those for promotion of hypocotyl elongation remain largely unknown. Elongation of hypocotyl cells has been studied as a model for elucidating the contribution of cellular expansion to plant organ growth.[7] *ZTL*-overexpressing plants have elongated hypocotyls when grown at 22°C with continuous white light.[3,4] *ztl* mutants are indistinguishable from the wild type in the dark, but they have short hypocotyls when grown at 22°C with continuous white light.[8] The difference in hypocotyl length between the *ztl* mutant and wild-type seedlings was more significant when they were grown at 28°C with continuous white light.[8] Thus, ZTL functions as a positive regulator in warmth-induced hypocotyl elongation under white light. In this study, we report our microarray analysis, real-time quantitative reverse-transcription PCR (qRT-PCR) results and auxin inhibitor experiments using *ztl* mutant and wild-type seedlings to support the idea that auxin and auxin-inducible genes are involved in the hypocotyl elongation mediated by ZTL.

Seeds of 2 *ztl* T-DNA insertion mutants, *ztl-3* and *ztl-105*,[9] and the wild-type Columbia accession were sown on 1/2-basal-salt Murashige and Skoog agar (0.8% w/v) medium without sucrose and incubated at 4°C for 7 d in the dark. The seeds were then incubated at 22°C for 3 d and then 28°C for 5 d with continuous white light (80 $\mu mol \cdot m^{-2} \cdot s^{-1}$) as reported.[8] Total RNA was isolated from 8-day-old *ztl-3, ztl-105* and wild-type seedlings (2 biological replicates: Col1 and Col2) using an RNeasy Plant Mini Kit (Qiagen, Valencia, CA, USA). The microarray experiment was performed using *Arabidopsis* (V4) Gene Expression Microarrays 4 × 44K (G2519F-021169) (Agilent Technologies, Böblingen, Germany) as previously described.[10] A total of 134 genes were upregulated (average fold change > 2.0; $p < 0.01$) and 204 genes were downregulated (average fold change < −2.0; $p < 0.01$) in *ztl* mutants. These genes are listed in Table S1 and S2. Downregulation of *ZTL* in *ztl* mutants (AT5G57360; average fold change −63.0) validated this microarray analysis. The downregulation of the clock genes *PSEUDO RESPONSE REGULATOR9* (*PRR9*)[11,12] (AT2G46790; average fold change −14.0), *LATE ELONGATED HYPOCOTYL* (*LHY*)[12,13] (AT1G01060; average fold change −4.7), *CIRCADIAN CLOCK ASSOCIATED1* (*CCA1*)[12,14] (AT2G46830; 3 probes: average fold changes −2.9, −2.5 and −2.4) in *ztl* mutants was consistent with the involvement of ZTL in circadian clock regulation. Pathway analysis of upregulated and downregulated 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. As for the upregulated genes, no group was detected with a significant *P*-value (<0.05) (data not shown). Among the downregulated genes, 24 genes involved in the response to endogenous stimulus were detected as the group with the smallest *P*-value (3.3E-08; Table S3). Based on this grouping and the result from the Arabidopsis eFP Browser (http://bar.utoronto.ca/efp/cgi-bin/efpWeb.cgi), we constructed Table 1, which lists auxin-inducible genes downregulated in *ztl* seedlings. They included 7 *SMALL AUXIN UP RNA* (*SAUR*)[15,16] genes (*SAUR1, 9, 10, 22, 23, 46* and *68*), 4 *AUXIN/INDOLE-3-ACETIC ACID* (*AUX/IAA*)[15-17] genes (*IAA1, 5, 29* and *34*), a gene for indole-3-acetic acid-amido synthetase (*GH3.5*),[15,16,18] a gene for 1-aminocyclopropane-1-carboxylic acid synthase (*ASC4*),[19] *AUXIN-REGULATED GENE INVOLVED IN ORGAN SIZE* (*ARGOS*)[20] and *ARGOS-LIKE* (*ARL*).[21] Among these 15 genes, 13 were included in the group for response to endogenous stimulus and 12 were included in the group for response to auxin stimulus in Table S3**.**

We performed real-time quantitative reverse-transcription qRT-PCR to confirm the downregulation of 3 auxin-inducible genes, *SAUR22*, *SAUR23* and *IAA29*, in hypocotyls of 8-day-old *ztl* mutants in comparison with wild-type seedlings grown as for microarray analysis. RNA was isolated from hypocotyls with RNAiso Plus (Takara, Otsu, Japan). The reverse transcription reaction was conducted with an oligo dT primer and PrimeScript II (Takara). PCR was performed with a StepOnePlus Real-Time PCR System (Life Technologies, Carlsbad, CA). The PCR primers are listed in Table S4. 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 lower in both *ztl* mutant hypocotyls than in wild-type hypocotyls (Fig. 1), confirming that these genes are downregulated in the hypocotyls of 2 *ztl* mutants.

To assess the role of auxin in hypocotyl elongation in *ztl* mutants and wild-type seedlings, we used 3 auxin inhibitors. The *ztl* mutant and wild-type seedlings were grown as described above in the absence or presence of the auxin transport inhibitor *N*-1-naphthylphthalamic acid (NPA),[22] the auxin antagonist α-(phenyl ethyl-2-one)-indole-3-acetic acid (PEO-IAA)[23] or the auxin biosynthesis inhibitor 5-(4-chlorophenyl)-4*H*-1,2,4-triazole-3-thiol (YUCASIN).[24] In the presence of 1 μM NPA, 5 μM PEO-IAA or 25 μM YUCASIN, the hypocotyl lengths of wild-type seedlings were reduced, although their hypocotyls were still significantly longer than those of *ztl* mutants (Fig. 2). Enhanced hypocotyl elongation in wild-type seedlings was completely inhibited to *ztl* mutant levels by 5 μM NPA, 50 μM PEO-IAA or 100 μM YUCASIN. These results suggest the involvement of auxin in the hypocotyl elongation in seedlings mediated by ZTL.

Auxin regulates the expression of a large number of genes involved in growth, development and differentiation.[25] Among them, the early or primary auxin-inducible genes are grouped into at least 3 families: *AUX/IAA, GH3* and *SAUR* genes.[15,16] *AUX/IAA* genes encode transcriptional repressors and function in negative-feedback pathways to attenuate auxin responses.[17] *GH3* genes encode auxin-conjugating enzymes and function to attenuate auxin responses by downregulation of endogenous active auxin levels.[18] The expression of *SAUR* genes is usually associated with tissue elongation.[26,27] Among *SAUR* genes, members of 2 subfamilies, *SAUR19–24* and *SAUR61–68*, are postulated as positive effectors of cell expansion.[27-30] The sequences of *SAUR19–24* are also highly identical to one another and these 6 genes are located in a cluster on chromosome 5, suggesting their functional redundancy.[15,27] Plants overexpressing *SAUR19* have longer hypocotyls than wild-type plants under continuous light,[27] and plants overexpressing a *GFP-SAUR19, 21, 23* or *24* fusion gene also have elongated hypocotyls under long-day conditions.[28] SAUR19 stimulates plasma membrane H^+ -ATPase by inhibiting the activity of type 2C protein phosphatases, leading to cell expansion via an acid growth mechanism.[29] Thus, the downregulation of *SAUR22* and *23* detected by microarray analysis and confirmed by qRT-PCR may contribute to reducing hypocotyl elongation in *ztl* mutants. As for *SAUR61–68*, these genes are located in a cluster on chromosome 1 with high DNA sequence identity.[15,30] The positive function of SAUR63 in hypocotyl elongation was reported, although *SAUR68* may be a pseudogene, as it encodes a shorter open reading frame than other members in the gene subfamily.[30] Thus, the meaning of the downregulation of *SAUR68* in the hypocotyls of *ztl* mutants is unknown.

We observed downregulation of the expression of 2 genes for gibberellin biosynthesis emzymes, i.e. twenty-oxidase (*GA5*) (AT4G25420; average fold change −2.9) and ent-copalyl diphosphate synthase (GA1) (AT4G02780; average fold change −2.4), and 2 genes involved in brassinosteroid signaling, i.e BRASSINOSTEROID INSENSITIVE1 (BRI1) (AT4G39400; average fold change of −2.4) and BR ENHANCED EXPRESSION1 (BEE1) (AT1G18400; average fold change −2.3). These data suggest *ZTL*-dependent changes in gibberellin level and brassinosteroid signaling. Gibberellins stimulate cell elongation in *Arabidopsis* hypocotyls.[31] Brassinosteroids act on light-grown hypocotyl elongation independent of, but co-operatively with, gibberellins and auxin.[32] The downregulation of gene expression for gibberellin biosynthesis and brassinosteroid signaling in *ztl* seedlings suggests that these hormones also contribute to the effect of ZTL on hypocotyl elongation.

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Table 1. Auxin-inducible genes downregulated in *ztl* seedlings in comparison with wild-type seedlings

			ztl vs Col	
Array element	Gene Locus	Gene name	Fold change	P-value
A_84_P17344	AT2G22810	*ACS4*	-6.569	8.83.E-15
A_84_P16724	AT1G15050	*IAA34*	-5.317	9.89.E-13
A_84_P12605	AT2G18010	*SAUR10*	-3.601	0.00.E+00
A_84_P13527	AT2G37030	*SAUR46*	-3.333	6.83.E-07
A_84_P18064	AT1G15580	*IAA5*	-2.899	4.58.E-28
A_84_P843096	AT1G29490	*SAUR68*	-2.876	3.35.E-14
A_84_P55550	AT4G32280	*IAA29*	-2.756	6.87.E-09
A_84_P794374	AT4G27260	*GH3.5*	-2.585	6.11.E-25
A_84_P524502	AT3G59900	*ARGOS*	-2.541	5.04.E-44
A_84_P230289	AT2G44080	*ARL*	-2.268	3.87.E-16
A_84_P10124	AT4G14560	*IAA1*	-2.145	1.47.E-15
A_84_P21449	AT4G34770	*SAUR1*	-2.120	2.67.E-14
A_84_P12944	AT4G36110	*SAUR9*	-2.058	4.26.E-03
A_84_P94979	AT5G18060	*SAUR23*	-2.052	3.10.E-10
A_84_P141269	AT5G18050	*SAUR22*	-2.029	1.03.E-15

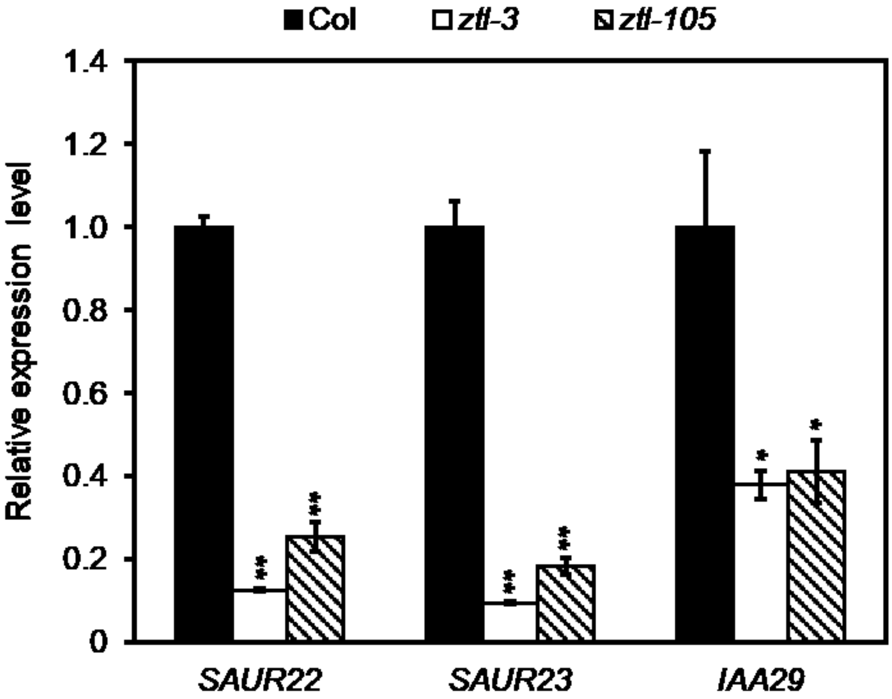

Figure 1. Expression of *SAUR22*, *SAUR23* and *IAA29* in hypocotyls of wild-type Columbia (Col) and 2 *ztl* mutant seedlings (*ztl-3* and *ztl-105*) quantified by real-time quantitative reverse-transcription PCR (qRT-PCR). Seedlings of wild-type Col plants and ztl mutants were grown on 1/2-basal-salt Murashige and Skoog agar (0.8% w/v) medium without sucrose for 3 d at 22°C and then for 5 d at 28°C with continuous white light (80 μmol·m−2·s−1). The expression levels were normalized using the actin transcript (*ACT2*) expression levels. The values for *ztl-3* and *ztl-105* are shown relative to wild-type Col. Error bars represent standard error of the mean (n = 3; technical replicates); *(P)< 0.05, **(P)< 0.01 (Student's t test) in comparison with wild-type Col.

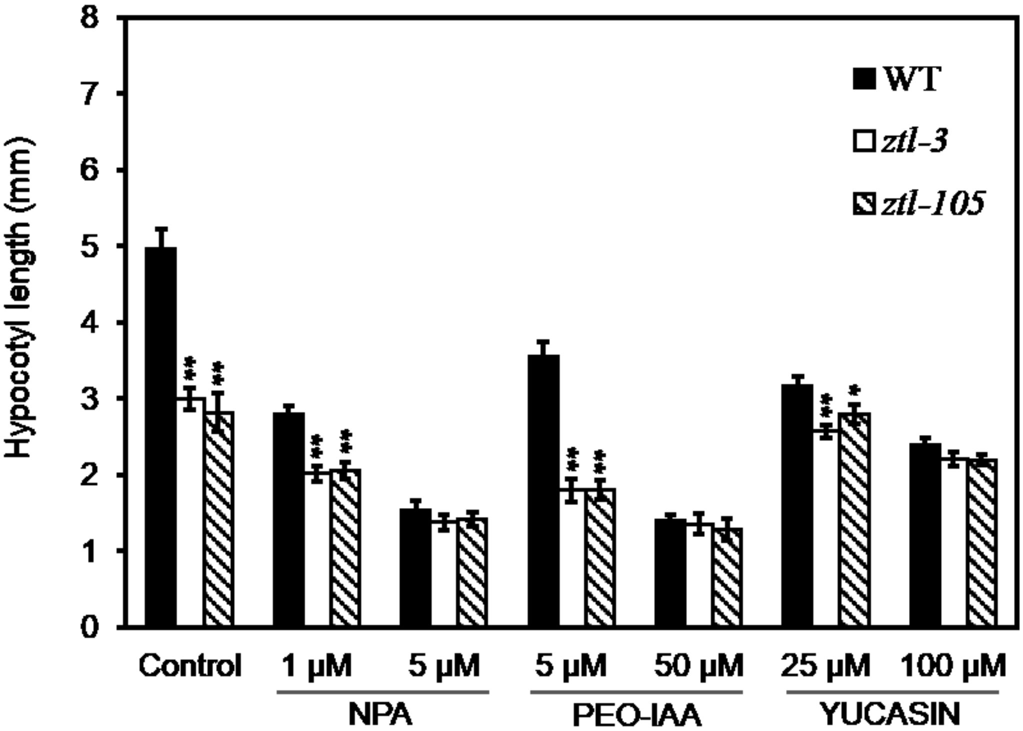

Figure 2. Inhibition of hypocotyl elongation by auxin inhibitors. Seedlings of wild-type Col plants and *ztl* mutants were grown for 3 d at 22°C and then for 5 d at 28°C with continuous white light (80 μmol·m−2·s−1) on 1/2-basal-salt Murashige and Skoog agar (0.8% w/v) medium without sucrose in the absence 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)-4H-1,2,4-triazole-3-thiol (YUCASIN). Error bars represent standard error of the mean (n = 5–10); *(P)< 0.05, **(P)< 0.01 (Student's t test) in comparison with wild-type Col.

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

			ztl vs Col		
Array element	Gene locus	Annotation	Log(Ratio)	Fold change	P-value
A_84_P862159	AT2G24850	TAT3 (TYROSINE AMINOTRANSFERASE 3); transaminase	1.422	26.424	6.00.E-05
A_84_P91639	AT2G39030	GCN5-related N-acetyltransferase (GNAT) family protein	1.369	23.382	2.00.E-05
A_84_P20045	AT1G57630	disease resistance protein (TIR class), putative	1.163	14.558	1.47.E-07
A_84_P21769	AT1G61120	terpene synthase/cyclase family protein	1.054	11.328	3.80.E-04
A_84_P767684	AT5G33395	transposable element gene	1.003	10.078	1.97.E-08
A_84_P762109	AT3G44006	unknown protein	0.938	8.660	1.10.E-04
A_84_P17866	AT1G01680	U-box domain-containing protein	0.924	8.396	9.60.E-08
A_84_P825539	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	0.896	7.875	3.40.E-04
A_84_P759938	AT3G25630	transposable element gene	0.873	7.469	6.10.E-04
A_84_P10609	AT2G24850	TAT3 (TYROSINE AMINOTRANSFERASE 3); transaminase	0.869	7.402	5.70.E-10
A_84_P609175	AT5G48860	unknown protein	0.841	6.934	7.80.E-04
A_84_P17546	AT3G44860	FAMT (FARNESOIC ACID CARBOXYL-O-METHYLTRANSFERASE); S-adenosylmethionine-dependent methyltransferase/ farnesoic acid O-methyltransferase	0.826	6.705	3.04.E-03
A_84_P301780	AT3G20975 AT3G20978	[AT3G20975, transposable element gene];[AT3G20978, other RNA]	0.817	6.566	3.30.E-04
A_84_P23754	AT1G33960	AIG1 (AVRRPT2-INDUCED GENE 1); GTP binding	0.792	6.198	1.01.E-06
A_84_P758871	AT3G43304 AT3G33197 AT3G37820	[AT3G43304, transposable element gene];[AT3G33197, transposable element gene];[AT3G37820, transposable element gene]	0.770	5.890	3.32.E-03
A_84_P21001	AT1G44130	nucellin protein, putative	0.766	5.840	2.00.E-05
A_84_P514216	AT3G46770	transcriptional factor B3 family protein	0.766	5.838	3.35.E-03
A_84_P11274	AT5G65080	AGL68/MAF5 (MADS AFFECTING FLOWERING 5); transcription factor	0.761	5.762	1.20.E-12
A_84_P720334	AT1G29680	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G45690.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47983.1); contains InterPro domain Protein of unknown function DUF1264 (InterPro:IPR010686)	0.759	5.736	4.17.E-03
A_84_P19362	AT3G46090	ZAT7; nucleic acid binding / transcription factor/ zinc ion binding	0.735	5.433	4.00.E-05
A_84_P13535	AT2G38240	oxidoreductase, 2OG-Fe(II) oxygenase family protein	0.734	5.420	3.37.E-03
A_84_P798365	AT1G45223	Encodes a ECA1 gametogenesis related family protein	0.732	5.400	6.38.E-03
A_84_P750060	AT1G36680	transposable element gene	0.732	5.398	7.10.E-03
A_84_P751391	AT1G21525	pseudogene of unknown protein	0.726	5.317	6.10.E-11
A_84_P792258	AT4G01080	no_match	0.725	5.304	1.00.E-05
A_84_P579882	AT3G28410	F-box family protein	0.717	5.212	6.27.E-03
A_84_P784679	AT5G45690	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G18920.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO47983.1); contains InterPro domain Protein of unknown function DUF1264 (InterPro:IPR010686)	0.717	5.209	6.86.E-03
A_84_P21945	AT1G32350	AOX1D (ALTERNATIVE OXIDASE 1D); alternative oxidase	0.710	5.134	1.63.E-03
A_84_P12794	AT3G57460	catalytic/ metal ion binding / metalloendopeptidase/ zinc ion binding	0.708	5.103	3.81.E-03
A_84_P764469	AT4G19690	IRT1 (IRON-REGULATED TRANSPORTER 1); cadmium ion transmembrane transporter/ iron ion transmembrane transporter/ manganese ion transmembrane transporter/ zinc ion transmembrane transporter	0.693	4.936	2.79.E-19
A_84_P818437	AT5G42380	CML37/CML39; calcium ion binding	0.691	4.905	4.30.E-04
A_84_P761066	AT3G05741	enzyme inhibitor/ pectinesterase	0.684	4.826	1.62.E-03
A_84_P14441	AT2G29460	ATGSTU4 (GLUTATHIONE S-TRANSFERASE 22); glutathione transferase	0.678	4.764	5.30.E-04
A_84_P756973	AT2G04032	ZIP7 (ZINC TRANSPORTER 7 PRECURSOR); cation transmembrane transp	0.661	4.582	1.13.E-24
A_84_P837346	AT4G39580	kelch repeat-containing F-box family protein	0.658	4.547	2.00.E-05
A_84_P825225	AT5G65080	AGL68/MAF5 (MADS AFFECTING FLOWERING 5); transcription factor	0.653	4.503	7.37.E-13
A_84_P11694	AT3G01830	calmodulin-related protein, putative	0.607	4.045	3.00.E-04
A_84_P828825	AT4G19690	IRT1 (IRON-REGULATED TRANSPORTER 1); cadmium ion transmembrane transporter/ iron ion transmembrane transporter/ manganese ion transmembrane transporter/ zinc ion transmembrane transporter	0.604	4.014	9.63.E-06
A_84_P762010	AT3G28899	unknown protein	0.593	3.916	3.22.E-23
A_84_P63390	AT4G31940	CYP82C4 (cytochrome P450, family 82, subfamily C, polypeptide 4); oxygen	0.584	3.840	1.07.E-03
A_84_P839943	AT1G36480	transposable element gene	0.578	3.781	7.61.E-03
A_84_P21058	AT2G36770	UDP-glucoronosyl/UDP-glucosyl transferase family protein	0.567	3.687	4.29.E-15
A_84_P11305	AT5G19810	proline-rich extensin-like family protein	0.555	3.593	1.89.E-03

A_84_P816558	AT5G20830	SUS1 (SUCROSE SYNTHASE 1); UDP-glycosyltransferase/ sucrose synthase	0.549	3.538	1.25.E-03
A_84_P19046	AT1G69920	ATGSTU12 (Arabidopsis thaliana Glutathione S-transferase (class tau) 12); gl	0.549	3.537	2.00.E-05
A_84_P306900	AT5G56430	F-box family protein	0.548	3.533	4.30.E-04
A_84_P17960	AT1G01580	FRO2 (FERRIC REDUCTION OXIDASE 2); ferric-chelate reductase	0.546	3.515	8.03.E-10
A_84_P587419	AT3G09922	IPS1 (INDUCED BY PHOSPHATE STARVATION1)	0.544	3.496	1.92.E-03
A_84_P16903	AT5G54610	ANK (ANKYRIN); protein binding	0.540	3.471	1.58.E-03
A_84_P23149	AT3G46660 AT3G46658	[AT3G46660, UDP-glucoronosyl/UDP-glucosyl transferase family protein];[A	0.539	3.463	1.38.E-03
A_84_P610569	AT3G12440	extensin family protein	0.537	3.444	3.57.E-03
A_84_P12212	AT1G56060	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G32190.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO68639.1); contains domain PD188784 (PD188784)	0.536	3.438	5.00.E-05
A_84_P839925	AT1G64480	CBL8 (CALCINEURIN B-LIKE PROTEIN 5)	0.531	3.398	3.64.E-03
A_84_P827123	AT3G61930	unknown protein	0.526	3.355	9.00.E-05
A_84_P184454	AT2G43220	DC1 domain-containing protein	0.524	3.339	1.20.E-04
A_84_P835133	AT5G10200	binding	0.522	3.328	1.38.E-03
A_84_P829727	AT5G13320	PBS3 (AVRPPHB SUSCEPTIBLE 3)	0.521	3.316	1.73.E-07
A_84_P850907	AT3G44790	meprin and TRAF homology domain-containing protein / MATH domain-con	0.519	3.300	2.63.E-03
A_84_P20466	AT4G26260	MIOX4 (MYO-INOSITOL OXYGENASE 4)	0.517	3.287	4.25.E-11
A_84_P821066	AT5G60910	AGL8 (AGAMOUS-LIKE 8); transcription factor	0.516	3.284	3.33.E-03
A_84_P766473	AT5G25260	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25250.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G64870.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO44306.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN77054.1); similar to 80C09_16 [Brassica rapa subsp. pekinensis] (GB:AAZ41827.1); contains domain PTHR13806:SF3 (PTHR13806:SF3); contains domain PTHR13806 (PTHR13806)	0.515	3.271	5.11.E-03
A_84_P13077	AT5G42380	CML37/CML39; calcium ion binding	0.512	3.249	4.00.E-04
A_84_P504165	AT4G17860	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G46200.1); similar to hypothetical protein 25.t00048 [Brassica oleracea] (GB:ABD64955.1); contains InterPro domain Protein of unknown function DUF239, plant (InterPro:IPR004314)	0.509	3.228	1.23.E-07
A_84_P599045	AT3G19320	leucine-rich repeat family protein	0.500	3.165	4.11.E-03
A_84_P765549	AT4G04077	other RNA	0.498	3.149	7.80.E-04
A_84_P11959	AT4G26930	MYB97 (myb domain protein 97); DNA binding / transcription factor	0.495	3.129	6.54.E-03
A_84_P795094	AT5G28850	calcium-binding EF hand family protein	0.493	3.112	8.80.E-04
A_84_P786320	AT5G35935	transposable element gene	0.491	3.096	3.14.E-17
A_84_P151248	AT4G27570	glycosyltransferase family protein	0.488	3.079	3.06.E-03
A_84_P249495	AT5G52760	heavy-metal-associated domain-containing protein	0.488	3.076	8.83.E-03
A_84_P19925	AT1G03020	glutaredoxin family protein	0.486	3.061	1.57.E-42
A_84_P844502	AT4G03180	similar to unnamed protein product [Vitis vinifera] (GB:CAO22413.1)	0.486	3.060	7.00.E-05
A_84_P787266	AT5G26170	WRKY50 (WRKY DNA-binding protein 50); transcription factor	0.483	3.039	5.00.E-05
A_84_P848499	AT5G35935	transposable element gene	0.481	3.024	8.90.E-21
A_84_P836925	AT5G35935	no_match	0.477	2.997	7.09.E-27
A_84_P573065	AT2G28210	carbonic anhydrase family protein	0.476	2.993	7.51.E-15
A_84_P582920	AT2G45760	BAP2 (BON ASSOCIATION PROTEIN 2)	0.473	2.972	2.86.E-06
A_84_P762318	AT3G08636	unknown protein	0.469	2.942	2.75.E-03
A_84_P18416	AT3G46080	zinc finger (C2H2 type) family protein	0.463	2.904	1.70.E-04
A_84_P511918	AT3G01175	similar to structural constituent of ribosome [Arabidopsis thaliana] (TAIR:AT5G39785.1); similar to structural constituent of ribosome [Arabidopsis thaliana] (TAIR:AT5G39785.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO14994.1); contains InterPro domain Protein of unknown function DUF1666 (InterPro:IPR012870)	0.461	2.890	1.10.E-04
A_84_P19960	AT1G78390	NCED9 (NINE-CIS-EPOXYCAROTENOID DIOXYGENASE 9)	0.456	2.857	5.10.E-04
A_84_P869713	AT5G52760	heavy-metal-associated domain-containing protein	0.451	2.823	1.52.E-03
A_84_P535912	AT3G13500	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G55365.1)	0.450	2.819	6.62.E-03
A_84_P543581	AT1G30660	toprim domain-containing protein	0.447	2.798	5.80.E-04
A_84_P19559	AT1G15010	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G01300.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO42242.1)	0.442	2.769	1.85.E-15
A_84_P569671	AT3G48640	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66670.2); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G66670.1)	0.442	2.768	4.65.E-03
A_84_P22612	AT5G62730	proton-dependent oligopeptide transport (POT) family protein	0.440	2.754	1.89.E-06
A_84_P758274	AT2G38304	unknown protein	0.437	2.737	7.15.E-03
A_84_P17209	AT1G31690	copper ion binding	0.437	2.736	4.43.E-08

A_84_P20281	AT3G22910	calcium-transporting ATPase, plasma membrane-type, putative / Ca(2+)-ATPa	0.433	2.710	4.77.E-14
A_84_P14958	AT5G40010	AATP1 (AAA-ATPASE 1); ATP binding / ATPase	0.431	2.695	1.58.E-03
A_84_P20214	AT3G10900	(1-4)-beta-mannan endohydrolase, putative	0.425	2.663	2.20.E-03
A_84_P101246	AT5G22530	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G22520.1)	0.422	2.640	3.98.E-03
A_84_P22377	AT4G30430	TET9 (TETRASPANIN9)	0.422	2.640	5.50.E-04
A_84_P58550	AT1G53325	F-box family protein-related	0.420	2.628	3.77.E-03
A_84_P232569	AT3G03530	NPC4 (NONSPECIFIC PHOSPHOLIPASE C4); hydrolase, acting on ester bo	0.405	2.541	2.00.E-05
A_84_P17676	AT4G37990	ELI3-2 (ELICITOR-ACTIVATED GENE 3)	0.404	2.538	5.33.E-03
A_84_P21712	AT1G54940	PGSIP4 (PLANT GLYCOGENIN-LIKE STARCH INITIATION PROTEIN 4); transferase, transferring glycosyl groups	0.404	2.534	3.27.E-03
A_84_P842974	AT1G67455	F-box family protein	0.404	2.534	4.48.E-03
A_84_P762827	AT3G60176	other RNA	0.401	2.520	3.11.E-03
A_84_P15487	AT3G09620	DEAD/DEAH box helicase, putative	0.401	2.516	6.73.E-03
A_84_P12107	AT5G28000	Bet v I allergen family protein	0.389	2.448	6.99.E-03
A_84_P13961	AT5G13320	PBS3 (AVRPPHB SUSCEPTIBLE 3)	0.385	2.428	9.92.E-03
A_84_P18423	AT3G47480	calcium-binding EF hand family protein	0.381	2.404	6.00.E-05
A_84_P17313	AT2G37770	aldo/keto reductase family protein	0.377	2.385	6.00.E-05
A_84_P829672	AT1G09932	phosphoglycerate/bisphosphoglycerate mutase-related	0.374	2.368	1.00.E-05
A_84_P845406	AT3G47340	ASN1 (DARK INDUCIBLE 6)	0.373	2.360	4.59.E-22
A_84_P24036	AT3G27070	TOM20-1 (TRANSLOCASE OUTER MEMBRANE 20-1)	0.373	2.359	4.43.E-03
A_84_P564785	AT1G14250	nucleoside phosphatase family protein / GDA1/CD39 family protein	0.366	2.323	5.71.E-21
A_84_P830570	AT5G56370	F-box family protein	0.365	2.318	1.50.E-04
A_84_P752834	AT1G54445	Encodes a defensin-like (DEFL) family protein.	0.360	2.289	4.79.E-03
A_84_P12970	AT4G17660	protein kinase, putative	0.359	2.287	8.40.E-03
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}	0.356	2.269	1.50.E-23
A_84_P751658	AT1G47620	CYP96A8 (cytochrome P450, family 96, subfamily A, polypeptide 8); oxygen	0.347	2.224	3.34.E-03
A_84_P602531	AT2G46880	ATPAP14/PAP14; acid phosphatase/ protein serine/threonine phosphatase	0.347	2.222	2.39.E-03
A_84_P786552	AT2G20870	cell wall protein precursor, putative	0.345	2.215	2.54.E-03
A_84_P866267	AT3G55500	ATEXPA16 (ARABIDOPSIS THALIANA EXPANSIN A16)	0.345	2.213	5.78.E-06
A_84_P847367	AT1G02205	CER1 (ECERIFERUM 1)	0.345	2.213	6.30.E-04
A_84_P11901	AT1G06100	fatty acid desaturase family protein	0.335	2.162	6.83.E-08
A_84_P727700	AT1G47265	unknown protein	0.330	2.139	1.86.E-06
A_84_P812380	AT3G30775	no_match	0.329	2.134	1.07.E-09
A_84_P223559	AT2G14560	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G33840.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO48825.1); contains InterPro domain Protein of unknown function DUF567 (InterPro:IPR007612)	0.329	2.134	8.96.E-03
A_84_P11318	AT1G35310	MLP168 (MLP-LIKE PROTEIN 168)	0.327	2.123	7.50.E-04
A_84_P836357	AT4G04990	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G61260.1); contains InterPro domain Protein of unknown function DUF761, plant (InterPro:IPR008480)	0.327	2.123	1.43.E-09
A_84_P750006	AT1G75250	myb family transcription factor	0.327	2.122	2.18.E-25
A_84_P23919	AT2G35980	YLS9 (YELLOW-LEAF-SPECIFIC GENE 9)	0.327	2.122	6.93.E-06
A_84_P564068	AT1G77655	unknown protein	0.326	2.119	7.56.E-03
A_84_P250315	AT2G18660	EXLB3 (EXPANSIN-LIKE B3 PRECURSOR)	0.325	2.113	4.07.E-03
A_84_P62310	AT3G43095	transposable element gene	0.324	2.107	6.24.E-03
A_84_P768104	AT5G44973	Encodes a defensin-like (DEFL) family protein.	0.323	2.102	4.00.E-05
A_84_P22549	AT5G46350	WRKY8 (WRKY DNA-binding protein 8); transcription factor	0.317	2.075	3.20.E-04
A_84_P10711	AT2G39330	jacalin lectin family protein	0.317	2.074	1.16.E-07
A_84_P20285	AT3G13660	disease resistance response	0.314	2.058	9.82.E-06
A_84_P21264	AT3G48360	BT2 (BTB AND TAZ DOMAIN PROTEIN 2); protein binding / transcription factor/ transcription regulator	0.313	2.056	7.00.E-05

A_84_P18377	AT3G24420	hydrolase, alpha/beta fold family protein	0.313	2.055	9.00.E-10
A_84_P767376	AT5G32572	transposable element gene	0.312	2.053	3.70.E-04
A_84_P10838	AT3G11080	disease resistance family protein	0.310	2.043	3.60.E-03
A_84_P179234	AT5G46770	unknown protein	0.310	2.042	5.60.E-04
A_84_P10328	AT5G65070	MAF4 (MADS AFFECTING FLOWERING 4); transcription factor	0.309	2.036	2.13.E-13
A_84_P555267	AT2G22460	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G65340.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN78584.1); contains InterPro domain Protein of unknown function DUF617, plant (InterPro:IPR006460)	0.309	2.035	7.88.E-06
A_84_P23070	AT3G22740	HMT3 (Homocysteine S-methyltransferase 3); homocysteine S-methyltransfera	0.308	2.031	4.09.E-13
A_84_P103716	AT5G03350	legume lectin family protein	0.305	2.016	1.05.E-10
A_84_P54570	AT3G61930	unknown protein	0.304	2.015	2.50.E-03
A_84_P18198	AT2G16660	nodulin family protein	0.302	2.005	6.54.E-06

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

			ztl vs Col		
Array element	Gene locus	Annotation	Log(Ratio)	Fold Change	P-value
A_84_P23534	AT5G57360	ZTL (ZEITLUPE); ubiquitin-protein ligase	-1.799	-63.003	1.25.E-29
A_84_P11480	AT1G53490 AT1G53480	[AT1G53490, DNA binding];[AT1G53480, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03090.1)]	-1.468	-29.345	7.32.E-34
A_84_P725341	AT1G53490 AT1G53480	[AT1G53490, DNA binding];[AT1G53480, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G03090.1)]	-1.353	-22.561	2.10.E-25
A_84_P22942	AT2G41260	M17	-1.201	-15.881	6.73.E-11
A_84_P608048	AT4G10895	Expressed protein	-1.179	-15.111	4.98.E-06
A_84_P126821	AT2G46790	PRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription regulator	-1.146	-13.985	0.00.E+00
A_84_P20623	AT5G37060	ATCHX24 (cation/hydrogen exchanger 24); monovalent cation:proton antipor	-1.120	-13.183	1.25.E-06
A_84_P760310	AT3G28157	transposable element gene	-1.072	-11.810	7.36.E-06
A_84_P12696	AT1G26790	Dof-type zinc finger domain-containing protein	-1.059	-11.446	1.28.E-26
A_84_P14029	AT5G44440	FAD-binding domain-containing protein	-1.055	-11.355	1.24.E-10
A_84_P12579	AT2G21910	CYP96A5 (cytochrome P450, family 96, subfamily A, polypeptide 5); oxygen	-1.053	-11.297	2.57.E-24
A_84_P607723	AT2G01560	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G45800.1); contains InterPro domain Conserved hypothetical protein CHP01589, plant (InterPro:IPR006476)	-0.992	-9.807	3.00.E-05
A_84_P757840	AT2G05995	other RNA	-0.908	-8.095	8.84.E-24
A_84_P15597	AT3G50330	HEC2 (HECATE 2); DNA binding / transcription factor	-0.870	-7.409	7.83.E-08
A_84_P765788	AT4G32342	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G25360.1); similar to unknown [Populus trichocarpa] (GB:ABK93715.1)	-0.863	-7.292	2.40.E-04
A_84_P113202	AT5G36820 AT5G36730	[AT5G36820, F-box family protein];[AT5G36730, F-box family protein]	-0.842	-6.942	1.39.E-03
A_84_P526328	AT4G19260	kelch repeat-containing protein	-0.827	-6.721	1.26.E-03
A_84_P17344	AT2G22810	ACS4 (1-AMINOCYCLOPROPANE-1-CARBOXYLATE SYNTHASE 4); 1-aminocyclopropane-1-carboxylate synthase	-0.818	-6.569	8.83.E-15
A_84_P16114	AT1G09350	ATGOLS3 (ARABIDOPSIS THALIANA GALACTINOL SYNTHASE 3); transferase, transferring glycosyl groups / transferase, transferring hexosyl groups	-0.811	-6.467	2.16.E-10
A_84_P758136	AT2G29263	unknown protein	-0.806	-6.396	2.51.E-03
A_84_P604992	AT1G54700	protein binding	-0.803	-6.347	3.07.E-03
A_84_P581278	AT3G55570	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G41761.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69142.1)	-0.779	-6.016	2.52.E-07
A_84_P761132	AT3G50925	Encodes a defensin-like (DEFL) family protein.	-0.765	-5.823	5.57.E-03
A_84_P266650	AT3G54510	early-responsive to dehydration protein-related / ERD protein-related	-0.758	-5.733	1.57.E-29
A_84_P758225	AT2G36053	unknown protein	-0.729	-5.362	9.19.E-03
A_84_P16724	AT1G15050	IAA34 (indoleacetic acid-induced protein 34); transcription factor	-0.726	-5.317	9.89.E-13
A_84_P524941	AT1G21320	nucleic acid binding / nucleotide binding	-0.724	-5.296	4.71.E-24
A_84_P15973	AT5G59120	ATSBT4.13; subtilase	-0.724	-5.295	3.83.E-03
A_84_P762597	AT3G27329 AT3G27331	[AT3G27329, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G27331.1); contains InterPro domain Plant self-incompatibility S1 (InterPro:IPR010264)];[AT3G27331, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G27329.1); contains InterPro domain Plant self-incompatibility S1 (InterPro:IPR010264)]	-0.723	-5.289	7.98.E-03
A_84_P595926	AT2G15660	AGL95; transcription factor	-0.716	-5.199	1.17.E-11
A_84_P23647	AT1G23510	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G23520.1); similar to hypothetical protein [Oryza sativa (japonica cultivar-group)] (GB:BAD23602.1); contains InterPro domain Protein of unknown function DUF220 (InterPro:IPR003863)	-0.714	-5.170	7.44.E-03
A_84_P16733	AT1G48130	ATPER1 (Arabidopsis thaliana 1-cysteine peroxiredoxin 1); antioxidant	-0.711	-5.142	2.65.E-06
A_84_P210738	AT1G65090	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G36100.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G36100.2); similar to hypothetical protein [Vitis vinifera] (GB:CAN81170.1)	-0.701	-5.019	2.44.E-03

A_84_P20477	AT4G28670	protein kinase family protein	-0.699	-5.000	1.61.E-03
A_84_P21050	AT2G41280	M10	-0.691	-4.908	8.00.E-04
A_84_P16823	AT1G01060	LHY (LATE ELONGATED HYPOCOTYL); DNA binding / transcription facto	-0.668	-4.655	0.00.E+00
A_84_P757623	AT2G24205	Encodes a ECA1 gametogenesis related family protein	-0.661	-4.582	9.41.E-03
A_84_P20824	AT1G23070	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G38360.2); similar to unnamed protein product [Vitis vinifera] (GB:CAO65220.1); contains InterPro domain Protein of unknown function DUF300 (InterPro:IPR005178)	-0.647	-4.435	3.00.E-05
A_84_P764623	AT4G15248	DNA binding / zinc ion binding	-0.643	-4.400	1.13.E-30
A_84_P565626	AT4G03160	similar to DNA binding [Arabidopsis thaliana] (TAIR:AT4G03170.1)	-0.639	-4.351	2.38.E-03
A_84_P150068	AT2G43140	DNA binding / transcription factor	-0.632	-4.283	1.77.E-38
A_84_P20020	AT1G18530	calmodulin, putative	-0.630	-4.271	1.50.E-04
A_84_P16827	AT5G26070	hydroxyproline-rich glycoprotein family protein	-0.630	-4.268	7.50.E-04
A_84_P751241	AT1G69590	pseudogene, similar to SAE1-S9-protein, blastp match of 31% identity and 1.7e-11 P-value to GP|4760708|dbj|BAA77394.1||AB012866 SAE1-S9-protein {Brassica rapa}	-0.621	-4.183	2.59.E-03
A_84_P16729	AT4G37770	ACS8 (1-Amino-cyclopropane-1-carboxylate synthase 8)	-0.611	-4.086	2.75.E-31
A_84_P18714	AT5G24860	FPF1 (FLOWERING PROMOTING FACTOR 1)	-0.606	-4.038	5.26.E-03
A_84_P12378	AT1G47540	trypsin inhibitor, putative	-0.601	-3.986	6.01.E-03
A_84_P838362	AT2G43140	DNA binding / transcription factor	-0.599	-3.969	2.01.E-31
A_84_P792837	AT5G57250 AT5G57240	[AT5G57250, similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT1G62910.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN75781.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49923.1); similar to Tetratricopeptide-like helical [Medicago truncatula] (GB:ABD28636.1); contains InterPro domain Pentatricopeptide repeat (InterPro:IPR002885)];[AT5G57240, oxysterol-binding family protein]	-0.598	-3.965	2.41.E-17
A_84_P12454	AT1G17810	BETA-TIP (BETA-TONOPLAST INTRINSIC PROTEIN); water channel	-0.595	-3.935	2.63.E-03
A_84_P14075	AT5G57250 AT5G57240	[AT5G57250, similar to pentatricopeptide (PPR) repeat-containing protein [Arabidopsis thaliana] (TAIR:AT1G62910.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN75781.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49923.1); similar to Tetratricopeptide-like helical [Medicago truncatula] (GB:ABD28636.1); contains InterPro domain Pentatricopeptide repeat (InterPro:IPR002885)];[AT5G57240, oxysterol-binding family protein]	-0.590	-3.887	7.29.E-15
A_84_P547483	AT3G27025	unknown protein	-0.589	-3.883	2.60.E-04
A_84_P757817	AT2G42388	other RNA	-0.585	-3.847	6.50.E-04
A_84_P581126	AT2G46790 AT2G46670	[AT2G46790, PRR9 (PSEUDO-RESPONSE REGULATOR 9); transcription regulator];[AT2G46670, pseudo-response regulator, putative / timing of CAB expression 1-like protein, putative]	-0.581	-3.810	3.00.E-05
A_84_P12346	AT1G78720	protein transport protein sec61, putative	-0.567	-3.688	1.40.E-04
A_84_P257260	AT2G47780	rubber elongation factor (REF) protein-related	-0.565	-3.672	5.38.E-11
A_84_P860611	AT2G36820	similar to unnamed protein product [Vitis vinifera] (GB:CAO62991.1)	-0.563	-3.654	4.20.E-04
A_84_P12605	AT2G18010	SAUR10	-0.556	-3.601	0.00.E+00
A_84_P11774	AT3G21360 AT3G21370	[AT3G21360, oxidoreductase];[AT3G21370, glycosyl hydrolase family 1 prote	-0.554	-3.582	5.70.E-04
A_84_P868236	AT5G44417	pseudogene, similar to CPRD2, blastp match of 42% identity and 7.0e-94 P-value to GP|13161397|dbj|BAB33033.1||AB056448 CPRD2 {Vigna unguiculata}	-0.553	-3.573	3.58.E-07
A_84_P17288	AT2G28490	cupin family protein	-0.549	-3.537	1.25.E-03
A_84_P17513	AT3G55580	regulator of chromosome condensation (RCC1) family protein	-0.547	-3.526	8.99.E-13
A_84_P11833	AT3G53830	regulator of chromosome condensation (RCC1) family protein / UVB-resistan	-0.547	-3.523	2.31.E-10
A_84_P519046	AT3G09450	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G28780.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO15627.1)	-0.544	-3.499	5.00.E-04
A_84_P821127	AT1G18890	ATCDPK1; calmodulin-dependent protein kinase/ kinase/ protein kinase	-0.543	-3.489	4.57.E-03
A_84_P756480	AT2G27870	transposable element gene	-0.541	-3.479	8.32.E-06
A_84_P121222	AT3G21330	basic helix-loop-helix (bHLH) family protein	-0.538	-3.454	1.34.E-09
A_84_P14446	AT2G19190	FRK1 (FLG22-INDUCED RECEPTOR-LIKE KINASE 1); kinase	-0.536	-3.439	2.90.E-04
A_84_P23812	AT1G13430	sulfotransferase family protein	-0.536	-3.438	8.78.E-11
A_84_P556409	AT3G60650	unknown protein	-0.536	-3.433	4.30.E-07
A_84_P750851	AT1G34230	transposable element gene	-0.533	-3.410	1.60.E-04
A_84_P792948	AT5G28919	similar to Expressed protein [Arabidopsis thaliana] (TAIR:AT3G01345.1)	-0.525	-3.350	5.91.E-03
A_84_P13527	AT2G37030	SAUR46	-0.523	-3.333	6.83.E-07
A_84_P22124	AT3G22640	cupin family protein	-0.519	-3.307	2.38.E-03
A_84_P19263	AT1G53690	DNA-directed RNA polymerases I, II, and III 7 kDa subunit, putative	-0.518	-3.293	3.04.E-21

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)	-0.516	-3.284	3.00.E-05
A_84_P787324	AT4G36280	ATP-binding region, ATPase-like domain-containing protein	-0.514	-3.269	4.95.E-03
A_84_P297904	AT2G41230	unknown protein	-0.514	-3.267	1.92.E-15
A_84_P21311	AT3G59260	pirin, putative	-0.513	-3.260	2.00.E-05
A_84_P12267	AT2G27375	transposable element gene	-0.509	-3.230	1.40.E-07
A_84_P79759	AT5G62280	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT2G45360.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO49726.1); contains InterPro domain Protein of unknown function DUF1442 (InterPro:IPR009902)	-0.507	-3.217	1.30.E-19
A_84_P16857	AT5G41890	GDSL-motif lipase/hydrolase family protein	-0.507	-3.215	3.20.E-03
A_84_P800880	AT5G07010	sulfotransferase family protein	-0.502	-3.177	1.98.E-09
A_84_P23852	AT2G42540	COR15A (COLD-REGULATED 15A)	-0.498	-3.145	7.34.E-11
A_84_P279060	AT3G12320	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G06980.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN75675.1)	-0.497	-3.140	2.76.E-32
A_84_P17085	AT1G05650	polygalacturonase, putative / pectinase, putative	-0.494	-3.120	6.17.E-03
A_84_P22821	AT1G49640	hydrolase	-0.492	-3.108	2.26.E-11
A_84_P584036	AT4G12360	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-0.492	-3.103	2.75.E-03
A_84_P271180	AT1G53490	DNA binding	-0.489	-3.081	0.00.E+00
A_84_P21248	AT3G44560	oxidoreductase, acting on the CH-CH group of donors	-0.484	-3.045	2.73.E-07
A_84_P762364	AT3G60647	unknown protein	-0.481	-3.027	1.12.E-03
A_84_P21360	AT1G69570 AT1G69572	[AT1G69570, Dof-type zinc finger domain-containing protein];[AT1G69572,	-0.479	-3.016	2.60.E-19
A_84_P541566	AT5G28646	WVD2 (wave-dampened2)	-0.477	-2.998	2.30.E-04
A_84_P23436	AT5G22500	acyl CoA reductase, putative / male-sterility protein, putative	-0.473	-2.971	3.44.E-07
A_84_P600521	AT1G48090	C2 domain-containing protein	-0.472	-2.968	5.66.E-03
A_84_P753180	AT1G35035	Encodes a Plant thionin family protein	-0.472	-2.968	1.81.E-03
A_84_P21493	AT5G02540	short-chain dehydrogenase/reductase (SDR) family protein	-0.472	-2.963	6.52.E-19
A_84_P242573	AT5G54470	zinc finger (B-box type) family protein	-0.471	-2.960	5.91.E-18
A_84_P751634	AT1G30150	transposable element gene	-0.470	-2.953	1.18.E-03
A_84_P16678	AT4G25420	GA5 (GA REQUIRING 5); gibberellin 20-oxidase/ gibberellin 3-beta-dioxygen	-0.469	-2.945	5.72.E-24
A_84_P17928	AT1G54980	invertase/pectin methylesterase inhibitor family protein	-0.466	-2.925	3.06.E-03
A_84_P17840	AT5G51930	glucose-methanol-choline (GMC) oxidoreductase family protein	-0.465	-2.920	5.23.E-03
A_84_P759241	AT3G30122	pseudogene similar to peptide chain release factor protein	-0.462	-2.900	6.22.E-12
A_84_P18064	AT1G15580	IAA5 (indoleacetic acid-induced protein 5); transcription factor	-0.462	-2.899	4.58.E-28
A_84_P544625	AT2G10560	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04860.1); similar to expressed protein [Oryza sativa (japonica cultivar-group)] (GB:ABF97907.1); similar to hypothetical protein OsJ_011438 [Oryza sativa (japonica cultivar-group)] (GB:EAZ27955.1); similar to Os03g0649000 [Oryza sativa (japonica cultivar-group)] (GB:NP_001050782.1)	-0.459	-2.881	2.92.E-03
A_84_P843096	AT1G29490	SAUR68	-0.459	-2.876	3.35.E-14
A_84_P19241	AT2G46830	CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor	-0.458	-2.870	1.25.E-35
A_84_P833445	AT1G26790	Dof-type zinc finger domain-containing protein	-0.456	-2.856	7.97.E-03
A_84_P216278	AT1G21210	WAK4 (WALL ASSOCIATED KINASE 4); protein serine/threonine kinase	-0.455	-2.850	1.69.E-03
A_84_P23950	AT1G07450	tropinone reductase, putative / tropine dehydrogenase, putative	-0.454	-2.846	2.76.E-28
A_84_P10076	AT4G28720	flavin-containing monooxygenase family protein / FMO family protein	-0.447	-2.802	2.93.E-39
A_84_P119242	AT5G45775	60S ribosomal protein L11 (RPL11D)	-0.447	-2.801	8.59.E-03
A_84_P768186	AT5G43285	Encodes a defensin-like (DEFL) family protein.	-0.446	-2.793	9.39.E-03
A_84_P19163	AT2G43050	ATPMEPCRD; pectinesterase	-0.446	-2.792	1.82.E-19
A_84_P10799	AT3G29190	lyase/ magnesium ion binding	-0.443	-2.774	8.00.E-04
A_84_P22463	AT5G10120	ethylene insensitive 3 family protein	-0.442	-2.765	4.80.E-04
A_84_P55550	AT4G32280	IAA29 (indoleacetic acid-induced protein 29); transcription factor	-0.440	-2.756	6.87.E-09
A_84_P207668	AT5G67060	HEC1 (HECATE 1); transcription factor	-0.432	-2.702	5.51.E-09
A_84_P582345	AT5G03590	GDSL-motif lipase/hydrolase protein-related	-0.426	-2.666	4.69.E-03
A_84_P18792	AT5G53870	plastocyanin-like domain-containing protein	-0.426	-2.665	2.08.E-24
A_84_P13566	AT2G47050	invertase/pectin methylesterase inhibitor family protein	-0.419	-2.623	3.00.E-05
A_84_P793763	AT3G57020	strictosidine synthase family protein	-0.418	-2.618	4.24.E-03
A_84_P792187	AT1G48720	no_match	-0.416	-2.604	3.14.E-03
A_84_P828837	AT1G07645	lactoylglutathione lyase family protein / glyoxalase I family protein	-0.415	-2.600	7.56.E-03
A_84_P794374	AT4G27260	GH3.5/WES1; indole-3-acetic acid amido synthetase	-0.412	-2.585	6.11.E-25
A_84_P523896	AT5G50335	unknown protein	-0.412	-2.585	7.28.E-28
A_84_P12395	AT1G32900	starch synthase, putative	-0.409	-2.567	1.29.E-25

A_84_P507058	AT5G57770 AT5G57760	[AT5G57770, similar to unnamed protein product [Vitis vinifera] (GB:CAO66578.1); contains InterPro domain Pleckstrin-like, plant (InterPro:IPR013666); contains InterPro domain Protein of unknown function DUF828, plant (InterPro:IPR008546)];[AT5G57760, unknown protein]	-0.405	-2.543	2.66.E-11
A_84_P18906	AT1G01590	FRO1 (FERRIC REDUCTION OXIDASE 1); ferric-chelate reductase	-0.405	-2.543	1.64.E-06
A_84_P12164	AT5G51030	short-chain dehydrogenase/reductase (SDR) family protein	-0.405	-2.543	1.01.E-14
A_84_P524502	AT3G59900	(ARGOS); unknown protein	-0.405	-2.541	5.04.E-44
A_84_P789543	AT5G57770 AT5G57760	[AT5G57770, similar to unnamed protein product [Vitis vinifera] (GB:CAO66578.1); contains InterPro domain Pleckstrin-like, plant (InterPro:IPR013666); contains InterPro domain Protein of unknown function DUF828, plant (InterPro:IPR008546)];[AT5G57760, unknown protein]	-0.404	-2.534	1.41.E-10
A_84_P23844	AT2G43870	polygalacturonase, putative / pectinase, putative	-0.403	-2.532	1.51.E-11
A_84_P22363	AT4G27360	dynein light chain, putative	-0.403	-2.530	7.30.E-15
A_84_P847991	AT2G46830	CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor	-0.403	-2.528	3.13.E-13
A_84_P549446	AT4G35720	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35690.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23717.1); contains InterPro domain Protein of unknown function DUF241, plant (InterPro:IPR004320)	-0.403	-2.527	1.90.E-06
A_84_P20292	AT3G02380	COL2 (CONSTANS-LIKE 2); transcription factor/ zinc ion binding	-0.401	-2.517	8.87.E-18
A_84_P585078	AT5G17780	hydrolase, alpha/beta fold family protein	-0.397	-2.494	1.40.E-45
A_84_P15595	AT3G49970	phototropic-responsive protein, putative	-0.397	-2.494	2.45.E-03
A_84_P16777	AT5G07010	sulfotransferase family protein	-0.396	-2.490	3.60.E-08
A_84_P10169	AT5G09970	CYP78A7 (cytochrome P450, family 78, subfamily A, polypeptide 7); oxygen	-0.396	-2.489	5.89.E-11
A_84_P796648	AT1G76610	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT1G21050.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN67637.1); contains InterPro domain Protein of unknown function DUF617, plant (InterPro:IPR006460)	-0.396	-2.486	6.00.E-05
A_84_P795830	AT1G21320	nucleic acid binding / nucleotide binding	-0.394	-2.476	1.33.E-12
A_84_P94969	AT5G06980	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G12320.1)	-0.393	-2.473	6.18.E-10
A_84_P52840	AT3G54500	similar to dentin sialophosphoprotein-related [Arabidopsis thaliana] (TAIR:AT5G64170.1); similar to dentin sialophosphoprotein-related [Arabidopsis thaliana] (TAIR:AT5G64170.2); similar to conserved hypothetical protein [Medicago truncatula] (GB:ABD28297.1)	-0.389	-2.448	8.17.E-12
A_84_P550153	AT3G30720	unknown protein	-0.389	-2.446	5.35.E-06
A_84_P820018	AT3G54500	no_match	-0.386	-2.434	6.31.E-28
A_84_P19451	AT4G02780	GA1 (GA REQUIRING 1); ent-copalyl diphosphate synthase	-0.384	-2.421	1.92.E-11
A_84_P844074	AT2G20250	unknown protein	-0.384	-2.421	8.10.E-04
A_84_P761999	AT5G04853 AT3G28674	[AT5G04853, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G28674.1); contains domain Multidrug efflux transporter AcrB transmembrane domain (SSF82866)];[AT3G28674, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G04853.1)]	-0.384	-2.420	4.60.E-04
A_84_P797535	AT4G39400	BRI1 (BRASSINOSTEROID INSENSITIVE 1); kinase	-0.381	-2.402	2.35.E-03
A_84_P250035	AT2G41250	haloacid dehalogenase-like hydrolase family protein	-0.380	-2.399	2.40.E-26
A_84_P20410	AT1G06080	ADS1 (DELTA 9 DESATURASE 1); oxidoreductase	-0.379	-2.396	8.41.E-10
A_84_P21330	AT3G44900	ATCHX4 (CATION/H+ EXCHANGER 4); monovalent cation:proton antiporte	-0.378	-2.388	2.05.E-06
A_84_P167173	AT4G25480	DREB1A (DEHYDRATION RESPONSE ELEMENT B1A); DNA binding / transcription activator/ transcription factor	-0.377	-2.381	3.15.E-06
A_84_P19825	AT5G04190	PKS4 (PHYTOCHROME KINASE SUBSTRATE 4)	-0.376	-2.376	1.14.E-07
A_84_P22571	AT5G52310	COR78 (COLD REGULATED 78)	-0.376	-2.375	5.47.E-06
A_84_P17710	AT5G02760	protein phosphatase 2C family protein / PP2C family protein	-0.375	-2.373	2.81.E-20
A_84_P841143	AT3G28170	unknown protein	-0.375	-2.369	3.10.E-07
A_84_P502380	AT4G19970	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G44820.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO46707.1); contains domain PTHR10483:SF6 (PTHR10483:SF6); contains domain PTHR10483 (PTHR10483)	-0.374	-2.364	5.78.E-12
A_84_P847314	AT2G46830	CCA1 (CIRCADIAN CLOCK ASSOCIATED 1); transcription factor	-0.373	-2.363	7.61.E-06
A_84_P22704	AT1G62450	Rho GDP-dissociation inhibitor family protein	-0.371	-2.352	1.80.E-04
A_84_P21523	AT1G18400	BEE1 (BR ENHANCED EXPRESSION 1); transcription factor	-0.370	-2.344	3.22.E-12
A_84_P753771	AT1G61575	ATP binding / protein kinase	-0.367	-2.326	1.00.E-05
A_84_P15502	AT3G14370	WAG2; kinase	-0.364	-2.310	1.46.E-32
A_84_P23021	AT2G29090	CYP707A2 (cytochrome P450, family 707, subfamily A, polypeptide 2); oxyge	-0.361	-2.298	4.70.E-10
A_84_P815985	AT5G22500	acyl CoA reductase, putative / male-sterility protein, putative	-0.356	-2.272	2.10.E-04
A_84_P13987	AT5G25190	ethylene-responsive element-binding protein, putative	-0.356	-2.269	8.69.E-07
A_84_P230289	AT2G44080	ARL (ARGOS-LIKE)	-0.356	-2.268	3.87.E-16

A_84_P22852	AT1G01520	myb family transcription factor	-0.355	-2.264	1.33.E-13
A_84_P761408	AT3G44042	transposable element gene	-0.353	-2.257	1.20.E-04
A_84_P831446	AT5G17780	hydrolase, alpha/beta fold family protein	-0.353	-2.256	7.63.E-29
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)	-0.352	-2.250	6.31.E-03
A_84_P761088	AT3G11773	electron carrier/ protein disulfide oxidoreductase	-0.352	-2.248	2.42.E-03
A_84_P792000	AT3G27503	SCRL19 (SCR-Like 19)	-0.351	-2.242	9.88.E-03
A_84_P789302	AT1G26945	no_match	-0.350	-2.237	8.76.E-26
A_84_P766132	AT5G39200 AT5G39170 AT5G39140	[AT5G39200, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39140.1); similar to hypothetical protein [Vitis vinifera] (GB:CAN77667.1)];[AT5G39170, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39140.1); similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39200.1)];[AT5G39140, similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39200.1)]	-0.348	-2.229	5.81.E-03
A_84_P792687	AT1G48145	no_match	-0.346	-2.219	2.90.E-03
A_84_P790159	AT5G38000	NADP-dependent oxidoreductase, putative	-0.346	-2.218	3.99.E-06
A_84_P10579	AT1G78970	LUP1 (LUPEOL SYNTHASE 1); lupeol synthase	-0.346	-2.217	5.92.E-12
A_84_P586474	AT2G39855	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G55646.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO69100.1)	-0.345	-2.214	1.01.E-06
A_84_P861080	AT3G20395	protein binding / zinc ion binding	-0.343	-2.205	3.33.E-26
A_84_P19887	AT1G80760	NIP6;1 (NOD26-like intrinsic protein 6;1); water channel	-0.342	-2.197	1.01.E-06
A_84_P108502	AT2G02120	LCR70/PDF2.1 (Low-molecular-weight cysteine-rich 70); protease inhibitor	-0.341	-2.194	5.20.E-04
A_84_P764577	AT4G14819	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT3G22540.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO71190.1); contains InterPro domain Protein of unknown function DUF1677, plant (InterPro:IPR012876)	-0.341	-2.191	2.82.E-06
A_84_P19525	AT4G27310	zinc finger (B-box type) family protein	-0.339	-2.184	1.33.E-11
A_84_P767553	AT5G37940 AT5G38000	[AT5G37940, NADP-dependent oxidoreductase, putative];[AT5G38000, NADP-dependent oxidoreductase, putative]	-0.338	-2.178	4.00.E-05
A_84_P16492	AT3G21150	zinc finger (B-box type) family protein	-0.338	-2.178	2.94.E-17
A_84_P734890	AT2G07784	transposable element gene	-0.337	-2.171	4.10.E-07
A_84_P21616	AT5G49700	DNA-binding protein-related	-0.332	-2.147	8.86.E-13
A_84_P10124	AT4G14560	IAA1 (INDOLE-3-ACETIC ACID INDUCIBLE); transcription factor	-0.332	-2.145	1.47.E-15
A_84_P793924	AT3G14310	ATPME3 (Arabidopsis thaliana pectin methylesterase 3)	-0.329	-2.135	1.10.E-04
A_84_P544465	AT1G26945	transcription regulator	-0.329	-2.134	5.34.E-12
A_84_P762938	AT4G22545	pseudogene of unknown protein	-0.328	-2.129	4.17.E-08
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 (PTHR13542)	-0.327	-2.125	1.70.E-04
A_84_P21449	AT4G34770	SAUR1	-0.326	-2.120	2.67.E-14
A_84_P21047	AT2G38530	LTP2 (LIPID TRANSFER PROTEIN 2); lipid binding	-0.325	-2.114	5.89.E-15
A_84_P13439	AT2G39980	transferase family protein	-0.323	-2.105	7.68.E-13
A_84_P761811	AT3G20395	protein binding / zinc ion binding	-0.323	-2.103	1.49.E-15
A_84_P787999	AT3G29370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39240.1)	-0.321	-2.092	1.52.E-09
A_84_P11973	AT4G30110	HMA2 (Heavy metal ATPase 2); cadmium-transporting ATPase	-0.318	-2.080	1.42.E-06
A_84_P552783	AT3G28170	unknown protein	-0.317	-2.076	2.00.E-05
A_84_P828261	AT1G51580	KH domain-containing protein	-0.317	-2.076	6.00.E-05
A_84_P23889	AT1G04880	high mobility group (HMG1/2) family protein / ARID/BRIGHT DNA-binding domain-containing protein	-0.314	-2.061	1.22.E-03
A_84_P795880	AT2G41230	unknown protein	-0.314	-2.059	1.14.E-07
A_84_P12944	AT4G36110	SAUR9	-0.314	-2.058	4.26.E-03
A_84_P94979	AT5G18060	SAUR23	-0.312	-2.052	3.10.E-10
A_84_P122462	AT5G53980	ATHB52 (ARABIDOPSIS THALIANA HOMEOBOX PROTEIN 52); transcrip	-0.312	-2.050	3.06.E-06
A_84_P797355	AT4G36110	auxin-responsive protein, putative	-0.311	-2.048	1.40.E-04

A_84_P23423	AT5G14360	ubiquitin family protein	-0.311	-2.047	3.45.E-12
A_84_P809041	AT2G38530	LTP2 (LIPID TRANSFER PROTEIN 2); lipid binding	-0.311	-2.046	7.78.E-23
A_84_P843083	AT1G76530	auxin efflux carrier family protein	-0.310	-2.042	7.80.E-06
A_84_P591083	AT3G51410	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT4G35680.1); similar to unnamed protein product [Vitis vinifera] (GB:CAO23714.1); contains InterPro domain Protein of unknown function DUF241, plant (InterPro:IPR004320)	-0.310	-2.042	1.00.E-05
A_84_P18533	AT4G12470	protease inhibitor/seed storage/lipid transfer protein (LTP) family protein	-0.308	-2.034	6.65.E-12
A_84_P141269	AT5G18050	SAUR22	-0.307	-2.029	1.03.E-15
A_84_P12114	AT5G37590	binding	-0.307	-2.029	1.53.E-03
A_84_P144819	AT3G29370	similar to unknown protein [Arabidopsis thaliana] (TAIR:AT5G39240.1)	-0.307	-2.028	1.34.E-06
A_84_P838948	AT1G01520	myb family transcription factor	-0.307	-2.025	1.31.E-07
A_84_P582351	AT5G05965	unknown protein	-0.305	-2.018	1.14.E-09
A_84_P10225	AT5G37960	oxidoreductase-related	-0.304	-2.014	8.00.E-05
A_84_P11811	AT3G48970	copper-binding family protein	-0.304	-2.013	5.13.E-10

Table S3. Pathway analysis of genes down-regulated in *ztl* mutants performed with the Gene Functional Classification Tool in DAVID Bioinfomatics Resources 6.7.

Annotation Cluster 1: Enrichment Score: 4.525889916481404			
Term	Count	%	PValue
response to endogenous stimulus	24	15.894	3.31.E-08
response to hormone stimulus	23	15.232	4.49.E-08
response to auxin stimulus	14	9.272	2.24.E-07
response to organic substance	25	16.556	2.39.E-07
intracellular signaling cascade	13	8.609	4.56.E-03
hormone-mediated signaling	9	5.960	6.58.E-03
cellular response to hormone stimulus	9	5.960	6.58.E-03
auxin mediated signaling pathway	4	2.649	3.96.E-02
Annotation Cluster 2: Enrichment Score: 3.866677277370593			
Term	Count	%	PValue
response to light stimulus	13	8.609	4.17.E-05
response to radiation	13	8.609	5.78.E-05
response to abiotic stimulus	20	13.245	1.80.E-04
response to red or far red light	7	4.636	7.88.E-04
Annotation Cluster 3: Enrichment Score: 1.8837448032489852			
Term	Count	%	PValue
photoperiodism	4	2.649	2.14.E-03
response to gibberellin stimulus	5	3.311	7.24.E-03
photoperiodism, flowering	3	1.987	2.35.E-02
vegetative to reproductive phase transition	3	1.987	8.01.E-02
Annotation Cluster 4: Enrichment Score: 1.778121309358034			
Term	Count	%	PValue
reproductive structure development	12	7.947	7.07.E-03
reproductive developmental process	12	7.947	1.42.E-02
post-embryonic development	11	7.285	4.62.E-02
Annotation Cluster 5 Enrichment Score: 1.503590992991188			
Term	Count	%	PValue
seed dormancy	3	1.987	3.54.E-03
dormancy process	3	1.987	3.54.E-03
seed maturation	3	1.987	4.63.E-03
reproductive process in a multicellular organism	3	1.987	3.96.E-02
multicellular organism reproduction	3	1.987	4.40.E-02
seed development	4	2.649	5.29.E-01
fruit development	4	2.649	5.60.E-01

Annotation Cluseter 6: Enrichment Score: 1.4835674934001872			
Term	Count	%	PValue
cold acclimation	3	1.987	7.20.E-03
response to cold	5	3.311	6.32.E-02
response to temperature stimulus	6	3.974	7.78.E-02

Annotation Cluster 7: Enrichment Score: 0.9776664968316278			
Term	Count	%	PValue
terpenoid metabolic process	4	2.649	2.52.E-02
isoprenoid metabolic process	4	2.649	5.52.E-02
terpenoid biosynthetic process	3	1.987	8.97.E-02
lipid biosynthetic process	6	3.974	1.29.E-01
isoprenoid biosynthetic process	3	1.987	1.64.E-01

Annotation Cluster 8: Enrichment Score: 0.6237420273710536			
Term	Count	%	PValue
response to osmotic stress	6	3.974	1.14.E-01
response to abscisic acid stimulus	4	2.649	2.77.E-01
response to salt stress	4	2.649	4.25.E-01

Annotation Cluster 9: Enrichment Score: 0.6164503682770265			
Term	Count	%	PValue
cell growth	4	2.649	1.59.E-01
regulation of cell size	4	2.649	1.78.E-01
regulation of cellular component size	4	2.649	1.97.E-01
growth	4	2.649	2.11.E-01
cell morphogenesis	3	1.987	3.88.E-01
cellular component morphogenesis	3	1.987	4.39.E-01

Annotation Cluster 10: Enrichment Score: 0.3828576108384531			
Term	Count	%	PValue
lipid biosynthetic process	6	3.974	1.29.E-01
organic acid biosynthetic process	3	1.987	7.43.E-01
carboxylic acid biosynthetic process	3	1.987	7.43.E-01

Annotation Cluster 11: Enrichment Score: 0.08674813161172817			
Term	Count	%	PValue
defense response to fungus	3	1.987	7.31.E-01
response to fungus	3	1.987	7.77.E-01
defense response	4	2.649	9.66.E-01

Annotation Cluster 12: Enrichment Score: 0.01166466285060844			
Term	Count	%	PValue
phosphate metabolic process	5	3.311	9.69.E-01
phosphorus metabolic process	5	3.311	9.69.E-01
protein amino acid phosphorylation	4	2.649	9.72.E-01
phosphorylation	4	2.649	9.84.E-01

Table S4. PCR primers used for expression analysis.

Gene	Primer sequence
ACT2_F	GGTAACATTGTGCTCAGTGGTGG
ACT2_R	AACGACCTTAATCTTCATGCTGC
SAUR22_F	CCTTCTTTCAAGCTCTGCTCAGT
SAUR22_R	TTGGAGCCGAGAAGTCACATT
SAUR23_F	AGTGTACGTAGGAGAGAGCCAGAA
SAUR23_R	ATCGGATGATCGAACCCAAA
IAA29_F	CTTCCAAGGGAAAGAGGGTGAC
IAA29_R	TTCCGCAAAGATCTTCCATGTAAC

Chapter 3

ZEITLUPE enhances expression of *PIF4* and *YUC8* in the upper aerial parts of *Arabidopsis* seedlings to positively regulate hypocotyl elongation

Abstract

ZTL is a blue light receptor that possesses a light-oxygen-voltage-sensing (LOV) domain, an F-box motif, and a kelch repeat domain. ZTL promotes hypocotyl elongation under high temperature (28 °C) in *Arabidopsis thaliana*; however, the mechanism of this regulation is unknown. Here, we divided seedlings into hypocotyls and upper aerial parts, and performed microarray analyses. In hypocotyl, 1062 genes were down-regulated in *ztl* mutants (*ztl-3* and *ztl-105*) compared with wild type; some of these encoded enzymes involved in cell wall modification, consistent with reduced hypocotyl elongation. In upper aerial parts, 1038 genes were down-regulated in the *ztl* mutants compared with wild type; these included genes involved in auxin synthesis and auxin response. Furthermore, the expression of the *PHYTOCHROME INTERACTING FACTOR 4* (*PIF4*) gene, which encodes a transcription factor known to positively regulate *YUCCA* gene*s* (*YUCs*), was also decreased. Genetic analysis revealed that overexpression of *PIF4* and *YUC8* could restore the loss of hypocotyl length in the *ztl* mutants. Our results suggest that the *ZTL* induces expression of *YUC8* via *PIF4* in upper aerial parts and promotes hypocotyl elongation.

Key words: Hypocotyl elongation・ZTL・IAA・YUC・PIF・phyB

Introduction

Plants use light not only as an energy source, but also as an environmental signal for growth and development. Many genes and proteins are known to be involved in light signaling, including photoreceptors. *Arabidopsis thaliana* has the following photoreceptors: phytochromes A to E (phyA–E), which absorb red and far red light (Sharrock and Quail 1989; Clack et al. 1994); UV-B Resistance 8 (UVR8), which absorbs Ultraviolet-B radiation (UV-B) (Kami et al. 2010; Heijde and Ulm 2012); cryptochromes 1 and 2 (CRY1 and 2), phototropins 1 and 2 (PHOT1 and 2) and ZEITLUPE (ZTL) / LOV KELCH PROTEIN2 (LKP2) / FLAVIN-BINDING KELCH REPEAT F-BOX 1 (FKF1), which absorb blue light (Lin 2002; Briggs and Christie 2002; Kiyosue and Wada 2000; Nelson et al. 2000; Schultz et al. 2001; Somers et al. 2000). ZTL has a light-oxygen-voltage-sensing (LOV) domain in the N-terminal region, an F-box motif, and 6 kelch repeats in the C-terminal region. The LOV domain binds flavin mononucleotide and has photochemical properties like those of phototropins (Demarsy and Fankhauser 2009). The F-box motif is involved in the formation of the Cul1–Rbx1–Skp1–F-box (SCF) complex, which functions as an E3 ubiquitin ligase (Vierstra 2003). Kelch repeats form a β-propeller structure, which is involved in protein–protein interactions (Adams et al. 2000).

ZTL is involved in the regulation of circadian rhythm and photoperiodic flowering and the regulation of hypocotyl elongation under light conditions (Zoltowski and Imaizumi 2014; Miyazaki 2015). The *ztl* mutant has a long-period circadian rhythm (Kevei et al. 2006) and bloom early under short-day conditions (Takase et al. 2011). In regulating circadian rhythm, ZTL acts as a component of the E3 ubiquitin ligase complex, leading to degradation of TIMING OF CAB EXPRESSION 1 (TOC1) and

PSEUDO-RESPONSE REGULATOR 5 (PRR5) via the proteasome pathway (Más et al. 2003; Yasuhara et al. 2004; Kiba et al. 2007; Fujiwara et al. 2008). In regulating photoperiodic flowering, it may be involved in degradation of flowering inhibitors such as CYCLING DOF FACTOR 2 (CDF2) via the proteasome pathway (Fornara et al. 2009).

Hypocotyl elongation has long been studied as a model for elucidating the mechanism of plant growth (Gendreau et al. 1997). In a process involving auxin, hypocotyl elongation occurs when cells that have absorbed water enlarge in the vertical direction. In hypocotyl treated with auxin, the cell membrane proton pump is activated and the cell wall is acidified. Subsequently, EXPANSIN (EXP), a protein that causes loosening of the cell wall, acts to induce an increase in cell volume (Cosgrove 2000).

ZTL positively regulates hypocotyl elongation under light conditions (Saitoh et al. 2015a, b). *ZTL* ox plants, which overexpress *ZTL*, have long hypocotyls, whereas *ztl* loss of function mutants have short hypocotyls (Saitoh et al. 2015a, b). The difference in hypocotyl length between wild type (WT) and the *ztl* mutants is greater at 28 °C than at 22 °C (Miyazaki et al. 2015). In contrast, under dark conditions, the *ztl* mutants show hypocotyl elongation to the same extent as WT (Miyazaki et al. 2015). In our previous microarray analysis of the whole seedlings of WT and the *ztl* mutants under continuous light and high temperature conditions, we identified genes whose expression was decreased in the *ztl* mutants compared with WT. The identified genes included 7 *SMALL AUXIN UP RNA (SAUR)* and 4 *AUXIN / INDOLE-3-ACETIC ACID (AUX / IAA)* genes, suggesting abnormal auxin signaling in the *ztl* mutants (Saitoh et al. 2015b). Furthermore, experiments with auxin inhibitors revealed that auxin signal suppression was involved in the phenotype of the short hypocotyl of the *ztl* mutants (Saitoh et al.

2015b). Auxin is synthesized at specific locations, and then transported to the site of action by polar transport (Petrásek and Friml 2009). In hypocotyl elongation, auxin is produced mainly in the cotyledon and is transported along the hypocotyl (Keuskamp et al. 2010; Kohnen et al. 2016).

In this study, we performed microarray analysis of WT and the *ztl* mutant seedlings divided into hypocotyl and upper aerial parts to clarify where ZTL controls auxin signals in *A. thaliana*.

Results

Hypocotyl growth kinetics

We have previously shown that T-DNA insertion mutants for *ZTL* have short hypocotyls, which is especially evident at a high ambient temperature, 28 °C (Miyazaki et al. 2015). Here, to find the time point with the largest difference between the *ztl* mutants (*ztl-3* and *ztl-105*) and WT (Columbia-0 accession), we measured the hypocotyl lengths for 10 days after incubation (DAI): i.e., after transfer of the seeds from the dark to light (Fig. 1). In this experiment, under continuous white light, seeds were germinated at 22 °C for the first 3 days and then transferred to 28 °C for 7 days. All seeds had germinated by 2 DAI and the reduced growth of hypocotyls in the *ztl* mutants compared with WT began to be observed at 3 DAI. After the transfer to 28 °C, the hypocotyls remained shorter in the *ztl* mutants than in WT, with the maximum difference being 1.6 mm (*ztl-3*) and 1.7 mm (*ztl-105*) at 8 DAI. At this time point, all seedlings (WT, *ztl-3*, and *ztl-105*) showed two expanded green cotyledons and two small true leaves, indicating that they are at the same developmental stage (Fig. S1). Thus, we used seedlings at 8 DAI in subsequent experiments.

Gene expression profile of hypocotyls of *ztl* seedlings

We performed microarray analysis using total RNA extracted from the hypocotyls of WT, *ztl-3*, and *ztl-105* plants at 8 DAI. A total of 1062 genes were down-regulated (average fold change < -2.0; Table S1) and 638 genes were up-regulated (average fold change > 2.0; Table S2) in both *ztl-3* and *ztl-105* mutants vs. WT. Annotation groups of the down-regulated and up-regulated genes are shown in Tables S3 and S4, respectively. Down-regulation of *ZTL* in the *ztl* mutants (AT5G57360; average fold change, -6.2) validated this microarray analysis. Pathway analysis classified the up- and down-regulated genes into several groups. Among them, the "regulation of transcription" group with 83 genes showed the smallest average *P*-value (5.37E-15). This group included genes for negative regulators of hypocotyl elongation such as *AUXIN/INDOLE-3-ACETIC ACID 20* (*IAA20*), *EARLY FLOWERING 3* (*ELF3*), and *TRANSCRIPTION FACTOR 2* (*TCP2*) (Sato and Yamamoto, 2008; Reed et al., 2000; He et al., 2016), which were up-regulated in the *ztl* mutants compared with WT. Among gene groups down-regulated in the *ztl* mutants, the cell wall modification group with 14 genes showed the smallest average *P*-value (1.70E-05; Table S3). This group includes 6 *EXPANSIN* (*EXP*) genes (*EXP A5*, *A8*, *A11*, *B1*, *B3*, and *EXP-like B1*), 5 *PECTINESTERASE* genes (*PME 2*, *16*, *35, 40*, and *41*), and *TRYPTOPHAN SYNTHASE ALPHA CHAIN 3* (*TRP3*), *BETA-GALACTOSIDASE 6* (*BGAL6*), and *XYLOGLUCAN ENDOTRANSGLUCOSYLASE 33* (*XTH33*), which is consistent with the reduced growth of hypocotyl in the *ztl* mutants.

To verify the results of the microarray analysis, we performed quantitative reverse-transcription PCR (qRT-PCR) analysis of several of the genes described above. As expected from the microarray results, the expression levels of *IAA20*, *ELF3*, and *TCP2* were significantly increased in the *ztl* mutants (Fig. S2), while those of *EXP8*, *PME2*, *BGAL6*, and *XTH33* were significantly reduced in the *ztl* mutants, compared with WT (Fig. 2a).

Gene expression profile of upper aerial parts including cotyledons and apical meristem of the *ztl* seedlings

The phenotypes of WT plants treated with auxin inhibitor 5-(4-chlorophenyl)-4H-1,2,4-triazole-3thiol (yucasin), 1-N-naphthylphthalamic acid (NPA), or α- (phenylethyl-2-one)-indole-3-acetic acid (PEO-IAA)] can mimic the *ztl* mutant phenotypes in hypocotyl at 28 °C (Saito et al. 2015b), suggesting that auxin plays a key role in promoting hypocotyl elongation by *ZTL* at this temperature. However, most auxin-related genes were not significantly differentially expressed in the microarray analysis of hypocotyls of *ztl* seedlings vs. WT described above. Thus, the change in early auxin signaling may occur in organs other than hypocotyl. To test this hypothesis, we extracted total RNA from the cotyledons and apical meristem (i.e., upper aerial parts) of WT and the *ztl* mutants at 8 DAI, and performed microarray analysis. A total of 469 genes were up-regulated (average fold change > 2.0; Table S5) in the upper aerial parts of both the *ztl* mutants vs. WT, but no functional clusters was detected with a significant *P*-value ($P < 0.05$; Table S6). On the other hand, 1038 genes were down-regulated (average fold change < -2.0; Table S7) in both the *ztl* mutants vs. WT; the annotation groups of the down-regulated genes are shown in Table S8.

In the upper aerial parts of the *ztl* mutants, genes involved in response to endogenous stimulus were down-regulated compared with WT. Among the down-regulated genes, 61 genes involved in the response to endogenous stimulus had the smallest *P*-value (2.7E-8). This group included 16 *SMALL AUXIN UP RNA* (*SAUR*) genes (*SAUR10*, *19–22*, *24–27*, *29*, *52*, *61–64*, and *66*) and 7 *AUXIN/INDOLE-3-ACETICACID* (*AUX/IAA*) genes (*IAA1*, *5*, *6*, *14*, *19*, *29*, and *30*). We performed qRT-PCR to confirm the down-regulation of three auxin-inducible genes, *SAUR22, IAA19*, and *IAA29*. As expected, the expression of these genes was significantly decreased in the upper aerial parts of both the *ztl* mutants compared with WT (Fig. 2b). Next, we focused on the genes in the cluster with the second smallest *P*-value (5.6E-07): i.e., 20 genes involved in the response to red or far red light (Table S8. This group included *PIF4* and *PIF5*, which encode transcription factors that positively regulate hypocotyl elongation. Because PIF4 promotes transcription of *YUC* auxin synthase genes (Franklin et al. 2011; Sun et al. 2012), we list the microarray results for *YUC* and other auxin synthase genes in Table 1. In *A. thaliana*, the auxin IAA is synthesized from tryptophan by four pathways i.e., the tryptamine (TAM) pathway, the indole-3-acetamide (IAM) pathway, the indole-3-pyruvic acid (IPA) pathway and the indole-3-acetaldoxime (IAOx) pathway. In the upper aerial parts, we found that expression levels of *TAR3, YUC3, YUC8*, and *YUC9* of the IPA pathway were decreased in both the *ztl* mutants compared with WT. Expression levels of genes in other auxin synthetic pathways were not reduced in the mutants (Fig. S3). We performed qRT-PCR to confirm the down-regulation of *PIF4*, *PIF5*, and four auxin biosynthesis genes, *TAR3*, *YUC3*, *YUC8*, and *YUC9*; the expression of these genes was significantly decreased in the upper aerial parts of both the *ztl* mutants vs. WT (Fig. 2b).

Promoter activities for *pYUC8:GUS* and *pDR5:GUS* are reduced in the *ztl* mutants

PIF4 binds to and activates the *YUC8* gene promoter (Sun et al. 2012). The above microarray and qRT-PCR analyses indicate that *PIF4* transcript levels were decreased in the *ztl* mutants compared with WT. Therefore, the short-hypocotyl phenotype of the *ztl* mutants may be caused by reduced *YUC8* expression. To investigate this possibility, we measured the promoter activity of *YUC8* when located upstream of the β-glucuronidase (*GUS*) gene in a reporter construct. Consistent with the above hypothesis, *GUS* expression was decreased by 69% for *ztl-3* and 65% for *ztl-105* (Fig. 3a), and GUS activity was decreased by 59% for *ztl-3* and 43% for *ztl-105* (Fig. 3b) compared with WT. In the histochemical analysis, the GUS staining of *pYUC8:GUS* was observed at the tips of the cotyledons in WT background, but was not detected in the *ztl* mutant background (Fig. 3c).

Microarray analysis and qRT-PCR suggested that the auxin-responsive gene expression was decreased in the *ztl* mutants compared with WT. These results suggest that the promoter activity of auxin-responsive genes in general may be decreased. To test this possibility, we used the *pDR5:GUS* construct, which comprises tandem auxin-responsive *cis* elements (AuxRE) and GUS (Ulmasov et al. 1997). Similar to the result for *YUC8*, *GUS* expression was decreased by 48% for *ztl-3* and 46% for *ztl-105* (Fig. 3a), and GUS activity and decreased by 90% for *ztl-3* and 69% for *ztl-105* mutants (Fig. 3b) compared with WT. *pDR5:GUS* staining was observed in the cotyledons, hypocotyl, and root (Fig. 3d) in the WT background, but not in the *ztl* mutant background. This result provides further evidence that the promoter activity of auxin-responsive genes in general may be decreased in the *ztl* mutants compared with WT.

ZTL **may affect the amplitude but not the rhythm of auxin-responsive gene expression**

In the microarray and qRT-PCR analyses described above, we found that the expression levels of auxin-responsive genes *SAUR22*, *IAA19*, and *IAA29* were decreased in the *ztl* mutants compared with WT (Fig. 2b and Table S8). Expression of *IAA19* is positively correlated with hypocotyl elongation (Pierik et al. 2009). Therefore, we considered that effect on *IAA19* expression could be used as an indirect indicator of effect on hypocotyl elongation. For that purpose, we used *pIAA19:ELuc-PEST*as an auxin-responsive reporter (Yamamoto et al. 2017).

The luciferase activity of *pIAA19:ELuc-PEST* in the WT background oscillated in an approximately 24-h cycle (Fig. 4a). Similar oscillation was observed when the construct was in the *ztl-3* or *ztl-105* mutant background; however, across the entire experiment (240 h) the LUC activity was substantially lower than in the WT background (Fig. 4b and c, Table 2). In the WT background, the maximum peak was observed at the 6th cycle (mean ± SD, 11602 ± 1575 photons/30s) (Table 2). Whereas in the *ztl* mutant background, the maximum peak was observed at the 7th cycle (3312 ± 1906 photons/30s) for *ztl-3* and the 6th cycle (3028 ± 1182 photons/30s) for *ztl-105*. Furthermore, the trough of the 6th cycle in the WT background was higher than the maximum peak of the *ztl* mutant background. By contrast the period was not significantly different between WT (mean ± SD. 24.39 ± 1.62 h) and the *ztl* mutants (*ztl*-3, 24.04 ± 0.60 h; *ztl*-105, 24.16 ± 0.70 h). These data suggest that *ZTL* affects the amplitude but not the rhythm of the expression of auxin-responsive genes.

PIF4, YUC8 and phyB are involved in the regulation of hypocotyl elongation by ZTL

The above microarray and qRT-PCR analyses and experiments using *pYUC8:GUS* suggested that YUC8 promotes hypocotyl elongation by ZTL. To explore this further, we performed gene overexpression analysis of *YUC8*. Overexpression of this gene promoted hypocotyl growth in both the WT background (*YUC8 ox*) and the *ztl* mutant background (*ztl-3* and *ztl-105 YUC8 ox*) to a similar extent (Fig. 5). Because the microarray and qRT-PCR analyses also suggested that PIF4, a known regulator of *YUC8* transcription (Franklin et al. 2011; Sun et al. 2012), promotes hypocotyl elongation, we additionally performed gene overexpression analysis of *PIF4*. Like *YUC8*, the hypocotyl lengths in plants overexpressing *PIF4* in the WT background (*PIF4 ox*) were similar to those in plants overexpressing the gene in the *ztl-3* or *ztl-105 PIF4 ox* background. These results indicate that PIF4 and YUC8 act downstream of ZTL.

Degradation of PIF4 protein is mediated by phyB (Huq, and Quail 2002 ; Lorrain et al. 2008). To investigate whether negative regulation of PIF4 by phyB is involved in the promotion of hypocotyl elongation by ZTL, we measured the hypocotyl length of a *phyb* mutant and a *ztl phyb* double mutant. Hypocotyls in the *phyb* mutant were significantly longer than those in WT, and similar to those in *ztl phyb* (Fig. 5). This finding suggests that phyB acts downstream of ZTL in hypocotyl elongation.

Discussion

By combining expression analysis and phenotype analysis, here we show that auxin synthesis in the upper aerial parts may be involved in the promotion of hypocotyl elongation by ZTL in *A. thaliana*. Our results suggest that ZTL positively regulates the expression of *PIF4* and *YUC8* in the upper aerial parts and promotes hypocotyl elongation by increasing the flow of auxin from its site of production (i.e., upper aerial parts) to the hypocotyl (Fig. S4).

Previously, we performed microarray analysis using WT and *ztl* whole seedlings (Saitoh et al. 2015b), most of which comprises the two cotyledons. Here we conducted microarray analysis of seedlings divided into hypocotyl and upper aerial parts. More genes that were differentially expressed between the *ztl* mutants and WT were detected in the analysis of hypocotyls than in the previous study of whole seedlings: i.e., gene expression of 7 *SAURs* and 4 *IAAs* were reduced (average fold change < -2.0) in the whole seedling, whereas gene expression of 16 *SAURs* and 7 *IAAs* were reduced (average fold change < -2.0) in upper aerial parts in the *ztl* mutants compared with WT. Expression of the genes encoding the transcription factors PIF4 was decreased in the upper aerial parts in the *ztl* mutants compared with WT; this protein directly bind to the G-box motif of the promoter of *YUC8*, a gene involved in auxin synthesis, to promote transcription under high temperature conditions (Sun et al. 2012). In the *ztl* mutants, decreased *pYUC8:GUS* gene expression and GUS activity suggest that PIF4 acts on the *YUC8* promoter downstream of ZTL and may regulate *YUC8* expression. We previously studied the effects of auxin inhibitors, yucasin, NPA, and PEO-IAA on hypocotyl elongation (Saitoh et al. 2015b). Yucasin inhibits the function of YUCs in the auxin synthesis pathway (Nishimura et al. 2014); NPA is an auxin polar transport inhibitor (Bernasconi et al. 1996); and PEO-IAA is an antagonist of the auxin receptor, which results in an auxin-deficient phenotype (Hayashi et al., 2012). There was no difference in the hypocotyl length between the WT and the *ztl* mutants in any of the three treatment groups (Saitoh et al. 2015b). This suggests that auxin synthesis, polar transport, and auxin receptor activity influence the regulation of hypocotyl elongation by ZTL. These results also support the hypothesis that ZTL positively regulates the expression of *PIF4* and *YUC8* in upper aerial parts and promotes hypocotyl elongation by the flow of auxin from upper aerial parts (production site) to the hypocotyl (Fig. S4). The fact that *ztl PIF4* ox and *ztl YUC8* ox have long hypocotyls fits this hypothesis. The finding that PIF4 directly activates expression of *YUC8*, and expression of *YUC8* increases at high temperature (Koini et al. 2009; Sun et al. 2012) does not contradict this hypothesis.

As was the case for whole seedlings, microarray analysis of hypocotyl and upper aerial parts showed decreased expression of auxin-responsive genes in the *ztl* mutants compared with WT (Saitoh et al. 2015b). This was confirmed by RT-PCR for *IAA19*, *IAA29*, and *SAUR22*. Furthermore, the lower promoter activity of *pDR5:GUS* in the *ztl* mutants compared with WT suggests that the promoter activity of not only *IAA19*, *IAA29*, and *SAUR22* but all auxin-responsive genes is decreased in the *ztl* mutants compared with WT.

IAA19 is known as an early auxin-responsive gene (Nakamura et al. 2003). A mutant of *IAA19* (*massugu2*, *msg2*) exhibits aberrant hypocotyl gravity and phototropic responses (Tatematsu et al. 2004). In addition, expression of *IAA19* is positively correlated with hypocotyl elongation in the shade avoidance response (Pierik et al. 2009). Because (a) the expression of *IAA19* was decreased in the *ztl* mutants compared with WT by microarray analysis and qRT-PCR, and (b) ZTL acts as a component of a circadian clock (*ztl* mutants have a longer circadian rhythm cycle and bloom early in short-day conditions; Jarillo et al. 2001; Takase et al. 2011), we measured the period and amplitude of IAA19 expression over time by using the *pIAA19:ELuc-PEST* construct in both WT and the *ztl* mutants. We found that the period was similar between WT and *ztl* mutants, but the amplitude was consistently lower in the *ztl* mutants than WT over time. This finding suggests that the expression of *IAA19* does not decrease only at certain times, but rather is consistently decreased in the *ztl* mutants compared with WT.

While auxin involvement has been discussed, gibberellins are also known to promote cell elongation in hypocotyls of *A. thaliana* (Cowling and Harberd 1999). In the microarray analysis, genes involved in gibberellin biosynthesis showed reduced expression in the upper aerial parts of the *ztl* mutants compared with WT. This finding suggests that gibberellins may also be involved in the regulation of hypocotyl elongation by ZTL, but this requires further investigation.

The difference in hypocotyl length between WT and *ztl* mutants is greater under red light than under blue light (Somers et al. 2004). Because ZTL is a blue photoreceptor, this seems contradictory to the fact that ZTL promotes hypocotyl elongation under red light. The key to resolving this contradiction is the involvement of the red light photoreceptor phyB, which is converted from the inactive Pr type to the active Pfr type under red light (Furuya 1993; Quail et al. 1995). Pfr type phyB interacts directly with PIF4 via an active phytochrome binding (APB) motif (Huq and Quail 2002; Khanna et al. 2007). PIF4 is phosphorylated by a phyB-mediated signaling pathway under red light and targeted for 26S proteasome degradation (Lorrain et al. 2008). Hypocotyls in the *phyb* mutant were significantly longer than those in WT, and similar to those in *ztl phyb* (Fig. 5). Therefore, phyB may act downstream of ZTL and regulate auxin synthesis via PIF4. However, the mechanism by which phyB is involved in the regulation of hypocotyl elongation by ZTL requires further study.

Materials and methods

Plant materials and growth conditions

Columbia-0 (Col-0) accession of *Arabidopsis thaliana* was used as WT. The *pDR5:GUS* (Oono et al. 2003), *pYUC8:GUS* (Hentrich et al. 2013), *YUC8* ox (Hentrich et al. 2013) and *PIF4* ox (Nozue et al. 2007) plants were crossed with *ztl* plants to produce *pDR5:GUS ztl*, *pYUC8:GUS ztl, ztl YUC8* ox, and *ztl PIF4* ox plants (where *ztl* was either *ztl-3* or *ztl-105*).The mutant *phyb-9* (Neff et al. 1998) was obtained from the Arabidopsis Biological Resource Center at Madison, WI, USA. To obtain double mutants, *ztl-3* and *ztl-105* was crossed with *phyb-9*, and the resulting F3 double homozygote was used for analysis. To introduce the *pIAA19:ELuc-PEST* construct (Yamamoto et al. 2017) into *ztl* mutants, we crossed a homozygous line harboring a single transgene for this construct with homozygous *ztl* mutants. Segregated F3 plants were used for the study.

Seeds were surface sterilized and placed on half-strength MS medium (0.8% w/v agar) without sucrose, and incubated at 4 °C for 7 days in the dark before germination. The seeds were then transferred (0 DAI) to 22 °C and incubated for 3 days followed by 28 °C for 5 days under continuous white light (80 μmol/m^2/s) as reported previously (Miyazaki et al. 2015).

Measurement of hypocotyl length

Images of seedlings grown on agar plates were taken with a CanoScan 9000F scanner (Canon, Tokyo, Japan) at 1 to 10 days. Hypocotyl lengths were determined from the images by using Scion Image software (Scion Corp., Frederick, MD, USA).

Microarray analysis

Hypocotyls and upper aerial parts, which include cotyledons and apical meristems, were separately sampled in 8 DAI seedlings of *ztl-3* and *ztl-105* mutants and WT. Total RNA was prepared using the RNeasy Plant Mini Kit (QIAGEN, Valencia, CA, USA). Microarray experiments were performed using Arabidopsis (V4) Gene Expression Microarrays 4 x 44K (Agilent Technologies, Böblingen, Germany). Genes with a fold change of >2 or <-2 were used for pathway analysis in DAVID Bioinformatics 75 Resources 6.7 (http://david.abcc.ncifcrf.gov/home.jsp) (Huang et al. 2009a, b). Gene annotations were retrieved from TAIR (http://www.arabidopsis.org/).

qRT-PCR analysis

Total RNA was isolated with the RNeasy Plant Mini Kit and used for cDNA synthesis by reverse transcription reaction with Prime Script II (Takara, Otsu, Japan) and oligo-dT primer. qRT-PCR was performed with the SYBR Green method using a Step One Plus

Real-Time PCR System (Life Technologies, Carlsbad, CA, USA). PCR primers are listed in Table S9. Gene expression levels were normalized by those of *ACTIN2* (*ACT2*).

GUS activity assay

GUS activity was examined in tissue extracts by fluorometric quantitation of 4-methylumbelliferone generated from its glucuronide precursor (GUS substrate) using a standard protocol (Jefferson et al. 1986).

Histochemical localization of GUS activity was conducted by incubating seedlings in GUS-staining solution (1 mg/mL 5-bromo-4-chloro-3-indolyl-glucuronic acid, 0.03% Triton X-100, and 0.1 M sodium phosphate buffer pH 7.0) overnight at 37 °C. GUS-stained samples were cleared with 70% ethanol and observed under a light microscope (Leica, Wetzlar, Germany).

Bioluminescence analysis

The luciferase activity of the individual seedlings was monitored every 30 minutes for 30 seconds with a multi-channel bioluminescence-monitoring apparatus (Okamoto et al. 2007). Periods of the bioluminescence rhythm were estimated using RAP software

(Okamoto et al. 2005).

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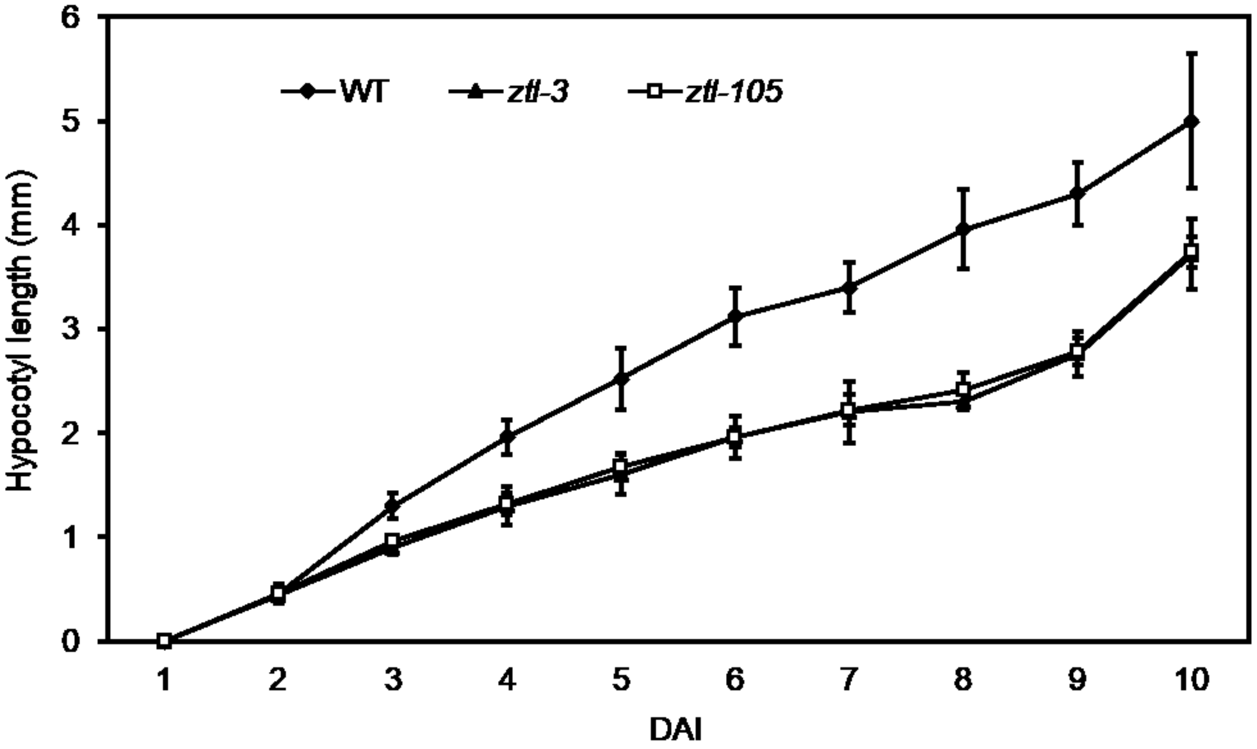


Fig. 1 Seedling growth
WT and *ztl* mutant (*ztl-3* and *ztl-105*) seeds were incubated at 4 °C in the dark and germinated under continuous white light (80 μmol·m^{-2}·s^{-1}) at 22 °C for 3 days. The horizontal axes show days after incubation (DAI).The seedlings were then grown at 28 °C for 7 days. Data are means ± SD (n = 10)

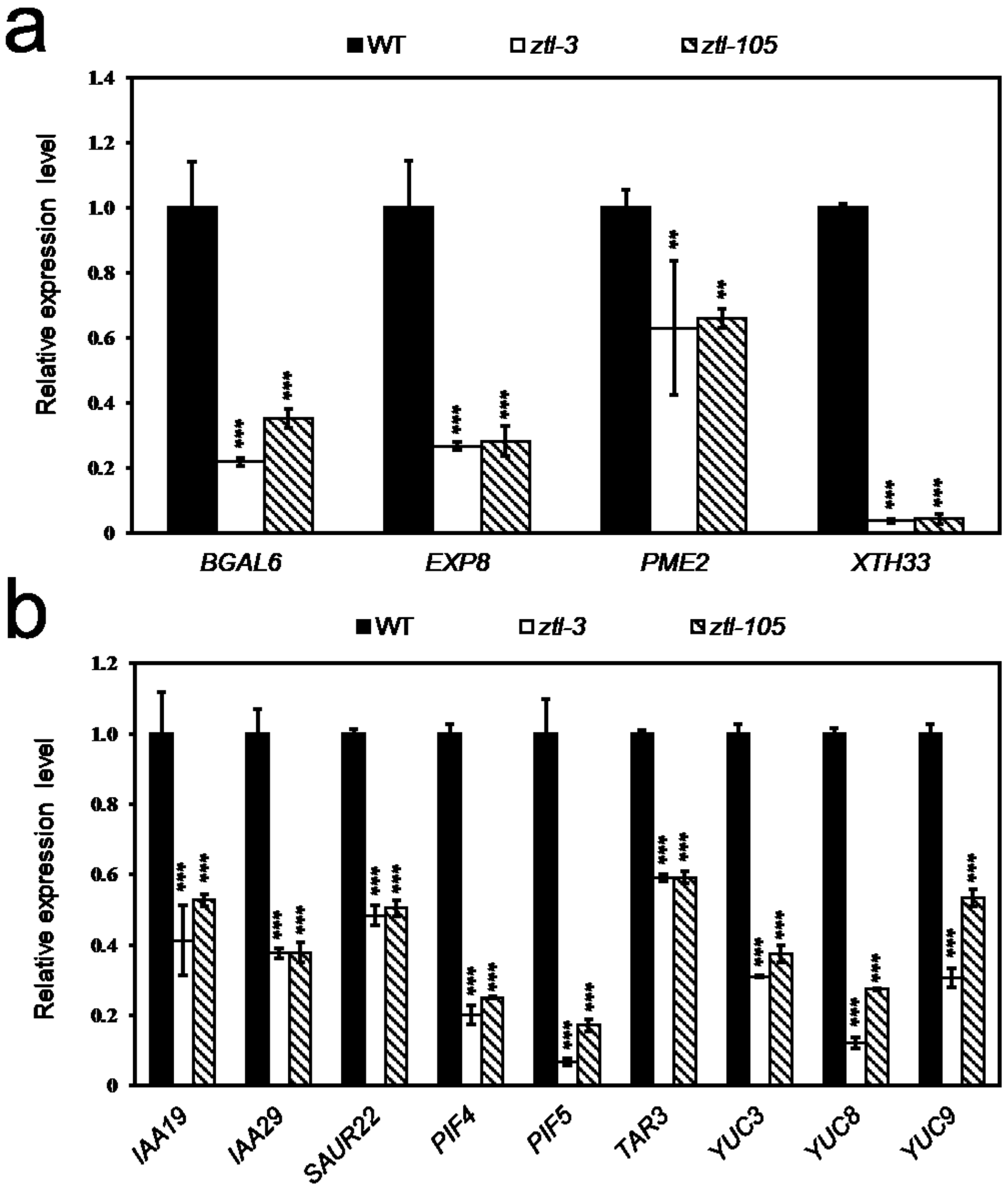


Fig. 2 Quantitative reverse-transcription PCR analysis

Quantitative reverse-transcription (qRT-PCR) analysis results for WT and *ztl-3* and *ztl-105* mutants. (a) Hypocotyls of 8 DAI WT and *ztl* mutants and (b) upper aerial parts comprising cotyledons and apical meristem of 8 DAI WT *ztl* mutants were examined. *ACTIN2 (ACT2)* was used as a control. Data are means ± SD (n = 3); ***P* < 0.01 and ****P* < 0.001 vs. WT (Student's *t*-test)

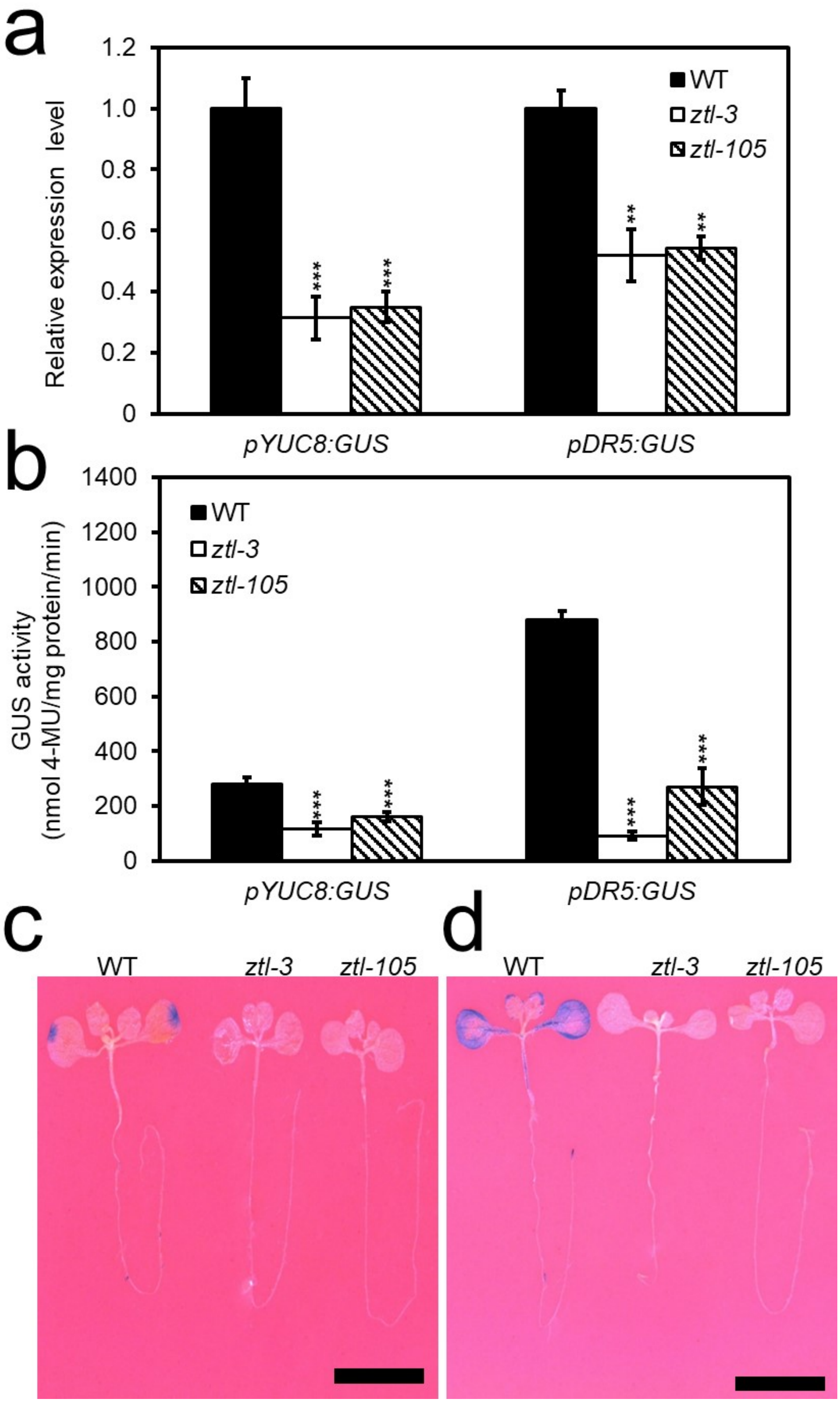


Fig. 3 Promoter:GUS assays
(a) qRT-PCR analysis of *GUS* gene in WT and *ztl-3* and *ztl-105* mutant seedlings at 8 DAI. *ACTIN2 (ACT2)* was used as a control. (b) GUS activity assay of WT and *ztl* mutant seedlings. (a, b) Data are means ± SD. (n = 3). $^{**}P < 0.01$ and $^{***}P < 0.001$ vs. WT (Student's *t*-test). (c, d) Histochemical staining of transgenic *Arabidopsis thaliana* seedlings expressing *pYUC8:GUS* (c) or *pDR5:GUS* (d). Scale bars = 5 mm

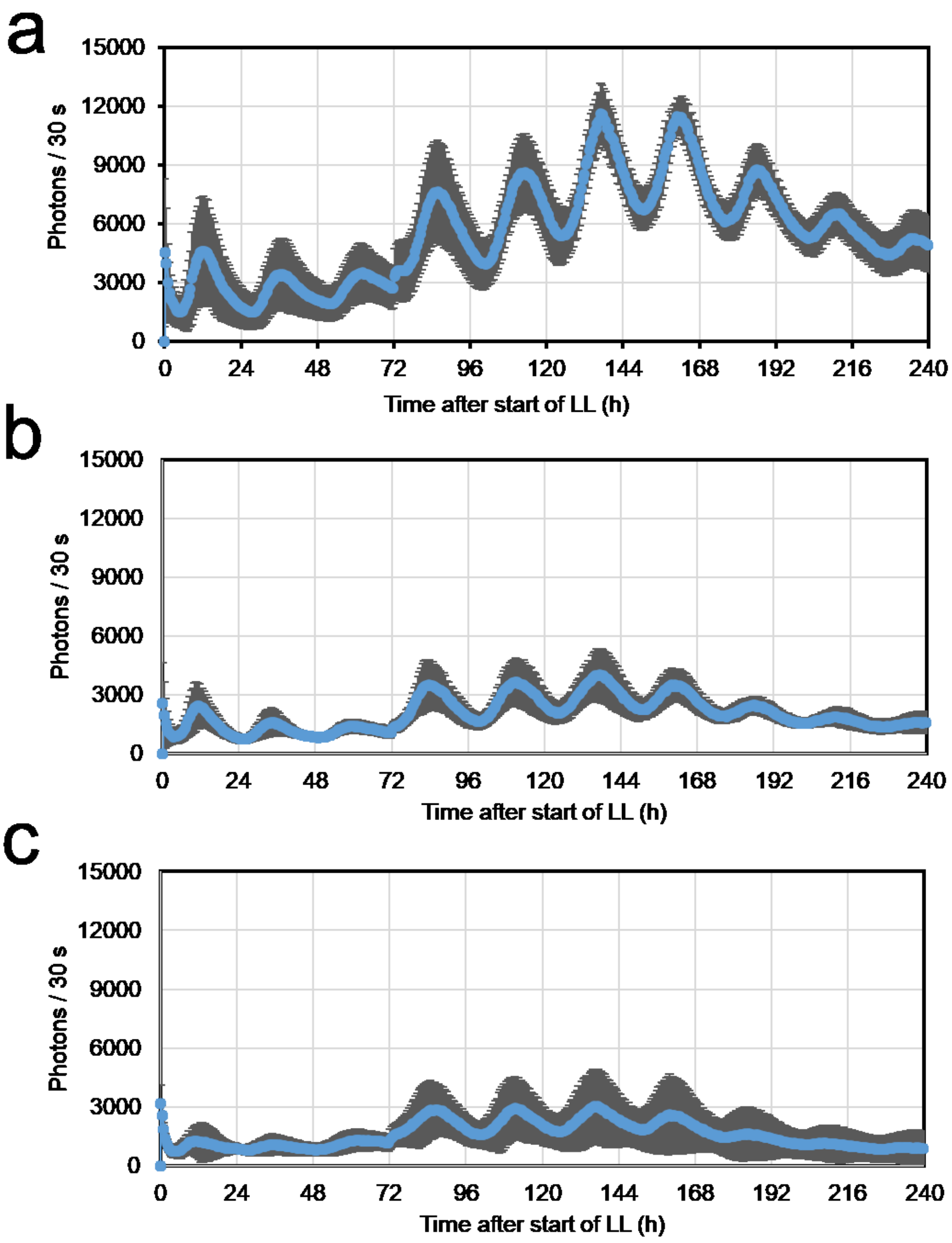


Fig. 4 Measurement of *pIAA19:ELuc-PEST* luciferase activity
Luciferase activities (photons/30s) of WT and *ztl-3* and *ztl-105* mutant seedlings at 0-10 days after low temperature treatment. (a) *pIAA19:ELuc-PEST*, (b) *pIAA19:ELuc-PEST ztl-3*, (c) *pIAA19:ELuc-PEST ztl-105*. LL, continuous light.

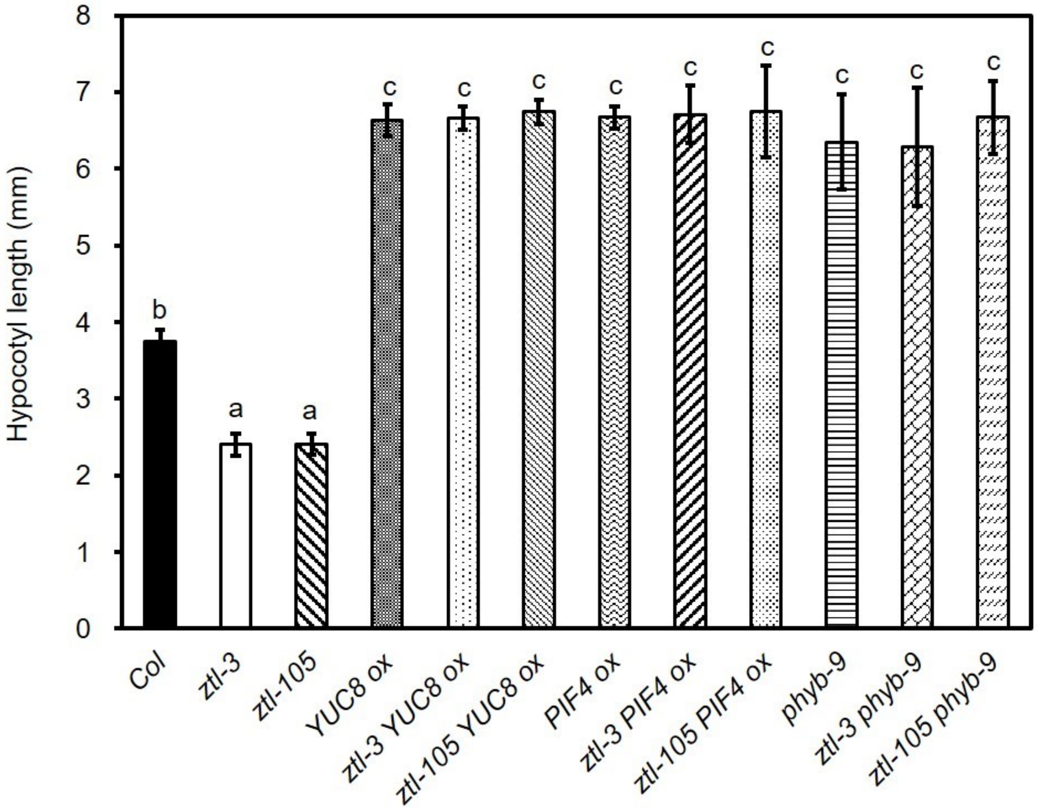


Fig. 5 Hypocotyl length
Hypocotyl lengths were measured in seedlings of WT and the indicated mutants at 8 DAI (days after incubation). Data are means ± SD (n = 10); different letters indicate statistically significant differences (*P* < 0.05, Tukey's test)

Table 1. Results of microarray analysis of auxin synthesis genes in upper aerial parts.

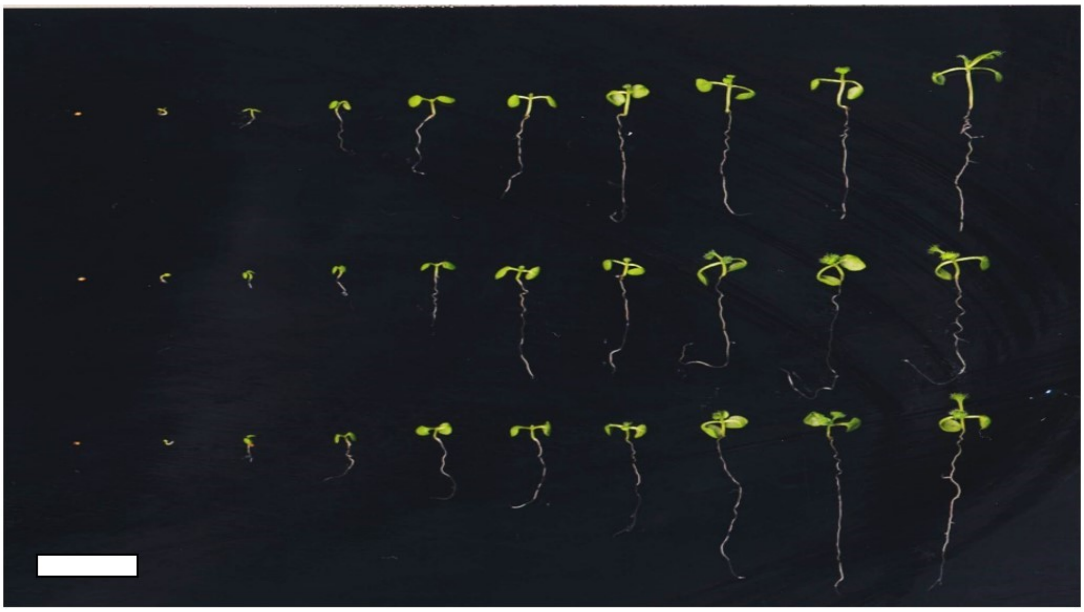
			ztl-3 vs WT	*ztl-105* vs WT
Array Element	Gene Locus	Gene Name	Log (Ratio)	
A_84_P22386	At4g32540	*YUC1*	-1.7	0
A_84_P16644	At4g13260	*YUC2*	-0.6	-0.6
A_84_P18949	At1g04610	*YUC3*	-2.9	-2.9
A_84_P18684	At5g11320	*YUC4*	-1.9	-0.8
A_84_P23485	At5g43890	*YUC5*	-0.1	-0.5
A_84_P11154	At5g25620	*YUC6*	-0.9	-0.4
A_84_P23869	At2g33230	*YUC7*	0	-2.8
A_84_P10076	At4g28720	*YUC8*	-2.9	-2.4
A_84_P19909	At1g04180	*YUC9*	-2.5	-1.1
A_84_P18152	At1g48910	*YUC10*	0.2	0
A_84_P18098	At1g21430	*YUC11*	-0.6	0
A_84_P19052	At1g70560	*TAA1*	0.9	0.9
A_84_P17563	At1g23320	*TAR1*	2.2	0.1
A_84_P10057	At4g24670	*TAR2*	-0.3	-0.3
A_84_P10523	At1g34040	*TAR3*	-1.2	-2.8
A_84_P23603	At1g34060	*TAR4*	-0.6	-1
A_84_P188054	At3g54640	*TSA1*	0.90	0
A_84_P18578	At4g27070	*TSB2*	0.9	-0.2
A_84_P798815	At4g39950	*CYP79B2*	1.2	0.1
A_84_P22022	At2g22330	*CYP79B3*	0.2	-0.6
A_84_P829748	At5g20960	*AAO1*	1.1	0
A_84_P21247	At3g44310	*NIT1*	0.5	0
A_84_P245685	At3g44300	*NIT2*	2.2	0.4
A_84_P22193	At3g44320	*NIT3*	1.2	0.3
A_84_P10196	At5g22300	*NIT4*	0.9	-0.1
A_84_P148728	At1g08980	*AMI1*	0	-0.1
A_84_P857638	At2g30770	*CYP71A13*	0.8	-1

Table 2. Peak value and trough values of each cycle of *pIAA19:ELuc-PEST* luciferase activity (see Fig. 4). Unit is photons/30s.

Cycle		1	2	3	4	5
pIAA19:ELuc-PEST	Peak	4613 ± 2775	3401 ± 1830	3459 ± 1455	7647 ± 2633	8256 ± 1956
	Trough	1483 ± 849	1904 ± 847	2719 ± 1039	3969 ± 1337	5396 ± 1494
pIAA19:ELuc-PEST/ztl-3	Peak	1192 ± 1004 ***	740 ± 514 ***	862 ± 556 ***	2335 ± 1536 **	2677 ± 1612 ***
	Trough	333 ± 230 ***	477 ± 312 ***	650 ± 416 **	1106 ± 677 **	1412 ± 857 ***
pIAA19:ELuc-PEST/ztl-105	Peak	1201 ± 958 ***	1087 ± 721 ***	1309 ± 714 ***	2835 ± 907 ***	2928 ± 1045 ***
	Trough	801 ± 230	802 ± 312 **	1160 ± 416 **	1564 ± 677 **	1716 ± 857 ***

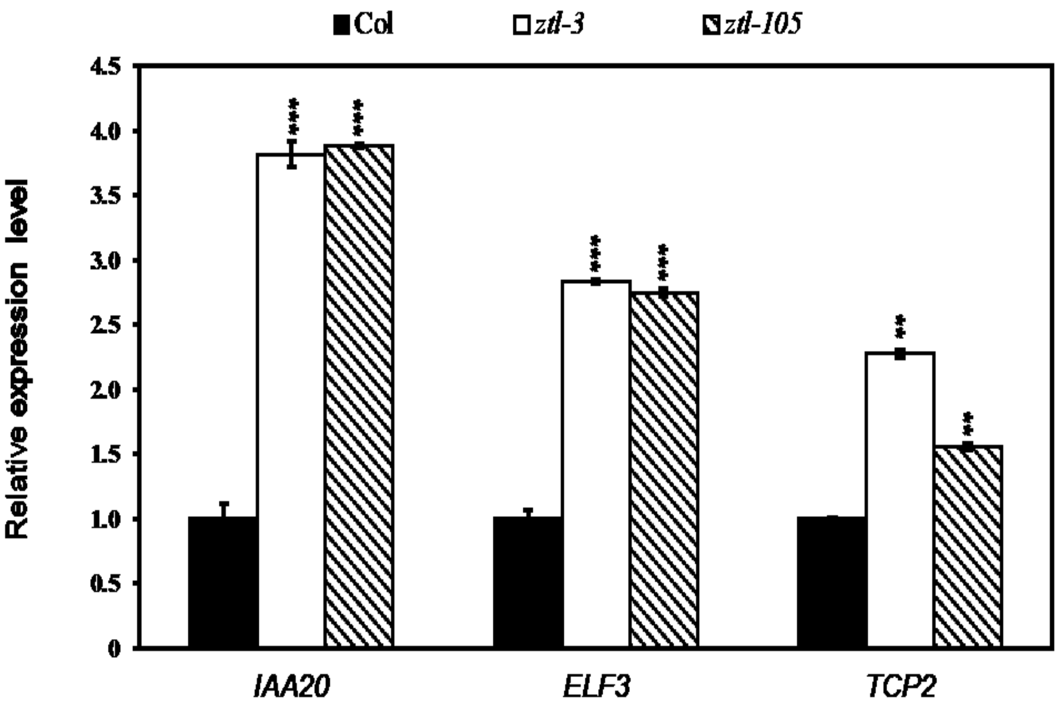
Cycle		6	7	8	9	10
pIAA19:ELuc-PEST	Peak	11602 ± 1575	11441 ± 951	8770 ± 1294	6503 ± 1044	5250 ± 1430
	Trough	6722 ± 1054	6114 ± 920	5298 ± 941	4398 ± 1066	4278 ± 1166
pIAA19:ELuc-PEST/ztl-3	Peak	3312 ± 1909 ***	3371 ± 1955 ***	2329 ± 1335 ***	1591 ± 938 ***	1371 ± 893 ***
	Trough	1651 ± 966 ***	1468 ± 873 ***	1210 ± 701 ***	1058 ± 637 ***	1150 ± 880 ***
pIAA19:ELuc-PEST/ztl-105	Peak	3028 ± 1182 ***	2564 ± 881 ***	1623 ± 637 ***	1155 ± 484 ***	924 ± 437 ***
	Trough	1820 ± 966 ***	1428 ± 873 ***	1061 ± 701 ***	826 ± 637 ***	700 ± 880 ***

Data are means ± SD (n = 10-16) **, $P < 0.01$; ***, $P < 0.001$ (Student's *t*-test).



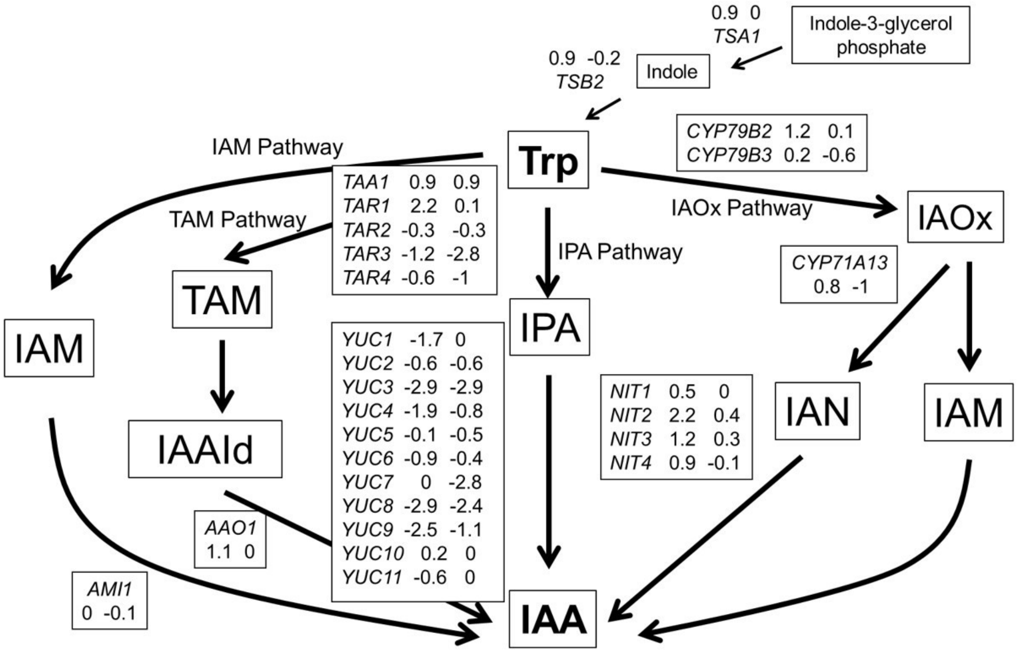
Supplemental Fig. 1 Seedling growth

Seedlings from 1 to 10 DAI. Top is wild type, middle is *ztl-3*, and bottom is *ztl-105*. Scale bar = 1 cm.



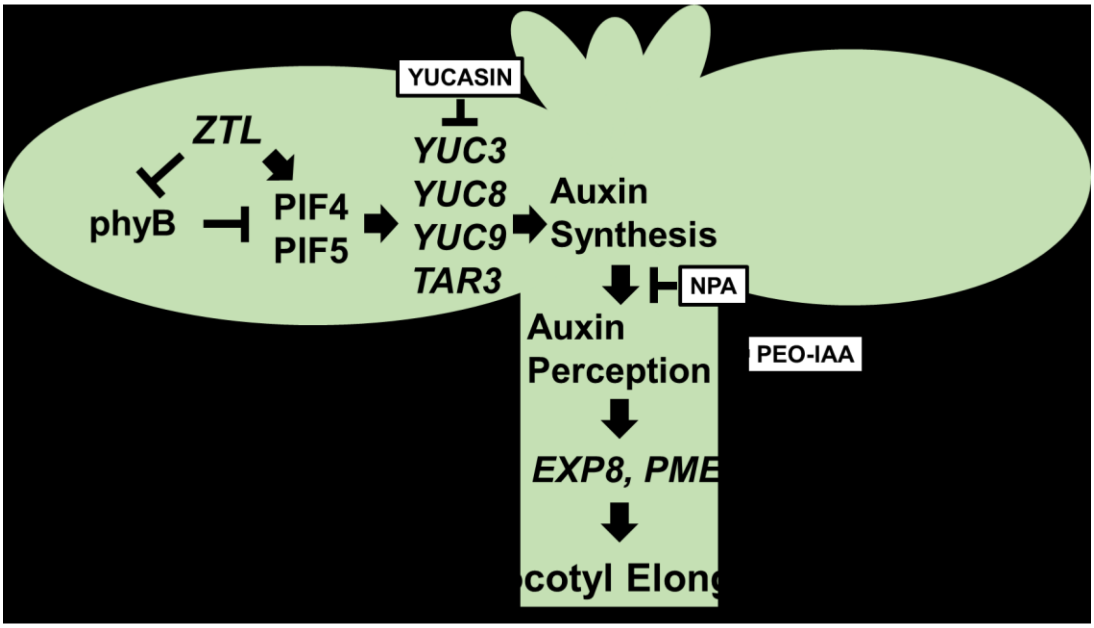
Supplemental Fig. 2 Quantitative reverse-transcription PCR analysis

qRT-PCR analysis results of WT and 2 mutants. Hypocotyls of 8 DAI WT and ztl mutants were used. ACTIN2 (ACT2) was used as a control. Error bars represent standard deviations (n = 3); **P <0.01 and ***P <0.001 (Student's t-test) in comparison with WT.



Supplemental Fig. 3 Microarray analysis of genes related to auxin synthesis.

Four pathways for the synthesis of IAA from Trp are depicted. Numbers shown in duplicate are gene expression levels [log (ratio)] for *ztl* mutants (left, *ztl*-3; right *ztl*-105) vs. wild type.



Supplemental Fig. 4 Schema of ZTL stimulation of the expression of genes related to auxin synthesis, resulting in promotion of hypocotyl elongation.

Supplemental Table 1. Probe values for down-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (hypocotyl)

Probe Name	Col1	*ztl3*	Log Ratio	Col2	*ztl105*	Log Ratio
A_84_P11530	90099.7	20876.2	-2.1	82571.3	33775.2	-1.3
A_84_P87299	41.5	2.9	-3.8	42.3	2.9	-3.9
A_84_P21392	1300.8	421.6	-1.6	2488.1	416	-2.6
A_84_P519500	15.1	4.2	-1.8	39.7	5.8	-2.8
A_84_P763873	7.4	3.4	-1.1	38.1	7	-2.4
A_84_P586644	3211.4	1051	-1.6	2672.2	420.9	-2.7
A_84_P822593	2176.1	621	-1.8	2789.5	1308.4	-1.1
A_84_P20686	183.1	3.3	-5.8	36.8	7.6	-2.3
A_84_P17435	25791.9	7700.4	-1.7	28376.1	11614.4	-1.3
A_84_P797928	11.7	4.1	-1.5	10.8	4.4	-1.3
A_84_P869955	87.3	36	-1.3	104.7	42.8	-1.3
A_84_P522798	8.9	3.3	-1.4	26.9	3.2	-3.1
A_84_P790159	470.9	35.5	-3.7	438.8	80.3	-2.4
A_84_P220358	49.5	20.3	-1.3	53.8	21.7	-1.3
A_84_P17231	114.8	32.1	-1.8	142.3	47.5	-1.6
A_84_P794265	9	4.3	-1.1	13.1	6.3	-1
A_84_P831568	559.8	270	-1.1	972.6	359.7	-1.4
A_84_P22225	978.5	374.1	-1.4	877	359.3	-1.3
A_84_P769252	90.3	12.5	-2.9	111	14.8	-2.9
A_84_P576778	11.4	3.7	-1.6	23.1	4.9	-2.2
A_84_P842485	22.5	10.5	-1.1	82.9	13.8	-2.6
A_84_P845426	43	17.9	-1.3	36.7	17.3	-1.1
A_84_P837084	91.6	34.8	-1.4	117.2	25.5	-2.2
A_84_P608698	8.6	2.9	-1.6	22.1	4.6	-2.3
A_84_P11966	12.1	2.9	-2	25.2	4.9	-2.4
A_84_P11474	11.1	3	-1.9	11.6	3.2	-1.9
A_84_P11195	3909.1	1056.5	-1.9	5509.4	2211.9	-1.3
A_84_P825877	10.2	2.9	-1.8	28.1	4.3	-2.7
A_84_P813024	60.1	26.2	-1.2	84.6	35.4	-1.3
A_84_P731112	8.8	3.6	-1.3	10.9	3	-1.8
A_84_P786781	385.3	131.5	-1.6	481.4	139.4	-1.8
A_84_P824053	4092.5	690.8	-2.6	3836.9	1096.5	-1.8
A_84_P512014	6.6	3.2	-1	11	5.3	-1
A_84_P18192	90.8	18.3	-2.3	107.4	38.2	-1.5
A_84_P11349	6	2.9	-1	15.2	5.8	-1.4
A_84_P18673	8362.4	1161.7	-2.8	5932.1	2771.9	-1.1
A_84_P22815	222.6	92.5	-1.3	568.7	145.2	-2
A_84_P23356	17.9	5.5	-1.7	7.1	3.1	-1.2
A_84_P59580	1391.3	525	-1.4	1946.5	925.9	-1.1

A_84_P22788	17	5	-1.8	15.5	5.9	-1.4
A_84_P762938	1571.8	171.2	-3.2	1114.4	522	-1.1
A_84_P189964	502	70.4	-2.8	499.9	219.8	-1.2
A_84_P15762	5611.9	2091	-1.4	8118.6	3596	-1.2
A_84_P15912	6554.9	3182.1	-1	7492.9	2736.7	-1.5
A_84_P806064	50534.3	8984.5	-2.5	44158.3	12647.1	-1.8
A_84_P765453	9.6	3	-1.7	16.3	4.2	-2
A_84_P523893	12.7	5.8	-1.1	11.9	3.7	-1.7
A_84_P12782	32.1	2.9	-3.5	24.4	11.5	-1.1
A_84_P22369	143.7	40.8	-1.8	97.8	36.9	-1.4
A_84_P754674	23.6	5.2	-2.2	32.7	5.9	-2.5
A_84_P788766	1244.4	552.9	-1.2	2410	734.5	-1.7
A_84_P282270	4001.5	888.9	-2.2	3166.1	1437.7	-1.1
A_84_P786467	82.4	9	-3.2	170.4	29.1	-2.6
A_84_P17929	10869.3	2331.9	-2.2	10787.3	2338.6	-2.2
A_84_P833194	7.4	2.9	-1.4	15.7	2.9	-2.4
A_84_P12761	27.6	3.1	-3.1	25.8	3.2	-3
A_84_P507895	22.7	3.2	-2.8	32.7	5.4	-2.6
A_84_P21360	2834.9	71	-5.3	2587.2	71.5	-5.2
A_84_P15926	399.9	115.7	-1.8	482.8	237	-1
A_84_P72884	70	24.3	-1.5	153	31.3	-2.3
A_84_P23534	6177.8	3.6	-10.8	5625.5	338.3	-4.1
A_84_P211128	1408.1	157.2	-3.2	1084.6	255.7	-2.1
A_84_P862370	5624.4	2653.1	-1.1	6619.9	3216.4	-1
A_84_P13432	5279.2	2128.7	-1.3	11977	2249.9	-2.4
A_84_P11358	3730.1	1854.4	-1	6892.2	1901.2	-1.9
A_84_P15844	164	44.7	-1.9	123.8	33.5	-1.9
A_84_P814302	958.6	468.7	-1	1712.2	682.3	-1.3
A_84_P12421	6457.9	1250.7	-2.4	5289.7	2162.8	-1.3
A_84_P838299	29.4	14.1	-1.1	73.3	9.7	-2.9
A_84_P10189	945.3	344.7	-1.5	828.3	406.3	-1
A_84_P17068	182.5	83.3	-1.1	244.4	104	-1.2
A_84_P18792	509.4	74.8	-2.8	690	52.9	-3.7
A_84_P827060	23.2	9.2	-1.3	23.3	3.3	-2.8
A_84_P860931	55.8	26.3	-1.1	94.1	42.6	-1.1
A_84_P24123	78.6	38.5	-1	118.9	52.4	-1.2
A_84_P829441	40.6	15.6	-1.4	33.9	16	-1.1
A_84_P11196	9.7	3.3	-1.6	8.6	2.9	-1.6
A_84_P843816	801.1	66.2	-3.6	665.3	225	-1.6
A_84_P23512	2277.3	348.1	-2.7	2595.4	319.2	-3
A_84_P778751	18.9	3.5	-2.4	27.7	6	-2.2
A_84_P20149	2751.1	678.4	-2	1816.2	828.2	-1.1
A_84_P23806	802.4	160.7	-2.3	900.4	349.8	-1.4
A_84_P847920	13735.3	3181.8	-2.1	10132.8	4688.4	-1.1
A_84_P231009	170.1	42.7	-2	313.8	62	-2.3

A_84_P16241	15569.5	5098.7	-1.6	17983.2	8799.3	-1
A_84_P169853	8.4	2.8	-1.6	12.6	5.7	-1.1
A_84_P764364	9.3	2.9	-1.7	5.7	2.9	-1
A_84_P786801	242.5	111.9	-1.1	260.1	101.7	-1.4
A_84_P20932	21.2	3.3	-2.7	19.1	6.8	-1.5
A_84_P571469	32.4	16	-1	91.4	20.6	-2.2
A_84_P10547	9.5	3.1	-1.6	34.5	3.1	-3.5
A_84_P869312	8.7	3.2	-1.4	11.2	5.1	-1.1
A_84_P12382	398.5	189.3	-1.1	381.5	158.3	-1.3
A_84_P806680	191.2	82	-1.2	280.8	97.2	-1.5
A_84_P89649	31.4	6.7	-2.2	170.8	5.2	-5
A_84_P805164	473.3	81.3	-2.5	490	71.4	-2.8
A_84_P17709	16.6	6.6	-1.3	17	3.7	-2.2
A_84_P830028	392.3	50.3	-3	480.8	44.9	-3.4
A_84_P858191	3761.3	1732.3	-1.1	5781.5	2366.5	-1.3
A_84_P265400	1453.1	648.3	-1.2	2042.6	701.9	-1.5
A_84_P760178	203.4	77.2	-1.4	319.1	43.3	-2.9
A_84_P532174	206.6	65.4	-1.7	217.8	103.3	-1.1
A_84_P11171	40.5	12.1	-1.7	63.7	4.8	-3.7
A_84_P16647	277	71.4	-2	221.7	89.1	-1.3
A_84_P10464	94	16.4	-2.5	108.1	20.3	-2.4
A_84_P90379	8.4	3.1	-1.4	13.7	3.1	-2.1
A_84_P145939	711.3	351.2	-1	1199.5	493.4	-1.3
A_84_P750037	46.6	22.5	-1.1	175.1	19.3	-3.2
A_84_P308053	9.7	3	-1.7	21.3	3	-2.8
A_84_P513467	10.9	3.4	-1.7	11.3	3.2	-1.8
A_84_P847349	59.2	29.5	-1	91.9	22.4	-2
A_84_P18763	2543.4	447.4	-2.5	1839.1	737.3	-1.3
A_84_P282290	2031.2	646.2	-1.7	2015.3	891	-1.2
A_84_P191914	66.7	15.3	-2.1	62.4	15	-2.1
A_84_P810056	31775.4	10250	-1.6	48220.6	17271.3	-1.5
A_84_P288904	176.8	51.1	-1.8	211.4	70	-1.6
A_84_P10586	35.9	17.2	-1.1	103.4	17.7	-2.5
A_84_P20395	26	8.4	-1.6	38.5	13.7	-1.5
A_84_P18655	386	42	-3.2	258.2	98.1	-1.4
A_84_P18230	668.7	209.5	-1.7	767.2	374.1	-1
A_84_P825382	1784.6	693	-1.4	1079.8	435.6	-1.3
A_84_P858917	39.7	8.5	-2.2	50	21.6	-1.2
A_84_P756427	720.7	39.3	-4.2	466.5	165.2	-1.5
A_84_P868891	56403.8	24116.3	-1.2	96907.8	14037.7	-2.8
A_84_P24129	6.4	3	-1.1	9.4	3	-1.7
A_84_P15243	1910.5	701	-1.4	2176.1	903	-1.3
A_84_P21709	879.9	346	-1.3	917.3	417	-1.1
A_84_P544996	13.5	6.6	-1	13.7	6.6	-1
A_84_P825792	891.6	320	-1.5	2389.2	388.6	-2.6

A_84_P13787	406.8	160.8	-1.3	1553.8	169.4	-3.2
A_84_P10436	32.8	12.5	-1.4	111.4	23.4	-2.2
A_84_P22755	74.4	19.3	-1.9	1190.4	10.1	-6.9
A_84_P786892	6797.8	1471.6	-2.2	8149.4	1650.8	-2.3
A_84_P850014	318.7	132.9	-1.3	695.7	266	-1.4
A_84_P107372	3614.6	1307.5	-1.5	3505.6	1347.9	-1.4
A_84_P802975	4841.7	1677.1	-1.5	6229.4	1207	-2.4
A_84_P752757	11.4	2.9	-2	14.3	2.8	-2.3
A_84_P16082	3089.2	507.2	-2.6	2418.8	625	-2
A_84_P163493	1847.7	335.6	-2.5	2826.9	398.1	-2.8
A_84_P608861	1480.2	532.5	-1.5	1276.6	555.9	-1.2
A_84_P156975	484.1	212.6	-1.2	557.6	235.1	-1.2
A_84_P14780	9.1	4	-1.2	7.6	2.8	-1.4
A_84_P555814	49.5	17.5	-1.5	62.4	24.1	-1.4
A_84_P581125	14	7	-1	12.6	5.1	-1.3
A_84_P12500	12.3	3.9	-1.7	6.2	2.8	-1.2
A_84_P547579	12.7	3.2	-2	23.9	7	-1.8
A_84_P12560	7887	2793.9	-1.5	6464.3	2700.3	-1.3
A_84_P561646	789.6	273.3	-1.5	1046.1	488.4	-1.1
A_84_P812910	70.6	8.3	-3.1	37.1	12	-1.6
A_84_P15425	2028.3	448	-2.2	2889.4	593.7	-2.3
A_84_P236563	85.1	41.2	-1	235.5	37.3	-2.7
A_84_P16607	3523	1071.3	-1.7	4569.2	1681.8	-1.4
A_84_P608304	3380.5	1424.2	-1.2	3325.1	1129.9	-1.6
A_84_P750319	27.6	4	-2.8	31	9.2	-1.7
A_84_P21103	615.1	227	-1.4	781.2	280.8	-1.5
A_84_P765197	30.1	13.6	-1.1	26.3	13	-1
A_84_P859317	5650.4	1504.8	-1.9	9383.4	2718.5	-1.8
A_84_P192044	35.8	17.5	-1	126.6	20.1	-2.7
A_84_P23582	1373	585.7	-1.2	1155.8	394.9	-1.5
A_84_P15126	6841.8	1553.5	-2.1	7252.4	2561	-1.5
A_84_P538534	68.7	25.5	-1.4	161.6	34.5	-2.2
A_84_P310283	12.8	5.4	-1.2	16.3	2.8	-2.6
A_84_P561987	376.1	174	-1.1	464	193.8	-1.3
A_84_P90469	16788	3101.9	-2.4	10604.7	4594.4	-1.2
A_84_P831167	2330	930.6	-1.3	1968.3	609.4	-1.7
A_84_P19490	6538.1	1405.8	-2.2	4835	2343.8	-1
A_84_P104616	12828.2	4197	-1.6	15487.6	6005.7	-1.4
A_84_P788914	2956	529.9	-2.5	3285.6	1063	-1.6
A_84_P180334	55.4	11	-2.3	40.7	14.1	-1.5
A_84_P784921	62.3	12.8	-2.3	109	13.1	-3.1
A_84_P826876	1015.9	344.7	-1.6	1174.6	477.8	-1.3
A_84_P15411	187.6	33.8	-2.5	115.6	40.7	-1.5
A_84_P22494	5652.8	1568	-1.9	4408.7	1634.1	-1.4
A_84_P518116	290	123.8	-1.2	587.6	174.9	-1.7

A_84_P302890	2324	842.1	-1.5	3276.8	1461.9	-1.2
A_84_P755290	10.3	2.9	-1.8	9.8	2.8	-1.8
A_84_P847209	7084.4	3193.9	-1.1	9891.5	3079.6	-1.7
A_84_P786235	1727.5	314.6	-2.5	2166.8	467.4	-2.2
A_84_P826337	72.7	25.1	-1.5	79.4	31	-1.4
A_84_P851378	70946.2	20824.9	-1.8	92699.9	26824.6	-1.8
A_84_P547123	39.7	6.5	-2.6	36.9	17	-1.1
A_84_P810240	92699.9	46175.1	-1	131341.7	52152	-1.3
A_84_P23218	1010.6	467.9	-1.1	1543.3	610.3	-1.3
A_84_P12471	593.3	267.7	-1.1	895.8	408.1	-1.1
A_84_P92139	78	19.1	-2	57.9	25.2	-1.2
A_84_P790636	25.9	2.8	-3.2	18	4.6	-2
A_84_P88029	475.4	215.1	-1.1	1354.9	245.4	-2.5
A_84_P857259	93598.2	28165.5	-1.7	125636.1	35109.3	-1.8
A_84_P23846	7087.5	2046.5	-1.8	7084.4	2241.2	-1.7
A_84_P787198	1051.9	490	-1.1	1500.1	705.6	-1.1
A_84_P761383	7.3	2.7	-1.4	12.8	2.8	-2.2
A_84_P507009	278.6	18.7	-3.9	181.3	34.1	-2.4
A_84_P242573	229.5	40.9	-2.5	176.8	26.7	-2.7
A_84_P11622	4206.4	1608.5	-1.4	6324.1	2288.2	-1.5
A_84_P20053	122.8	58.7	-1.1	127.8	63.5	-1
A_84_P240515	446.6	153.4	-1.5	621.6	193.1	-1.7
A_84_P606561	41	12.7	-1.7	468.4	6	-6.3
A_84_P20858	66.2	23.2	-1.5	352.5	19.9	-4.1
A_84_P802502	8.7	3.5	-1.3	35	5.2	-2.7
A_84_P587419	15	3	-2.3	13.3	3	-2.2
A_84_P751365	9743	4685.8	-1.1	14529.7	6491.6	-1.2
A_84_P81529	3649.2	1138.5	-1.7	3801	1388.1	-1.5
A_84_P303690	8.2	2.9	-1.5	7.9	2.7	-1.5
A_84_P556238	113.6	36.6	-1.6	114.8	49.6	-1.2
A_84_P756100	9.6	3.8	-1.3	8.8	4.1	-1.1
A_84_P23464	61.4	10.4	-2.6	70	3.8	-4.2
A_84_P298084	59.4	25.8	-1.2	86.2	29.2	-1.6
A_84_P557668	23.5	3.5	-2.8	32	6	-2.4
A_84_P19687	219.2	42.4	-2.4	187.1	39.8	-2.2
A_84_P833445	27	3	-3.2	22.7	2.9	-3
A_84_P18265	1813.2	396.7	-2.2	1568.3	433.8	-1.9
A_84_P599862	6778.2	1137.3	-2.6	5831.4	2248.6	-1.4
A_84_P790750	154.5	44.7	-1.8	154.5	59.6	-1.4
A_84_P575512	154.8	76.4	-1	432.9	87.3	-2.3
A_84_P281230	1860.3	889	-1.1	1817.6	746.4	-1.3
A_84_P821420	2619.5	302.2	-3.1	2524.1	407.1	-2.6
A_84_P836527	29.9	7	-2.1	89.1	16.5	-2.4
A_84_P14793	11.5	2.9	-2	18.3	3.7	-2.3
A_84_P266650	860.2	49.3	-4.1	732	83.8	-3.1

A_84_P785814	321.7	126.4	-1.3	443.3	154	-1.5
A_84_P21555	19	7.7	-1.3	20.7	5.4	-1.9
A_84_P12457	65.4	11.7	-2.5	34	6.8	-2.3
A_84_P76044	13	3.8	-1.8	10.3	2.7	-1.9
A_84_P593312	192.8	90.5	-1.1	256	117.9	-1.1
A_84_P22659	536.3	193.5	-1.5	403.6	151.5	-1.4
A_84_P24055	30.2	9.9	-1.6	29	8.9	-1.7
A_84_P765747	48.7	15.7	-1.6	46.2	19.4	-1.3
A_84_P12727	68.6	22	-1.6	74.5	29.5	-1.3
A_84_P14263	1886.2	802.8	-1.2	1753.2	790.4	-1.1
A_84_P826328	382.5	155.4	-1.3	715.6	281.8	-1.3
A_84_P868534	2096.2	778	-1.4	1913.4	746.2	-1.4
A_84_P572154	33.6	9.9	-1.8	73.5	17.8	-2
A_84_P542440	1087.8	273.5	-2	2096.9	222	-3.2
A_84_P812936	302.5	89	-1.8	619.1	82.3	-2.9
A_84_P222439	416	124.6	-1.7	441.9	171.5	-1.4
A_84_P19474	108.8	32.3	-1.8	204.3	31	-2.7
A_84_P827866	103.3	50.9	-1	176.1	74	-1.3
A_84_P568614	22.6	10.9	-1	19	6	-1.7
A_84_P21961	7929	1939.7	-2	6513.9	2176.1	-1.6
A_84_P843096	50.3	4.9	-3.4	83.8	17.7	-2.2
A_84_P23329	17237.6	7834.6	-1.1	20200.6	7110.3	-1.5
A_84_P121162	1026.1	418.1	-1.3	1232.5	607.7	-1
A_84_P577310	348.6	163.6	-1.1	465.5	186.2	-1.3
A_84_P16227	2347.4	638.7	-1.9	1939.7	921	-1.1
A_84_P784554	68.9	16.3	-2.1	41.3	18	-1.2
A_84_P860230	42125.7	13823.8	-1.6	33407	11854.1	-1.5
A_84_P23719	43.8	5.7	-2.9	82.2	14.1	-2.5
A_84_P12305	91.3	4	-4.5	22.5	3.7	-2.6
A_84_P23973	40246.7	11131.8	-1.9	37397.7	16788	-1.2
A_84_P13379	470.7	75.5	-2.6	430.8	157.1	-1.5
A_84_P18059	66.6	27.8	-1.3	83.3	35.7	-1.2
A_84_P149828	1177.3	508	-1.2	1292.7	634.4	-1
A_84_P180884	71.6	7.4	-3.3	58.7	5.2	-3.5
A_84_P788550	21386.3	7809.7	-1.5	28100.6	12234.6	-1.2
A_84_P785087	2872.6	1258.9	-1.2	3532.3	1685.8	-1.1
A_84_P12696	197.3	2.8	-6.1	98	2.8	-5.1
A_84_P89919	13.3	2.7	-2.3	61.8	2.7	-4.5
A_84_P861110	1623.3	610	-1.4	2331.5	864	-1.4
A_84_P820222	119.5	54.3	-1.1	215.8	42	-2.4
A_84_P752264	56.9	27.3	-1.1	65.7	21.7	-1.6
A_84_P12011	1793.5	624	-1.5	2252.9	748.3	-1.6
A_84_P514027	174.7	84.9	-1	319	103	-1.6
A_84_P825910	706.8	139.4	-2.3	532.8	207.3	-1.4
A_84_P802547	386.2	160.5	-1.3	424.8	178.2	-1.3

A_84_P66174	37.4	9.3	-2	52.3	23.1	-1.2
A_84_P119892	207	73.1	-1.5	222.7	97.6	-1.2
A_84_P861830	507.2	245.6	-1	746.7	363.6	-1
A_84_P20622	106.4	38.7	-1.5	93.3	42.1	-1.1
A_84_P137179	1647.3	747.1	-1.1	2142.5	781.1	-1.5
A_84_P729644	133.5	4.5	-4.9	136.6	7.4	-4.2
A_84_P603991	15.3	2.6	-2.6	19.8	6.3	-1.6
A_84_P855865	4356	1760.5	-1.3	6152.4	2506	-1.3
A_84_P537312	1993.2	982.2	-1	5331.8	1036.8	-2.4
A_84_P11569	8524.2	1451.3	-2.6	11315	3383.2	-1.7
A_84_P837235	1121.1	277.8	-2	1237.9	245.7	-2.3
A_84_P20881	11.6	2.8	-2.1	11.3	5.5	-1
A_84_P15932	553.5	60.6	-3.2	195	50.3	-2
A_84_P91139	447.9	213.6	-1.1	681.4	319	-1.1
A_84_P823096	73.4	17.3	-2.1	51	19.9	-1.4
A_84_P22675	236.6	104.3	-1.2	842	97.7	-3.1
A_84_P830899	687.9	278.6	-1.3	1133.1	442.6	-1.4
A_84_P829045	2662.6	464.2	-2.5	2225.3	629	-1.8
A_84_P12549	1739.1	738.2	-1.2	1998	907.7	-1.1
A_84_P846994	913.5	152.8	-2.6	1198.9	346.6	-1.8
A_84_P16676	19.4	6.2	-1.6	56.7	2.9	-4.3
A_84_P763492	163.9	2.9	-5.8	182.2	25.7	-2.8
A_84_P603012	148.8	51	-1.5	210.4	101.3	-1.1
A_84_P839463	223.7	85	-1.4	446.3	122.3	-1.9
A_84_P16900	80.5	39.7	-1	135.2	48.5	-1.5
A_84_P17820	10	3.7	-1.4	13.7	5.6	-1.3
A_84_P19773	209.2	96.6	-1.1	285.1	137.9	-1
A_84_P758488	298.9	93.8	-1.7	249.6	94.6	-1.4
A_84_P839184	29.5	14.2	-1.1	32.7	14.1	-1.2
A_84_P20632	2233.8	661.1	-1.8	2505.4	699.8	-1.8
A_84_P764623	7385.5	378.2	-4.3	5396.9	456.3	-3.6
A_84_P823385	1195.8	575.7	-1.1	1846.5	632.9	-1.5
A_84_P515003	89.2	30.8	-1.5	171.9	24.5	-2.8
A_84_P11644	2243.4	473.2	-2.2	2412.4	851.1	-1.5
A_84_P814887	514.7	253.2	-1	670.2	122.7	-2.4
A_84_P20461	17.7	2.6	-2.8	10.8	2.5	-2.1
A_84_P10096	26.5	3.2	-3	56.5	9.5	-2.6
A_84_P823166	14103.7	4877	-1.5	16464.7	7249.9	-1.2
A_84_P585099	5.9	2.6	-1.2	5.3	2.5	-1.1
A_84_P18858	50.4	18.4	-1.5	242.9	22.7	-3.4
A_84_P17723	5669.2	2610.4	-1.1	8287.4	3772.4	-1.1
A_84_P791049	14.4	6.2	-1.2	18.3	2.5	-2.9
A_84_P120842	27.7	8	-1.8	22	4.5	-2.3
A_84_P21113	67.6	21.3	-1.7	54.6	14	-2
A_84_P507571	602.1	158.9	-1.9	716.4	248.2	-1.5

A_84_P816739	190.5	84.4	-1.2	341.9	67	-2.4
A_84_P839634	983.1	448.2	-1.1	2092.5	587.5	-1.8
A_84_P13249	7.2	2.8	-1.4	9.2	3.2	-1.5
A_84_P19588	4605.1	1643.3	-1.5	9201.8	1777	-2.4
A_84_P11805	3510.9	251.7	-3.8	2840.8	416.8	-2.8
A_84_P752862	478.4	62.5	-2.9	375.6	78.2	-2.3
A_84_P829873	241.3	100	-1.3	308.6	151.4	-1
A_84_P240805	3100.4	480.8	-2.7	3266.2	436.1	-2.9
A_84_P536936	41	13.5	-1.6	27.3	5.3	-2.4
A_84_P10736	211.6	87.9	-1.3	338.4	109	-1.6
A_84_P11583	10070.2	2226.8	-2.2	8847.9	4411.5	-1
A_84_P184234	4031.3	1250	-1.7	4603.8	1750.4	-1.4
A_84_P23724	1005.8	476.8	-1.1	942.4	409.5	-1.2
A_84_P137629	2852.9	198.5	-3.8	1870.8	294.2	-2.7
A_84_P859652	8342	3035.9	-1.5	8508	4012.8	-1.1
A_84_P18029	185.9	49.7	-1.9	181.9	78.2	-1.2
A_84_P94929	21.8	2.6	-3.1	31.8	2.6	-3.6
A_84_P255680	43837.4	9832.2	-2.2	66999.3	19578.3	-1.8
A_84_P857281	3476.5	1370.4	-1.3	6661.7	1801.4	-1.9
A_84_P15281	1077.4	521.3	-1	1277.1	393.5	-1.7
A_84_P784679	9.9	2.8	-1.8	12.9	3.5	-1.9
A_84_P788919	105.8	19.5	-2.4	190.4	49.8	-1.9
A_84_P841882	159594.8	71378.1	-1.2	167281.3	56176.5	-1.6
A_84_P235073	2058.6	525.6	-2	1731.7	720.1	-1.3
A_84_P10474	12.3	4.8	-1.4	12.5	2.8	-2.2
A_84_P554535	6.3	2.7	-1.2	9.9	3.2	-1.6
A_84_P296664	1350.5	662.2	-1	7418.3	638.1	-3.5
A_84_P797706	2478.8	905.1	-1.5	3417.5	1500.5	-1.2
A_84_P12031	260.1	92.6	-1.5	212.2	103.3	-1
A_84_P24041	11791	4534.7	-1.4	11416.8	4016.2	-1.5
A_84_P16850	881	418.6	-1.1	3255	518.3	-2.7
A_84_P20549	5709.7	2488.1	-1.2	8474.3	3587.7	-1.2
A_84_P14783	8935.6	3671.3	-1.3	14148.9	4143.6	-1.8
A_84_P189624	173767.2	43540.9	-2	166716.3	78104.3	-1.1
A_84_P754183	6.7	2.8	-1.3	12.7	5.1	-1.3
A_84_P845859	19568	6971.7	-1.5	24948	10526.1	-1.2
A_84_P845705	36.5	4.3	-3.1	29.5	12.1	-1.3
A_84_P10281	7.5	2.5	-1.6	7.4	2.5	-1.6
A_84_P74664	703.1	125.8	-2.5	797.2	250.6	-1.7
A_84_P751111	122.8	58.6	-1.1	192.1	58.9	-1.7
A_84_P17624	278.6	110.4	-1.3	434.3	138.1	-1.7
A_84_P11877	9.8	3.3	-1.5	8.5	2.5	-1.8
A_84_P832842	36	11.4	-1.7	21.8	10.1	-1.1
A_84_P14852	8.3	2.6	-1.7	5.6	2.6	-1.1
A_84_P795530	144.1	41.2	-1.8	126.4	42.1	-1.6

A_84_P830062	516.3	184.4	-1.5	717.9	181	-2
A_84_P14879	21.8	4.9	-2.1	15.2	6.5	-1.2
A_84_P751557	9.2	2.7	-1.8	33.8	2.7	-3.6
A_84_P539913	93.5	32.8	-1.5	112	30.3	-1.9
A_84_P16627	31.4	8.2	-1.9	14.8	5	-1.6
A_84_P579221	19.2	2.6	-2.9	22	2.6	-3.1
A_84_P16385	16.5	2.5	-2.7	9.2	2.5	-1.9
A_84_P279940	315	88.2	-1.8	319.5	148.4	-1.1
A_84_P522811	323.4	141.4	-1.2	508.6	201.9	-1.3
A_84_P763376	323.1	159.3	-1	387.9	159.4	-1.3
A_84_P739163	1274.5	631.4	-1	1822.6	751	-1.3
A_84_P839829	217.8	101.2	-1.1	435.6	105.5	-2
A_84_P824880	75	24.4	-1.6	88.4	12.7	-2.8
A_84_P820618	8	3	-1.4	7.9	2.5	-1.7
A_84_P15040	1663.5	366.4	-2.2	3053.7	275.8	-3.5
A_84_P10208	25843	8829.6	-1.5	25356.4	8543	-1.6
A_84_P850782	228.2	64.5	-1.8	435.4	62.4	-2.8
A_84_P845992	16.2	7.4	-1.1	23.2	7.7	-1.6
A_84_P16685	386.5	155.3	-1.3	341.6	119.5	-1.5
A_84_P760622	3376.7	1250.9	-1.4	3393.2	1579.4	-1.1
A_84_P155935	6.8	3	-1.2	11.8	2.6	-2.2
A_84_P257990	3277.9	907.3	-1.9	2482.8	1096.7	-1.2
A_84_P14326	10.6	2.5	-2.1	7.6	2.5	-1.6
A_84_P762645	880.6	338.9	-1.4	1154.5	552.7	-1.1
A_84_P21670	7917.5	3691.7	-1.1	8183	2290.1	-1.8
A_84_P233529	1431.6	429.9	-1.7	1522.8	715.2	-1.1
A_84_P20292	12458.1	2610.6	-2.3	8124.4	3763.7	-1.1
A_84_P126241	1889.7	234	-3	927.9	395.7	-1.2
A_84_P14753	12905.8	5879.9	-1.1	17103.5	8124.4	-1.1
A_84_P20788	188	27.2	-2.8	447.9	48.9	-3.2
A_84_P18366	3241.7	1121.3	-1.5	4815.9	1338.8	-1.8
A_84_P17987	201.6	89.8	-1.2	128.8	54.1	-1.3
A_84_P23544	1022.1	250.7	-2	997.9	352.2	-1.5
A_84_P20167	36	11.2	-1.7	41.2	18	-1.2
A_84_P19887	1864.3	386.5	-2.3	1363.2	538.7	-1.3
A_84_P307510	946.8	341.6	-1.5	1017	264.1	-1.9
A_84_P273780	4141.4	928.8	-2.2	4609.2	1549.9	-1.6
A_84_P139499	27527.5	9448.3	-1.5	42987.7	12927.7	-1.7
A_84_P22910	9.4	2.7	-1.8	6.7	2.7	-1.3
A_84_P226239	3487.3	1199.2	-1.5	3513.9	1281.2	-1.5
A_84_P83309	227.9	89.9	-1.3	247.3	112	-1.1
A_84_P251495	196.6	77.5	-1.3	296.2	97.6	-1.6
A_84_P840600	16.9	4.9	-1.8	24.5	5	-2.3
A_84_P20687	18.8	6.5	-1.5	19.4	8.7	-1.2
A_84_P13541	8561.3	3390.3	-1.3	6853.4	2692.4	-1.3

A_84_P15144	1547.8	329.4	-2.2	1528.2	317	-2.3
A_84_P853518	10132.8	4720.7	-1.1	15537.4	5451	-1.5
A_84_P22911	18625.9	9060.4	-1	20058.6	9727.4	-1
A_84_P253335	56.3	15.8	-1.8	52.8	23.3	-1.2
A_84_P830457	9.3	3.8	-1.3	13.8	2.4	-2.5
A_84_P813495	975.7	73.1	-3.7	714.2	226.9	-1.7
A_84_P102716	157.8	75.4	-1.1	249.7	83.9	-1.6
A_84_P12395	5152.8	468.8	-3.5	3488.3	700.5	-2.3
A_84_P12057	13.5	2.6	-2.4	38.4	6.4	-2.6
A_84_P812476	38501.2	14043.4	-1.5	39378.5	10341.6	-1.9
A_84_P17561	168.4	28.3	-2.6	102.8	32.3	-1.7
A_84_P806069	272	50	-2.4	324	81.3	-2
A_84_P16655	89.6	39.8	-1.2	119	54	-1.1
A_84_P593050	36.5	7.9	-2.2	31.1	14.6	-1.1
A_84_P23923	1091.5	115.5	-3.2	932.6	246	-1.9
A_84_P785851	38.5	9.2	-2.1	17.6	8.7	-1
A_84_P96296	1650.8	461.8	-1.8	1713.4	679.7	-1.3
A_84_P281090	352.1	175.8	-1	424.2	205.3	-1
A_84_P18119	2259	863.8	-1.4	1912.6	561.2	-1.8
A_84_P845902	747.5	331	-1.2	541.5	230.6	-1.2
A_84_P790373	79.5	14.4	-2.5	71.5	27.5	-1.4
A_84_P766967	8.8	2.5	-1.8	31.4	5.7	-2.5
A_84_P857373	13.9	3.8	-1.9	12.6	6	-1.1
A_84_P765172	306.2	30.4	-3.3	134.4	63.8	-1.1
A_84_P23838	9050.2	4090.6	-1.1	9484.4	2460.6	-1.9
A_84_P17179	50.6	11.8	-2.1	34.3	8.4	-2
A_84_P18129	325.5	77.8	-2.1	339.8	107.2	-1.7
A_84_P512914	17.1	3.3	-2.4	33	2.5	-3.7
A_84_P17981	39.9	15.1	-1.4	12.3	4	-1.6
A_84_P535279	44.3	19	-1.2	85	14.3	-2.6
A_84_P786144	58.2	18.5	-1.7	61.7	30.8	-1
A_84_P19994	21.8	3.4	-2.7	49.3	2.6	-4.2
A_84_P814388	1274.6	631.2	-1	1426.6	534.4	-1.4
A_84_P19163	10089.7	1066.5	-3.2	12180	1872.8	-2.7
A_84_P761982	13.6	3.7	-1.9	15.4	7.5	-1
A_84_P14556	4165.1	1515.7	-1.5	5067.8	1702.7	-1.6
A_84_P573108	50.4	15.6	-1.7	97.2	31.7	-1.6
A_84_P20172	12325.9	3512.3	-1.8	12314.4	5216.7	-1.2
A_84_P613051	12	5.6	-1.1	9.7	4.7	-1.1
A_84_P127161	1909.9	694.1	-1.5	1069.5	432.8	-1.3
A_84_P563624	11.9	2.8	-2.1	11.3	2.6	-2.1
A_84_P178234	114.4	25.1	-2.2	50.1	21.4	-1.2
A_84_P754636	24.2	4.7	-2.4	9.9	4.8	-1
A_84_P15068	5789.8	989.9	-2.5	6802.9	2226.8	-1.6
A_84_P707765	19	5.8	-1.7	14	4.5	-1.6

A_84_P173901	232.8	31.7	-2.9	199.5	75.2	-1.4
A_84_P22977	3406	1617.3	-1.1	3973.7	1499	-1.4
A_84_P16270	42.4	20.3	-1.1	23	8.5	-1.4
A_84_P10865	8.8	2.6	-1.8	16.7	2.6	-2.7
A_84_P737847	104	25.9	-2	88.6	33.9	-1.4
A_84_P808706	2485.8	1081.5	-1.2	3229.6	1061	-1.6
A_84_P561086	870.5	258.6	-1.8	623.2	172.8	-1.9
A_84_P515468	24.6	11.6	-1.1	30.6	10.2	-1.6
A_84_P546863	31.3	3.1	-3.4	9.9	3.4	-1.6
A_84_P613622	1203.7	468.3	-1.4	1213	494.3	-1.3
A_84_P520839	53.2	19.8	-1.4	83.8	31.9	-1.4
A_84_P12035	2614.9	1146.8	-1.2	2834.9	1364	-1.1
A_84_P533889	6.4	2.5	-1.4	23.5	2.6	-3.2
A_84_P52840	16372.2	2481.7	-2.7	11168.5	4523.6	-1.3
A_84_P19255	1063.3	264.4	-2	1728.8	539.2	-1.7
A_84_P785012	1248.1	360.7	-1.8	1631.8	397.6	-2
A_84_P21842	10223.7	1705.2	-2.6	6337.7	2892.1	-1.1
A_84_P10083	397	122.7	-1.7	622.7	180	-1.8
A_84_P14689	101.6	35.6	-1.5	104	42.8	-1.3
A_84_P843757	58.5	15.8	-1.9	45.5	17.4	-1.4
A_84_P579600	1365.1	313.5	-2.1	1451.7	444.9	-1.7
A_84_P533079	9.3	2.5	-1.9	12.8	2.5	-2.3
A_84_P13905	8.1	2.5	-1.7	5.1	2.5	-1
A_84_P786590	1286.4	355.9	-1.9	1012.6	482.7	-1.1
A_84_P719271	23	9.5	-1.3	25.1	10.5	-1.3
A_84_P761630	32.6	10.5	-1.6	35.2	13.2	-1.4
A_84_P17486	43.4	12.3	-1.8	34.9	15.5	-1.2
A_84_P750177	8061.7	1610.8	-2.3	9532.6	3313.5	-1.5
A_84_P94999	23.1	10	-1.2	48.7	10.7	-2.2
A_84_P834455	119	36.8	-1.7	70	30.7	-1.2
A_84_P241075	7.2	2.5	-1.6	8.6	3	-1.5
A_84_P762010	989.4	180.6	-2.5	899.7	364.8	-1.3
A_84_P16766	94.8	27.9	-1.8	83.4	23.8	-1.8
A_84_P94969	19988.5	1798.1	-3.5	14711	2128.4	-2.8
A_84_P820052	248.8	53.4	-2.2	223.6	92.4	-1.3
A_84_P528212	10.7	4.4	-1.3	60.1	2.6	-4.5
A_84_P725162	250.1	119.3	-1.1	1402.9	129.8	-3.4
A_84_P117182	2814.1	192.3	-3.9	2406.9	708.9	-1.8
A_84_P522239	13.8	6.1	-1.2	14.5	2.4	-2.6
A_84_P763076	1819.5	907.4	-1	1953.8	859.7	-1.2
A_84_P10878	811.8	258.7	-1.6	803.7	297.8	-1.4
A_84_P755803	7.9	2.4	-1.7	45.1	12.3	-1.9
A_84_P186814	22.8	4.7	-2.3	51.1	2.4	-4.4
A_84_P596315	1629.6	794	-1	1602.1	653.6	-1.3
A_84_P751116	232.3	4.1	-5.8	9	2.5	-1.9

A_84_P17983	7.8	2.6	-1.6	7.5	2.5	-1.6
A_84_P556074	1310.4	350	-1.9	1234.5	409.8	-1.6
A_84_P20420	554.2	158.7	-1.8	1135.4	151.7	-2.9
A_84_P517600	587	282.1	-1.1	544.1	262.6	-1.1
A_84_P22686	285.5	139.3	-1	383	171.2	-1.2
A_84_P12278	2422.3	863.1	-1.5	3627.5	624.8	-2.5
A_84_P784278	205.3	87.3	-1.2	183.1	52.8	-1.8
A_84_P14454	18.1	2.4	-2.9	7.1	2.8	-1.3
A_84_P842083	125.1	47	-1.4	215	52	-2
A_84_P16874	664.3	317.2	-1.1	1641	331.7	-2.3
A_84_P820018	1517.7	216.9	-2.8	772.3	355.5	-1.1
A_84_P16471	14.7	2.5	-2.6	10	2.5	-2
A_84_P21915	8893.6	1713.3	-2.4	7996.9	3222.5	-1.3
A_84_P768727	2549.7	791.8	-1.7	1665.7	639.8	-1.4
A_84_P807008	53564.9	25791.9	-1.1	65032.4	28667.4	-1.2
A_84_P297064	941.2	451.4	-1.1	1699.3	397.2	-2.1
A_84_P275610	317.7	142.5	-1.2	848.7	181.5	-2.2
A_84_P17557	1138.7	351.3	-1.7	1599.4	585.7	-1.4
A_84_P187764	213.7	103.5	-1	291.3	109.8	-1.4
A_84_P832994	65.6	32.1	-1	151	58.2	-1.4
A_84_P838635	74.9	26.1	-1.5	118.9	51.3	-1.2
A_84_P15458	3739.4	1408.6	-1.4	4012.8	1851.3	-1.1
A_84_P768403	202.7	34.8	-2.5	197.7	93.8	-1.1
A_84_P830153	8.3	2.5	-1.7	6.4	2.5	-1.3
A_84_P12692	2699.6	844.3	-1.7	3785.9	1498	-1.3
A_84_P10935	40.3	9.6	-2.1	43.4	19.7	-1.1
A_84_P591196	86.9	41.4	-1.1	98.8	45.8	-1.1
A_84_P21386	1864.5	390.9	-2.3	2544.3	837.9	-1.6
A_84_P14033	358.3	42.6	-3.1	385.2	148.8	-1.4
A_84_P846903	664.7	112.4	-2.6	664.1	215.1	-1.6
A_84_P15454	303.5	84.5	-1.8	782.5	203.8	-1.9
A_84_P807083	7.3	2.5	-1.5	9.9	2.6	-2
A_84_P853770	6305.1	2718.5	-1.2	10143.8	3847.1	-1.4
A_84_P203658	36.2	14.6	-1.3	74.5	8.4	-3.2
A_84_P20880	179.4	73.1	-1.3	261.2	90.4	-1.5
A_84_P71554	7.4	3.5	-1.1	14.9	5	-1.6
A_84_P14137	1002	138.2	-2.9	535.7	150.1	-1.8
A_84_P544019	2526	1222.5	-1	2636.6	568.4	-2.2
A_84_P23789	88.1	34.1	-1.4	180.4	70.8	-1.3
A_84_P515517	7.7	2.5	-1.7	10.1	2.4	-2.1
A_84_P22462	37.1	6	-2.6	24.6	2.4	-3.4
A_84_P23012	23.1	3.4	-2.8	33.9	2.4	-3.8
A_84_P787734	490.7	137.2	-1.8	706.5	211	-1.7
A_84_P847118	110	45.8	-1.3	164.2	63.2	-1.4
A_84_P831705	577.3	158.5	-1.9	672	287.9	-1.2

A_84_P16644	92.2	35.9	-1.4	101.6	39.9	-1.3
A_84_P789317	3591.3	1513.7	-1.2	4293.4	1915.5	-1.2
A_84_P24047	158	45.2	-1.8	129.7	36.3	-1.8
A_84_P11001	175.2	81.7	-1.1	473.7	107.9	-2.1
A_84_P572184	24.3	11.6	-1.1	28.8	13.6	-1.1
A_84_P16440	2064.9	547.8	-1.9	1427.1	569.8	-1.3
A_84_P856227	931	230.5	-2	860.3	331.8	-1.4
A_84_P15831	408.6	91.3	-2.2	503.3	224.2	-1.2
A_84_P765361	12.8	2.7	-2.2	13.3	6.5	-1
A_84_P11893	4652.3	2180.8	-1.1	5454.2	1645.9	-1.7
A_84_P754935	6.5	2.5	-1.4	8.7	4.3	-1
A_84_P507242	4798.7	1680.8	-1.5	5331.1	2371.4	-1.2
A_84_P283860	59.9	29	-1	197.7	32.7	-2.6
A_84_P15904	2908.1	334.1	-3.1	2724.6	491.6	-2.5
A_84_P528977	120.1	12.4	-3.3	93.1	10.5	-3.2
A_84_P20322	7.7	2.4	-1.7	6.4	2.4	-1.4
A_84_P10747	1843.6	560	-1.7	1717.7	781.9	-1.1
A_84_P175401	789.1	169.2	-2.2	937.9	232.3	-2
A_84_P856574	9082.7	2649	-1.8	9094.3	2857.8	-1.7
A_84_P10252	15473.6	5048.9	-1.6	14734.1	5355	-1.5
A_84_P17122	3336	1413.5	-1.2	3481.5	1090.6	-1.7
A_84_P761647	26.4	9.8	-1.4	35	15.6	-1.2
A_84_P13675	33889.1	13558.3	-1.3	36844.8	18090.4	-1
A_84_P181744	36.3	3.2	-3.5	4.9	2.4	-1
A_84_P96816	268	71.4	-1.9	297.8	59	-2.3
A_84_P766418	12.5	3.7	-1.7	201.8	27.5	-2.9
A_84_P840571	6.9	2.5	-1.5	292	2.6	-6.8
A_84_P612689	30.6	2.5	-3.6	7.4	2.5	-1.6
A_84_P13400	7.6	2.5	-1.6	11.5	2.4	-2.3
A_84_P761667	106.4	47.8	-1.2	359	48.3	-2.9
A_84_P115622	2141.9	1066.9	-1	2070.8	804.3	-1.4
A_84_P769609	72.4	23.4	-1.6	77.7	12	-2.7
A_84_P22923	150.2	39.9	-1.9	164.5	60	-1.5
A_84_P15484	5975.3	2690.8	-1.2	6129.7	2874.3	-1.1
A_84_P801247	8.3	2.4	-1.8	8.5	2.4	-1.8
A_84_P287550	5680.1	1928.6	-1.6	7005.2	3149.6	-1.2
A_84_P761641	24.3	2.5	-3.3	27.2	10.2	-1.4
A_84_P17163	26.9	2.4	-3.5	15.1	6.4	-1.2
A_84_P799025	25	10.9	-1.2	35.3	16.5	-1.1
A_84_P15536	70034.2	30584.2	-1.2	76584	33270.2	-1.2
A_84_P526317	194.6	78.3	-1.3	294.1	121.2	-1.3
A_84_P825000	7.9	2.4	-1.7	22.7	7.7	-1.6
A_84_P23628	65.3	26.3	-1.3	63.3	19.4	-1.7
A_84_P827867	11.8	5.7	-1	14	2.5	-2.5
A_84_P842382	176.5	85.4	-1	425.1	90.4	-2.2

A_84_P851319	2248.6	739.6	-1.6	2219.9	1080.6	-1
A_84_P502404	104.2	47.3	-1.1	85.6	20.8	-2
A_84_P13475	20.2	2.5	-3	77.3	2.5	-4.9
A_84_P16254	278.4	111.1	-1.3	341.2	131.2	-1.4
A_84_P21046	931.8	103.1	-3.2	1299.1	241.2	-2.4
A_84_P17453	6.2	2.4	-1.4	10.5	2.6	-2
A_84_P19006	3414.8	1517.4	-1.2	4451.6	2223.7	-1
A_84_P22425	338.4	103	-1.7	211.2	75.2	-1.5
A_84_P15367	46	17.9	-1.4	362.2	10.9	-5.1
A_84_P869688	129.5	2.4	-5.8	96.1	17.3	-2.5
A_84_P14195	351.7	2.4	-7.2	65.6	15.6	-2.1
A_84_P17015	2350	640.2	-1.9	2407.4	931.6	-1.4
A_84_P765604	16.4	7.1	-1.2	24.6	9.5	-1.4
A_84_P832980	82.8	37	-1.2	84.1	33.8	-1.3
A_84_P19718	557.8	240.3	-1.2	520.4	194.4	-1.4
A_84_P869667	3615.8	833.7	-2.1	5157.6	982.8	-2.4
A_84_P13501	97.4	31.3	-1.6	78	36.7	-1.1
A_84_P568309	8.8	4.1	-1.1	17.1	5.8	-1.6
A_84_P855563	147.4	64.9	-1.2	238.3	108.7	-1.1
A_84_P10687	56.5	2.4	-4.5	37.5	7.2	-2.4
A_84_P840120	223.7	66.6	-1.7	239.8	78.4	-1.6
A_84_P814238	23085.4	6377.7	-1.9	19956.3	9115.9	-1.1
A_84_P50100	2712.6	183.7	-3.9	2046.2	388.5	-2.4
A_84_P17058	5290.4	1492.5	-1.8	5784.2	2343.3	-1.3
A_84_P246705	38441.8	2745.2	-3.8	52783.9	12608.2	-2.1
A_84_P557530	202.2	64.2	-1.7	338.5	109.5	-1.6
A_84_P21263	40	5.8	-2.8	41.1	18.6	-1.1
A_84_P22981	253.6	67.6	-1.9	215.9	85.6	-1.3
A_84_P855785	8770.4	3900	-1.2	14360	5381.9	-1.4
A_84_P768049	6.6	2.4	-1.5	13.5	3.7	-1.9
A_84_P22020	11460.9	5357.9	-1.1	11250.4	4906.9	-1.2
A_84_P591926	49.3	11.5	-2.1	35.1	15.6	-1.2
A_84_P15616	18.7	7.7	-1.3	16.4	7.4	-1.1
A_84_P821825	17.7	4.6	-1.9	19.4	6.7	-1.5
A_84_P808187	4585	1427.5	-1.7	6630.4	2619.8	-1.3
A_84_P101346	5532.1	2003.9	-1.5	7251.4	2378.9	-1.6
A_84_P89869	2087.5	985.5	-1.1	5652.8	1005.6	-2.5
A_84_P511284	69.8	34.3	-1	113.5	45.5	-1.3
A_84_P22300	870.8	79.5	-3.5	1547.7	189.8	-3
A_84_P821159	399.3	104.5	-1.9	390.2	192.5	-1
A_84_P808228	197528.6	86912.9	-1.2	193135.3	83227.5	-1.2
A_84_P279270	23.2	5.1	-2.2	34	6.3	-2.4
A_84_P19905	23.1	2.4	-3.3	17.5	3.9	-2.2
A_84_P24102	4113.6	1393.4	-1.6	2881	1287.6	-1.2
A_84_P15851	24315.4	4758.2	-2.4	18171.5	4610	-2

A_84_P16449	398.9	168.4	-1.2	272.6	104.5	-1.4
A_84_P15991	5.9	2.6	-1.2	12.9	5.5	-1.2
A_84_P559359	14468.4	3429.2	-2.1	10185.3	3488.3	-1.5
A_84_P130716	697.7	325.2	-1.1	1330.3	388.3	-1.8
A_84_P12982	701.1	334.8	-1.1	1125.5	471.6	-1.3
A_84_P858659	11938.2	4271.6	-1.5	16498.4	6399	-1.4
A_84_P95079	745.2	284.1	-1.4	2022.2	409.7	-2.3
A_84_P507728	134.4	7.6	-4.1	102.8	25.8	-2
A_84_P130466	8982.3	3557.1	-1.3	7703	3846.6	-1
A_84_P859998	689.1	156.1	-2.1	1202.1	323.3	-1.9
A_84_P19901	439.1	208.5	-1.1	419	174	-1.3
A_84_P10495	226.2	78.4	-1.5	117.3	42.2	-1.5
A_84_P10458	209.8	93.3	-1.2	601	131.5	-2.2
A_84_P758278	59.8	17.2	-1.8	83.4	39	-1.1
A_84_P580219	340.3	130.8	-1.4	330.8	147.6	-1.2
A_84_P20333	7022.5	2774.1	-1.3	9517.3	3109	-1.6
A_84_P610462	630.1	312.5	-1	986	427.5	-1.2
A_84_P287570	10424	4469.9	-1.2	13484.3	4395.9	-1.6
A_84_P16608	915.2	396	-1.2	1096.2	537.4	-1
A_84_P20497	173.4	74.3	-1.2	265.6	110.9	-1.3
A_84_P757762	147.4	33.2	-2.2	101.6	34.5	-1.6
A_84_P10947	15134.1	5754.6	-1.4	16899.4	6648.3	-1.3
A_84_P769063	18.7	4.9	-1.9	24.8	6.5	-1.9
A_84_P801733	17.1	8.5	-1	24.2	5.2	-2.2
A_84_P16907	540.1	205.8	-1.4	604.2	207.6	-1.5
A_84_P831613	157.7	63.4	-1.3	440.9	89	-2.3
A_84_P159845	24875.5	8364.5	-1.6	21083.7	9414.5	-1.2
A_84_P787769	10.5	4.7	-1.2	16	5.6	-1.5
A_84_P299940	82.9	32.7	-1.3	67.4	32.8	-1
A_84_P557122	19.3	3.5	-2.4	46.3	2.4	-4.3
A_84_P15357	529.6	258.8	-1	797.4	268.2	-1.6
A_84_P16474	222.7	55.8	-2	229.8	107.6	-1.1
A_84_P12712	15.1	2.6	-2.5	20.2	4.9	-2
A_84_P57310	5396.9	1307.2	-2	6195.3	2979.5	-1.1
A_84_P14996	88.9	22.6	-2	94.8	36.4	-1.4
A_84_P11369	8.5	2.4	-1.8	13.3	2.4	-2.5
A_84_P767020	23.1	11.3	-1	48.4	11.9	-2
A_84_P10200	60.5	29	-1.1	104	36.8	-1.5
A_84_P577170	432	66	-2.7	407.6	81.7	-2.3
A_84_P21138	1324.1	560.3	-1.2	1630	532.7	-1.6
A_84_P540848	5404.3	507.8	-3.4	4211	1030.7	-2
A_84_P824075	2696.3	42.3	-6	2351.6	444.8	-2.4
A_84_P836102	151.2	28.8	-2.4	198.1	73.8	-1.4
A_84_P18953	220.4	96.5	-1.2	398.9	151.7	-1.4
A_84_P17266	2077.1	718.7	-1.5	3448.7	1125.9	-1.6

A_84_P751155	12.1	5.3	-1.2	11.4	4.2	-1.4
A_84_P591780	1200.1	296.5	-2	1445.3	503.1	-1.5
A_84_P819325	787.2	250.5	-1.7	1395.2	510	-1.5
A_84_P155475	6151.3	660.5	-3.2	4881	1007.9	-2.3
A_84_P190054	1864.1	897.2	-1.1	2056.6	446.4	-2.2
A_84_P751713	11.4	4.2	-1.5	15.3	7.3	-1.1
A_84_P11757	1123.2	478.6	-1.2	1692.5	613.8	-1.5
A_84_P769315	25.8	9.5	-1.4	94.8	16.6	-2.5
A_84_P14733	41406.3	7569.3	-2.5	39073.9	10242.6	-1.9
A_84_P22457	561	274.8	-1	944.8	323.8	-1.5
A_84_P21311	55.7	8.7	-2.7	47.3	17.8	-1.4
A_84_P272660	316.2	146.9	-1.1	391.4	120.5	-1.7
A_84_P828091	89.8	18.5	-2.3	134.8	35.2	-1.9
A_84_P195914	911.6	134.3	-2.8	658.5	230.4	-1.5
A_84_P807545	38112.2	12611.4	-1.6	41041	18486.1	-1.2
A_84_P809869	68672.9	20080.6	-1.8	88660.8	25422.6	-1.8
A_84_P157075	823.3	237.5	-1.8	834.4	413	-1
A_84_P821812	285.8	81.6	-1.8	240.7	85.7	-1.5
A_84_P730499	38.3	16.6	-1.2	38.2	8	-2.3
A_84_P754942	31.1	14.7	-1.1	54.1	23.3	-1.2
A_84_P788567	214	79.9	-1.4	371.1	141.9	-1.4
A_84_P19241	8805.1	1339.8	-2.7	6144.9	2178.2	-1.5
A_84_P14626	178.5	82.8	-1.1	354.8	93.5	-1.9
A_84_P16678	141.5	12.9	-3.5	168.2	41.6	-2
A_84_P21904	75.9	21.1	-1.9	114.8	49.7	-1.2
A_84_P19344	102.2	42.1	-1.3	119.6	31.9	-1.9
A_84_P159165	9.9	4.8	-1	59.9	7	-3.1
A_84_P264320	182.3	61.5	-1.6	154.1	56.5	-1.4
A_84_P221276	20	6.8	-1.5	18.6	7.8	-1.2
A_84_P17176	56.2	16.8	-1.7	58.5	24.1	-1.3
A_84_P801001	3896.1	1235	-1.7	5333.2	761.4	-2.8
A_84_P169473	86.4	22.3	-2	106.9	22.8	-2.2
A_84_P828432	705.6	249.5	-1.5	698.5	213	-1.7
A_84_P21673	15591.1	6739	-1.2	31705.6	3574.5	-3.1
A_84_P808177	1782.2	486.4	-1.9	1767.8	310.9	-2.5
A_84_P574554	556.9	257.9	-1.1	678.6	286.8	-1.2
A_84_P12200	615	200.8	-1.6	1400.9	251.9	-2.5
A_84_P601177	138.2	62.9	-1.1	278.5	64.4	-2.1
A_84_P21662	11.9	3.6	-1.7	68	5.9	-3.5
A_84_P764629	42.1	4.5	-3.2	58.5	18.1	-1.7
A_84_P514265	82.3	37.6	-1.1	194.9	53.4	-1.9
A_84_P786411	4040.6	589.2	-2.8	2052.6	1020	-1
A_84_P11833	195.6	22.4	-3.1	165.3	49.9	-1.7
A_84_P10144	152.5	56.9	-1.4	141.4	57.1	-1.3
A_84_P18078	11.8	4.5	-1.4	13.4	5.2	-1.4

A_84_P16943	12698.2	3983.3	-1.7	14914.9	3237	-2.2
A_84_P15811	258.5	90.2	-1.5	369.1	175.3	-1.1
A_84_P23557	2472.8	370.8	-2.7	2044.3	592.5	-1.8
A_84_P132675	20.7	6	-1.8	22.8	10.3	-1.1
A_84_P21222	112.9	22.7	-2.3	154.5	45.8	-1.8
A_84_P20630	298.5	48.7	-2.6	290.4	129.5	-1.2
A_84_P786806	233.1	114.1	-1	250.1	80.8	-1.6
A_84_P522289	15.7	3.5	-2.2	38.9	5.9	-2.7
A_84_P17377	9.8	2.6	-1.9	9.1	2.5	-1.8
A_84_P64944	110.7	24.8	-2.2	83.5	16.2	-2.4
A_84_P511590	206.4	62.1	-1.7	332	107.5	-1.6
A_84_P791657	890.6	400.1	-1.2	606.6	288.5	-1.1
A_84_P755608	10.6	2.9	-1.9	7.2	2.6	-1.5
A_84_P563250	21.8	9.9	-1.1	7.2	2.7	-1.4
A_84_P853304	141.3	46.2	-1.6	128.1	60.4	-1.1
A_84_P284920	2014.9	682.8	-1.6	1475.1	666.2	-1.1
A_84_P14122	7.4	2.7	-1.5	5.9	2.8	-1.1
A_84_P833480	216.6	91	-1.3	287.2	128.8	-1.2
A_84_P22952	19798.4	6538.1	-1.6	19260.8	8362.4	-1.2
A_84_P811603	1644.5	555.1	-1.6	1817.2	610.7	-1.6
A_84_P605545	553.7	59.4	-3.2	322.4	69	-2.2
A_84_P19369	14705.9	1242.2	-3.6	10420.8	1848	-2.5
A_84_P24148	2201.3	186.1	-3.6	1810	304.2	-2.6
A_84_P266040	198.3	76.1	-1.4	253	50	-2.3
A_84_P545837	50.9	17.6	-1.5	163.7	17.8	-3.2
A_84_P11217	27.5	7.6	-1.9	42.2	5.5	-3
A_84_P830707	13.7	4.8	-1.5	20.7	10.2	-1
A_84_P848977	45.9	9.1	-2.3	123.3	8.5	-3.9
A_84_P799420	11953.3	4149.6	-1.5	20727.9	5697.2	-1.9
A_84_P857089	382.8	47	-3	269.1	66.7	-2
A_84_P238533	209	91.7	-1.2	411.9	111.4	-1.9
A_84_P788524	312.5	153.4	-1	586.9	178.5	-1.7
A_84_P518710	17.1	3.4	-2.3	17.6	8.3	-1.1
A_84_P816936	4844.6	2312	-1.1	6591.2	3218.2	-1
A_84_P205218	154.2	3.8	-5.4	41.6	8.4	-2.3
A_84_P187174	668.5	303.1	-1.1	473.5	194.3	-1.3
A_84_P12898	17.5	5.9	-1.6	18.8	5.7	-1.7
A_84_P302850	7874.4	1299.4	-2.6	16974.6	3470	-2.3
A_84_P305070	10030.6	1410.1	-2.8	4568.4	2004.6	-1.2
A_84_P822840	303.4	146.1	-1.1	669.6	86.9	-2.9
A_84_P18161	103.7	36.1	-1.5	121	52	-1.2
A_84_P18027	125636.1	36879.4	-1.8	146953.4	45042.5	-1.7
A_84_P235463	580.7	264.1	-1.1	1525.6	337.7	-2.2
A_84_P583210	4551.6	436.1	-3.4	9772.3	1987.4	-2.3
A_84_P862797	215994.6	79394.9	-1.4	264256.2	119419.6	-1.1

A_84_P14349	75.7	37.7	-1	156.6	44.2	-1.8
A_84_P23770	11713.1	2699.9	-2.1	15511.8	4853.3	-1.7
A_84_P115752	30299.1	10370.8	-1.5	31612.6	7989.3	-2
A_84_P544339	474.5	149.5	-1.7	494.3	228.7	-1.1
A_84_P280570	157.4	77.7	-1	180.4	50.9	-1.8
A_84_P579790	128.4	14.2	-3.2	223.1	21.1	-3.4
A_84_P606765	25.1	12.1	-1.1	122	7.4	-4.1
A_84_P597565	77.6	30.2	-1.4	188.6	34.4	-2.5
A_84_P761718	30.3	6.2	-2.3	20.4	9.1	-1.2
A_84_P556874	32.8	10.7	-1.6	67.5	15.9	-2.1
A_84_P22626	22	6.3	-1.8	31.7	11.6	-1.5
A_84_P14951	2153.2	184.8	-3.5	1877.4	264.8	-2.8
A_84_P751920	6.1	2.9	-1.1	13.9	4.3	-1.7
A_84_P79449	1834.1	890.8	-1	1734	827.5	-1.1
A_84_P806966	9053.5	1507.6	-2.6	10622.6	3721.5	-1.5
A_84_P286130	161.8	80.3	-1	349.8	88	-2
A_84_P540652	130.6	28.8	-2.2	128.9	58.5	-1.1
A_84_P544696	71.6	29.6	-1.3	119.9	28.8	-2.1
A_84_P518902	10.3	5.1	-1	69.3	9.3	-2.9
A_84_P13943	5558.4	1999.2	-1.5	5636.2	1916.5	-1.6
A_84_P733222	129.7	38.7	-1.7	133.2	59.3	-1.2
A_84_P20824	26.8	5.1	-2.4	29	2.5	-3.5
A_84_P861798	2922.9	1280.1	-1.2	6315.5	1448.4	-2.1
A_84_P297814	248.8	115.9	-1.1	348.7	163.5	-1.1
A_84_P279060	9038.6	490.7	-4.2	6422.5	591.9	-3.4
A_84_P19003	1255.2	570.5	-1.1	4549.8	682.9	-2.7
A_84_P545036	644.1	140.8	-2.2	761.2	284	-1.4
A_84_P17611	22.8	2.8	-3	19	2.8	-2.8
A_84_P17156	42.2	18.2	-1.2	76.4	14.7	-2.4
A_84_P131066	33.5	15.3	-1.1	72	26.9	-1.4
A_84_P18126	1402.7	688.5	-1	2049.4	666.1	-1.6
A_84_P74014	15598.7	6898	-1.2	20118.1	3604.5	-2.5
A_84_P840305	168.4	63.3	-1.4	205.7	101.4	-1
A_84_P13426	310	2.6	-6.9	238.8	3	-6.3
A_84_P24132	896.9	376.3	-1.3	652.6	290.8	-1.2
A_84_P19295	206.7	6.1	-5.1	267.3	87.3	-1.6
A_84_P553871	10.9	4.3	-1.3	17.9	7.2	-1.3
A_84_P502546	281.5	16	-4.1	295.7	24.5	-3.6
A_84_P23686	97.5	41.8	-1.2	261.6	48.1	-2.4
A_84_P575955	18.7	2.8	-2.8	23.8	4.6	-2.4
A_84_P851088	255.3	52.8	-2.3	212.6	67.7	-1.7
A_84_P808696	267433	93815.6	-1.5	268310.7	96907.8	-1.5
A_84_P537401	610	286.6	-1.1	1104.5	372.4	-1.6
A_84_P600850	396.7	134.5	-1.6	475.4	92.7	-2.4
A_84_P11135	1308.6	383	-1.8	1236	489	-1.3

A_84_P14194	5158.3	1349.3	-1.9	5793.7	1935.7	-1.6
A_84_P574446	249.1	120.6	-1	429.3	96.3	-2.2
A_84_P17327	25.7	2.7	-3.3	15.5	7.1	-1.1
A_84_P80109	1122.4	438.4	-1.4	1420.3	670.5	-1.1
A_84_P20157	83.7	31.8	-1.4	113.7	43.9	-1.4
A_84_P22825	87.6	15.7	-2.5	80.4	30.9	-1.4
A_84_P18880	36.9	15.4	-1.3	62	21.8	-1.5
A_84_P808697	2375.1	203.5	-3.5	1766.5	288.1	-2.6
A_84_P504795	489.1	209	-1.2	971.9	314.7	-1.6
A_84_P17407	17.9	2.8	-2.7	24.3	2.8	-3.1
A_84_P12139	1634.4	531.6	-1.6	2958	702.5	-2.1
A_84_P10400	1309.2	383.5	-1.8	1659.8	505.7	-1.7
A_84_P19525	2837	529.7	-2.4	3560.9	717.1	-2.3
A_84_P752590	2977.6	576.3	-2.4	2601.9	1029.5	-1.3
A_84_P15207	10834.7	4096.9	-1.4	10956.4	5105	-1.1
A_84_P831103	1953.8	692.8	-1.5	2373.3	947.9	-1.3
A_84_P601663	27.3	2.6	-3.4	26.7	9.8	-1.4
A_84_P767553	2065.1	150.9	-3.8	1501.6	356.8	-2.1
A_84_P769343	12.6	2.9	-2.1	15.1	2.9	-2.4
A_84_P16751	16680.5	5585	-1.6	16792.3	3982.4	-2.1
A_84_P13270	20.7	4.3	-2.3	29.2	7.6	-1.9
A_84_P21184	1285.3	608.9	-1.1	1645.9	298	-2.5
A_84_P10014	77.8	9.3	-3.1	99.5	25.9	-1.9
A_84_P15049	17.4	2.7	-2.7	110.8	2.7	-5.4
A_84_P815477	127	42.4	-1.6	132.1	60	-1.1
A_84_P89429	582	123.5	-2.2	597.4	205.1	-1.5
A_84_P592920	54.7	12	-2.2	144.1	27.4	-2.4
A_84_P13832	240.4	112.9	-1.1	360.4	155.7	-1.2
A_84_P606494	85	29.9	-1.5	237.4	43.8	-2.4
A_84_P13983	9535.3	1430.1	-2.7	6411.9	1469.4	-2.1
A_84_P200454	1475.1	582.8	-1.3	1908.5	847.5	-1.2
A_84_P23056	6	2.8	-1.1	20	2.8	-2.8
A_84_P87419	1814.2	483	-1.9	2562.1	707.3	-1.9
A_84_P20949	1665.1	827.8	-1	1735	838	-1
A_84_P16618	446.2	182.2	-1.3	784.8	274.1	-1.5
A_84_P15529	11	4	-1.4	16.6	2.7	-2.6
A_84_P502806	359.7	95.9	-1.9	449.7	155.9	-1.5
A_84_P829317	156.9	43.7	-1.8	214.3	88.5	-1.3
A_84_P13771	1875.4	689.4	-1.4	2728.9	1338.4	-1
A_84_P834687	230.3	78.7	-1.5	190.2	83.5	-1.2
A_84_P834162	796	367.3	-1.1	3378	426.9	-3
A_84_P561066	44.4	17.8	-1.3	30.6	8.6	-1.8
A_84_P751343	806.1	337.2	-1.3	940.1	393.2	-1.3
A_84_P829521	1122.9	461.9	-1.3	1649.6	604.4	-1.4
A_84_P602364	44.4	21.8	-1	41.9	7.5	-2.5

A_84_P288490	2474.2	416.1	-2.6	2787.1	465	-2.6
A_84_P764077	1215.1	311.7	-2	1538.9	452.8	-1.8
A_84_P12148	19.5	3	-2.7	22.4	2.9	-2.9
A_84_P816631	459.4	207.3	-1.1	707.2	193.9	-1.9
A_84_P168383	17.1	5.8	-1.6	21.4	5.8	-1.9
A_84_P798680	13.3	5.3	-1.3	9.8	3	-1.7
A_84_P567982	138.7	67.2	-1	105.7	42.4	-1.3
A_84_P16857	35.2	5.8	-2.6	33	10.9	-1.6
A_84_P107712	841.8	310.8	-1.4	1073.4	359.8	-1.6
A_84_P23518	29.4	3.9	-2.9	10.3	3.9	-1.4
A_84_P20307	105.2	48.1	-1.1	155	76.7	-1
A_84_P519840	36.7	10.6	-1.8	117.2	13.7	-3.1
A_84_P15535	57.6	21.4	-1.4	123.8	35.3	-1.8
A_84_P115172	704	267.1	-1.4	797.8	385	-1.1
A_84_P795651	1206	525.1	-1.2	1681.6	621.2	-1.4
A_84_P826634	142	45.8	-1.6	88.8	44	-1
A_84_P759248	945.1	194.3	-2.3	658.7	273.8	-1.3
A_84_P18772	164.5	52.3	-1.7	157.6	32.9	-2.3
A_84_P556078	23.5	6.2	-1.9	17.6	7	-1.3
A_84_P12722	331	149.5	-1.1	330.9	111.1	-1.6
A_84_P857209	5594.1	2018.2	-1.5	8898.8	3062	-1.5
A_84_P831236	38.2	17.4	-1.1	102.2	10.1	-3.3
A_84_P18818	125.9	2.9	-5.4	27.3	2.9	-3.2
A_84_P167173	861.4	378.8	-1.2	991.2	247.9	-2
A_84_P300170	18	3.9	-2.2	26.9	9.8	-1.5
A_84_P19161	1879.2	464.2	-2	4198.9	462.6	-3.2
A_84_P501388	659.6	264.6	-1.3	941.6	310.6	-1.6
A_84_P11383	18.6	3	-2.6	7.5	3	-1.3
A_84_P829971	74.3	34.9	-1.1	125.8	44.4	-1.5
A_84_P561984	6.8	3	-1.2	43.1	3	-3.8
A_84_P512454	8.1	2.9	-1.5	7	2.8	-1.3
A_84_P10001	152.4	28.6	-2.4	157.4	78.2	-1
A_84_P19297	1171.8	580	-1	1628.3	500.7	-1.7
A_84_P14089	1322.4	641.6	-1	2237.3	853.8	-1.4
A_84_P509353	639.4	84.8	-2.9	763.8	248.7	-1.6
A_84_P20704	190.7	59.4	-1.7	257	33.7	-2.9
A_84_P603863	5.8	2.8	-1.1	8.3	3.7	-1.2
A_84_P816904	4419	484.3	-3.2	914	400.9	-1.2
A_84_P13061	62.9	17.8	-1.8	111.5	4.2	-4.7
A_84_P22004	50.3	13.2	-1.9	7.1	2.9	-1.3
A_84_P847991	905.8	130.6	-2.8	552	274.7	-1
A_84_P13433	82.8	33.7	-1.3	82.4	36	-1.2
A_84_P558384	18.3	7.7	-1.2	33.7	3.1	-3.4
A_84_P508571	39.7	17.6	-1.2	99.2	23.2	-2.1
A_84_P757845	19.9	9.8	-1	11.2	3.8	-1.6

A_84_P21369	26.8	8.3	-1.7	36.8	11.9	-1.6
A_84_P569290	6.2	3	-1	11.4	3	-1.9
A_84_P10642	1728.2	523.2	-1.7	1495.2	625.9	-1.3
A_84_P13197	13.7	4.3	-1.7	14	2.8	-2.3
A_84_P845159	19.6	2.8	-2.8	6.8	3.2	-1.1
A_84_P769485	80.6	18.8	-2.1	79.5	20.5	-2
A_84_P761618	39.1	17	-1.2	41.5	16.3	-1.3
A_84_P19126	7.2	3.3	-1.1	19.5	2.8	-2.8
A_84_P15660	68.4	24.2	-1.5	65	31.3	-1.1
A_84_P23751	7.1	2.8	-1.3	7.2	2.8	-1.4
A_84_P17513	178.7	18.7	-3.3	110	26.4	-2.1
A_84_P24136	60	14.9	-2	105.2	13	-3
A_84_P12413	6.7	3	-1.2	9	3	-1.6
A_84_P761666	1277.2	369.3	-1.8	1150	450.6	-1.4
A_84_P23045	9807.6	4138.6	-1.2	13274.4	5037.6	-1.4
A_84_P22080	47	5.9	-3	37.7	3.1	-3.6
A_84_P605408	30.4	12.2	-1.3	50.9	9	-2.5
A_84_P520318	543.4	164.6	-1.7	584.8	268.8	-1.1
A_84_P13818	1076.9	439.1	-1.3	1288.8	639.4	-1
A_84_P810284	127.5	63	-1	243.4	57	-2.1
A_84_P18780	637.1	231.2	-1.5	958.3	371.7	-1.4
A_84_P789523	53630.9	823.8	-6	44807.2	436.5	-6.7
A_84_P12680	6055.7	1682	-1.8	4622.9	2104.4	-1.1
A_84_P765578	34.6	3.7	-3.2	16.1	5	-1.7
A_84_P542466	1384.2	460.3	-1.6	1803.6	480.8	-1.9
A_84_P12008	1034.8	209.3	-2.3	742.8	275	-1.4
A_84_P808711	3749.7	571.6	-2.7	4043.8	723.3	-2.5
A_84_P821818	39.4	12.4	-1.7	57.2	14	-2
A_84_P23445	365.8	101.7	-1.8	384.9	150.8	-1.4
A_84_P126821	66.6	5.1	-3.7	45.4	2.8	-4
A_84_P16475	4183.4	841.7	-2.3	3406.6	737.8	-2.2
A_84_P723748	239.7	72.5	-1.7	258.4	98.1	-1.4
A_84_P820541	4138.6	1423.5	-1.5	5366	1533.6	-1.8
A_84_P16570	65.8	30.1	-1.1	116.8	30.4	-1.9
A_84_P750690	311.5	152.9	-1	848.3	156.9	-2.4
A_84_P867201	363.7	82.5	-2.1	719.6	62.7	-3.5
A_84_P561018	44.6	18	-1.3	52.9	16.4	-1.7
A_84_P275700	20.4	3	-2.8	16.7	3.2	-2.4
A_84_P23387	600.7	225.9	-1.4	3203.1	327.1	-3.3
A_84_P20921	46	6.3	-2.9	56.4	2.8	-4.3
A_84_P21894	998.9	169.5	-2.6	1080.6	283.6	-1.9
A_84_P833862	21442.8	6548.6	-1.7	16239.8	7872.4	-1
A_84_P868627	22848.7	11134.1	-1	53098.5	5529.4	-3.3
A_84_P844091	7.4	2.9	-1.3	7.9	3.2	-1.3
A_84_P521842	34.1	11.7	-1.5	61.3	19.7	-1.6

A_84_P22211	10666.8	2835.6	-1.9	7029.2	3401.2	-1
A_84_P12619	6340.6	1940	-1.7	9568.3	3500	-1.5
A_84_P603366	163.3	78.5	-1.1	227	87	-1.4
A_84_P827928	122.9	57.3	-1.1	143.2	40.9	-1.8
A_84_P14250	183.6	59	-1.6	315.1	131.3	-1.3
A_84_P546117	376.7	161.8	-1.2	457.2	136	-1.7
A_84_P15103	9.7	2.8	-1.8	9.5	2.8	-1.8
A_84_P20572	246.4	23.3	-3.4	194.2	64.6	-1.6
A_84_P242653	26.1	6.5	-2	29.5	9.3	-1.7
A_84_P207798	8.5	2.9	-1.5	44.1	2.9	-3.9
A_84_P243945	5858.5	993.7	-2.6	6748.9	696.7	-3.3
A_84_P21511	411.5	130.5	-1.7	325	160.9	-1
A_84_P750433	24.4	3.8	-2.7	26.5	3	-3.2
A_84_P762563	160.6	54.1	-1.6	184.5	48.8	-1.9
A_84_P18364	878.3	297	-1.6	1278.3	522.4	-1.3
A_84_P20231	25.9	4.5	-2.5	29.5	11.1	-1.4
A_84_P804836	1127.3	547.2	-1	1800.7	657.4	-1.5
A_84_P98146	5912.1	2451.1	-1.3	6446	2705.3	-1.3
A_84_P824560	5060.1	1451.6	-1.8	5312.3	2099.1	-1.3
A_84_P834131	89	6.9	-3.7	71.8	10.1	-2.8
A_84_P17296	18.5	6.2	-1.6	20.4	2.9	-2.8
A_84_P17196	6.8	2.9	-1.2	20.4	2.9	-2.8
A_84_P11909	666.5	89.3	-2.9	930.7	163.6	-2.5
A_84_P769455	47.5	22.9	-1	189.3	20.4	-3.2
A_84_P150008	9.7	3.4	-1.5	25.2	7.7	-1.7
A_84_P20763	517.7	152	-1.8	571.4	247.4	-1.2
A_84_P10441	3799.5	818.6	-2.2	3425.7	1644.3	-1.1
A_84_P859712	1662.7	531.2	-1.6	1655.7	765.9	-1.1
A_84_P759661	211.8	31.3	-2.8	200	77.9	-1.4
A_84_P18331	29.5	4.1	-2.8	15	4.5	-1.7
A_84_P194234	2434.1	1111.8	-1.1	3179	1506.2	-1.1
A_84_P23749	2600.4	1055.5	-1.3	2263.1	784.2	-1.5
A_84_P560489	643.5	266.4	-1.3	789	390.2	-1
A_84_P805287	50.6	17.8	-1.5	97.6	25.8	-1.9
A_84_P862999	8883.5	3808.9	-1.2	14096.9	5111.5	-1.5
A_84_P506967	12.8	6.3	-1	77.2	5.5	-3.8
A_84_P853705	9.2	3.4	-1.4	10.1	3.7	-1.4
A_84_P130356	36.3	9.9	-1.9	22.9	6.6	-1.8
A_84_P828261	22.9	3	-2.9	18.7	8.7	-1.1
A_84_P13697	10.2	3	-1.8	8.3	3	-1.5
A_84_P859915	187.1	91.8	-1	297.3	97	-1.6
A_84_P22699	9.1	3.8	-1.2	7.2	2.9	-1.3
A_84_P801437	5275.2	1924.8	-1.5	8342	2825	-1.6
A_84_P16843	33.4	10.7	-1.6	46.6	10.2	-2.2
A_84_P520879	9.2	3.9	-1.2	8.3	3.2	-1.4

A_84_P19022	16.5	8	-1	23.9	3.2	-2.9
A_84_P835531	277.4	17	-4	123.9	40.7	-1.6
A_84_P22306	35.4	14.8	-1.3	84.7	13.8	-2.6
A_84_P129946	120.7	24.3	-2.3	79.8	21.7	-1.9
A_84_P260340	20703.3	2312.9	-3.2	12841.7	5087	-1.3
A_84_P20360	23.6	8.3	-1.5	53.7	10.6	-2.3
A_84_P15319	44561.1	7293.8	-2.6	46504.1	13155.4	-1.8
A_84_P19051	1376.9	590.7	-1.2	1213.9	305.7	-2
A_84_P20553	177.5	71.1	-1.3	483.2	76.2	-2.7
A_84_P832535	10.3	3	-1.8	9.3	3.1	-1.6
A_84_P553654	8.8	2.9	-1.6	8.9	2.9	-1.6
A_84_P172851	228.5	106.9	-1.1	674.2	88.9	-2.9
A_84_P807753	174581.6	60241.1	-1.5	191436.6	92316.4	-1.1
A_84_P24057	260.7	88.8	-1.6	450	102.3	-2.1
A_84_P859145	5222.4	2268.7	-1.2	8074.6	3470.9	-1.2
A_84_P750390	155.2	18.5	-3.1	204	32.7	-2.6
A_84_P838052	2704	995.6	-1.4	4304.5	2003.9	-1.1
A_84_P855428	631.3	297	-1.1	911.7	312.9	-1.5
A_84_P20577	267.2	84.1	-1.7	528.1	120.3	-2.1
A_84_P11844	15	2.9	-2.4	16.5	2.9	-2.5
A_84_P21829	161.2	37.7	-2.1	248.3	109	-1.2
A_84_P559896	1205.9	265.9	-2.2	819.4	293.3	-1.5
A_84_P14542	758	285.1	-1.4	1034.1	339.8	-1.6
A_84_P18574	211.4	101.1	-1.1	267.1	119.7	-1.2
A_84_P532498	493.7	130.2	-1.9	721.5	203.1	-1.8
A_84_P789572	315.4	147	-1.1	491.6	210.3	-1.2
A_84_P751783	997.2	400.3	-1.3	4193.7	596.2	-2.8
A_84_P836756	12.9	3	-2.1	26.9	3.1	-3.1
A_84_P820316	156.2	71.4	-1.1	179.3	45.1	-2
A_84_P555663	36591.1	591	-6	32397.5	332.9	-6.6
A_84_P191234	989.7	455.4	-1.1	764.3	337.3	-1.2
A_84_P19563	436.3	171	-1.4	1616.2	214.4	-2.9
A_84_P20372	2124.9	916.4	-1.2	2350.8	1114.3	-1.1
A_84_P21695	462.6	175	-1.4	751.2	279.7	-1.4
A_84_P10702	9000.7	2755	-1.7	9102.3	4175.3	-1.1
A_84_P525395	1106.1	391.3	-1.5	1217.9	476	-1.4
A_84_P522895	1994.4	984.8	-1	2772.9	1265.2	-1.1
A_84_P12475	24.5	2.9	-3.1	14.8	2.9	-2.3
A_84_P183184	201.7	37.2	-2.4	95.9	42.9	-1.2
A_84_P203368	47.4	7.2	-2.7	52.2	16.8	-1.6
A_84_P284610	223.2	106.4	-1.1	566.2	125.2	-2.2
A_84_P16790	2063.7	666.7	-1.6	2814.6	831.4	-1.8
A_84_P20771	63.3	14.7	-2.1	971.3	19.5	-5.6
A_84_P839599	45.2	3.1	-3.9	20.2	7.4	-1.5
A_84_P595814	224.4	59	-1.9	231.8	84.1	-1.5

A_84_P10779	13.3	5.4	-1.3	20.1	3.2	-2.6
A_84_P24121	1918.2	910	-1.1	3674.6	1109.8	-1.7
A_84_P21341	8734.9	2830.1	-1.6	8205.7	1774	-2.2
A_84_P13857	282.7	125.2	-1.2	248.8	73.8	-1.8
A_84_P55740	6.5	3.2	-1	7.1	3.2	-1.1
A_84_P603792	611.3	265.4	-1.2	975.6	325.2	-1.6
A_84_P176434	118.9	44.9	-1.4	111.2	41.3	-1.4
A_84_P16114	112.7	3.1	-5.2	33	7.5	-2.1
A_84_P788181	725.8	254	-1.5	2456.3	182.7	-3.7
A_84_P16076	35	3.6	-3.3	31.3	11	-1.5
A_84_P541401	75.6	37.7	-1	499.7	42.5	-3.6
A_84_P16823	9944.9	1225.8	-3	6410.8	1658.7	-2
A_84_P22625	943.7	364	-1.4	754.2	308.1	-1.3
A_84_P10296	23349.7	10045.8	-1.2	24732.4	11285.9	-1.1
A_84_P847684	128.6	47.4	-1.4	200.6	74.5	-1.4
A_84_P285150	651.8	131.7	-2.3	627.4	234.9	-1.4
A_84_P847692	220682.4	56589.5	-2	233463.9	61428.5	-1.9
A_84_P14934	81190.6	34961.8	-1.2	64784.1	31969.8	-1
A_84_P838576	11.1	3.2	-1.8	16	3.3	-2.3
A_84_P250035	17163	3724.7	-2.2	14077	4451.2	-1.7
A_84_P859628	22.1	4.5	-2.3	23.2	3.1	-2.9
A_84_P834970	6.5	3.1	-1	7.1	3.3	-1.1
A_84_P192414	411.7	183.5	-1.2	562.5	173.8	-1.7
A_84_P14874	3007.5	1150	-1.4	4537.2	2258.2	-1
A_84_P12113	1431.3	166.2	-3.1	1627.8	310	-2.4
A_84_P17642	417	195.3	-1.1	423.7	188.1	-1.2
A_84_P105626	33	4.7	-2.8	7.4	3.3	-1.1
A_84_P21567	93.3	29	-1.7	43.6	9.9	-2.1
A_84_P831286	493.9	210.7	-1.2	660.2	272.6	-1.3
A_84_P851624	14341	4159.2	-1.8	16634.9	3880.6	-2.1
A_84_P869566	940.6	429.7	-1.1	1545.1	534.1	-1.5
A_84_P293384	941	365.5	-1.4	781.7	389.7	-1
A_84_P522670	55.6	18.6	-1.6	79	18	-2.1

Supplemental Table 2. Probe values for up-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (hypocotyl)

Probe Name	Col1	*ztl3*	Log Ratio	Col2	*ztl105*	Log Ratio
A_84_P721670	125.2	980.7	3	115.9	525.1	2.2
A_84_P224829	82.3	827.9	3.3	52	175	1.8
A_84_P546611	3.2	16.5	2.4	3.5	81.3	4.5
A_84_P507384	74.8	568.2	2.9	77.8	169.2	1.1
A_84_P792453	18	46.9	1.4	11.6	23.8	1
A_84_P592635	3.2	116.8	5.2	4.7	44.4	3.2
A_84_P104666	5.7	17.7	1.6	3.2	6.5	1
A_84_P15062	129.9	488.5	1.9	99.2	260.6	1.4
A_84_P793001	120.4	401.1	1.7	76.1	225.3	1.6
A_84_P19710	16.3	35.6	1.1	3.2	12.1	1.9
A_84_P816743	77.4	188.5	1.3	76.8	166.8	1.1
A_84_P758144	4.7	10.1	1.1	6.4	15.4	1.3
A_84_P11108	14	45	1.7	9	26.3	1.6
A_84_P755572	4.2	18.9	2.2	4.3	9.8	1.2
A_84_P19999	3.1	35.4	3.5	3.2	8.8	1.5
A_84_P784980	63.6	921.9	3.9	57.9	153	1.4
A_84_P185924	903.8	1945.8	1.1	656.8	1415.2	1.1
A_84_P16974	6934.8	48295.9	2.8	8303.6	28436	1.8
A_84_P67324	3913.7	8574.3	1.1	3791.1	9702.1	1.4
A_84_P791084	65.4	398.1	2.6	104.4	246.2	1.2
A_84_P10365	9.7	37.2	1.9	3.3	49.2	3.9
A_84_P582318	18.9	141.4	2.9	12	34.3	1.5
A_84_P22576	29.6	92.1	1.6	17.6	39.4	1.2
A_84_P833401	4.5	21.2	2.2	3.4	8.8	1.4
A_84_P809337	17509.8	42038.6	1.3	19622.2	43490.9	1.1
A_84_P115322	6.3	19.8	1.6	3.2	11	1.8
A_84_P17018	4.4	21.6	2.3	6.7	15.3	1.2
A_84_P714286	44.3	136.7	1.6	44.3	174.8	2
A_84_P12575	1470	3010.7	1	1599.8	3297.4	1
A_84_P527390	127.1	299.8	1.2	75.3	152.3	1
A_84_P798104	4.5	9.6	1.1	3.9	13.9	1.8
A_84_P17184	8.8	28.8	1.7	11.5	26.7	1.2
A_84_P23342	1593.1	7065.5	2.1	2188.9	5494.4	1.3
A_84_P12960	7.1	116.2	4	24.7	77.6	1.6
A_84_P15209	154.6	1014.1	2.7	73.8	423.6	2.5
A_84_P16735	589	3835.3	2.7	709.4	2358.6	1.7
A_84_P54840	9.9	65.5	2.7	9.5	29.5	1.6
A_84_P761811	371	1496.6	2	409.9	1108.8	1.4
A_84_P17398	1437.9	3700.2	1.4	1307.7	4643.1	1.8
A_84_P600454	4.4	71.8	4	3	32.4	3.4
A_84_P20736	22.9	181.8	3	17.2	65.2	1.9
A_84_P809332	296.1	947.7	1.7	437	874.6	1
A_84_P18695	66.6	149.8	1.2	47.5	109.7	1.2
A_84_P216998	1331.6	2761.2	1.1	752.8	1768.8	1.2

A_84_P22521	26.8	153.7	2.5	10.6	57.2	2.4
A_84_P840864	2.8	5.7	1	4.1	8.8	1.1
A_84_P98606	2.8	6.1	1.1	2.9	6.9	1.3
A_84_P14787	378.3	5800.5	3.9	284.5	3803.3	3.7
A_84_P18069	231.8	988.3	2.1	273.5	768	1.5
A_84_P23353	16.7	36.6	1.1	8.9	22.5	1.3
A_84_P503102	46.2	398.9	3.1	52	197.1	1.9
A_84_P223919	2514.4	6677.9	1.4	2574.4	5541.2	1.1
A_84_P10999	450.6	1187.7	1.4	430.6	938.3	1.1
A_84_P180664	6.1	23.4	2	3	22.3	2.9
A_84_P12371	868	2589.2	1.6	851.9	2129.1	1.3
A_84_P601310	99.2	241.6	1.3	67.3	139.2	1
A_84_P750943	6.6	34.2	2.4	10.5	42.4	2
A_84_P769115	3.1	12.1	2	4.2	8.7	1.1
A_84_P767684	457.3	1902	2.1	316.5	638.6	1
A_84_P858347	44	230.6	2.4	38.5	95.7	1.3
A_84_P840901	4.8	13.8	1.5	3.2	14.2	2.1
A_84_P264030	2367.3	5452.1	1.2	2139.4	4804	1.2
A_84_P812380	365.5	2465.6	2.8	344.7	1229	1.8
A_84_P554758	36.7	107.6	1.6	23.5	48.7	1.1
A_84_P848499	517.9	3508	2.8	418	4198.3	3.3
A_84_P511454	116.9	2227.2	4.3	216.1	1297	2.6
A_84_P194874	1794.3	4133.2	1.2	1352.2	3752.5	1.5
A_84_P10395	912.3	4660.2	2.4	996	2797.6	1.5
A_84_P15163	10.2	28.8	1.5	5.3	21.9	2
A_84_P812071	9.1	28.1	1.6	11.1	1002	6.5
A_84_P18380	76.5	266.3	1.8	78.4	320.5	2
A_84_P15944	2.7	43.5	4	2.8	7.8	1.5
A_84_P860716	17.1	47	1.5	14.9	35.2	1.2
A_84_P815531	4.3	15.3	1.8	2.8	17.8	2.7
A_84_P863936	370.2	1220.9	1.7	270	581	1.1
A_84_P595174	9.8	26.3	1.4	4.6	19.4	2.1
A_84_P19671	112	268.3	1.3	93.5	215.6	1.2
A_84_P850547	551.2	1608.8	1.5	455.3	1318	1.5
A_84_P21718	3.1	10.8	1.8	3.2	11.1	1.8
A_84_P20714	1496.6	4949.8	1.7	1776.7	3577.4	1
A_84_P751246	13.1	54.8	2.1	11.2	26.1	1.2
A_84_P798478	15.8	80.7	2.4	5.7	55.7	3.3
A_84_P11250	1561.8	5010.9	1.7	2152.2	4446.2	1
A_84_P119322	66.8	311.3	2.2	45.3	133	1.6
A_84_P183724	301.5	2144.6	2.8	292.9	607.8	1.1
A_84_P17322	5	13.3	1.4	2.8	12.4	2.2
A_84_P20712	19.2	225.6	3.6	10.9	42.9	2
A_84_P149348	192.5	1041	2.4	152.5	369.2	1.3
A_84_P765520	215.8	434.2	1	202.5	462	1.2

A_84_P235603	31.4	100.5	1.7	22.3	46.7	1.1
A_84_P527444	59.9	147.5	1.3	37.9	104.1	1.5
A_84_P760632	4535.8	22054.1	2.3	3906	10079.7	1.4
A_84_P125471	20.2	74.4	1.9	11.8	35.6	1.6
A_84_P12882	10.7	46.9	2.1	7.7	16.8	1.1
A_84_P17710	253.5	563	1.2	418.1	927.5	1.1
A_84_P159675	3.4	7.4	1.1	3	7.2	1.2
A_84_P18726	316.7	713.4	1.2	307.3	805.5	1.4
A_84_P609095	2.6	6.9	1.4	2.7	6.2	1.2
A_84_P759212	17.6	40.5	1.2	2.8	17.2	2.6
A_84_P795460	5.5	21.2	1.9	6.3	26.8	2.1
A_84_P10054	88.9	409.3	2.2	34.8	289.2	3.1
A_84_P13287	69.1	360.5	2.4	51.5	149	1.5
A_84_P789641	3.3	7.4	1.2	3.9	13.3	1.8
A_84_P146119	360.9	875.8	1.3	342.2	986	1.5
A_84_P522076	66.3	246	1.9	43.9	116.7	1.4
A_84_P788162	7.9	19.9	1.3	7.9	19	1.3
A_84_P19487	28.8	402.4	3.8	18.7	60.3	1.7
A_84_P828342	115.6	987.4	3.1	168.7	787.9	2.2
A_84_P256030	11.5	25	1.1	7.4	18.7	1.3
A_84_P10157	47.2	122.1	1.4	28	111.4	2
A_84_P528833	53.5	1409.6	4.7	13.6	97.9	2.8
A_84_P14774	58	209.2	1.9	55	149.7	1.4
A_84_P163603	3.1	7	1.2	2.7	5.6	1.1
A_84_P14930	8.4	66.5	3	8	22.8	1.5
A_84_P103766	254.5	3137	3.6	79.7	383.1	2.3
A_84_P761907	25.9	137	2.4	32	79.2	1.3
A_84_P12955	3.7	21.7	2.5	2.7	13.8	2.3
A_84_P792837	116.1	951.4	3	77.7	323.7	2.1
A_84_P838935	10.5	21.1	1	9.9	32.4	1.7
A_84_P21066	3.8	22.8	2.6	9.7	26	1.4
A_84_P834863	2.7	22.3	3.1	2.7	5.7	1.1
A_84_P17145	65.7	391.6	2.6	79.8	193.9	1.3
A_84_P18091	22.7	103.8	2.2	26.6	95.6	1.8
A_84_P526945	2.6	15.8	2.6	2.7	13	2.3
A_84_P728206	478.2	1096.1	1.2	320.7	1138.8	1.8
A_84_P846200	64.7	366.7	2.5	76	177.1	1.2
A_84_P511862	145.2	698.2	2.3	108.8	343.8	1.7
A_84_P14721	4.1	20.5	2.3	2.9	9.8	1.7
A_84_P21881	6.6	27.3	2.1	2.9	7.2	1.3
A_84_P541789	13.8	242.8	4.1	38.8	121	1.6
A_84_P20376	21.7	194	3.2	19.3	41.8	1.1
A_84_P13635	58.6	228.2	2	57.5	286	2.3
A_84_P588837	26.1	289.2	3.5	24	177.8	2.9
A_84_P756276	10385.5	29377.5	1.5	16778.3	34398.6	1

A_84_P22664	7.9	51.9	2.7	5.3	13.7	1.4
A_84_P16455	17.4	314.8	4.2	14.6	49.1	1.8
A_84_P832442	64.2	195.5	1.6	44.8	104.4	1.2
A_84_P127211	266.4	1252.8	2.2	236.3	559.2	1.2
A_84_P257500	4.3	20.1	2.2	3.8	8.4	1.2
A_84_P763748	5.3	12.6	1.3	2.6	17.2	2.7
A_84_P754212	2.6	14.6	2.5	4.7	47.6	3.3
A_84_P21883	4.2	40.1	3.2	3.8	9.5	1.3
A_84_P14601	1715.3	3812.4	1.2	1259.1	3921	1.6
A_84_P244235	3844.5	9229.3	1.3	3380	12937.3	1.9
A_84_P13770	577	1350.2	1.2	544.2	1103	1
A_84_P22124	18.2	262.8	3.9	10.2	111.2	3.4
A_84_P755918	55.2	173.2	1.6	10.1	32.6	1.7
A_84_P230699	124	613.3	2.3	153.9	308.5	1
A_84_P13120	75.6	165.2	1.1	64.5	140.4	1.1
A_84_P11522	2.6	13	2.3	2.6	21.4	3
A_84_P516094	17123.4	35145.6	1	18514.5	37063.2	1
A_84_P762469	5.7	61	3.4	4.2	25	2.6
A_84_P184024	41.2	97.5	1.2	29	59.8	1
A_84_P601609	436.7	937.2	1.1	439.3	1053.6	1.3
A_84_P18143	4.8	19.1	2	2.9	10.6	1.8
A_84_P16027	21.1	147.3	2.8	18.3	131	2.8
A_84_P806316	2.8	15.5	2.5	4.5	18	2
A_84_P828455	32.8	173.3	2.4	32.9	136.1	2.1
A_84_P862018	5.1	45.5	3.2	4.5	23.1	2.4
A_84_P505607	4.7	9.6	1	3	12.5	2.1
A_84_P12020	8.7	30.9	1.8	2.7	8.5	1.6
A_84_P850839	21.7	52.4	1.3	13.1	55.8	2.1
A_84_P789673	4.7	68.6	3.9	4.3	13	1.6
A_84_P16754	16.5	71.2	2.1	20	77.2	1.9
A_84_P247395	1104.5	3197.1	1.5	1286.1	2853.4	1.1
A_84_P840778	3.4	10.9	1.7	5.1	48.5	3.2
A_84_P758386	16.5	36.2	1.1	19.4	42.9	1.1
A_84_P192824	467.3	1008.2	1.1	418.2	1191.5	1.5
A_84_P799804	2.5	11.3	2.2	2.8	5.8	1
A_84_P793823	3.3	10.9	1.7	2.8	9.7	1.8
A_84_P752986	36.3	123.7	1.8	41.2	89.2	1.1
A_84_P20310	18.7	75.5	2	11.5	68.8	2.6
A_84_P811911	4993	12654.6	1.3	6333.5	17046.4	1.4
A_84_P800404	3.9	9.6	1.3	4.8	10.6	1.1
A_84_P603801	7.9	16.7	1.1	3	7.6	1.4
A_84_P19361	2.6	7.9	1.6	2.6	6.4	1.3
A_84_P270820	3.3	12.4	1.9	2.6	8.7	1.8
A_84_P588044	7	28.4	2	3.9	14.3	1.9
A_84_P15984	1845.8	4598.4	1.3	1753.7	4871.9	1.5

A_84_P596337	3.4	32.8	3.3	2.6	8	1.6
A_84_P756592	2.5	38.8	3.9	2.6	14.6	2.5
A_84_P564716	13.3	56.8	2.1	21.8	52.7	1.3
A_84_P16865	8.8	57.7	2.7	7.7	26.1	1.8
A_84_P762878	4	37.1	3.2	3.7	10.9	1.6
A_84_P766114	3.2	9.9	1.6	2.9	13.5	2.2
A_84_P792258	8.3	228.9	4.8	3.2	119.9	5.2
A_84_P190534	23	186.7	3	39.3	135.5	1.8
A_84_P850437	14.6	29.7	1	12.4	25.4	1
A_84_P815580	15.9	38.6	1.3	7.7	25.4	1.7
A_84_P20677	916.4	3902.2	2.1	619.8	1484.2	1.3
A_84_P17794	320.1	6660.4	4.4	561.2	1176.5	1.1
A_84_P23406	435.5	1154.3	1.4	375.4	1117.6	1.6
A_84_P21088	19.3	230.2	3.6	22	105.1	2.3
A_84_P17045	2051.2	15919.5	3	2817.8	9537.1	1.8
A_84_P860044	593	8495.4	3.8	196.5	3606.4	4.2
A_84_P515906	2.6	7.4	1.5	2.6	16	2.6
A_84_P852477	24.2	347.3	3.8	3.3	14.7	2.1
A_84_P843385	21.7	88.7	2	17.1	44	1.4
A_84_P760097	297	687.1	1.2	172.7	420.2	1.3
A_84_P11229	2.5	24.9	3.3	2.5	15.1	2.6
A_84_P755250	129.4	1819.2	3.8	75.7	427.1	2.5
A_84_P761538	105.9	428.1	2	34.6	213.4	2.6
A_84_P757419	2.6	6.4	1.3	3.3	24.6	2.9
A_84_P769164	10.5	33.5	1.7	8.4	31.1	1.9
A_84_P14928	8.5	38.3	2.2	2.8	30.8	3.5
A_84_P803062	163.6	847.5	2.4	109.4	504.9	2.2
A_84_P834182	226.3	1498.8	2.7	163.3	445.7	1.4
A_84_P506389	4.8	81.5	4.1	12.1	24.6	1
A_84_P754704	2.4	5.8	1.3	2.5	6.8	1.4
A_84_P186734	81.4	177.2	1.1	56.7	121.3	1.1
A_84_P521243	5.2	14.4	1.5	5	12.9	1.4
A_84_P843181	87.5	462.8	2.4	99.8	223.7	1.2
A_84_P231259	155.2	543.9	1.8	95.5	303.8	1.7
A_84_P750559	92.3	534.7	2.5	55.4	125	1.2
A_84_P811364	8.4	48.3	2.5	5.6	16.9	1.6
A_84_P586725	75.8	173.1	1.2	65.1	192.3	1.6
A_84_P10787	31.5	65.5	1.1	29.1	63.1	1.1
A_84_P817769	3.5	7.8	1.1	2.5	5.8	1.2
A_84_P243255	32.2	135.7	2.1	46.6	125.7	1.4
A_84_P800898	175	1250.5	2.8	229	699.5	1.6
A_84_P169283	548.3	4929.7	3.2	787.5	1807	1.2
A_84_P23107	2.5	30.6	3.6	17.8	36.7	1
A_84_P15503	345.6	1653.7	2.3	623.8	1838.1	1.6
A_84_P847491	3.3	7.9	1.2	2.6	5.3	1.1

A_84_P819167	2.6	8.7	1.7	2.7	6.4	1.3
A_84_P842669	5.5	62.5	3.5	6.1	15.1	1.3
A_84_P19836	5.1	19.6	1.9	2.8	6	1.1
A_84_P21010	12.6	82.4	2.7	14.4	139.1	3.3
A_84_P17553	203.3	1494.2	2.9	146.9	686.7	2.2
A_84_P241225	18.1	482.6	4.7	22.6	58.5	1.4
A_84_P257800	2.6	11.9	2.2	2.6	7.2	1.5
A_84_P517322	131.1	643.2	2.3	84	255.8	1.6
A_84_P80329	14.3	353	4.6	34.2	262.3	2.9
A_84_P11512	3.4	31.5	3.2	2.4	9.2	1.9
A_84_P834670	120.7	490.1	2	116.7	529.5	2.2
A_84_P859103	30566.7	69362.6	1.2	34221.9	85239.1	1.3
A_84_P866419	2.6	6.2	1.3	3.5	7.1	1
A_84_P790736	80.9	521.4	2.7	52.5	215.4	2
A_84_P592843	2.4	9	1.9	2.5	5.3	1.1
A_84_P553447	3.4	7	1	5	15.6	1.6
A_84_P279900	13.6	81.5	2.6	27.2	58	1.1
A_84_P756228	12.1	36.2	1.6	14.8	43.9	1.6
A_84_P757480	8.5	65	2.9	5.1	11.1	1.1
A_84_P19131	124.4	828.5	2.7	106.4	736.1	2.8
A_84_P18193	74.8	179.1	1.3	27.7	61.8	1.2
A_84_P15672	6.1	16.5	1.4	2.7	7.2	1.4
A_84_P830520	469.1	1456.6	1.6	418.9	1053.1	1.3
A_84_P839331	5.2	36.8	2.8	12.7	60.3	2.3
A_84_P12832	9.2	102	3.5	8.5	35.7	2.1
A_84_P843011	13	236.8	4.2	14.4	95.4	2.7
A_84_P765821	4.7	32.6	2.8	3	8.8	1.6
A_84_P293424	158.2	519.1	1.7	65.3	133.7	1
A_84_P784935	99.7	775.9	3	59	288.4	2.3
A_84_P119582	2030.6	7585.9	1.9	2083.4	5887.6	1.5
A_84_P750699	18.7	41.2	1.1	6.3	18.4	1.5
A_84_P185784	35.7	338.3	3.2	39.4	168.9	2.1
A_84_P23823	30	235.2	3	18.2	76.8	2.1
A_84_P211958	2357	16468	2.8	2191.7	4910	1.2
A_84_P100456	24.4	335.5	3.8	25.9	124.4	2.3
A_84_P529724	3122.1	14664	2.2	3271.7	11007	1.8
A_84_P797027	39.3	88.6	1.2	41.1	82.1	1
A_84_P15284	10.6	111.4	3.4	11.1	40.3	1.9
A_84_P15135	11	43.9	2	2.4	11.4	2.2
A_84_P14854	11466.6	23609.4	1	8102.8	16331.2	1
A_84_P800107	74.5	207.5	1.5	61.5	162.7	1.4
A_84_P852577	915.8	4451.2	2.3	1587.2	3292.8	1.1
A_84_P21230	3187.2	36645.9	3.5	2565	13694.4	2.4
A_84_P22432	79.7	283.2	1.8	78.9	167.3	1.1
A_84_P812064	63037	157557.6	1.3	61838.7	123787.6	1

A_84_P15400	2136.8	5269.7	1.3	2211.5	4712.6	1.1
A_84_P520864	76.2	172.5	1.2	79.4	168.7	1.1
A_84_P156015	398.3	3453.2	3.1	252.4	1033.8	2
A_84_P174821	4805.8	27638.3	2.5	2897.9	12760	2.1
A_84_P758763	27.8	130.7	2.2	20	47	1.2
A_84_P17749	49.7	181.2	1.9	18.1	59.7	1.7
A_84_P824264	705.7	1730.1	1.3	461.5	1031.6	1.2
A_84_P118712	424.7	1549.2	1.9	433.1	1397.5	1.7
A_84_P784903	2.5	58.8	4.5	2.6	7.8	1.6
A_84_P23970	53.9	248.4	2.2	36.8	89.7	1.3
A_84_P15827	1516.4	5895.9	2	1446.7	3021.1	1.1
A_84_P763669	13	29.8	1.2	5.5	15	1.4
A_84_P22629	143.5	306.3	1.1	118.6	385.3	1.7
A_84_P188764	886.1	2333.8	1.4	594.7	2700.5	2.2
A_84_P20316	10.4	38	1.9	19.1	42.1	1.1
A_84_P23556	6.7	65.2	3.3	5.6	20.6	1.9
A_84_P847244	3.8	22	2.5	4.1	11.9	1.5
A_84_P766531	10.5	78	2.9	7.8	24.6	1.7
A_84_P12100	538	12510.4	4.5	367.3	884.6	1.3
A_84_P762857	69.3	595.8	3.1	66.7	259.3	2
A_84_P14772	20.2	56.3	1.5	21.9	54.3	1.3
A_84_P608981	4.7	57.5	3.6	4.8	21	2.1
A_84_P16068	1675	9147	2.4	1541.6	13049.6	3.1
A_84_P860427	2.4	22.7	3.2	2.4	9	1.9
A_84_P14436	4.9	89.4	4.2	3.3	25.3	3
A_84_P859660	3.7	8.4	1.2	4.6	111.9	4.6
A_84_P788885	1805.4	6850.3	1.9	1853.8	5885.7	1.7
A_84_P764817	2.4	22.1	3.2	2.4	6.2	1.4
A_84_P765683	347.3	951.2	1.5	417.6	1020.8	1.3
A_84_P828934	97.3	790.9	3	82.8	335.8	2
A_84_P13939	40.6	336.8	3.1	66	146.3	1.1
A_84_P20135	2.4	6	1.3	3.1	13.1	2.1
A_84_P576326	2.4	92.4	5.3	2.4	7.8	1.7
A_84_P10265	195.4	571.8	1.5	114.3	377	1.7
A_84_P810094	7020.7	17627.8	1.3	7645.2	16858.8	1.1
A_84_P15293	645.9	2141.9	1.7	256.4	843.8	1.7
A_84_P827080	241.2	584.5	1.3	188.4	604.7	1.7
A_84_P10073	1533.8	5024.8	1.7	1831.6	4417.8	1.3
A_84_P789465	341.2	1020.3	1.6	463.8	1089.8	1.2
A_84_P600168	600.4	1428.3	1.3	559.1	1190.5	1.1
A_84_P16611	1332.1	3972.8	1.6	1573.2	3220	1
A_84_P511795	20.6	80.7	2	34.4	160.1	2.2
A_84_P23900	2.5	6	1.3	2.6	9.2	1.8
A_84_P794998	2.4	7.3	1.6	2.4	5.4	1.2
A_84_P301610	10.1	28.5	1.5	2.8	14.7	2.4

A_84_P18980	2.5	13.3	2.4	2.6	16	2.6
A_84_P845020	2.5	7.2	1.5	3.1	10.7	1.8
A_84_P595141	119.1	1191.3	3.3	89.3	207.8	1.2
A_84_P811360	1509.3	20058.6	3.7	479	9013.5	4.2
A_84_P855860	8.8	26.4	1.6	7.7	22.1	1.5
A_84_P71564	3540.4	7085.6	1	2133.6	4769.7	1.2
A_84_P789655	2.5	6.1	1.3	4.5	9.4	1.1
A_84_P15172	10.5	26.9	1.4	8.1	17.3	1.1
A_84_P21340	6.4	15.6	1.3	2.4	18.1	2.9
A_84_P12234	370.9	3567	3.3	273.8	557.3	1
A_84_P70284	3893.1	9999.1	1.4	3298.2	8915.3	1.4
A_84_P767924	6.4	32.5	2.3	2.5	8	1.7
A_84_P786412	1055.7	2655.6	1.3	898.8	2141.2	1.3
A_84_P800855	187.2	693.8	1.9	175	469.9	1.4
A_84_P225239	76.8	555.6	2.9	48.9	160.8	1.7
A_84_P18294	4.7	86.7	4.2	7.1	16.9	1.2
A_84_P21437	35.2	343.8	3.3	25.3	60.7	1.3
A_84_P18057	2.5	5	1	2.5	5.8	1.2
A_84_P21080	604.5	5029.2	3.1	444.1	975.8	1.1
A_84_P796838	7.6	19.9	1.4	6.6	15.3	1.2
A_84_P755464	4.6	206.4	5.5	17.9	79.6	2.2
A_84_P546148	272.4	947.3	1.8	223.7	450.5	1
A_84_P721340	2.5	5.2	1.1	6.2	14.1	1.2
A_84_P836925	150.5	712.9	2.2	144.3	736.3	2.4
A_84_P794609	32	202.9	2.7	45.2	124.6	1.5
A_84_P14024	347.9	1766.5	2.3	215.5	556.2	1.4
A_84_P19239	91.5	382.8	2.1	61.5	180.4	1.6
A_84_P160283	128935.3	332953.2	1.4	122727.4	278226.6	1.2
A_84_P21517	97.6	768.8	3	63.8	338.1	2.4
A_84_P20976	192.3	2240.2	3.5	146.1	382.2	1.4
A_84_P838729	4.2	9.6	1.2	2.4	13.4	2.5
A_84_P312543	2898.5	9136	1.7	3080.8	7109	1.2
A_84_P68424	2.4	44.9	4.2	2.4	15.2	2.7
A_84_P840855	2.4	20.1	3	2.4	6.6	1.4
A_84_P18851	5.9	24.4	2.1	2.5	5.6	1.2
A_84_P87509	6.8	19.9	1.6	6.6	13.4	1
A_84_P791663	14.3	59.2	2	15.6	35.7	1.2
A_84_P551242	475.9	1048.3	1.1	412.8	885.5	1.1
A_84_P822097	51.8	113.1	1.1	47.2	102.1	1.1
A_84_P12029	1945.5	4618.6	1.2	1340	4309.5	1.7
A_84_P220658	11346.3	23066.7	1	10178.3	20824.9	1
A_84_P15029	10657.5	22344.9	1.1	9498.8	24361.1	1.4
A_84_P562958	132.9	643.8	2.3	88.8	231.2	1.4
A_84_P18941	74.7	282	1.9	71.4	161.9	1.2
A_84_P799663	8	28	1.8	8.4	24.7	1.6

A_84_P805958	4684.6	14083	1.6	7470.6	18040.4	1.3
A_84_P600706	3.5	12.5	1.8	5.3	14	1.4
A_84_P18334	26.3	278.2	3.4	25.8	64.9	1.3
A_84_P13690	2.7	13.7	2.3	2.6	5.3	1
A_84_P17346	25.8	55.6	1.1	10.1	34.2	1.8
A_84_P854253	2.6	29.8	3.5	2.7	8.4	1.7
A_84_P511427	2.5	9.6	1.9	2.8	7.6	1.5
A_84_P607294	82.2	183.4	1.2	87.4	181	1.1
A_84_P12677	20.9	47.2	1.2	12.7	27.1	1.1
A_84_P11817	2.5	6.2	1.3	2.5	5.1	1
A_84_P760300	27	138.2	2.4	20.7	46.5	1.2
A_84_P528380	93.5	369.7	2	62.9	194.4	1.6
A_84_P563378	487.2	989.7	1	324.1	674.5	1.1
A_84_P612892	99.4	511.7	2.4	127.3	400.2	1.7
A_84_P858361	84738.5	249460.5	1.6	80080.1	200688	1.3
A_84_P862707	569.2	1343.8	1.2	639.1	1743.1	1.4
A_84_P764738	6.2	30.9	2.3	10	43.4	2.1
A_84_P530188	34.9	72.2	1	31.1	180.1	2.5
A_84_P132365	5.2	15.2	1.6	5.3	14.8	1.5
A_84_P767270	172.8	2000.1	3.5	150.1	1206	3
A_84_P22784	36.8	167	2.2	22.8	66.2	1.5
A_84_P10647	8	18.2	1.2	3.4	16.6	2.3
A_84_P195704	4.9	14.7	1.6	3.8	11	1.5
A_84_P14468	105.2	290	1.5	101.4	235.7	1.2
A_84_P758971	2.6	7.9	1.6	2.6	6.4	1.3
A_84_P21090	13.9	120.4	3.1	2.8	64.3	4.5
A_84_P265480	1016	3334.6	1.7	724.3	2820.3	2
A_84_P270980	3.2	7.3	1.2	4.3	8.9	1.1
A_84_P844790	2.5	5.3	1.1	2.5	6.5	1.4
A_84_P272560	130.6	643.3	2.3	68.9	331.9	2.3
A_84_P841206	4.4	13.1	1.6	5.6	25.6	2.2
A_84_P224339	2.6	11.5	2.2	5.2	16.2	1.6
A_84_P204118	482.6	1359.2	1.5	469.7	1167.8	1.3
A_84_P55300	4.7	9.9	1.1	5.4	18.8	1.8
A_84_P596833	4.4	33.5	2.9	4.3	12.7	1.6
A_84_P563065	11.4	124.4	3.4	2.4	20.8	3.1
A_84_P16170	2.5	7	1.5	2.7	6.8	1.3
A_84_P12393	30	106.8	1.8	14.4	65.3	2.2
A_84_P846493	3.1	27.6	3.1	2.6	9.6	1.9
A_84_P855617	324	3008.8	3.2	572.5	1637.7	1.5
A_84_P857666	111.3	235.1	1.1	105.1	257.7	1.3
A_84_P806641	14352.6	38481.7	1.4	11344.6	27638.3	1.3
A_84_P837793	4.9	48.1	3.3	3.1	7.7	1.3
A_84_P55930	3.7	19.9	2.4	2.9	6.8	1.2
A_84_P575989	5.5	11.6	1.1	3.6	8.1	1.2

A_84_P818368	2.6	7.5	1.5	3.6	7.6	1.1
A_84_P22940	11.4	23.8	1.1	12.4	28.7	1.2
A_84_P757276	2.5	5.1	1	2.5	54.2	4.5
A_84_P521588	2.5	39.6	4	6.5	31.8	2.3
A_84_P18647	3.7	8.7	1.2	2.5	18.5	2.9
A_84_P579705	2.5	6.5	1.4	2.6	10.3	2
A_84_P16730	50.7	2423.2	5.6	45.8	220.7	2.3
A_84_P847302	52.5	1857.5	5.1	151.7	475.6	1.6
A_84_P859664	1096.1	2695.4	1.3	556.2	1479.7	1.4
A_84_P826049	2.7	42.1	4	4.2	9.9	1.2
A_84_P297454	2666.6	6886.9	1.4	2377.3	5479.7	1.2
A_84_P167633	2.7	9.3	1.8	2.7	6.6	1.3
A_84_P759744	12.5	197.5	4	9.9	20.7	1.1
A_84_P209848	368.3	1368	1.9	346.6	991.8	1.5
A_84_P16274	2.6	13.8	2.4	6.4	25.6	2
A_84_P811421	292.9	663.3	1.2	350.9	743.3	1.1
A_84_P23485	6.6	21.5	1.7	9	26.6	1.6
A_84_P839984	4.4	31	2.8	8.6	18.7	1.1
A_84_P862902	9.6	22.7	1.2	9.2	23.5	1.4
A_84_P156125	2911.2	8238.1	1.5	2030.6	4479.7	1.1
A_84_P512786	20.5	72.2	1.8	19.6	45.6	1.2
A_84_P205268	2.7	44.8	4.1	4.7	10.7	1.2
A_84_P12333	4.5	28.4	2.7	8.5	17.5	1
A_84_P838408	9.7	28.9	1.6	6.9	14.4	1.1
A_84_P571918	9.4	26.9	1.5	4.4	13.9	1.7
A_84_P133775	1029.7	2839	1.5	1016.7	2330	1.2
A_84_P595614	7.3	18	1.3	10.1	22.8	1.2
A_84_P16778	118.5	499.2	2.1	82.9	234	1.5
A_84_P803284	83.4	640	2.9	70.1	169.7	1.3
A_84_P549693	2.6	5.8	1.2	2.5	6.5	1.4
A_84_P23561	1476.6	3504.2	1.2	721.6	1962.1	1.4
A_84_P797786	48.7	231	2.2	32.1	75.9	1.2
A_84_P21719	4.1	38.3	3.2	6.6	34.4	2.4
A_84_P210868	407.3	1578.4	2	324.6	850.6	1.4
A_84_P21593	62.2	154.6	1.3	36.6	89.5	1.3
A_84_P13741	7.3	198.9	4.8	4.9	25.2	2.4
A_84_P17124	114.6	235.6	1	86.8	177.9	1
A_84_P18409	33.1	74.7	1.2	49.2	107.3	1.1
A_84_P23860	65.4	249.3	1.9	62.7	307	2.3
A_84_P534390	160	368.8	1.2	121.8	278.8	1.2
A_84_P15000	2.7	7	1.4	3.2	7	1.1
A_84_P18172	94.6	445.4	2.2	133.7	319.4	1.3
A_84_P20252	5331.8	15097.4	1.5	4528.4	10871.6	1.3
A_84_P22153	4055.7	28785.1	2.8	3932.2	14447.8	1.9
A_84_P249125	584.5	1285.1	1.1	548.1	1340	1.3

A_84_P20899	80.7	582.3	2.9	76.3	257	1.8
A_84_P17298	65	152.1	1.2	40.8	106.3	1.4
A_84_P158795	1769.4	3790	1.1	1399.4	3773.7	1.4
A_84_P217138	21245.3	53517.3	1.3	21196.7	46023.3	1.1
A_84_P23291	130.9	792.3	2.6	152.9	412.8	1.4
A_84_P16837	6.8	22.9	1.8	4.7	14.2	1.6
A_84_P512226	3.9	13.4	1.8	4.9	28.3	2.5
A_84_P24017	11.8	118.2	3.3	3.9	39.5	3.4
A_84_P837591	2.7	8.5	1.7	4.6	12.1	1.4
A_84_P11772	15.4	81	2.4	31.8	105.7	1.7
A_84_P91299	877.7	7280.8	3.1	992.8	6621.6	2.7
A_84_P164883	398	3029.6	2.9	352.1	1681.5	2.3
A_84_P11473	2791	6723.9	1.3	2681.3	6274	1.2
A_84_P17798	8.3	21.4	1.4	2.6	13.1	2.3
A_84_P22728	2904.6	12493.9	2.1	3005.6	7387.6	1.3
A_84_P787353	5662.5	15693.1	1.5	4539.7	9819	1.1
A_84_P733288	4.7	10.9	1.2	6.5	16.8	1.4
A_84_P791532	31.6	153.4	2.3	36.1	158.5	2.1
A_84_P799760	160.8	550.9	1.8	238	654.7	1.5
A_84_P15640	36	112.2	1.6	27.7	81.5	1.6
A_84_P844220	280.7	587.3	1.1	278	647.1	1.2
A_84_P22039	229.6	534.4	1.2	215.6	433	1
A_84_P17628	39.9	427.9	3.4	39.5	216.6	2.5
A_84_P822209	1407.1	4510.7	1.7	1713.3	3573.1	1.1
A_84_P828648	50.2	200.7	2	15.1	30.3	1
A_84_P12346	37.7	117.4	1.6	37.2	103.2	1.5
A_84_P766178	17.6	75.2	2.1	26.1	56.6	1.1
A_84_P753180	2.8	7.1	1.4	2.8	12.1	2.1
A_84_P861444	133.9	729	2.4	62.3	244.4	2
A_84_P88889	2.6	13.6	2.4	2.6	11.8	2.2
A_84_P275920	60.3	456.6	2.9	23.8	141.7	2.6
A_84_P842776	2.6	7.8	1.6	6.8	19.1	1.5
A_84_P22166	110	1809.2	4	92.5	197.4	1.1
A_84_P14053	2.8	18.2	2.7	2.8	7.9	1.5
A_84_P565344	3.1	70.4	4.5	3.5	31.9	3.2
A_84_P24157	373.2	1030	1.5	219.6	1027.7	2.2
A_84_P716749	20.1	41.8	1.1	14.9	39.7	1.4
A_84_P803506	212.3	1424	2.7	211.5	669.5	1.7
A_84_P204968	152.6	1593.9	3.4	137.3	416.6	1.6
A_84_P21972	3.3	16.2	2.3	2.9	13.5	2.2
A_84_P565260	30.9	93.1	1.6	25.5	73.3	1.5
A_84_P789200	1232.8	9507.7	2.9	1053	13869.1	3.7
A_84_P825221	3.4	26.9	3	4	11.6	1.5
A_84_P211628	2111.1	8787.3	2.1	2893.8	7155.8	1.3
A_84_P244315	209.6	715.5	1.8	256.9	627.1	1.3

A_84_P20734	3.1	6.5	1.1	2.8	14.1	2.3
A_84_P22100	2.8	9.2	1.7	2.8	7.2	1.4
A_84_P20927	5.8	13.8	1.3	6.4	12.9	1
A_84_P21132	2.6	11.6	2.1	5.2	11.5	1.2
A_84_P521040	2.7	14.9	2.5	2.7	13.8	2.3
A_84_P508523	3.8	18.6	2.3	3	8.6	1.5
A_84_P297344	63.2	440.2	2.8	68.2	378.2	2.5
A_84_P21831	1385.4	8244.1	2.6	1790.9	4152.9	1.2
A_84_P11046	996.8	8611	3.1	826	1756.8	1.1
A_84_P605779	80.1	487.8	2.6	52.5	120.2	1.2
A_84_P15118	2.8	13.4	2.3	3.2	10.3	1.7
A_84_P595866	3.9	11.3	1.5	2.7	9.9	1.9
A_84_P827841	5.5	20.1	1.9	4.2	11.3	1.4
A_84_P15517	363.5	4981.2	3.8	125.2	2052.4	4
A_84_P826232	70.5	301.8	2.1	66.4	320.2	2.3
A_84_P786320	661.2	3920.4	2.6	520.6	4534.3	3.1
A_84_P766952	2.6	32.1	3.6	2.7	9.8	1.9
A_84_P142169	23	255.8	3.5	12.5	34.2	1.5
A_84_P14249	1525.8	6013.6	2	1662	4352.3	1.4
A_84_P14354	4.5	17.5	1.9	3.8	9.7	1.4
A_84_P17613	26.1	60.2	1.2	9.4	26.9	1.5
A_84_P19256	297.1	1018.1	1.8	216.8	998.3	2.2
A_84_P20306	4	14.6	1.8	3.6	10.7	1.6
A_84_P827473	286.3	2454.1	3.1	385.5	2686.9	2.8
A_84_P15399	2.6	6.5	1.3	2.7	5.6	1
A_84_P18266	6.1	20.4	1.7	3.7	13.8	1.9
A_84_P767462	53.6	111.1	1.1	23.2	59.1	1.4
A_84_P200074	16	61	1.9	12.1	53.9	2.2
A_84_P15528	303.7	725.8	1.3	265.3	545	1
A_84_P15821	22.9	95.3	2.1	11.9	44.3	1.9
A_84_P12945	21.3	156.7	2.9	12.3	57.7	2.2
A_84_P19616	11.9	24.7	1.1	2.7	8	1.6
A_84_P757967	4.5	12.5	1.5	2.7	9.6	1.8
A_84_P852163	372.1	809.8	1.1	419.7	884.2	1.1
A_84_P11357	260	1590.5	2.6	186.6	501.1	1.4
A_84_P568573	2.8	6.5	1.2	2.8	6.7	1.3
A_84_P14695	4.4	10.4	1.2	2.8	9	1.7
A_84_P13946	16.3	66.4	2	8.2	21.6	1.4
A_84_P16724	36.9	246.1	2.7	44.4	128.4	1.5
A_84_P838093	2.7	12.1	2.2	4	9.9	1.3
A_84_P801373	125.4	866.9	2.8	64.7	557.9	3.1
A_84_P849144	1046.3	2769.1	1.4	611.7	1642.2	1.4
A_84_P516292	42.3	411.7	3.3	38.6	83	1.1
A_84_P557335	355	710.7	1	313.9	757.6	1.3
A_84_P21757	202.1	1642.2	3	159.4	493.6	1.6

A_84_P766522	2.8	12	2.1	2.9	12.8	2.1
A_84_P712672	570.5	2598.5	2.2	621.2	1754.7	1.5
A_84_P238673	1059.6	3138.5	1.6	582.6	2021.8	1.8
A_84_P816193	2089.4	15292.1	2.9	2863	9019.3	1.7
A_84_P59870	38.7	144.1	1.9	34.2	74.3	1.1
A_84_P12872	107.6	887.4	3	46.7	169	1.9
A_84_P840519	3	6.4	1.1	3.8	22.7	2.6
A_84_P19559	3836.3	19334.4	2.3	4208.4	8773.3	1.1
A_84_P514216	9.5	22.1	1.2	18	41.4	1.2
A_84_P21705	1306.7	2920.5	1.2	1572.3	3790	1.3
A_84_P764001	11.5	34.6	1.6	9.4	26.9	1.5
A_84_P75644	1698.2	11535.2	2.8	4151	9319	1.2
A_84_P186194	108.4	445.1	2	88.7	200.1	1.2
A_84_P573393	1466.2	5281.4	1.8	1041.2	2232.2	1.1
A_84_P79105	16.1	125.9	3	5.6	22.1	2
A_84_P13573	658.6	2733.8	2.1	852.6	2556.8	1.6
A_84_P22475	155.5	482.9	1.6	151	366.5	1.3
A_84_P14504	3.8	9.6	1.3	5.3	40.5	2.9
A_84_P861080	582.8	2312.5	2	630	1566.9	1.3
A_84_P509484	40.5	128.7	1.7	12.1	48.2	2
A_84_P836826	2.8	6.3	1.2	5.1	10.5	1.1
A_84_P18915	9.6	87	3.2	8.5	21.3	1.3
A_84_P840742	9	19	1.1	3	29.7	3.3
A_84_P21229	294.6	1554.1	2.4	338.2	770.8	1.2
A_84_P752283	3.3	8.6	1.4	4.5	36.3	3
A_84_P18467	19604.3	59529.9	1.6	16644.6	39451.2	1.2
A_84_P521890	11.6	25.4	1.1	14.5	59.2	2
A_84_P18132	2.8	9.4	1.7	6.7	28.2	2.1
A_84_P13692	6	12.1	1	6.5	17.9	1.5
A_84_P511918	26	137.8	2.4	21.3	88.1	2
A_84_P788325	104.7	954.9	3.2	83.6	189.4	1.2
A_84_P522474	3.1	7.3	1.2	4	8.9	1.2
A_84_P769278	4.4	23	2.4	3	10.1	1.7
A_84_P12640	322	1810	2.5	551.8	1582.5	1.5
A_84_P71314	10.2	20.4	1	9.5	95.8	3.3
A_84_P539298	3.1	7.7	1.3	3.9	9.6	1.3
A_84_P540757	5.7	16	1.5	10.8	25.4	1.2
A_84_P164953	1229.7	3256.8	1.4	1231.6	3757.4	1.6
A_84_P853677	7.9	16.4	1.1	9.4	25.4	1.4
A_84_P14060	23.5	256.9	3.4	21	57.8	1.5
A_84_P14828	616.8	1822.8	1.6	429.9	880.4	1
A_84_P20057	3.5	27.3	3	6.4	15.8	1.3
A_84_P753967	3.1	11.7	1.9	3.5	15.7	2.2
A_84_P789339	101.7	479.3	2.2	67.8	228.2	1.8
A_84_P836671	5	21.8	2.1	4.4	12.9	1.6

A_84_P144479	52	858.7	4	46.2	111.9	1.3
A_84_P22812	65.1	311.8	2.3	63.5	163.2	1.4
A_84_P590289	7.4	20.6	1.5	4.3	9.2	1.1
A_84_P93089	7.9	58.8	2.9	9.9	20	1
A_84_P20466	87	1618	4.2	150.4	620.7	2
A_84_P848183	317.4	849.7	1.4	216.5	463.2	1.1
A_84_P232979	5.1	11.3	1.1	2.9	6.2	1.1
A_84_P17957	92.5	239.1	1.4	105.6	233.3	1.1
A_84_P580415	17.7	69.6	2	13.6	28.4	1.1
A_84_P81409	5314.9	13363.2	1.3	6052.2	12357.9	1
A_84_P239845	3.2	9.1	1.5	3.3	9.2	1.5
A_84_P58700	2.9	16.7	2.5	9.9	27.4	1.5
A_84_P832673	3369.7	17067.9	2.3	4105	13217.9	1.7
A_84_P825864	15.5	170.3	3.5	16.9	38.2	1.2
A_84_P166733	2362.3	6779.6	1.5	1928.3	4002.9	1.1
A_84_P840276	140.2	364.8	1.4	94.7	334.6	1.8
A_84_P515118	7.8	24.1	1.6	4.7	19	2
A_84_P803202	2824.1	32979.1	3.5	1983.1	11836.7	2.6
A_84_P15595	11	27.5	1.3	8.3	47.7	2.5
A_84_P304550	3.4	37.8	3.5	12.1	41	1.8
A_84_P807037	146.1	519.7	1.8	132.9	336	1.3
A_84_P820317	24.2	140	2.5	21.1	42.3	1
A_84_P558649	12.4	24.7	1	8.4	26.4	1.6
A_84_P764437	2.9	233.1	6.3	2.9	23.9	3
A_84_P830991	2.9	14.7	2.3	2.9	9.1	1.6
A_84_P534517	6.5	47.1	2.9	8.3	32.9	2
A_84_P838751	63.9	185.2	1.5	65	152.1	1.2
A_84_P856007	352.9	727	1	413	929.7	1.2
A_84_P22942	226.8	913.2	2	105.8	339.1	1.7
A_84_P12454	7.3	32.8	2.2	11.3	24.9	1.1
A_84_P20369	281	12579.5	5.5	995.5	2138.4	1.1
A_84_P20216	7.1	22.5	1.7	21.3	50.4	1.2
A_84_P76869	5.7	24.4	2.1	2.9	8	1.4
A_84_P798429	78.1	183.8	1.2	65.7	229.4	1.8
A_84_P756150	4.3	13.9	1.7	3	14.5	2.3
A_84_P565014	6.3	28.3	2.2	3	6.3	1
A_84_P818855	521.4	2390.6	2.2	528.3	1086.4	1
A_84_P14680	3.2	20.8	2.7	5.3	14.2	1.4
A_84_P852565	4	10.4	1.4	3.3	17.7	2.4
A_84_P242693	3.3	29	3.2	15.6	34.7	1.2
A_84_P786059	137.3	319.5	1.2	91.1	297.4	1.7
A_84_P603904	202.3	633.2	1.6	80.8	320.8	2
A_84_P18892	220	548.3	1.3	273	553.4	1
A_84_P63350	12.2	77.1	2.7	6	21.5	1.9
A_84_P102376	1683.4	4085.3	1.3	1249.5	3177.5	1.3

A_84_P22670	28.4	63.4	1.2	35.4	72.5	1
A_84_P811412	426.5	921.8	1.1	511.4	1091.9	1.1
A_84_P14075	165.8	1201.8	2.9	101.7	437.9	2.1
A_84_P755144	3	7.2	1.3	3	11.8	2
A_84_P753902	17.8	61	1.8	11.1	81.8	2.9
A_84_P18328	1232.1	2646.7	1.1	1269.7	2580.6	1
A_84_P10494	215.8	1501.1	2.8	179.9	396.3	1.1
A_84_P795300	9.3	28.2	1.6	9.1	29	1.7
A_84_P808649	120.3	525.7	2.1	71.8	367.9	2.4

Supplemental Table 3. Cluster analysis of down-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (hypocotyl)

Annotation Cluster 1: Enrichment Score: 3.850345417203327			
Term	Count	%	PValue
cell wall modification	14	1.963534	1.70E-05
cell wall organization	18	2.524544	2.95E-04
external encapsulating structure organization	18	2.524544	5.62E-04
Annotation Cluster 2: Enrichment Score: 2.477696476341466			
Term	Count	%	PValue
secondary metabolic process	25	3.506311	6.09E-05
cellular amino acid derivative metabolic process	17	2.384292	9.54E-04
phenylpropanoid metabolic process	12	1.683029	0.001853
lignan metabolic process	4	0.56101	0.005691
lignan biosynthetic process	4	0.56101	0.005691
cellular amino acid derivative biosynthetic process	12	1.683029	0.006108
phenylpropanoid biosynthetic process	9	1.262272	0.010518
aromatic compound biosynthetic process	10	1.402525	0.067366
Annotation Cluster 3: Enrichment Score: 2.4059617973062943			
Term	Count	%	PValue
cellular response to nutrient levels	8	1.12202	0.00113
cellular response to phosphate starvation	6	0.841515	0.001613
response to nutrient levels	8	1.12202	0.00287
cellular response to extracellular stimulus	8	1.12202	0.00287
cellular response to starvation	7	0.981767	0.002972
response to starvation	7	0.981767	0.004753
response to extracellular stimulus	8	1.12202	0.006168
cellular response to stress	17	2.384292	0.043223

Annotation Cluster 4: Enrichment Score: 1.8247151147506977			
Term	Count	%	PValue
cell wall modification	14	1.963534	1.70E-05
plant-type cell wall modification	8	1.12202	7.68E-05
plant-type cell wall loosening	6	0.841515	0.001248
plant-type cell wall organization	8	1.12202	0.002314
plant-type cell wall modification during multidimensional cel	4	0.56101	0.022246
regulation of cellular component size	12	1.683029	0.024892
cell wall modification during multidimensional cell growth	4	0.56101	0.027089
cell growth	11	1.542777	0.029628
unidimensional cell growth	9	1.262272	0.030635
developmental growth involved in morphogenesis	9	1.262272	0.030635
regulation of cell size	11	1.542777	0.04066
developmental growth	9	1.262272	0.061647
growth	11	1.542777	0.064768
multidimensional cell growth	4	0.56101	0.092677
cell morphogenesis	9	1.262272	0.116777
cellular component morphogenesis	9	1.262272	0.177074
sexual reproduction	4	0.56101	0.195216

Annotation Cluster 5: Enrichment Score: 1.3689163556330588			
Term	Count	%	PValue
multidrug transport	6	0.841515	0.031191
drug transport	6	0.841515	0.039589
response to drug	6	0.841515	0.041418
transmembrane transport	10	1.402525	0.065396

Annotation Cluster 6: Enrichment Score: 1.3271613418007489			
Term	Count	%	PValue
response to hydrogen peroxide	9	1.262272	0.006247
response to reactive oxygen species	9	1.262272	0.017308
cellular response to stress	17	2.384292	0.043223
cellular response to hydrogen peroxide	6	0.841515	0.049239
hydrogen peroxide catabolic process	6	0.841515	0.049239
hydrogen peroxide metabolic process	6	0.841515	0.055638
cellular response to reactive oxygen species	6	0.841515	0.072345
cellular response to oxidative stress	6	0.841515	0.074934
response to oxidative stress	12	1.683029	0.076318
response to inorganic substance	19	2.664797	0.085477
oxygen and reactive oxygen species metabolic process	6	0.841515	0.112995

Annotation Cluster 7: Enrichment Score: 1.1781363547521817			
Term	Count	%	PValue
lignin metabolic process	6	0.841515	0.017995
lignin catabolic process	3	0.420757	0.059062
phenylpropanoid catabolic process	3	0.420757	0.059062
aromatic compound catabolic process	3	0.420757	0.139149
cellular amino acid derivative catabolic process	3	0.420757	0.147256
Annotation Cluster 8: Enrichment Score: 1.1221426863168174			
Term	Count	%	PValue
glycosinolate biosynthetic process	4	0.56101	0.029704
glucosinolate biosynthetic process	4	0.56101	0.029704
S-glycoside biosynthetic process	4	0.56101	0.029704
sulfur compound biosynthetic process	7	0.981767	0.039895
carbohydrate biosynthetic process	11	1.542777	0.076574
glycosinolate metabolic process	4	0.56101	0.083599
glucosinolate metabolic process	4	0.56101	0.083599
S-glycoside metabolic process	4	0.56101	0.083599
sulfur metabolic process	8	1.12202	0.107619
glycoside metabolic process	5	0.701262	0.134442
glycoside biosynthetic process	4	0.56101	0.177455
cellular carbohydrate biosynthetic process	7	0.981767	0.284926
Annotation Cluster 9: Enrichment Score: 1.0069635730745474			
Term	Count	%	PValue
response to abscisic acid stimulus	13	1.823282	0.036725
response to hormone stimulus	30	4.207574	0.056145
response to endogenous stimulus	31	4.347826	0.076409
response to auxin stimulus	12	1.683029	0.171231
response to organic substance	31	4.347826	0.342128
Annotation Cluster 10: Enrichment Score: 0.9426859839872416			
Term	Count	%	PValue
regulation of timing of transition from vegetative to reproduct	3	0.420757	0.059062
regulation of timing of meristematic phase transition	3	0.420757	0.059062
regulation of development, heterochronic	3	0.420757	0.131145
regulation of meristem development	3	0.420757	0.370585
Annotation Cluster 11: Enrichment Score: 0.8186180969346792			
Term	Count	%	PValue
photoperiodism	4	0.56101	0.066683
photoperiodism, flowering	3	0.420757	0.214786
vegetative to reproductive phase transition	4	0.56101	0.244412

Annotation Cluster 12: Enrichment Score: 0.8163027714785701			
Term	Count	%	PValue
response to gibberellin stimulus	9	1.262272	0.006903
response to salicylic acid stimulus	6	0.841515	0.275719
response to jasmonic acid stimulus	6	0.841515	0.302978
response to ethylene stimulus	4	0.56101	0.941664
Annotation Cluster 13: Enrichment Score: 0.8006266554248845			
Term	Count	%	PValue
response to light stimulus	16	2.244039	0.134525
response to abiotic stimulus	35	4.908836	0.138072
response to radiation	16	2.244039	0.161297
response to red or far red light	7	0.981767	0.209391
Annotation Cluster 14: Enrichment Score: 0.7734333145083384			
Term	Count	%	PValue
glucan catabolic process	4	0.56101	0.062727
glucan metabolic process	8	1.12202	0.064915
polysaccharide metabolic process	10	1.402525	0.073253
polysaccharide catabolic process	5	0.701262	0.095495
cellulose catabolic process	3	0.420757	0.123253
cellular polysaccharide metabolic process	6	0.841515	0.29384
cellular glucan metabolic process	5	0.701262	0.331237
cellulose metabolic process	3	0.420757	0.452317
carbohydrate catabolic process	5	0.701262	0.707954
Annotation Cluster 15: Enrichment Score: 0.6852960343868292			
Term	Count	%	PValue
fatty acid metabolic process	9	1.262272	0.131174
fatty acid biosynthetic process	7	0.981767	0.170326
organic acid biosynthetic process	13	1.823282	0.249751
carboxylic acid biosynthetic process	13	1.823282	0.249751
lipid biosynthetic process	13	1.823282	0.268768
Annotation Cluster 16: Enrichment Score: 0.5726596227782237			
Term	Count	%	PValue
gravitropism	3	0.420757	0.232135
response to gravity	3	0.420757	0.258298
tropism	3	0.420757	0.319271

Annotation Cluster 17: Enrichment Score: 0.5371217087253822			
Term	Count	%	PValue
response to osmotic stress	13	1.823282	0.22223
response to jasmonic acid stimulus	6	0.841515	0.302978
response to salt stress	11	1.542777	0.36343
Annotation Cluster 18: Enrichment Score: 0.5277281167851636			
Term	Count	%	PValue
sulfur compound biosynthetic process	7	0.981767	0.039895
sulfur metabolic process	8	1.12202	0.107619
sulfur amino acid metabolic process	4	0.56101	0.250705
methionine metabolic process	3	0.420757	0.319271
sulfur amino acid biosynthetic process	3	0.420757	0.327909
aspartate family amino acid metabolic process	3	0.420757	0.498386
amine biosynthetic process	6	0.841515	0.527398
cellular amino acid biosynthetic process	5	0.701262	0.629238
nitrogen compound biosynthetic process	8	1.12202	0.955097
Annotation Cluster 19: Enrichment Score: 0.4892065729622252			
Term	Count	%	PValue
regulation of transcription	57	7.99439	0.10159
regulation of transcription, DNA-dependent	26	3.646564	0.573441
regulation of RNA metabolic process	26	3.646564	0.584843
Annotation Cluster 20: Enrichment Score: 0.4470157996883969			
Term	Count	%	PValue
response to inorganic substance	19	2.664797	0.085477
response to metal ion	9	1.262272	0.681883
response to cadmium ion	7	0.981767	0.782333
Annotation Cluster 21: Enrichment Score: 0.2889905050697123			
Term	Count	%	PValue
auxin mediated signaling pathway	5	0.701262	0.294124
intracellular signaling cascade	22	3.085554	0.303719
cellular response to hormone stimulus	8	1.12202	0.884133
hormone-mediated signaling	8	1.12202	0.884133
Annotation Cluster 22: Enrichment Score: 0.24341628447450608			
Term	Count	%	PValue
base-excision repair	3	0.420757	0.123253
DNA repair	3	0.420757	0.928156
response to DNA damage stimulus	3	0.420757	0.938557
DNA metabolic process	4	0.56101	0.989592

Annotation Cluster 23: Enrichment Score: 0.2189748936833288			
Term	Count	%	PValue
root development	6	0.841515	0.493456
root system development	6	0.841515	0.493456
shoot system development	5	0.701262	0.904853

Annotation Cluster 24: Enrichment Score: 0.1578959321539985			
Term	Count	%	PValue
transition metal ion transport	3	0.420757	0.513186
metal ion transport	6	0.841515	0.707504
ion transport	11	1.542777	0.723659
cation transport	7	0.981767	0.888953

Annotation Cluster 25: Enrichment Score: 0.1377034541159062			
Term	Count	%	PValue
membrane fusion	3	0.420757	0.172104
small GTPase mediated signal transduction	4	0.56101	0.366001
membrane organization	3	0.420757	0.718997
cellular macromolecule localization	5	0.701262	0.927819
protein transport	8	1.12202	0.942843
establishment of protein localization	8	1.12202	0.942843
protein localization	8	1.12202	0.954483
intracellular protein transport	4	0.56101	0.957516
intracellular transport	6	0.841515	0.958276
cellular protein localization	4	0.56101	0.965117
vesicle-mediated transport	4	0.56101	0.968132

Annotation Cluster 26: Enrichment Score: 0.13737919008918278			
Term	Count	%	PValue
cell division	5	0.701262	0.56674
regulation of cell cycle	3	0.420757	0.746608
cell cycle	4	0.56101	0.914926

Annotation Cluster 27: Enrichment Score: 0.12082724580850283			
Term	Count	%	PValue
post-embryonic development	20	2.805049	0.620704
reproductive developmental process	19	2.664797	0.62074
reproductive structure development	17	2.384292	0.647498
seed development	8	1.12202	0.884133
fruit development	8	1.12202	0.909247
embryonic development ending in seed dormancy	6	0.841515	0.939302

Annotation Cluster 28: Enrichment Score: 0.029335639594597146			
Term	Count	%	PValue
macromolecule catabolic process	15	2.103787	0.732887
protein catabolic process	9	1.262272	0.963031
cellular macromolecule catabolic process	9	1.262272	0.968932
modification-dependent macromolecule catabolic process	8	1.12202	0.975743
modification-dependent protein catabolic process	8	1.12202	0.975743
proteolysis involved in cellular protein catabolic process	8	1.12202	0.977432
cellular protein catabolic process	8	1.12202	0.979316

Annotation Cluster 29: Enrichment Score: 0.0030671883958797576			
Term	Count	%	PValue
protein amino acid phosphorylation	17	2.384292	0.982021
phosphorylation	17	2.384292	0.995389
phosphate metabolic process	18	2.524544	0.997243
phosphorus metabolic process	18	2.524544	0.997278

Cluster 1-1: cell wall modification			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log2 Ratio	Log2 Ratio
A_84_P16943	AT3G54640	TRYPTOPHAN SYNTHASE ALPHA CHAIN	-1.7	-2.2
A_84_P21670	AT5G63800	Beta-galactosidase 6	-1.1	-1.8
A_84_P21915	AT1G20190	Expansin-A11	-2.4	-1.3
A_84_P12680	AT3G29030	Expansin-A5	-1.8	-1.1
A_84_P11569	AT2G40610	Expansin-A8	-2.6	-1.7
A_84_P18192	AT2G20750	Expansin-B1	-2.3	-1.5
A_84_P57310	AT4G28250	Expansin-B3	-2	-1.1
A_84_P19588	AT4G17030	Expansin-like B1	-1.5	-2.4
A_84_P12382	AT1G53830	Pectinesterase 2, PME2	-1.1	-1.3
A_84_P19163	AT2G43050	Probable pectinesterase/pectinesterase inhibit	-3.2	-2.7
A_84_P24148	AT3G59010	Probable pectinesterase/pectinesterase inhibit	-3.6	-2.6
A_84_P20395	AT4G02320	Probable pectinesterase/pectinesterase inhibit	-1.6	-1.5
A_84_P21341	AT4G02330	Probable pectinesterase/pectinesterase inhibit	-1.6	-2.2
A_84_P18029	AT1G10550	Probable xyloglucan endotransglucosylase/hyd	-1.9	-1.2

Cluster 1-2: cell wall organization			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P11383	AT1G65570	polygalacturonase family protein	-2.6	-1.3
A_84_P10687	AT2G43880	putative polygalacturonase /pectinase	-4.5	-2.4
A_84_P17557	AT4G02290	GLYCOSYL HYDROLASE 9B13, Endogluca	-1.7	-1.4
A_84_P18129	AT1G19940	Endoglucanase 2	-2.1	-1.7
A_84_P20788	AT1G71380	Endoglucanase 9	-2.8	-3.2
A_84_P21915	AT1G20190	Expansin-A11	-2.4	-1.3
A_84_P12680	AT3G29030	Expansin-A5	-1.8	-1.1
A_84_P11569	AT2G40610	Expansin-A8	-2.6	-1.7
A_84_P18192	AT2G20750	Expansin-B1	-2.3	-1.5
A_84_P57310	AT4G28250	Expansin-B3	-2	-1.1
A_84_P12382	AT1G53830	Pectinesterase 2, PME2	-1.1	-1.3
A_84_P19163	AT2G43050	Probable pectinesterase/pectinesterase inhibit	-3.2	-2.7
A_84_P24148	AT3G59010	Probable pectinesterase/pectinesterase inhibit	-3.6	-2.6
A_84_P20395	AT4G02320	Probable pectinesterase/pectinesterase inhibit	-1.6	-1.5
A_84_P21341	AT4G02330	Probable pectinesterase/pectinesterase inhibit	-1.6	-2.2
A_84_P297064	AT1G65310	Probable xyloglucan endotransglucosylase/hyd	-1.1	-2.1
A_84_P10083	AT4G30290	Probable xyloglucan endotransglucosylase/hyd	-1.7	-1.8
A_84_P18029	AT1G10550	Probable xyloglucan endotransglucosylase/hyd	-1.9	-1.2

Cluster 1-3: external encapsulating structure organization			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P11383	AT1G65570	polygalacturonase family protein	-2.6	-1.3
A_84_P10687	AT2G43880	putative polygalacturonase /pectinase	-4.5	-2.4
A_84_P17557	AT4G02290	GLYCOSYL HYDROLASE 9B13, Endogluca	-1.7	-1.4
A_84_P18129	AT1G19940	Endoglucanase 2	-2.1	-1.7
A_84_P20788	AT1G71380	Endoglucanase 9	-2.8	-3.2
A_84_P21915	AT1G20190	Expansin-A11	-2.4	-1.3
A_84_P12680	AT3G29030	Expansin-A5	-1.8	-1.1
A_84_P11569	AT2G40610	Expansin-A8	-2.6	-1.7
A_84_P18192	AT2G20750	Expansin-B1	-2.3	-1.5
A_84_P57310	AT4G28250	Expansin-B3	-2	-1.1
A_84_P12382	AT1G53830	Pectinesterase 2, PME2	-1.1	-1.3
A_84_P19163	AT2G43050	Probable pectinesterase/pectinesterase inhibit	-3.2	-2.7
A_84_P24148	AT3G59010	Probable pectinesterase/pectinesterase inhibit	-3.6	-2.6
A_84_P20395	AT4G02320	Probable pectinesterase/pectinesterase inhibit	-1.6	-1.5
A_84_P21341	AT4G02330	Probable pectinesterase/pectinesterase inhibit	-1.6	-2.2
A_84_P297064	AT1G65310	Probable xyloglucan endotransglucosylase/hyd	-1.1	-2.1
A_84_P10083	AT4G30290	Probable xyloglucan endotransglucosylase/hyd	-1.7	-1.8
A_84_P18029	AT1G10550	Probable xyloglucan endotransglucosylase/hyd	-1.9	-1.2

Cluster 2-1: secondary metabolic process			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P19003	AT1G02950	GLUTATHIONE S-TRANSFERASE 31, GLU	-1.1	-2.7
A_84_P23719	AT1G16490	MYB DOMAIN PROTEIN 58, MYB58, ATM	-2.9	-2.5
A_84_P23724	AT1G17180	GLUTATHIONE S-TRANSFERASE TAU 25	-1.1	-1.2
A_84_P23356	AT1G27140	GLUTATHIONE S-TRANSFERASE 13, GLU	-1.7	-1.2
A_84_P13432	AT1G32100	PINORESINOL REDUCTASE 1, PRR1	-1.3	-2.4
A_84_P22788	AT1G65870	Disease resistance-responsive (dirigent-like p	-1.8	-1.4
A_84_P20921	AT1G77520	O-methyltransferase family protein	-2.9	-4.3
A_84_P12475	AT1G78360	GLUTATHIONE S-TRANSFERASE TAU 21	-3.1	-2.3
A_84_P11530	AT1G78370	GLUTATHIONE S-TRANSFERASE TAU 20	-2.1	-1.3
A_84_P107712	AT2G21100	Disease resistance-responsive (dirigent-like p	-1.4	-1.6
A_84_P17266	AT2G41300	STRICTOSIDINE SYNTHASE-LIKE 1, SSL1	-1.5	-1.6
A_84_P11909	AT4G11210	disease resistance-responsive, dirigent domai	-2.9	-2.5
A_84_P24132	AT3G55120	Chalcone--flavonone isomerase 1	-1.3	-1.2
A_84_P18772	AT5G47990	Cytochrome P450 705A5	-1.7	-2.3
A_84_P19718	AT5G48000	Cytochrome P450 708A2	-1.2	-1.4
A_84_P90469	AT1G16410	Dihomomethionine N-hydroxylase	-2.4	-1.2
A_84_P21842	AT1G65860	Flavin-containing monooxygenase FMO GS-O	-2.6	-1.1
A_84_P16082	AT1G62540	Flavin-containing monooxygenase FMO GS-O	-2.6	-2
A_84_P22004	AT2G36790	Flavonol-3-O-glycoside-7-O-glucosyltransfer	-1.9	-1.3
A_84_P16678	AT4G25420	Gibberellin 20 oxidase 1	-3.5	-2
A_84_P15811	AT5G01190	Laccase-10	-1.5	-1.1
A_84_P23387	AT5G03260	Laccase-11	-1.4	-3.3
A_84_P15454	AT2G29130	Laccase-2	-1.8	-1.9
A_84_P17435	AT1G62800	Probable branched-chain-amino-acid aminotra	-1.7	-1.3
A_84_P18574	AT4G26220	Probable caffeoyl-CoA O-methyltransferase A	-1.1	-1.2

Cluster 2-2: cellular amino acid derivative metabolic process			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P307510	AT4G08040	1-aminocyclopropane-1-carboxylate synthase	-1.5	-1.9
A_84_P23719	AT1G16490	MYB DOMAIN PROTEIN 58, MYB58, ATM	-2.9	-2.5
A_84_P13432	AT1G32100	PINORESINOL REDUCTASE 1, PRR1	-1.3	-2.4
A_84_P22788	AT1G65870	Disease resistance-responsive (dirigent-like p	-1.8	-1.4
A_84_P20921	AT1G77520	O-methyltransferase family protein	-2.9	-4.3
A_84_P107712	AT2G21100	Disease resistance-responsive (dirigent-like p	-1.4	-1.6
A_84_P16943	AT3G54640	TRYPTOPHAN SYNTHASE ALPHA CHAIN	-1.7	-2.2
A_84_P11909	AT4G11210	disease resistance-responsive, dirigent domain	-2.9	-2.5
A_84_P24132	AT3G55120	Chalcone--flavonone isomerase 1	-1.3	-1.2
A_84_P14263	AT1G26630	Eukaryotic translation initiation factor 5A-1	-1.2	-1.1
A_84_P22004	AT2G36790	Flavonol-3-O-glycoside-7-O-glucosyltransfera	-1.9	-1.3
A_84_P15811	AT5G01190	Laccase-10	-1.5	-1.1
A_84_P23387	AT5G03260	Laccase-11	-1.4	-3.3
A_84_P15454	AT2G29130	Laccase-2	-1.8	-1.9
A_84_P15049	AT1G55180	Phospholipase D epsilon	-2.7	-5.4
A_84_P18574	AT4G26220	Probable caffeoyl-CoA O-methyltransferase A	-1.1	-1.2
A_84_P23582	AT5G15950	S-adenosylmethionine decarboxylase proenzym	-1.2	-1.5

Cluster 3-1: cellular response to nutrient levels			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P14033	AT1G66270	BGLU21	-3.1	-1.4
A_84_P21894	AT1G68740	Encodes PHO1;H1, a member of the PHO1 fam	-2.6	-1.9
A_84_P557122	AT2G45130	SPX DOMAIN GENE 3, SPX3	-2.4	-4.3
A_84_P587419	AT3G09922	INDUCED BY PHOSPHATE STARVATION	-2.3	-2.2
A_84_P18673	AT5G07690	MYB DOMAIN PROTEIN 29, MYB29	-2.8	-1.1
A_84_P19887	AT1G80760	Aquaporin NIP6-1	-2.3	-1.3
A_84_P13475	AT2G11810	Monogalactosyldiacylglycerol synthase 3, chlo	-3	-4.9
A_84_P15049	AT1G55180	Phospholipase D epsilon	-2.7	-5.4

Cluster 4-1: cell wall modification			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P16943	AT3G54640; AT1G52410		-1.7	-2.2
A_84_P21670	AT5G63800	Beta-galactosidase 6	-1.1	-1.8
A_84_P21915	AT1G20190	Expansin-A11	-2.4	-1.3
A_84_P12680	AT3G29030	Expansin-A5	-1.8	-1.1
A_84_P11569	AT2G40610	Expansin-A8	-2.6	-1.7
A_84_P18192	AT2G20750	Expansin-B1	-2.3	-1.5
A_84_P57310	AT4G28250	Expansin-B3	-2	-1.1
A_84_P19588	AT4G17030	Expansin-like B1	-1.5	-2.4
A_84_P12382	AT1G53830	Pectinesterase 2	-1.1	-1.3
A_84_P19163	AT2G43050	Probable pectinesterase/pectinesterase inhibito	-3.2	-2.7
A_84_P24148	AT3G59010	Probable pectinesterase/pectinesterase inhibito	-3.6	-2.6
A_84_P20395	AT4G02320	Probable pectinesterase/pectinesterase inhibito	-1.6	-1.5
A_84_P21341	AT4G02330	Probable pectinesterase/pectinesterase inhibito	-1.6	-2.2
A_84_P18029	AT1G10550	Probable xyloglucan endotransglucosylase/hyd	-1.9	-1.2

Cluster 5-1: multidrug transport			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P518710	AT1G15160	MATE efflux family protein	-2.3	-1.1
A_84_P233529	AT4G22790	RESISTANT TO HIGH CO2, RHC1	-1.7	-1.1
A_84_P11135	AT5G17700	MATE efflux family protein	-1.8	-1.3
A_84_P16843	AT5G38030	MATE efflux family protein	-1.6	-2.2
A_84_P561086	AT5G44050	MATE efflux family protein	-1.8	-1.9
A_84_P168383	AT5G49130	BIGE1B	-1.6	-1.9

Cluster 6-1: response to hydrogen peroxide			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P23846	AT2G47180	GALACTINOL SYNTHASE 1, GOLS1	-1.8	-1.7
A_84_P23544	AT5G59720	HEAT SHOCK PROTEIN 18.2, HSP18.2	-2	-1.5
A_84_P19563	AT4G35970	L-ascorbate peroxidase 5, peroxisomal	-1.4	-2.9
A_84_P14454	AT2G39040	Peroxidase 24	-2.9	-1.3
A_84_P21103	AT2G41480	Peroxidase 25	-1.4	-1.5
A_84_P10441	AT1G05260	Peroxidase 3	-2.2	-1.1
A_84_P15912	AT5G42180	Peroxidase 64	-1	-1.5
A_84_P17122	AT1G44970	Peroxidase 9	-1.2	-1.7
A_84_P21184	AT3G17790	Purple acid phosphatase 17	-1.1	-2.5

Supplemental Table 4 Cluster analysis of up-regulated genes in microarray analysis, ztl-3/ztl-105 mutants compared with WT (hypocotyl)

Annotation Cluster 1: Enrichment Score: 9.726836590927762			
Term	Count	%	PValue
regulation of transcription	83	20.6467662	5.3676E-15
transcription	55	13.681592	5.4964E-10
regulation of transcription, DNA-dependent	46	11.4427861	1.886E-08
regulation of RNA metabolic process	46	11.4427861	2.2246E-08
Annotation Cluster 2: Enrichment Score: 4.390941933613232			
Term	Count	%	PValue
shoot development	17	4.22885572	2.6451E-05
shoot system development	17	4.22885572	3.0124E-05
phyllome development	14	3.48258706	4.6748E-05
leaf development	13	3.23383085	7.3303E-05
Annotation Cluster 3: Enrichment Score: 3.0456287866733156			
Term	Count	%	PValue
reproductive structure development	27	6.71641791	0.00029978
flower development	13	3.23383085	0.00062559
reproductive developmental process	27	6.71641791	0.00129506
post-embryonic development	27	6.71641791	0.00270465
Annotation Cluster 4: Enrichment Score: 2.7220238687033977			
Term	Count	%	PValue
regulation of development, heterochronic	7	1.74129353	4.9777E-06
regulation of meristem development	6	1.49253731	0.00237252
regulation of timing of meristematic phase transition	3	0.74626866	0.03310053
regulation of timing of transition from vegetative to repr	3	0.74626866	0.03310053
Annotation Cluster 5: Enrichment Score: 2.485130228888129			
Term	Count	%	PValue
regulation of development, heterochronic	7	1.74129353	4.9777E-06
positive regulation of development, heterochronic	3	0.74626866	0.0057143
shoot morphogenesis	8	1.99004975	0.01423842
leaf morphogenesis	4	0.99502488	0.28315795

Annotation Cluster 6: Enrichment Score: 2.11194174409844			
Term	Count	%	PValue
two-component signal transduction system (phosphorela	11	2.73631841	0.00417196
cytokinin mediated signaling	5	1.24378109	0.00948882
response to cytokinin stimulus	6	1.49253731	0.01165795
Annotation Cluster 7: Enrichment Score: 1.8695986143104801			
Term	Count	%	PValue
response to organic substance	37	9.2039801	0.00038935
response to hormone stimulus	30	7.46268657	0.00079054
response to endogenous stimulus	31	7.71144279	0.00114094
two-component signal transduction system (phosphorela	11	2.73631841	0.00417196
cellular response to hormone stimulus	15	3.73134328	0.01618084
hormone-mediated signaling	15	3.73134328	0.01618084
response to auxin stimulus	11	2.73631841	0.06254117
ethylene mediated signaling pathway	6	1.49253731	0.16412805
intracellular signaling cascade	18	4.47761194	0.18931858
response to ethylene stimulus	7	1.74129353	0.27015233
Annotation Cluster 8: Enrichment Score: 1.849217797802634			
Term	Count	%	PValue
regionalization	8	1.99004975	0.00090578
pattern specification process	8	1.99004975	0.00285685
adaxial/abaxial axis specification	3	0.74626866	0.04070858
adaxial/abaxial pattern formation	3	0.74626866	0.06218803
axis specification	3	0.74626866	0.08661819
Annotation Cluster 9: Enrichment Score: 1.513893982017802			
Term	Count	%	PValue
flower development	13	3.23383085	0.00062559
floral whorl development	6	1.49253731	0.03461344
carpel development	4	0.99502488	0.05047722
floral organ development	6	1.49253731	0.06049211
gynoecium development	4	0.99502488	0.06682631
post-embryonic organ development	6	1.49253731	0.18679368

Annotation Cluster 10: Enrichment Score: 1.4732430574721704			
Term	Count	%	PValue
stomatal complex development	4	0.99502488	0.0084685
shoot morphogenesis	8	1.99004975	0.01423842
stomatal complex morphogenesis	3	0.74626866	0.02953186
post-embryonic morphogenesis	3	0.74626866	0.35930915

Annotation Cluster 11: Enrichment Score: 1.135124275103342			
Term	Count	%	PValue
inositol catabolic process	3	0.74626866	0.00168874
polyol catabolic process	3	0.74626866	0.01183994
L-ascorbic acid metabolic process	3	0.74626866	0.01984663
L-ascorbic acid biosynthetic process	3	0.74626866	0.01984663
syncytium formation	3	0.74626866	0.02289808
polyol metabolic process	4	0.99502488	0.02829792
inositol metabolic process	3	0.74626866	0.03310053
water-soluble vitamin biosynthetic process	4	0.99502488	0.07275005
water-soluble vitamin metabolic process	4	0.99502488	0.08205718
vitamin biosynthetic process	4	0.99502488	0.12012851
vitamin metabolic process	4	0.99502488	0.13147021
cellular carbohydrate catabolic process	5	1.24378109	0.23344378
carbohydrate catabolic process	5	1.24378109	0.45855606
alcohol catabolic process	3	0.74626866	0.58982776
carboxylic acid biosynthetic process	6	1.49253731	0.82757412
organic acid biosynthetic process	6	1.49253731	0.82757412

Annotation Cluster 12: Enrichment Score: 0.937799546353004			
Term	Count	%	PValue
cytokinin metabolic process	3	0.74626866	0.04473536
cellular hormone metabolic process	3	0.74626866	0.09707343
hormone metabolic process	4	0.99502488	0.12386749
regulation of hormone levels	4	0.99502488	0.32968044

Annotation Cluster 13: Enrichment Score: 0.5681426330141817			
Term	Count	%	PValue
lignin metabolic process	4	0.99502488	0.09863241
phenylpropanoid metabolic process	6	1.49253731	0.15320347
secondary metabolic process	11	2.73631841	0.18464538
cellular amino acid derivative metabolic process	7	1.74129353	0.33977321
phenylpropanoid biosynthetic process	4	0.99502488	0.37152654
cellular amino acid derivative biosynthetic process	5	1.24378109	0.42067892
aromatic compound biosynthetic process	4	0.99502488	0.71161512

Annotation Cluster 14: Enrichment Score: 0.37305578106314324			
Term	Count	%	PValue
response to cold	7	1.74129353	0.20595968
response to temperature stimulus	7	1.74129353	0.56082031
response to abiotic stimulus	20	4.97512438	0.65800125
Annotation Cluster 15: Enrichment Score: 0.29326249777811053			
Term	Count	%	PValue
fruit development	10	2.48756219	0.35776912
seed development	8	1.99004975	0.60492685
embryonic development ending in seed dormancy	7	1.74129353	0.60940608
Annotation Cluster 16: Enrichment Score: 0.1495354325040088			
Term	Count	%	PValue
cell death	5	1.24378109	0.63035531
death	5	1.24378109	0.63035531
programmed cell death	3	0.74626866	0.89582436
Annotation Cluster 17: Enrichment Score: 0.14881575603248642			
Term	Count	%	PValue
response to abiotic stimulus	20	4.97512438	0.65800125
response to light stimulus	8	1.99004975	0.68325133
response to radiation	8	1.99004975	0.7165253
response to red or far red light	3	0.74626866	0.78831219
Annotation Cluster 18: Enrichment Score: 0.059894088974012945			
Term	Count	%	PValue
growth	4	0.99502488	0.79250811
cell growth	3	0.74626866	0.88211975
regulation of cell size	3	0.74626866	0.90005428
regulation of cellular component size	3	0.74626866	0.91542692
Annotation Cluster 19: Enrichment Score: 0.004894541727678365			
Term	Count	%	PValue
protein amino acid phosphorylation	12	2.98507463	0.97642441
phosphorylation	12	2.98507463	0.99206467
phosphate metabolic process	13	3.23383085	0.99336131
phosphorus metabolic process	13	3.23383085	0.99342706

Annotation Cluster 20: Enrichment Score: 0.0038678398687665484			
Term	Count	%	PValue
protein transport	4	0.99502488	0.99045757
establishment of protein localization	4	0.99502488	0.99045757
protein localization	4	0.99502488	0.99248677

Annotation Cluster 21: Enrichment Score: 3.7139384588572456E-4			
Term	Count	%	PValue
cellular macromolecule catabolic process	4	0.99502488	0.99776208
modification-dependent protein catabolic process	3	0.74626866	0.99927826
modification-dependent macromolecule catabolic proce	3	0.74626866	0.99927826
proteolysis involved in cellular protein catabolic proce	3	0.74626866	0.99933423
cellular protein catabolic process	3	0.74626866	0.99939578
macromolecule catabolic process	4	0.99502488	0.99944275
protein catabolic process	3	0.74626866	0.99952619

Cluster 1-1: regulation of transcription			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log2 Ratio	Log2 Ratio
A_84_P164953	AT1G49720	ABSCISIC ACID-INSENSITIVE 5-like protein	1.4	1.6
A_84_P516094	AT1G26665	Mediator complex, subunit Med10	1	1
A_84_P21517	AT1G31310	hydroxyproline-rich glycoprotein-like protein	3	2.4
A_84_P21593	AT1G49830	basic helix-loop-helix (bHLH) DNA-binding sup	1.3	1.3
A_84_P21883	AT1G68320	MYB DOMAIN PROTEIN 62, MYB62	3.2	1.3
A_84_P125471	AT2G21235	Basic-leucine zipper (bZIP) transcription factor	1.9	1.6
A_84_P17322	AT2G32460	MYB DOMAIN PROTEIN 101, MYB101	1.4	2.2
A_84_P186194	AT2G35640	homeodomain-like superfamily protein	2	1.2
A_84_P265480	AT2G36400	GROWTH-REGULATING FACTOR 3, GRF3	1.7	2
A_84_P565344	AT4G24150	GROWTH-REGULATING FACTOR 8, GRF8	4.5	3.2
A_84_P534390	AT4G37740	GROWTH-REGULATING FACTOR 2, GRF2	1.2	1.2
A_84_P225239	AT3G13960	GROWTH-REGULATING FACTOR 5, GRF5	2.9	1.7
A_84_P13635	AT3G18400	NAC DOMAIN CONTAINING PROTEIN 58, N	2	2.3
A_84_P18334	AT3G06490	MYB DOMAIN PROTEIN 108, MYB108	3.4	1.3
A_84_P23107	AT3G24310	MYB DOMAIN PROTEIN 305, MYB305	3.6	1
A_84_P18409	AT3G44290	NAC DOMAIN CONTAINING PROTEIN 60, N	1.2	1.1
A_84_P24157	AT3G61250	MYB DOMAIN PROTEIN 17, MYB17	1.5	2.2
A_84_P12832	AT4G02670	INDETERMINATE(ID)-DOMAIN12, IDD12	3.5	2.1
A_84_P557335	AT4G12750	homeodomain-like transcriptional regulator	1	1.3
A_84_P21437	AT4G31805	POLAR LOCALIZATION DURING ASYMMET	3.3	1.3
A_84_P16735	AT4G39070	B-BOX DOMAIN PROTEIN 20, BBX20	2.7	1.7
A_84_P17794	AT5G39610	NAC DOMAIN CONTAINING PROTEIN 6, NA	4.4	1.1
A_84_P13120	AT5G54230	MYB DOMAIN PROTEIN 49, MYB49	1.1	1.1
A_84_P11250	AT5G59570	BROTHER OF LUX ARRHYTHMO, BOA	1.7	1
A_84_P17613	AT4G22950	Agamous-like MADS-box protein AGL19	1.2	1.5
A_84_P18294	AT2G46990	Auxin-responsive protein IAA20	4.2	1.2
A_84_P16724	AT1G15050	Auxin-responsive protein IAA34	2.7	1.5
A_84_P142169	AT4G00180	Axial regulator YABBY 3	3.5	1.5
A_84_P516292	AT2G26580	Axial regulator YABBY 5	3.3	1.1
A_84_P562958	AT3G06220	B3 domain-containing protein At3g06220	2.3	1.4
A_84_P127211	AT3G18960	B3 domain-containing protein At3g18960	2.2	1.2
A_84_P546148	AT4G01580	B3 domain-containing protein At4g01580	1.8	1
A_84_P514216	AT3G46770	B3 domain-containing protein REM22	1.2	1.2
A_84_P549693	AT4G31690	B3 domain-containing protein REM9	1.2	1.4
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA2	3.2	1.1
A_84_P21090	AT1G75430	BEL1-like homeodomain protein 11	3.1	4.5
A_84_P17145	AT1G63030	Dehydration-responsive element-binding protein	2.6	1.3
A_84_P13741	AT3G57600	Dehydration-responsive element-binding protein	4.8	2.4
A_84_P23823	AT1G28360	Ethylene-responsive transcription factor 12	3	2.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P19239	AT1G44830	Ethylene-responsive transcription factor ERF014	2.1	1.6
A_84_P20976	AT1G19210	Ethylene-responsive transcription factor ERF017	3.5	1.4
A_84_P14249	AT1G36060	Ethylene-responsive transcription factor ERF055	2	1.4
A_84_P11046	AT4G34410	Ethylene-responsive transcription factor ERF109	3.1	1.1
A_84_P15503	AT3G22830	Heat stress transcription factor A-6b	2.3	1.6
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	2.1	1.9
A_84_P20736	AT5G66700	Homeobox-leucine zipper protein ATHB-53	3	1.9

A_84_P159675	AT1G64100	Pentatricopeptide repeat-containing protein At1g	1.1	1.2
A_84_P23291	AT4G23550	Probable WRKY transcription factor 29	2.6	1.4
A_84_P14772	AT4G22070	Probable WRKY transcription factor 31	1.5	1.3
A_84_P15672	AT4G04450	Probable WRKY transcription factor 42	1.4	1.4
A_84_P12393	AT1G79510	Probable WRKY transcription factor 61	1.8	2.2
A_84_P18695	AT5G15130	Probable WRKY transcription factor 72	1.2	1.2
A_84_P232979	AT5G06070	Probable transcriptional regulator RABBIT EA	1.1	1.1
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2, CUC2	1.6	1.2
A_84_P67324	AT2G25930	Protein EARLY FLOWERING 3, ELF3	1.1	1.4
A_84_P55930	AT5G61850	Protein LEAFY	2.4	1.2
A_84_P595141	AT1G30135	Protein TIFY 5A	3.3	1.2
A_84_P20316	AT1G48500	Protein TIFY 6A	1.9	1.1
A_84_P15135	AT1G30950	Protein UNUSUAL FLORAL ORGANS, UFO	2	2.2
A_84_P14721	AT1G14600	Putative Myb family transcription factor At1g14	2.3	1.7
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATH	2.1	1.9
A_84_P167633	AT3G15270	Squamosa promoter-binding-like protein 5	1.8	1.3
A_84_P275920	AT1G02065	Squamosa promoter-binding-like protein 8	2.9	2.6
A_84_P576326	AT5G53210	Transcription factor SPEECHLESS	5.3	1.7
A_84_P13946	AT5G08070	Transcription factor TCP17	2	1.4
A_84_P19487	AT4G18390	Transcription factor TCP2	3.8	1.7
A_84_P17124	AT1G53230	Transcription factor TCP3	1	1
A_84_P20712	AT5G60970	Transcription factor TCP5	3.6	2
A_84_P17553	AT4G01460	Transcription factor bHLH57	2.9	2.2
A_84_P16837	AT5G35770	Transcriptional regulator STERILE APETALA	1.8	1.6
A_84_P22812	AT1G74890	Two-component response regulator ARR15	2.3	1.4
A_84_P21088	AT2G40670	Two-component response regulator ARR16	3.6	2.3
A_84_P14680	AT3G56380	Two-component response regulator ARR17	2.7	1.4
A_84_P10395	AT1G19050	Two-component response regulator ARR7	2.4	1.5
A_84_P15984	AT5G61380	Two-component response regulator-like APRR1	1.3	1.5
A_84_P16455	AT3G18010	WUSCHEL-related homeobox 1	4.2	1.8
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2
A_84_P596337	AT3G11260	WUSCHEL-related homeobox 5	3.3	1.6
A_84_P526945	AT2G33880	WUSCHEL-related homeobox 9	2.6	2.3
A_84_P18069	AT1G49130	Zinc finger protein CONSTANS-LIKE 8	2.1	1.5
A_84_P13573	AT3G07650	Zinc finger protein CONSTANS-LIKE 9	2.1	1.6

Cluster 1-2: transcription			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P164953	AT1G49720	ABSCISIC ACID-INSENSITIVE 5-like protein	1.4	1.6
A_84_P17613	AT4G22950	Agamous-like MADS-box protein AGL19	1.2	1.5
A_84_P18294	AT2G46990	Auxin-responsive protein IAA20	4.2	1.2
A_84_P16724	AT1G15050	Auxin-responsive protein IAA34	2.7	1.5
A_84_P562958	AT3G06220	B3 domain-containing protein At3g06220	2.3	1.4
A_84_P127211	AT3G18960	B3 domain-containing protein At3g18960	2.2	1.2
A_84_P546148	AT4G01580	B3 domain-containing protein At4g01580	1.8	1
A_84_P514216	AT3G46770	B3 domain-containing protein REM22	1.2	1.2
A_84_P549693	AT4G31690	B3 domain-containing protein REM9	1.2	1.4
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA2	3.2	1.1
A_84_P21090	AT1G75430	BEL1-like homeodomain protein 11	3.1	4.5
A_84_P17145	AT1G63030	Dehydration-responsive element-binding protein	2.6	1.3
A_84_P13741	AT3G57600	Dehydration-responsive element-binding protein	4.8	2.4
A_84_P23823	AT1G28360	Ethylene-responsive transcription factor 12	3	2.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P19239	AT1G44830	Ethylene-responsive transcription factor ERF014	2.1	1.6
A_84_P20976	AT1G19210	Ethylene-responsive transcription factor ERF017	3.5	1.4
A_84_P14249	AT1G36060	Ethylene-responsive transcription factor ERF055	2	1.4
A_84_P11046	AT4G34410	Ethylene-responsive transcription factor ERF109	3.1	1.1
A_84_P15503	AT3G22830	Heat stress transcription factor A-6b	2.3	1.6
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	2.1	1.9
A_84_P20736	AT5G66700	Homeobox-leucine zipper protein ATHB-53	3	1.9
A_84_P23291	AT4G23550	Probable WRKY transcription factor 29	2.6	1.4
A_84_P14772	AT4G22070	Probable WRKY transcription factor 31	1.5	1.3
A_84_P15672	AT4G04450	Probable WRKY transcription factor 42	1.4	1.4
A_84_P12393	AT1G79510	Probable WRKY transcription factor 61	1.8	2.2
A_84_P18695	AT5G15130	Probable WRKY transcription factor 72	1.2	1.2
A_84_P232979	AT5G06070	Probable transcriptional regulator RABBIT EAR	1.1	1.1
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2	1.6	1.2
A_84_P67324	AT2G25930	Protein EARLY FLOWERING 3	1.1	1.4
A_84_P55930	AT5G61850	Protein LEAFY	2.4	1.2
A_84_P595141	AT1G30135	Protein TIFY 5A	3.3	1.2
A_84_P20316	AT1G48500	Protein TIFY 6A	1.9	1.1
A_84_P15135	AT1G30950	Protein UNUSUAL FLORAL ORGANS	2	2.2
A_84_P14721	AT1G14600	Putative Myb family transcription factor At1g146	2.3	1.7
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATHB	2.1	1.9
A_84_P167633	AT3G15270	Squamosa promoter-binding-like protein 5	1.8	1.3
A_84_P275920	AT1G02065	Squamosa promoter-binding-like protein 8	2.9	2.6
A_84_P576326	AT5G53210	Transcription factor SPEECHLESS	5.3	1.7
A_84_P13946	AT5G08070	Transcription factor TCP17	2	1.4
A_84_P19487	AT4G18390	Transcription factor TCP2	3.8	1.7
A_84_P17124	AT1G53230	Transcription factor TCP3	1	1

A_84_P20712	AT5G60970	Transcription factor TCP5	3.6	2
A_84_P17553	AT4G01460	Transcription factor bHLH57	2.9	2.2
A_84_P16837	AT5G35770	Transcriptional regulator STERILE APETALA	1.8	1.6
A_84_P22812	AT1G74890	Two-component response regulator ARR15	2.3	1.4
A_84_P21088	AT2G40670	Two-component response regulator ARR16	3.6	2.3
A_84_P14680	AT3G56380	Two-component response regulator ARR17	2.7	1.4
A_84_P10395	AT1G19050	Two-component response regulator ARR7	2.4	1.5
A_84_P15984	AT5G61380	Two-component response regulator-like APRR1	1.3	1.5
A_84_P16455	AT3G18010	WUSCHEL-related homeobox 1	4.2	1.8
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2
A_84_P596337	AT3G11260	WUSCHEL-related homeobox 5	3.3	1.6
A_84_P526945	AT2G33880	WUSCHEL-related homeobox 9	2.6	2.3

Cluster 1-3: regulation of transcription, DNA-dependent			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P164953	AT1G49720	ABSCISIC ACID-INSENSITIVE 5-like protein	1.4	1.6
A_84_P516094	AT1G26665	Mediator complex, subunit Med10	1	1
A_84_P21883	AT1G68320	MYB DOMAIN PROTEIN 62, MYB62	3.2	1.3
A_84_P125471	AT2G21235	Basic-leucine zipper (bZIP) transcription factor	1.9	1.6
A_84_P17322	AT2G32460	MYB DOMAIN PROTEIN 101, MYB101	1.4	2.2
A_84_P18334	AT3G06490	MYB DOMAIN PROTEIN 108, MYB108	3.4	1.3
A_84_P23107	AT3G24310	MYB DOMAIN PROTEIN 305, MYB305	3.6	1
A_84_P24157	AT3G61250	MYB DOMAIN PROTEIN 17, MYB17	1.5	2.2
A_84_P557335	AT4G12750	homeodomain-like transcriptional regulator	1	1.3
A_84_P21437	AT4G31805	POLAR LOCALIZATION DURING ASYMME	3.3	1.3
A_84_P17613	AT4G22950	Agamous-like MADS-box protein AGL19	1.2	1.5
A_84_P562958	AT3G06220	B3 domain-containing protein At3g06220	2.3	1.4
A_84_P127211	AT3G18960	B3 domain-containing protein At3g18960	2.2	1.2
A_84_P546148	AT4G01580	B3 domain-containing protein At4g01580	1.8	1
A_84_P514216	AT3G46770	B3 domain-containing protein REM22	1.2	1.2
A_84_P549693	AT4G31690	B3 domain-containing protein REM9	1.2	1.4
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA	3.2	1.1
A_84_P21090	AT1G75430	BEL1-like homeodomain protein 11	3.1	4.5
A_84_P17145	AT1G63030	Dehydration-responsive element-binding protein	2.6	1.3
A_84_P13741	AT3G57600	Dehydration-responsive element-binding protein	4.8	2.4
A_84_P23823	AT1G28360	Ethylene-responsive transcription factor 12	3	2.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P19239	AT1G44830	Ethylene-responsive transcription factor ERF01	2.1	1.6
A_84_P20976	AT1G19210	Ethylene-responsive transcription factor ERF01	3.5	1.4
A_84_P14249	AT1G36060	Ethylene-responsive transcription factor ERF05	2	1.4
A_84_P11046	AT4G34410	Ethylene-responsive transcription factor ERF10	3.1	1.1
A_84_P15503	AT3G22830	Heat stress transcription factor A-6b	2.3	1.6
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	2.1	1.9
A_84_P20736	AT5G66700	Homeobox-leucine zipper protein ATHB-53	3	1.9
A_84_P23291	AT4G23550	Probable WRKY transcription factor 29	2.6	1.4
A_84_P14772	AT4G22070	Probable WRKY transcription factor 31	1.5	1.3
A_84_P15672	AT4G04450	Probable WRKY transcription factor 42	1.4	1.4
A_84_P12393	AT1G79510	Probable WRKY transcription factor 61	1.8	2.2
A_84_P18695	AT5G15130	Probable WRKY transcription factor 72	1.2	1.2
A_84_P15135	AT1G30950	Protein UNUSUAL FLORAL ORGANS	2	2.2
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATH	2.1	1.9
A_84_P22812	AT1G74890	Two-component response regulator ARR15	2.3	1.4
A_84_P21088	AT2G40670	Two-component response regulator ARR16	3.6	2.3
A_84_P14680	AT3G56380	Two-component response regulator ARR17	2.7	1.4
A_84_P10395	AT1G19050	Two-component response regulator ARR7	2.4	1.5
A_84_P15984	AT5G61380	Two-component response regulator-like APRR1	1.3	1.5
A_84_P16455	AT3G18010	WUSCHEL-related homeobox 1	4.2	1.8
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2
A_84_P596337	AT3G11260	WUSCHEL-related homeobox 5	3.3	1.6
A_84_P526945	AT2G33880	WUSCHEL-related homeobox 9	2.6	2.3

Cluster 1-4: regulation of RNA metabolic process			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P164953	AT1G49720	ABSCISIC ACID-INSENSITIVE 5-like protein	1.4	1.6
A_84_P516094	AT1G26665	Mediator complex, subunit Med10	1	1
A_84_P21883	AT1G68320	MYB DOMAIN PROTEIN 62, MYB62	3.2	1.3
A_84_P125471	AT2G21235	Basic-leucine zipper (bZIP) transcription factor	1.9	1.6
A_84_P17322	AT2G32460	MYB DOMAIN PROTEIN 101, MYB101	1.4	2.2
A_84_P18334	AT3G06490	MYB DOMAIN PROTEIN 108, MYB108	3.4	1.3
A_84_P23107	AT3G24310	MYB DOMAIN PROTEIN 305, MYB305	3.6	1
A_84_P24157	AT3G61250	MYB DOMAIN PROTEIN 17, MYB17	1.5	2.2
A_84_P557335	AT4G12750	homeodomain-like transcriptional regulator	1	1.3
A_84_P21437	AT4G31805	POLAR LOCALIZATION DURING ASYMMET	3.3	1.3
A_84_P17613	AT4G22950	Agamous-like MADS-box protein AGL19	1.2	1.5
A_84_P562958	AT3G06220	B3 domain-containing protein At3g06220	2.3	1.4
A_84_P127211	AT3G18960	B3 domain-containing protein At3g18960	2.2	1.2
A_84_P546148	AT4G01580	B3 domain-containing protein At4g01580	1.8	1
A_84_P514216	AT3G46770	B3 domain-containing protein REM22	1.2	1.2
A_84_P549693	AT4G31690	B3 domain-containing protein REM9	1.2	1.4
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA2	3.2	1.1
A_84_P21090	AT1G75430	BEL1-like homeodomain protein 11	3.1	4.5
A_84_P17145	AT1G63030	Dehydration-responsive element-binding protein	2.6	1.3
A_84_P13741	AT3G57600	Dehydration-responsive element-binding protein	4.8	2.4
A_84_P23823	AT1G28360	Ethylene-responsive transcription factor 12	3	2.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P19239	AT1G44830	Ethylene-responsive transcription factor ERF014	2.1	1.6
A_84_P20976	AT1G19210	Ethylene-responsive transcription factor ERF017	3.5	1.4
A_84_P14249	AT1G36060	Ethylene-responsive transcription factor ERF055	2	1.4
A_84_P11046	AT4G34410	Ethylene-responsive transcription factor ERF109	3.1	1.1
A_84_P15503	AT3G22830	Heat stress transcription factor A-6b	2.3	1.6
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	2.1	1.9
A_84_P20736	AT5G66700	Homeobox-leucine zipper protein ATHB-53	3	1.9
A_84_P23291	AT4G23550	Probable WRKY transcription factor 29	2.6	1.4
A_84_P14772	AT4G22070	Probable WRKY transcription factor 31	1.5	1.3
A_84_P15672	AT4G04450	Probable WRKY transcription factor 42	1.4	1.4
A_84_P12393	AT1G79510	Probable WRKY transcription factor 61	1.8	2.2
A_84_P18695	AT5G15130	Probable WRKY transcription factor 72	1.2	1.2
A_84_P15135	AT1G30950	Protein UNUSUAL FLORAL ORGANS	2	2.2
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATHB	2.1	1.9
A_84_P22812	AT1G74890	Two-component response regulator ARR15	2.3	1.4
A_84_P21088	AT2G40670	Two-component response regulator ARR16	3.6	2.3
A_84_P14680	AT3G56380	Two-component response regulator ARR17	2.7	1.4
A_84_P10395	AT1G19050	Two-component response regulator ARR7	2.4	1.5
A_84_P15984	AT5G61380	Two-component response regulator-like APRR1	1.3	1.5
A_84_P16455	AT3G18010	WUSCHEL-related homeobox 1	4.2	1.8
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2
A_84_P596337	AT3G11260	WUSCHEL-related homeobox 5	3.3	1.6
A_84_P526945	AT2G33880	WUSCHEL-related homeobox 9	2.6	2.3

Cluster 2-1: shoot development			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P265480	AT2G36400	GROWTH-REGULATING FACTOR 3,GRF3	1.7	2
A_84_P225239	AT3G13960	GROWTH-REGULATING FACTOR 5,GRF5	2.9	1.7
A_84_P565344	AT4G24150	GROWTH-REGULATING FACTOR 8, GRF8	4.5	3.2
A_84_P534390	AT4G37740	GROWTH-REGULATING FACTOR 2, GRF2	1.2	1.2
A_84_P16778	AT5G07180	ERECTA-LIKE 2, ERL2	2.1	1.5
A_84_P238673	AT5G28640	GRF1-INTERACTING FACTOR 1, GIF1, AN3	1.6	1.8
A_84_P23556	AT5G62230	ERECTA-LIKE 1, ERL1	3.3	1.9
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA2	3.2	1.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2	1.6	1.2
A_84_P10494	AT1G80080	Protein TOO MANY MOUTHS	2.8	1.1
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATHB	2.1	1.9
A_84_P13946	AT5G08070	Transcription factor TCP17	2	1.4
A_84_P17124	AT1G53230	Transcription factor TCP3	1	1
A_84_P20712	AT5G60970	Transcription factor TCP5	3.6	2
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2

Cluster 3-1: reproductive structure development			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P17628	AT4G26200	1-aminocyclopropane-1-carboxylate synthase 7,	3.4	2.5
A_84_P11512	AT1G13400	JAGGED-LIKE, JGL	3.2	1.9
A_84_P18193	AT2G35300	LATE EMBRYOGENESIS ABUNDANT 18, LE	1.3	1.2
A_84_P211628	AT2G40080	EARLY FLOWERING 4, ELF4	2.1	1.3
A_84_P15528	AT3G20440	EMBRYO DEFECTIVE 2729, EMB2729	1.3	1
A_84_P12945	AT4G36260	SHI RELATED SEQUENCE 2, SRS2	2.9	2.2
A_84_P16778	AT5G07180	ERECTA-LIKE 2, ERL2	2.1	1.5
A_84_P16865	AT5G44310	Late embryogenesis abundant protein (LEA) fam	2.7	1.8
A_84_P23556	AT5G62230	ERECTA-LIKE 1, ERL1	3.3	1.9
A_84_P264030	AT5G63420	EMBRYO DEFECTIVE 2746, EMB2746	1.2	1.2
A_84_P224829	AT2G45190	Axial regulator YABBY 1	3.3	1.8
A_84_P142169	AT4G00180	Axial regulator YABBY 3	3.5	1.5
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA2	3.2	1.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P15163	AT1G65620	LOB domain-containing protein 6	1.5	2
A_84_P22432	AT5G01040	Laccase-8	1.8	1.1
A_84_P17798	AT5G40420	Oleosin 21.2 kDa	1.4	2.3
A_84_P232979	AT5G06070	Probable transcriptional regulator RABBIT EAR	1.1	1.1
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2	1.6	1.2
A_84_P67324	AT2G25930	Protein EARLY FLOWERING 3	1.1	1.4
A_84_P55930	AT5G61850	Protein LEAFY	2.4	1.2
A_84_P15135	AT1G30950	Protein UNUSUAL FLORAL ORGANS	2	2.2
A_84_P275920	AT1G02065	Squamosa promoter-binding-like protein 8	2.9	2.6
A_84_P16837	AT5G35770	Transcriptional regulator STERILE APETALA	1.8	1.6
A_84_P21972	AT1G46480	WUSCHEL-related homeobox 3	2.3	2.2
A_84_P526945	AT2G33880	WUSCHEL-related homeobox 9	2.6	2.3

Cluster 4-1: regulation of development, heterochronic			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P17613	AT4G22950	Agamous-like MADS-box protein AGL19	1.2	1.5
A_84_P17145	AT1G63030	Dehydration-responsive element-binding protein	2.6	1.3
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2	1.6	1.2
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATHB	2.1	1.9
A_84_P13946	AT5G08070	Transcription factor TCP17	2	1.4
A_84_P17124	AT1G53230	Transcription factor TCP3	1	1
A_84_P20712	AT5G60970	Transcription factor TCP5	3.6	2

Cluster 5-1: regulation of development, heterochronic			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P17613	AT4G22950	Agamous-like MADS-box protein AGL19	1.2	1.5
A_84_P17145	AT1G63030	Dehydration-responsive element-binding protein	2.6	1.3
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2	1.6	1.2
A_84_P15821	AT5G03790	Putative homeobox-leucine zipper protein ATHB	2.1	1.9
A_84_P13946	AT5G08070	Transcription factor TCP17	2	1.4
A_84_P17124	AT1G53230	Transcription factor TCP3	1	1
A_84_P20712	AT5G60970	Transcription factor TCP5	3.6	2

Cluster 6-1: two-component signal transduction system			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P23823	AT1G53910	Ethylene-responsive transcription factor 12	3	2.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P19239	AT1G44830	Ethylene-responsive transcription factor ERF014	2.1	1.6
A_84_P20976	AT1G19210	Ethylene-responsive transcription factor ERF017	3.5	1.4
A_84_P14249	AT1G36060	Ethylene-responsive transcription factor ERF055	2	1.4
A_84_P11046	AT4G34410	Ethylene-responsive transcription factor ERF109	3.1	1.1
A_84_P22812	AT1G74890	Two-component response regulator ARR15	2.3	1.4
A_84_P21088	AT2G40670	Two-component response regulator ARR16	3.6	2.3
A_84_P14680	AT3G56380	Two-component response regulator ARR17	2.7	1.4
A_84_P10395	AT1G19050	Two-component response regulator ARR7	2.4	1.5
A_84_P15984	AT5G61380	Two-component response regulator-like APRR1	1.3	1.5

Cluster 7-1: response to organic substance			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P164953	AT3G19290	ABSCISIC ACID-INSENSITIVE 5-like protein	1.4	1.6
A_84_P12371	AT1G16510	SMALL AUXIN UPREGULATED 41, SAUR41	1.6	1.3
A_84_P17184	AT1G43040	SMALL AUXIN UPREGULATED RNA 58, SA	1.7	1.2
A_84_P21883	AT1G68320	MYB DOMAIN PROTEIN 62, MYB62	3.2	1.3
A_84_P13287	AT1G75580	SMALL AUXIN UPREGULATED RNA 51, SA	2.4	1.5
A_84_P17322	AT2G32460	MYB DOMAIN PROTEIN 101, MYB101	1.4	2.2
A_84_P12640	AT3G01420	ALPHA-DIOXYGENASE 1, DIOX1	2.5	1.5
A_84_P18334	AT3G06490	MYB DOMAIN PROTEIN 108, MYB108	3.4	1.3
A_84_P156125	AT3G61190	BON ASSOCIATION PROTEIN 1, BAP1	1.5	1.1
A_84_P24157	AT3G61250	MYB DOMAIN PROTEIN 17, MYB17	1.5	2.2
A_84_P14854	AT4G15910	DROUGHT-INDUCED 21, DI21	1	1
A_84_P12029	AT4G37220	Cold acclimation protein WCOR413 family	1.2	1.7
A_84_P16735	AT4G39070	B-BOX DOMAIN PROTEIN 20, BBX20	2.7	1.7
A_84_P231259	AT5G12330	LATERAL ROOT PRIMORDIUM 1, LRP1	1.8	1.7
A_84_P80329	AT5G50700	HYDROXYSTEROID DEHYDROGENASE 1,	4.6	2.9
A_84_P527444	AT5G50760	SMALL AUXIN UPREGULATED RNA 55, SA	1.3	1.5
A_84_P13120	AT5G54230	MYB DOMAIN PROTEIN 49, MYB49	1.1	1.1
A_84_P18294	AT2G46990	Auxin-responsive protein IAA20	4.2	1.2
A_84_P16724	AT1G15050	Auxin-responsive protein IAA34	2.7	1.5
A_84_P23823	AT1G53910	Ethylene-responsive transcription factor 12	3	2.1
A_84_P10999	AT4G23750	Ethylene-responsive transcription factor CRF2	1.4	1.1
A_84_P19239	AT1G44830	Ethylene-responsive transcription factor ERF01	2.1	1.6
A_84_P20976	AT1G19210	Ethylene-responsive transcription factor ERF01	3.5	1.4
A_84_P14249	AT1G36060	Ethylene-responsive transcription factor ERF05	2	1.4
A_84_P11046	AT4G34410	Ethylene-responsive transcription factor ERF10	3.1	1.1
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	2.1	1.9
A_84_P20736	AT5G66700	Homeobox-leucine zipper protein ATHB-53	3	1.9
A_84_P564716	AT1G03850	Monothiol glutaredoxin-S13	2.1	1.3
A_84_P23291	AT4G23550	Probable WRKY transcription factor 29	2.6	1.4
A_84_P67324	AT2G25930	Protein EARLY FLOWERING 3	1.1	1.4
A_84_P55930	AT5G61850	Protein LEAFY	2.4	1.2
A_84_P10494	AT1G80080	Protein TOO MANY MOUTHS	2.8	1.1
A_84_P22812	AT1G74890	Two-component response regulator ARR15	2.3	1.4
A_84_P21088	AT2G40670	Two-component response regulator ARR16	3.6	2.3
A_84_P14680	AT3G56380	Two-component response regulator ARR17	2.7	1.4
A_84_P10395	AT1G19050	Two-component response regulator ARR7	2.4	1.5
A_84_P596337	AT3G11260	WUSCHEL-related homeobox 5	3.3	1.6

Cluster 8-1: regionalization			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P22784	AT1G14760	KNOX ARABIDOPSIS THALIANA MEINOX,	2.2	1.5
A_84_P12945	AT4G36260	SHI RELATED SEQUENCE 2, SRS2	2.9	2.2
A_84_P18294	AT2G46990	Auxin-responsive protein IAA20	4.2	1.2
A_84_P224829	AT2G45190	Axial regulator YABBY 1	3.3	1.8
A_84_P15163	AT1G65620	LOB domain-containing protein 6	1.5	2
A_84_P22576	AT5G53950	Protein CUP-SHAPED COTYLEDON 2	1.6	1.2
A_84_P603904	AT5G63090	Protein LATERAL ORGAN BOUNDARIES	1.6	2
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2

Cluster 9-1: flower development			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P11512	AT1G13400	JAGGED-LIKE, JGL	3.2	1.9
A_84_P12945	AT4G36260	SHI RELATED SEQUENCE 2, SRS2	2.9	2.2
A_84_P16778	AT5G07180	ERECTA-LIKE 2, ERL2	2.1	1.5
A_84_P23556	AT5G62230	ERECTA-LIKE 1, ERL1	3.3	1.9
A_84_P23970	AT2G46870	B3 domain-containing transcription factor NGA1	2.2	1.3
A_84_P20376	AT3G61970	B3 domain-containing transcription factor NGA2	3.2	1.1
A_84_P15163	AT1G65620	LOB domain-containing protein 6	1.5	2
A_84_P232979	AT5G06070	Probable transcriptional regulator RABBIT EAR	1.1	1.1
A_84_P55930	AT5G61850	Protein LEAFY	2.4	1.2
A_84_P15135	AT1G30950	Protein UNUSUAL FLORAL ORGANS	2	2.2
A_84_P275920	AT1G02065	Squamosa promoter-binding-like protein 8	2.9	2.6
A_84_P16837	AT5G35770	Transcriptional regulator STERILE APETALA	1.8	1.6
A_84_P21972	AT2G28610	WUSCHEL-related homeobox 3	2.3	2.2

Cluster 10-1: stomatal complex development			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio)	Log (Ratio)
A_84_P16778	AT5G07180	ERECTA-LIKE 2, ERL2	2.1	1.5
A_84_P23556	AT5G62230	ERECTA-LIKE 1, ERL1	3.3	1.9
A_84_P10494	AT1G80080	Protein TOO MANY MOUTHS	2.8	1.1
A_84_P576326	AT5G53210	Transcription factor SPEECHLESS	5.3	1.7

Supplemental Table 5. Probe values for up-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (upper aerial parts)

Probe Name	Col1	*ztl3*	Log Ratio	Col2	*ztl105*	Log Ratio
A_84_P17470	11.1	65.4	2.6	9.4	21.7	1.2
A_84_P765100	446.9	1463.5	1.7	429.7	1437.5	1.7
A_84_P751278	7.7	29	1.9	11.5	27.6	1.3
A_84_P11288	459.8	936.3	1	455.1	1293.9	1.5
A_84_P56650	2721.6	8770.4	1.7	3597	8114.3	1.2
A_84_P787864	179.8	440.5	1.3	187.3	401.7	1.1
A_84_P22146	38.8	233.7	2.6	45.2	121.8	1.4
A_84_P560172	13.7	41.7	1.6	13.3	37.1	1.5
A_84_P841191	2.9	8.2	1.5	3.5	7.9	1.2
A_84_P813024	28.8	70.4	1.3	54.2	126.6	1.2
A_84_P21908	17.3	73.1	2.1	17.1	70.5	2
A_84_P753493	14.4	34.9	1.3	15.6	71	2.2
A_84_P795807	22.4	215.9	3.3	31.9	74.7	1.2
A_84_P542377	9	46.1	2.4	3.7	18.9	2.3
A_84_P548849	26.9	274.8	3.4	37.7	82.1	1.1
A_84_P800029	12.5	26.9	1.1	12.9	38	1.6
A_84_P796276	14.7	44.7	1.6	12	69.6	2.5
A_84_P18367	105.8	232.7	1.1	131.4	10666.8	6.3
A_84_P755537	5.2	10.8	1.1	6.2	13.2	1.1
A_84_P784525	560.9	1627	1.5	502.3	1711.9	1.8
A_84_P838876	19	98	2.4	29.7	66.7	1.2
A_84_P800216	3.3	11	1.7	3.9	7.8	1
A_84_P12761	3.4	7.9	1.2	5.1	12.9	1.3
A_84_P16506	4219.3	11180.9	1.4	4233.9	9554.4	1.2
A_84_P795946	52.2	224.2	2.1	57.2	166.3	1.5
A_84_P18792	148.6	1437.2	3.3	192.3	1287.8	2.7
A_84_P10039	7891	33644.8	2.1	10769.5	22612.3	1.1
A_84_P823929	1780.4	8861.7	2.3	2633.6	7536.7	1.5
A_84_P514511	2.9	8.8	1.6	3.1	16.7	2.4
A_84_P222669	40023.9	173393.1	2.1	38782.4	84036.6	1.1
A_84_P714286	99.5	365	1.9	114	313.9	1.5
A_84_P572099	4.1	9.8	1.2	3	30.6	3.4
A_84_P17184	2.9	16.5	2.5	4.5	21.5	2.3
A_84_P16735	1039.9	4617.5	2.2	1155.1	3506.2	1.6
A_84_P762490	2.9	13.1	2.2	3	6.2	1
A_84_P560934	26.2	53.7	1	33.5	76.3	1.2
A_84_P804259	846.2	4158.2	2.3	786	1679.3	1.1
A_84_P812535	147.1	1944.7	3.7	109.2	394.1	1.9
A_84_P532174	8.9	19.1	1.1	15.2	44.2	1.5

A_84_P249255	3.7	11.4	1.6	6.2	15.5	1.3
A_84_P519326	3.5	10.8	1.6	3.5	11.5	1.7
A_84_P22521	154.9	515.9	1.7	86.5	190.2	1.1
A_84_P756720	2.8	6.2	1.1	2.8	6	1.1
A_84_P524292	551.5	1254.3	1.2	558.4	1368.6	1.3
A_84_P717727	137.5	295	1.1	217.4	436.8	1
A_84_P758461	3	12.6	2.1	3	7.7	1.4
A_84_P232159	88.3	212.7	1.3	85.7	205.6	1.3
A_84_P832802	66.2	280.2	2.1	39.2	106.4	1.4
A_84_P752023	14.1	36.3	1.4	10.2	29.5	1.5
A_84_P12604	5.7	12.6	1.2	7.8	16.6	1.1
A_84_P11140	96.6	1802.6	4.2	206.6	1503.9	2.9
A_84_P21126	1295.4	4039.3	1.6	1404.5	3069.9	1.1
A_84_P805516	300.2	1064.1	1.8	325.6	893.2	1.5
A_84_P12863	51.9	431.3	3.1	41.8	111.7	1.4
A_84_P812380	2002.9	6889.6	1.8	2615.7	6250	1.3
A_84_P848499	228.1	2170.5	3.3	241.4	2211.2	3.2
A_84_P511454	415.2	3974.1	3.3	244.8	631.1	1.4
A_84_P611100	14.6	47.8	1.7	22.9	47.8	1.1
A_84_P15944	111.5	420.5	1.9	107.1	265.7	1.3
A_84_P15976	3.1	12.6	2	3.1	6.3	1
A_84_P789874	3.1	20.5	2.7	3.1	10.9	1.8
A_84_P17963	931.5	5915.4	2.7	1560.2	5852.1	1.9
A_84_P700126	4	16.3	2	4.5	17.7	2
A_84_P510789	2.8	6.8	1.3	4	10.1	1.3
A_84_P20714	4743.2	11271.3	1.2	5722.7	14648	1.4
A_84_P21379	72	210.9	1.6	72.2	148.8	1
A_84_P819058	30.9	66.8	1.1	34.8	70.5	1
A_84_P839037	25.7	54.4	1.1	29.7	64.2	1.1
A_84_P793237	36.9	78.7	1.1	32.4	66.2	1
A_84_P11250	1709.4	4169.7	1.3	1672.8	4390.1	1.4
A_84_P17322	13	32.4	1.3	6.5	17.7	1.4
A_84_P21267	34.4	165.8	2.3	49.9	129.6	1.4
A_84_P235603	138.9	554.5	2	131.6	332.6	1.3
A_84_P23228	26.2	290.8	3.5	38.2	143	1.9
A_84_P853428	692.6	3195.8	2.2	595.8	1209.6	1
A_84_P20959	1122.3	2457.1	1.1	1889.1	4123	1.1
A_84_P17442	109.1	286.3	1.4	107.6	218.4	1
A_84_P753154	17.5	104	2.6	22.4	90.8	2
A_84_P761276	54.8	464	3.1	41.9	104.4	1.3
A_84_P577620	40.1	227	2.5	48	115	1.3
A_84_P606215	183.4	532.7	1.5	234.2	507	1.1
A_84_P22847	114.8	1744.7	3.9	127.9	409.3	1.7
A_84_P295664	2.7	10.2	1.9	2.8	7.5	1.4
A_84_P828342	287.8	1323.1	2.2	231	520.2	1.2

A_84_P198904	2.7	15.4	2.5	5.9	13.9	1.3
A_84_P573235	3	6.3	1.1	3.7	24.8	2.7
A_84_P20644	83.4	234.9	1.5	133.6	376.5	1.5
A_84_P791775	2.8	9.6	1.8	4.9	18.2	1.9
A_84_P791097	143	978.2	2.8	177.1	381.8	1.1
A_84_P768725	33.8	225.7	2.7	69.3	233.1	1.8
A_84_P805550	6.1	13.5	1.1	8.8	31.7	1.8
A_84_P557668	7.2	24.8	1.8	11.2	27.4	1.3
A_84_P796812	2.8	5.6	1	2.8	11.9	2.1
A_84_P22203	3.7	27.1	2.9	5.6	26.5	2.2
A_84_P20706	350.4	932.8	1.4	423.2	864.2	1
A_84_P549947	207.9	843.4	2	370	968.3	1.4
A_84_P823098	754	2575.7	1.8	899.7	2108.5	1.2
A_84_P96076	130.6	303.3	1.2	161.9	445.7	1.5
A_84_P537212	17.6	82.5	2.2	9.8	37	1.9
A_84_P22664	81.7	432	2.4	74.4	230.6	1.6
A_84_P860859	15.1	32.3	1.1	13.7	27.7	1
A_84_P761328	11.6	62.6	2.4	6.8	28.3	2.1
A_84_P289374	100.9	441.2	2.1	119	238.5	1
A_84_P244235	1996.1	5037.6	1.3	1881.3	6129.4	1.7
A_84_P833279	3.2	9	1.5	2.6	8.7	1.7
A_84_P18526	17.3	38.3	1.1	2.8	8.8	1.6
A_84_P18989	861.7	2899.9	1.8	832.8	3033.6	1.9
A_84_P792813	4.8	26.7	2.5	4.6	10.1	1.1
A_84_P230039	17.8	88.1	2.3	19	39.9	1.1
A_84_P16226	1967.6	7531	1.9	2254.6	4711.8	1.1
A_84_P16027	53.6	250.1	2.2	42	330.2	3
A_84_P828455	10.9	140.3	3.7	3.5	34.5	3.3
A_84_P262840	84.6	215.8	1.4	89.3	188.6	1.1
A_84_P22924	180.1	1242.1	2.8	244	555.3	1.2
A_84_P10163	26.5	64.5	1.3	51	131.6	1.4
A_84_P23038	64.2	165.3	1.4	84.8	197.5	1.2
A_84_P12398	27	109	2	51.5	106.3	1
A_84_P702630	5.8	12.9	1.1	5.9	14.3	1.3
A_84_P55910	84.1	195	1.2	76.4	207.5	1.4
A_84_P23912	125.8	410.9	1.7	133.8	309.5	1.2
A_84_P756592	10.4	82.3	3	7.2	17.3	1.3
A_84_P814887	801.7	1928.1	1.3	1542.5	3398.1	1.1
A_84_P833585	8.5	40.6	2.3	12.8	26.7	1.1
A_84_P564716	11.7	69.4	2.6	15.2	52.2	1.8
A_84_P15691	186.5	898.4	2.3	309.1	1045.8	1.8
A_84_P756551	12.1	58.8	2.3	14.8	34.6	1.2
A_84_P792258	2.6	144	5.8	5.2	41.4	3
A_84_P190534	63.4	292.2	2.2	55.4	128.3	1.2
A_84_P11223	15.1	33.2	1.1	8.7	26.7	1.6

A_84_P754101	4.3	10.1	1.2	4	10.3	1.4
A_84_P22934	5	12.1	1.3	4.2	13.6	1.7
A_84_P21574	11.4	25.1	1.1	10.9	63.7	2.5
A_84_P770206	10.6	27.7	1.4	7.6	18.9	1.3
A_84_P506633	38	139.3	1.9	51.7	113.3	1.1
A_84_P787728	4.9	86.5	4.2	9.5	38.8	2
A_84_P769325	23.8	50.1	1.1	49.5	111.1	1.2
A_84_P860044	401.2	1115.2	1.5	140.2	386.4	1.5
A_84_P798791	20.4	47.5	1.2	23.4	49.2	1.1
A_84_P10863	1863.9	5519.4	1.6	1545.9	3626.9	1.2
A_84_P762727	6	88.9	3.9	9.6	33.9	1.8
A_84_P10624	1361.7	8334.7	2.6	2046.9	5177.1	1.3
A_84_P20938	175.7	1167.1	2.7	107.6	303.1	1.5
A_84_P18698	2.8	9	1.7	2.7	6.3	1.2
A_84_P543246	935.9	1939.4	1.1	1063.6	2162.1	1
A_84_P791958	14.3	115.5	3	20.1	50.9	1.3
A_84_P861779	15.9	34.2	1.1	20.4	42.5	1.1
A_84_P790164	1153.6	3802.4	1.7	1699.9	4088.1	1.3
A_84_P580265	115.9	253.5	1.1	73.8	226.8	1.6
A_84_P14315	51	309.4	2.6	54.6	160.7	1.6
A_84_P11109	2.5	7.7	1.6	10.8	25.1	1.2
A_84_P559543	16.5	102.3	2.6	24.9	80.5	1.7
A_84_P753853	6.2	18.3	1.6	17.6	35.8	1
A_84_P750392	75.4	437.8	2.5	90.1	299	1.7
A_84_P257110	6	13.2	1.1	2.4	6	1.3
A_84_P21010	12.5	118.4	3.2	12.3	142.3	3.5
A_84_P248115	1305.8	3655.3	1.5	1294.7	3569.7	1.5
A_84_P231139	14.1	59.2	2.1	9.1	27.7	1.6
A_84_P762597	2.4	9.4	2	7.7	19.3	1.3
A_84_P80329	37.5	78.9	1.1	30.8	92.6	1.6
A_84_P837245	3.5	13.2	1.9	2.4	5.4	1.2
A_84_P19801	3.5	18.2	2.4	3.6	9.6	1.4
A_84_P13415	24.2	71.6	1.6	26.8	113.1	2.1
A_84_P753826	2.6	12	2.2	2.7	25.9	3.3
A_84_P61310	4.5	21	2.2	2.6	40.3	3.9
A_84_P19131	391.2	900.8	1.2	305.3	955.3	1.6
A_84_P11816	47.2	265.8	2.5	122.3	387.8	1.7
A_84_P13311	1269.8	4681.1	1.9	1401.3	4737.3	1.8
A_84_P839331	2.5	32.3	3.7	7.3	15.1	1.1
A_84_P22830	2.4	7.6	1.7	2.7	14.2	2.4
A_84_P799871	6	136.3	4.5	2.5	5.2	1.1
A_84_P788151	56.5	212.8	1.9	74.6	175.8	1.2
A_84_P22612	20	68.3	1.8	33.3	139.1	2.1
A_84_P596827	19.5	89.5	2.2	31.5	67	1.1
A_84_P572181	2.5	7.5	1.6	5	12.1	1.3

A_84_P211958	4429.8	25088.5	2.5	1769.4	3889.5	1.1
A_84_P751391	103.1	1410.3	3.8	117.4	236.6	1
A_84_P174151	120.2	422.4	1.8	109.5	279.2	1.3
A_84_P839743	9.9	57.1	2.5	8.1	33.4	2
A_84_P15284	75.3	296.8	2	67.1	148.8	1.1
A_84_P536494	3.6	15.6	2.1	2.9	13.8	2.2
A_84_P791037	2.4	7.8	1.7	2.4	8.5	1.8
A_84_P765147	5	10.8	1.1	4.7	9.8	1.1
A_84_P12389	396.7	1293.9	1.7	379	915.4	1.3
A_84_P19768	115.6	325.7	1.5	124.4	341.5	1.5
A_84_P10838	21.3	50.7	1.3	22.4	64.9	1.5
A_84_P849804	25	122.6	2.3	55.5	154.1	1.5
A_84_P191734	3.1	8.4	1.4	2.4	8.6	1.9
A_84_P22432	130.9	570.6	2.1	182.5	626.6	1.8
A_84_P794692	28.5	132.6	2.2	30.9	81	1.4
A_84_P217968	2.5	7.3	1.6	2.5	5.7	1.2
A_84_P513790	2.4	7.3	1.6	2.5	6.4	1.3
A_84_P752371	2.5	78.3	5	2.5	23.2	3.2
A_84_P571762	3.5	15.1	2.1	4.7	10.5	1.2
A_84_P760264	2.4	4.7	1	2.4	6	1.4
A_84_P15946	428.8	1061	1.3	486.2	1085.8	1.2
A_84_P10275	2.4	11.6	2.3	2.4	5.2	1.1
A_84_P800077	2.5	9.2	1.9	2.5	7.9	1.6
A_84_P795102	2.4	6.6	1.5	2.8	11	1.9
A_84_P793397	9	46.4	2.4	7.5	17.1	1.2
A_84_P243155	5.4	15.9	1.6	10.7	131.4	3.6
A_84_P11438	558.5	1471.2	1.4	568.7	1268.5	1.2
A_84_P848243	20.8	44	1.1	20.2	45.3	1.2
A_84_P843355	17.4	37.9	1.1	24.9	66.8	1.4
A_84_P13706	150.4	621.4	2	287.3	626.9	1.1
A_84_P860427	14.1	57	2	9.8	30.8	1.6
A_84_P560739	4.4	9.8	1.1	3.3	7.7	1.2
A_84_P14061	2.5	10.4	2	2.5	6.2	1.3
A_84_P752155	2.4	7	1.5	7.1	14.3	1
A_84_P823027	10.5	131.6	3.6	4.3	9.9	1.2
A_84_P752711	2.4	39.2	4	2.4	5	1.1
A_84_P590571	14.1	34.6	1.3	10.7	25.9	1.3
A_84_P756221	4.6	11.5	1.3	3.2	9.1	1.5
A_84_P610683	4.5	9.6	1.1	3.2	7.6	1.2
A_84_P20176	1098.4	5392	2.3	1015.3	2073.3	1
A_84_P754341	310.3	846.7	1.4	364.1	795.2	1.1
A_84_P787293	2.4	12.8	2.4	2.9	16.5	2.5
A_84_P10497	9.4	38.7	2	7.9	24.5	1.6
A_84_P799083	2.4	60.9	4.7	2.8	18.7	2.7
A_84_P752706	2.5	40.8	4.1	5	63.6	3.7

A_84_P831544	4.8	13.2	1.5	5.2	10.5	1
A_84_P21550	1279.7	4285.7	1.7	1579.8	4211.5	1.4
A_84_P829667	19.8	44	1.1	24	62.4	1.4
A_84_P599972	4	19.1	2.2	2.6	10.7	2.1
A_84_P22809	11.2	22.6	1	10.2	34.3	1.8
A_84_P511795	11.3	73.5	2.7	14	31.9	1.2
A_84_P805655	258.2	1204.2	2.2	476.1	1372.7	1.5
A_84_P14218	142.9	1200.1	3.1	212.8	569.9	1.4
A_84_P13477	84.7	384.8	2.2	66.6	141.7	1.1
A_84_P811360	929.2	2485.8	1.4	319.6	875.5	1.5
A_84_P23422	42.7	164.6	1.9	60	126.7	1.1
A_84_P826766	121	371.2	1.6	146.1	295.1	1
A_84_P592992	2.4	6.1	1.3	2.4	12	2.3
A_84_P12550	277.4	2607.4	3.2	328.1	680.6	1.1
A_84_P851082	36.7	108.7	1.6	69.5	143.6	1
A_84_P22837	8.4	20.2	1.3	2.5	6.5	1.4
A_84_P13112	9.1	98.6	3.4	5.7	17.4	1.6
A_84_P791857	3.5	7.3	1.1	2.5	5.7	1.2
A_84_P23378	2.5	12	2.3	2.5	6.5	1.4
A_84_P832916	78.5	329.3	2.1	57.9	185.5	1.7
A_84_P19380	19.4	68	1.8	32.7	90.4	1.5
A_84_P13955	144.2	745.2	2.4	157.8	383.9	1.3
A_84_P770385	24	64.2	1.4	18.2	45.2	1.3
A_84_P818172	957	7118.6	2.9	1343	4131.9	1.6
A_84_P755464	7.6	41.5	2.4	8.7	26.6	1.6
A_84_P15427	2.9	6	1.1	2.4	19	3
A_84_P836925	81.6	661.4	3	88.4	727	3
A_84_P784755	15	30.4	1	11.6	33.7	1.5
A_84_P856686	2.4	82.5	5.1	3.6	7.2	1
A_84_P529562	2.4	6	1.3	4.1	9	1.1
A_84_P852419	2.4	10.8	2.2	3.4	9.5	1.5
A_84_P765092	4	24.8	2.6	4.6	18.6	2
A_84_P529840	38.7	113.8	1.6	58.4	128.4	1.1
A_84_P535721	10.9	143.6	3.7	61.4	136	1.1
A_84_P769137	3.3	7.6	1.2	2.6	15.1	2.5
A_84_P555128	87.1	479.4	2.5	65	158.9	1.3
A_84_P19658	56.1	348.2	2.6	47.6	138.6	1.5
A_84_P10856	55.9	551.4	3.3	85.4	173.4	1
A_84_P753993	2.5	7.5	1.6	3	9	1.6
A_84_P835092	2.4	32.5	3.7	3.6	9.3	1.4
A_84_P21943	13074.3	38541.6	1.6	15497.2	33112.8	1.1
A_84_P258360	15.9	46.9	1.6	15.1	35.5	1.2
A_84_P844215	4.2	10	1.2	6.1	14.8	1.3
A_84_P121762	333.7	933.3	1.5	445.4	891.8	1
A_84_P798640	6.3	13.3	1.1	3.1	9.1	1.5

A_84_P751062	4.1	16	2	6	12.3	1
A_84_P551607	171.8	399.6	1.2	123.6	282.5	1.2
A_84_P572262	341.4	1255.6	1.9	362.4	752.1	1.1
A_84_P847936	22.7	61.9	1.4	20.2	64.3	1.7
A_84_P19508	24959	83693.4	1.7	44667.4	105042.8	1.2
A_84_P855610	554.5	3527.4	2.7	884.2	2219.2	1.3
A_84_P708146	2.6	9.7	1.9	2.6	6.7	1.4
A_84_P12677	10.7	165.9	4	12.5	71.9	2.5
A_84_P750540	24.6	57.8	1.2	21.9	46.4	1.1
A_84_P791176	24.1	209.7	3.1	26.6	68.8	1.4
A_84_P574116	3.1	9.6	1.6	3	9.5	1.7
A_84_P612892	255.1	706.5	1.5	254.9	733.2	1.5
A_84_P767439	12.3	26.8	1.1	12	34.9	1.5
A_84_P530188	28.1	60.3	1.1	35.7	95.3	1.4
A_84_P767270	2217.7	17071.7	2.9	1623.8	8819.8	2.4
A_84_P14666	209.3	1004	2.3	181	378.2	1.1
A_84_P83359	4.7	9.5	1	8.8	22.1	1.3
A_84_P14044	3.8	7.9	1.1	3.5	10.2	1.5
A_84_P844408	20.5	73.8	1.8	17.7	61.3	1.8
A_84_P224339	3.9	14.4	1.9	2.5	166.7	6.1
A_84_P800699	64.4	137.7	1.1	112.4	278.9	1.3
A_84_P15038	105.9	216.5	1	112	278.8	1.3
A_84_P12941	17.3	62.5	1.9	12.6	289.8	4.5
A_84_P502029	14.1	29.3	1.1	15.4	33.3	1.1
A_84_P847323	200.3	815.9	2	385.5	1003.5	1.4
A_84_P11125	147	567.2	1.9	141.5	336.5	1.2
A_84_P836547	3.9	27.3	2.8	5.6	12.8	1.2
A_84_P136115	67368.3	223436.6	1.7	84528.8	219468.1	1.4
A_84_P575989	2.6	15.6	2.6	2.6	12	2.2
A_84_P753747	114.7	567.5	2.3	115.9	268.5	1.2
A_84_P81249	2.6	5.6	1.1	3	10.7	1.8
A_84_P757276	3.4	14	2	5.1	20.6	2
A_84_P18647	2.5	5.6	1.2	2.5	11.5	2.2
A_84_P727700	18.7	39.4	1.1	26	81	1.6
A_84_P522030	561.1	1282.8	1.2	828.9	3574.1	2.1
A_84_P805609	14404.7	48700.7	1.8	26008.5	65697.1	1.3
A_84_P541541	10.7	22.6	1.1	16.3	52	1.7
A_84_P12694	8.2	24.9	1.6	6.4	21.7	1.8
A_84_P12488	2.5	13.5	2.4	2.5	12.7	2.4
A_84_P764897	83.2	270.7	1.7	54	120.6	1.2
A_84_P513341	2.6	9.4	1.8	3	8.4	1.5
A_84_P513574	97.3	242.3	1.3	40.9	122.3	1.6
A_84_P10303	20	64.3	1.7	19.3	49.4	1.4
A_84_P512786	10.2	52.6	2.4	6.3	19.6	1.6
A_84_P569671	479.2	1103.3	1.2	486	973.7	1

A_84_P143569	66.1	341	2.4	49.2	203.1	2
A_84_P735806	23.1	77.2	1.7	59.7	140.8	1.2
A_84_P838408	61.1	373.8	2.6	69.7	238.2	1.8
A_84_P571918	38.4	151.1	2	35.7	76.9	1.1
A_84_P752110	2.7	8	1.6	3.2	13.9	2.1
A_84_P17377	2.6	13.8	2.4	4.4	21.6	2.3
A_84_P14924	47.2	174.2	1.9	39.7	86.3	1.1
A_84_P23561	86.1	201.2	1.2	25.8	53.8	1.1
A_84_P23516	323.9	773.5	1.3	342	743.4	1.1
A_84_P268980	338.9	1277.4	1.9	443.9	1129.6	1.3
A_84_P859748	5.8	15	1.4	3.9	19.4	2.3
A_84_P850983	7.6	77.8	3.3	8.3	28.4	1.8
A_84_P66894	4.7	19.7	2.1	5.9	12.5	1.1
A_84_P16847	2.6	6.1	1.2	2.6	5.6	1.1
A_84_P859689	92699.9	300907.4	1.7	117686.3	307444.2	1.4
A_84_P826445	67.1	158.5	1.2	95.1	191.6	1
A_84_P765781	7.5	86.9	3.5	11.8	27.3	1.2
A_84_P755041	2.6	9.8	1.9	4.1	13.1	1.7
A_84_P14157	2.7	7.5	1.5	3.8	8.1	1.1
A_84_P18172	69.9	404.4	2.5	43.4	145.5	1.7
A_84_P77129	184.5	479.3	1.4	153.7	373.2	1.3
A_84_P22153	17610.8	53475.3	1.6	21442.8	50534.3	1.2
A_84_P500297	115.2	722	2.6	121.2	245.2	1
A_84_P606349	693.2	2888.8	2.1	827	1707.1	1
A_84_P853815	3.9	18.5	2.2	2.6	22.8	3.2
A_84_P786039	73.3	312.5	2.1	97.8	265.3	1.4
A_84_P785309	47.9	107.2	1.2	62.4	126.1	1
A_84_P545938	45.5	274.5	2.6	56	113.8	1
A_84_P802055	2.6	6.4	1.3	2.5	20.9	3
A_84_P12090	2.6	11	2.1	2.6	7.6	1.6
A_84_P557570	4.6	10.4	1.2	6.6	14.9	1.2
A_84_P88649	91.7	333.3	1.9	81	162.3	1
A_84_P24172	2.6	6.3	1.3	3.9	10.2	1.4
A_84_P230389	267.8	1396.6	2.4	260.2	558.5	1.1
A_84_P22019	14.5	80.8	2.5	15.9	36.6	1.2
A_84_P21375	12.3	25.2	1	8.6	21	1.3
A_84_P88749	16.6	33.6	1	12.5	32	1.4
A_84_P842776	2.6	17.6	2.7	2.6	17.7	2.8
A_84_P289314	67.7	253.8	1.9	81.4	169.4	1.1
A_84_P578562	7.8	17.1	1.1	5.7	18.5	1.7
A_84_P20450	293.9	620	1.1	263.4	604.5	1.2
A_84_P83469	395.8	1334.5	1.8	367.2	886.8	1.3
A_84_P803506	1145	4615.5	2	1606.3	3774.6	1.2
A_84_P811601	270.6	790	1.5	367.8	868	1.2
A_84_P23558	3.9	10.1	1.4	4.3	9.6	1.2

A_84_P528317	2.7	13.9	2.4	2.7	10.6	2
A_84_P855665	70	279.2	2	132.5	352.2	1.4
A_84_P861435	2.7	14.1	2.4	2.7	11.6	2.1
A_84_P789200	255.4	6860.6	4.7	480.7	7522.8	4
A_84_P842195	3.5	13.1	1.9	2.7	16.5	2.6
A_84_P550058	169.4	822.8	2.3	181.5	426.1	1.2
A_84_P23794	3.9	8	1	2.8	7.4	1.4
A_84_P298514	1427.5	4983.3	1.8	1373	3861.7	1.5
A_84_P20927	6.7	15.2	1.2	2.7	17.6	2.7
A_84_P841116	2.7	6.9	1.4	2.7	11.9	2.2
A_84_P21864	342.9	1195	1.8	433.9	1296.2	1.6
A_84_P852428	480.9	1241.7	1.4	371.5	806.8	1.1
A_84_P10614	58.8	204.2	1.8	108.8	232.2	1.1
A_84_P824802	681.3	1717.7	1.3	542.3	1259.6	1.2
A_84_P15118	10.4	58.5	2.5	9.4	34.9	1.9
A_84_P759912	2.7	5.9	1.1	3.4	9	1.4
A_84_P13708	96.9	513.6	2.4	125.8	543.4	2.1
A_84_P15517	239	711.3	1.6	83.9	260.2	1.6
A_84_P594466	129.6	759.2	2.6	162.3	361.9	1.2
A_84_P786320	281.9	2668	3.2	301.7	2792	3.2
A_84_P14249	1893.9	10373.7	2.5	3107.8	9044.8	1.5
A_84_P185874	130.8	766.9	2.6	144.8	327.6	1.2
A_84_P107692	3.7	11.6	1.6	2.8	8.5	1.6
A_84_P20386	1529.3	6033.4	2	1982.6	4305.9	1.1
A_84_P826034	103.8	345.6	1.7	161.7	349.1	1.1
A_84_P23146	2.7	8.6	1.6	2.7	7.7	1.5
A_84_P13929	4.3	8.7	1	2.7	7.8	1.5
A_84_P20416	2.8	19.8	2.8	2.8	7.3	1.4
A_84_P12345	987.4	2871.2	1.5	1035.2	2080.2	1
A_84_P857919	19.4	52.4	1.4	19.3	44.3	1.2
A_84_P761767	49.4	340.9	2.8	53.5	108.7	1
A_84_P306270	2.8	7.3	1.4	2.7	13.7	2.3
A_84_P19972	111.5	1958.4	4.1	76.4	234.4	1.6
A_84_P753880	8.7	62.7	2.8	6.3	19.6	1.6
A_84_P18184	2.9	36.8	3.6	2.9	6.3	1.1
A_84_P598819	4.4	39.5	3.2	6.1	13.3	1.1
A_84_P17031	3541.6	17772.4	2.3	5324.4	14760.2	1.5
A_84_P22990	5.2	26.1	2.3	9.3	30.8	1.7
A_84_P764652	9.5	42.7	2.2	5.8	63.7	3.5
A_84_P855388	11.7	39.5	1.8	7.3	20.7	1.5
A_84_P846972	16.5	72.4	2.1	14.9	33.5	1.2
A_84_P754529	20.4	43.5	1.1	5.7	12.7	1.2
A_84_P761415	102.3	254.7	1.3	119.1	716	2.6
A_84_P59870	14.1	50	1.8	14.5	32.7	1.2
A_84_P20335	181.8	423.5	1.2	211.2	513.6	1.3

A_84_P704042	21.9	67.1	1.6	15.3	32.2	1.1
A_84_P843668	3	11.6	1.9	3.7	11.5	1.6
A_84_P836976	22.5	89.1	2	20.6	41.3	1
A_84_P509388	174.3	470.8	1.4	236.8	504.4	1.1
A_84_P603863	4.3	14.6	1.8	5.1	10.9	1.1
A_84_P14929	7.1	17.4	1.3	3.2	10.2	1.7
A_84_P764001	7.8	52.3	2.7	6.3	21	1.7
A_84_P765863	9.2	20.7	1.2	10.5	29.7	1.5
A_84_P796287	31.8	102.9	1.7	44.1	129.7	1.6
A_84_P816073	695.8	1911.6	1.5	860.3	1744.7	1
A_84_P13573	1086.9	2492.9	1.2	995.5	3143.7	1.7
A_84_P521818	5.7	21.7	1.9	3.1	7.1	1.2
A_84_P59020	46.8	225.5	2.3	24.6	67.5	1.5
A_84_P21229	2613.8	5375.3	1	2355.8	5292	1.2
A_84_P767727	3.6	19	2.4	3.1	8.3	1.4
A_84_P23171	1127.7	2966.3	1.4	1536.9	3252	1.1
A_84_P10406	33	146.4	2.1	28.2	58.1	1
A_84_P754300	31.7	135.5	2.1	41	122.8	1.6
A_84_P539588	8.8	22.4	1.4	3.1	16.9	2.5
A_84_P785546	3.8	21.2	2.5	6.5	17.7	1.5
A_84_P769278	3.1	9.7	1.6	3.1	9.2	1.6
A_84_P12640	89.2	396.4	2.2	46.2	137.2	1.6
A_84_P11913	3.2	14.9	2.2	3.2	14.9	2.2
A_84_P787664	6.7	18.1	1.4	6.3	16.6	1.4
A_84_P542646	2052.9	16203.1	3	2441.9	7713	1.7
A_84_P15149	3.3	17	2.4	3.2	10.6	1.7
A_84_P275310	3.3	13	2	3.2	8.2	1.4
A_84_P18920	86.7	250.9	1.5	92.6	295.3	1.7
A_84_P860087	8917.9	38441.8	2.1	10280.8	23367.9	1.2
A_84_P753967	6	17.6	1.6	4.1	23.7	2.5
A_84_P789339	87.2	618.9	2.8	80.4	219	1.4
A_84_P225309	134.5	712.4	2.4	167.6	370.4	1.1
A_84_P760826	110.3	360.1	1.7	145.2	407.1	1.5
A_84_P761121	3.2	6.7	1.1	2.9	9.9	1.8
A_84_P13709	765	4336.9	2.5	925.7	2484.1	1.4
A_84_P13801	229.1	2813.1	3.6	164.7	603.2	1.9
A_84_P22833	3.4	11.4	1.7	6.1	16.7	1.5
A_84_P130356	34.5	73	1.1	31.4	67.4	1.1
A_84_P798132	4.7	11.8	1.3	6.6	17.7	1.4
A_84_P169963	80.3	208	1.4	166.4	390.6	1.2
A_84_P804630	2.9	12.5	2.1	4.6	10.8	1.2
A_84_P853443	18.9	45.3	1.3	18.4	48.8	1.4
A_84_P500750	1773.1	3696.6	1.1	2941.7	7642.7	1.4
A_84_P12563	178.2	828.5	2.2	340	683.7	1
A_84_P106762	33.9	80.4	1.2	34.4	83	1.3

A_84_P222339	54.8	120.9	1.1	71.1	194.7	1.5
A_84_P793199	24.1	79.7	1.7	36.9	76.1	1
A_84_P17690	9	19.1	1.1	2.9	7.6	1.4
A_84_P837280	110.3	323.7	1.6	153.1	399.1	1.4
A_84_P787513	91.2	210.8	1.2	69.4	218.2	1.7
A_84_P566794	3.2	10.3	1.7	5.7	15.1	1.4
A_84_P835838	48.5	226.8	2.2	84.3	256	1.6
A_84_P559372	96.3	356.7	1.9	110.1	261.5	1.2
A_84_P756150	13.4	51.8	2	14.3	31	1.1
A_84_P784927	3.1	7.4	1.3	3	10.2	1.8
A_84_P12940	243.3	961	2	218.3	633.2	1.5
A_84_P767469	6.9	23.8	1.8	9.9	31	1.7
A_84_P551975	3	21.1	2.8	2.9	6.9	1.2
A_84_P19697	227	883	2	252.9	552.3	1.1
A_84_P277930	3.2	25.6	3	3.1	25.6	3
A_84_P536643	3	6.8	1.2	3.7	8.5	1.2
A_84_P786059	5.3	100.3	4.3	6.9	30.9	2.2
A_84_P568028	3.3	15.5	2.2	3.2	6.5	1
A_84_P509518	3	12.1	2	3	8.4	1.5
A_84_P800204	2.9	7.9	1.4	2.9	14.1	2.3
A_84_P16680	5.1	77.1	3.9	14.2	46.8	1.7
A_84_P21567	4	22.6	2.5	5.6	14.4	1.4
A_84_P795300	8.4	26.4	1.7	7.5	24.3	1.7
A_84_P827279	3	9.3	1.6	3	10.1	1.8
A_84_P828140	3	8.1	1.4	3	13.6	2.2

Supplemental Table 6. Cluster analysis of up-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (upper aerial parts)

Annotation Cluster 1: Enrichment Score: 1.102128561315216			
Term	Count	%	PValue
death	7	2.67175573	0.03324021
cell death	7	2.67175573	0.03324021
programmed cell death	5	1.90839695	0.15970398
apoptosis	4	1.52671756	0.22122919
Annotation Cluster 2: Enrichment Score: 0.9526957335276258			
Term	Count	%	PValue
cellular homeostasis	7	2.67175573	0.02139165
homeostatic process	7	2.67175573	0.04801576
cellular metal ion homeostasis	3	1.14503817	0.06201147
metal ion homeostasis	3	1.14503817	0.06201147
cellular cation homeostasis	3	1.14503817	0.13798028
cell redox homeostasis	4	1.52671756	0.1548947
cation homeostasis	3	1.14503817	0.17760824
cellular ion homeostasis	3	1.14503817	0.17760824
cellular chemical homeostasis	3	1.14503817	0.18098956
ion homeostasis	3	1.14503817	0.22219574
chemical homeostasis	3	1.14503817	0.3094608
Annotation Cluster 3: Enrichment Score: 0.8572424636062304			
Term	Count	%	PValue
cell wall organization	8	3.05343511	0.0159813
external encapsulating structure organization	8	3.05343511	0.02104051
glucan metabolic process	4	1.52671756	0.17085989
cellular glucan metabolic process	3	1.14503817	0.32680094
polysaccharide metabolic process	4	1.52671756	0.3411484
cell wall modification	3	1.14503817	0.36451225
cellular polysaccharide metabolic process	3	1.14503817	0.42761751
Annotation Cluster 4: Enrichment Score: 0.8404851000721124			
Term	Count	%	PValue
phenylpropanoid metabolic process	6	2.29007634	0.02047854
phenylpropanoid biosynthetic process	4	1.52671756	0.12041242
lignin metabolic process	3	1.14503817	0.12525984
cellular amino acid derivative metabolic proce	6	2.29007634	0.12540744
cellular amino acid derivative biosynthetic pro	4	1.52671756	0.27670056
aromatic compound biosynthetic process	4	1.52671756	0.33081432
secondary metabolic process	6	2.29007634	0.36889643

Annotation Cluster 5: Enrichment Score: 0.7791525349225715			
Term	Count	%	PValue
response to organic substance	17	6.48854962	0.08702186
response to hormone stimulus	13	4.96183206	0.14930941
response to endogenous stimulus	13	4.96183206	0.20858878
response to abscisic acid stimulus	5	1.90839695	0.28208719
Annotation Cluster 6: Enrichment Score: 0.6095779185971728			
Term	Count	%	PValue
response to oxidative stress	7	2.67175573	0.05445969
response to hydrogen peroxide	3	1.14503817	0.30249941
response to reactive oxygen species	3	1.14503817	0.38139922
response to inorganic substance	6	2.29007634	0.58010799
Annotation Cluster 7: Enrichment Score: 0.32663666862298774			
Term	Count	%	PValue
cell morphogenesis	4	1.52671756	0.31272849
cellular component morphogenesis	4	1.52671756	0.37206588
growth	4	1.52671756	0.4103226
developmental growth involved in morphogene	3	1.14503817	0.43407666
unidimensional cell growth	3	1.14503817	0.43407666
developmental growth	3	1.14503817	0.50836073
cell growth	3	1.14503817	0.60223225
regulation of cell size	3	1.14503817	0.63200769
regulation of cellular component size	3	1.14503817	0.66003355
Annotation Cluster 8: Enrichment Score: 0.19937177339594506			
Term	Count	%	PValue
regulation of transcription	22	8.39694656	0.35320002
regulation of transcription, DNA-dependent	11	4.19847328	0.58225951
regulation of RNA metabolic process	11	4.19847328	0.5894041
intracellular signaling cascade	8	3.05343511	0.62169972
hormone-mediated signaling	4	1.52671756	0.77845063
cellular response to hormone stimulus	4	1.52671756	0.77845063
transcription	10	3.81679389	0.88065198
Annotation Cluster 9: Enrichment Score: 0.13000960432363975			
Term	Count	%	PValue
response to light stimulus	5	1.90839695	0.64483426
response to radiation	5	1.90839695	0.6709841
response to abiotic stimulus	8	3.05343511	0.94147947

Annotation Cluster 10: Enrichment Score: 0.015607358020655961			
Term	Count	%	PValue
protein amino acid phosphorylation	7	2.67175573	0.94247912
phosphorus metabolic process	8	3.05343511	0.96205762
phosphorylation	7	2.67175573	0.97074409
phosphate metabolic process	7	2.67175573	0.98399522
Annotation Cluster 11: Enrichment Score: 0.00366070081170899			
Term	Count	%	PValue
reproductive developmental process	4	1.52671756	0.98400534
reproductive structure development	3	1.14503817	0.99320996
post-embryonic development	3	1.14503817	0.99765268

Supplemental Table 7. Probe values for down-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (upper aerial parts)

Probe Name	Col1	*ztl3*	Log Ratio	Col2	*ztl105*	Log Ratio
A_84_P13493	21.5	3	-2.8	10.7	5.3	-1
A_84_P723122	644.9	283.6	-1.2	481.7	185.4	-1.4
A_84_P837838	10.8	3.8	-1.5	9.4	3.3	-1.5
A_84_P764933	9238.1	1487.8	-2.6	3180.8	1574	-1
A_84_P599908	21.1	5.6	-1.9	15.5	4.2	-1.9
A_84_P507254	11.5	5.4	-1.1	9.2	3.2	-1.5
A_84_P21392	1276.5	217.9	-2.6	1066.3	301.9	-1.8
A_84_P216298	482.9	77.6	-2.6	162.9	80.8	-1
A_84_P754363	15.3	4.2	-1.8	10.8	4.1	-1.4
A_84_P602497	99.2	36	-1.5	82.3	35.3	-1.2
A_84_P78679	503.4	219.7	-1.2	427.2	188	-1.2
A_84_P17435	5878.6	1875.4	-1.6	4362.5	1863	-1.2
A_84_P847448	14.2	5.5	-1.4	13.9	6.1	-1.2
A_84_P13518	98.7	39.9	-1.3	99.9	49	-1
A_84_P84109	10.8	3.3	-1.7	20.1	3.2	-2.7
A_84_P590126	37.4	9.9	-1.9	27.5	6	-2.2
A_84_P14212	90.7	18.6	-2.3	151.8	24.4	-2.6
A_84_P15966	14.8	4.3	-1.8	7.3	3.5	-1
A_84_P750003	32.7	10.6	-1.6	30	9.6	-1.6
A_84_P790159	10.4	3.6	-1.5	27.4	6.6	-2
A_84_P810835	66937.5	32810.9	-1	75344.6	29891.5	-1.3
A_84_P17231	21.5	7.4	-1.5	19.3	7.8	-1.3
A_84_P21636	34.3	10.7	-1.7	29.6	10.2	-1.5
A_84_P831568	133.4	46.4	-1.5	162.7	66.2	-1.3
A_84_P764046	135.2	51.8	-1.4	120.9	45.4	-1.4
A_84_P15002	4245.8	1539.4	-1.5	4328	1284	-1.8
A_84_P89979	5201.5	2158.8	-1.3	4225.8	2063.7	-1
A_84_P14851	10.4	4.3	-1.3	8.7	3.6	-1.3
A_84_P520558	835.9	211	-2	505.4	197.1	-1.4
A_84_P763570	346	17.3	-4.3	45.4	17.9	-1.3
A_84_P857782	60.3	12.2	-2.3	36.5	5.6	-2.7
A_84_P824053	2260.5	461.9	-2.3	1747.4	584.9	-1.6
A_84_P18192	47.8	18.8	-1.3	71.3	33.7	-1.1
A_84_P19081	1132	335.1	-1.8	773.3	295.7	-1.4
A_84_P144819	1474.8	320	-2.2	1804	419.9	-2.1
A_84_P18673	1022.3	196.4	-2.4	740.1	209.2	-1.8
A_84_P586474	479.9	154.4	-1.6	483.9	147.6	-1.7
A_84_P847314	197	52.2	-1.9	147.2	48.3	-1.6
A_84_P12387	13.7	4.2	-1.7	12.5	3.8	-1.7
A_84_P22463	38.6	14.9	-1.4	19.6	6.5	-1.6
A_84_P283390	1478.1	619.8	-1.3	2382.9	688.7	-1.8
A_84_P762938	75.9	34.1	-1.2	86.9	32.1	-1.4
A_84_P11764	11.4	3.3	-1.8	15.2	3.8	-2
A_84_P802510	16.1	4.1	-2	18.7	8.7	-1.1

A_84_P15762	918.6	353.1	-1.4	824.8	375.8	-1.1
A_84_P563750	127.2	54	-1.2	99.3	47.6	-1.1
A_84_P753614	1097.8	494.1	-1.2	1068.3	422	-1.3
A_84_P806064	44365.5	13274.4	-1.7	45248.7	13164.8	-1.8
A_84_P806987	139261.8	66006.2	-1.1	155245.7	69954.4	-1.2
A_84_P605859	18.5	7.8	-1.2	15.7	7.5	-1.1
A_84_P765453	15	3	-2.3	16.6	3.9	-2.1
A_84_P784871	5036.6	2136.5	-1.2	4302.3	2147.7	-1
A_84_P16776	270.7	63.7	-2.1	263.5	92.6	-1.5
A_84_P18949	88	11.6	-2.9	100.1	13	-2.9
A_84_P203128	16429	8208.1	-1	13254.9	5624.9	-1.2
A_84_P24160	1114.2	401.4	-1.5	1092.3	342.4	-1.7
A_84_P784686	21235.4	7133	-1.6	16203.1	8051	-1
A_84_P786467	31.4	4.2	-2.9	27.8	3.6	-2.9
A_84_P17929	4942.1	808.7	-2.6	6410.8	665.4	-3.3
A_84_P585437	19	5.2	-1.9	21.3	8.8	-1.3
A_84_P834039	13.3	6.5	-1	14.6	6.9	-1.1
A_84_P14635	585.3	112.3	-2.4	295.6	100.2	-1.6
A_84_P820492	12892.6	6436.5	-1	10622.6	4788.5	-1.1
A_84_P21360	1239.7	180.1	-2.8	1273.7	151.4	-3.1
A_84_P15926	59.3	22.1	-1.4	57.5	16.6	-1.8
A_84_P23534	5387.2	42.3	-7	5149.6	125.8	-5.4
A_84_P12704	2301.8	895.4	-1.4	2309	807	-1.5
A_84_P10105	892.8	339.8	-1.4	869.6	302.9	-1.5
A_84_P258350	175011.5	28752.7	-2.6	121846.1	45789.7	-1.4
A_84_P833206	45.2	10.3	-2.1	60.2	14.2	-2.1
A_84_P13432	2171.2	663.1	-1.7	2021.3	521.3	-2
A_84_P11358	508.1	218.6	-1.2	466.4	202.5	-1.2
A_84_P593573	251.6	108	-1.2	208.3	98.8	-1.1
A_84_P792384	29.5	11.1	-1.4	30.7	12.9	-1.3
A_84_P838299	24.3	6.6	-1.9	20.7	9.1	-1.2
A_84_P10189	555.3	207.1	-1.4	401.5	152.7	-1.4
A_84_P17068	65.9	17.6	-1.9	74.7	23.3	-1.7
A_84_P549850	2237.1	956.8	-1.2	2120.3	1041.2	-1
A_84_P104886	267.9	69	-2	349.8	149.2	-1.2
A_84_P857762	658.7	265.9	-1.3	653.4	220	-1.6
A_84_P829441	27.6	3.4	-3	22.3	3.2	-2.8
A_84_P582022	111.2	49.1	-1.2	101.6	49.4	-1
A_84_P19780	38	3	-3.7	43.6	8	-2.4
A_84_P11230	206.4	27	-2.9	197.5	26	-2.9
A_84_P23806	188.2	31.3	-2.6	112.4	47.1	-1.3
A_84_P12894	7556	2283.6	-1.7	5438.4	2695.7	-1
A_84_P16241	4993	1699.3	-1.6	6017.3	2289.1	-1.4
A_84_P19845	15.7	3	-2.4	22	9.7	-1.2
A_84_P507766	460.2	173.8	-1.4	405.4	117.9	-1.8
A_84_P22571	43540.9	2065.1	-4.4	26378.7	5302.6	-2.3
A_84_P762197	4715.1	1038.8	-2.2	3145.2	1479.2	-1.1
A_84_P21277	62.3	23.1	-1.4	75.6	28.5	-1.4
A_84_P571469	7	3.1	-1.2	11.2	3.1	-1.9
A_84_P10547	11.2	3.2	-1.8	18.4	5.2	-1.8

A_84_P761609	28.1	8.2	-1.8	20.8	2.9	-2.8
A_84_P233609	28	13.1	-1.1	24.4	11.1	-1.1
A_84_P89649	22.9	7.2	-1.7	20.7	3.2	-2.7
A_84_P16910	168	74.1	-1.2	164.8	58.9	-1.5
A_84_P279980	1695.6	491.5	-1.8	1922	792.3	-1.3
A_84_P17960	77	25.3	-1.6	52.5	19.3	-1.4
A_84_P703913	1274.6	543.4	-1.2	1152.6	523	-1.1
A_84_P211388	15.4	3.3	-2.2	17.2	3.2	-2.4
A_84_P21026	35084.8	11321.4	-1.6	19972.8	8524.2	-1.2
A_84_P799489	28	9.2	-1.6	22.2	7.8	-1.5
A_84_P22733	47.1	21.9	-1.1	48.7	22.8	-1.1
A_84_P784216	1424.4	455.8	-1.6	1697.2	299.8	-2.5
A_84_P10464	16.9	2.9	-2.5	16	6.3	-1.3
A_84_P145939	286.3	117.3	-1.3	308.5	121.2	-1.3
A_84_P750037	52.8	17.3	-1.6	47.3	17.8	-1.4
A_84_P22188	54.4	26	-1.1	61.3	21.9	-1.5
A_84_P23046	436.7	83.2	-2.4	233.2	75.9	-1.6
A_84_P18763	3041.2	1475.1	-1	4219.3	1207.8	-1.8
A_84_P147788	72	14	-2.4	49.9	6.4	-3
A_84_P21643	2650.9	897.2	-1.6	2220.7	1019.2	-1.1
A_84_P180664	42.1	10.6	-2	43.7	11.7	-1.9
A_84_P10586	29	14.5	-1	27.7	4.3	-2.7
A_84_P20395	8.7	2.9	-1.6	10.9	2.9	-1.9
A_84_P18655	139.2	17.5	-3	116.2	19.4	-2.6
A_84_P832877	68.8	24.4	-1.5	92.4	30	-1.6
A_84_P167393	7.4	3.4	-1.1	7.9	3.2	-1.3
A_84_P599301	303.6	150.1	-1	300.7	126.7	-1.2
A_84_P868891	81603.1	29233.9	-1.5	86152.7	23856.7	-1.9
A_84_P21181	1003.7	408.5	-1.3	790.7	379.3	-1.1
A_84_P14974	14.5	6.1	-1.3	10.2	3	-1.8
A_84_P825792	229.5	61.7	-1.9	303.9	69.1	-2.1
A_84_P13787	171.2	71.3	-1.3	151.2	57	-1.4
A_84_P66364	101.3	25	-2	61.5	13.6	-2.2
A_84_P10436	21.4	3.2	-2.8	23.1	4	-2.5
A_84_P22755	165.8	60.8	-1.4	168.8	46.2	-1.9
A_84_P786892	3879.6	1933.8	-1	4269.3	1774	-1.3
A_84_P850014	241.8	85.5	-1.5	252.5	117.3	-1.1
A_84_P840901	9.9	3.8	-1.4	11	3.3	-1.8
A_84_P107372	1955.1	892.8	-1.1	1653.7	779.4	-1.1
A_84_P21252	230.7	73.5	-1.7	195.5	91.5	-1.1
A_84_P13165	47	21.4	-1.1	60.1	24.2	-1.3
A_84_P10124	2132.9	649	-1.7	2459.3	661.9	-1.9
A_84_P21302	29.9	14.2	-1.1	36.1	16.7	-1.1
A_84_P20793	31.7	7	-2.2	24.5	2.9	-3.1
A_84_P787920	21.3	7.1	-1.6	30.5	4.2	-2.9
A_84_P12198	1206	519.4	-1.2	1021.5	477.8	-1.1
A_84_P16322	125.2	61.5	-1	118.6	49	-1.3
A_84_P275660	344.1	133.9	-1.4	377.1	125.2	-1.6
A_84_P599932	16.9	5.5	-1.6	15.8	4.4	-1.8
A_84_P19451	29.7	9.1	-1.7	28	8	-1.8

A_84_P17547	82.7	21.8	-1.9	78.4	29	-1.4
A_84_P18380	20.7	5.8	-1.8	9.2	3.4	-1.5
A_84_P12560	6339.7	2793.9	-1.2	5606.1	2624.8	-1.1
A_84_P19214	250.1	108.4	-1.2	238.9	115.9	-1
A_84_P561646	416.3	123	-1.8	448.4	162.7	-1.5
A_84_P767724	13525.2	5520.3	-1.3	9809.8	3987.6	-1.3
A_84_P210388	109.7	28.7	-1.9	115.7	38.3	-1.6
A_84_P574263	30.4	14.5	-1.1	15.3	6.7	-1.2
A_84_P790292	27.1	6	-2.2	40.6	11	-1.9
A_84_P302670	50.5	14.7	-1.8	45.5	22.1	-1
A_84_P200834	418.6	163.1	-1.4	373.6	130.1	-1.5
A_84_P13182	524.5	194.2	-1.4	530.9	164.9	-1.7
A_84_P537376	120.6	37.1	-1.7	134.3	57.4	-1.2
A_84_P17278	476.5	217.8	-1.1	359.7	149.9	-1.3
A_84_P14515	11.5	2.8	-2	8.9	2.8	-1.6
A_84_P20800	934	321.2	-1.5	760.2	288.7	-1.4
A_84_P13909	300.9	113.1	-1.4	353.7	156.7	-1.2
A_84_P50530	3204.9	402.6	-3	1483.3	460.9	-1.7
A_84_P813784	172.8	78.4	-1.1	150.7	72.1	-1.1
A_84_P19713	850.3	274.2	-1.6	1058.7	413.4	-1.4
A_84_P192044	42.2	16.8	-1.3	42.2	15.6	-1.4
A_84_P799914	504.2	61.5	-3	356	62.4	-2.5
A_84_P23582	3925.6	809.8	-2.3	3019.7	701.6	-2.1
A_84_P15126	2905.5	1046.8	-1.5	3076.9	1158.5	-1.4
A_84_P285010	185	61.9	-1.6	180.8	55.4	-1.7
A_84_P815985	913	299.7	-1.6	933.4	318.7	-1.6
A_84_P786422	2304.3	772.3	-1.6	1823.1	849.7	-1.1
A_84_P17328	5441.7	1578.2	-1.8	3820.2	1220	-1.6
A_84_P159675	9.5	3.1	-1.6	12.8	4.5	-1.5
A_84_P19490	6065	2483.2	-1.3	8109.7	2966.8	-1.5
A_84_P20970	43.6	19.3	-1.2	46.7	12.1	-1.9
A_84_P23026	10.5	3.2	-1.7	6.3	3.1	-1
A_84_P757054	840.3	304	-1.5	689.4	264.7	-1.4
A_84_P788914	367.5	106.1	-1.8	261.4	115.9	-1.2
A_84_P180334	10.7	3.2	-1.8	8.7	3	-1.6
A_84_P834342	9.7	2.9	-1.7	6.5	3.2	-1.1
A_84_P207668	67.2	33.2	-1	77.1	35.4	-1.1
A_84_P818053	71.5	18	-2	77	15.1	-2.4
A_84_P15411	138	61	-1.2	96.4	46.9	-1
A_84_P305320	545	233.5	-1.2	519.1	251.4	-1
A_84_P275630	262.6	90.6	-1.5	209.5	101.9	-1
A_84_P518116	117.3	49.8	-1.2	147.5	39.5	-1.9
A_84_P302890	428.5	160.7	-1.4	347.4	170.9	-1
A_84_P10627	6956.3	1209.2	-2.5	3739.4	1442.3	-1.4
A_84_P583074	31.8	6.7	-2.3	24.4	8.4	-1.5
A_84_P18494	311	111.9	-1.5	301.9	101.7	-1.6
A_84_P856901	2467.6	1124.6	-1.1	3160	1375.2	-1.2
A_84_P754439	31	15.1	-1	39.4	10.1	-2
A_84_P140239	31.9	7.4	-2.1	27.5	9.1	-1.6
A_84_P856001	14128.3	2452.3	-2.5	11684.7	3543	-1.7

A_84_P584775	34.8	13	-1.4	46.7	18.1	-1.4
A_84_P12207	270	119.6	-1.2	324.7	119.2	-1.4
A_84_P291544	60.1	16.6	-1.9	65	19.6	-1.7
A_84_P828945	14.8	6.1	-1.3	38.9	4	-3.3
A_84_P23992	3567.9	397.4	-3.2	2244.6	380.9	-2.6
A_84_P511310	18.5	3.1	-2.6	17.8	2.7	-2.7
A_84_P88029	352.8	170.9	-1	335.5	108.2	-1.6
A_84_P514938	2846.9	929.5	-1.6	2017.1	980.7	-1
A_84_P760043	5.9	2.9	-1	7.4	3	-1.3
A_84_P52460	10.3	2.7	-1.9	8.2	4.1	-1
A_84_P861883	6568.8	2867.4	-1.2	6481.2	2372.2	-1.5
A_84_P11207	2097.9	606.7	-1.8	2324.7	1078.5	-1.1
A_84_P22636	109.5	23.9	-2.2	90.7	25.2	-1.8
A_84_P242573	210.7	17.5	-3.6	177.2	13.1	-3.8
A_84_P11622	1654.5	547.2	-1.6	1635.7	640.8	-1.4
A_84_P20020	9.7	4.8	-1	12.1	5.1	-1.3
A_84_P733994	25.6	12.7	-1	36.6	10.6	-1.8
A_84_P606561	74.2	27.6	-1.4	64.2	19.9	-1.7
A_84_P804582	50221.2	21514.3	-1.2	43344.4	18082.4	-1.3
A_84_P310253	15.4	2.8	-2.5	40.2	2.8	-3.8
A_84_P754657	52.9	25.9	-1	53.1	21.5	-1.3
A_84_P14433	750	359.9	-1.1	797.8	348.1	-1.2
A_84_P12605	125.1	41.8	-1.6	150.6	65.9	-1.2
A_84_P831464	376.3	174.9	-1.1	330.6	155.5	-1.1
A_84_P12451	15.5	3	-2.4	14.5	4.8	-1.6
A_84_P62840	675.5	206.5	-1.7	353.4	155.5	-1.2
A_84_P10178	5244.8	2281.2	-1.2	8116.5	3319.3	-1.3
A_84_P19687	475	176.9	-1.4	531	214.6	-1.3
A_84_P23644	343	125.7	-1.4	314.1	96.8	-1.7
A_84_P18265	111.1	26.3	-2.1	79.9	19.4	-2
A_84_P14023	4648.5	1934.9	-1.3	3974.1	1808.7	-1.1
A_84_P599862	883	202.8	-2.1	896.5	173.4	-2.4
A_84_P790750	12.7	4.9	-1.4	16.5	2.9	-2.5
A_84_P575512	119.5	39.8	-1.6	138.5	34.3	-2
A_84_P281230	1947.1	667.2	-1.5	1763.6	716.6	-1.3
A_84_P836527	22	10.2	-1.1	20.3	7.5	-1.4
A_84_P602945	13.5	2.9	-2.2	19.6	2.9	-2.7
A_84_P546682	122.7	58.1	-1.1	104.9	39	-1.4
A_84_P266650	459.3	48.1	-3.3	608	34.1	-4.2
A_84_P178184	1097.1	445.7	-1.3	1006	417.6	-1.3
A_84_P13344	3768.2	1659.2	-1.2	4077.8	1856.4	-1.1
A_84_P790894	323.7	143.7	-1.2	276.8	89.2	-1.6
A_84_P13885	563	268.9	-1.1	448	165.7	-1.4
A_84_P716147	6.7	2.8	-1.2	9.1	2.8	-1.7
A_84_P504518	123.6	52.8	-1.2	115.2	41.2	-1.5
A_84_P604601	29.8	13.8	-1.1	17.6	7.2	-1.3
A_84_P15978	704.8	303.6	-1.2	764.9	297.3	-1.4
A_84_P784578	609.2	298.3	-1	628.6	260.6	-1.3
A_84_P266910	617.4	258.7	-1.3	544.4	233.5	-1.2
A_84_P826328	169.5	66.7	-1.3	168.2	66.9	-1.3

A_84_P572154	10.2	4.4	-1.2	9.2	2.7	-1.8
A_84_P19909	197.8	35.9	-2.5	257.3	122.2	-1.1
A_84_P812936	71.3	20.3	-1.8	104.1	22.7	-2.2
A_84_P10978	149.8	67.5	-1.1	131	51.8	-1.3
A_84_P860746	312.1	145.9	-1.1	306	109.1	-1.5
A_84_P750195	274.5	102	-1.4	239	80.9	-1.6
A_84_P21961	7698.7	3815.5	-1	8611	3698.4	-1.2
A_84_P843096	12.3	2.7	-2.2	24.4	2.7	-3.2
A_84_P593738	5454.2	2413.2	-1.2	4907.6	1707.7	-1.5
A_84_P23329	13214.1	5628.9	-1.2	11887.6	5780.1	-1
A_84_P298204	2474.3	937.9	-1.4	2256.8	809	-1.5
A_84_P838362	6.4	2.9	-1.2	6.4	2.9	-1.1
A_84_P137739	5099.6	1759.7	-1.5	3713.4	1694.7	-1.1
A_84_P839478	24.1	3.1	-3	20.4	8.8	-1.2
A_84_P13379	376.1	81.7	-2.2	512.2	128.9	-2
A_84_P257260	3824.6	873.9	-2.1	2863.9	990.6	-1.5
A_84_P10985	60.8	25.2	-1.3	60.1	19.9	-1.6
A_84_P12696	25.3	2.8	-3.2	12.3	2.9	-2.1
A_84_P820222	574.4	92.1	-2.6	616.8	64.1	-3.3
A_84_P829892	8.4	2.7	-1.6	10.4	4.2	-1.3
A_84_P825910	570.8	90.1	-2.7	381	87.8	-2.1
A_84_P802547	2417	629.6	-1.9	2918.9	604.9	-2.3
A_84_P10579	905.8	239	-1.9	875.7	279.3	-1.6
A_84_P600829	469.5	138.1	-1.8	294.4	130.5	-1.2
A_84_P22795	1290.2	309.1	-2.1	1046.5	297.4	-1.8
A_84_P11569	2208.2	973.9	-1.2	3964.3	1447.6	-1.5
A_84_P14585	4303.8	1704.5	-1.3	4436.5	1802.8	-1.3
A_84_P12020	134.2	18.8	-2.8	80.7	25.1	-1.7
A_84_P127071	1568.3	371.5	-2.1	861.7	411.3	-1.1
A_84_P16754	104.6	37.1	-1.5	69.1	33.6	-1
A_84_P846994	139.2	38.8	-1.8	109.6	46.5	-1.2
A_84_P14191	18.3	2.8	-2.7	6.9	2.8	-1.3
A_84_P20080	25777.6	10471.3	-1.3	23456.2	11518.5	-1
A_84_P510538	8	2.6	-1.6	6.8	2.6	-1.4
A_84_P20377	817.3	293.1	-1.5	828.4	280.6	-1.6
A_84_P839463	7.8	2.6	-1.6	5.8	2.6	-1.1
A_84_P761616	51.6	11	-2.2	23.8	2.8	-3.1
A_84_P18335	3356.2	884.3	-1.9	2463.6	679.6	-1.9
A_84_P806562	78512.8	38979.3	-1	86912.9	40432.6	-1.1
A_84_P791422	453.5	226.3	-1	354.7	167.9	-1.1
A_84_P516993	21.2	8.8	-1.3	18.5	8.4	-1.1
A_84_P758488	237.1	64.5	-1.9	175.7	71.6	-1.3
A_84_P20632	1612.7	621.2	-1.4	1408.9	649.9	-1.1
A_84_P19808	165.6	59.5	-1.5	159.3	54.8	-1.5
A_84_P764623	1427.4	266.5	-2.4	1017.9	209.5	-2.3
A_84_P253265	734.5	277.8	-1.4	648.7	183.1	-1.8
A_84_P515003	79.5	23.6	-1.8	98.5	23.1	-2.1
A_84_P754856	17.2	5.3	-1.7	9.6	3.6	-1.4
A_84_P761238	8.2	2.6	-1.7	19.9	2.6	-2.9
A_84_P11360	782.5	256.4	-1.6	1151.4	248.3	-2.2

A_84_P18969	1286.8	533.4	-1.3	1433.9	436.5	-1.7
A_84_P11428	6.3	2.8	-1.1	9.7	2.8	-1.8
A_84_P79809	798.4	297.3	-1.4	659.3	293.3	-1.2
A_84_P16825	1820.8	667.2	-1.4	1487.5	609.6	-1.3
A_84_P526191	24.9	6.5	-1.9	20.9	7.8	-1.4
A_84_P857480	59908.2	19038.3	-1.7	48630.8	24287.9	-1
A_84_P823166	4624.4	1319.9	-1.8	4537.2	1370.7	-1.7
A_84_P196604	843.4	385.8	-1.1	938.3	363.8	-1.4
A_84_P769426	41.3	13	-1.7	62	30	-1
A_84_P18858	27.5	13.6	-1	29.7	9.7	-1.6
A_84_P17723	2430	883.1	-1.5	2252	1055.7	-1.1
A_84_P15784	327.8	93.9	-1.8	265.9	77.7	-1.8
A_84_P120842	29.2	12.1	-1.3	23.9	4.9	-2.3
A_84_P159445	6.9	2.6	-1.4	9.1	4.5	-1
A_84_P519725	637.6	262.3	-1.3	504.1	251.7	-1
A_84_P14620	47.7	14	-1.8	39.1	14	-1.5
A_84_P501207	38.3	5.4	-2.8	16.6	8	-1.1
A_84_P18669	25.6	10.4	-1.3	21.4	10.6	-1
A_84_P544465	1807.4	568.5	-1.7	1802.6	610.9	-1.6
A_84_P21376	11.2	2.6	-2.1	20.6	6.7	-1.6
A_84_P11104	307.1	140.5	-1.1	284.2	137.8	-1
A_84_P22775	236.4	71.8	-1.7	226.9	77.6	-1.5
A_84_P19588	937.1	315.7	-1.6	1164.3	241.5	-2.3
A_84_P559351	310	123.3	-1.3	264.8	129.8	-1
A_84_P789302	386.5	148.6	-1.4	417.7	160	-1.4
A_84_P19990	646.7	293.9	-1.1	559.7	267.2	-1.1
A_84_P794288	4293.4	1650.8	-1.4	2906.4	1115.4	-1.4
A_84_P240805	6446	1947.5	-1.7	7207.9	1739.9	-2.1
A_84_P536936	13.2	2.5	-2.4	6.9	2.6	-1.4
A_84_P230529	15885.8	6551.8	-1.3	18052.5	7220.6	-1.3
A_84_P10736	61.8	21.1	-1.5	59.9	20.6	-1.5
A_84_P798436	1127	380.2	-1.6	1673.3	480.3	-1.8
A_84_P137629	2962.1	628.4	-2.2	2979.5	536.5	-2.5
A_84_P11030	919.1	152.8	-2.6	581.2	163.8	-1.8
A_84_P834747	117.8	51.8	-1.2	109.8	52.7	-1.1
A_84_P543942	9.8	3.5	-1.5	33.6	4.4	-2.9
A_84_P255680	1060.7	402	-1.4	816.9	380.6	-1.1
A_84_P19641	22.5	8.3	-1.4	18.9	4.1	-2.2
A_84_P857281	1304.2	375.8	-1.8	1169.8	329.9	-1.8
A_84_P603116	443.1	154.3	-1.5	447.3	203.4	-1.1
A_84_P784679	21.5	3.2	-2.8	62.5	7	-3.2
A_84_P788919	47.3	20.2	-1.2	90.4	39.5	-1.2
A_84_P22129	121.5	34.1	-1.8	73.4	31.3	-1.2
A_84_P235073	3889.1	1269.7	-1.6	4849.9	1347.9	-1.8
A_84_P22076	3581.1	1114.3	-1.7	2891.7	1051	-1.5
A_84_P296664	1145.2	436.1	-1.4	1072.3	343.3	-1.6
A_84_P13975	232.6	106	-1.1	230.4	106	-1.1
A_84_P12031	375.3	69.1	-2.4	443.2	110.4	-2
A_84_P761538	1585.2	572.9	-1.5	1163.6	571.4	-1
A_84_P10076	142.1	19.7	-2.9	212.2	41.4	-2.4

A_84_P20549	2112	797.5	-1.4	2204.5	780.7	-1.5
A_84_P750600	5.6	2.7	-1	6.7	2.8	-1.3
A_84_P18717	1100.1	499.6	-1.1	1108.5	532.2	-1.1
A_84_P827648	2359.9	1054.3	-1.2	1947.1	754.8	-1.4
A_84_P179004	70	21.7	-1.7	65.9	24.8	-1.4
A_84_P24034	17.3	8.4	-1	18.9	5.2	-1.9
A_84_P10266	3328	1106.2	-1.6	4026.5	1434.1	-1.5
A_84_P761632	6	2.5	-1.3	7.2	2.5	-1.5
A_84_P522242	803	271.9	-1.6	621.4	203.3	-1.6
A_84_P21605	85.4	6.2	-3.8	56.3	11.7	-2.3
A_84_P13813	460.4	14.9	-4.9	393.4	32.2	-3.6
A_84_P751111	59.7	27.9	-1.1	69.4	23.8	-1.5
A_84_P14725	11.8	2.7	-2.1	8.2	2.7	-1.6
A_84_P20968	13.8	5.7	-1.3	10.4	2.6	-2
A_84_P573423	64.4	19	-1.8	91.1	24.8	-1.9
A_84_P795530	476.8	199.8	-1.3	507.3	214.9	-1.2
A_84_P145159	1623.9	290.7	-2.5	1502.7	296.5	-2.3
A_84_P554482	235.2	61.3	-1.9	245	91.6	-1.4
A_84_P10257	112	45.6	-1.3	140	69.6	-1
A_84_P611528	8.1	2.5	-1.7	6.8	2.5	-1.4
A_84_P858602	204.2	71.6	-1.5	248.9	87.7	-1.5
A_84_P751557	9.4	2.7	-1.8	8.4	2.7	-1.6
A_84_P764577	80.7	12.1	-2.7	88	24.4	-1.8
A_84_P311113	491.9	158.7	-1.6	676.7	257.8	-1.4
A_84_P12579	42.2	16.6	-1.3	52	24.2	-1.1
A_84_P579221	9.4	2.6	-1.9	7.5	2.6	-1.5
A_84_P509274	7	2.5	-1.5	16.5	2.5	-2.7
A_84_P19599	19.3	6.5	-1.6	13	4.6	-1.5
A_84_P23649	21.8	7.2	-1.6	22.3	2.7	-3
A_84_P21770	222.2	51	-2.1	218	53.2	-2
A_84_P23253	51.8	22.5	-1.2	85.7	35.6	-1.3
A_84_P552987	17.5	4.9	-1.8	28	7.7	-1.9
A_84_P23436	4463.3	1512.1	-1.6	4937.8	1473.1	-1.7
A_84_P839829	217	71.6	-1.6	206.1	65	-1.7
A_84_P18484	10.5	2.6	-2	6.2	2.6	-1.3
A_84_P15040	1149.5	184.4	-2.6	992.1	263.4	-1.9
A_84_P100746	24361.1	7983.2	-1.6	18927	6455.3	-1.6
A_84_P850782	54.6	14.2	-1.9	70	20.5	-1.8
A_84_P760622	1873.5	417.7	-2.2	1779.7	595.1	-1.6
A_84_P761903	10.5	2.8	-1.9	12	5.7	-1.1
A_84_P19619	164.5	34.1	-2.3	90.6	44	-1
A_84_P603549	74.6	28.8	-1.4	70.9	27.9	-1.3
A_84_P763269	161	79.1	-1	145.8	52.3	-1.5
A_84_P20292	8022.7	2126.5	-1.9	6791.1	2466.8	-1.5
A_84_P126241	1096.6	164	-2.7	762.8	340.7	-1.2
A_84_P754081	7.2	2.7	-1.4	76.3	2.7	-4.8
A_84_P18297	47.4	15.3	-1.6	57	21.1	-1.4
A_84_P14572	6.2	3	-1.1	5.6	2.6	-1.1
A_84_P19887	1464	260	-2.5	959.7	205.9	-2.2
A_84_P21493	1637.7	706.4	-1.2	3346.9	985	-1.8

A_84_P14899	2492.5	1088.5	-1.2	2050.5	947.5	-1.1
A_84_P526328	55	2.5	-4.5	10.6	2.5	-2.1
A_84_P814282	330.5	39.6	-3.1	163.9	79	-1.1
A_84_P834210	135.3	38.1	-1.8	111.5	51	-1.1
A_84_P587696	106.4	40.4	-1.4	93.3	34.8	-1.4
A_84_P15894	24.5	2.5	-3.3	6	2.5	-1.3
A_84_P551649	231	93.8	-1.3	181.3	79.3	-1.2
A_84_P835897	172.1	50.7	-1.8	135.2	60.6	-1.2
A_84_P12513	4845.1	1215.6	-2	4099.8	1402.9	-1.5
A_84_P570783	398.7	171.4	-1.2	269.6	125.3	-1.1
A_84_P826231	19.5	8.9	-1.1	21.7	9.4	-1.2
A_84_P761805	5.3	2.4	-1.1	5.8	2.4	-1.3
A_84_P813455	1072	432.6	-1.3	1085.4	357.3	-1.6
A_84_P11024	7403	3443.2	-1.1	8541.2	3463.2	-1.3
A_84_P836421	24.5	2.4	-3.3	18.1	8.8	-1
A_84_P787591	219.5	67.2	-1.7	173.5	77.5	-1.2
A_84_P13987	2120.6	908.7	-1.2	2720.2	951.9	-1.5
A_84_P102716	39.7	16.7	-1.2	38.8	14.3	-1.4
A_84_P12395	2825	462.2	-2.6	2403.6	468.2	-2.4
A_84_P534217	668.6	322.2	-1.1	591.1	229	-1.4
A_84_P764568	5	2.4	-1	38.1	2.4	-4
A_84_P791730	75.9	14.6	-2.4	49.5	20.3	-1.3
A_84_P806069	426	140.9	-1.6	524.8	153.4	-1.8
A_84_P13686	495.4	186.9	-1.4	324.9	159.3	-1
A_84_P831529	97.8	12.4	-3	9.6	2.6	-1.9
A_84_P23923	278.6	46	-2.6	174.3	51.5	-1.8
A_84_P810688	108033.9	15424.2	-2.8	77335.7	24579.1	-1.7
A_84_P592414	69.4	31.8	-1.1	80.5	29.6	-1.4
A_84_P769350	2670.7	798.2	-1.7	1589.5	723.9	-1.1
A_84_P18657	247.5	91.9	-1.4	224	97.6	-1.2
A_84_P840645	6.1	3	-1	6.6	2.5	-1.4
A_84_P822179	27935.7	12166.3	-1.2	20036.6	9272.9	-1.1
A_84_P210918	1142.4	468	-1.3	1030.7	472.4	-1.1
A_84_P18271	805	188.9	-2.1	821.1	208.8	-2
A_84_P14448	612.9	286.5	-1.1	528.9	200.2	-1.4
A_84_P19971	10.3	2.5	-2	5.7	2.5	-1.2
A_84_P790373	25.6	2.4	-3.4	14.5	6.6	-1.1
A_84_P755191	21.2	4	-2.4	6.5	2.6	-1.3
A_84_P557066	62.9	21.1	-1.6	54.4	26	-1.1
A_84_P765172	26.6	2.6	-3.4	16.7	5.7	-1.6
A_84_P23838	26294.5	3791.6	-2.8	20071.8	2445.3	-3
A_84_P19414	224.2	73.7	-1.6	234.3	92.4	-1.3
A_84_P205328	22.7	2.6	-3.1	16.5	2.6	-2.6
A_84_P512914	17.5	2.6	-2.7	6.8	2.5	-1.4
A_84_P18064	358.3	75	-2.3	319	114	-1.5

A_84_P14274	5978.8	684.1	-3.1	5927.3	887.1	-2.7
A_84_P831400	979.7	167.2	-2.6	597	155.6	-1.9
A_84_P535279	20.5	3.1	-2.7	18.1	5.2	-1.8
A_84_P16890	29.7	2.6	-3.5	35.5	2.6	-3.8
A_84_P825325	2220.7	976.6	-1.2	2342.5	931.6	-1.3
A_84_P14556	3074.4	1126.6	-1.4	3382.7	1301.1	-1.4
A_84_P810442	52663	24972.4	-1.1	56279	26395.9	-1.1
A_84_P613604	72	29.5	-1.3	68.6	27.7	-1.3
A_84_P11053	453.6	53.4	-3.1	128.6	64.2	-1
A_84_P855052	172.9	66.4	-1.4	190.4	62.4	-1.6
A_84_P20987	49	22.8	-1.1	32.9	16.1	-1
A_84_P11975	528.4	120.4	-2.1	381.8	97.5	-2
A_84_P127161	2479.6	890	-1.5	1983.6	979.4	-1
A_84_P837804	86.8	22	-2	93.3	36.7	-1.3
A_84_P604467	559.5	220.2	-1.3	450.5	221.2	-1
A_84_P178234	101.2	28.9	-1.8	91.5	30.7	-1.6
A_84_P12954	710.4	265.2	-1.4	677.5	329.3	-1
A_84_P801897	12.4	5.1	-1.3	7.7	2.8	-1.4
A_84_P868217	4011.5	1436.3	-1.5	4012.8	1168.5	-1.8
A_84_P210738	19.6	5.7	-1.8	13.6	2.4	-2.5
A_84_P22142	45.9	19	-1.3	37.1	14.1	-1.4
A_84_P808706	15776.2	3654.7	-2.1	19506.5	4163.6	-2.2
A_84_P839149	316.7	131.7	-1.3	391.2	129.2	-1.6
A_84_P764601	6.3	2.6	-1.3	6.4	3	-1.1
A_84_P826714	1577.6	464.1	-1.8	968.2	416.5	-1.2
A_84_P520839	24.5	6	-2	20.7	8.8	-1.2
A_84_P23648	371.5	180.4	-1	350.1	162.8	-1.1
A_84_P52840	12881	3150.1	-2	11338	3312.9	-1.8
A_84_P581126	54.7	6.8	-3	50.3	4.3	-3.6
A_84_P10083	210.6	97.9	-1.1	302.7	95.9	-1.7
A_84_P579600	263.6	90.2	-1.5	225.7	83.1	-1.4
A_84_P10849	60.5	28.9	-1.1	50.3	25.1	-1
A_84_P533306	53	19.4	-1.4	44	14.6	-1.6
A_84_P800107	172.4	54.3	-1.7	123.9	59.3	-1.1
A_84_P74474	134	66.5	-1	140	56.6	-1.3
A_84_P549255	27.4	10.4	-1.4	34	3.7	-3.2
A_84_P516448	36.7	13.5	-1.4	40.1	10.7	-1.9
A_84_P283170	32.2	11.2	-1.5	6.9	2.5	-1.5
A_84_P93859	6.7	2.4	-1.5	15.6	3.4	-2.2
A_84_P23347	4356.7	1762.7	-1.3	3583	1683.9	-1.1
A_84_P545880	29.7	7.4	-2	130.7	17.1	-2.9
A_84_P238433	126.6	23.1	-2.5	49.4	22.2	-1.2
A_84_P20532	29.5	13.4	-1.1	24	11	-1.1
A_84_P19195	1004.9	357.4	-1.5	799.8	382.1	-1.1
A_84_P147028	1232.5	252.2	-2.3	1273.8	455.7	-1.5

A_84_P17486	5.3	2.5	-1.1	6.8	2.5	-1.4
A_84_P12558	38.1	11.1	-1.8	33.3	9.4	-1.8
A_84_P17282	14.8	2.4	-2.6	5.3	2.4	-1.2
A_84_P11320	46.2	16.5	-1.5	51.9	14.6	-1.8
A_84_P822770	26	7.2	-1.8	6.8	2.6	-1.4
A_84_P567973	6.2	2.5	-1.3	10.5	2.5	-2.1
A_84_P762010	825.9	136.9	-2.6	1018.2	459.4	-1.1
A_84_P544235	98.1	34.4	-1.5	74.9	37.4	-1
A_84_P94969	19625	3132.2	-2.6	21123	2406.9	-3.1
A_84_P801256	6845.9	3199.9	-1.1	5961.2	2397.5	-1.3
A_84_P286710	1884.7	448.1	-2.1	1365.8	346.2	-2
A_84_P766510	101.6	47.3	-1.1	143	61.8	-1.2
A_84_P20420	122.6	42	-1.5	181.7	39.7	-2.2
A_84_P842083	19.2	8.3	-1.2	15.6	6	-1.4
A_84_P12256	37.6	17.6	-1.1	21	5.7	-1.9
A_84_P820018	1189.8	373.3	-1.7	1009	271.3	-1.9
A_84_P21915	1660.3	683.4	-1.3	2371.4	1111	-1.1
A_84_P768727	1345.8	326.7	-2	670.9	318	-1.1
A_84_P807008	104280.9	40621.9	-1.4	121216.8	48962.4	-1.3
A_84_P22479	148.6	65.7	-1.2	240.3	70.6	-1.8
A_84_P593782	2082.9	873.3	-1.3	1917.1	824.8	-1.2
A_84_P60230	155.7	59.7	-1.4	126.5	46.9	-1.4
A_84_P12692	624.6	239.7	-1.4	751.4	289.7	-1.4
A_84_P556364	627.4	280.4	-1.2	558	260.5	-1.1
A_84_P21386	55.4	22.8	-1.3	74.8	24.2	-1.6
A_84_P10333	168.5	49.8	-1.8	139.9	62	-1.2
A_84_P15454	83.9	6.9	-3.6	28.9	9.7	-1.6
A_84_P504860	5.3	2.4	-1.1	50.6	2.4	-4.4
A_84_P846194	1923	662.4	-1.5	1782.6	710.1	-1.3
A_84_P530576	34.6	5	-2.8	13.7	3.1	-2.1
A_84_P118982	1329.1	623.8	-1.1	1241.6	613.1	-1
A_84_P22105	175.3	71.8	-1.3	162.7	63.6	-1.4
A_84_P203658	64.6	26.8	-1.3	66.5	19.9	-1.7
A_84_P10613	11775.6	770	-3.9	8973.3	899.7	-3.3
A_84_P13006	12701.2	5872.4	-1.1	11408.6	5035	-1.2
A_84_P23851	1861.5	762.4	-1.3	1627.6	644.4	-1.3
A_84_P16077	1864.5	644.2	-1.5	1372.2	494.5	-1.5
A_84_P14137	551.3	100.2	-2.5	565	76.4	-2.9
A_84_P21826	117.1	33	-1.8	123.1	33.4	-1.9
A_84_P23789	91.7	15.5	-2.6	120	27.5	-2.1
A_84_P22462	28.3	2.4	-3.6	23	2.4	-3.3
A_84_P23012	12.3	2.4	-2.4	9.6	2.4	-2
A_84_P789317	2177.1	504.2	-2.1	2195.5	732.9	-1.6
A_84_P546356	519.2	104.1	-2.3	395.5	162.9	-1.3
A_84_P756407	899.2	425.2	-1.1	683.9	334.9	-1
A_84_P11001	104.1	44	-1.2	101.9	43.5	-1.2
A_84_P18561	2064.5	606.2	-1.8	1366.5	586.9	-1.2
A_84_P20016	189.5	82.9	-1.2	105	38.4	-1.5
A_84_P17207	181	80.2	-1.2	218.1	31.1	-2.8
A_84_P10523	14.9	6.3	-1.2	17.6	2.5	-2.8

A_84_P293404	88.9	4.7	-4.2	7.1	2.5	-1.5
A_84_P817244	3614.6	1049.4	-1.8	2741.5	1242.5	-1.1
A_84_P856574	6025.9	2081.1	-1.5	5164.4	2277.3	-1.2
A_84_P753017	30.7	7.6	-2	44.5	15	-1.6
A_84_P15074	747	372.8	-1	705.1	249.1	-1.5
A_84_P13763	744	285.7	-1.4	648.9	293.5	-1.1
A_84_P560513	119.8	21.9	-2.4	118.5	35.4	-1.7
A_84_P836138	38.8	11.3	-1.8	39.2	13.4	-1.5
A_84_P97476	6110.4	1946.1	-1.7	6911.8	1234.2	-2.5
A_84_P762507	27.3	7.8	-1.8	9	2.4	-1.9
A_84_P10979	974.9	331.8	-1.6	1033.8	284.1	-1.9
A_84_P754114	5.7	2.4	-1.2	5.2	2.4	-1.1
A_84_P96816	139.6	41.1	-1.8	118.9	55.7	-1.1
A_84_P851976	12497.8	4366.8	-1.5	15393.6	4763.2	-1.7
A_84_P549107	49.3	17.6	-1.5	42.2	17.9	-1.2
A_84_P23812	7.4	2.7	-1.5	15.1	3.9	-1.9
A_84_P507142	7.3	2.5	-1.5	6.2	2.5	-1.3
A_84_P841491	12.2	5.7	-1.1	11.7	2.5	-2.2
A_84_P18312	3211.1	644.4	-2.3	2175	888.3	-1.3
A_84_P552861	17.9	2.4	-2.9	19.1	6.8	-1.5
A_84_P20410	6556.8	2295	-1.5	10459.4	3422.8	-1.6
A_84_P259090	121	37.3	-1.7	148.3	51.2	-1.5
A_84_P861274	27607.7	13585.8	-1	33332.9	16651.6	-1
A_84_P805566	975.6	328.5	-1.6	1176	218.1	-2.4
A_84_P15213	1656	593.7	-1.5	1508.4	624.3	-1.3
A_84_P287550	2074.3	486.9	-2.1	1184.8	249.8	-2.2
A_84_P768186	9.3	2.6	-1.8	10.8	4.2	-1.4
A_84_P251255	443	161.9	-1.5	432.2	187	-1.2
A_84_P526317	71.2	32.2	-1.1	82.3	39.3	-1.1
A_84_P13886	15.8	6.3	-1.3	14	5.4	-1.4
A_84_P12234	18231.1	7462.5	-1.3	19956.3	9435	-1.1
A_84_P809484	181.4	43.5	-2.1	160.8	50	-1.7
A_84_P804120	15	2.4	-2.6	10.4	2.5	-2.1
A_84_P240095	55.2	19.9	-1.5	52.1	19.9	-1.4
A_84_P842382	85	40.6	-1.1	87.2	28.8	-1.6
A_84_P513461	8.4	2.9	-1.5	15.9	2.5	-2.7
A_84_P127021	36.3	17.8	-1	35.9	17.9	-1
A_84_P786477	1794.7	428.8	-2.1	940.7	467.1	-1
A_84_P869953	197.7	69.8	-1.5	208.1	61.4	-1.8
A_84_P17520	636.1	167.8	-1.9	516.1	163.2	-1.7
A_84_P21478	29	11.7	-1.3	22.9	10	-1.2
A_84_P11494	30791.9	14492.7	-1.1	31085.4	15158.2	-1
A_84_P22151	1706.8	624.5	-1.5	1376.2	573.9	-1.3
A_84_P15367	119.6	43.3	-1.5	121.9	30.6	-2
A_84_P851538	128.5	45.6	-1.5	229.6	24.2	-3.2
A_84_P19734	6959.8	2405.9	-1.5	5012.8	2255.3	-1.2
A_84_P189534	19.7	9.5	-1	67.2	9.2	-2.9
A_84_P196504	1267.2	277.7	-2.2	1449.6	536.6	-1.4
A_84_P11609	47.4	18.9	-1.3	39.3	13.6	-1.5
A_84_P14690	12441	4754.4	-1.4	13446.1	4575.6	-1.6

A_84_P840120	13.1	2.7	-2.3	21.1	5.9	-1.9
A_84_P50100	3294.9	1037.6	-1.7	4546.9	751.8	-2.6
A_84_P246705	2220.1	351.8	-2.7	1552.5	555.7	-1.5
A_84_P732491	224	104.2	-1.1	248.4	100.9	-1.3
A_84_P84909	10526.1	4900.8	-1.1	6495.8	2928.7	-1.1
A_84_P164223	3518.3	1472.2	-1.3	3850.8	1676.8	-1.2
A_84_P18851	99.9	32.8	-1.6	65.9	28.2	-1.2
A_84_P101346	1859.5	833.1	-1.2	1426.3	695.4	-1
A_84_P23570	6.7	2.6	-1.4	8.5	2.6	-1.7
A_84_P89869	1134.2	516.5	-1.1	1091.6	409.2	-1.4
A_84_P817337	7.6	2.4	-1.7	8.6	4.1	-1.1
A_84_P15505	23	2.5	-3.2	7.7	2.5	-1.6
A_84_P14739	60.9	25.5	-1.3	67.4	30.2	-1.2
A_84_P806566	84528.8	39746.7	-1.1	88021.7	40182.7	-1.1
A_84_P15851	9517.3	4223.2	-1.2	13062.9	5753.6	-1.2
A_84_P824563	1341.9	417.9	-1.7	938.9	423.6	-1.1
A_84_P83919	7173.8	2836.6	-1.3	5972.7	2554.4	-1.2
A_84_P16449	454.7	74.6	-2.6	295.8	67.9	-2.1
A_84_P23323	910.5	334.5	-1.4	788.2	234.5	-1.7
A_84_P130716	345.6	128.6	-1.4	346.3	113.9	-1.6
A_84_P12982	59.2	25.4	-1.2	61.7	29.8	-1.1
A_84_P159095	1956.2	801.4	-1.3	1273.2	598.4	-1.1
A_84_P166633	2270.8	928.6	-1.3	2107.2	780.3	-1.4
A_84_P867334	1771.9	674.9	-1.4	1810	580	-1.6
A_84_P20399	2538.5	1118.8	-1.2	2308	881	-1.4
A_84_P10495	101.9	30.6	-1.7	58.3	22.6	-1.4
A_84_P10458	110.6	45.8	-1.3	121.4	45.1	-1.4
A_84_P830759	12.4	2.7	-2.2	10.9	5.3	-1
A_84_P22747	18	4.9	-1.9	6.5	2.7	-1.3
A_84_P20497	52.3	17	-1.6	56.7	14.8	-1.9
A_84_P754199	149.4	61	-1.3	170.7	56.9	-1.6
A_84_P12921	2858.1	994.2	-1.5	2675.8	1170.5	-1.2
A_84_P568745	171.7	55.7	-1.6	219.5	93	-1.2
A_84_P21553	161.8	53.6	-1.6	172	48.4	-1.8
A_84_P765839	472.5	209.5	-1.2	611.3	258.1	-1.2
A_84_P10859	102.8	41.1	-1.3	104.2	46.1	-1.2
A_84_P751876	1142.7	245.6	-2.2	1246.1	423.7	-1.6
A_84_P582075	249.3	102.6	-1.3	231.5	115.1	-1
A_84_P11449	632.3	280.3	-1.2	588.8	270.6	-1.1
A_84_P11587	10980.3	3354.1	-1.7	9673.7	3651	-1.4
A_84_P188254	411.1	168.2	-1.3	379.9	143.5	-1.4
A_84_P817628	32.5	15.5	-1.1	45.3	18.4	-1.3
A_84_P57310	728	220.9	-1.7	658.6	298.8	-1.1
A_84_P18879	28.3	8.2	-1.8	39.4	11.1	-1.8
A_84_P730385	3034.5	1278.8	-1.2	2105.4	855.1	-1.3
A_84_P17310	16.4	2.4	-2.8	11.9	3.3	-1.9
A_84_P851677	29356.6	10750.1	-1.4	38613.8	13324.5	-1.5
A_84_P602046	68.6	6.1	-3.5	84.7	13.9	-2.6
A_84_P769477	7.7	2.4	-1.7	5.1	2.4	-1.1
A_84_P22706	171	58.2	-1.6	170.1	68.2	-1.3

A_84_P540848	685.6	188.1	-1.9	817.3	260.7	-1.6
A_84_P796859	11.8	5.3	-1.1	12.7	2.5	-2.3
A_84_P22906	389	37.2	-3.4	325.8	34.5	-3.2
A_84_P750244	14.8	5.5	-1.4	18	4.9	-1.9
A_84_P852482	89.3	22.9	-2	70.8	28.3	-1.3
A_84_P582351	1644.8	737.8	-1.2	1461.7	666.5	-1.1
A_84_P14468	764.8	308.7	-1.3	826.3	177.4	-2.2
A_84_P18953	90.4	29.3	-1.6	102.6	32.5	-1.7
A_84_P15797	115	12.8	-3.2	61.7	13.3	-2.2
A_84_P757156	5.5	2.6	-1.1	7	2.5	-1.5
A_84_P23852	5177.1	160.7	-5	3164.3	181.5	-4.1
A_84_P819325	371.7	145.4	-1.4	566.5	194.6	-1.5
A_84_P507561	39.7	5.8	-2.8	40.8	5.3	-2.9
A_84_P765048	15228	4300.1	-1.8	8891.1	2301.4	-1.9
A_84_P556409	8.8	2.5	-1.8	10	2.5	-2
A_84_P10075	164.7	65.8	-1.3	143	63.2	-1.2
A_84_P14848	2275.2	882.6	-1.4	2111.6	740.1	-1.5
A_84_P13631	519.8	129.8	-2	309.8	108.6	-1.5
A_84_P14733	38501.2	11247	-1.8	40302.3	11321.4	-1.8
A_84_P826648	1117.8	485.6	-1.2	1364	484.6	-1.5
A_84_P10415	446.7	191	-1.2	449.1	170.4	-1.4
A_84_P17242	7686.7	2391.8	-1.7	4999.4	2103.5	-1.2
A_84_P188574	54543.8	25502.1	-1.1	38979.3	19307.7	-1
A_84_P812992	701.9	288.9	-1.3	647.2	301.9	-1.1
A_84_P15600	1206.5	506.4	-1.3	995.1	457.3	-1.1
A_84_P55930	9.5	2.5	-1.9	5.8	2.6	-1.2
A_84_P856597	277.8	123.9	-1.2	223.1	109.6	-1
A_84_P22852	1351	492.2	-1.5	1002.5	481.9	-1.1
A_84_P576905	3766.2	1214.7	-1.6	3960.9	1709.4	-1.2
A_84_P157075	240.2	98.6	-1.3	251.7	91.3	-1.5
A_84_P19241	4933.8	1352.1	-1.9	3884.5	1311.8	-1.6
A_84_P15870	29340.1	9532.6	-1.6	22283.1	9993.3	-1.2
A_84_P16678	67.5	20.7	-1.7	74.6	28	-1.4
A_84_P12496	44	19.4	-1.2	48.5	20.1	-1.3
A_84_P550347	36.4	9.1	-2	34.2	11.3	-1.6
A_84_P200484	318	121.8	-1.4	237	70.5	-1.7
A_84_P755699	22.2	8.9	-1.3	16	5.8	-1.5
A_84_P169473	44.9	9.2	-2.3	74.7	8.5	-3.1
A_84_P21673	27265.8	9400.3	-1.5	29920.6	8194.4	-1.9
A_84_P18221	254.8	38	-2.7	235.6	53.1	-2.1
A_84_P859880	31.5	10.3	-1.6	33.8	9.5	-1.8
A_84_P808177	1814.2	175	-3.4	996	253.2	-2
A_84_P14336	621.6	226.9	-1.5	990.4	101.4	-3.3
A_84_P818204	2249.6	804.6	-1.5	2143.4	701.7	-1.6
A_84_P235303	12.2	2.5	-2.3	12.8	3.1	-2
A_84_P12200	224.7	96.3	-1.2	255.8	86.4	-1.6
A_84_P19198	10.5	2.6	-2	9.9	2.5	-2
A_84_P764629	5.6	2.5	-1.1	6.9	2.5	-1.5
A_84_P757143	50.8	14.4	-1.8	49.6	20.4	-1.3
A_84_P11833	314.3	56.4	-2.5	358.5	78.9	-2.2

A_84_P810125	1497.6	118.8	-3.7	957.1	187.1	-2.4
A_84_P18778	613.8	208.6	-1.6	506.3	163.7	-1.6
A_84_P16943	6505.3	2721.2	-1.3	6818.3	2202.1	-1.6
A_84_P15811	80.5	29.8	-1.4	83.9	28.3	-1.6
A_84_P23557	1293.2	268.3	-2.3	1004.6	308.3	-1.7
A_84_P854328	7529.6	3620.5	-1.1	5664.9	2547.7	-1.2
A_84_P522289	76	2.6	-4.9	12	5.8	-1.1
A_84_P11660	7	2.8	-1.3	11.7	4.6	-1.4
A_84_P10042	28.1	5.4	-2.4	19.4	9.5	-1
A_84_P217028	9.2	2.5	-1.9	9.7	2.5	-2
A_84_P511590	73.5	35.3	-1.1	70.9	25.2	-1.5
A_84_P845241	5.4	2.5	-1.1	5.6	2.5	-1.2
A_84_P563250	48	12.6	-1.9	17.6	6	-1.5
A_84_P853304	450.5	62.5	-2.8	278.6	93.3	-1.6
A_84_P223759	1176.2	447.4	-1.4	1122.4	503.6	-1.2
A_84_P23021	335	114.3	-1.6	256.9	106.9	-1.3
A_84_P19176	20.6	6.9	-1.6	11.2	2.6	-2.1
A_84_P820553	324.9	78.8	-2	277.3	52.3	-2.4
A_84_P13338	1804.2	483.2	-1.9	1190.8	463.6	-1.4
A_84_P19369	11698	1494.9	-3	10147.6	1214.7	-3.1
A_84_P206178	13.6	5.5	-1.3	12.5	5	-1.3
A_84_P545837	60.8	22.7	-1.4	72.5	30.4	-1.3
A_84_P17492	27.1	10.8	-1.3	20.2	6.5	-1.6
A_84_P857089	560.7	175	-1.7	621.6	153.2	-2
A_84_P24056	2858.9	1230.8	-1.2	2120.9	923.3	-1.2
A_84_P788524	85.6	40.3	-1.1	96.9	41.6	-1.2
A_84_P23860	47.6	10.7	-2.2	96.9	12.8	-2.9
A_84_P10794	1330.7	453.5	-1.6	1508.9	375	-2
A_84_P152798	1542.2	303.4	-2.3	1676	561	-1.6
A_84_P238393	242	111.7	-1.1	220.1	105.6	-1.1
A_84_P532625	52.3	24.9	-1.1	45.8	19.6	-1.2
A_84_P272980	1583	328.6	-2.3	1687.9	580.3	-1.5
A_84_P302850	2485.1	257.3	-3.3	2474.3	300.2	-3
A_84_P11752	11.1	2.8	-2	11.3	2.6	-2.1
A_84_P22438	48.3	20.8	-1.2	52.5	14.6	-1.9
A_84_P518257	10.5	2.7	-2	13.1	2.6	-2.3
A_84_P805621	31143.7	9422	-1.7	31536	7038.2	-2.2
A_84_P121222	266	42.2	-2.7	344.1	60.1	-2.5
A_84_P583210	411.9	70.2	-2.6	310.1	103.7	-1.6
A_84_P10711	741.3	290.6	-1.4	875.8	193	-2.2
A_84_P739044	18.2	2.8	-2.7	16.6	2.6	-2.7
A_84_P544339	129.9	36.5	-1.8	82.8	40.5	-1
A_84_P579790	5.9	2.7	-1.1	17	2.6	-2.7
A_84_P606765	27.7	9.6	-1.5	26.2	10.2	-1.4
A_84_P20961	194.6	87.8	-1.1	168.8	68.8	-1.3
A_84_P597565	17.3	8.3	-1.1	23.7	7.2	-1.7
A_84_P12366	7427	2362	-1.7	6840.2	2127.2	-1.7
A_84_P13066	27459.2	12686.7	-1.1	25485	11726	-1.1
A_84_P18962	167.8	72.5	-1.2	195.1	72	-1.4
A_84_P16982	779.5	134.2	-2.5	216.3	102.7	-1.1

A_84_P787999	1781.5	369.9	-2.3	2072.5	464.1	-2.2
A_84_P24090	120.8	54.1	-1.2	130.5	53.8	-1.3
A_84_P753015	52.7	22.7	-1.2	49.9	21.1	-1.2
A_84_P16029	2249.4	844.9	-1.4	2065.8	734.4	-1.5
A_84_P17028	1399.9	301.9	-2.2	907.9	371.1	-1.3
A_84_P11686	2399.5	860.8	-1.5	1916.8	815.5	-1.2
A_84_P806966	2043.9	964.3	-1.1	3710.5	1348.9	-1.5
A_84_P813271	11.3	4.6	-1.3	15.8	4.1	-1.9
A_84_P815283	43.5	15.2	-1.5	81.5	15.5	-2.4
A_84_P815281	35	9.5	-1.9	60.2	17	-1.8
A_84_P20824	34.3	3.2	-3.4	38	4.7	-3
A_84_P796648	53.8	13.1	-2	50.1	15	-1.7
A_84_P214578	23.9	6.1	-2	22.6	7.5	-1.6
A_84_P18975	3120.7	1224.8	-1.3	3952.1	1908.5	-1.1
A_84_P297814	16.4	2.7	-2.6	6.9	2.6	-1.4
A_84_P279060	7553.6	678.1	-3.5	6619.9	589.4	-3.5
A_84_P767554	108.8	9.9	-3.5	52.1	17.7	-1.6
A_84_P547483	100.9	15.7	-2.7	71.1	17.8	-2
A_84_P545036	87.9	28.7	-1.6	76.2	33.4	-1.2
A_84_P22256	2162.1	581.2	-1.9	1442.5	719.5	-1
A_84_P788047	85.3	41.5	-1	110.8	40.9	-1.4
A_84_P849853	19135.1	9012.2	-1.1	17247.3	8112.7	-1.1
A_84_P16734	171.9	57.5	-1.6	188.2	63.5	-1.6
A_84_P19295	37	8.8	-2.1	94.3	21.3	-2.1
A_84_P841268	14.2	2.6	-2.4	14	6.1	-1.2
A_84_P557734	6.7	2.7	-1.3	155.4	4.8	-5
A_84_P826478	28.6	10.9	-1.4	44.5	10.2	-2.1
A_84_P14702	70.7	15	-2.2	89.5	22.2	-2
A_84_P70944	6047.6	2869	-1.1	4519.3	2142.7	-1.1
A_84_P13368	3097.8	1004.9	-1.6	2285.9	646.4	-1.8
A_84_P545700	58.3	13.1	-2.2	66.4	14.9	-2.2
A_84_P12012	240.1	83.4	-1.5	199.1	87.6	-1.2
A_84_P560726	899.4	365.6	-1.3	1149	513.3	-1.2
A_84_P150068	27.2	11.5	-1.2	28.9	6.3	-2.2
A_84_P752730	1302.1	638.7	-1	742.8	283.9	-1.4
A_84_P16852	4474.8	1392	-1.7	4260	1500.1	-1.5
A_84_P11441	304.3	141.8	-1.1	246.4	118.5	-1.1
A_84_P80109	88	28.6	-1.6	77.2	33	-1.2
A_84_P834918	6.7	2.9	-1.2	7.5	2.8	-1.4
A_84_P23176	2417.7	942.4	-1.4	2322.1	859.9	-1.4
A_84_P22825	24.3	8.7	-1.5	25.5	11.3	-1.2
A_84_P22594	32.9	12.7	-1.4	36.9	17.6	-1.1
A_84_P23363	2583.5	1272.7	-1	3169	1400.9	-1.2
A_84_P808697	2037.4	530.9	-1.9	2313.5	494.6	-2.2
A_84_P504795	176.3	60.7	-1.5	194.9	60.5	-1.7

A_84_P17407	9.6	2.9	-1.7	15.3	3.8	-2
A_84_P20499	329.6	120.9	-1.4	287.2	102.1	-1.5
A_84_P12139	746.6	244.9	-1.6	674	211.9	-1.7
A_84_P765785	16.3	2.7	-2.6	8.1	2.6	-1.6
A_84_P19525	3926.6	965.3	-2	4595.9	832.6	-2.5
A_84_P22100	95.2	22.7	-2.1	66	32.8	-1
A_84_P23814	3003.9	1401.9	-1.1	2536.3	1154.3	-1.1
A_84_P13266	31	2.8	-3.5	7	2.7	-1.4
A_84_P521040	26.3	2.7	-3.3	28.9	8.1	-1.8
A_84_P563787	16.1	5.4	-1.6	6.5	2.7	-1.3
A_84_P533825	8.6	3	-1.5	6.7	3	-1.2
A_84_P19943	3612.3	1017	-1.8	2138.6	1068	-1
A_84_P767553	43.7	14.6	-1.6	70	17.5	-2
A_84_P12622	28.4	14	-1	27.4	9.4	-1.5
A_84_P786948	61.4	18.4	-1.7	45.2	22.4	-1
A_84_P795916	37.9	10.4	-1.9	11.4	2.7	-2.1
A_84_P754278	11.4	2.8	-2	10.3	3	-1.8
A_84_P13270	9.5	3	-1.7	14.6	3	-2.3
A_84_P605779	1953	729.7	-1.4	1769.3	750.7	-1.2
A_84_P826232	99.2	5.6	-4.2	100.7	17.5	-2.5
A_84_P10014	27.6	12.2	-1.2	39.3	16.7	-1.2
A_84_P19565	832.8	346.6	-1.3	672.7	281.6	-1.3
A_84_P15049	26.3	8.6	-1.6	17.9	7.2	-1.3
A_84_P592920	9.7	2.7	-1.8	16.3	4.5	-1.8
A_84_P122532	76.8	22.2	-1.8	61.9	22.7	-1.4
A_84_P761565	19.4	7.6	-1.3	18.9	8.7	-1.1
A_84_P22979	65.9	26.2	-1.3	91.3	28.5	-1.7
A_84_P13832	30.4	2.9	-3.4	19	2.9	-2.7
A_84_P841862	2529.6	370.7	-2.8	1251.5	411.5	-1.6
A_84_P21494	5642.8	1655.7	-1.8	5644.6	1152.5	-2.3
A_84_P13136	10.6	2.8	-1.9	10.2	4.8	-1.1
A_84_P13983	3974.1	1517.4	-1.4	3263.1	1390.8	-1.2
A_84_P14918	6.5	2.7	-1.3	22.3	2.7	-3.1
A_84_P754916	9	3.1	-1.6	18.8	9.3	-1
A_84_P23056	22.4	3	-2.9	52.2	2.9	-4.2
A_84_P100496	4756	1973.2	-1.3	4746.2	1523.2	-1.6
A_84_P16618	361.2	172.4	-1.1	431	213.1	-1
A_84_P150708	5729	2324.7	-1.3	5019.9	2153.8	-1.2
A_84_P16800	8.4	3.1	-1.4	11.9	3	-2
A_84_P141269	2822.5	732.8	-1.9	3464.4	1246.7	-1.5
A_84_P502806	160.2	34.3	-2.2	107.7	39.8	-1.4
A_84_P840707	242.2	56.3	-2.1	231.7	61.7	-1.9
A_84_P23348	799	277.9	-1.5	768.7	357.4	-1.1
A_84_P834687	276.3	116.6	-1.2	277.2	80.1	-1.8
A_84_P570804	248.3	92.4	-1.4	243.6	77.9	-1.6
A_84_P14280	33.1	14.3	-1.2	21.1	10.1	-1.1
A_84_P839293	48.2	3.1	-4	9.7	4.5	-1.1
A_84_P509017	20.2	6.3	-1.7	68.6	11.7	-2.6
A_84_P829521	379.1	149	-1.3	311.7	152	-1
A_84_P24021	42843.6	9413.4	-2.2	46643	10923.8	-2.1

A_84_P837705	7.4	2.8	-1.4	106.6	5.5	-4.3
A_84_P288490	5569.5	1634.4	-1.8	6511.6	1420.3	-2.2
A_84_P23123	1758.9	772.5	-1.2	2364.4	808.7	-1.5
A_84_P754468	30.1	6.3	-2.3	11.6	2.7	-2.1
A_84_P14757	5.9	2.8	-1	11.9	2.7	-2.1
A_84_P860828	450.8	210.6	-1.1	375.8	141.1	-1.4
A_84_P20117	20.2	9.6	-1.1	15.1	6.8	-1.2
A_84_P16857	71.3	15.2	-2.2	75.8	34.6	-1.1
A_84_P514181	20.6	4.6	-2.2	21.2	10.5	-1
A_84_P13923	3885.8	1857.1	-1.1	3665.4	1812.6	-1
A_84_P19825	702.2	249.7	-1.5	930.7	283	-1.7
A_84_P826593	81.4	24.9	-1.7	68.7	30.2	-1.2
A_84_P751663	13.1	5.1	-1.4	15.2	5.2	-1.5
A_84_P20307	35.5	11.2	-1.7	42	17.9	-1.2
A_84_P519840	13.1	6	-1.1	13.6	6	-1.2
A_84_P13548	830.7	245.3	-1.8	708.9	283.5	-1.3
A_84_P593798	29	13.3	-1.1	23.5	9.3	-1.3
A_84_P750062	8	3	-1.4	7.6	2.7	-1.5
A_84_P160313	7.4	2.9	-1.3	8	2.7	-1.6
A_84_P574525	10.4	3.2	-1.7	11.5	5.1	-1.2
A_84_P24038	17.4	3.2	-2.5	8	3.1	-1.4
A_84_P596819	47.4	23.7	-1	44.3	19.2	-1.2
A_84_P802777	8.7	2.8	-1.6	11.1	2.7	-2
A_84_P10329	1571.9	699.9	-1.2	1195.1	515.8	-1.2
A_84_P594594	282.3	81.7	-1.8	279.1	72.7	-1.9
A_84_P803243	46.3	13.1	-1.8	40	12.9	-1.6
A_84_P816625	4054.1	1909.7	-1.1	3176.6	1318.2	-1.3
A_84_P14703	2315.1	847	-1.5	1698.2	767.3	-1.1
A_84_P167173	4377.6	520.8	-3.1	3565.4	443.6	-3
A_84_P19161	2355.2	792	-1.6	2408.4	667.6	-1.9
A_84_P244675	58.3	27	-1.1	55.5	20.3	-1.4
A_84_P501388	497.5	160.4	-1.6	483.5	140.3	-1.8
A_84_P608949	1615.7	538.8	-1.6	1121.2	492.3	-1.2
A_84_P800587	30.2	10.7	-1.5	17.3	8.4	-1.1
A_84_P292994	1919.7	926.6	-1.1	2276	914	-1.3
A_84_P768863	467.8	159.8	-1.5	332.3	107.6	-1.6
A_84_P820867	721.6	298.5	-1.3	761.6	307.3	-1.3
A_84_P13860	6.3	2.9	-1.1	14.2	2.9	-2.3
A_84_P844663	16.5	8.2	-1	45.2	14.2	-1.7
A_84_P509353	102.7	47	-1.1	136.8	41.9	-1.7
A_84_P20704	239.1	22.8	-3.4	156.3	42.7	-1.9
A_84_P767389	6.8	2.8	-1.3	6.8	2.7	-1.3
A_84_P804208	99.1	37.3	-1.4	36.6	16.8	-1.1
A_84_P93449	355	169.5	-1.1	287.8	121.6	-1.2
A_84_P761129	12.9	6.1	-1.1	10.4	5.2	-1
A_84_P832423	615.6	27.6	-4.5	7.5	2.8	-1.4
A_84_P847991	525.3	123.4	-2.1	412.7	141.5	-1.5
A_84_P10469	196.6	91.4	-1.1	200.5	77.8	-1.4
A_84_P23101	1158.5	379	-1.6	696.2	271.9	-1.4
A_84_P558384	7.3	3.2	-1.2	13.1	3.1	-2.1

A_84_P507386	22.6	5.6	-2	45.4	6.7	-2.8
A_84_P538813	116.6	47.1	-1.3	499	50.6	-3.3
A_84_P535484	31.5	10.9	-1.5	37.4	15	-1.3
A_84_P20629	429.5	35.4	-3.6	53.9	26.9	-1
A_84_P10080	220.1	105.9	-1.1	246.6	87.3	-1.5
A_84_P579536	68.2	5.8	-3.6	57	9.3	-2.6
A_84_P19459	55.4	17.1	-1.7	413.2	29	-3.8
A_84_P11841	264.9	66.8	-2	245.7	120.3	-1
A_84_P10642	2023.6	825.9	-1.3	2288.2	592.8	-1.9
A_84_P763660	492.1	2.9	-7.4	8.9	2.8	-1.7
A_84_P769485	31.6	15.6	-1	21	9.6	-1.1
A_84_P841791	24.4	7.8	-1.6	7.1	3	-1.2
A_84_P14963	1026.1	261.8	-2	905.5	334.4	-1.4
A_84_P23993	6.3	2.9	-1.1	21.8	2.9	-2.9
A_84_P761618	49.4	24.5	-1	45.4	10.3	-2.1
A_84_P581530	6.5	2.9	-1.2	8.8	2.8	-1.6
A_84_P17513	100.4	12.6	-3	87.9	15.1	-2.5
A_84_P24136	50.3	18.7	-1.4	42.7	19.2	-1.2
A_84_P20056	46.7	2.9	-4	9	2.8	-1.7
A_84_P586802	2464.9	1000.1	-1.3	2295	1026.5	-1.2
A_84_P55550	1285.7	87.4	-3.9	2159.5	229.4	-3.2
A_84_P23045	4647.7	1691	-1.5	3956	1671.2	-1.2
A_84_P14587	2813.1	904	-1.6	2427.5	1057.1	-1.2
A_84_P516878	353.9	121.2	-1.5	324.2	131.3	-1.3
A_84_P605408	26.2	9.2	-1.5	19.6	6.3	-1.6
A_84_P141439	13908.2	4727.2	-1.6	13666.6	3999.1	-1.8
A_84_P17974	5922.9	1832.9	-1.7	3949.6	1256.3	-1.7
A_84_P826986	889.6	374.6	-1.2	803.8	308.7	-1.4
A_84_P22866	3719.3	698.2	-2.4	2650.9	905.4	-1.5
A_84_P18547	9.4	2.9	-1.7	11.2	3.2	-1.8
A_84_P18780	66.9	27	-1.3	61.8	29.5	-1.1
A_84_P16979	39	10.3	-1.9	8.4	3	-1.5
A_84_P12749	125.8	60	-1.1	111.7	42.3	-1.4
A_84_P842320	179.1	72.2	-1.3	256.1	95.9	-1.4
A_84_P17440	19.4	3.1	-2.7	8.9	3	-1.6
A_84_P727405	11.6	3	-2	7.2	2.9	-1.3
A_84_P769532	29.9	9.4	-1.7	31.8	10.8	-1.6
A_84_P768411	8.1	3.3	-1.3	28.7	2.8	-3.3
A_84_P808711	8466.2	2443.4	-1.8	10521.8	2036.9	-2.4
A_84_P19743	1262.1	356.8	-1.8	1072	379	-1.5
A_84_P286640	875.5	149.6	-2.5	543.4	165.6	-1.7
A_84_P126821	117	4.9	-4.6	91.1	2.8	-5
A_84_P22349	54.7	24.3	-1.2	46.3	8.7	-2.4
A_84_P16475	3258.3	1077.9	-1.6	2380.7	743.1	-1.7
A_84_P21000	201.5	68.5	-1.6	162.2	58.3	-1.5
A_84_P13057	2496.5	654.5	-1.9	2191.7	654.9	-1.7
A_84_P18269	338.4	121.5	-1.5	276.3	136.1	-1
A_84_P71314	24.7	6.7	-1.9	23.4	8.9	-1.4
A_84_P11342	47145.6	19354.6	-1.3	34838.6	15728.2	-1.1
A_84_P750690	212	95.7	-1.1	186.6	91.4	-1

A_84_P11065	34.5	13.3	-1.4	47.4	21.5	-1.1
A_84_P23387	352.1	133.3	-1.4	350.6	115.3	-1.6
A_84_P291304	12506.3	3209.7	-2	13348.3	3333.2	-2
A_84_P297634	3675.9	1763.8	-1.1	4535.8	2072.5	-1.1
A_84_P868627	41835.2	14744	-1.5	46667.5	13886.7	-1.7
A_84_P19272	195.3	81.2	-1.3	175.4	44.9	-2
A_84_P12779	162.8	78.4	-1.1	140.6	60.2	-1.2
A_84_P21135	410.5	96.8	-2.1	440.1	148.4	-1.6
A_84_P606188	1371.1	117.4	-3.5	661.6	134.4	-2.3
A_84_P19657	237.7	118.7	-1	292.4	143.3	-1
A_84_P21248	1140.2	371.7	-1.6	797.1	316.2	-1.3
A_84_P575245	345.8	163.6	-1.1	284.4	135.4	-1.1
A_84_P838453	214.5	74.6	-1.5	185.7	87.4	-1.1
A_84_P285230	3320	1432.5	-1.2	2721.6	1071.1	-1.3
A_84_P243945	6212.6	1758	-1.8	6942.6	1768.2	-2
A_84_P22556	142.3	58.9	-1.3	127.4	56.6	-1.2
A_84_P549446	381.2	72	-2.4	215	107.2	-1
A_84_P818278	1068.7	480.8	-1.2	975.1	453.2	-1.1
A_84_P515014	253.3	106.2	-1.3	216.9	61	-1.8
A_84_P130806	6.8	3.3	-1	6.5	3.2	-1
A_84_P769455	61.7	30	-1	67.5	27.9	-1.3
A_84_P851812	39.8	3	-3.7	14.3	4.7	-1.6
A_84_P10699	151.4	74	-1	160.4	70.8	-1.2
A_84_P803335	1476.7	132.2	-3.5	688.2	143.2	-2.3
A_84_P145309	65.5	29.4	-1.2	53.3	22.5	-1.2
A_84_P17663	35.2	13	-1.4	26.6	6.9	-2
A_84_P762142	1261.1	479.1	-1.4	690.7	295.7	-1.2
A_84_P793175	9.8	3.1	-1.7	11	3.4	-1.7
A_84_P14098	25.3	9.2	-1.5	13.4	6.2	-1.1
A_84_P13263	29.6	7.7	-1.9	17.5	6.5	-1.4
A_84_P506967	20.4	6.1	-1.7	19.2	5.6	-1.8
A_84_P14449	3362.1	850.6	-2	2398	781.1	-1.6
A_84_P19141	27	3.1	-3.1	18.1	6.2	-1.5
A_84_P853705	10.2	2.9	-1.8	18.5	5	-1.9
A_84_P556726	523	244	-1.1	416.5	203.5	-1
A_84_P17344	12.4	3	-2.1	32.6	2.9	-3.5
A_84_P768715	31	3.2	-3.3	35.7	5.5	-2.7
A_84_P737916	46.2	20.8	-1.2	35.5	16.9	-1.1
A_84_P806997	117015.8	45914	-1.3	144828.5	55600.7	-1.4
A_84_P23247	18.2	3.2	-2.5	23.3	11.5	-1
A_84_P102366	57.8	25.7	-1.2	47.4	19.7	-1.3
A_84_P573240	60.2	14.5	-2.1	55.9	23.8	-1.2
A_84_P23070	1575.1	505.5	-1.6	898.8	345.6	-1.4
A_84_P161343	802.8	308.4	-1.4	606.7	283.3	-1.1
A_84_P237883	19103.3	8561.3	-1.2	16137.6	7730.9	-1.1
A_84_P834773	205.9	72.1	-1.5	210.7	92.1	-1.2
A_84_P835531	256.6	44.2	-2.5	182.8	44.1	-2.1
A_84_P22306	20.3	7.3	-1.5	17.9	4.9	-1.9
A_84_P10874	2652.3	77.9	-5.1	1118	106	-3.4
A_84_P260340	992.2	449.3	-1.1	1421.3	544.3	-1.4

A_84_P20360	11.3	3	-1.9	17.4	3.9	-2.1
A_84_P162983	22161.3	7725.2	-1.5	25964.6	8384.3	-1.6
A_84_P112782	41.6	14.6	-1.5	47	11.2	-2.1
A_84_P20553	119.5	44.9	-1.4	115.7	41.9	-1.5
A_84_P172851	131.6	46.2	-1.5	145.3	40	-1.9
A_84_P24057	1109	311.4	-1.8	1213.3	308.1	-2
A_84_P786520	393	147.7	-1.4	294.5	127	-1.2
A_84_P750390	110.4	23.4	-2.2	157.7	37.3	-2.1
A_84_P591116	26.9	5.7	-2.2	15.3	7.3	-1.1
A_84_P20577	55.2	20.9	-1.4	75	16.9	-2.1
A_84_P844479	9.3	3.4	-1.4	9.8	3.2	-1.6
A_84_P194044	41.3	16.4	-1.3	41.9	18.8	-1.2
A_84_P52180	24.1	8.6	-1.5	13.6	3.5	-2
A_84_P789572	119.7	59.4	-1	135.5	63.1	-1.1
A_84_P751783	533.7	171	-1.6	510.5	148.3	-1.8
A_84_P593014	182.5	89	-1	167	73.3	-1.2
A_84_P10702	1017.8	361.5	-1.5	806.8	266	-1.6
A_84_P16621	20.6	5.1	-2	21.1	5	-2.1
A_84_P12475	6.1	3	-1	6.8	2.9	-1.2
A_84_P308073	3618.7	1044.1	-1.8	2359.4	1081.5	-1.1
A_84_P523896	1503.1	349.8	-2.1	1321.9	384.9	-1.8
A_84_P758419	85.1	39.6	-1.1	85.6	32.8	-1.4
A_84_P284610	186.3	69.3	-1.4	161.5	63.5	-1.3
A_84_P20771	127.8	42.4	-1.6	121.1	28.5	-2.1
A_84_P301340	1078.5	405.4	-1.4	847.9	381.7	-1.2
A_84_P736161	1214.7	79.7	-3.9	186.3	62	-1.6
A_84_P595814	119.3	10.6	-3.5	105.8	20.5	-2.4
A_84_P24121	710.9	287.5	-1.3	664.5	246.5	-1.4
A_84_P20210	861.1	177.8	-2.3	490.1	217.1	-1.2
A_84_P841601	8.4	3.2	-1.4	7.7	3.3	-1.2
A_84_P787196	13.9	4.3	-1.7	12.4	5.1	-1.3
A_84_P16699	40.5	15.4	-1.4	25.5	11.1	-1.2
A_84_P551816	10.6	5.2	-1	15.2	4.5	-1.8
A_84_P16114	357.7	3.9	-6.5	284.9	3.5	-6.4
A_84_P788181	1458.6	492.7	-1.6	1617.8	436	-1.9
A_84_P841062	6.6	3.2	-1.1	8.7	2.9	-1.6
A_84_P541401	72.2	27.4	-1.4	82.8	32.4	-1.4
A_84_P16823	3814.2	1010.8	-1.9	2961.7	997.2	-1.6
A_84_P766364	65.7	15.4	-2.1	20.9	8.2	-1.3
A_84_P10296	26624.2	10266	-1.4	25887.1	9474.2	-1.5
A_84_P19392	65.4	24.5	-1.4	69.1	34.1	-1
A_84_P115902	81.2	27.2	-1.6	98.6	34.7	-1.5
A_84_P847692	256203	101913	-1.3	272751.6	97608.2	-1.5
A_84_P808818	18155.3	5859.7	-1.6	18237.3	4320.3	-2.1
A_84_P23867	12.1	4.4	-1.5	11	3.8	-1.5
A_84_P832177	6.8	3.1	-1.1	8.6	3	-1.5
A_84_P20327	8.8	3.9	-1.2	7.8	3.4	-1.2
A_84_P11000	43.9	13.7	-1.7	49.5	18	-1.5
A_84_P10799	504	207.8	-1.3	364.9	78.1	-2.2
A_84_P17637	9040.8	2192.4	-2	5293.1	2069.3	-1.4

A_84_P18911	44.1	15.2	-1.5	52.7	15.7	-1.7
A_84_P841973	727.5	263.5	-1.5	583.2	250.8	-1.2
A_84_P17175	354.4	89.2	-2	398.1	147.6	-1.4
A_84_P63754	2200.8	894.6	-1.3	2783.5	882.6	-1.7
A_84_P16548	29	8.1	-1.8	33.7	12.4	-1.4
A_84_P23654	22760.1	8508	-1.4	17328.2	7703	-1.2
A_84_P565128	13.6	3.2	-2.1	12	4.9	-1.3
A_84_P11099	1979.7	953.5	-1.1	1548.2	748.7	-1
A_84_P851624	1751	560.6	-1.6	2207.6	493.7	-2.2

Supplemental Table 8. Cluster analysis of down-regulated genes in microarray analysis, *ztl-3/ztl-105* mutants compared with WT (upper aerial parts)

Annotation Cluster 1: Enrichment Score: 6.395116037422884			
Term	Count	%	PValue
response to endogenous stimulus	61	8.37912088	2.7E-08
response to auxin stimulus	31	4.25824176	5.9E-08
response to hormone stimulus	53	7.28021978	0.00000235
response to organic substance	62	8.51648352	0.00000702
Annotation Cluster 2: Enrichment Score: 4.863686385135738			
Term	Count	%	PValue
response to red or far red light	20	2.74725275	0.00000056
response to abiotic stimulus	64	8.79120879	0.00000298
response to light stimulus	30	4.12087912	0.000109
response to radiation	30	4.12087912	0.000193
Annotation Cluster 3: Enrichment Score: 4.507582420379099			
Term	Count	%	PValue
response to red or far red light	20	2.74725275	0.00000056
response to red light	9	1.23626374	0.000206
response to far red light	8	1.0989011	0.00026
Annotation Cluster 4: Enrichment Score: 2.915235714334651			
Term	Count	%	PValue
phenylpropanoid catabolic process	6	0.82417582	0.0000962
lignin catabolic process	6	0.82417582	0.0000962
aromatic compound catabolic process	7	0.96153846	0.000131
cellular amino acid derivative catabolic proce	6	0.82417582	0.00138271
cellular amino acid derivative metabolic proc	18	2.47252747	0.00367767
lignin metabolic process	7	0.96153846	0.01160416
phenylpropanoid metabolic process	10	1.37362637	0.05489424
Annotation Cluster 5: Enrichment Score: 2.84054453061101			
Term	Count	%	PValue
secondary cell wall biogenesis	6	0.82417582	0.00013
plant-type cell wall biogenesis	7	0.96153846	0.00431628
cell wall biogenesis	8	1.0989011	0.00536274

Annotation Cluster 6: Enrichment Score: 2.597274741756561			
Term	Count	%	PValue
cell wall organization	20	2.74725275	0.000519
external encapsulating structure organization	20	2.74725275	0.00101962
cell wall modification	11	1.51098901	0.00626039
polysaccharide metabolic process	14	1.92307692	0.01232364

Annotation Cluster 7: Enrichment Score: 2.4252166346225668			
Term	Count	%	PValue
regulation of transcription	97	13.3241758	5.76E-07
regulation of transcription, DNA-dependent	36	4.94505495	0.29793765
regulation of RNA metabolic process	36	4.94505495	0.30871936

Annotation Cluster 8: Enrichment Score: 1.886146835639398			
Term	Count	%	PValue
post-embryonic development	43	5.90659341	0.000598
reproductive structure development	37	5.08241758	0.00152623
reproductive developmental process	38	5.21978022	0.00436995
fruit development	20	2.74725275	0.07145282
seed development	19	2.60989011	0.08429013
embryonic development ending in seed dorma	15	2.06043956	0.20057238

Annotation Cluster 9: Enrichment Score: 1.5985917889387538			
Term	Count	%	PValue
glycoside biosynthetic process	7	0.96153846	0.00928707
glucosinolate biosynthetic process	5	0.68681319	0.00956681
glycosinolate biosynthetic process	5	0.68681319	0.00956681
S-glycoside biosynthetic process	5	0.68681319	0.00956681
glycoside metabolic process	7	0.96153846	0.03617498
glucosinolate metabolic process	5	0.68681319	0.03892575
S-glycoside metabolic process	5	0.68681319	0.03892575
glycosinolate metabolic process	5	0.68681319	0.03892575
sulfur metabolic process	10	1.37362637	0.06377456
sulfur compound biosynthetic process	7	0.96153846	0.09335431

Annotation Cluster 10: Enrichment Score: 1.5966764466075574

Term	Count	%	PValue
carbohydrate biosynthetic process	19	2.60989011	0.000492
cellular carbohydrate biosynthetic process	15	2.06043956	0.00133087
cellular polysaccharide metabolic process	12	1.64835165	0.00556463
glycoside biosynthetic process	7	0.96153846	0.00928707
polysaccharide metabolic process	14	1.92307692	0.01232364
cellular glucan metabolic process	9	1.23626374	0.02900603
glucan metabolic process	10	1.37362637	0.03323374
glycoside metabolic process	7	0.96153846	0.03617498
cellular polysaccharide biosynthetic process	7	0.96153846	0.08112908
polysaccharide biosynthetic process	7	0.96153846	0.09335431
glucan biosynthetic process	5	0.68681319	0.17612758
cellulose metabolic process	4	0.54945055	0.29555287
cellulose biosynthetic process	3	0.41208791	0.30536007

Annotation Cluster 11: Enrichment Score: 1.5712267624467662

Term	Count	%	PValue
hyperosmotic salinity response	6	0.82417582	0.00726547
hyperosmotic response	6	0.82417582	0.01380213
response to salt stress	15	2.06043956	0.19280123

Annotation Cluster 12: Enrichment Score: 1.342870481768334

Term	Count	%	PValue
cell wall biogenesis	8	1.0989011	0.00536274
cellular cell wall macromolecule metabolic p	3	0.41208791	0.05370437
cell wall macromolecule metabolic process	5	0.68681319	0.05774068
cell wall polysaccharide metabolic process	3	0.41208791	0.06959655
cellular polysaccharide biosynthetic process	7	0.96153846	0.08112908
polysaccharide biosynthetic process	7	0.96153846	0.09335431

Annotation Cluster 13: Enrichment Score: 1.1091974042776358

Term	Count	%	PValue
red or far red light signaling pathway	9	1.23626374	0.000524
red, far-red light phototransduction	4	0.54945055	0.14365039
detection of light stimulus	4	0.54945055	0.14365039
phototransduction	4	0.54945055	0.14365039
detection of abiotic stimulus	4	0.54945055	0.17185455
detection of external stimulus	4	0.54945055	0.20146526
detection of stimulus	4	0.54945055	0.31966375

Annotation Cluster 14: Enrichment Score: 1.0339782894844969			
Term	Count	%	PValue
plant-type cell wall loosening	6	0.82417582	0.00327483
cell wall modification	11	1.51098901	0.00626039
plant-type cell wall organization	8	1.0989011	0.00768406
plant-type cell wall modification	6	0.82417582	0.00971922
syncytium formation	3	0.41208791	0.06147341
developmental growth involved in morphogen	9	1.23626374	0.08720049
unidimensional cell growth	9	1.23626374	0.08720049
developmental growth	9	1.23626374	0.15751543
plant-type cell wall modification during multi	3	0.41208791	0.17539289
cell growth	10	1.37362637	0.17578957
cell wall modification during multidimensiona	3	0.41208791	0.19664366
regulation of cell size	10	1.37362637	0.21734684
regulation of cellular component size	10	1.37362637	0.26222771
cell morphogenesis	9	1.23626374	0.26357034
growth	10	1.37362637	0.29358407
cellular component morphogenesis	9	1.23626374	0.36408266
multidimensional cell growth	3	0.41208791	0.39066581
sexual reproduction	3	0.41208791	0.57039916

Annotation Cluster 15: Enrichment Score: 0.9964015039319278			
Term	Count	%	PValue
methionine metabolic process	5	0.68681319	0.05431971
aspartate family amino acid metabolic proces	6	0.82417582	0.05638592
ethylene biosynthetic process	3	0.41208791	0.1146153
ethylene metabolic process	3	0.41208791	0.1146153
alkene biosynthetic process	3	0.41208791	0.12433474
cellular alkene metabolic process	3	0.41208791	0.12433474
sulfur amino acid metabolic process	5	0.68681319	0.17036927

Annotation Cluster 16: Enrichment Score: 0.9879861984149876			
Term	Count	%	PValue
intracellular signaling cascade	34	4.67032967	0.02459862
auxin mediated signaling pathway	8	1.0989011	0.05564328
hormone-mediated signaling	16	2.1978022	0.28567084
cellular response to hormone stimulus	16	2.1978022	0.28567084

Annotation Cluster 17: Enrichment Score: 0.8794203102758386			
Term	Count	%	PValue
regulation of timing of transition from vegetati	3	0.41208791	0.08679761
regulation of timing of meristematic phase tra	3	0.41208791	0.08679761
regulation of development, heterochronic	3	0.41208791	0.18597484
regulation of meristem development	4	0.54945055	0.21669506

Annotation Cluster 18: Enrichment Score: 0.8205473894709745			
Term	Count	%	PValue
flower development	15	2.06043956	0.00837828
floral whorl development	6	0.82417582	0.198349
gynoecium development	4	0.54945055	0.21669506
post-embryonic organ development	8	1.0989011	0.26510436
floral organ development	6	0.82417582	0.2965346
carpel development	3	0.41208791	0.42149242

Annotation Cluster 19: Enrichment Score: 0.8069726735363173			
Term	Count	%	PValue
amino acid transport	5	0.68681319	0.12695234
amine transport	5	0.68681319	0.13209958
organic acid transport	5	0.68681319	0.18783806
carboxylic acid transport	5	0.68681319	0.18783806

Annotation Cluster 20: Enrichment Score: 0.7026299745626389			
Term	Count	%	PValue
response to gibberellin stimulus	7	0.96153846	0.13551482
gibberellin-mediated signaling	3	0.41208791	0.23991734
gibberellic acid mediated signaling	3	0.41208791	0.23991734

Annotation Cluster 21: Enrichment Score: 0.6380327581935898			
Term	Count	%	PValue
photoperiodism	4	0.54945055	0.11088981
response to gibberellin stimulus	7	0.96153846	0.13551482
photoperiodism, flowering	3	0.41208791	0.29448314
vegetative to reproductive phase transition	3	0.41208791	0.63376766

Annotation Cluster 22: Enrichment Score: 0.6068700905582817			
Term	Count	%	PValue
biogenic amine metabolic process	5	0.68681319	0.09347233
biogenic amine biosynthetic process	4	0.54945055	0.11088981
amine biosynthetic process	10	1.37362637	0.14422708
organic acid biosynthetic process	16	2.1978022	0.21463688
carboxylic acid biosynthetic process	16	2.1978022	0.21463688
cellular amino acid biosynthetic process	8	1.0989011	0.29249078
heterocycle biosynthetic process	4	0.54945055	0.74585207
nitrogen compound biosynthetic process	11	1.51098901	0.92948883

Annotation Cluster 23: Enrichment Score: 0.5068205706028447			
Term	Count	%	PValue
terpenoid metabolic process	6	0.82417582	0.15894955
terpenoid biosynthetic process	5	0.68681319	0.19378522
terpene metabolic process	3	0.41208791	0.29448314
isoprenoid metabolic process	6	0.82417582	0.35424343
isoprenoid biosynthetic process	5	0.68681319	0.42126166
lipid biosynthetic process	12	1.64835165	0.67232993
Annotation Cluster 24: Enrichment Score: 0.23371340590737458			
Term	Count	%	PValue
transmembrane receptor protein tyrosine kinas	5	0.68681319	0.52935834
enzyme linked receptor protein signaling path	5	0.68681319	0.52935834
cell surface receptor linked signal transductio	5	0.68681319	0.71016662
Annotation Cluster 25: Enrichment Score: 0.21154629557148896			
Term	Count	%	PValue
cellular response to extracellular stimulus	4	0.54945055	0.42324873
response to extracellular stimulus	4	0.54945055	0.5137706
cellular response to nutrient levels	3	0.41208791	0.60303646
response to nutrient levels	3	0.41208791	0.68960005
cellular response to stress	8	1.0989011	0.96819482
Annotation Cluster 26: Enrichment Score: 0.20928910101165435			
Term	Count	%	PValue
photosynthesis, light harvesting	3	0.41208791	0.23991734
photosynthesis, light reaction	3	0.41208791	0.71479071
photosynthesis	4	0.54945055	0.88967839
generation of precursor metabolites and energ	8	1.0989011	0.95360829
Annotation Cluster 27: Enrichment Score: 0.15697070061690832			
Term	Count	%	PValue
meiotic cell cycle	3	0.41208791	0.54467428
gametophyte development	6	0.82417582	0.64642768
pollen development	4	0.54945055	0.73171384
cell cycle	5	0.68681319	0.91436398
Annotation Cluster 28: Enrichment Score: 0.153568188353182			
Term	Count	%	PValue
two-component signal transduction system (ph	7	0.96153846	0.61636772
ethylene mediated signaling pathway	5	0.68681319	0.73617385
response to ethylene stimulus	7	0.96153846	0.76291326

Annotation Cluster 29: Enrichment Score: 0.15275832380725257			
Term	Count	%	PValue
lipid biosynthetic process	12	1.64835165	0.67232993
fatty acid biosynthetic process	5	0.68681319	0.68710778
fatty acid metabolic process	6	0.82417582	0.7535598
Annotation Cluster 30: Enrichment Score: 0.13689851619919985			
Term	Count	%	PValue
metal ion transport	9	1.23626374	0.45745402
transition metal ion transport	3	0.41208791	0.63376766
ion transport	12	1.64835165	0.85802569
cation transport	9	1.23626374	0.87586164
monovalent inorganic cation transport	3	0.41208791	0.94906094
Annotation Cluster 31: Enrichment Score: 0.12760756870504			
Term	Count	%	PValue
response to oxidative stress	9	1.23626374	0.60406417
response to hydrogen peroxide	4	0.54945055	0.66898249
response to reactive oxygen species	4	0.54945055	0.78065498
response to inorganic substance	10	1.37362637	0.97861703
Annotation Cluster 32: Enrichment Score: 0.06089195730864939			
Term	Count	%	PValue
response to fungus	11	1.51098901	0.82855204
defense response to fungus	10	1.37362637	0.82907145
defense response	23	3.15934066	0.95589981
Annotation Cluster 33: Enrichment Score: 0.05003481528405651			
Term	Count	%	PValue
hexose metabolic process	4	0.54945055	0.84774949
glucose metabolic process	3	0.41208791	0.85708404
monosaccharide metabolic process	4	0.54945055	0.91033193
generation of precursor metabolites and energ	8	1.0989011	0.95360829

Annotation Cluster 34: Enrichment Score: 0.0027518543044451754			
Term	Count	%	PValue
cellular macromolecule localization	5	0.68681319	0.97886397
intracellular protein transport	4	0.54945055	0.98782847
cellular protein localization	4	0.54945055	0.99063054
intracellular transport	4	0.54945055	0.99942437
protein transport	5	0.68681319	0.99971511
establishment of protein localization	5	0.68681319	0.99971511
protein localization	5	0.68681319	0.99981345

Annotation Cluster 35: Enrichment Score: 0.002341621852032989			
Term	Count	%	PValue
macromolecule catabolic process	13	1.78571429	0.981483
cellular macromolecule catabolic process	10	1.37362637	0.99082133
modification-dependent protein catabolic proc	8	1.0989011	0.99697827
modification-dependent macromolecule catab	8	1.0989011	0.99697827
proteolysis involved in cellular protein catab	8	1.0989011	0.99727071
cellular protein catabolic process	8	1.0989011	0.99758601
ubiquitin-dependent protein catabolic process	3	0.41208791	0.99775495
protein catabolic process	8	1.0989011	0.99822905

Annotation Cluster 36: Enrichment Score: 0.0015173277842208742			
Term	Count	%	PValue
protein amino acid phosphorylation	21	2.88461539	0.98977661
phosphorylation	21	2.88461539	0.99804318
phosphate metabolic process	22	3.02197802	0.99912325
phosphorus metabolic process	22	3.02197802	0.99913715

Cluster 1-1: response to endogenous stimulus			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log2 Ratic	Log2 Ratic
A_84_P17344	AT2G22810	1-aminocyclopropane-1-carboxylate synthase 4, ACS4	-2.1	-3.5
A_84_P23570	AT5G65800	1-aminocyclopropane-1-carboxylate synthase 5, ACS5	-1.4	-1.7
A_84_P23812	AT1G13430	ARABIDOPSIS THALIANA SULFOTRANSFERASE 4C, ATST4C	-1.5	-1.9
A_84_P13338	AT1G18710	ATMYB47, MYB DOMAIN PROTEIN 47, MYB47	-1.9	-1.4
A_84_P291304	AT1G29395	COLD REGULATED 314 INNER MEMBRANE 1, COLD REGULATED 314 THYLAKOID MEMBRANE 1, COLD REGULATED 414 THYLAKOID MEMBRANE 1, COR413-TM1, COR413IM1, COR414-TM1	-2	-2
A_84_P16823	AT1G01060	LATE ELONGATED HYPOCOTYL, LHY	-1.9	-1.6
A_84_P537376	AT1G29420	SMALL AUXIN UPREGULATED RNA 61, SAUR61	-1.7	-1.2
A_84_P10257	AT1G29430	SMALL AUXIN UPREGULATED RNA 62, SAUR62	-1.3	-1
A_84_P19713	AT1G29450	SMALL AUXIN UPREGULATED RNA 64, AUR64	-1.6	-1.4
A_84_P11207	AT1G29500	SMALL AUXIN UPREGULATED RNA 66, SAUR66	-1.8	-1.1
A_84_P17068	AT1G75590	SMALL AUXIN UPREGULATED RNA 52, SAUR52	-1.9	-1.7
A_84_P12605	AT2G18010	SMALL AUXIN UPREGULATED RNA 10, SAUR10	-1.6	-1.2
A_84_P21026	AT2G33380	ARABIDOPSIS THALIANA CALEOSIN 3, ATCLO3	-1.6	-1.2
A_84_P14449	AT2G34810	FAD-binding Berberine family protein	-2	-1.6
A_84_P19241	AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1, ATCCA1, CCA1	-1.9	-1.6
A_84_P21135	AT3G03820	SMALL AUXIN UP RNA 29, SAUR29	-2.1	-1.6
A_84_P18297	AT3G03840	SMALL AUXIN UP RNA 27, SAUR27	-1.6	-1.4
A_84_P554482	AT3G03850	SMALL AUXIN UP RNA 26, SAUR26	-1.9	-1.4
A_84_P11752	AT3G30210	ATMYB121, MYB DOMAIN PROTEIN 121, MYB121	-2	-2.1
A_84_P20399	AT4G03400	DFL2, DWARF IN LIGHT 2, GH3-10	-1.2	-1.4
A_84_P308073	AT4G12030	BASS5, BAT5, BILE ACID TRANSPORTER 5, BILE ACID : SODIUM SYMPORTER FAMILY PROTEIN 5	-1.8	-1.1
A_84_P21376	AT4G13790	SMALL AUXIN UPREGULATED RNA 25, SAUR25	-2.1	-1.6
A_84_P16734	AT4G38850	ARABIDOPSIS COLUMBIA SAUR GENE 1, ARABIDOPSIS THALIANA SMALL AUXIN UPREGULATED 15, ATSAUR15, SAUR-AC1, SAUR15, SAUR_AC1, SMALL AUXIN UP RNA 1 FROM ARABIDOPSIS THALIANA ECOTYPE COLUMBIA, SMALL AUXIN UPREGULATED 15	-1.6	-1.6
A_84_P18673	AT5G07690	ATMYB29, MYB DOMAIN PROTEIN 29, MYB29, PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 2, PMG2	-2.4	-1.8
A_84_P19619	AT5G07700	ATMYB76, MYB DOMAIN PROTEIN 76, MYB76	-2.3	-1
A_84_P196504	AT5G18010	SMALL AUXIN UP RNA 19, SAUR19	-2.2	-1.4
A_84_P147028	AT5G18020	SMALL AUXIN UP RNA 20, SAUR20	-2.3	-1.5
A_84_P152798	AT5G18030	SMALL AUXIN UP RNA 21, SAUR21	-2.3	-1.6
A_84_P141269	AT5G18050	SMALL AUXIN UP RNA 22, SAUR22	-1.9	-1.5
A_84_P272980	AT5G18080	SMALL AUXIN UP RNA 24, SAUR24	-2.3	-1.5
A_84_P279980	AT1G29440	SMALL AUXIN UP RNA 63, SAUR63	-1.8	-1.3
A_84_P606561	AT5G59845	Gibberellin-regulated family protein	-1.4	-1.7
A_84_P11622	AT2G21050	Auxin transporter-like protein 2, LAX2	-1.6	-1.4
A_84_P10124	AT4G14560	Auxin-responsive protein IAA1	-1.7	-1.9
A_84_P23363	AT4G14550	Auxin-responsive protein IAA14	-1	-1.2
A_84_P14556	AT3G15540	Auxin-responsive protein IAA19	-1.4	-1.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P14702	AT3G62100	Auxin-responsive protein IAA30	-2.2	-2
A_84_P18064	AT1G15580	Auxin-responsive protein IAA5	-2.3	-1.5
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P18763	AT5G45820	CBL-interacting serine/threonine-protein kinase 20	-1	-1.8
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P10874	AT3G50970	Dehydrin Xero 2	-5.1	-3.4
A_84_P11587	AT2G39800	Delta-1-pyrroline-5-carboxylate synthetase A	-1.7	-1.4

A_84_P19451	AT4G02780	Ent-copalyl diphosphate synthase, chloroplastic	-1.7	-1.8
A_84_P13987	AT1G50640	Ethylene-responsive transcription factor ERF003	-1.2	-1.5
A_84_P10627	AT2G20880	Ethylene-responsive transcription factor ERF053	-2.5	-1.4
A_84_P17637	AT4G28140	Ethylene-responsive transcription factor ERF054	-2	-1.4
A_84_P16678	AT4G25420	Gibberellin 20 oxidase 1	-1.7	-1.4
A_84_P12894	AT4G24960	HVA22-like protein d	-1.7	-1
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	-1.5	-1
A_84_P13518	AT1G19640	Jasmonate O-methyltransferase	-1.3	-1
A_84_P22571	AT5G52310	Low-temperature-induced 78 kDa protein	-4.4	-2.3
A_84_P20704	AT5G59320	Non-specific lipid-transfer protein 3	-3.4	-1.9
A_84_P55930	AT5G61850	Protein LEAFY	-1.9	-1.2
A_84_P22463	AT5G10120	Putative ETHYLENE INSENSITIVE 3-like 4 protein	-1.4	-1.6
A_84_P258350	AT5G15970	Stress-induced protein KIN2	-2.6	-1.4
A_84_P14336	AT1G72260	Thionin-2.1	-1.5	-3.3
A_84_P19845	AT3G27810	Transcription factor MYB21	-2.4	-1.2
A_84_P97476	AT5G24780	Vegetative storage protein 1	-1.7	-2.5
A_84_P141439	AT5G24770	Vegetative storage protein 2	-1.6	-1.8

Cluster 1-2: response to auxin stimulus			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log2 Ratic	Log2 Ratic
A_84_P17344	AT2G22810	1-aminocyclopropane-1-carboxylate synthase 4, ACS4	-2.1	-3.5
A_84_P16823	AT1G01060	LATE ELONGATED HYPOCOTYL, LHY	-1.9	-1.6
A_84_P537376	AT1G29420	SMALL AUXIN UPREGULATED RNA 61, SAUR61	-1.7	-1.2
A_84_P10257	AT1G29430	SMALL AUXIN UPREGULATED RNA 62, SAUR62	-1.3	-1
A_84_P19713	AT1G29450	SMALL AUXIN UPREGULATED RNA 64, AUR64	-1.6	-1.4
A_84_P11207	AT1G29500	SMALL AUXIN UPREGULATED RNA 66, SAUR66	-1.8	-1.1
A_84_P17068	AT1G75590	SMALL AUXIN UPREGULATED RNA 52, SAUR52	-1.9	-1.7
A_84_P12605	AT2G18010	SMALL AUXIN UPREGULATED RNA 10, SAUR10	-1.6	-1.2
A_84_P21376	AT4G13790	SMALL AUXIN UPREGULATED RNA 25, SAUR25	-2.1	-1.6
A_84_P21135	AT3G03820	SMALL AUXIN UP RNA 29, SAUR29	-2.1	-1.6
A_84_P18297	AT3G03840	SMALL AUXIN UP RNA 27, SAUR27	-1.6	-1.4
A_84_P554482	AT3G03850	SMALL AUXIN UP RNA 26, SAUR26	-1.9	-1.4
A_84_P279980	AT1G29440	SMALL AUXIN UP RNA 63, SAUR63	-1.8	-1.3
A_84_P196504	AT5G18010	SMALL AUXIN UP RNA 19, SAUR19	-2.2	-1.4
A_84_P147028	AT5G18020	SMALL AUXIN UP RNA 20, SAUR20	-2.3	-1.5
A_84_P152798	AT5G18030	SMALL AUXIN UP RNA 21, SAUR21	-2.3	-1.6
A_84_P141269	AT5G18050	SMALL AUXIN UP RNA 22, SAUR22	-1.9	-1.5
A_84_P272980	AT5G18080	SMALL AUXIN UP RNA 24, SAUR24	-2.3	-1.5
A_84_P20399	AT4G03400	DFL2, DWARF IN LIGHT 2, GH3-10	-1.2	-1.4
A_84_P16734	AT4G38850	ARABIDOPSIS COLUMBIA SAUR GENE 1, ARABIDOPSIS THALIANA SMALL AUXIN UPREGULATED 15, ATSAUR15, SAUR-AC1, SAUR15, SAUR_AC1, SMALL AUXIN UP RNA 1 FROM ARABIDOPSIS THALIANA ECOTYPE COLUMBIA, SMALL AUXIN UPREGULATED 15	-1.6	-1.6
A_84_P19619	AT5G07700	ATMYB76, MYB DOMAIN PROTEIN 76, MYB76	-2.3	-1
A_84_P19241	AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1, ATCCA1, CCA1	-1.9	-1.6
A_84_P11622	AT2G21050	Auxin transporter-like protein 2, LAX2	-1.6	-1.4
A_84_P10124	AT4G14560	Auxin-responsive protein IAA1	-1.7	-1.9
A_84_P23363	AT4G14550	Auxin-responsive protein IAA14	-1	-1.2
A_84_P14556	AT3G15540	Auxin-responsive protein IAA19	-1.4	-1.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P14702	AT3G62100	Auxin-responsive protein IAA30	-2.2	-2
A_84_P18064	AT1G15580	Auxin-responsive protein IAA5	-2.3	-1.5
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	-1.5	-1

Cluster 1-3: response to hormone stimulus			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P17344	AT2G22810	1-aminocyclopropane-1-carboxylate synthase 4, ACS4	-2.1	-3.5
A_84_P23570	AT5G65800	1-aminocyclopropane-1-carboxylate synthase 5, ACS5	-1.4	-1.7
A_84_P16823	AT1G01060	LATE ELONGATED HYPOCOTYL, LHY	-1.9	-1.6
A_84_P23812	AT1G13430	ARABIDOPSIS THALIANA SULFOTRANSFERASE 4C, ATST4C, ST4C, SULFOTRANSFERASE 4C	-1.5	-1.9
A_84_P291304	AT1G29395	COLD REGULATED 314 INNER MEMBRANE 1, COLD REGULATED 314 THYLAKOID MEMBRANE 1, COLD REGULATED 414 THYLAKOID MEMBRANE 1, COR413-TM1, COR413IM1, COR414-TM1	-2	-2
A_84_P537376	AT1G29420	SMALL AUXIN UPREGULATED RNA 61, SAUR61	-1.7	-1.2
A_84_P10257	AT1G29430	SMALL AUXIN UPREGULATED RNA 62, SAUR62	-1.3	-1
A_84_P279980	AT1G29440	SMALL AUXIN UP RNA 63, SAUR63	-1.8	-1.3
A_84_P19713	AT1G29450	SMALL AUXIN UPREGULATED RNA 64, AUR64	-1.6	-1.4
A_84_P11207	AT1G29500	SMALL AUXIN UPREGULATED RNA 66, SAUR66	-1.8	-1.1
A_84_P17068	AT1G75590	SMALL AUXIN UPREGULATED RNA 52, SAUR52	-1.9	-1.7
A_84_P12605	AT2G18010	SMALL AUXIN UPREGULATED RNA 10, SAUR10	-1.6	-1.2
A_84_P21026	AT2G33380	ARABIDOPSIS THALIANA CALEOSIN 3, ATCLO3, ATRD20, CALEOSIN 3, CLO-3, CLO3, PEROXYGENASE 3, PXG3, RD20, RESPONSIVE TO DESICCATION 20	-1.6	-1.2
A_84_P19241	AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1, ATCCA1, CCA1	-1.9	-1.6
A_84_P21135	AT3G03820	SMALL AUXIN UP RNA 29, SAUR29	-2.1	-1.6
A_84_P18297	AT3G03840	SMALL AUXIN UP RNA 27, SAUR27	-1.6	-1.4
A_84_P554482	AT3G03850	SMALL AUXIN UP RNA 26, SAUR26	-1.9	-1.4
A_84_P11752	AT3G30210	ATMYB121, MYB DOMAIN PROTEIN 121, MYB121	-2	-2.1
A_84_P20399	AT4G03400	DFL2, DWARF IN LIGHT 2, GH3-10	-1.2	-1.4
A_84_P21376	AT4G13790	SMALL AUXIN UPREGULATED RNA 25, SAUR25	-2.1	-1.6
A_84_P16734	AT4G38850	ARABIDOPSIS COLUMBIA SAUR GENE 1, ARABIDOPSIS THALIANA SMALL AUXIN UPREGULATED 15, ATSAUR15, SAUR-AC1, SAUR15, SAUR_AC1, SMALL AUXIN UP RNA 1 FROM ARABIDOPSIS THALIANA ECOTYPE COLUMBIA, SMALL AUXIN UPREGULATED 15	-1.6	-1.6
A_84_P18673	AT5G07690	ATMYB29, MYB DOMAIN PROTEIN 29, MYB29, PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 2, PMG2	-2.4	-1.8
A_84_P19619	AT5G07700	ATMYB76, MYB DOMAIN PROTEIN 76, MYB76	-2.3	-1
A_84_P196504	AT5G18010	SMALL AUXIN UP RNA 19, SAUR19	-2.2	-1.4
A_84_P147028	AT5G18020	SMALL AUXIN UP RNA 20, SAUR20	-2.3	-1.5
A_84_P152798	AT5G18030	SMALL AUXIN UP RNA 21, SAUR21	-2.3	-1.6
A_84_P141269	AT5G18050	SMALL AUXIN UP RNA 22, SAUR22	-1.9	-1.5
A_84_P272980	AT5G18080	SMALL AUXIN UP RNA 24, SAUR24	-2.3	-1.5
A_84_P606561	AT5G59845	Gibberellin-regulated family protein	-1.4	-1.7
A_84_P11622	AT2G21050	Auxin transporter-like protein 2, LAX2	-1.6	-1.4
A_84_P10124	AT4G14560	Auxin-responsive protein IAA1	-1.7	-1.9
A_84_P23363	AT4G14550	Auxin-responsive protein IAA14	-1	-1.2
A_84_P14556	AT3G15540	Auxin-responsive protein IAA19	-1.4	-1.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P14702	AT3G62100	Auxin-responsive protein IAA30	-2.2	-2
A_84_P18064	AT1G15580	Auxin-responsive protein IAA5	-2.3	-1.5
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P18763	AT5G45820	CBL-interacting serine/threonine-protein kinase 20	-1	-1.8
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P10874	AT3G50970	Dehydrin Xero 2	-5.1	-3.4
A_84_P11587	AT2G39800	Delta-1-pyrroline-5-carboxylate synthetase A	-1.7	-1.4
A_84_P19451	AT4G02780	Ent-copalyl diphosphate synthase, chloroplastic	-1.7	-1.8

A_84_P13987	AT1G50640	Ethylene-responsive transcription factor ERF003	-1.2	-1.5
A_84_P10627	AT2G20880	Ethylene-responsive transcription factor ERF053	-2.5	-1.4
A_84_P17637	AT4G28140	Ethylene-responsive transcription factor ERF054	-2	-1.4
A_84_P16678	AT4G25420	Gibberellin 20 oxidase 1	-1.7	-1.4
A_84_P12894	AT4G24960	HVA22-like protein d	-1.7	-1
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	-1.5	-1
A_84_P22571	AT5G52310	Low-temperature-induced 78 kDa protein	-4.4	-2.3
A_84_P20704	AT5G59320	Non-specific lipid-transfer protein 3	-3.4	-1.9
A_84_P55930	AT5G61850	Protein LEAFY	-1.9	-1.2
A_84_P22463	AT5G10120	Putative ETHYLENE INSENSITIVE 3-like 4 protein	-1.4	-1.6
A_84_P258350	AT5G15970	Stress-induced protein KIN2	-2.6	-1.4

Cluster 1-4: response to organic substance			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P17344	AT2G22810	1-aminocyclopropane-1-carboxylate synthase 4, ACS4	-2.1	-3.5
A_84_P23570	AT5G65800	1-aminocyclopropane-1-carboxylate synthase 5, ACS5	-1.4	-1.7
A_84_P16823	AT1G01060	LATE ELONGATED HYPOCOTYL, LHY	-1.9	-1.6
A_84_P23812	AT1G13430	ARABIDOPSIS THALIANA SULFOTRANSFERASE 4C, ATST4C, ST4C, SULFOTRANSFERASE 4C	-1.5	-1.9
A_84_P13338	AT1G18710	ATMYB47, MYB DOMAIN PROTEIN 47, MYB47	-1.9	-1.4
A_84_P291304	AT1G29395	COLD REGULATED 314 INNER MEMBRANE 1, COLD REGULATED 314 THYLAKOID MEMBRANE 1, COLD REGULATED 414 THYLAKOID MEMBRANE 1, COR413-TM1, COR413IM1, COR414-TM1	-2	-2
A_84_P537376	AT1G29420	SMALL AUXIN UPREGULATED RNA 61, SAUR61	-1.7	-1.2
A_84_P10257	AT1G29430	SMALL AUXIN UPREGULATED RNA 62, SAUR62	-1.3	-1
A_84_P279980	AT1G29440	SMALL AUXIN UP RNA 63, SAUR63	-1.8	-1.3
A_84_P19713	AT1G29450	SMALL AUXIN UPREGULATED RNA 64, AUR64	-1.6	-1.4
A_84_P11207	AT1G29500	SMALL AUXIN UPREGULATED RNA 66, SAUR66	-1.8	-1.1
A_84_P17068	AT1G75590	SMALL AUXIN UPREGULATED RNA 52, SAUR52	-1.9	-1.7
A_84_P12605	AT2G18010	SMALL AUXIN UPREGULATED RNA 10, SAUR10	-1.6	-1.2
A_84_P21026	AT2G33380	ARABIDOPSIS THALIANA CALEOSIN 3, ATCLO3, ATRD20, CALEOSIN 3, CLO-3, CLO3, PEROXYGENASE 3, PXG3, RD20, RESPONSIVE TO DESICCATION 20	-1.6	-1.2
A_84_P14449	AT2G34810	FAD-binding Berberine family protein	-2	-1.6
A_84_P19241	AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1, ATCCA1, CCA1	-1.9	-1.6
A_84_P21135	AT3G03820	SMALL AUXIN UP RNA 29, SAUR29	-2.1	-1.6
A_84_P18297	AT3G03840	SMALL AUXIN UP RNA 27, SAUR27	-1.6	-1.4
A_84_P554482	AT3G03850	SMALL AUXIN UP RNA 26, SAUR26	-1.9	-1.4
A_84_P11752	AT3G30210	ATMYB121, MYB DOMAIN PROTEIN 121, MYB121	-2	-2.1
A_84_P20399	AT4G03400	DFL2, DWARF IN LIGHT 2, GH3-10	-1.2	-1.4
A_84_P308073	AT4G12030	BASS5, BAT5, BILE ACID TRANSPORTER 5, BILE ACID : SODIUM SYMPORTER FAMILY PROTEIN 5	-1.8	-1.1
A_84_P21376	AT4G13790	SMALL AUXIN UPREGULATED RNA 25, SAUR25	-2.1	-1.6
A_84_P16734	AT4G38850	ARABIDOPSIS COLUMBIA SAUR GENE 1, ARABIDOPSIS THALIANA SMALL AUXIN UPREGULATED 15, ATSAUR15, SAUR-AC1, SAUR15, SAUR_AC1, SMALL AUXIN UP RNA 1 FROM ARABIDOPSIS THALIANA ECOTYPE COLUMBIA, SMALL AUXIN UPREGULATED 15	-1.6	-1.6
A_84_P18673	AT5G07690	ATMYB29, MYB DOMAIN PROTEIN 29, MYB29, PRODUCTION OF METHIONINE-DERIVED GLUCOSINOLATE 2, PMG2	-2.4	-1.8
A_84_P19619	AT5G07700	ATMYB76, MYB DOMAIN PROTEIN 76, MYB76	-2.3	-1
A_84_P196504	AT5G18010	SMALL AUXIN UP RNA 19, SAUR19	-2.2	-1.4
A_84_P147028	AT5G18020	SMALL AUXIN UP RNA 20, SAUR20	-2.3	-1.5
A_84_P152798	AT5G18030	SMALL AUXIN UP RNA 21, SAUR21	-2.3	-1.6
A_84_P141269	AT5G18050	SMALL AUXIN UP RNA 22, SAUR22	-1.9	-1.5
A_84_P272980	AT5G18080	SMALL AUXIN UP RNA 24, SAUR24	-2.3	-1.5
A_84_P606561	AT5G59845	Gibberellin-regulated family protein	-1.4	-1.7
A_84_P11622	AT2G21050	Auxin transporter-like protein 2, LAX2	-1.6	-1.4
A_84_P10124	AT4G14560	Auxin-responsive protein IAA1	-1.7	-1.9
A_84_P23363	AT4G14550	Auxin-responsive protein IAA14	-1	-1.2
A_84_P14556	AT3G15540	Auxin-responsive protein IAA19	-1.4	-1.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P14702	AT3G62100	Auxin-responsive protein IAA30	-2.2	-2

A_84_P18064	AT1G15580	Auxin-responsive protein IAA5	-2.3	-1.5
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P18763	AT5G45820	CBL-interacting serine/threonine-protein kinase 20	-1	-1.8
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P10874	AT3G50970	Dehydrin Xero 2	-5.1	-3.4
A_84_P11587	AT2G39800	Delta-1-pyrroline-5-carboxylate synthetase A	-1.7	-1.4
A_84_P19451	AT4G02780	Ent-copalyl diphosphate synthase, chloroplastic	-1.7	-1.8
A_84_P13987	AT1G50640	Ethylene-responsive transcription factor ERF003	-1.2	-1.5
A_84_P10627	AT2G20880	Ethylene-responsive transcription factor ERF053	-2.5	-1.4
A_84_P17637	AT4G28140	Ethylene-responsive transcription factor ERF054	-2	-1.4
A_84_P16678	AT4G25420	Gibberellin 20 oxidase 1	-1.7	-1.4
A_84_P12894	AT4G24960	HVA22-like protein d	-1.7	-1
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	-1.5	-1
A_84_P13518	AT1G19640	Jasmonate O-methyltransferase	-1.3	-1
A_84_P22571	AT5G52310	Low-temperature-induced 78 kDa protein	-4.4	-2.3
A_84_P20704	AT5G59320	Non-specific lipid-transfer protein 3	-3.4	-1.9
A_84_P55930	AT5G61850	Protein LEAFY	-1.9	-1.2
A_84_P22463	AT5G10120	Putative ETHYLENE INSENSITIVE 3-like 4 protein	-1.4	-1.6
A_84_P17547	AT3G56770	Putative transcription factor bHLH107	-1.9	-1.4
A_84_P258350	AT5G15970	Stress-induced protein KIN2	-2.6	-1.4
A_84_P14336	AT1G72260	Thionin-2.1	-1.5	-3.3
A_84_P19845	AT3G27810	Transcription factor MYB21	-2.4	-1.2
A_84_P97476	AT5G24780	Vegetative storage protein 1	-1.7	-2.5
A_84_P141439	AT5G24770	Vegetative storage protein 2	-1.6	-1.8

Cluster 2-1: response to red or far red light			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log2 Ratio	Log2 Ratio
A_84_P240805	AT2G05100	LIGHT-HARVESTING CHLOROPHYLL B-BINDING 2, LHCB2	-1.7	-2.1
A_84_P23852	AT2G42540	COLD-REGULATED 15A, COR15A, ATCOR15A	-5	-4.1
A_84_P164223	AT2G42870	HELIX-LOOP-HELIX 1, HLH1, PHY RAPIDLY REGULATED 1, PAR1	-1.3	-1.2
A_84_P24021	AT3G27690	LIGHT-HARVESTING CHLOROPHYLL B-BINDING 2, LHCB2	-2.2	-2.1
A_84_P21376	AT4G13790	SMALL AUXIN UPREGULATED RNA 25, SAUR25	-2.1	-1.6
A_84_P62840	AT4G14690	LIGHT-HARVESTING CHLOROPHYLL B-BINDING 2, LHCB2	-1.7	-1.2
A_84_P19825	AT5G04190	PHYTOCHROME KINASE SUBSTRATE 4, PKS4	-1.5	-1.7
A_84_P13983	AT5G24120	SIGMA FACTOR 5, ATSIG5	-1.4	-1.2
A_84_P23021	AT2G29090	CYTOCHROME P450,Abscisic acid 8'-hydroxylase 2, CYP707A2	-1.6	-1.3
A_84_P23534	AT5G57360	ZEITLUPE, ZTL	-7	-5.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P23436	AT4G15090	Protein FAR-RED IMPAIRED RESPONSE 1	-1.6	-1.7
A_84_P18969	AT1G22770	Protein GIGANTEA	-1.3	-1.7
A_84_P14733	AT1G06040	Salt tolerance protein	-1.8	-1.8
A_84_P19845	AT3G27810	Transcription factor MYB21	-2.4	-1.2
A_84_P162983	AT2G43010	Transcription factor PIF4	-1.5	-1.6
A_84_P14690	AT3G59060	Transcription factor PIF5	-1.4	-1.6
A_84_P21494	AT5G02810	Two-component response regulator-like APRR7	-1.8	-2.3
A_84_P126821	AT2G46790	Two-component response regulator-like APRR9	-4.6	-5

Cluster 3-1: response to red or far red light			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P240805	AT2G05100	LIGHT-HARVESTING CHLOROPHYLL B-BINDING 2, LHCB2	-1.7	-2.1
A_84_P23852	AT2G42540	COLD-REGULATED 15A, COR15A, ATCOR15A	-5	-4.1
A_84_P164223	AT2G42870	HELIX-LOOP-HELIX 1, HLH1, PHY RAPIDLY REGULATED 1, PAR1	-1.3	-1.2
A_84_P24021	AT3G27690	LIGHT-HARVESTING CHLOROPHYLL B-BINDING 2, LHCB2	-2.2	-2.1
A_84_P21376	AT4G13790	SMALL AUXIN UPREGULATED RNA 25, SAUR25	-2.1	-1.6
A_84_P62840	AT4G14690	LIGHT-HARVESTING CHLOROPHYLL B-BINDING 2, LHCB2	-1.7	-1.2
A_84_P19825	AT5G04190	PHYTOCHROME KINASE SUBSTRATE 4, PKS4	-1.5	-1.7
A_84_P13983	AT5G24120	SIGMA FACTOR 5, ATSIG5	-1.4	-1.2
A_84_P23021	AT2G29090	CYTOCHROME P450,Abscisic acid 8'-hydroxylase 2, CYP707A2	-1.6	-1.3
A_84_P23534	AT5G57360	Adagio protein 1	-7	-5.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P23436	AT4G15090	Protein FAR-RED IMPAIRED RESPONSE 1	-1.6	-1.7
A_84_P18969	AT1G22770	Protein GIGANTEA	-1.3	-1.7
A_84_P14733	AT1G06040	Salt tolerance protein	-1.8	-1.8
A_84_P19845	AT3G27810	Transcription factor MYB21	-2.4	-1.2
A_84_P162983	AT2G43010	Transcription factor PIF4	-1.5	-1.6
A_84_P14690	AT3G59060	Transcription factor PIF5	-1.4	-1.6
A_84_P21494	AT5G02810	Two-component response regulator-like APRR7	-1.8	-2.3
A_84_P126821	AT2G46790	Two-component response regulator-like APRR9	-4.6	-5

Cluster 4-1: phenylpropanoid catabolic process			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P15811	AT5G01190	Laccase-10	-1.4	-1.6
A_84_P23387	AT5G03260	Laccase-11	-1.4	-1.6
A_84_P22594	AT5G58910	Laccase-16	-1.4	-1.1
A_84_P15978	AT5G60020	Laccase-17	-1.2	-1.4
A_84_P15454	AT2G29130	Laccase-2	-3.6	-1.6
A_84_P10699	AT2G38080	Laccase-4	-1	-1.2

Cluster 5-1: secondary cell wall biogenesis			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P23323	AT1G43790	TRACHEARY ELEMENT DIFFERENTIATION-RELATED 6, TED6	-1.4	-1.7
A_84_P504795	AT2G37090	IRREGULAR XYLEM 9, IRX9	-1.5	-1.7
A_84_P515014	AT5G48920	TRACHEARY ELEMENT DIFFERENTIATION-RELATED 7, TED7	-1.3	-1.8
A_84_P13182	AT5G17420	Cellulose synthase A catalytic subunit 7 [UDP-forming]	-1.4	-1.7
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P10699	AT2G38080	Laccase-4	-1	-1.2

Cluster 6-1: cell wall organization			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P12256	AT1G56710	pectin lyase-like protein	-1.1	-1.9
A_84_P259090	AT5G54690	GALACTURONOSYLTRANSFERASE 12, GAUT12, IRX8	-1.7	-1.5
A_84_P13182	AT5G17420	Cellulose synthase A catalytic subunit 7 [UDP-forming]	-1.4	-1.7
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P11000	AT4G24010	Cellulose synthase-like protein G1	-1.7	-1.5
A_84_P14433	AT2G32990	Endoglucanase 11	-1.1	-1.2
A_84_P21915	AT1G20190	Expansin-A11	-1.3	-1.1
A_84_P11841	AT3G55500	Expansin-A16	-2	-1
A_84_P11569	AT2G40610	Expansin-A8	-1.2	-1.5
A_84_P18192	AT2G20750	Expansin-B1	-1.3	-1.1
A_84_P57310	AT4G28250	Expansin-B3	-1.7	-1.1
A_84_P21636	AT5G55590	Pectinesterase QRT1	-1.7	-1.5
A_84_P17520	AT1G24070	Probable mannan synthase 10	-1.9	-1.7
A_84_P575245	AT5G16190	Probable mannan synthase 11	-1.1	-1.1
A_84_P593738	AT3G43270	Probable pectinesterase/pectinesterase inhibitor 32	-1.2	-1.5
A_84_P10859	AT3G47400	Probable pectinesterase/pectinesterase inhibitor 33	-1.3	-1.2
A_84_P20395	AT4G02320	Probable pectinesterase/pectinesterase inhibitor 40	-1.6	-1.9
A_84_P16322	AT2G14620	Probable xyloglucan endotransglucosylase/hydrolase protein 10	-1	-1.3
A_84_P14848	AT4G14130	Probable xyloglucan endotransglucosylase/hydrolase protein 15	-1.4	-1.5
A_84_P10083	AT4G30290	Probable xyloglucan endotransglucosylase/hydrolase protein 19	-1.1	-1.7

Cluster 7-1: regulation of transcription			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P16823	AT1G01060	LATE ELONGATED HYPOCOTYL, LHY	-1.9	-1.6
A_84_P22852	AT1G01520	ALTERED SEED GERMINATION 4, ASG4	-1.5	-1.1
A_84_P14280	AT1G08290	WIP DOMAIN PROTEIN 3, WIP3	-1.2	-1.1
A_84_P23806	AT1G13600	BASIC LEUCINE-ZIPPER 58, BZIP58	-2.6	-1.3
A_84_P13338	AT1G18710	ATMYB47, MYB DOMAIN PROTEIN 47, MYB47	-1.9	-1.4
A_84_P544465	AT1G26945	PACLOBUTRAZOL RESISTANCE 6, PRE6	-1.7	-1.6
A_84_P22438	AT1G62700	VASCULAR RELATED NAC-DOMAIN PROTEIN 5, VND5	-1.2	-1.9
A_84_P11441	AT1G65910	NAC DOMAIN CONTAINING PROTEIN 28, NAC028	-1.1	-1.1
A_84_P574525	AT2G01810	RING/FYVE/PHD zinc finger superfamily protein	-1.7	-1.2
A_84_P93859	AT2G12900	BASIC LEUCINE-ZIPPER 33, BZIP33	-1.5	-2.2
A_84_P12622	AT2G27300	ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 40, NTL8	-1	-1.5
A_84_P22105	AT3G04030	MYR2	-1.3	-1.4
A_84_P22188	AT3G08500	MYB DOMAIN PROTEIN 83, MYB83	-1.1	-1.5
A_84_P22142	AT3G17730	NAC DOMAIN CONTAINING PROTEIN 57, NAC057	-1.3	-1.4
A_84_P23101	AT3G21890	B-BOX DOMAIN PROTEIN 31, BBX31	-1.6	-1.4
A_84_P509353	AT3G28857	PACLOBUTRAZOL RESISTANCE 5, PRE5	-1.1	-1.7
A_84_P11752	AT3G30210	MYB DOMAIN PROTEIN 121, MYB121	-2	-2.1
A_84_P17486	AT3G49760	BASIC LEUCINE-ZIPPER 5, BZIP5	-1.1	-1.4
A_84_P21302	AT3G56660	BASIC REGION/LEUCINE ZIPPER MOTIF PROTEIN 49, BZIP49	-1.1	-1.1
A_84_P19525	AT4G27310	B-BOX DOMAIN PROTEIN 28, BBX28	-2	-2.5
A_84_P10075	AT4G28500	NAC DOMAIN CONTAINING PROTEIN 73, NAC073	-1.3	-1.2
A_84_P587696	AT5G03510	C2H2-type zinc finger protein	-1.4	-1.4
A_84_P18673	AT5G07690	MYB DOMAIN PROTEIN 29, MYB29	-2.4	-1.8
A_84_P19619	AT5G07700	MYB DOMAIN PROTEIN 76, MYB76	-2.3	-1
A_84_P16979	AT5G11050	MYB DOMAIN PROTEIN 64, MYB64	-1.9	-1.5
A_84_P281230	AT5G15160	BASIC HELIX-LOOP-HELIX PROTEIN 134, BHLH134, BNQ2	-1.5	-1.3
A_84_P13983	AT5G24120	SIGMA FACTOR 5	-1.4	-1.2
A_84_P19687	AT5G39860	BASIC HELIX-LOOP-HELIX PROTEIN 136, BHLH136, BNQ1	-1.4	-1.3
A_84_P167393	AT5G42630	ABERRANT TESTA SHAPE, ATS, KAN4, KANADI 4	-1.1	-1.3
A_84_P242573	AT5G54470	B-BOX DOMAIN PROTEIN 29, BBX29	-3.6	-3.8
A_84_P14098	AT5G62320	MYB DOMAIN PROTEIN 99, MYB99	-1.5	-1.1
A_84_P544339	AT5G64530	ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 104, XND1	-1.8	-1
A_84_P10333	AT5G66300	ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 105, VND3	-1.8	-1.2
A_84_P23534	AT5G57360	Adagio protein 1, ZTL	-7	-5.4
A_84_P20117	AT2G45650	Agamous-like MADS-box protein AGL6	-1.1	-1.2
A_84_P52180	AT5G60910	Agamous-like MADS-box protein AGL8	-1.5	-2
A_84_P10124	AT4G14560	Auxin-responsive protein IAA1	-1.7	-1.9
A_84_P23363	AT4G14550	Auxin-responsive protein IAA14	-1	-1.2
A_84_P14556	AT3G15540	Auxin-responsive protein IAA19	-1.4	-1.4
A_84_P55550	AT4G32280	Auxin-responsive protein IAA29	-3.9	-3.2
A_84_P14702	AT3G62100	Auxin-responsive protein IAA30	-2.2	-2
A_84_P18064	AT1G15580	Auxin-responsive protein IAA5	-2.3	-1.5
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P538813	AT4G34060	DEMETER-like protein 3	-1.3	-3.3

A_84_P167173	AT4G25480	Dehydration-responsive element-binding protein 1A	-3.1	-3
A_84_P14918	AT5G18450	Dehydration-responsive element-binding protein 2G	-1.3	-3.1
A_84_P21360	AT1G69570	Dof zinc finger protein DOF1.10	-2.8	-3.1
A_84_P12696	AT1G26790	Dof zinc finger protein DOF1.3	-3.2	-2.1
A_84_P266910	AT1G47655	Dof zinc finger protein DOF1.6	-1.3	-1.2
A_84_P13686	AT3G45610	Dof zinc finger protein DOF3.2	-1.4	-1
A_84_P19369	AT2G38530	Dof zinc finger protein DOF3.3	-3	-3.1
A_84_P20632	AT5G39660	Dof zinc finger protein DOF5.2	-1.4	-1.1
A_84_P12198	AT5G60200	Dof zinc finger protein DOF5.3	-1.2	-1.1
A_84_P23557	AT5G23040	Dof zinc finger protein DOF5.5	-2.3	-1.7
A_84_P13987	AT1G50640	Ethylene-responsive transcription factor ERF003	-1.2	-1.5
A_84_P10627	AT2G20880	Ethylene-responsive transcription factor ERF053	-2.5	-1.4
A_84_P17637	AT4G28140	Ethylene-responsive transcription factor ERF054	-2	-1.4
A_84_P311113	AT5G43840	Heat stress transcription factor A-6a	-1.6	-1.4
A_84_P16754	AT4G36740	Homeobox-leucine zipper protein ATHB-40	-1.5	-1
A_84_P11104	AT5G06710	Homeobox-leucine zipper protein HAT14	-1.1	-1
A_84_P18494	AT1G12260	NAC domain-containing protein 7	-1.5	-1.6
A_84_P10469	AT1G54160	Nuclear transcription factor Y subunit A-5	-1.1	-1.4
A_84_P159675	AT1G64100	Pentatricopeptide repeat-containing protein At1g64100	-1.6	-1.5
A_84_P18969	AT1G22770	Protein GIGANTEA	-1.3	-1.7
A_84_P55930	AT5G61850	Protein LEAFY	-1.9	-1.2
A_84_P13266	AT1G80740	Putative DNA (cytosine-5)-methyltransferase CMT1	-3.5	-1.4
A_84_P22463	AT5G10120	Putative ETHYLENE INSENSITIVE 3-like 4 protein	-1.4	-1.6
A_84_P17547	AT3G56770	Putative transcription factor bHLH107	-1.9	-1.4
A_84_P17440	AT3G21880	Putative zinc finger protein CONSTANS-LIKE 12	-2.7	-1.6
A_84_P12560	AT2G31380	Salt tolerance-like protein	-1.2	-1.1
A_84_P22151	AT3G25710	Transcription factor AIG1	-1.5	-1.3
A_84_P207668	AT5G67060	Transcription factor HEC1	-1	-1.1
A_84_P19141	AT2G47460	Transcription factor MYB12	-3.1	-1.5
A_84_P19845	AT3G27810	Transcription factor MYB21	-2.4	-1.2
A_84_P162983	AT2G43010	Transcription factor PIF4	-1.5	-1.6
A_84_P14690	AT3G59060	Transcription factor PIF5	-1.4	-1.6
A_84_P10547	AT1G68800	Transcription factor TCP12	-1.8	-1.8
A_84_P302890	AT4G36060	Transcription factor bHLH11	-1.4	-1
A_84_P23649	AT1G31050	Transcription factor bHLH111	-1.6	-3
A_84_P70944	AT1G61660	Transcription factor bHLH112	-1.1	-1.1
A_84_P16621	AT4G05170	Transcription factor bHLH114	-2	-2.1
A_84_P150068	AT2G43140	Transcription factor bHLH129	-1.2	-2.2
A_84_P16699	AT4G29930	Transcription factor bHLH27	-1.4	-1.2
A_84_P21605	AT5G46830	Transcription factor bHLH28	-3.8	-2.3
A_84_P19990	AT1G68810	Transcription factor bHLH30	-1.1	-1.1
A_84_P121222	AT3G21330	Transcription factor bHLH87	-2.7	-2.5
A_84_P22306	AT1G06170	Transcription factor bHLH89	-1.5	-1.9
A_84_P13165	AT5G65320	Transcription factor bHLH99	-1.1	-1.3
A_84_P21494	AT5G02810	Two-component response regulator-like APRR7	-1.8	-2.3
A_84_P126821	AT2G46790	Two-component response regulator-like APRR9	-4.6	-5
A_84_P20968	AT1G20700	WUSCHEL-related homeobox 14	-1.3	-2
A_84_P502806	AT1G46480	WUSCHEL-related homeobox 4	-2.2	-1.4
A_84_P11024	AT4G29190	Zinc finger CCCH domain-containing protein 49	-1.1	-1.3
A_84_P20292	AT3G02380	Zinc finger protein CONSTANS-LIKE 2	-1.9	-1.5
A_84_P10296	AT5G57660	Zinc finger protein CONSTANS-LIKE 5	-1.4	-1.5
A_84_P235073	AT1G73870	Zinc finger protein CONSTANS-LIKE 7	-1.6	-1.8
A_84_P18657	AT5G03150	Zinc finger protein JACKDAW	-1.4	-1.2

Cluster 8-1: post-embryonic development			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P16823	AT1G01060	LATE ELONGATED HYPOCOTYL, LHY	-1.9	-1.6
A_84_P17175	AT1G32560	LATE EMBRYOGENESIS ABUNDANT 4-1, LEA4-1	-2	-1.4
A_84_P605859	AT1G47485	C-TERMINALLY ENCODED PEPTIDE 1, CEP1	-1.2	-1.1
A_84_P147788	AT1G49320	UNKNOWN SEED PROTEIN LIKE 1, USPL1	-2.4	-3
A_84_P14274	AT1G52690	LATE EMBRYOGENESIS ABUNDANT 7, LEA7	-3.1	-2.7
A_84_P12451	AT1G72100	late embryogenesis abundant domain-containing protein	-2.4	-1.6
A_84_P22979	AT1G75520	SHI-RELATED SEQUENCE 5, SRS5	-1.3	-1.7
A_84_P579221	AT2G01280	MATERNAL EFFECT EMBRYO ARREST 65, MEE65	-1.9	-1.5
A_84_P12622	AT2G27300	ARABIDOPSIS NAC DOMAIN CONTAINING PROTEIN 40, NTL8	-1	-1.5
A_84_P14448	AT2G34790	MATERNAL EFFECT EMBRYO ARREST 23, MEE23	-1.1	-1.4
A_84_P18221	AT2G36640	EMBRYONIC CELL PROTEIN 63, ECP63	-2.7	-2.1
A_84_P22906	AT2G42560	late embryogenesis abundant domain-containing protein	-3.4	-3.2
A_84_P19241	AT2G46830	CIRCADIAN CLOCK ASSOCIATED 1, CCA1	-1.9	-1.6
A_84_P17492	AT3G51060	SHI RELATED SEQUENCE 1, SRS1	-1.3	-1.6
A_84_P19392	AT3G53040	putative late embryogenesis abundant protein	-1.4	-1
A_84_P10042	AT4G21020	Late embryogenesis abundant protein (LEA) family protein	-2.4	-1
A_84_P573423	AT4G36600	Late embryogenesis abundant (LEA) protein	-1.8	-1.9
A_84_P604601	AT4G37140	ARABIDOPSIS THALIANA METHYL ESTERASE 20, ATMES20	-1.1	-1.3
A_84_P16776	AT5G06760	LATE EMBRYOGENESIS ABUNDANT 4-5, LEA4-5	-2.1	-1.5
A_84_P167393	AT5G42630	ABERRANT TESTA SHAPE, ATS	-1.1	-1.3
A_84_P23021	AT2G29090	Abscisic acid 8'-hydroxylase 2	-1.6	-1.3
A_84_P23534	AT5G57360	Adagio protein 1, ZTL	-7	-5.4
A_84_P20117	AT2G45650	Agamous-like MADS-box protein AGL6	-1.1	-1.2
A_84_P52180	AT5G60910	Agamous-like MADS-box protein AGL8	-1.5	-2
A_84_P23363	AT4G14550	Auxin-responsive protein IAA14	-1	-1.2
A_84_P14556	AT3G15540	Auxin-responsive protein IAA19	-1.4	-1.4
A_84_P13379	AT1G52830	Auxin-responsive protein IAA6	-2.2	-2
A_84_P13763	AT3G63440	Cytokinin dehydrogenase 6	-1.4	-1.1
A_84_P16678	AT4G25420	Gibberellin 20 oxidase 1	-1.7	-1.4
A_84_P12894	AT4G24960	HVA22-like protein d	-1.7	-1
A_84_P23867	AT1G63990	Meiotic recombination protein SPO11-2	-1.5	-1.5
A_84_P10415	AT1G52030	Myrosinase-binding protein-like At1g52030	-1.2	-1.4
A_84_P18494	AT1G12260	NAC domain-containing protein 7	-1.5	-1.6
A_84_P22129	AT3G27660	Oleosin 20.3 kDa	-1.8	-1.2
A_84_P15049	AT1G55180	Phospholipase D epsilon	-1.6	-1.3
A_84_P18969	AT1G22770	Protein GIGANTEA	-1.3	-1.7
A_84_P55930	AT5G61850	Protein LEAFY	-1.9	-1.2
A_84_P11342	AT1G01470	Putative desiccation-related protein LEA14	-1.3	-1.1
A_84_P14733	AT1G06040	Salt tolerance protein	-1.8	-1.8
A_84_P207668	AT5G67060	Transcription factor HEC1	-1	-1.1
A_84_P19845	AT3G27810	Transcription factor MYB21	-2.4	-1.2
A_84_P162983	AT2G43010	Transcription factor PIF4	-1.5	-1.6
A_84_P20968	AT1G20700	WUSCHEL-related homeobox 14	-1.3	-2

Cluster 9-1: glycoside biosynthetic process			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P308073	AT4G12030	BILE ACID TRANSPORTER 5, BAT5	-1.8	-1.1
A_84_P570783	AT5G10100	TREHALOSE-6-PHOSPHATE PHOSPHATASE I, TPPI	-1.2	-1.1
A_84_P16852	AT1G55740	CBL-interacting serine/threonine-protein kinase 10	-1.7	-1.5
A_84_P17028	AT1G62560	Flavin-containing monooxygenase FMO GS-OX3	-2.2	-1.3
A_84_P17974	AT1G62570	Flavin-containing monooxygenase FMO GS-OX4	-1.7	-1.7
A_84_P15870	AT4G39210	Methylthioalkylmalate synthase 1, chloroplastic	-1.6	-1.2
A_84_P17435	AT3G19710	Probable branched-chain-amino-acid aminotransferase 4	-1.6	-1.2

Cluster 10-1: carbohydrate biosynthetic process			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P16114	AT1G09350	GALACTINOL SYNTHASE 3, GOLS3	-6.5	-6.4
A_84_P19272	AT1G53100	protein plant cadmium resistance 10	-1.3	-2
A_84_P17929	AT1G56600	GALACTINOL SYNTHASE 2, GOLS2	-2.6	-3.3
A_84_P504795	AT2G37090	IRREGULAR XYLEM 9, IRX9	-1.5	-1.7
A_84_P308073	AT4G12030	BILE ACID TRANSPORTER 5, BAT5	-1.8	-1.1
A_84_P570783	AT5G10100	TREHALOSE-6-PHOSPHATE PHOSPHATASE I, TPPI	-1.2	-1.1
A_84_P169473	AT5G30500	GALACTINOL SYNTHASE 10, GOLS10	-2.3	-3.1
A_84_P259090	AT5G54690	IRREGULAR XYLEM 8, IRX8	-1.7	-1.5
A_84_P16852	AT1G55740	CBL-interacting serine/threonine-protein kinase 10	-1.7	-1.5
A_84_P13182	AT5G17420	Cellulose synthase A catalytic subunit 7 [UDP-forming]	-1.4	-1.7
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P11000	AT4G24010	Cellulose synthase-like protein G1	-1.7	-1.5
A_84_P17028	AT1G62560	Flavin-containing monooxygenase FMO GS-OX3	-2.2	-1.3
A_84_P17974	AT1G62570	Flavin-containing monooxygenase FMO GS-OX4	-1.7	-1.7
A_84_P12954	AT4G39210	Glucose-1-phosphate adenylyltransferase large subunit 3, chloroplastic	-1.4	-1
A_84_P12513	AT2G22240	Inositol-3-phosphate synthase isozyme 2	-2	-1.5
A_84_P15870	AT4G39210	Methylthioalkylmalate synthase 1, chloroplastic	-1.6	-1.2
A_84_P17435	AT3G19710	Probable branched-chain-amino-acid aminotransferase 4	-1.6	-1.2
A_84_P12395	AT1G32900	Probable granule-bound starch synthase 1, chloroplastic/amyloplastic	-2.6	-2.4

Cluster 11-1: hyperosmotic salinity response			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P14587	AT3G14440	9-cis-epoxycarotenoid dioxygenase NCED3, chloroplastic	-1.6	-1.2
A_84_P11587	AT2G39800	Delta-1-pyrroline-5-carboxylate synthetase A	-1.7	-1.4
A_84_P12894	AT4G24960	HVA22-like protein d	-1.7	-1
A_84_P22571	AT5G52310	Low-temperature-induced 78 kDa protein	-4.4	-2.3
A_84_P12921	AT4G30650	UPF0057 membrane protein At4g30650	-1.5	-1.2
A_84_P141439	AT5G24770	Vegetative storage protein 2	-1.6	-1.8

Cluster 12-1: cell wall biogenesis			*ztl-3*	*ztl-105*
Array Element	Gene Locus	Annotation	Log (Ratio	Log (Ratio
A_84_P23323	AT1G43790	TRACHEARY ELEMENT DIFFERENTIATION-RELATED 6, TED6	-1.4	-1.7
A_84_P504795	AT2G37090	IRREGULAR XYLEM 9, IRX9	-1.5	-1.7
A_84_P570804	AT5G16490	ROP-INTERACTIVE CRIB MOTIF-CONTAINING PROTEIN 4, RIC4	-1.4	-1.6
A_84_P515014	AT5G48920	TRACHEARY ELEMENT DIFFERENTIATION-RELATED 7, TED7	-1.3	-1.8
A_84_P259090	AT5G54690	GALACTURONOSYLTRANSFERASE 12, GAUT12, IRX8	-1.7	-1.5
A_84_P13182	AT5G17420	Cellulose synthase A catalytic subunit 7 [UDP-forming]	-1.4	-1.7
A_84_P10979	AT4G18780	Cellulose synthase A catalytic subunit 8 [UDP-forming]	-1.6	-1.9
A_84_P10699	AT2G38080	Laccase-4	-1	-1.2

Supplemental Table 9. Primer sequences for qRT-PCR

Gene	Primer sequence
ACT2_F	GGTAACATTGTGCTCAGTGGTGG
ACT2_R	AACGACCTTAATCTTCATGCTGC
BGAL6_F	GTCTGGTCTTCGGGTTGTGTTTG
BGAL6_R	TGGATGGAACCGGAGAAGAGAAG
EXP8_F	GAACTCATGGAGACGACGGAGG
EXP8_R	ACCTCGGGTCATCGTTACACTTC
PME2_F	TTATTGGCCTCCATAGTCGGAATCG
PME2_R	TCCGGGTATAGTGTTGAGCTGC
XTH33_F	ACACAGCAGGAAATTCACAACACC
XTH33_R	GAGAGTGAGCTTAGCGAGGGAG
IAA19_F	GAGCATGGATGGTGTGCCTTAT
IAA19_R	TTCGCAGTTGTCACCATCTTTC
IAA29_F	CTTCCAAGGGAAAGAGGGTGAC
IAA29_R	TTCCGCAAAGATCTTCCATGTAAC
SAUR22_F	CCTTCTTTCAAGCTCTGCTCAG
SAUR22_R	TTGGAGCCGAGAAGTCACATT
PIF4_F	GTTGTTGACTTTGCTGTCCCGC
PIF4_R	CGACTCAGCCGATGGAGATGTT
PIF5_F	CGCCGGAGATCCAAATCCCAACAT
PIF5_R	GCGGGAAATCAGACCGTGCAACAA
TAR3_F	GCTGGGCATTAGTAAAAGAGAAAACTG
TAR3_R	CGAAAAACGCGTAGACATGGAAAA
YUC3_F	ATTCAGTACCTTGAGTCCTACGCAG
YUC3_R	ATTTAGCGGACTGGACTGTCTCG
YUC8_F	ATCAACCCTAAGTTCAACGAGTG
YUC8_R	CTCCCGTAGCCACCACAAG
YUC9_F	CTCCCGTAGCCACCACAAG
YUC9_R	CCACTTCATCATCATCAC
IAA20_F	TGTCTCTTAATGGCTACCGCGACT
IAA20_R	TCAGCCCAGAGAATGGATGCGT
ELF3_F	GGAAAGCCATTGCCAATCAA
ELF3_R	ATCCGGTGATGCAGCAATAAGT
TCP2_F	GGGTTTAATTCTCGGGTCG
TCP2_R	CGCCGTTGGATTCTGCC

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